# Foundations of Cognition: Loosely coupled oscillators as correlates of affective states within the central complex of the fruit-fly (*Drosophila melanogaster*)

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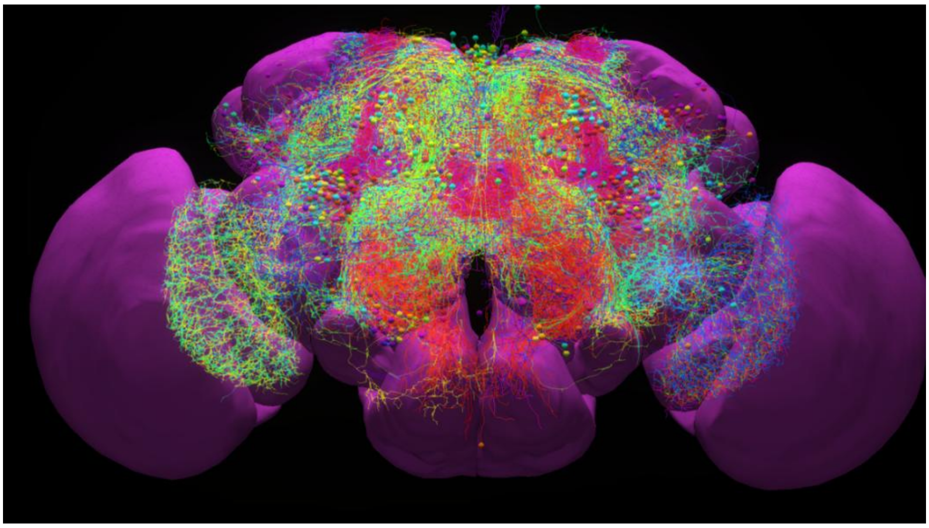

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# I. Abstract

Affective Neuroscience is a field that explores the neural mechanisms underlying emotions and affective (proto-emotions) states. Seeking behavior, one of the seven affects proposed by Jaak Panksepp, plays a vital role in exploration, learning, and decision-making. This thesis investigates the neural mechanisms that underlie this enigmatic drive through an integrative approach that combines principles from various domains of science, including Comparative Neuroanatomy, Computational Affective Neuroscience, and study of dynamic systems such as Loosely Coupled Oscillators.

By examining homologous brain structures across species, with a particular interest in those regions that might plausibly be involved in the neural processes associated with seeking behavior, and employing computational models in neuroscience, this research aims to shed light on the complex interplay between neural activity and affective responses. My work seeks to elucidate plausible mechanisms governing SEEK (capitalized in this context), ultimately enhancing our understanding of brain function and providing insights into the neural basis of emotional responses.

By simulating neuronal motifs and circuits within the mid-brain and basal brain systems of the fruit fly, this thesis aims to provide insights into brain functions related to SEEK. This work contributes to the ongoing discourse on Cognitive Neuroscience and Artificial Intelligence (AI) by employing analytical and computational tools of neuroscience and signal analysis to bridge the explanatory gap in understanding of SEEK and seeking behavior. This thesis employs a novel computational framework to identify stable oscillatory points in pairs of excitatory and inhibitory neurons in the fan-shaped body of Drosophila, aiding in the pathfinding and testing of neural circuits associated with SEEK behavior.

The study's key achievement is the identification of these stable points, revealing dynamic neural interactions and contributing to the understanding of neural oscillations in the fan-shaped body's architecture. The framework is efficient and reproducible for future studies. Additionally, the research explores the significance of SEEK in cognition, utilizing Drosophila's central nervous system to probe the neurophysiological mechanisms underlying SEEK behavior. The thesis also demonstrates how Spiking Neural Network models support the investigation of SEEK and affective neuroscience. Lastly, it examines how SEEK's relationship to Wilson-Cowan-like motifs and behavior can be applied to the Free Energy Principle and Bayesian Inference, providing insights into brain function and decision-making. The future direction of the thesis states that further experimental validation is needed to strengthen these findings.

By advancing our knowledge of seeking behavior, this research could have far-reaching implications for various fields such as robotics, artificial intelligence, psychology, and neuroscience. By creating more accurate models of emotional processes in AI systems, we can develop machines that exhibit adaptability, efficiency, and human-like decision-making capabilities. This work's findings could pave the way for a new generation of AI systems capable of understanding and responding to emotional stimuli in a more nuanced manner, thereby improving their ability to function effectively in complex, dynamic environments.

## II. List of Abbreviations

**CNS** (Central Nervous System): The seat of cognition, where thoughts, perceptions, memories, and emotions are processed.
**FB** (Fan-shaped Body): A region in the insect central brain analogous to the mammalian striatum.
**PB** (Protocerebral Bridge): A region in the insect central brain corresponding to the caudate nucleus and putamen in mammals. It is a part of the central complex.
**EB** (Ellipsoid Body): A region in the insect central brain corresponding to the external and internal globus pallidus in mammals. It is related to vision and head direction.
**NO** (Noduli): They play a crucial role in guiding the formation and differentiation of various wing structures. It is part of the central complex.
**CX** (Central Complex): A region in the insect central brain which includes the FB, PB, EB and NO.
**LAL** (Large Amygdral Area): A region in the insect central brain analogous to the mammalian globus pallidus, involved in amnesia-related functions.
**IMP** (Intermediate neural Protocerebra): A region located in the insect brain that acts as an intermediate pathway for processing sensory and environmental information, bridging sensory inputs with more complex cognitive functions.
**ILP** (Inferior lateral Protocerebra): Another brain region within insects involved in processing specific types of sensory or behavioral information, possibly acting as a gatekeeper or organizer of sensory data.
**VLP** (Ventrolateral Protocerebra): A specific lateral and ventral region within the insect brain. This area is part of the protocerebral domain, which forms the basis of higher-order brain structures.
**SMP** (Superior medial Protocerebrum): A key structure in the insect brain that processes learned visual information and outputs signals to higher-order brain regions like the mushroom bodies (MB), which are analogous to mammalian hippocampi. This helps shape memory, learning, and perception.
**MB** (Mushroom Body): A brain region in insects corresponding to the mammalian hippocampus, involved in encoding spatial and olfactory information, storing learned experiences, and facilitating complex cognitive functions like navigation and memory.
**PPL1**(protocerebral posterior lateral region 1): Dopamine Neurons which are homologous to those in the substantia nigra in humans.
**PPM3**(protocerebral posterior medial region 3): Dopamine Neurons which are homologous to those in the substantia nigra in humans.
**TH**(Thalamus): A region of the brain that acts as a bridge between sensory input (from the eyes, ears, skin, etc.) and the rest of the brain.

**GPe** (External Globus Pallidus): A part of the human basal ganglia involved in motor control and cognitive functions.
**GPi** (Internal Globus Pallidus): A part of the human basal ganglia responsible for inhibiting the thalamus indirectly, affecting cerebral areas.
**mAChR-B(**Muscarinic acetylcholine receptor**)**: Receptor in neurons, functioning in various physiological processes such as smooth muscle contraction and secretion.
**VLPO** (Ventral Lateral Prefrontal Operculatum): A subregion within the prefrontal cortex, located ventrally (ventral) and laterally (lateral), involved in higher-order functions such as attention, decision-making, and emotional processing.
**MnPO** (Medial Prefrontal Operculatum): Another subdivision of the prefrontal cortex, situated in the medial portion, contributing to sensory integration, motor planning, and associative learning.
**SLD** (Small-l Bundles or Sensory Laminar Divisions): Refers to subdivisions within the somatosensory cortex that organize the arrangement of sensory nerve fibers, playing a key role in sensory processing.
**PC** (Precentral Gyrus): A central area in the frontal lobe responsible for integrating and interpreting sensory information from both hemispheres of the brain, involved in higher-order sensory functions.
**vPAG** (Ventral Periaqueductal Gray) refers to a subdivision within the midbrain, specifically located in the ventral region of the periaqueductal gray areas. These structures are involved in regulating mood and anxiety.
**LC (**Locus Coeruleus**):** A small structure within the midbrain that plays a vital role in regulating mood, particularly helping to maintain a calm and peaceful state of mind.
**LDT** (Lost Dark Triangle or Lateral Dorsal Triangle): Refers to subdivisions within the thalamus, particularly involved in sensory processing from higher-order brain areas to lower-level sensory cortices.
**PPT** (Posterior Prefrontal Transversalis): Located posteriorly in the prefrontal cortex, this area is associated with executive functions such as planning, decision-making, and impulse control.
**AI** (Artificial Intelligence): The simulation of human intelligence through artificial systems.
**AGI** (Artificial General Intelligence): AI that can generalize information across domains, without domain-specific expertise similar to that of a human.
**OR**(Objective Reduction): A theory that suggests that higher-level cognitive functions emerge from underlying quantum processes.
**LLM** (Large Language Model): A large neural network designed to learn representations of language quickly, often used in text generation and understanding.
**AN**(Affective Neuroscience): A branch of neuroscience that posits cognition is centered in the basal brain structures of animals, particularly focusing on the mid-brain and other subcortical regions.
**CN**(Cognitive Neuroscience): A branch of neuroscience that argues that the cortex, especially the prefrontal cortex, is the primary location of cognitive processes.
**NCC**(Neural Correlate of Consciousness): A concept that suggests specific neural activity patterns in the brain are associated with conscious experience.

**GWT** (Global Workspace Theory): A neurocognitive model that explains how information from various brain regions integrates through a global workspace to create conscious experiences during perception.
**IIT**(Integrated Information Theory): A theory that posits that consciousness corresponds to the capacity of a system to integrate information.
**KL-Divergence**(Kullback-Leibler Divergence): A measure of how one probability distribution diverges from a second, reference probability distribution.
**FEP** (Free Energy Principle):A theory that posits that living organisms maintain their functional states by continuously expending energy to sustain life processes such as growth, reproduction, and adaptation.
**fMRI**(Functional Magnetic Resonance Imaging): A non-invasive neuroimaging technique used to measure brain activity by detecting changes in blood flow.
**EEG** (Electroencephalography): A technique that measures electrical activity in the brain using electrodes.
**LIF**(Leaky Integrate and Fire): A mathematical model of neurons that accumulate incoming signals (integrating) until they reach a threshold, causing them to fire an action potential.
**StNN**(Stochastic Neural Networks): Networks that integrate randomness into their architecture and learning processes to enhance modeling of biological neural systems.
**RWA**(Random Weights Assignment) A method where random weights are assigned within a network to facilitate exploration of a broader solution space, thereby improving generalization capabilities.
**SCN**(Stochastic Configuration Networks): Neural networks that utilize random assignments of input weights during the configuration process, allowing for dynamic adjustments based on data variability (Wang & Li, 2017).
**SDE**(Stochastic Differential Equations): Mathematical equations used to model systems that are subject to random influences or noise.
**NeuralFMU**(Neural Functional Mock-up Units): A model that focuses on the structural integration of FMUs (Functional Mock-up Units) into neural networks, enabling seamless interaction between physical modeling and machine learning.
**NeuralODE**(neural ordinary differential equations) An advanced model that extends the concept of integrating neural networks with physical systems by combining neural networks with ordinary differential equations to enhance computational efficiency and interpretability in dynamic system modeling.
**PINNs**(Physics-informed neural networks): Neural networks that incorporate physical principles into their training process, often used as a contrast to traditional methods in the context of hybrid models like those described.

## III. Attestation of Authorship

I hereby declare that this submission is my own work and that, to the best of my knowledge and belief, it contains no material previously published or written by another person (except where explicitly defined in the acknowledgements), nor material which to a substantial extant has been submitted for the award of any other degree or diploma of a university or other institution of higher learning.

# IV. Acknowledgements

I would like to express gratitude to my advisor for their continuous support, guidance, and encouragement throughout the course of my research and thesis writing. Their insightful feedback and expertise have been invaluable in shaping this work.

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# Chapter 1 Introduction

The fruit fly (*Drosophila melanogaster*) represents an invaluable model organism for studying the neural mechanisms underlying animal behavior. Recent advancements in neuroscience have provided deeper insights into how seeking behavior—a fundamental aspect of sensory processing and decision-making—arises from neuronal activity (Panksepp, 1998; Jaak Panksepp, 2011a). For example, an organism's drive to find food when hungry is an example of SEEK. This affect (proto-emotion) has been identified as playing a pivotal role in exploration, learning, and decision-making, making it essential to understanding the intricacies of animal behavior (Solms, 2021).

Central to understanding SEEK is the role of sleep and arousal. These states are closely tied to the activity of specific neuron groups, including those in the central complex (CX) of the fruit fly nervous system (van Swinderen, 2007). Arousal, the state of increased physiological and cognitive activation, is an integral part of the seeking system, driving individuals towards novel stimuli and goals (Panksepp & Biven, 2012). Cognition thus encompasses a range of processes, with sleep and arousal being fundamental to the behavioral repertoire of most animals, and these states are crucial for maintaining consciousness, which is a characteristic of complex nervous systems across species(Anthoney et al., 2023; Barron & Klein, 2016; Frith, 2019; Hulse et al., 2021; Kirszenblat & van Swinderen, 2019; Jaak Panksepp, 2011b; Panksepp, 2016a; Panksepp & Biven, 2012; Solms, 2017b, 2021; Solms & Turnbull, 2007; van Alphen et al., 2013).

The size of the fruit fly brain is also a benefit for research. The fruit fly's brain size—approximately 200,000 neurons is manageable while maintaining sufficient complexity to mimic higher-order animal behaviors(Raji & Potter, 2021). Advanced imaging techniques like electron microscopy have enabled unprecedented resolution in mapping neural circuits within the entire brain. Recent studies using datasets such as the Hemibrain project(Hulse et al., 2021) have provided detailed synaptic connectivity maps, revealing pathways essential for behavior generation.

Despite these advancements, bridging the gap between neuronal activity and behavioral outcomes remains challenging. The fruit fly's connectome is intricate, with variability in connectivity weights and temporal dynamics complicating computational modeling efforts (Hulse et al., 2021). Thus, understanding processes across the Central Nervous System (CNS) regions requires methods that reveal underlying brain activity leading to observed behavior. One method is to investigate coupled oscillators within organisms' nervous systems, essential for controlling behaviors like sleep, arousal, and locomotion(Grabowska et al., 2020; Tainton-Heap et al., 2021). Invertebrate brains may have simpler oscillatory activity richness, but local field potential (LFP) neuronal recordings of oscillations associated with sensory and motor processing indicate the presence of coupled oscillatory mechanisms(Gray, 1994; Hulse et al., 2021). For clarity, LFP is a measure of aggregate electrical potential across a population of neurons in a specific brain region over time. Even with all this, the functional purpose of many neurons remains poorly understood, further hindering our ability to predict behavior from neural activity.

To address these challenges, my thesis posits that certain neural circuits in the fruit fly's Fan-shaped Body (FB), a central neuropil in the fruit fly brain, act as loosely coupled oscillators, controlling affects like SEEK. This entails identifying specific Neurons of Interest (NOIs) based on metrics that are predictive of oscillatory patterns, similar to those observed in Wilson-Cowan or Morris-Lecar type neuronal models(Ashwin et al., 2016). The thesis also introduces a novel framework that posits integration with computational tools such as Bayesian brain models, which suggests that the FB may perform Bayesian inference by estimating environmental probabilities based on sensory inputs.

Note that while biological assays of neurons during in-vivo activity can either prove or disprove the hypothesis that SEEK emerges from Wilson-Cowan motifs within the CX, this thesis at this time can only propose in-silico evidence to show that the hypothesis is plausible (i.e. not impossible). The proposed evidence includes the presence of SEEK cells within the CX and the possibility that a Wilson-Cowan motif serves as a strong candidate for the neuromechanical mechanism underlying SEEK function. Although further research is required to test this hypothesis, it offers a potential explanation for how SEEK and associated neurons may contribute to the processing of information across the fly's afferent sensory systems.

## 1.0 Background and Motivation

The enigma surrounding the origin of a living being's subjective experience in the world continues to intrigue researchers. This question, often considered one of the most significant challenges, delves into the realm of information technology, cognitive neuroscience, and philosophy (Chalmers, 2007). The pursuit of general artificial intelligence and an explanation for the "hard problem" of consciousness as proposed by David Chalmers remains a topic of great interest. However, there is ongoing debate about the underlying factors driving general intelligence, assuming it is a system that transcends neurophysiological processes within the brain. I believe SEEK may shed light on this debate.

Unraveling why the SEEK affect may serve as an objective account for affects and cognition in insects necessitates a detailed explanation. To provide a coherent explanation, I employ a novel computational framework composed of multiple technical domains and their corresponding research methods. As Vilas et al. highlight(Vilas et al., 2021), addressing cognitive phenomena, or phenomenal consciousness, often leads to explananda that lack unity, offering only a rudimentary understanding of the underlying mechanisms. This issue is known as the Explananda Problem. Consequently, this thesis limits its scope to investigate how cognition might function in simpler organisms like the fruit fly, Drosophila *melanogaster*.

Understanding why the SEEK affect within insects may represent an objective account for affects and cognition takes some explaining. I thus begin by employing a novel computational framework, made up of several technical domains along with their associated research methods that provide a sufficient explanation. As Vilas points out, addressing cognition (phenomenal consciousness) leads to explananda that lack unity and provide only a vague understanding of what exactly needs to be explained. This general issue is referred to as the Explananda Problem. Therefore, the general question of what manifests cognition in complex organisms like humans shall remain outside the scope of this thesis. Within the thesis, a narrower, if not more reasonable, working hypothesis is raised to explore how cognition might work in animals such as the fruit fly, Drosophila *melanogaster*.

Computer models of animal cognition are well suited for exploring the hard problem for two basic reasons. There has been some progress in computer science to address the hard problem of consciousness as defined by Chalmers(Chalmers, 2017). It's fair to say that there's been good progress using deep learning and neural networks to address some aspects of AI, but it must be understood that even with all such progress to date, Artificial General Intelligence (AGI intelligence that possesses the ability to understand, learn, and apply knowledge across a broad range of tasks, similar to a human mind), like the one in living organisms with a brain, has not been achieved(Friston, 2024; Haikonen, 2020; Hossenfelder, 2024; Ma, 2022; Marcus, 2008). In fact, current research has arguably no immediate way to achieve AGI in the near future using standard approaches based on either classical AI or newer techniques in deep learning(Haikonen, 2020; Hossenfelder, 2024). It would seem that researchers lack a correct understanding of the problem at hand, often made more difficult by the many aspects of consciousness that must be explained. These things that need to be explained are referred to as explananda leading to an explanatory gap. The thesis does not intend to make a breakthrough discovery that brings all matters to rest, only to shed light on the topic by focusing current technology on the simplest meaningful example of biological affective systems.

Finding neuronal circuits that are capable of "SEEK" (one of the thesis goals) would allow for the possible creation of homologue circuits in a non-biological system that behave like living organisms and should create true AGI. While there are systems like Large Language Models (LLMs) that simulate what humans can do, an AGI that acts as a true analogue would usher in a new area of AGI-based systems. These systems, like LLMs, would have far-reaching and profound effects on various industries, enhancing and transforming their operations in significant ways. For example, in healthcare, AGI could help doctors make more accurate diagnoses by analyzing vast amounts of medical data quickly and accurately. In manufacturing, AGI could optimize production processes, leading to increased efficiency and cost savings. Similarly, in transportation, AGI-powered self-driving cars could revolutionize the industry yet again, reducing accidents and traffic congestion. Therefore, it is crucial to understand that AGI, like Large Language Models today, would contribute to advancements and improvements across a broad range of industries.

## 1.1 Research Objectives and Goals

1. Employ a novel computational framework to help locate (i.e. Pathfinding) and test candidate neural circuits for SEEK.

2. Understand the significance of affects, such as SEEK, leveraging Drosophila's CNS and well-established research methodologies to investigate the neurophysiological mechanisms underlying SEEK behavior.
3. Demonstrate how Spiking Neural Network computational models support the investigation of SEEK and affective neuroscience.
4. Determine how SEEK's relation to Wilson-Cowan like motif and behavior can be applied to the Free Energy Principle (FEP), and Bayesian Inference.

## 1.2 Structure of the Thesis

This section provides an overview of each chapter, elucidating how they interconnect to form a cohesive narrative around the research question and objectives. The thesis begins with an Introduction (Chapter 1) that lays the groundwork by presenting the background and motivation for the study, followed by objectives. It sets the stage for the reader, outlining what to expect and why the research is significant.

The Literature Review (Chapter 2) delves into existing theoretical perspectives on cognition, brain structure across species, and computational models, constructing a foundation upon which the study is built.

The thesis' methodology (Chapter 3) is based on my framework to model and analyze a circuit mechanism within the Fan-shaped Body (FB), a core neuropil within the CX of fruit fly. The multistep framework includes methods for: identifying NOIs; calculating synaptic weights, modelling neural connectivity using graphs; developing neural circuit model diagrams; simulating NOIs, and performing signal analysis. This methodological rigor ensures the study's credibility and reliability. The proposed methodology is illustrated in Fig. 1.

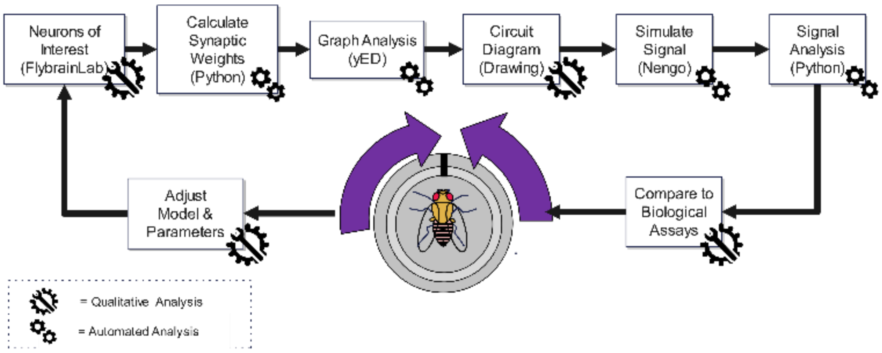


**Fig. 1.** An overview of the workflow used by the Framework. Top-left are Neurons of interest are loaded into the FlybrainLab(Lazar, Turkcan, et al., 2021)

Following this, the Results chapter (Chapter 4) presents key findings, such as the identification of loosely coupled oscillators, and compares these findings with existing literature. The implications of these results for behavior, affective cognitive processes, and Bayesian brain theories are also discussed, paving the way for future experimental approaches.

Finally, the thesis concludes by summarizing the contributions of the study, acknowledging its limitations, and suggesting areas for further research. The Appendices provide additional methodological details and supplementary information, while the References section lists all the sources cited throughout the thesis.

# Chapter 2 Literature Review

The following literature review integrates philosophical, neuroscientific, and computational perspectives relevant to cognition and consciousness. While the philosophical sections (e.g., Mind–Brain Identity Theory, Integrated Information Theory, and Phenomenology) provide conceptual grounding for the overall research question, they are not required for understanding the technical modelling that follows. Readers primarily interested in the computational framework may skim these sections, as subsequent chapters summarize only the components that directly inform the modelling approach. This structure preserves conceptual rigor while allowing streamlined reading for diverse audiences.

The exploration of SEEK affects as the root of core subjective experience, or cognition, through the lens of loosely coupled oscillators, necessitates a comprehensive understanding of several foundational topics. As demonstrated in **Fig. 2**, this literature review will delve into four primary areas: what is cognition? what are the characteristics of cognition? how does cognition work? and where does cognition exist in the brain? These high-level topics will be dissected through various theoretical and empirical lenses, including epistemology and realism, theory of mind, Bayesian and algebraic approaches, and electromagnetic theories such as quantum consciousness.

In exploring the foundational areas of cognition, characteristics of cognition, how cognition operates, and its existence in the brain, we establish the necessary philosophical groundwork for understanding the interplay between affects and cognitive processes through oscillators. Our focus on deterministic physicalism is guided by the need to analyze neural correlates within the mid-brain, aligning with methodologies that explore oscillatory interactions in cognition. This perspective ensures a coherent and logically consistent approach, particularly when considering complex theories such as quantum consciousness or Bayesian models, thereby providing a structured foundation for our research objectives.

Again, while a broad range of topics will be reviewed, the primary focus of this thesis is grounded in deterministic physicalism, particularly the neural correlates of SEEK affects in the mid-brain. The SEEK affect, as conceptualized by Jaak Panksepp(Panksepp, 1998), refers to a primal emotional system that drives exploratory behavior and the pursuit of goals, often associated with feelings of curiosity and anticipation. This system is crucial for understanding emotional states across species, as it is linked to the neural mechanisms underlying social attachments and the experience of pleasure derived from seeking rewards(Coenen et al., 2011; Davis et al., 2003; Ikemoto & Panksepp, 1999; Panksepp, 2007; Jaak Panksepp, 2011a; Panksepp, 2016a, 2016b; Panksepp et al., 2002; Solms, 2021).

Consequently, some areas, such as Integrated Information Theory (IIT) and other less empirically supported or non-falsifiable theories, will not be heavily delved into.

For justification, please refer to the section below entitled, ‘Comparison with Existing Literature’.

The mechanisms of cognition will be investigated primarily through the lens of physicalism, and the localization of cognitive processes will be explored within the context of affective and cognitive neuroscience, particularly focusing on the mid-brain and cortex. Additionally, this review will cover computational neurophysiology, providing a rationale for combining physicalism with computational approaches. The discussion will extend to comparative neuroanatomy, highlighting homologue brain structures across species, and the role of SEEK affect as a foundational element of cognition. By integrating insights from various theoretical models, including Bayesian brain theories, neural network models, and dynamical systems, this section aims to present a holistic view of cognition, its characteristics, mechanisms, and neural substrates.

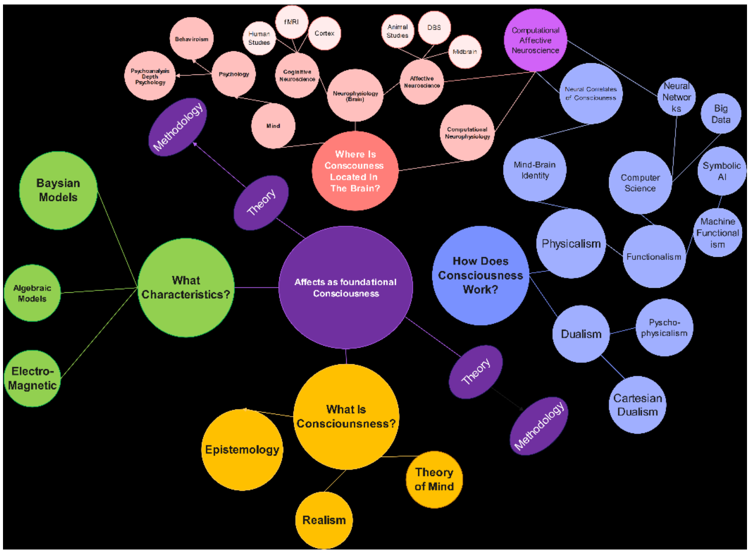


**Fig. 2.** A Mind-map overview showing the scientific problem of “Affects as foundational consciousness) at the center with outward layers demonstrating theories and methodologies explored by the thesis.

## 2.0 What is Cognition?

Much has been theorized over the last few centuries, but many notions are grouped under an umbrella theory called, “Theory of Mind”. And while it is possible to fill entire books about this branch of theories, the thesis highlights two central theoretical branches: Cognitive and Phenomenological consciousness. Of the two, Cognitive theory deals with what Chalmers calls, “the easy problem”(Chalmers, 2017). This refers to a modern understanding of how incoming sensory information travels through the central nervous system and an organism’s ability to respond. For example, consider how light travels through the eyes and into the retina and then through the nervous system to be interpreted by the visual cortex. While the mechanical process for sight is by no means easy to explain, it is explainable (within certain constraints) using well-established scientific methods. The ability to explain such mechanistic processes is precisely why Chalmers refers to this as the “Easy Problem”.

The most interesting theory here is Phenomenology. There are countless books on the subject that have inspired many theorists(Armstrong, 2017; Chalmers, 2017; D.C. Dennett, 2018; Dreyfus et al., 1986; Heidegger & Stambaugh, 1996; Hepburn et al., 1964; Merleau-Ponty & Landes, 2013; Sartre & Richmond, 2022; Searle, 2004; Zahavi, 2003), but to sum things in short, Phenomenology attempts to explain the phenomena known as consciousness. Phenomenology can be considered as a method of exploring subjective experience. Why is this important? One may be familiar with the general understanding of feelings and one’s own personal subjective experience, but in scientific terms it seems almost incomprehensible for most people to consider how a biological process can give rise to subjective experience. There remains a large explanatory gap, and this is precisely why Chalmers calls all this “the hard problem”

But Chalmers is only one of many who’ve tried to tackle all this. Heidegger was central to the exploration of Phenomenology as a branch of Intentionalism(Hepburn et al., 1964). And by applying his ontology, it might be possible to argue how affects within the brain represent a conscious phenomenon, and by doing so, give rise to an organism’s subjective experience. This thought should simply be kept in the back of one’s mind as other research methodologies are explored. Philosophy is indeed useful describing the problem to be solved, but it won’t suffice to employ any philosophy that escapes empirical falsification. Thus, the thesis will utilize the questions raised by philosophy but not pursue answers within the philosophical domain. Instead, the thesis moves to other domains that provide modern, objective scientific methodologies that can be used to test the hypothesis posited here.

## 2.0 Epistemology and Realism.

Epistemology, the study of knowledge, seeks to understand the nature, origin, and limits of human knowledge(Audi, 1998). It addresses some key questions such as: What is knowledge? How is knowledge acquired? And what do people know? Various epistemological theories offer different perspectives on these questions(Steup, 2024). Empiricism, for instance, posits that knowledge comes primarily from sensory experience, while rationalism argues that reason and intellect are the primary sources of knowledge. Constructivism suggests that knowledge is constructed by individuals through their interactions with the world and others. These diverse epistemological frameworks provide a foundation for exploring how researchers come to understand complex phenomena, including cognitive processes and affects.

In the context of this thesis, which aims to explain affects through loosely coupled oscillations, it is essential to consider how these frameworks can inform our understanding of cognitive processes. A key concept here is the idea of SEEK affects, which may serve as a foundational element in cognition. By exploring how specific affects, such as "seek", contribute to the formation of knowledge, one can bridge the gap between epistemological theories and empirical evidence.

Realism, in philosophy, posits that reality exists independently of our perceptions or beliefs(Chakravartty, 2017). This thesis aligns with the realist perspective, suggesting that there are objective neural correlates of SEEK affects in the mid-brain that can be studied and understood. While epistemological theories offer valuable insights into how knowledge is formed and validated, the realist stance taken here asserts that there is a tangible, observable reality that underpins cognitive and affective processes.

However, it is important to recognize the limitations of epistemological approaches when applied to the study of the mind and brain. While the brain is an extraordinary organ capable of understanding the external world, it faces inherent challenges when attempting to introspect and comprehend its own functioning. The notion that there is a reality outside the human mind is only partially helpful in understanding the intricacies of cognitive processes. The brain's self-referential limitations mean that while most people can observe and measure neural activity, understanding the subjective experience and internal mechanisms remains a complex endeavor. This thesis acknowledges these challenges and focuses on empirical, observable data to elucidate the neural correlates of SEEK affects, while remaining aware of the broader epistemological context.

## 2.1 Theory of Mind

Theory of Mind is a multifaceted concept that explores the ability to attribute mental states—such as beliefs, intents, desires, emotions, and knowledge—to oneself and others. This philosophical and psychological construct has been examined by numerous thinkers, including Immanuel Kant, René Descartes, and Baruch Spinoza. Theory of Mind encompasses various sub-theories, each offering unique perspectives on how the mind operates. Computational Theory of Mind suggests that cognitive processes are akin to computational operations(Müller, 2009). Mind-Brain Identity Theory posits that mental states are identical to brain states(Polák & Marvan, 2018). Phenomenological Theories focus on the subjective experience of consciousness(Sytsma, 2009), while Game Theory examines strategic interactions where individuals' decisions are influenced by their understanding of others' mental states(Wang et al., 2024). These diverse approaches provide a rich tapestry of insights into the nature of cognition and consciousness.

Within the context of this thesis, Mind-Brain Identity Theory is particularly favored. This theory, supported by many scholars, posits that mental states are identical to brain states(Polger, 2004). Essentially, it argues that every mental state or process corresponds directly to a physical state or process in the brain(Polák & Marvan, 2018). This perspective aligns with the deterministic physicalism that underpins this research, suggesting that cognitive functions and subjective experiences can be fully explained by neural activities. Mind-Brain Identity Theory works well within a scientific reductive approach because it allows for the decomposition of complex mental phenomena into their neural components. By treating mental states as brain states, researchers can utilize empirical methods to investigate the neural correlates of consciousness (NCC)(Frith, 2019; Långsjö et al., 2012; Michel & Morales, 2019). This approach facilitates the identification of specific neuronal patterns and structures, such as those in the mid-brain, that are associated with SEEK affects and other cognitive processes. By focusing on these neural substrates, this thesis aims to provide a detailed and scientifically grounded explanation of how core subjective experiences arise from brain activity.

While Theory of Mind is a multifaceted set of theories, many of its aspects overlap with other sections of this literature review. The understanding of affects and cognition is divided into four major topics: What is cognition? What characteristics does it have? How does cognition work? And where might cognition exist in the brain/mid-brain? It is challenging to delve into “what” cognition is without touching on these other areas. Therefore, the discussion of “what” cognition is will be relegated to more abstract concepts with broad interpretations, rather than delving into actual mechanistic explanations. This approach allows for a comprehensive yet focused exploration of cognition, aligning with the overarching goals of this thesis.

## 2.1 Characteristics of Cognition

This section of the thesis refers to the fundamental properties that define cognitive processes, encompassing how information is processed, represented, and transformed within the mind. These characteristics provide a framework for understanding the nature of thought, perception, memory, decision-making, and learning. Various theoretical approaches have been proposed to characterize cognition, each offering unique insights into its underpinnings.

One prominent approach is the Bayesian framework, which integrates probability theory with information processing, often associated with the Free Energy Principle (FEP)(Friston & Kiebel, 2009). This perspective suggests that cognitive systems operate as adaptive agents, minimizing "free energy" by continually updating beliefs and predictions based on sensory input. Another influential framework is Integrated Information Theory (IIT)(Tononi, 2008), which posits that cognition arises from the maximization of whole-system information, emphasizing the interdependence of neural elements in generating conscious experience. Additionally, some researchers have drawn parallels between cognitive processes and physical phenomena, such as electromagnetic interactions or quantum principles, proposing that consciousness itself might emerge from complex dynamics akin to those observed at the quantum level(Hameroff, 2007).

While these approaches reflect different theoretical perspectives, they share common ground in their emphasis on adaptability, efficiency, and the integration of information across multiple scales. By adopting a multidimensional approach that incorporates insights from these diverse frameworks, this study aims to elucidate the universal characteristics of cognition while exploring how these principles manifest in concrete biological systems.

### 2.1.1 Bayesian Approaches.

Bayesian theories of cognition, such as the Bayesian Brain Theory, propose that cognition is fundamentally about probabilistic inference(Stubbs & Friston, 2024). According to these theories, the brain constructs and continuously updates an internal model of the world based on incoming sensory information. This model allows the brain to predict future states and make decisions that are generative in nature. Different versions of Bayesian theories include the Predictive Coding framework, which suggests that the brain minimizes prediction errors by constantly comparing its predictions with actual sensory input(Pezzulo et al., 2022). Central to the thesis is the Free Energy Principle (FEP), which posits that the brain minimizes a quantity called "free energy" to maintain a stable internal state and adapt to environmental changes.

The Free Energy Principle (FEP) is a comprehensive theory that explains how biological systems, including the brain, maintain homeostasis and adapt to their environment(Brouillet & Friston, 2023; Friston et al., 2017; Friston & Frith, 2015; Millidge, 2019a, 2019b; Parr et al., 2022; Stubbs & Friston, 2024; Whyte & Smith, 2020). The principle is mathematically expressed as minimizing the free energy, which can be broken down into several components. For more detail the reader is directed to the Appendix section, but in short, the equation for free energy is typically written as:

$$F = -\langle \ln p\,(\tilde{y}(\alpha) \mid \vartheta\,)\rangle_q + D\big(q(\vartheta)|p(\vartheta)\big) \tag{1}$$

Here, $\mathrm{p}(\tilde{\mathrm{y}}(\alpha) \mid \vartheta\,)$ represents the likelihood of sensory input given the hidden states, and $\mathrm{q}(\vartheta)$ represents the approximate posterior distribution of hidden states. The first term, $-\langle \ln \mathrm{p}\,(\tilde{\mathrm{y}}(\alpha) \mid \vartheta\,)\rangle_{\mathrm{q}}$, is the expected log probability of the sensory input under the variational (ensemble) density, which is a function of action variables $\alpha$. Minimizing this term corresponds to maximizing the log probability of the sensory input, meaning the system will reconfigure itself to sample incoming sensory inputs that are most likely under the ensemble density. The second term, $\mathrm{D}\big(\mathrm{q}(\vartheta)\big|\mathrm{p}(\vartheta)\big)$, is the Kullback-Leibler (KL) divergence (see the Appendix for more details) between the approximate posterior $\mathrm{q}(\vartheta)$ and the prior $\mathrm{p}(\vartheta)$. This term measures the difference between the brain's model of the world and the actual sensory input. By minimizing free energy, the system ensures that its internal model aligns closely with the external environment.

Due to its inherent circularity, this process necessitates that the system adheres to its self-generated expectations. In essence, the system selectively interacts with causes in its surroundings based on its anticipated encounters. These expectations are bounded by the physical states the system can occupy, thus defining the ensemble density. Systems with low free energy can only explore portions of the environment that they can represent using their repertoire of physical states. Since the free energy is minimal, the inferred causes closely mirror the actual environmental conditions. As a result, the system's physical state must be sustainable under these conditions. The Free Energy Principle offers a robust foundation for comprehending how biological systems, including the brain, maintain stability and adapt to their environment by minimizing free energy.

The Free Energy Principle offers a pathway for incorporating neuromechanistic explanations for the input, output, and KL-divergence minimization functions that it calls for. Minimization of free energy can be seen as a decrease in KL-divergence if one considers two distributions: one representing the model of the outside world as seen via external sensory input, and the other representing the desired state of the world to achieve homeostatic balance in the organism(Friston et al., 2017; Parr et al., 2022). In this way, FEP provides a framework that can be broken down into abstract concepts and equated to real neurophysiological data. By aligning the brain's internal model with external reality, FEP helps explain how cognitive processes are optimized to maintain stability and adapt to changes, offering a robust theoretical foundation for understanding the characteristics of cognition.

### 2.1.2 Algebraic Approaches (Integrated Information Theory).

Algebraic approaches to understanding cognition involve using mathematical frameworks to describe and analyze cognitive processes. One prominent theory within this domain is Integrated Information Theory (IIT), developed by Giulio Tononi. IIT seeks to explain consciousness by quantifying the amount of integrated information within a system(Tononi, 2008). According to IIT, consciousness corresponds to the capacity of a system to integrate information, and this capacity can be measured using a mathematical quantity called $\Phi$ (phi). The theory posits that systems with higher $\Phi$ values have higher levels of consciousness(Barrett & Seth, 2011; Cerullo, 2015; Oizumi et al., 2014; Oizumi, Amari, et al., 2016). Other algebraic theories include the Global Workspace Theory (GWT), which uses a mathematical model to describe how information is broadcast across different parts of the brain(Baars & Franklin, 2009; Shanahan, 2006).

Integrated Information Theory is built on two main concepts: differentiation and integration(Tononi, 2008). Differentiation refers to the ability of a system to produce a large repertoire of distinct states, while integration refers to the system's ability to combine these states into a unified whole. To understand these concepts, consider a simple example: a digital camera sensor. Each pixel in the sensor can be in one of many states (differentiation), but the sensor, as a whole, integrates these states to produce a coherent image (integration). In the context of the brain, IIT suggests that consciousness arises from the integration of information across different neural networks. The theory uses complex mathematical formulations to calculate $\Phi$, which represents the degree of integrated information within the system.

While IIT offers a compelling theoretical framework, it has several limitations. One major challenge is its computational intractability for complex systems. Calculating $\Phi$ for a large network of neurons is extremely difficult, making it impractical for real-world applications(Cerullo, 2015). Additionally, IIT lacks a concrete mechanism for cognition, relying instead on the assumption that consciousness emerges intrinsically from any system with integrated information, regardless of its composition(Barrett & Seth, 2011). Prominent researchers like Christof Koch and David Chalmers support IIT, arguing that it provides a promising framework for understanding consciousness by linking it to measurable physical properties. Koch, for instance, views IIT as the most promising fundamental theory of consciousness(Koch, 2018, 2021). On the other hand, Scott Aaronson argues emphatically that IIT “unavoidably predicts vast amounts of consciousness in physical systems that no sane person would regard as particularly ‘conscious’ at all”(Aaronson, 2014 ). Barrett and Seth also criticizes IIT for mathematical formulations that may not capture the full complexity of conscious experience(Barrett & Seth, 2011). These critiques highlight the theory's practical limitations and the need for more concrete mechanistic explanations.

In contrast to all this, this thesis posits that cognition can be explained by oscillators created by neurons, a concrete physical phenomenon observed in biological systems. If this hypothesis is proven true, it would suggest that similar processes could potentially be replicated in non-biological systems, though this would require a great deal of further research. Thus, while IIT provides valuable insights, its practical limitations and lack of mechanistic detail highlight the need for alternative approaches to understanding cognition.

## 2.2 Electromagnetic Approaches (Quantum Consciousness).

Electromagnetic approaches to understanding consciousness propose that consciousness arises from electromagnetic fields generated by neural activity. One prominent subset of these theories is Quantum Consciousness, which suggests that quantum mechanical phenomena, such as entanglement and superposition, play a crucial role in brain function and consciousness(Hameroff & Penrose, 2016). This idea posits that classical physics alone cannot fully explain consciousness and that quantum effects at the microscopic level within neurons could be key to understanding conscious experience. Stuart Hameroff and Roger Penrose have proposed the Orchestrated Objective Reduction (Orch OR) theory, which posits that microtubules within neurons provide an environment for quantum properties to emerge(Hameroff & Penrose, 2014). According to this theory, quantum computations within these microtubules contribute to the generation of consciousness.

The theory of Quantum Consciousness has both proponents and critics. Bohm and Hiley's work(Hiley & Pylkkänen, 2022) laid the groundwork by introducing the concept of active information and the implicate order, which they believed could bridge the gap between mind and matter. Building on this, Stuart Hameroff and Roger Penrose developed the OR theory, which posits that consciousness arises from quantum computations within microtubules inside neurons(Hameroff & Penrose, 2007, 2014; Hameroff & Penrose, 2016). They argue that these quantum processes are orchestrated by cellular structures and are fundamental to conscious experience. However, critics like Daniel Dennett along with other researchers have been vocal in their opposition. Dennett, contends that the theory does not provide a testable hypothesis and fails to offer a solid philosophical basis for making predictions(Keating, 2024). One of the most significant arguments against Quantum Mind theory is the assertion that quantum effects, as prescribed by Orch OR, cannot occur in the warm, wet environment of the brain, where decoherence would rapidly destroy any quantum states (Hossenfelder, 2022; Lawrence Kuhn, 2022; Litt et al., 2006).

Given the claims of the theory and lack of compelling evidence and the speculative nature of Quantum Consciousness, this thesis considers such theories to be speculative at best. Instead, the thesis relies on more well-established neuronal dynamics to explain cognition. The focus is on deterministic physicalism and the role of neural oscillators in generating cognitive processes. While Quantum Consciousness offers intriguing theoretical insights, its practical limitations and the absence of concrete mechanisms for cognition make it less viable for explaining cognitive phenomena. Future research may explore the potential of quantum effects in non-biological systems, but for now, this thesis prioritizes empirical, observable data from known neuronal dynamics.

## 2.3 Mechanisms of Cognition

In this section we explore the question of "how" cognition might work at a high level. This entails two large philosophical domains: Physicalism, that explains cognitive processes (like perception, memory, or decision-making) as arising from physical brain activity, and Dualism, that explores how mental states or subjective experiences (e.g., awareness or intention) might interact with the physical brain in a non-reducible way.

### 2.3.1 Dualism vs Physicalism.

Dualism and Physicalism represent two distinct approaches to understanding the mechanisms of cognition. Dualism posits that the mind and body are separate entities, with the mind existing as a non-physical phenomenon that does not supervene upon the brain or central nervous system (CNS). This view, historically associated with René Descartes(Hatfield, 2024), suggests that mental states are not reducible to physical states and that the mind can exist independently of the body. In contrast, Physicalism(Stoljar, 2024) asserts that all mental states and processes are entirely dependent on physical states and processes within the brain and CNS. According to Physicalism, cognition and consciousness arise from the interactions of neurons and synapses, and there is no need to invoke non-physical entities to explain mental phenomena.

David Chalmers is a modern-day proponent of Dualism(Chalmers, 1998), particularly known for his formulation of the "hard problem of consciousness," which questions how and why physical processes in the brain give rise to subjective experiences(Chalmers, 2017). However, this thesis rejects Dualism, aligning with the views of prominent researchers who argue against it. Critics like Daniel Dennett and John Searle contend that Dualism fails to provide a plausible mechanism for how non-physical phenomena could interact with the physical body. They argue that if the mind were truly non-physical, it would be inexplicable how it could influence physical actions, which are clearly observable and measurable(Dennett, 2003; Daniel C. Dennett, 2018; Searle, 2004). This lack of explanatory power and empirical support leads many in the scientific community to favor Physicalism over Dualism.

Physicalism is clearly favored by this thesis, but it encompasses a range of theories, some of which have evolved over time. Within this framework, two main groups are Functionalism and Mind-Brain Identity Theory. Mind-Brain Identity Theory, supported by researchers like Christof Koch, posits that mental states are identical to brain states and that consciousness arises from specific neuronal activities(Koch, 2018). However, this theory faces the challenge of explaining in detail how subjective experiences emerge from neurodynamic activity.

On the other hand, Functionalism, including Machine Functionalism, suggests that mental states are defined by their functional roles rather than their physical substrates.

This approach has seen limited success in AI, with symbolic AI and Large Language Models (LLMs) achieving milestones like the Turing test(Dodig-Crnkovic, 2023). However, critics like Gary Marcus argue that functional analogs of cognitive systems are not equivalent to conscious organisms(Marcus, 2008, 2018). Marcus points out that despite advances in computational power, achieving Artificial General Intelligence (AGI) remains elusive, as functional analogs do not capture the full complexity of human cognition(Fridman, 2019). This thesis, therefore, emphasizes the importance of understanding cognition through concrete neuronal dynamics rather than abstract functional analogs.

## 2.4 Localization of Cognition in the Brain

In this section we look at the question of “where” cognition might exist in the CNS. This area of research is broken into two main domains, Affective Neuroscience and Cognitive neuroscience. Both areas of research believe that cognition is in the CNS but differs on the general location.

### 2.4.1 Affective vs Cognitive Neuroscience.

Affective Neuroscience (AN) is a branch of neuroscience that posits cognition is centered in the basal brain structures of animals, particularly focusing on the mid-brain and other subcortical regions. This field contrasts with Cognitive Neuroscience (CN), which argues that the cortex, especially the prefrontal cortex, is the primary location of cognitive processes. Researchers like Mark Solms, Jaak Panksepp (Damasio et al., 2013; Panksepp, 2007; Solms, 2021) argue that these subcortical regions are crucial for survival and have been conserved throughout evolution, providing a fundamental basis for cognition. On the other hand, researchers such as Richard Lane, Ryan Smith, Joseph LeDoux, and Lisa Feldman Barrett support CN, presenting evidence that higher-order cognitive functions, such as decision-making, planning, and abstract thinking, are predominantly mediated by cortical circuits (Barrett & Bliss-Moreau, 2009; Feldman Barrett & Lida, 2024; LeDoux, 2023; Smith & Lane, 2016). These researchers highlight the complexity and flexibility of cortical networks, which are essential for advanced cognitive tasks.

The divergence in these perspectives often stems from the types of evidence each group relies on. Proponents of AN frequently base their arguments on animal studies, which allow for invasive techniques and detailed examination of subcortical structures(Panksepp et al., 2017). These studies provide compelling evidence of the role of basal brain regions in fundamental cognitive and emotional processes. In contrast, CN relies heavily on human studies, utilizing non-invasive imaging techniques like fMRI and EEG to explore cortical activity during cognitive tasks. This approach offers insights into the functioning of the human brain but often lacks the granularity of animal studies. The reliance on different types of experimental evidence makes it challenging to reconcile these two areas of neuroscience, as each provides a unique but partial view of the brain's cognitive architecture.

A central tenet of both CN and AN is the degree of phylogenetic continuity between animals and humans. Both theories agree that evolutionary pressures across the animal kingdom have conserved similar mechanisms in the brain to enhance fitness and survival(Jaak Panksepp, 2011a). This continuity suggests that many cognitive processes observed in humans have their roots in the animal brain, shaped by the need to navigate and adapt to environmental challenges. However, CN places more emphasis on the unique adaptations and capabilities that have evolved in humans, particularly those related to complex social behaviors and higher-order cognitive functions(Panksepp, 2016b). CN also highlights that humans have developed more complex emotions and cognitive capabilities due to their advanced cortical structures. Researchers like Jonathan Haidt have explored emotions such as guilt, contempt, and pride, which are crucial for social group dynamics and are more complex than the basic affects studied in AN(Rozin & Haidt, 2013). These complex emotions are seen as adaptations that provide humans with sophisticated tools for navigating social environments.

While CN involves the initiation of cognitive reactions to environmental changes, with a significant focus on the interactions between the basal brain regions and the prefrontal cortex, AN researchers argue that while this might be true for humans, it is not sufficient to explain basic cognition and affective states in all animals. AN posits that fundamental emotional processes are rooted in subcortical structures, which are conserved across species and are essential for basic survival functions. The difference in focus between CN and AN often stems from the fact that cognition, affects, and emotions are not fully understood, leading to different interpretations of the evidence.

Thus, the distinction between what is "necessary" and what is "sufficient" to explain cognition is a central area of disagreement between CN and AN. CN justifies its focus on the neocortex by arguing that self-reflective thinking about one's cognitive and emotional state is a hallmark of human cognition. In contrast, AN maintains that basic affects are the primary mechanisms by which organisms interact with their environment and achieve homeostatic balance.

As stated above, this thesis adopts the AN position, arguing that fundamental affective processes are sufficient to explain core cognition. By emphasizing the role of base affects, this approach provides a more parsimonious explanation for cognitive phenomena across different species, highlighting the evolutionary continuity of these processes.

### 2.4.2 Affective Neurophysiology and SEEK

Affective Neuroscience is a field that explores the neural mechanisms underlying emotions and affective states. Researchers like Mark Solms, Jaak Panksepp, and Antonio Damasio have significantly contributed to defining the term "affect"(Panksepp et al., 2017). Affect refers to the intrinsic emotional experiences that arise from the integration of sensory input with internal physiological states. Panksepp identified seven primary emotional systems, which he termed affects: SEEK, RAGE, FEAR, PANIC, PLAY, CARE, and LUST(Panksepp, 2007). These affects are considered fundamental to survival and are deeply rooted in the brain's subcortical structures. SEEK involves the drive to explore and engage with the environment, RAGE is associated with anger and frustration, FEAR relates to anxiety and threat responses, PANIC involves separation distress, PLAY is linked to social joy and interaction, CARE pertains to nurturing behaviors, and LUST is related to sexual arousal and reproduction.

Ikemoto and Panksepp and proposed that the subcortical midline structures, particularly the mid-brain, are the location of the subjective self, composed of neurons with affective properties(Ikemoto & Panksepp, 1999). This theory suggests that core cognition and affective experiences are rooted in these ancient brain regions. Evidence supporting this view comes from studies showing that lesions in subcortical areas can induce coma, indicating their crucial role in maintaining consciousness and basic cognitive functions. Researchers like Parr, Solms, and Pezzulo have reported that damage to the cortex does not necessarily eliminate cognition(Merker, 2007; Parr et al., 2022; Solms, 2017b). This is exemplified by cases of hydranencephaly, where individuals are born without a functioning cortex but still exhibit core cognitive functions, although they are significantly impaired in learning and higher-order cognitive tasks.

Alcaro, Panksepp, and Coenen categorize affects into three types: homeostatic/visceral affects, instinctual/emotional affects, and sensorial affects(Alcaro & Panksepp, 2011; Coenen et al., 2011). Homeostatic affects refer to internal bodily states, such as hunger and thirst, which are crucial for maintaining physiological balance. Instinctual/emotional affects include basic emotional responses like fear and attachment, which are essential for survival and social bonding. Sensorial affects encompass rudimentary perceptual experiences with affective value, such as the feeling of touch, hearing calming or startling sounds, and sensing warmth or coldness. These emotional affects are innate and not learned, distinguishing them from the broader concept of emotions, which are often shaped by cultural and social influences over a person's lifetime(Solms, 2017a). This distinction underscores the foundational role of affects in driving behavior and maintaining homeostasis across species.

The concept of affects as the core of the subjective self has its roots in the early 20th century with Carl Jung, who proposed that the self emerges from an innate dynamic structure that encompasses the fundamental motivations of our "brain-mind," resulting in both instinctual behaviors and primordial psychological experiences. (Jung et al., 2016). This idea has been further developed and promoted in the 21st century by researchers like Jaak Panksepp and Mark Solms. Panksepp, often referred to as the father of Affective Neuroscience, conducted extensive experiments using electrical stimulation, pharmacological challenges, and brain lesions in mammals to map out primary emotional systems.

Panksepp and Solms have conducted various experiments to support their theories. For instance, Panksepp's work with electrical stimulation of the brain demonstrated that activating certain subcortical regions could elicit specific emotional responses in animals(Coenen et al., 2011). These findings were further supported by studies showing that lesions in subcortical areas, such as the mid-brain, could induce coma, indicating their critical role in maintaining consciousness and core cognitive functions(Solms, 2021). Additionally, cases of hydranencephaly, where individuals are born without a functioning cortex but still exhibit core cognitive functions, provide compelling evidence for the importance of subcortical structures in cognition.

Among the primary affects identified by Panksepp, SEEK stands out as a special affect that acts as the foundational basis for an organism's subjective self. SEEK is associated with the drive to explore and engage with the environment, and it underpins the core of reward and arousal systems. Panksepp and Solms argue that SEEK is fundamental to an organism's desire to interact with the world, making it a key affect for understanding cognition(Panksepp et al., 2017). The SEEK system is believed to be the primary mechanism through which organisms achieve homeostatic balance and adapt to their environment. This thesis posits that uncovering the neural mechanisms underlying the SEEK affect is crucial for developing a general explanation of cognition. By focusing on the SEEK system, this research aims to provide a concrete neuromechanical explanation for how core cognitive processes arise from affective states.

### 2.4.3 Research Rationale

#### 2.4.3.1 Justification for Combining Physicalism and Computational Neurophysiology

The focus of this thesis on Computational Affective Neuroscience is grounded in the robust framework it provides for exploring the neural mechanisms underlying cognition. By adopting a combined perspective combination of realism, Bayesian and affective neuroscience (see **Fig. 3**), this research posits that cognitive processes can be fully explained by the physical interactions of neurons and synapses. This approach is particularly compelling when combined with computational neurophysiology, which allows for the modeling and simulation of complex neural dynamics. The hypothesis that coupled oscillators can explain the SEEK affect within the central complex (CX) of Drosophila offers a promising avenue for understanding core cognition. Computational models enable the detailed examination of how neural oscillations contribute to affective states, providing in-silico evidence that supports the hypothesis.

One of the significant benefits of focusing on computational approaches is the ability to generate testable predictions that can be validated through biological experiments. For instance, in-silico models of coupled oscillators can be used to simulate the neural activity associated with the SEEK affect. These simulations can then guide experimental designs, such as patch clamp recordings, to measure the electrical activity of neurons in the CX of Drosophila. By comparing the computational predictions with empirical data, researchers can refine their models and gain deeper insights into the neural mechanisms of cognition. This iterative process of modeling and experimentation enhances the reliability and validity of any testable findings.

Moreover, computational methods offer several advantages that are often cited by biological scientists. These include the ability to handle large datasets, perform complex analyses, and explore hypotheses that may be difficult or impossible to test experimentally. Computational models can integrate data from various sources, such as genetic, anatomical, and physiological studies, to provide a comprehensive understanding of neural systems. Additionally, they allow for the exploration of parameter spaces and the identification of critical variables that influence neural dynamics. This holistic approach not only advances our knowledge of the brain but also facilitates the development of new experimental techniques and technologies. For more details on this, the reader is directed to the section below on Future Experimental Approaches.

The Hemibrain dataset from the Janelia Research Campus is a crucial resource for this research, providing detailed anatomical and functional data on Drosophila neurons. Future versions of the Hemibrain dataset will offer even more detailed information, and broader datasets will become available, enabling the generation of new models(Hulse et al., 2021). For example, the Janelia team has also developed the MANC (Male Adult Nerve Cord) dataset, which includes neurons from the ventral nerve cord (VNC). Combining the Hemibrain and MANC datasets could allow for more complex and fully integrated simulations that map sensory input to CX cognition and motor output in the legs or wings. While such a comprehensive dataset is not yet available, the techniques proposed in this thesis can be easily adapted to incorporate these future datasets, paving the way for more advanced and holistic models of neural function.

**Fig. 3.** Combined theories and methods that form the basis of the thesis.

### 2.4.4 Computational Affective Neuroscience

Computational Affective Neuroscience is an interdisciplinary field that combines principles from neuroscience, psychology, and computational modeling to understand the neural mechanisms underlying emotions and affective behaviors. By simulating neuronal motifs and circuits, particularly within the mid-brain and basal brain systems, researchers aim to elucidate how these neural dynamics correlate with specific behaviors. This approach not only enhances our understanding of brain function but also provides insights into the complex interplay between neural activity and emotional responses.

In this thesis, the focus will be on simulating a neuronal analog of SEEK observed in Drosophila. SEEKING is a fundamental motivational system that drives organisms to explore their environment and seek out resources. By modeling the neuronal circuits involved in this behavior, one can gain a deeper understanding of the underlying neural dynamics and how they contribute to the expression of SEEKING. While the primary focus is on this specific behavior, the principles and methodologies discussed are applicable to a wide range of affective behaviors across different species.

Research in Computational Affective Neuroscience often favors model organisms with well-understood central nervous systems (CNS)(Panksepp et al., 2017). These models, such as fruit flies, mice, and zebrafish, provide a robust framework for conducting biological experiments that can validate computational models. This thesis favors using fruit flies because their connectome is better documented than any other organism at the moment. Additionally, there are no ethical considerations with fruit flies, as they can be freely bred, experimented upon, and euthanized. This makes it relatively easier to conduct both in-silico and in-vivo assays. The ability to confirm or falsify results through empirical data is crucial for advancing our understanding of affective neuroscience and ensuring the accuracy of computational simulations.

Several technical frameworks are available for simulating neuronal circuits, each with its strengths and community support. Notable platforms include FlybrainLab, Virtual Flybrain, NEURON, NEST, Brian, Nengo, and DynaSim(Casalegno et al., 2016; Enochson et al., 2022; Kulkarni et al., 2021; Lazar, Liu, et al., 2021). These tools offer robust and stable environments for modeling neural systems, supported by active user communities that contribute to their continuous improvement and functionality. This thesis will leverage these platforms to ensure reliable and reproducible results, benefiting from the collective expertise and ongoing development within these communities.

## 2.5 Homologue Brain Structures Across Species

### 2.5.1 Insects and Basic Consciousness: Subjective Experience

The topic of basic consciousness and subjective experience in insects is a subject of ongoing debate within the scientific community. While some researchers argue that invertebrates, including insects, do not possess emotional states homologous to human emotions, others believe that these creatures exhibit fundamental affective states(Barron & Klein, 2016; Perry & Barron, 2013). This thesis posits that to engage in meaningful discussions about insect consciousness, it is essential to distinguish between complex emotions and more basic affective states.

Complex emotions, such as those observed in humans, great apes, and even dogs, are learned over time and are influenced by social and environmental factors. These emotions involve higher cognitive processes and are often shaped by individual experiences and interactions. In contrast, “affects,” sometimes referred to as emotional primitives by researchers like Anderson, are more basic and innate(Anderson, 2022). Affects are fundamental emotional responses that are hardwired into the brain and are crucial for survival. They are not learned but are instead intrinsic to the organism’s neural architecture. According to Panksepp, affects are primary emotional systems that are deeply rooted in the brain’s subcortical regions(Fabbro et al., 2015; Jaak Panksepp, 2011a, 2011b; Panksepp, 2013; Panksepp, 2016a, 2016b; Panksepp et al., 2017). Barron supports this view by suggesting that these basic affective states are the foundation of cognition and are integral to the emergence of consciousness(Barron et al., 2015; Barron & Klein, 2016; Barron & Plath, 2017).

In the context of invertebrates, Barron posits that insects may possess rudimentary affective states that guide their behavior. While these states may not be homologous to human emotions, they serve similar functional roles in regulating behavior and ensuring survival. Barron and Klien further argue that insects have the capacity for the most basic aspect of consciousness: subjective experience(Barron & Klein, 2016). They propose that subjective experience is supported by integrated structures in the mid-brain, which create a neural simulation of the state of the mobile animal in space. This perspective aligns with Panksepp’s ideas and suggests that the origins of consciousness may lie in animals that perform simple, unremarkable behaviors. Evidence supporting this view includes the work of Strausfeld(Strausfeld & Hirth, 2013), who demonstrated that the central complex (CX) in insect brains processes sensory information and executes command functions over the behavioral system. These findings highlight the importance of the CX in providing subjective location and navigation, reinforcing the idea that insects possess a form of basic consciousness.

### 2.5.2 SEEK Affect: Foundation of Cognition

The SEEK affect, as described by Jaak Panksepp, is considered special because it is a foundational affect that underpins cognition and allows organisms to engage with their environment(Panksepp & Biven, 2012). Panksepp places significant emphasis on the SEEK affect due to several key reasons that highlight its importance in the neural and behavioral landscape of organisms. Firstly, the SEEK affect is deeply rooted in the brain’s subcortical regions, particularly within the mesolimbic and mesocortical pathways(Panksepp, 1998, 2010). These neural circuits are responsible for generating a sense of curiosity and motivation, driving organisms to explore their surroundings and seek out resources. This exploratory behavior is crucial for survival, as it enables organisms to find food, shelter, and mates. By engaging in SEEKING behavior, organisms can adapt to changing environments and improve their chances of survival. Secondly, Panksepp argues that the SEEK affect is fundamental to learning and memory. When an organism engages in SEEKING behavior, it encounters new stimuli and experiences that are encoded in the brain. This process of exploration and discovery leads to the formation of new neural connections and the strengthening of existing ones, facilitating learning and cognitive development(J. Panksepp, 2011; Panksepp, 2013). The SEEK affect thus serves as a driving force behind the acquisition of knowledge and the ability to adapt to new situations.

Additionally, the SEEK affect is closely linked to positive emotional states. Panksepp's research suggests that the activation of SEEKING circuits in the brain is associated with feelings of anticipation and excitement. These positive emotions reinforce SEEKING behavior, encouraging organisms to continue exploring and engaging with their environment(J. Panksepp, 2011). This positive reinforcement mechanism ensures that organisms remain motivated to seek out new opportunities and challenges, further enhancing their cognitive abilities. Moreover, the SEEK affect plays a crucial role in goal-directed behavior. By generating a sense of purpose and direction, the SEEK affect enables organisms to set and pursue goals(Panksepp & Biven, 2012). This goal-directed behavior is essential for problem-solving and decision-making, as it allows organisms to plan and execute actions that lead to desired outcomes. The ability to set and achieve goals is a hallmark of higher cognitive functions, and the SEEK affect provides the motivational foundation for these processes.

In summary, Panksepp emphasizes the SEEK affect as the foundation of cognition due to its role in driving exploratory behavior, facilitating learning and memory, promoting positive emotional states, and enabling goal-directed behavior. By understanding the importance of the SEEK affect, researchers can gain deeper insights into the neural mechanisms underlying cognition and the ways in which organisms interact with their environment.

### 2.5.3 Integrated Structures in the Mid-brain

This section reviews the neurophysiological similarities between arthropod central complex (CX) and vertebrate basal ganglia. They share striking analogies in their neural architecture and functional roles, and both systems are analogous in processing sensory input and generating motor commands. These findings illuminate a deep homology between insect and mammalian motor control systems, highlighting shared neural mechanisms for sensory processing, motor command generation, and learning.

### 2.5.4 Neural Simulation of the State of the Mobile Animal in Space.

Research in animals such as mice and Drosophila has provided compelling evidence that the mid-brain and central complex (CX) are crucial centers of the central nervous system (CNS) for determining an animal's location in the environment and its orientation relative to goal-based locations(Bayraktar et al., 2010; Hulse et al., 2021). These integrated structures in the mid-brain create a neural simulation of the state of the mobile animal in space, enabling effective navigation and goal-directed behavior.

The Jayaraman, Dan, and Hulse labs at the Janelia Research Campus have made significant contributions to our understanding of these neural mechanisms. In addition, the Wilson lab in Harvard Their work focuses on the CX in Drosophila, a higher brain region responsible for sensory-guided decision-making, navigation, and motor control(Hulse et al., 2021). By using advanced techniques such as two-photon calcium imaging, whole-cell patch clamp electrophysiology, optogenetics, and computational modeling, they have established causal links between the dynamics of neural circuits and the behavioral decisions that Drosophila makes during navigation. The fly central complex (CX), ellipsoid body (EB), protocerebral bridge (PB), fan-shaped body (FB), and lateral accessory lobes (LALs) create a compass-like structure of neurons that innervate wedges of the EB representing particular heading vectors. Compass neurons, receiving input from the anterior visual pathway, are essential for fruit flies to establish and maintain personal heading preferences in relation to a solitary visual landmark. Additionally, these inputs have been associated with flies' capacity to recollect specific orientations relative to a vanishing visual landmark.

One of the key findings from the Jayaraman lab is the role of the CX in representing visual space for orientation and navigation(Franconville et al., 2018). Their research has shown that specific neural populations within the CX are responsible for processing sensory information and integrating it with past experiences and internal states to guide behavior(Hulse et al., 2021) . This neural representation of space allows Drosophila to navigate complex environments and make adaptive decisions based on goal locations. Huston and Jayaraman highlighted that insect neural circuits perform both hard-wired and learned sensorimotor transformations, modulating their neural processing based on internal variables such as the animal’s behavioral state and external ones like the time of day(Huston & Jayaraman, 2011).

Other researchers have also contributed to this field by studying the mid-brain and CX in various model organisms. For example, studies by Heinze and Homberg have demonstrated that the mid-brain structures, such as the superior colliculus, play a critical role in spatial orientation and goal-directed behavior(Heinze & Homberg, 2007). These structures integrate sensory inputs and generate motor commands that guide the animal’s movements towards specific targets. Similarly, research by Weir et al. (Weir et al., 2014)and Seelig and Jayaraman(Seelig & Jayaraman, 2013) on the Drosophila CX has revealed its importance in coordinating locomotor behavior and maintaining spatial orientation.

And finally, Wilson has also made significant contributions to our understanding of neural mechanisms, particularly in the context of navigation and olfactory processing in Drosophila. Her work Drosophila navigation highlights the intricate relationship between neural connectivity and computational functions in arthropod brains. She comments that the CX exhibits several characteristics comparable to those of primate and rodent brains; the head direction system is a prime example of this overlap. Yet, the CX shares many traits with the control system of an autonomous robot or a miniature self-driving vehicle; it can be fully explained using concepts from dynamical systems and control theory. As such, arthropod brains inhabit an intriguing intermediate zone between human brains and artificial intelligence. Clearly Wilson sees research in CX bridging the gap between human cognitive processes and artificial intelligence(Wilson, 2023). This perspective is crucial for understanding how neural networks facilitate navigation strategies, especially in the context of spatial memory and cue integration, although the specific details of these mechanisms may vary across studies. Additionally, Wilson's research has made a significant impact on the understanding of neural mechanisms in Drosophila. For example, she has explored olfactory representations in the Drosophila AL (Wilson et al., 2004), where she elucidates how olfactory signals are processed and transformed within the brain, contributing to our understanding of sensory integration and neural coding.

Overall, the integrated structures in the mid-brain and CX are essential for creating a neural simulation of the state of the mobile animal in space. Understanding the mechanisms of such simulation provides a foundation for comprehending the navigation mechanics and behaviors of Drosophila. This insight is critical to the research presented in this thesis, as it suggests that these behaviors are intrinsically linked to homeostasis and are influenced by SEEK affects.

### 2.5.5 Substructures of the Central Complex and Basal Ganglia.

The insect CX is a vital brain region found in insects, including Drosophila melanogaster, composed of stereotyped neurons that extend into distinct substructures(Franconville et al., 2018). This complex plays a crucial role in various behaviors such as directed locomotion, sleep regulation, and context-dependent spatial navigation(Hulse et al., 2021). The CX comprises four main regions: the protocerebral bridge, the fan-shaped body, the ellipsoid body, and the noduli(Kato et al., 2022). These substructures are interconnected and contribute to functions like locomotion, flight, and visual pattern memory(Bayraktar et al., 2010). The CX is highly conserved across insect species and serves as a navigational center in the insect brain(Honkanen et al., 2023).

In comparison, the basal ganglia in mammals share deep homology with the insect CX(Strausfeld & Hirth, 2013). Both structures derive from basal forebrain lineages specified by evolutionarily conserved genetic programs, resulting in interconnected neuropils and nuclei located in the midline of the forebrain-midbrain boundary region(Strausfeld & Hirth, 2013). The basal ganglia in mammals are involved in motor control, learning, and decision-making processes(Strausfeld & Hirth, 2013). Similarly, the insect CX plays a crucial role in coordinating motor behaviors, spatial navigation, and sensory integration in insects(Hulse et al., 2021; Okubo et al., 2020; Wilson, 2023).

The CX in insects and the basal ganglia in mammals exhibit similarities in their organization and function. Both structures are involved in the integration of sensory information, motor control, and decision-making processes(Strausfeld & Hirth, 2013). The CX in insects has been implicated in behaviors such as flight control, visual pattern memory, and spatial navigation(Bayraktar et al., 2010). Similarly, the basal ganglia in mammals play a key role in motor coordination, habit formation, and action selection (Strausfeld & Hirth, 2013). Despite the evolutionary distance between insects and mammals, the CX and basal ganglia share common features in their neural circuitry and function.

Moreover, studies have shown that the CX in insects, particularly in Drosophila, is essential for locomotor control and navigation(Fisher et al., 2019; Sullivan, 2019). This brain region serves as a model system for investigating the mechanisms underlying circuit development and function(Frighetto et al., 2022; Sullivan, 2019). By manipulating genetic pathways in neural lineages, researchers have been able to rewire the Drosophila brain and gain insights into the neural circuits involved in locomotion and navigation(Fisher et al., 2019; Sullivan, 2019). This research highlights the importance of the CX in orchestrating complex behaviors in insects.

In summary, the insect CX and the mammalian basal ganglia exhibit structural and functional similarities despite their evolutionary divergence. Both play critical roles in motor control, decision-making, and sensory integration. Studying the CX in insects like Drosophila provides valuable insights into the neural circuits underlying complex behaviors and may offer parallels to understanding the basal ganglia in mammals.

### 2.5.6 Relation of Arthropod CX and Vertebrate Basal Ganglia.

The parallels between the neural organization of the mammalian basal ganglia and the insect CX reveal parallels in their structure and function. Strausfeld & Hirth have done analysis to support a deep homology between the arthropod CX and vertebrate basal ganglia, elucidating their shared embryonic origins and structural parallels(Strausfeld & Hirth, 2013). These analogies highlight the deep homology between these two systems, suggesting that they share a common evolutionary origin and perform similar roles in regulating behavior.

Strausfeld & Hirth claim that, as seen in **Fig. 4**, the striatum in mammals, which includes the caudate nucleus and putamen, corresponds to the fan-shaped body (FB) and protocerebral bridge (PB) in insects. These regions are involved in processing sensory information and generating motor commands. The external and internal globus pallidus (GPe, GPi) in mammals correspond to the ellipsoid body (EB) in insects. Both structures play a crucial role in modulating motor activity through inhibitory pathways. Inputs to the striatum in mammals come from sensory and association cortices, the hippocampus, and the amygdala(Choi et al., 2017). Similarly, inputs to the FB and PB in insects derive from sensory intermediate and inferior lateral protocerebra (IMP, ILP) and the associative superior medial protocerebrum (SMP)(Strausfeld & Hirth, 2013). The SMP receives learned visual cues and outputs from the mushroom bodies (MB), which correspond to the mammalian hippocampus(Strausfeld & Hirth, 2013).

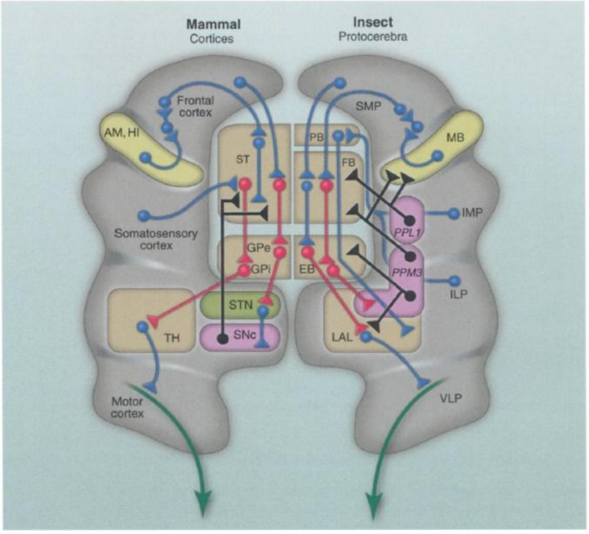


**Fig. 4.** The above is figure 2 from Hirth and Strausfeld's paper entitled Deep Homology of Arthropod Central Complex and Vertebrate Basal Ganglia(Strausfeld & Hirth, 2013). The proposed parallels between the neural architecture of mammalian basal ganglia and the insect CX reveal several significant similarities. In mammals, the striatum, encompassing the caudate nucleus and putamen, corresponds to the fan-shaped body (FB) and protocerebral bridge (PB) in insects. The external and internal globus pallidus (GPe, GPi) in mammals correspond to the ellipsoid body (EB) in insects. Inhibitory pathways are depicted in red, dopaminergic pathways in black, and other pathways (excitatory or modulatory) in blue.

The PB, FB, and EB in insects are linked by excitatory columnar neurons, many of which extend to the lateral accessory lobes (LAL)(Hulse et al., 2021) which are important for motor control. GABAergic outputs from the EB provide the LAL and its associated neuropils. The LAL is compared to the vertebrate thalamus (TH), which is supplied by the globus pallidus(Strausfeld & Hirth, 2013). Both the TH and LAL supply motor centers, with the TH connecting to the motor cortices in mammals and the LAL connecting to the inferior and ventrolateral protocerebra (ILP, VLP) in insects(Strausfeld & Hirth, 2013). Dopamine pathways in insects, extending from the PPM3 and PPL1 domains to the FB and EB, correspond to the dopamine innervation of the striatum from the SNc in mammals(Hulse et al., 2021). These pathways are crucial for modulating motor activity and reinforcing behavior.

While the above correspondences documented by Hulse, Hirth and Strausfeld provide a compelling framework, it is important to note that many of these relationships between neuropils were established without the detailed map of the Drosophila connectome that has recently become available. The first complete electron microscopy-based connectome of the Drosophila CX, encompassing all its neurons and circuits at synaptic resolution, has unveiled new neuron types, novel sensory and motor pathways, and network motifs. This thorough connectome offers a more precise blueprint for elucidating the exact neuronal pathways and their roles.

Furthermore, while ortholog conservation can be a compelling reason to establish relationships between the biological phenotypes they underpin, there are reasons to consider the possibility of functional divergence over millions of years of evolution. For a deeper understanding of orthologs and functional divergence, the reader is directed to the section below entitled ‘Comparison with Existing Literature’. Nonetheless, while there are indeed good reasons to see similarities between the CNS of vertebrates and arthropods, the mapping given by Strausfeld will most likely need to be modified as a better understanding of exact neuronal pathways are discovered. This thesis is one step in this direction, contributing to the ongoing refinement of our knowledge of these complex neural systems.

## 2.6 Networks Supporting Sleep and Wakefulness Across Species

Sleep in mammals is regulated by a complex interplay of neural circuits that promote either wakefulness or sleep. Key wake-promoting projections originate from neurons in the upper brainstem, including cholinergic neurons that provide major input to the thalamus, and monoaminergic and glutamatergic neurons that innervate the hypothalamus, basal forebrain, and cerebral cortex(D. W. Pfaff, 2019; Saper et al., 2010; Solms, 2021). The orexin neurons in the lateral hypothalamus reinforce activity in these brainstem arousal pathways and directly excite the cerebral cortex and basal forebrain (**Fig. 5**).

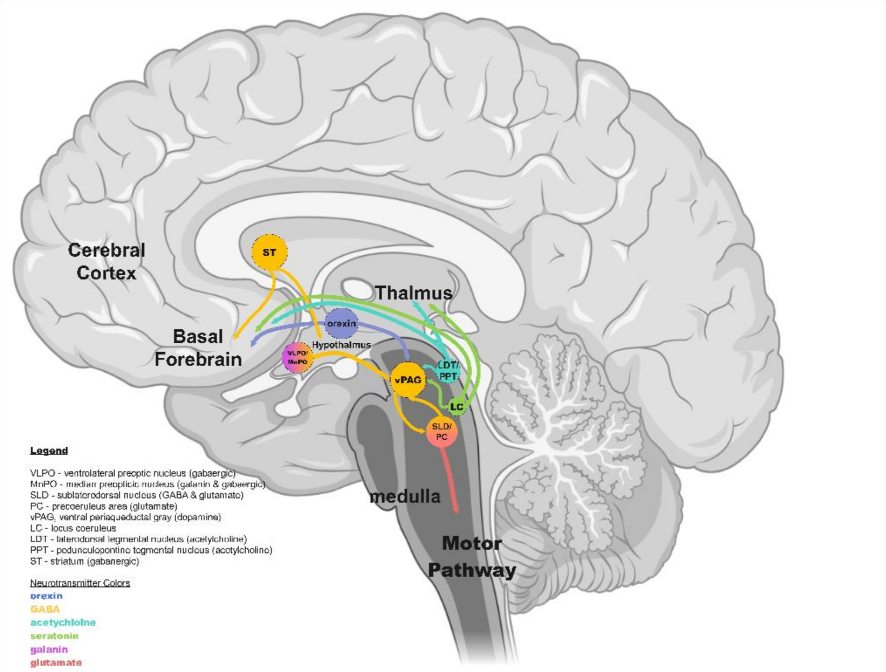


**Fig. 5.** The above is based data from Figure 1 and 2 from Saper's paper 'Sleep State Switching'(Saper et al., 2010) and show major Wake and sleep promoting neurons in the upper brainstem. Cholinergic neurons (aqua) provide the input to the thalamus, whereas monoaminergic and glutamatergic neurons (green, magenta and orange) provide direct innervation of the hypothalamus, basal forebrain, and cerebral cortex. Hypothalamic orexin neurons (blue) innervate brainstem arousal pathways and excite the cerebral cortex and basal forebrain. Sleep-promoting pathways (yellow) from the ventrolateral (VLPO) and median (MnPO) preoptic nuclei inhibit pathways in both the hypothalamus and the brainstem. However, the sublaterodorsal nucleus (SLD) ascending arousal system also inhibits the vPAG and VLPO. Important here is the mutually inhibitory relationship of the arousal and sleep-promoting pathways producing a purported flip-flop switch, which can generate transition between waking and sleeping states.

On the other hand, sleep-promoting pathways arise from the ventrolateral preoptic (VLPO) and median preoptic nuclei (MnPO) (Han et al., 2014). These GABAergic pathways inhibit components of the ascending arousal pathways in both the hypothalamus and brainstem. The ascending sublaterodorsal region (SLD) arousal systems can also inhibit the VLPO(Kroeger et al., 2018), creating a mutually inhibitory relationship that functions as a "flip-flop" switch(Liu et al., 2012). This switch allows for rapid and complete transitions between waking and sleeping states. In a similar way, Galanin plays a crucial role in the ventrolateral preoptic nucleus (VLPO) in promoting sleep. Galanin is a neuropeptide that exhibits a diverse range of functions in the nervous system. Research indicates that galanin can have both inhibitory and excitatory effects depending on the specific context and location within the nervous system of both mammals and invertebrates (Einstein et al., 2013; Kerr et al., 2000). Studies have shown that sleep-active neurons in the VLPO, which are considered a neuronal substrate of sleep homeostasis, contain galanin. Galanin-containing neurons express c-Fos during recovery sleep after sleep deprivation, indicating their involvement in sleep regulation(Tsai et al., 2009). Galaninergic neurons in the VLPO are responsible for promoting non-rapid eye movement (NREM) sleep, as selective activation of these neurons increases NREM sleep, while their inhibition decreases NREM sleep, highlighting their pivotal role in sleep promotion(Kroeger et al., 2018).

The Striatum also plays a crucial role in this sleep mechanism. It is particularly important when comparing mammals to invertebrates. According to Strausfeld(Strausfeld & Hirth, 2013), the Striatum is homologous to the Fan Shaped Body (FB) in Drosophila, a central neuropil that contains sleep and arousal networks. This homology suggests that the Striatum's role in sleep regulation is evolutionarily conserved and critical for understanding sleep mechanisms across species.

Highlighting the mutually inhibitory neurons between the VLPO and the hypothalamus is not only essential but offers interesting parallels between mammals and invertebrates. Disinhibition via the innervation of two inhibitory neurons is seen in the well-studied sleep circuit within the dorsal layer of the Fan Shaped Body in Drosophila(Dissel et al., 2022). The VLPO and hypothalamus interaction, as described by Saper, mirrors some characteristics of the FB's sleep circuit that will be discussed in more detail in later sections. This parallel in comparable frameworks is important for understanding sleep regulation in both mammals and invertebrates.

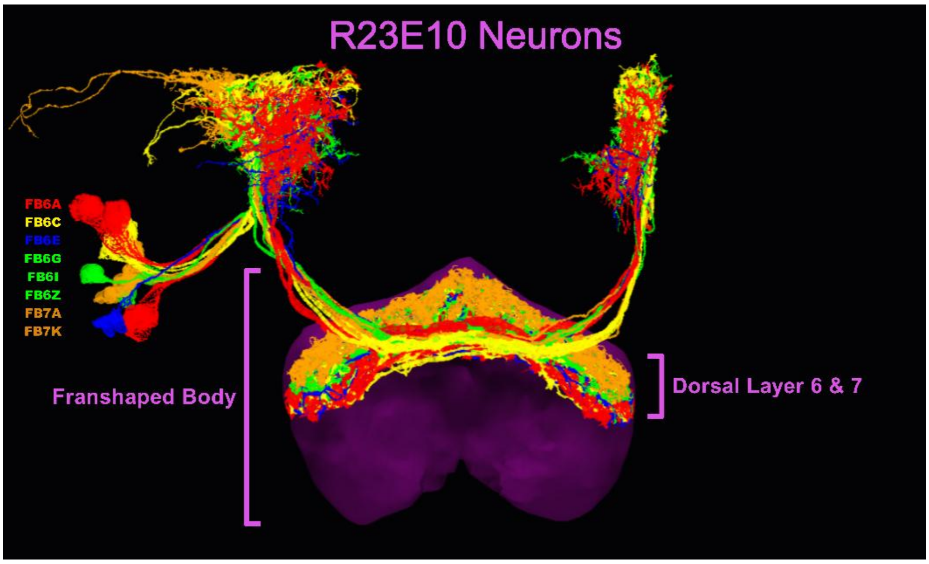


**Fig. 6.** The R23E10 line in Drosophila demonstrates the dorsal fan-shaped body circuit within the central brain, notably symbolized by the R23E10-gal4 line, which serves as the executor arm of the sleep homeostat(Berry et al., 2015). The use of this line to suppress the mAChR-B gene in dFB neurons has led to heightened arousal and reduced sleep.

## 2.7 Overview of the Fan-shaped Body (FB) and Central Complex

The Drosophila central complex (CX) is a vital region within the central nervous system (CNS) responsible for various fundamental behaviors in Drosophila(Young & Armstrong, 2010). Comprising several key neuropils, the CX plays a significant role in behaviors such as locomotion, flight, and visual pattern memory(Bayraktar et al., 2010; Olsen & Wilson, 2008; Wilson, 2023)(**Fig. 7**). This complex structure consists of four interconnected substructures situated along the midline of the protocerebrum: the protocerebral bridge (PB), the fan-shaped body (FB), the paired noduli (NO), and the ellipsoid body (EB)(Bayraktar et al., 2010; Hulse et al., 2021). The CX has been implicated in a range of functions, including spatial navigation, context-dependent action selection, and flexible navigation(Hulse et al., 2021; Wilson, 2023). It is a major neuropil in the adult brain of Drosophila and is essential for various behavioral outputs(Young & Armstrong, 2010).

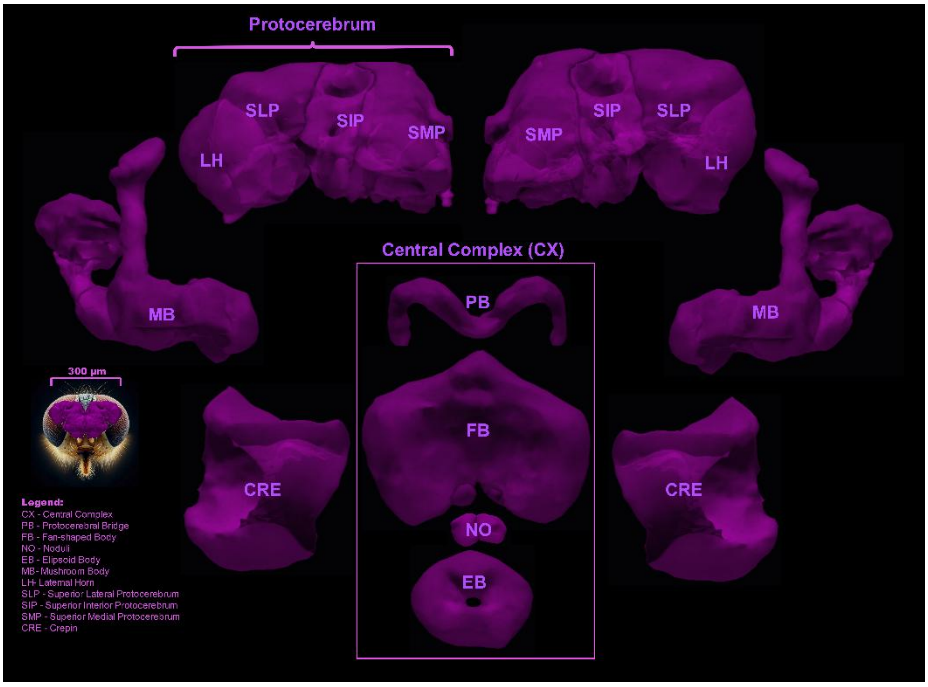


**Fig. 7.** Major Neuropils of Drosophila melanogaster with highlights of the Central Complex

The CX is also known to be modulated by various neuromodulators, such as dopamine and serotonin, indicating that functional connectivity within this region is influenced by the brain state(Franconville et al., 2018). Furthermore, the CX exhibits oscillatory activity that is phase-locked to attended visual features, highlighting the dynamic nature of neural activity in this region (Grabowska et al., 2020). This means that the timing of neural oscillations in the CX aligns with specific visual stimuli, which is crucial for processing and responding to these stimuli. The connectome of the Drosophila CX reveals network motifs—recurrent, interconnected patterns of neurons that are suitable for flexible navigation and context-dependent action selection, emphasizing the intricate neural circuitry within this brain region(Hulse et al., 2021).

Neuronal architecture studies have provided insights into the organization of the CX in Drosophila melanogaster, shedding light on the structural composition of this critical brain region (Hanesch et al., 1989; Hulse et al., 2021). The CX is a well-defined set of neuropils located in the midline of the protocerebrum and is implicated in a variety of behaviors (Young & Armstrong, 2010). Additionally, the CX has been linked to the regulation of sleep and arousal states in Drosophila, with studies demonstrating that different neuronal populations within this region play distinct roles in controlling these behavioral states (Anthoney et al., 2023; Liu et al., 2023; Van De Poll et al., 2023; Van De Poll & van Swinderen, 2021). For instance, specific subsets of neurons within the CX influence arousal thresholds during different sleep stages, thereby regulating nighttime sleep (Chen et al., 2019).

Moreover, the CX of Drosophila serves as an excellent model system for exploring the mechanisms underlying circuit development and function, particularly in relation to locomotor control and navigation (Sullivan, 2019). The CX is part of a larger network of brain regions involved in sensory processing, motor output, and higher-order cognitive functions (Frye & Dickinson, 2004). Understanding the neural circuitry of the CX is crucial for unraveling the neural computations that underlie various behaviors in Drosophila (Takemura et al., 2013). By analyzing the connectivity-based neuronal classification within the Drosophila brain, researchers have identified key communication pathways that contribute to the functional interactions within this complex neural network (Mehta et al., 2022).

In conclusion, the Drosophila CX is a core region within the CNS that plays a pivotal role in regulating a wide range of behaviors in Drosophila. From memory formation to sleep regulation and locomotor control, this complex brain region is essential for orchestrating various physiological and behavioral responses. The intricate neural circuitry within the CX underscores its importance in integrating sensory information, processing neural signals, and generating appropriate behavioral outputs. Further research into the structural and functional aspects of the CX will provide valuable insights into the neural mechanisms governing behavior in Drosophila.

## 2.8 SEEK, Sleep and Arousal Mechanisms in Drosophila

Before looking at the neuromechanistic system for sleep in Drosophila, it is very important to understand the sleep and arousal mechanisms across species when researching how affects manifest themselves. The SEEK system in invertebrates, particularly in Drosophila melanogaster, exhibits intriguing correlations with sleep and arousal systems, which are essential for understanding the broader implications of these mechanisms in both invertebrates and mammals. The SEEK system, as described by Panksepp, is part of a broader emotional framework that includes systems such as RAGE and FEAR, all of which are linked to metabolic activity in the brainstem of mammals (Panksepp, 2016a). This framework provides a foundation for exploring how similar systems may operate in invertebrates, particularly in relation to sleep and arousal.

First, the notion that affects like SEEK overlap with sleep and arousal stems from evidence showing that these behaviors share similar neural correlates with the basal ganglia of mammals. In mammals, the basal ganglia's subcortical structures, including the Locus Coeruleus (LC) and Periaqueductal Gray PAG(**Fig. 5**), share evolutionarily conserved functions that underscore their importance in both motor control and emotional processing's work in affective neuroscience emphasizes that these subcortical structures are integral to the emotional experiences shared across species, suggesting that the emotional systems of mammals are deeply rooted in their neuroanatomy(Jaak Panksepp, 2011a; Panksepp, 2016b).

The PAG plays a crucial role in the emotional processing of animals, particularly in the modulation of defensive responses and fear learning(Motta et al., 2017). According to Motta et al., the PAG is integral to the neural circuits that govern primal emotions, influencing both fear and reward-seeking behaviors and interacts with various brain regions, including the hippocampal formation and the amygdala, which are essential for emotional regulation and memory processing. This interaction underscores the PAG's significance in shaping complex emotional responses, as it integrates sensory information and emotional context to inform behavioral outcomes. Further, the neuroanatomical organization of the PAG reveals its connections with various brain regions involved in emotional processing, such as the amygdala and the prefrontal cortex. These connections facilitate the integration of emotional and cognitive processes, allowing for a nuanced response to emotional stimuli(D. Pfaff, 2019; Solms, 2021). For instance, the amygdala, known for its role in fear processing, communicates with the PAG to modulate fear responses based on contextual information (Coenen et al., 2011). Given all the above, neuronal interaction to and from the PAG highlights its role as a mediator between emotional arousal and behavioral responses.

The periaqueductal gray (PAG) in the mid-brain also plays a crucial role in modulating sleep and arousal. Research indicates that sleep stages are characterized by distinct electrophysiological patterns, with the PAG being integral to these processes in mammals(Linnman et al., 2012; Solms, 2019). The PAG is involved in regulating both sleep and wakefulness, influencing behavioral responsiveness and synaptic activity within the neural circuits that govern these states(Mitchell & Weinshenker, 2010). Additionally, sleep has been shown to restore cognitive functions and behavioral plasticity, further underscoring the PAG's role in sleep regulation and its impact on arousal mechanisms(Suckow et al., 2012).

Both the periaqueductal gray (PAG) in mammals and the fan-shaped body (FB) in Drosophila exhibit functional parallels in regulating affective states, sleep, and arousal. The PAG modulates emotions such as rage and fear, which are essential for survival and behavioral responses to threats(Panksepp, 2013). Similarly, the FB plays a crucial role in sleep regulation and arousal responses in Drosophila. Studies have shown that alterations in FB activity can significantly impact sleep duration and behavioral responsiveness(Faville et al., 2015; Yap et al., 2017). Furthermore, sleep in Drosophila has been linked to cognitive functions, including attention and memory. This suggests that both the PAG and FB contribute to emotional and cognitive processing through their respective roles in sleep and arousal mechanisms(van Alphen et al., 2021). Thus, the functional similarities between these brain regions underscore the evolutionary conservation of neural circuits involved in affective and cognitive regulation across species.

The conserved functionality between the periaqueductal gray (PAG) and the dorsal fan-shaped body (dFB) in Drosophila is further underscored by genetic experiments revealing that mutations affecting neurotransmitter signaling mechanisms yield similar behavioral outcomes. Specifically, studies have shown that the regulation of sleep and synaptic plasticity in Drosophila is influenced by neurotransmitter systems, including GABA and dopamine, which are also critical in mammalian systems (Andretic et al., 2005; Dissel et al., 2015; Larkin et al., 2015). For instance, the role of GABA-A receptors in modulating sleep states in Drosophila parallels the function of similar receptors in mammals, suggesting a conserved evolutionary mechanism(Dissel et al., 2015). Furthermore, the synaptic release machinery, particularly involving SNARE proteins, is implicated in both sleep regulation and neurotransmitter signaling across species, reinforcing the idea of functional conservation (van Swinderen & Kottler, 2014). These findings collectively highlight the genetic and neurochemical parallels between the PAG and dFB, emphasizing their roles in modulating sleep and behavioral responses through conserved signaling pathways.

As discussed earlier, the role of R23E10 neurons (**Fig. 6**) in the dorsal Fan-shaped Body of Drosophila in regulating arousal and affective behavior is increasingly supported by research. Activation of these neurons has been linked to sleep pressure and various emotional behaviors. For instance, studies have shown that sleep deprivation affects attention and arousal, indicating a complex interplay between sleep and behavioral responsiveness in Drosophila (Faville et al., 2015; Troup et al., 2018). Furthermore, the modulation of synaptic activity in specific neuronal circuits, including those involving GABA receptors, has been shown to influence sleep and arousal states (Dissel et al., 2015; Kirszenblat & van Swinderen, 2019). The findings suggest that R23E10 neurons may play a critical role in integrating sensory experiences and modulating sleep needs, thereby influencing emotional and arousal-related behaviors in Drosophila (van Alphen et al., 2021).

### 2.9 Computational Models in Neuroscience

Computational models in neuroscience serve as pivotal tools for understanding the intricate dynamics of neuronal networks and the neurodynamics of individual neurons. These models can be broadly categorized into several types, including Bayesian Brain Models, Neural Network Models, Statistical Models, and Hybrid Models. Each model type presents unique advantages and limitations, which are essential for researchers to consider when selecting the appropriate framework for their studies.

Bayesian Brain Models are particularly influential in the realm of perceptual inference and decision-making. These models posit that the brain functions similarly to a Bayesian inference system, continuously updating beliefs based on incoming sensory information. For instance, the work of Sokoloski illustrates how linear probabilistic population codes (LPPCs) can effectively capture the statistics of neural encoding and facilitate accurate Bayesian decoding within neural circuits, thereby providing insights into how information is processed in the brain(Sokoloski et al., 2021). In the context of Bayesian decoding, LPPCs facilitate accurate inference by integrating prior knowledge with the observed neural activity. The probabilistic nature of LPPCs allows for the incorporation of uncertainty in neural responses, which is crucial for making reliable predictions about sensory inputs or motor outputs.

LPPCs are not unlike the concept of predictive coding, as discussed by Yon et al., emphasizes that the brain generates predictions about sensory inputs and adjusts these predictions based on new evidence, effectively functioning as a "stubborn scientist" that resists change unless compelled by strong evidence (Yon et al., 2019). This framework aligns with the findings on how neural representations of probabilities can inform Bayesian inference processes, particularly in the context of auditory perception(Rich et al., 2015). Linear probabilistic population codes (LPPCs) and predictive coding share conceptual similarities, particularly in their Bayesian foundations for understanding neural processing. Both frameworks emphasize the role of prior knowledge and the integration of sensory information to form a coherent representation of the external world.

LPPCs and Predictive Coding models share foundational principles with Neural Network Models. Such deep learning architectures have gained prominence due to their ability to model complex relationships within data, demonstrating the application of deep neural networks in estimating nonlinear receptive fields of sensory neural responses, and highlighting the model's capacity to capture intricate mappings from stimuli to neural responses (Keshishian et al., 2020). Furthermore, draw parallels between deep learning and the mammalian neocortex, suggesting that the representations developed by deep neural networks closely resemble those observed in biological systems (Guerguiev et al., 2017). However, while these models are powerful, they often require substantial computational resources and large datasets, which can limit their accessibility and applicability in certain research contexts.

Statistical Models play a crucial role in understanding the connectivity and dynamics of neural networks. For example, dynamic causal modeling can estimate effective connectivity within large-scale resting brain networks, providing insights into the interactions among brain regions(Aranyi et al., 2022). This approach allows researchers to infer causal relationships based on observed neural activity, which is essential for elucidating the mechanisms underlying various cognitive functions. Moreover, the integration of statistical methods with neural data can enhance the interpretability of findings, as demonstrated by McGee and Grill, who developed a quantitative simulation of bladder control mechanisms that incorporates neural activity modeling(McGee & Grill, 2016).

Hybrid Models represent a synthesis of various computational approaches, combining elements from different modeling paradigms to address complex neurobiological questions. For instance, the research by discusses the integration of statistical learning principles with neural representations, proposing a framework that accounts for uncertainty in perception and learning processes(Fiser et al., 2010). This hybrid approach allows for a more nuanced understanding of how the brain processes information and adapts to changing environments. Additionally, the exploration of inverse reinforcement learning by exemplifies how hybrid models can elucidate cognitive processes that are abstract and divorced from immediate sensory inputs, thereby expanding the scope of traditional reinforcement learning frameworks(Collette et al., 2017).

While there are many instrumental models that can be exploited to investigate neuronal activity, the limitations of each model type must also be acknowledged. Bayesian models, while robust in their theoretical foundations, can sometimes oversimplify the complexities of neural processing by assuming that the brain operates in a purely probabilistic manner. Similarly, neural network models may struggle with generalization when trained on limited datasets, leading to overfitting and reduced applicability in real-world scenarios. Statistical models, while powerful for connectivity analysis, may not fully capture the dynamic and nonlinear aspects of neural interactions. Hybrid models, although promising, can become overly complex and difficult to interpret, necessitating careful consideration of their design and implementation.

In conclusion, computational models in neuroscience provide invaluable frameworks for exploring the neurodynamics of neuronal networks and individual neurons. The diversity of model types, including Bayesian Brain Models, Neural Network Models, Statistical Models, and Hybrid Models, allows researchers to tailor their approaches to specific research questions and contexts. However, careful consideration of the strengths and limitations of each model type is essential for advancing our understanding of the brain's complex functions and mechanisms.

### 2.9.1 Bayesian Inference Models

The Bayesian modeling framework for decision-making (**Fig. 8**) is compelling due to its evolutionary implications and its role optimizing behavioral performance. Bayesian inference is posited to be a near-optimal algorithm that the mind applies in decision tasks prevalent in natural and daily life scenarios. This assertion is supported by various studies that highlight the effectiveness of Bayesian models in understanding neural processes and decision-making behaviors.

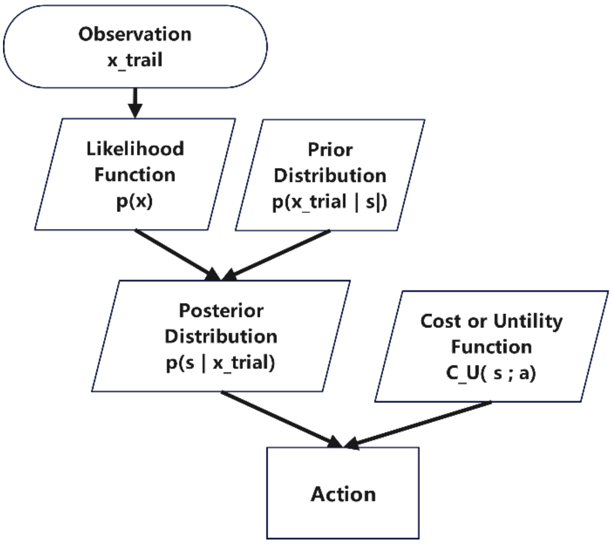


**Fig. 8.** Bayesian Model Logic Flow Chart

Bayesian models are fundamentally grounded in the principle of optimizing behavior based on available evidence. For instance, discusses how Bayesian decision models serve as a primer for understanding decision-making behavior in controlled environments, emphasizing that optimal behavior is inherently Bayesian, and even deviations from this optimality can be accounted for using Bayesian frameworks(Ma, 2019). Moreover, the application of Bayesian inference in neural coding and decision-making processes has been extensively documented. For instance, illustrates how Bayes filters can be implemented in neural circuits to estimate unknown stimulus dynamics, thereby facilitating intelligent interactions with the environment(Sokoloski, 2017). This reflects the adaptive nature of Bayesian models in processing information and making decisions based on probabilistic reasoning, which is crucial for survival and effective functioning in complex environments.

The relevance of Bayesian inference is further underscored by its role in the neural mechanisms underlying learning and memory. It can explore how the cellular architecture of memory modules in Drosophila supports stochastic input integration, which is essential for decision-making processes that involve associating stimuli with valence information(Hafez et al., 2023). This suggests that the evolutionary development of such neural architectures may have been influenced by the need for efficient decision-making strategies in fluctuating environments.

Bayes' rule, a foundational concept in probability theory and statistics, plays the central role in Bayesian models, particularly in decision-making processes where uncertainty is prevalent. The equation is as follows:

$$p(s \mid x_{\text{trial}}) = \frac{p(x_{\text{trial}} \mid s) p(s)}{p(x_{\text{trial}})} \tag{2}$$

Where $s$ is the world state variable and should be considered as a hypothesis estimated by an organism. $p(s)$ is referred to as the prior distribution. It represents the organism's expectations for different values of $s$. The numerator on the right side of the equation, $p(x_{\text{trial}} \mid s)$, is the likelihood function of the world state, $s$. This can be counterintuitive because within the context of Bayesian logic, the likelihood of the observation $x_{\text{trial}}$ given $s$ is the probability of the hypothesized state given an observation. On the left side of the equation, $p(s \mid x_{\text{trial}})$ denotes the posterior probability, or in other words it is an updated output to what extent (i.e. probability) the value $s$ is supported by the observed measurement $x_{\text{trial}}$ and the prior assumptions regarding the world state $s$. Finally, the right-side denominator $p(x_{\text{trial}})$ represents the possibility of $x$ without any consideration of $s$. Or more simply put, it is the probably of $x$ under all possible world states. The purpose of the denominator is to ensure that over the many trials, the aggregated value of the posterior adds up to 1, and in this sense the denominator acts as a normalization factor.

At its core, Bayes' rule allows for the updating of probabilities based on new evidence, which is essential for decision-makers who must navigate uncertain environments (see appendix for more details). The variable " $s$ " in the Bayes' equation represents a state of the world or a hypothesis held by the decision-maker, and the probabilities associated with $s$ reflect the decision-maker's degree of belief in various outcomes. Importantly, these probabilities are subjective and exist within the cognitive framework of the individual, making them inherently unobservable(Ma, 2019).

With an estimation of the world-state possible, Bayesian inference next plays an important role in decision-making processes, particularly through the formulation of cost functions that help quantify the consequences of various actions. The cost function, denoted as the following:

$$\mathbb{E}C(a) = \sum_s p(s \mid x_{\text{trial}})C(s,a) \tag{3}$$

The cost function in equation 3 is denoted on the right side by $C(s,a)$, where $s$ represents the state and $a$ the action, serves as a tool for decision-makers aiming to minimize potential losses associated with their choices. This framework is essential in Bayesian decision models, which emphasizes that optimal behavior is inherently Bayesian, allowing for the accommodation of suboptimal behaviors through various candidate models(Ma, 2019).

In the context of action selection, the principle of minimizing the cost function is closely tied to the concept of active inference, where actions are viewed as attempts to minimize the expected free energy. (Friston & Penny, 2011). The Bayesian framework thus provides a structured method for integrating prior knowledge with new evidence, ultimately guiding the selection of actions that are expected to yield the least costly outcomes.

Moreover, the application of Bayesian inference extends beyond theoretical constructs to practical implementations, such as neuro-prosthetics, where Bayesian methods are employed to optimize stimulus parameters for retinal implants. This demonstrates the versatility of Bayesian models in real-world scenarios, where the cost function can be tailored to account for uncertainties in biological systems(Oesterle et al., 2020). By leveraging Bayesian inference, researchers can derive posterior distributions that inform decision-making processes, thereby enhancing the efficacy of interventions in complex environments(Yon et al., 2019).

The relevance of cost functions in Bayesian inference is further underscored by their role in modeling neural responses and behaviors. For instance, studies have shown that neural circuits can be designed to implement Bayes filters, which effectively combine population responses with predictions of internal models to estimate dynamic stimuli (Sokoloski, 2017). This integration of Bayesian principles into neural computation highlights the importance of cost functions in shaping adaptive behaviors and optimizing decision-making in both biological and artificial systems.

The application of Bayes' rule extends into various fields, including neuroscience, where it has been employed to model neural processes and decision-making behaviors. For instance, demonstrated that Bayesian decoding can predict how neural activity influences perception and behavior, suggesting that a Bayesian framework can effectively "crack the neural code" in complex neural systems(Sokoloski et al., 2021). This aligns with the notion that decision-making, even in biological systems, can be framed through Bayesian inference, where the brain continuously updates its beliefs based on sensory inputs and prior knowledge (Yon et al., 2019).

### 2.9.2 Coupled Oscillators in Mathematical Circuit Representations.

Coupled oscillator theory provides a robust framework for understanding the dynamics of biological neural networks, particularly through concepts such as coupling, synchronization, and emergent dynamics. In the context of circadian rhythms, studies have shown that distinct groups of neurons can exhibit synchronized oscillatory behavior, which is crucial for maintaining rhythmic activities in organisms like Drosophila (Keny et al., 2007; Stoleru et al., 2004). The interactions among these oscillators can lead to phase locking, where oscillators synchronize their phases, enhancing the stability of the rhythmic patterns (Rashid & Kurata, 2020). Furthermore, stochastic models have been employed to describe the emergence of collective oscillations from individual cellular oscillators, highlighting the role of noise in synchronization processes (Gonze et al., 2004). This interplay between deterministic and stochastic elements is essential for understanding how biological systems achieve robust temporal patterns despite inherent variability (Gonze et al., 2004; Xu & Cai, 2009).

In the context of neural networks, oscillators can represent individual neurons or groups of neurons that exhibit rhythmic activity, with coupling referring to the interactions between these oscillators. Coupling can be excitatory or inhibitory and varies in strength and type, such as electrical or chemical synapses. Studies have shown that the coupling between distinct cellular oscillators can lead to the emergence of collective oscillations, which are observable at the macroscopic level, highlighting the importance of these interactions in neural dynamics(Singh et al., 2010). The role of coupling in circadian rhythms has also been explored, demonstrating how interlocked feedback oscillators contribute to robust oscillatory behavior(Rashid & Kurata, 2020). Thus, understanding the nature of coupling in neural networks is crucial for elucidating the mechanisms underlying rhythmic neuronal activity and its implications for broader neural functions.

Synchronization in coupled oscillator theory is a fundamental phenomenon observed in various neural processes(Strogatz, 2000), particularly in the coordination of motor activities and rhythmic patterns in the brain. This synchronization is crucial for the effective functioning of neural circuits, as it allows oscillators to adjust their rhythms to match one another, leading to coherent output across populations of neurons. For instance, studies have shown that the coupling between distinct cellular oscillators can give rise to collective oscillations, which are observable at the macroscopic level(Singh et al., 2010). Furthermore, the human motor system exhibits nonlinear coupling, where factors such as handedness and experience-dependent plasticity influence synchronization dynamics(Chen et al., 2010). Additionally, the interactions between circadian oscillators in organisms like Drosophila demonstrate how rhythmic patterns can be modulated by external stimuli, thereby enhancing synchronization among neuronal populations(Lazopulo et al., 2015).

Phase locking is a critical phenomenon in neural circuits, facilitating consistent phase relationships among oscillators, which is essential for sensory processing and information transfer. Research indicates that phase locking can enhance coherence in specific frequency bands, such as theta (4–10 Hz), which is crucial for motor control and sensory integration(Friston & Penny, 2011). For instance, significant phase-locking has been observed between oscillatory activities in the primary motor cortex and hand speed, suggesting a robust coupling that supports coordinated movement(Chen et al., 2010). Furthermore, the robustness of circadian rhythms, which also exhibit phase locking, highlights the importance of interlocked feedback loops in maintaining consistent oscillatory features despite external variations(Rashid & Kurata, 2020). This interplay of oscillatory dynamics underscores the fundamental role of phase locking in both sensory processing and motor coordination within neural circuits(Chen et al., 2010; Friston & Penny, 2011; Rashid & Kurata, 2020).

Coupled oscillators exhibit complex emergent dynamics, such as chaotic behavior and multi-stability, which arise from their interactions rather than their individual properties. For instance, Rashid & Kurata explored different coupling protocols in circadian clocks, revealing how these interactions can lead to robust oscillatory behaviors(Rashid & Kurata, 2020). Similarly, Singh et al. demonstrated that collective oscillations emerge from microscopic coupling between cellular oscillators, highlighting the significance of stochastic synchronization in biological systems(Singh et al., 2010). The intricate dynamics of these coupled systems can also lead to pattern formation, as evidenced by the coupling of external light with endogenous oscillators in Drosophila, which results in rhythmic locomotion patterns characterized by distinct morning and evening peaks(Lazopulo et al., 2015).

With many complex dynamics involved, Mathematical Neuronal models are fundamental to understanding the above dynamics of neural activity and communication within the brain. Among the prominent models studied in neuroscience are the Hodgkin-Huxley model, the Wilson-Cowan model, and the Kuramoto model, each contributing uniquely to our comprehension of neuronal behavior and synchronization.

The Hodgkin-Huxley model, developed to describe action potentials in neurons, provides a detailed representation of the ionic currents that underlie neuronal excitability(Hodgkin & Huxley, 1952). This model is crucial for understanding how neurons generate and propagate electrical signals, which is foundational for studying neuronal oscillations. The model's equations illustrate how the interplay between different ionic currents can lead to oscillatory behavior under certain conditions, thus serving as a basis for more complex models of neuronal dynamics(Catterall et al., 2012).

The Wilson-Cowan model extends this understanding by focusing on the interactions between excitatory and inhibitory populations of neurons(Wilson & Cowan, 1972). It captures the essence of how these populations can synchronize and produce oscillatory activity, which is particularly relevant in the context of brain rhythms observed in electroencephalography (EEG) studies. This model emphasizes the role of feedback loops and the balance between excitation and inhibition in generating oscillatory patterns, which are critical for cognitive functions such as motor, perception and attention (Chen et al., 2010; Penny et al., 2002). The synchronization phenomena described by Wilson and Cowan have been linked to various cognitive processes, highlighting the importance of oscillatory dynamics in neural communication(Linkenkaer-Hansen et al., 2001).

The Kuramoto model, on the other hand, provides a theoretical framework for understanding synchronization in large populations of coupled oscillators(Kuramoto, 1984). Initially motivated by physical systems, it has been adapted to describe neuronal networks where individual oscillators (neurons) can synchronize despite differences in their natural frequencies. This model has been instrumental in elucidating how collective behavior emerges from local interactions among neurons, leading to coherent oscillations that are essential for various brain functions (Singh et al., 2010; Strogatz, 2000). The Kuramoto model's insights into synchronization have implications for understanding pathological states, such as those seen in epilepsy, where abnormal synchronization can lead to seizures (Kazemi & Jamali, 2022).

The mathematical overview for all the models in this section are provided in the appendix section, but the Wilson-Cowan model is particularly well-suited for the thesis due to its simplicity and effectiveness in capturing essential neural dynamics. Unlike more complex models such as the Hodgkin-Huxley model, which can be applied to leaky integrate-and-fire (LIF) neurons commonly used for analyzing neuronal dynamics, the Wilson-Cowan model offers a more straightforward mathematical framework. This simplicity is advantageous as it allows for a clear and concise representation of the interactions between excitatory and inhibitory neurons, which are key features of the NOI in this study.

Despite its relative simplicity, the Wilson-Cowan model effectively incorporates the stochastic nature of neural activity and the cross-innervation between excitatory and inhibitory neurons, providing a realistic depiction of neural dynamics. Additionally, the model’s ability to represent population-level activity makes it particularly useful for studying the collective behavior of neural oscillators, which is a central focus of my thesis. By keeping mathematics simple yet meaningful, the Wilson-Cowan model enables a more accessible and interpretable analysis of the complex oscillatory behavior observed in the fan-shaped body of Drosophila.

### 2.9.3 Neural Network Models Used for Drosophila Research

Neural network models are computational programs that emulate the biological neural networks found in living organisms. These models are designed to recognize patterns, make decisions, and predict outcomes through interconnected nodes or neurons. Among the various types of neural networks, four primary categories stand out: feed-forward neural networks(FFNN), recurrent neural networks (RNNs), deep learning such as convolutional neural networks (CNNs), and biologically plausible spiking neural networks (SNNs). Each of these models has unique architectures and applications that cater to specific tasks in machine learning and artificial intelligence.

FFNNs are the simplest type of neural network architecture, where the information moves in one direction—from input nodes, through hidden nodes (if any), and finally to output nodes. This architecture is particularly effective for tasks such as image classification and regression analysis. Some studies have shown that while feedforward networks can perform well on straightforward tasks, they may struggle with more complex visual recognition tasks that require hierarchical feature extraction, as demonstrated by the limitations observed in simple three-layer CNNs for higher-variation object recognition tasks(Yamins et al., 2014). However, the performance of these networks can be significantly enhanced through the use of modern deep learning techniques, which allow for the training of deeper architectures that can capture more intricate patterns in data (He et al., 2016; Krizhevsky et al., 2017).

RNNs are designed to handle sequential data by maintaining a form of memory through feedback connections. This architecture is particularly useful for tasks involving time series data, natural language processing, and any application where context is crucial. RNNs can capture temporal dependencies in data, making them suitable for applications such as speech recognition and language modeling(Pfeiffer & Pfeil, 2018). However, RNNs can face challenges with long-term dependencies due to issues like vanishing gradients, which have led to the development of more advanced architectures such as Long Short-Term Memory (LSTM) networks and Gated Recurrent Units (GRUs)(Pfeiffer & Pfeil, 2018).

CNNs are specifically designed for processing grid-like data, such as images. They utilize convolutional layers that apply filters to the input data, allowing the network to learn spatial hierarchies of features automatically. CNNs have achieved remarkable success in various computer vision tasks, including image classification, object detection, and segmentation(Li et al., 2019). The architecture of CNNs enables them to effectively reduce the dimensionality of the input data while preserving important features, which is crucial for tasks that require high accuracy and efficiency (He et al., 2016; Krizhevsky et al., 2017). The success of CNNs in practical applications has been underscored by their performance in competitions such as the ImageNet challenge, where they have consistently outperformed traditional machine learning methods(Zhang et al., 2019).

SNNs represent a more biologically realistic approach to neural computation by incorporating the timing of spikes (action potentials) as a fundamental aspect of information processing. SNNs are particularly suited for tasks that require real-time processing and are often used in neuromorphic computing applications, where energy efficiency is paramount (Pfeiffer & Pfeil, 2018; Taherkhani et al., 2020). These networks can model the dynamics of biological neurons more closely than traditional artificial neural networks, allowing for the exploration of complex phenomena such as temporal coding and synaptic plasticity (Pfeiffer & Pfeil, 2018; Taherkhani et al., 2020). Despite their potential, SNNs face challenges in terms of training and scalability, which are active areas of research in the field of computational neuroscience (Pfeiffer & Pfeil, 2018; Taherkhani et al., 2020).

For the type of simulations that are entertained by this thesis, Leaky Integrate and Fire (LIF) models, a subset of SNN are exploited because they provide many benefits that are recognized with the neuroscience research community. Firstly, LIF models closely mimic the behavior of biological neurons by using discrete spikes to transmit information. This makes them a valuable tool for studying and understanding neural processes in the brain. LIF models also provide an abstract mathematical construct that retains the essential characteristics of biological neurons while simplifying the complex dynamics. This balance makes it easier to analyze and simulate large neural networks. Secondly, LIF models are very well suited to working with large data sets(Pfeiffer & Pfeil, 2018) generated within the neuroscience field. LIFs naturally incorporate the timing of spikes, allowing them to capture the temporal dynamics of neural activity. This is crucial for tasks that involve time-dependent data, such as sensory processing and motor control. Moreover, due to their event-driven nature, LIF models can be more energy-efficient compared to traditional neural networks(Pfeiffer & Pfeil, 2018). Neurons in LIF models only process information when they receive spikes, reducing unnecessary computations. This can lead to more efficient storage and processing of information. NeuCube is an example of modelling spatio-temporal brain data including fMRI and EEG based on SNN and LIF models(Kasabov et al., 2023).

Even though LIF models offer the above benefits, there are some negative issues that must be considered. Training LIF models can be more challenging compared to traditional neural networks(Pfeiffer & Pfeil, 2018). The non-differentiable nature of spikes makes it difficult to apply standard gradient-based optimization methods. Specialized training algorithms, such as spike-timing-dependent plasticity (STDP) and surrogate gradient methods, are often required(Pfeiffer & Pfeil, 2018). Also, even though computationally efficient, simulating LIF models can be computationally intensive for large-scale networks. The need to track and process individual spikes can lead to higher computational overhead compared to continuous-valued neural networks, and in such cases other models may be required. Finally, LIF models are simple compared to the biophysics of real neurons but can be sensitive to the choice of parameters, such as membrane time constants, threshold values, and synaptic weights(Gerstner & Kistler, 2002). Fine-tuning these parameters to achieve optimal performance can be a complex and time-consuming process(Taherkhani et al., 2020).

Details on the mathematics used for the above models can be found in the appendix of the thesis. However, a brief overview of LIF key differential equations is presented in this section because of its central importance to the thesis in general.

The LIF model is described by the following differential equation:

$$\tau_m \frac{dV}{dt} = -(V - E_L) + \frac{I}{g_L} \tag{4}$$

Where the membrane Potential V represents the membrane potential of the neuron and $E_L$ is the resting potential or leak potential and represents the baseline voltage of the neuron when there is no input current. This value is typically negative, indicating that the inside of the neuron is more negative compared to the outside. The variable $g_L$ is the membrane resistance. It determines how much the membrane potential changes in response to a given input current. Higher resistance means a larger change in potential for the same amount of current. $I$ is the input current and represents the synaptic inputs the neuron receives from other neurons. It can vary over time and can be excitatory (increasing $V$) or inhibitory (decreasing $(V)$. The membrane Time Constant $\tau_m$ is defined as $\tau_m = R_m C_m$, where $R_m$ is the membrane resistance and $C_m$ its capacitance. The time constant determines how quickly the membrane potential responds to changes in the input current. A larger $\tau_\mathrm{m}$ means the neuron integrates inputs over a longer period. The right side differential term $\frac{dV}{dt}$ represents the rate of change of the membrane potential over time. It indicates how quickly the membrane potential is changing at any given moment.

In the simulations used in this thesis, a neuron emits a spike when the membrane potential $V$crosses a fixed threshold $V_\mathrm{th}$. Immediately after a spike, $V$is reset to a lower reset potential $V_\mathrm{reset}$, and the membrane potential again evolves according to Eq. (4). This threshold and reset dynamics ensure that the model reproduces the integrate–fire behavior of biological neurons in a computationally tractable way.

The equation can be interpreted as follows. The term $-(V - E_L)$ represents the "leaky" part of the model. It shows that the membrane potential $V$ tends to decay towards the resting potential $E_L$ over time. This decay happens because of the natural leakage of ions through the membrane, even in the absence of input current. The term $\frac{I}{g_L}$ (which can also equivalent to $R_m I_t$) represents the effect of the input current on the membrane potential. When there is an input current causes a change in the membrane potential proportional to the membrane resistance.

In summary, neural network models encompass a diverse range of architectures, each tailored to specific types of data and tasks. Feedforward networks excel in straightforward pattern recognition, RNNs are adept at handling sequential data, CNNs are the go-to choice for image-related tasks, and SNN-LIFs offer a biologically inspired approach to neural computation. The thesis leverages LIFs for its many benefits described above but other models may be employed at a later stage.

As a final note, there are criticisms for all the above models, particularly in the context of their limitations and challenges. However, many of these criticisms overlap with the model types that follow so for brevity, they will be discussed in the following sections.

### 2.9.4 Stochastic Models

Stochastic neural networks (StNNs) integrate randomness into their architecture and learning processes, enhancing their ability to model biological neural systems. This randomness can stem from various sources, including random weights, biases, and noise in inputs or activations, which collectively contribute to improved robustness and generalization capabilities of the networks(Pfeiffer & Pfeil, 2018; Tavanaei et al., 2019; Wang & Li, 2017; Yu et al., 2021). Moreover, StNNs have been shown to outperform traditional models in specific tasks by leveraging their stochastic nature to explore a broader solution space, thus enhancing learning efficiency and adaptability(Florensa et al., 2017; Yu et al., 2021). This adaptability is particularly crucial in dynamic environments where variability is a constant factor, underscoring the relevance of stochastic approaches in both artificial and biological contexts(Hafez et al., 2023; Razetti et al., 2018).

For a more mathematically rigorous treatment, the reader is directed to the Appendix at the end of this document, but at a high level these models effectively incorporate randomness into neural computations through various mechanisms, enhancing their adaptability and performance in dynamic environments. There are several common methods employed: random weights and biases; noise integration; standard differential equations (SDEs); continuous paths. Each of these shall be discussed here briefly.

Random weights and biases allow models to explore a broader solution space and improve generalization capabilities. For instance, Stochastic Configuration Networks (SCNs) utilize random assignments of input weights, facilitating a flexible learning process that can dynamically adjust to data variability (Wang & Li, 2017; Yu et al., 2021). Research indicates that networks initialized with random weights can exhibit properties akin to those found in statistical mechanics, providing insights into the optimization landscape of deep learning models(Pennington & Worah, 2019). This perspective is supported by the findings of Bahri et al., who discuss the statistical mechanics underlying deep learning and how random configurations can influence information propagation within networks(Bahri et al., 2020). And finally, the interplay between random weights and the learning process is further emphasized by the work of Kazemi and Jamali, which explores the synchronization properties in neural models, highlighting the emergent behaviors that arise from such stochastic configurations(Kazemi & Jamali, 2022).

Stochastic models also integrate noise into their computations, simulating the uncertainty inherent in biological systems. This noise can manifest random fluctuations in activations or inputs, which helps the models to better mimic the behavior of biological neurons and enhances their robustness against overfitting(Pfeiffer & Pfeil, 2018). As example, the work by Song et al. highlights how stochastic processes can influence neural responses in biological systems, particularly in the context of visual phototransduction in Drosophila(Song et al., 2012). This is particularly relevant in the context of deep learning, where dropout techniques are employed to introduce randomness during training, thereby improving the model's performance on unseen data(Yu et al., 2021).

Stochastic Differential Equation (SDE) Models provide a rigorous mathematical framework for modeling the dynamics of neural networks under uncertainty(Florensa et al., 2017). These models are particularly useful for capturing the continuous-time evolution of neural states, incorporating both deterministic and stochastic components.

The application of SDEs in neuroscience allows researchers to simulate the behavior of neurons and neural populations under various conditions, including the effects of noise and external perturbations(Gonze et al., 2004). For example, the work by Razetti et al. presents a stochastic framework to model interactions within growing neuronal populations, illustrating how stochastic processes can influence neuronal morphology and connectivity(Razetti et al., 2018).

In the context of spiking neural networks (SNNs), the incorporation of continuous paths enables these models to simulate the dynamic interactions of neurons more accurately, allowing for a better understanding of how neural computations adapt to changing environments. They represent the intricate interactions and dependencies between variables over time, which is particularly important in biological systems where changes are often gradual and influenced by multiple factors(Razetti et al., 2018). Moreover, continuous path methods can facilitate the analysis of the stability and convergence of stochastic processes, providing insights that may not be readily apparent through SDEs alone. This is particularly relevant in reinforcement learning scenarios, where understanding the long-term behavior of policies and value functions is crucial for effective learning(Florensa et al., 2017).

The integration of the above stochastic elements into neural network models also has implications for understanding cognitive processes. The predictive coding framework, which posits that the brain continuously generates and updates predictions about sensory input, can be enhanced by incorporating stochastic elements. This perspective is articulated in the work of Friston, who discusses the role of active inference in cognitive processes, emphasizing how uncertainty and variability are fundamental to perception and action(Friston et al., 2017; Friston & Kiebel, 2009). By modeling the brain as a predictive machine that minimizes prediction errors, researchers can better understand how stochastic influences affect cognitive functions such as perception, decision-making, and learning(Parr et al., 2022).

Naturally there are criticisms of stochastic models, particularly in the context of their application in artificial intelligence and cognitive modeling. For example, researchers put forth that these models often introduce additional complexity, making them harder to interpret(Marcus, 2018), prone to overfitting and incorrect generalization(Davis & Marcus, 2015), and fall short of capturing the richness of human cognition(Dreyfus, 2007, 2016).

In summary, the foundational equations and concepts surrounding StNN models offer a rich framework for understanding the complexities of neural computations in the presence of randomness and uncertainty. By integrating insights from various fields, including neuroscience, mathematics, and computer science, researchers can develop more sophisticated models that reflect the intricacies of biological neural systems. The ongoing exploration of these models will yield further insights into both artificial intelligence and the fundamental principles of neural computation.

### 2.9.5 Hybrid Models

Hybrid models that integrate neural networks with physical models has led to the development of models such as NeuralFMU and Hybrid NeuralODE. These models represent a significant advancement in the field of machine learning, particularly in their ability to incorporate domain-specific knowledge into neural architectures(Thummerer et al., 2022). NeuralFMU focuses on the structural integration of Functional Mock-up Units (FMUs) into neural networks, allowing for a more seamless interaction between physical modeling and machine learning processes. This approach contrasts with traditional methods that evaluate physical models as part of the loss function during training, as seen in Physics-informed Neural Networks (PINNs)(Tobias Thummerer et al., 2021). The structural integration allows for a more holistic approach to modeling, where the neural network can learn from both data and physical principles simultaneously.

Hybrid NeuralODEs extend this concept by integrating neural ordinary differential equations (NeuralODEs) into real-world applications(Ko et al., 2022; Thummerer et al., 2022). This model leverages the strengths of both neural networks and differential equations, allowing for the modeling of dynamic systems in a way that is both computationally efficient and interpretable. The incorporation of physical equations into the loss function of neural networks, as proposed in the context of eigen-informed NeuralODEs, exemplifies how these models can be designed to evaluate eigenvalues and eigenvectors as part of their training process (Thummerer et al., 2022; Tobias Thummerer et al., 2021). This not only enhances the model's performance but also ensures that the learned representations are consistent with the underlying physical phenomena they aim to model.

The significance of these hybrid models lies in their ability to bridge the gap between data-driven approaches and traditional physics-based modeling. This is mathematically expressed by a foundational equation used in hybrid neural models called the Neural Ordinary Differential Equation (NeuralODE). This equation combines an Artificial Neural Networks (ANN) with an ODE solver, where the ANN defines the right-hand side of the ODE:

$$\frac{dh(t)}{dt} = f(h(t), \theta) \tag{5}$$

Where:
$h(t)$ represents the hidden state at time t,
$\frac{dh(t)}{dt}$ denotes the rate of change of the hidden state with respect to time,
$f(h(t), \theta)$ is a function that how the hiden state evolves over time, and
$\theta$ representing the parameters of the model.

This equation utilizes the strengths of both methodologies, allowing researchers to develop models that are not only accurate but also robust and interpretable. For instance, the work by Thummerer et al. highlights the potential of NeuralFMU to enhance the modeling of complex systems by integrating physical insights directly into the neural network architecture(Tobias Thummerer et al., 2021). This structural integration facilitates a more comprehensive understanding of the system dynamics, ultimately leading to improved predictive capabilities.

Moreover, the application space of these hybrid models is vast, ranging from neuroscience to engineering. In neuroscience, for example, the modeling of neural dynamics can benefit from the integration of physical principles that govern neuronal behavior. The ability to simulate large populations of neurons and their interactions through hybrid models allows for a more nuanced understanding of neural coding and information processing(Sokoloski et al., 2021), and as discussed in the context of neural coding, further enhances the model's ability to capture the temporal dynamics of neural responses(Kietzmann et al., 2019).

In addition to their theoretical implications, hybrid models like NeuralFMU and Hybrid NeuralODE also offer practical advantages in real-world applications. The ability to model complex systems with high-dimensional dynamics while maintaining computational efficiency is crucial in fields such as robotics, where real-time decision-making is essential. The integration of physical models into neural networks can lead to more reliable and interpretable outcomes, which is particularly important in safety-critical applications(Thummerer et al., 2022).

Furthermore, the exploration of stochastic elements within these hybrid frameworks can enhance their robustness against uncertainties and variabilities present in real-world data. The incorporation of stochastic processes into the training of neural networks allows for a more comprehensive understanding of the underlying data distributions, leading to improved generalization capabilities(Yu et al., 2021). This is particularly relevant in scenarios where data is noisy or incomplete, as the hybrid models can learn to account for these uncertainties while still adhering to the physical constraints imposed by the underlying models.

The ongoing research into hybrid models continues to reveal new insights and methodologies that can further enhance their capabilities. For instance, the exploration of deep learning techniques within spiking neural networks (SNNs) presents an exciting avenue for future research, as these models can potentially offer advantages in terms of efficiency and biological plausibility (Tavanaei et al., 2019; Thummerer et al., 2022; Yu et al., 2021). The combination of hybrid modeling approaches with SNNs could lead to the development of more sophisticated neural architectures that are capable of mimicking biological processes more closely.

In conclusion, the development of hybrid models such as NeuralFMU and Hybrid NeuralODE represents a significant advancement in the integration of machine learning with physical modeling. These models not only enhance the predictive capabilities of neural networks but also provide a framework for incorporating domain-specific knowledge into the learning process. However, this area uses neural networks, it employs NeuralODEs and NeuraFMUs which are, when you cast them plainly, resemble a form of plain old-fashioned AI (POFAI) which compares to rule-based systems, expert systems, and early forms of symbolic AI. Therefore, the limitations of Hybrid models inherit many criticisms of both neural networks and symbolic AI. As put forth by Dreyfus and Marcus, such models lack contextual understanding, overemphasize formal logic, fail when faced with novel situations outside of training data, simply complicate frameworks without addressing human understanding and reasoning, and fail to account for the embodied and situated nature of human existence(Davis & Marcus, 2015; Dreyfus, 2007, 2016; Marcus, 2018).

Nonetheless, as seen by the recent AI explosion in LLMs, research continues to evolve in this area, and the potential applications of these hybrid models will likely expand further, offering new solutions to complex problems across various fields.

### 2.9.6 Cognitive Architecture Models

Cognitive architecture serves to create and demonstrate frameworks for understanding the intricate processes and structures of the human mind, integrating insights from artificial intelligence (AI), psychology, and neuroscience(Baars & Franklin, 2009; Borst & Anderson, 2015; Laird, 2012; Sun, 2007). Among the prominent cognitive architectures are ACT-R, SOAR, CLARION, EPIC, and LIDA, each contributing unique perspectives on cognitive functions such as memory, learning, problem-solving, and decision-making.

ACT-R (Adaptive Control of Thought - Rational), developed by John R. Anderson, is a hybrid architecture that combines symbolic and subsymbolic processes to model cognitive tasks. It emphasizes the interplay between declarative and procedural knowledge, allowing for a nuanced understanding of human cognition, particularly in memory and learning contexts(Borst & Anderson, 2015). The architecture's ability to simulate various cognitive tasks makes it a valuable tool for researchers exploring the underlying mechanisms of human thought processes(Taatgen et al., 2005).

SOAR, created by Allen Newell, focuses on problem-solving and decision-making. It operates on the principle of production rules, which guide the agent's actions based on its current state and goals(Laird, 2012). This architecture has been instrumental in advancing our understanding of how humans approach complex tasks and make decisions, integrating both knowledge-based and heuristic strategies. The flexibility of SOAR allows it to adapt to different problem-solving scenarios, making it a robust model for cognitive research.

CLARION (Connectionist Learning with Adaptive Rule Induction ONline), developed by Ron Sun, merges neural network approaches with symbolic processing to simulate learning and reasoning tasks. This architecture highlights the importance of both implicit and explicit knowledge, allowing for a more comprehensive understanding of cognitive processes(Sun, 2007). By integrating connectionist and symbolic elements, CLARION provides insights into how humans learn from experience and adapt their knowledge to new situations(Sun, 2005, 2007).

EPIC (Executive-Process Interactive Control), formulated by Kieras and Meyer, explores human multitasking and attention allocation. It models the cognitive processes involved in managing multiple tasks simultaneously, shedding light on the limitations and capabilities of human attention(Kieras et al., 1999; Kieras et al., 1995; Meyer & Kieras, 1997). EPIC's focus on the interaction between cognitive processes and task demands offers valuable insights into the dynamics of multitasking in real-world scenarios.

The LIDA (Learning Intelligent Distribution Agent) model draws inspiration from the Global Workspace Theory, simulating complex cognitive processes such as perception, attention, and memory(Baars & Franklin, 2009). LIDA emphasizes the role of consciousness in cognitive functioning, proposing that conscious processes arise from the interaction of various cognitive subsystems(Baars & Franklin, 2009). This architecture provides a framework for understanding how conscious and non-conscious processes work together to facilitate adaptive behavior.

In summary, cognitive architectures like ACT-R, SOAR, CLARION, EPIC, and LIDA offer diverse frameworks for understanding the complexities of human cognition. By integrating principles from AI, psychology, and neuroscience, these models enhance our comprehension of cognitive processes, paving the way for advancements in both theoretical and applied domains. However, while cognitive architectures show some usefulness, critics of these various Global Workspace Theory (GWT) frameworks argue that these cognitive architectures often fail to accurately represent the underlying micro neuronal mechanisms that drive cognitive processes(Shanahan, 2006; Whyte & Smith, 2020). While models like ACT-R and EPIC are designed to mimic certain brain structures, they do not necessarily provide a faithful representation of the brain's actual architecture. This discrepancy raises concerns about the validity of these models in capturing the complexities of human cognition.

# Chapter 3 Methodology

## 3.0 Research Design

The thesis proposes a framework to model and analyze a circuit mechanism within the Fan-shaped Body (FB), a core neuropil within the CX of fruit fly. The multistep framework (**Fig. 1**) includes methods for: identifying NOIs; calculating synaptic weights, modelling neural connectivity using graphs; developing neural circuit model diagrams; simulating NOIs, and perform signal analysis. Each method within the framework is further elaborated in the following sections.

## 3.1 Methodology Framework

### 3.1.1 Justification for Selecting FB1G and FB4N

The selection of FB1G and FB4N as the primary Neurons of Interest (NOIs) in this study arises from a convergence of anatomical evidence, quantitative synaptic analysis, and computational modelling requirements. Although these justifications previously appeared across several sections of the chapter, they are consolidated here for clarity and coherence.

FB1G was identified as the initial NOI based on its exceptional synaptic prominence within the Fan-shaped Body (FB). Analysis of the Hemibrain dataset shows that FB1G provides between 7.5k and 10k synapses into layers 1–3 of the posterior FB, representing one of the densest projection patterns observed in this neuropil. Its anatomical connections reveal further importance: FB1G integrates signals from higher-order regions such as the Superior Protocerebrum and the Lateral Horn, the latter being functionally analogous to an affective processing hub. These pathways suggest that FB1G plays a major role in shaping information flow from sensory-affective sources into central complex circuitry.

Quantitative Z-score analysis further validates the centrality of FB1G. Heatmaps of neurotransmitter-specific connectivity demonstrate that FB1G forms statistically strong connections with several FB4 subtypes, including FB4A, FB4C, and most prominently FB4N. This makes FB4N a compelling postsynaptic partner. Additional filtering based on graph-analytic pruning removed weaker or less biologically plausible motifs, leaving FB4N as the principal inhibitory counterpart to FB1G. This conclusion is supported by p-value analysis, where the FB1G→FB4N connection ranks among the most significant synaptic relationships in the FB.

From a computational perspective, the excitatory-inhibitory pairing between FB1G (cholinergic) and FB4N (glutamatergic but functionally inhibitory within the FB context) provides an ideal two-population motif for Wilson–Cowan modelling. Their interaction supports the emergence of stable firing-rate equilibria, as later demonstrated through phase-plane analysis. The combination of structural prominence, statistical significance, and computational tractability thus makes FB1G and FB4N the most suitable candidates for the modelling framework employed in this thesis.

The remainder of Chapter 3 expands upon each of these points in detail, demonstrating how anatomical data, synaptic statistics, and computational modelling collectively justify the selection of these neuron types.

### 3.1.2 Neurons of Interest (NOI) - Qualitative Analysis

The first step in the framework is to leverage FlybrainLab, a software platform developed by Lazar et al(Lazar, Turkcan, et al., 2021), to investigate the connectome of the fruit fly. This platform offers a powerful approach to explore neuronal pathways (Lazar, Liu, et al., 2021; Lazar, Turkcan, et al., 2021) and facilitates the exploration of datasets, particularly the Hemibrain dataset, in a Python-based environment. FlybrainLab (see Detailed Methodological Procedure) integrates neuroanatomical, neurogenetic, and electrophysiological datasets with computational models from various researchers, allowing for validation and comparison within a unified platform(Lazar, Liu, et al., 2021). The User Interface offers an intuitive and automated workflow for 3D exploration and visualization of fly brain circuits, enabling interactive exploration of functional logic within selected circuits as part of setting up a general workspace. After the workspace has been loaded (**Fig. 9**), a search for NOIs is made from which to begin analysis.

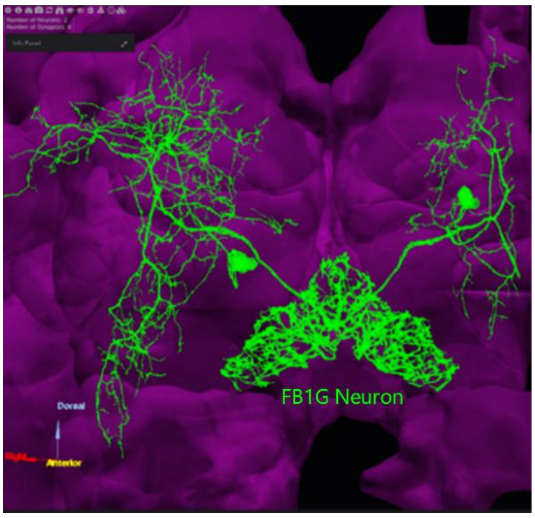


**Fig. 9.** An example of the FB1G (Fan-shaped Body, layer one, subtype G) neurons displayed in the FlybrainLab workspace.

The workspace shows the GUI 3D output of one specific neuron type named FB1G, which stands for: Fan-shaped Body, layer one, subtype G. Naming of neurons is unique to each dataset even though there is crossover at times. The choice of FB1G as a starting NOI was made by literature review and analysis within FlybrainLab that demonstrated FB1G's innervation that indirectly connects the Superior Protocerebrum (an analog of the mammalian cortex) including the Lateral Horn to the CX. This analysis is important because of the possibility that the Lateral Horn acts as an analog of the human amygdala(Bates et al., 2020) and outputs an olfactory response to more downstream neuropils (i.e. CX) in parallel to Mushroom Body Output Neurons (MBONs)(Bates et al., 2020).

Aiding the search for NOIs was data from the connectome paper by Hulse et al.(Hulse et al., 2021), where arborization of FB1G into the CX can be seen in **Fig. 10**.

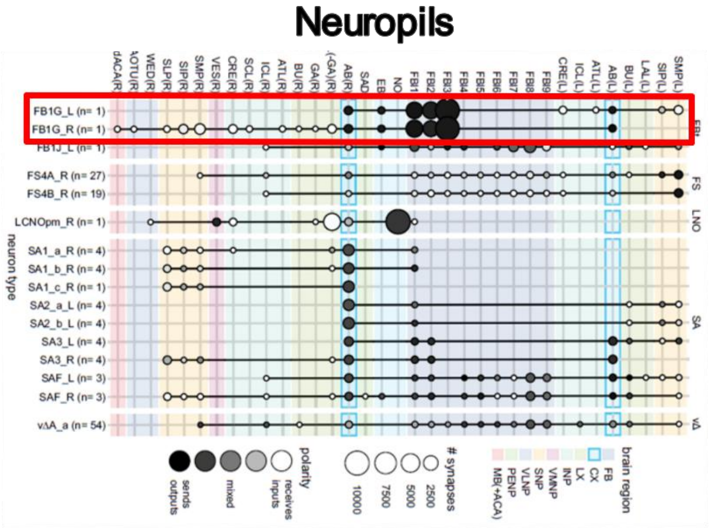


**Fig. 10.** Region arborization plots for each neuron type. Highlighted FB1G neurons highlighted in red show strong innervation to the FB (large round black circles) provides a large output to the lower FB layers. The figure is adopted from research by Hulse et al(Hulse et al., 2021) "A connectome of the Drosophila central complex reveals network motifs suitable for navigation and action selection.

In **Fig. 10** the highlighted area shows FB layers 1-3 in the posterior FB have between 7.5k and 10k synapses from FB1G, a synaptic density greater than any other neurons type. This data point is a compelling reason to focus on FB1G, even though other factors may exist. For example, it is known that the synaptic contact area, the amount of neurotransmitter released into the synaptic cleft, and the types and number of postsynaptic receptors all have an important role determining the degree of propagated signal strength between neurons(X.-J. Wang, 2010). However, those parameters in numerical form are not obtainable. Neither the Hemibrain dataset nor any other large dataset currently provides a detailed morphology of the synaptic microcircuitry per neuron. Thus, using only the number of synapses as an assumed measure of signal strength seems reasonable until more detailed information about the synaptome is published. Simply put, data availability in the underlying dataset is a limiting factor of analysis that can be performed computationally in silico.

Next, NOIs were loaded into the workspace using FlybrainLab's natural language search engine to explore circuit pathways, allowing connection tracing of the FB1G neuron towards the central target in the CX. This process is qualitative and involves researching literature and reviewing metrics. FlybrainLab's natural language engine speeds up the search process before automated analysis using Python algorithms.

In the current example, the search process used a cutoff of 30 synapses to determine significant pre- and post-synaptic connections, but this number can vary. A minimum number of synapses used as a cutoff is important to control the number of possible pathways and ensure that the final set of selected neurons and synapses are reasonable for identifying significant pathways to and from the CX.

### 3.1.3 Pathfinding Analysis based on synaptic Z-score

In the proposed Neuron Pathfinding Analysis step, a Python algorithm is implemented to identify significant neuronal connections based on synaptic weights. This automated process analyzes neurons in the FlybrainLab workspace, calculating weighted connections between them. The workspace contains several pre- and post-synaptic neurons, considered as NOIs. At least two neurons are required to assess synaptic strength. Comparison is made for innervation of two neurons to the synaptic distribution across all synaptic partners. For instance, if neuron A and B have 52 post synapses, one must compute how these compare to all of A’s potential postsynaptic connections. If A only connects to B, the 52 synapses represent 100% of A’s postsynaptic connectivity.

Most connections involve only a small number of synapses and are less than 5 (**Fig. 11**). Recognizing that greater synaptic connectivity facilitates stronger signal propagation across neurons(Scheffer et al., 2020), it is important to focus on larger synaptic connectivity, as defined above, as indicative of meaningful connections within the overall circuit. To objectively determine these higher degrees of connectivity, Z-score analysis is performed by taking a single neuron, listing out all its neuronal partners along with their associated number of synapses, and simply calculating its statistical Z-score. For clarity, a standard statistical Z-score is a measure that tells you how many standard deviations a data point is from the mean. It's a dimensionless quantity used to indicate the signed, fractional, number of standard deviations by which an event is above the mean value being measured. The formula for calculating a Z-score is:

$$z = \frac{x-\mu}{\sigma} \tag{6}$$

Where x the raw score (the data point in question), and μ is the population mean, and σ is the population standard deviation.

By examining Z-scores for individual neurons in relation to their pre- or post-synaptic partners, one can identify a limited set of neurons with notably high Z-scores. Fig**.** 11 shows a right skewed histogram where most of the synaptic connectivity is on the left side of the curve, with higher synaptic connectivity skewed to the right. To refine the investigation, one can filter out synaptic connections below an arbitrary Z-score threshold, resulting in a significantly reduced set of meaningful connections.

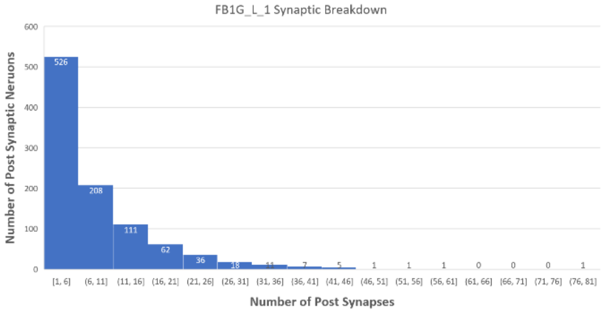


**Fig. 11.** A histogram of synaptic connectivity of the FB1G neuron with all its related postsynaptic partner neurons. The right skewedness demonstrates that most synaptic innervation occurs with only a small number of synapses. The smallest number of incoming postsynaptic neurons represent a very small percentage of the entire distribution.

Z-scores are not uniformly distributed across the connectome making the standard calculation hard to compare between neuron pairs. To overcome this, one must normalize the Z-scores (a number between zero and one) to facilitate comparison between neurons and draw initial conclusions about their pre- or post-synaptic connection and their proportional contribution to a neuron's overall connectivity. The normalization process involves the following formula:

$$Z_{\text{normalized}} = 1 - \frac{Z_{max} - Z}{Z_{max}} \tag{7}$$

### 3.1.4 Bidirectional Graph Analysis

Normalized Z-score calculations are integrated into a graph analysis method for visual utility. Given the Hemibrain dataset's vast neuron and synapse count, bidirectional graphs are crucial for understanding complex relations (Fornito et al., 2013). Here, methods using Graphviz and yWorks are applied. Python packages like NetworkX and Graphviz are used to construct these graphs. They incorporate interneuron Z-score weights into edge descriptions, providing a nuanced view of synaptic strength. Distinct colors for pre- and post-synaptic connections enhance discernment between strong and weak links. Z-score weights indicate connection significance. **Fig. 12** demonstrates four Z-score combination types: strong-strong; strong-weak; weak-strong; weak-weak. Colors range from red and yellow indicate weaker connections (Z-scores <= 0.5) to green and blue for stronger ones (Z-scores >=0.5).

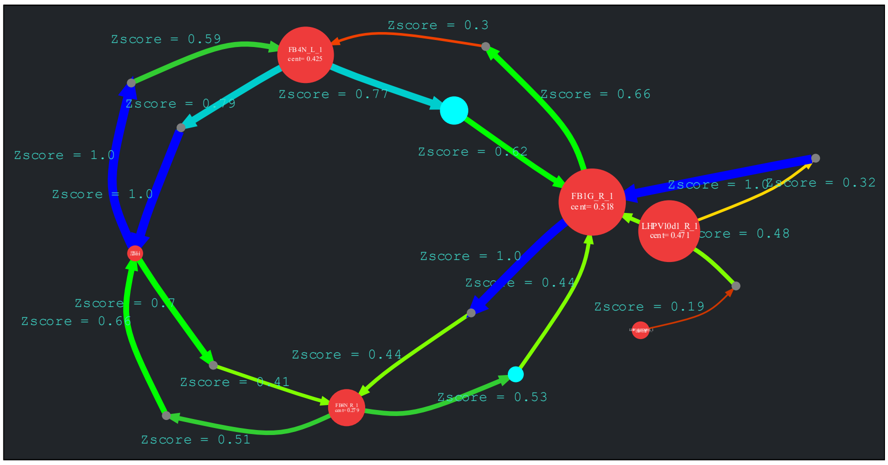


**Fig. 12.** A directional graph plot using normalized Z-scores to identify the weight of synaptic connectivity between neurons represented by the red nodes. Red edges indicate a low Z-score, while dark blue edges are the strongest. The size of nodes indicates centrality calculations of the red neuron nodes that measure the importance of the node within a network.

Z-score colored bidirectional graphs present necessary insights into the hierarchical organization of neural circuits, which in turn shed light on the desired functional architecture to simulate neuronal dynamics in later steps. But as the number of neurons and synapses increases, maintaining readability becomes a challenge. To address this, a final step converts the data from Graphviz's native format to GraphML—a widely used format that facilitates exchange with other software packages and employ yED, a tool developed by yWorks GmbH, which significantly enhances the visual inspection of hierarchical layouts. **Fig. 13** illustrates an example graph created using the yED software package where the model is simplified by restricting the number of edges to a single neuron type. Specifically, neurons can be grouped with similar root names—for instance, neurons labeled as FB1G_R_1 are interpreted as part of the broader FB1G category. By doing so graphs will be generated where each edge represents a neuron type rather than an individual neuron.

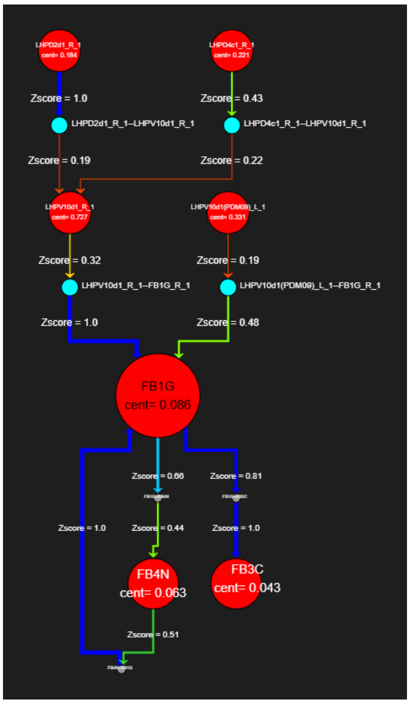


**Fig. 13.** A hierarchical layout using yED software. The readability is greatly improved over Graphviz.

After graph generation, an end-to-end circuit model is qualitatively created using a drawing application, as shown in **Fig. 14**. This model, derived from graphs tracing primary inputs from the Lateral Horn and Mushroom Body, is qualitative due to the high node and edge count. Despite some fidelity loss for readability, one gains insight and context within the model organism's biological framework and incorporates information about the source and target neuropils where neurons arborize, enriching our understanding of connectivity patterns. Instead of color-coding axons based on Z-scores, Z-score values are labeled at synaptic boutons and spikes, allowing direct assessment of synaptic junction connection strength. This convention of color-coding neurons by target neuropils aids pathway identification. While color choices may seem arbitrary, they enhance the connectome's visual accessibility.

In the Graph Analysis step, one can see that NOIs can be based on four pre- and post-synaptic Z-score categories: strong-strong, strong-weak, weak-strong, and weak-weak. For the sake of simplification, certain neurons are deemed less relevant to the hypothesis and removed from the final set of NOIs, but this isn't always straightforward. In this case weak-weak connections are excluded, and this left us with a circuit as seen in Fig. 14, FB1G and FB4N. It is worth noting that the process of simplification may remove connectivity relevant to the hypothesis. And while this possibility cannot be ruled out, one can consider the current methodology a first step toward understanding basic neuronal combinations. Future experiments can certainly expand the number and complexity of NOIs and determine how more complex networks behave differently than the simple framework presented here. See the discussion for amore detailed on this issue. Nonetheless, with a model of two NOIs decided upon, it is possible to move onto the next step of the Framework and test for evidence of oscillatory characteristics between the excitatory neuron FB1G and its postsynaptic inhibitory partner FB4N.

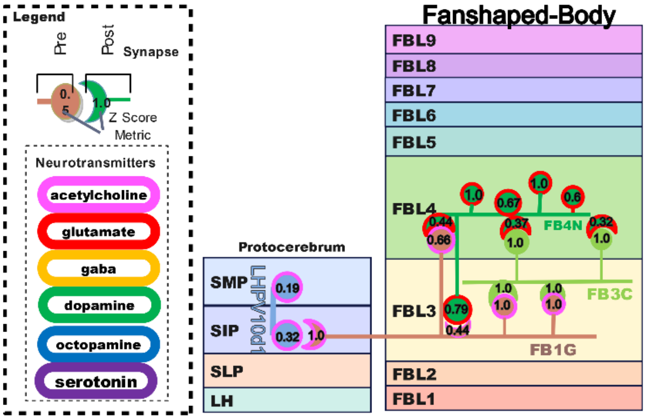


**Fig. 14.** Circuit Diagram of innervation between the CX and select neuropils in the fruit fly. Each colored area denotes a unique neuropil, with important sources of signal coming from the Superior Protocerebrum. The Fan-shaped Body is where incoming signals are processed.

### 3.1.5 Simulation

#### 3.1.5.1 LIF model using Excitatory and Inhibitory Neurons

To analyze the characteristics of a coupled oscillator network, it is necessary as a first step to simulate the frequency output of the NOI neural network (NOIs). The model employed by the thesis is a Leaky Integrate-and-Fire (LIF) model. The LIF model is a fundamental concept in computational neuroscience that describes in a computationally tractable way how neurons accumulate incoming synaptic currents over time, incorporating a leak factor, until a threshold is reached, triggering the firing of an action potential (Burkitt, 2006). This model is widely used in studying the spiking dynamics of neural networks under various conditions such as stimuli, tasks, or dynamic network states(Mazzoni et al., 2015). The basic equation for the LIF model is:

$$\tau_m \frac{dV}{dt} = -(\mathrm{V} - E_L) + \frac{I}{g_L} \tag{8}$$

where: V is the membrane potential, g is the leak conductance, $E_L$ is the resting potential, I is the external input current, and $\tau_m$ is the membrane time constant. In practice, each simulated neuron is treated as a spike generator when its membrane potential $V$ exceeds a threshold $V_{\mathrm{th}}$, the neuron is said to “fire”, and $V$ is instantaneously reset to a reset potential $V_{\text{reset}}$. Between spikes, the voltage continues to evolve according to the LIF dynamics in equation 8 above.

With the identification of two NOIs, FB1G and FB4N, using the above stated combination of literature, pathfinding analysis, graph analysis, and circuit modeling, the aim is to now simulate the NOIs within the FlybrainLab environment using the Nengo package which is graphical and imported as a Python package for simulating large-scale neural networks (see section 'Detailed Methodological Procedures'). However, it is worth noting that the methodology isn't exclusive to Nengo and can adapt to any neural simulation package. The process begins by importing the NOIs into the FlybrainLab workspace (**Fig. 9**), followed by autonomous generation of necessary nodes and edges for simulations.

Before proceeding, it's important to note that unlike the simplifications in the Pathfinding and Graph sections, all available neurons are used in each group to construct Nengo ensembles. The model isn't limited by neuron and synapse count, but it does restrict the simulation to one excitatory and one inhibitory neuron type, limiting the model to two dimensions. This facilitates Wilson-Cowan analysis, which treats many neurons within a similar ensemble as a single unit constrained to excitatory inhibitory types. This supports Phase-Plane analysis for visualizing network stability and avoids the need for compactification of extra data dimensions, which could obscure results(Xie et al., 2016). **Fig. 15** shows the output topology of the model's two neuron types.

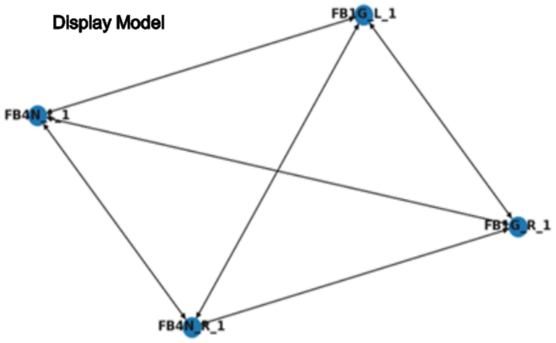


**Fig. 15.** Simplified version of the Nengo model graph. FB1G is cholinergic and FB4N being Glutamatergic which creates a four-way node integration.

With the above constraints in place the approach used by the thesis lies in establishing ensemble connections using a transfer function that mirrors, as accurately as possible, the biophysical parameters of the selected neurons. To do this, two key parameters, alpha and theta, are used within the Frequency-Current sigmoid transfer functions (F-I curve), a key component in artificial neural networks (i.e. Nengo), crucial for simulating the nonlinear behavior of neuron ensembles. The F-I curve in neuroscience illustrates the relationship between a neuron's firing rate F and the net synaptic current I it receives(Wilson & Cowan, 1972).

$$\mathrm{F}(\mathrm{I};\alpha,\theta) = \frac{1}{1+e^{-\alpha(\mathrm{I}-\theta)}} - \frac{1}{1+e^{\alpha\theta}} \tag{9}$$

Where: I is the simulated input to the function, an abstract value of current, θ determines the position of maximum slope before the sigmoid curve inverts toward its upper limit, α alpha determines the value of the overall slope between minimum and maximum. The theta value used within the sigmoid function is challenging to determine and is best fitted against biological assays or backward engineered via deep learning algorithms. Sadly, without such data at this time, the number must simply be estimated to a value between two random integers. The alpha function used is novel, and is derived from the Z-score connection weights using the following formula:

$$\alpha = \begin{cases} \frac{Z_{\text{nPost}}}{Z_{\text{nPre}}} & \text{if} \quad \frac{Z_{\text{nPost}}}{Z_{\text{nPre}}} > 1 \\ \frac{Z_{\text{nPost}}}{Z_{\text{nPre}}} + 1 & \text{if} \quad \frac{Z_{\text{nPost}}}{Z_{\text{nPre}}} < 1 \end{cases} \tag{10}$$

The product of pre- and post-synaptic Z-scores (i.e. $Z_{\text{nPre}}$ and $Z_{\text{nPost}}$ ) provides an analog for the alpha value in the sigmoid transfer function, representing gain and loss. clarifies alpha's role in gain within this function.

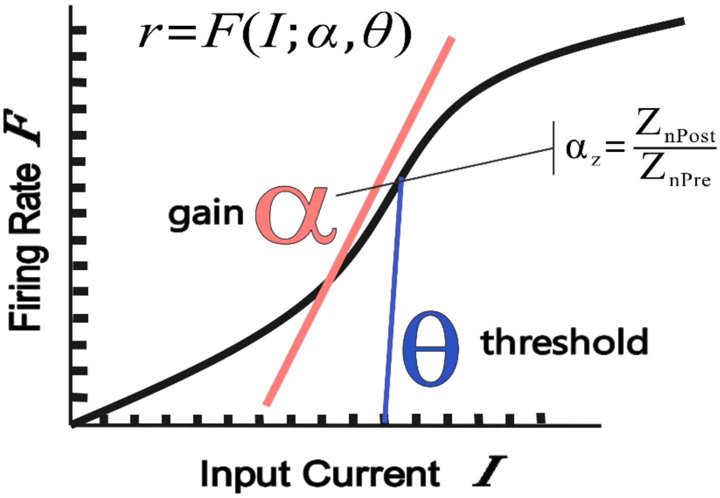


**Fig. 16.** Parameters of the FI curve sigmoid function, alpha and theta. Theta shifts the curve along the x-axis and is typically estimated. The alpha parameter influences the steepness of the curve and is derived from the product of Z-scores.

After configuring transfer functions and establishing neuron connections in Nengo, a simulated 10Hz input sine function is connected to the FB1G neurons. This choice is informed by the Hemibrain dataset's pre- and post-synaptic directional vector and confirmed by graph analysis.

### 3.1.5.2 Z-Score based Alpha Function

A central requirement in modelling neuronal ensembles within the Wilson–Cowan framework is the use of a nonlinear transfer function that converts synaptic input into a population-level firing rate. In this thesis, this nonlinearity is implemented using a sigmoidal Frequency–Current (F–I) curve: $S(x) = 1/(1 + e\hat{}(-\alpha(x - \theta))\ )$where $\boldsymbol{\alpha}$ deter mines the steepness (gain) of the response and θ represents the threshold at which the ensemble begins to transition from low to high firing probability. The gain parameter α is therefore essential: it controls the degree of nonlinearity that enables the coupled excitatory–inhibitory system to exhibit stable fixed points, oscillatory dynamics, or state transitions, depending on how input currents interact.

The Hemibrain connectome provides high-resolution information about synaptic counts but does not offer biophysical firing-rate curves, membrane properties, or experimentally measured gains for specific neuron types. Because a Wilson–Cowan-style model aggregates many individual neurons into a single excitatory or inhibitory ensemble, a biologically meaningful estimate of α is required to approximate how strongly each neuron class reacts to input.

Rather than assign α arbitrarily or treat it as a free parameter, the thesis uses existing synaptic statistics—specifically Z-scores—to derive a principled and repeatable estimate of gain from available connectomic structure.

Earlier sections introduced synaptic Z-scores as a way to describe how exceptional a given connection is relative to a neuron's entire distribution of synaptic partners. This makes Z-scores a natural candidate for approximating *relative influence* between neuron types.

To ensure that α reflects structural connectivity in a meaningful way, the gain parameter is defined as a ratio: $\alpha \propto Z\_\text{"}post\text{"}\ /Z\_\text{"}pre\text{"}$. This ratio captures complementary and asymmetrical aspects of neural interaction. If a postsynaptic neuron receives an unusually strong input relative to its overall distribution, it is reasonable to attribute a higher gain to its firing response. A high $Z_{\text{post}}$ therefore increases α, sharpening the sigmoidal response and making the neuron more sensitive to variation in upstream input. If a presynaptic neuron already projects strongly to many targets (i.e., has a high $Z_{\text{pre}}$), the postsynaptic neuron's response should not be overly amplified by a single dominant presynaptic source. The denominator tempers α so that broad presynaptic influence does not automatically inflate gain.

The α ratio expresses how *selectively* a neuron responds to strong incoming connections relative to how widely or strongly the upstream neuron distributes its output.

- A neuron with high selectivity but modest presynaptic broadcast strength yields high α.
- A neuron receiving strong input from a highly dominant presynaptic source yields moderated α.

This matches the role of α as a “gain modulator” of the postsynaptic response rather than a proxy for raw synaptic magnitude.

In the Wilson–Cowan equations, synaptic influences appear as weighted inputs such as: $W\_EE\ E - W\_EI\ I, W\_IE\ E - W\_II\ I,$ with inhibition represented through subtraction. The ratio-based α complements this structure:

- The presynaptic neuron's broad output (high $Z_{\text{pre}}$) reduces α, reflecting that broad drivers should not over-steepen the sigmoidal gain.
- The postsynaptic neuron's exceptional input (high $Z_{\text{post}}$) increases α, steepening the response curve where appropriate.

Thus, α acts as a structural-normalized, population-level gain term, ensuring that the nonlinearity of the response function is grounded in actual connectivity patterns rather than arbitrary tuning.

It is also worth pointing out that α must be constrained to α ≥ 1 because both Z-scores are normalized values in the range [0, 1], their ratio often produces α values below 1 unless the numerator is substantially larger than the denominator. While mathematically valid, α < 1 produces a very shallow sigmoid slope—almost linear—leading to:

- poor separation between active and inactive states,
- reduced nonlinearity in the EI interaction,
- failure to generate stable fixed points in phase-plane analysis.

To ensure biologically meaningful nonlinear behaviour, α is therefore constrained to $\alpha \geq 1$. This lower bound prevents degenerate transfer functions and guarantees the model maintains sufficient curvature to support the oscillatory or attractor-like dynamics that the simulation aims to reveal.

Importantly, this constraint concerns only the steepness of the sigmoidal activation. Inhibition itself remains encoded in the sign of synaptic weights, not in α. Although the α ratio is principled and connectome-derived, it remains an approximation. Definitive α values require electrophysiological recordings—such as patch-clamp measurements—from the specific FB neuron types modelled in this thesis. Such wet-lab data would allow:

- empirical fitting of gain curves,
- direct comparison with simulated firing rates,
- refinement or replacement of the Z-score-derived ratio.

The use of α as a structural surrogate is therefore provisional but scientifically defensible, providing a falsifiable, data-driven starting point until precise biophysical measurements become available.

#### 3.1.5.3 Alpha Values in Context of Wilson-Cowan

Although the Wilson–Cowan analysis presented in this thesis does not involve sweeping parameters across a wide range, the fixed parameter set used here is not arbitrary: all gain values are dynamically computed at runtime from biologically informed Z-score ratios, ensuring that the resulting α\alphaα values reflect the relative synaptic structure of FB1G and FB4N rather than being manually imposed. Importantly, this novel method of deriving α does not alter or violate any expected qualitative behavior of standard Wilson–Cowan dynamics. Instead, the analysis demonstrates that, under these structurally motivated parameters, a stable operating point for the excitatory–inhibitory motif is possible, and therefore not ruled out by either the theory or the connectome data available. A full discussion of parameter constraints, bifurcation considerations, and the rationale for not performing broad parameter sweeps can be found in Appendix D.

### 3.1.6 Stabilized Frequency Output with Respect to Time.

The result is a graph showing the Hz frequency firing rate over time, with each neuron color-coded for identification. **Fig. 17** is a sample output produced by the Nengo Simulation. A key aspect to observe here is the consistent rise and maintenance of a steady firing rate by the neurons throughout the simulation.

In this example, each ensemble receives a simple sinusoidal input current at a fixed frequency. This input is not intended to explore parameter ranges or induce bifurcation but instead serves as a minimal, rhythmic drive that allows us to verify that the simulated LIF ensembles converge to stable firing regimes. The WC-related parameters such as $w_{EE}, w_{EI}, w_{IE}, w_{II}$ and the α-derived gain values are held constant in this demonstration. The fluctuations observed in Fig. 17 therefore reflect the transient response of the LIF ensembles to this periodic input rather than any parametric variation within the Wilson–Cowan system.

This figure is presented before the introduction of the WC equations because its purpose is simply to show that the simulated FB1G and FB4N ensembles exhibit stable firing behavior under steady rhythmic input, establishing a baseline for the more formal phase-plane and fixed-point analysis that follows in the next section.

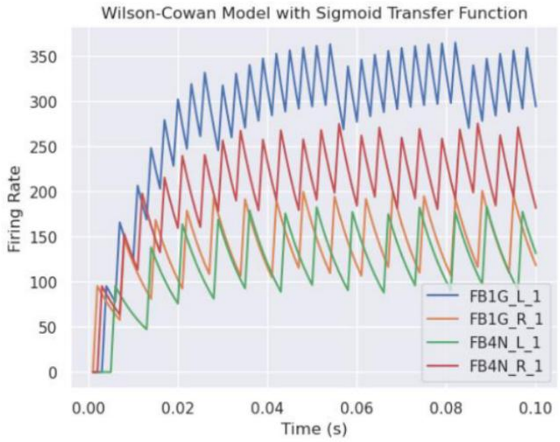


**Fig. 17.** Simulated firing rates of four ensembles, with Y values representing an abstract Hz rate which can be converted into values that make sense from a biological example.

In line with the Wilson-Cowan theory, one should anticipate that all firing rates will reach stable points if they exist. This expectation is based on the theory's premise that neurons within an excitatory-inhibitory network tend to stabilize their firing rates over time(Wilson & Cowan, 2021).

### 3.1.7 Signal Analysis

#### 3.1.7.1 Wilson-Cowan Model Review and Output using Neurons of Interest.

Coupled oscillator theory, commonly used for signal analysis, studies the dynamics of biological neural network models (Ashwin et al., 2016). Originating from Huygens' work, the theory has evolved and been applied to both biological and non-biological systems. Synchronous rhythms are key in coordinating neural activity across brain networks (X. J. Wang, 2010). The rhythmic activities of various systems, like cardiac pacemaker cells, neural circuits of central pattern generators, and circadian cells, exemplify pulse-coupled oscillators in both invertebrates and vertebrates.

After generating a stable signal with Nengo, the crucial final step is signal analysis. The Wilson-Cowan theory is now applied using a two-dimensional phase plane analysis. This approach is ideal for our study as it helps understand Loosely Coupled Oscillators. For a detailed discussion on Loosely Coupled Oscillators, please refer to the discussion section. The model is defined by a system of two first-order, nonlinear differential equations. These equations are discussed in more detail in the appendix (see appendix formula 39 and 40) but repeated here for readability:

$$\frac{dE}{dt} = -E + S(w_{EE}E - w_{EI}I + P_E) \tag{11}$$

$$\frac{dI}{dt} = -I + S(w_{IE}E - w_{II}I + P_I) \tag{12}$$

Here, E and I represent the average activity levels of the excitatory and inhibitory neurons, respectively. The parameters $w_{\mathrm{EE}}$, $w_{EI}$, $w_{IE}$ and $w_{II}$ denote the synaptic weights, reflecting the strength of connections within and between the two types of neurons. $I_E$ and $I_I$ are external inputs to the excitatory and inhibitory populations, respectively. These weights are used in the simulation and nullclines phase plane analysis. Currently, the weights (i.e., $Wee, Wei, Wie, Wii$ ) must be estimated due to the lack of clear computational datasets for specific neuron combinations. The function $S$ is a sigmoidal function that influences the input into a firing rate. Once again, the reader is directed to the appendix for more detail but the sigmoid function is repeated here for clarity:

$$\mathrm{S(x)} = \frac{1}{1+\mathrm{e}^{-\alpha(\mathrm{x}-\theta)}} \tag{13}$$

Because the differential equations above are not intuitive, **Fig. 18** makes the integration of the Wilson-Cowan model easier to understand.

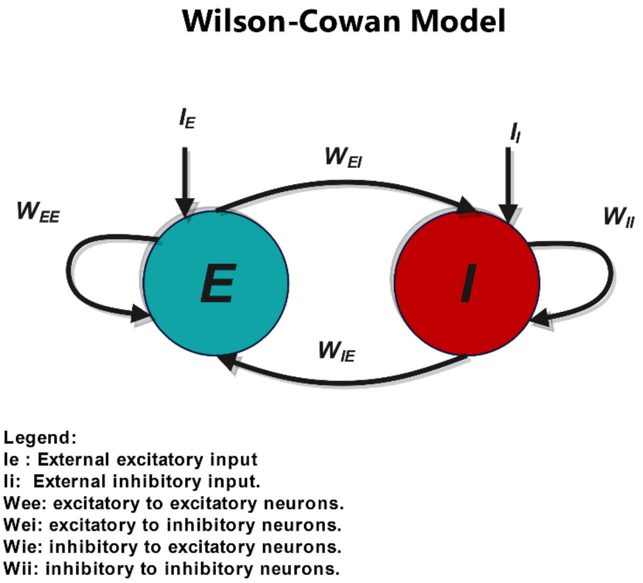


**Fig. 18.** Graphic showing the integration pattern of the Wilson-Cowan model.

The diagram's main goal is to depict the nullclines for both excitatory (E) and inhibitory (I) neurons, outlining the conditions that keep a neuron's activity constant over time.

#### 3.1.7.2 Phase Plane Analysis.

The parameters crucially shape neural network dynamics. Synaptic weights determine neuron influence, and external inputs can drive the network into various states. Understanding these parameters is key to interpreting the Wilson-Cowan model and the represented neural networks.

The Nengo simulation engine was chosen to model two neuron ensembles, FB1G and FB4N, within the fruit fly's FB. These neurons were identified as computationally significant through literature review, pathfinding techniques, and advanced modeling. They form a major part of the pathway connecting the FB to the Lateral Horn, an important neuropil in arousal(Bates et al., 2020; Huoviala et al., 2018). The simulation produced spiking neurons with stable firing rates over time, dynamically representing neural activity in the fruit fly's FB. Further analysis using 2D phase plane analysis revealed at least one stable point for each neuron type, approximately 0.61 for FB4N and 0.6 for FB1G. This suggests the presence of stable coupled oscillators within the network. This key finding allows for future comparisons with in-vivo neuron recordings in the fruit fly CX, enhancing our understanding of simulation parameters that accurately reflect individual neuron biophysics, contributing to computational neuroscience.

**Fig. 19** shows the resulting phase plane diagram indicating two nullclines following an expected pattern, with at least one intersecting point at roughly 0.7 and 0.6 for FB1G and FB4N respectively. These intersection points, also known as fixed points, can be either stable or unstable, depending on the local behavior of the system. In this case, calculations reveal one stable point, as confirmed by examining the flow directions of all possible (X, Y) values within the grid.

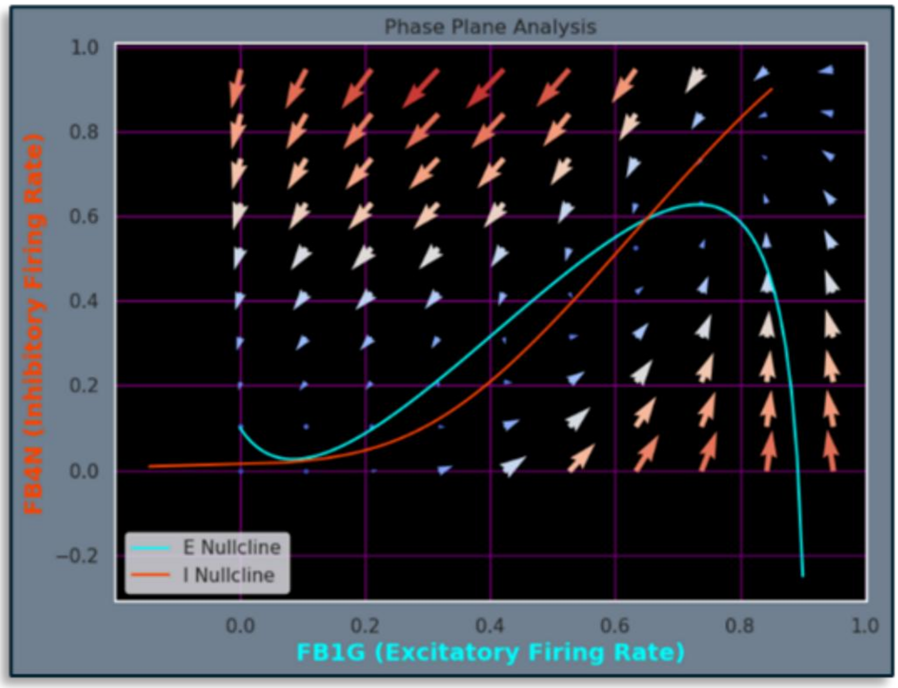


**Fig. 19.** The resulting phase plane model from the simulated results above. X and Y axis represent abstract frequencies produced by the simulated neurons. The two nullclines, FB1G and FB4N respectively, converge at the stable point. Arrows show the flow of any signal that is not located on the two nullcline.

This result demonstrates a failure to prove the null hypothesis and that it is not impossible for the two NOIs to form an oscillatory point within the CX of the fruit fly. A key next step would be to compare these results to actual recordings of the CX and Fan-shaped body. Doing so would clearly be relevant to important questions such the neuromechanistic explanation of cognitive functions within the CX and their relation to other brain theories such functions to Bayesian brain model.

### 3.1.8 Statistical Analysis

#### 3.1.8.1 Neurotransmitter Breakdown of Neurons Innervating the Fanshaped Body (FB)

The initial analysis focuses on the distribution of neurotransmitters among neurons that innervate the Fanshaped Body (FB). A pie chart representation (Figure **Fig. 20**) was constructed to visualize the proportion of different neurotransmitters. The most prominent neurotransmitter is glutamate, which constitutes approximately 88% of the innervating neurons.

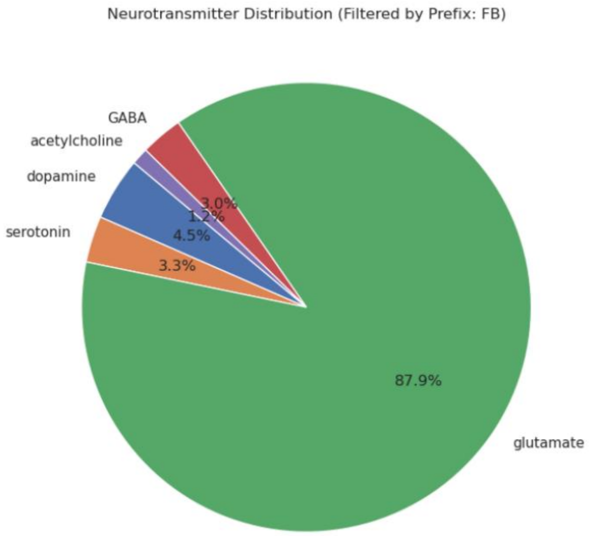


**Fig. 20.** Neurotransmitter Breakdown of Neurons Innervating the FB which shows a heavy predominance of glutamatergic neurons innervating the FB.

The dominance of glutamate in the FB is a significant finding for several reasons. Glutamate is commonly known as an excitatory neurotransmitter, but in the context of the FB, it may play a unique role. The results section will delve deeper into this hypothesis, proposing that these glutamatergic neurons could function as inhibitory elements crucial for maintaining stable points within the neural circuitry (see Interpretation of Results). This proposition aligns with the observed data and sets the stage for further exploration in subsequent sections.

### 3.1.8.2 Z-Score Heatmap for Acetylcholine to Glutamate Neuron Pairs

The second analysis involves a Z-score heatmap that depicts the innervation patterns between neurons using acetylcholine as the presynaptic neurotransmitter and glutamate as the postsynaptic neurotransmitter. This heatmap (Figure 2) highlights the neuron pairs that exhibit significant innervation, enabling us to identify key points of interaction within the neural network.

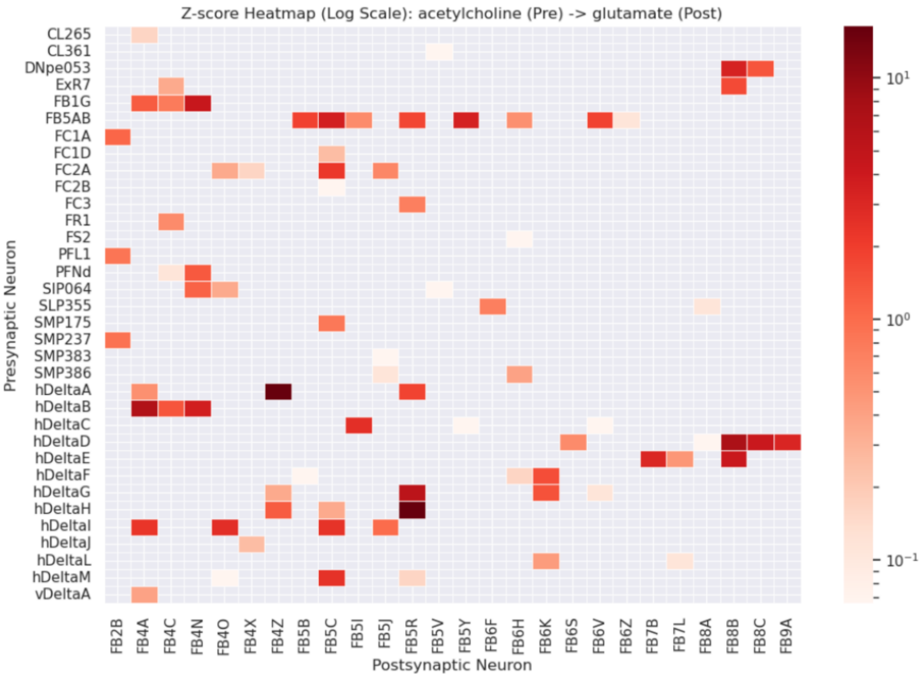


**Fig. 21.** Z-Score Heatmap for Acetylcholine to Glutamate Neuron Pairs with Pre and postsynaptic neurons along Y and X axis respectively. The scale used is logarithmic to allow easier identification of significant neuron pairs.

Notably, the heatmap reveals that FB1G strongly innervates with FB4A, FB4C, and FB4N. This significant innervation suggests that FB1G plays a pivotal role in the neural dynamics of the Fanshaped Body (FB). The concentration of interactions at FB1G aligns with previous qualitative observations of Z-score pathways originating from the lateral horn (LH). Furthermore, the heatmap uncovers additional neuron pairs with significant innervation patterns that warrant further investigation. These pairs exhibit stable points that could be critical for understanding the overall neural circuitry. The prominence of FB1G, as initially identified through qualitative inspection, is now quantitatively validated, confirming its importance while also presenting new avenues for exploration within the FB neural network.

### 3.1.8.3 P-Values of Significant Neuron Pairs

The final analysis presents a table of p-values generated from the Z-score calculations. These values indicate the statistical significance of the neuron pairs, with a focus on pairs that have p-values less than 0.05. The table (Table 1) below lists the significant neuron pairs, highlighting their p-values.

**Table 1.** P-Values of Significant Neuron Pairs

| Postsynaptic Neuron | Presynaptic Neuron | P-Value |
|---|---|---|
| hDeltaA | FB4Z | $2.836 \times 10^{-60}$ |
| hDeltaH | FB5R | $6.135 \times 10^{-60}$ |
| hDeltaD | FB8B | $7.862 \times 10^{-13}$ |
| hDeltaB | FB4A | $5.658 \times 10^{-11}$ |
| hDeltaG | FB5R | $4.464 \times 10^{-8}$ |
| FB1G | FB4N | $9.106 \times 10^{-6}$ |
| hDeltaE | FB8B | $2.144 \times 10^{-5}$ |
| hDeltaD | FB8C | $2.144 \times 10^{-5}$ |
| hDeltaB | FB4N | $2.284 \times 10^{-4}$ |
| FB5AB | FB5C | $3.290 \times 10^{-4}$ |
| FB5AB | FB5Y | $5.599 \times 10^{-4}$ |
| DNpe053 | FB8B | $7.899 \times 10^{-4}$ |
| hDeltaD | FB9A | $1.800 \times 10^{-3}$ |
| hDeltaE | FB7B | $2.110 \times 10^{-3}$ |
| hDeltaI | FB40 | $8.019 \times 10^{-3}$ |
| hDeltaC | FB5I | $9.207 \times 10^{-3}$ |
| hDeltaM | FB5C | $1.377 \times 10^{-2}$ |
| hDeltal | FB5C | $1.568 \times 10^{-2}$ |
| hDeltal | FB4A | $2.022 \times 10^{-2}$ |
| FC2A | FB5C | $2.586 \times 10^{-2}$ |

This table underscores the connection between FB1G and FB4N, which has a significant p-value of 9.106e-06, indicating a strong interaction. Additionally, the table reveals other significant pathways that deserve attention. These pathways suggest that while clearly significant, the FB1G-FB4N pair discussed above is not the only stable point within the FB. The variety of neuron pairs with significant p-values highlights the complexity and importance of these interactions in maintaining neural stability.

The existence of multiple significant neuron pairs underscores the importance of exploring various pathways within the FB. These interactions are critical for understanding the intricate dynamics of neural circuits and their role in maintaining stable points, which is essential for the overall function of the FB.

# Chapter 4 Results

## 4.0 Identification of Loosely Coupled Oscillators

The exploration of phase plane analysis within constraints of previous assumptions was achieved In Silico, and as seen in **Fig. 19** the resulting phase plane diagram indicating two nullclines following an expected pattern, with at least one intersecting point at roughly 0.7 and 0.6 for FB1G and FB4N respectively.

## 4.1 Interpretation of Results

Here we will review the objectives and goals stated at the beginning of the thesis and both discuss and interpret how the research and results employed within the thesis have been achieved. They are repeated here for simplicity:

1. Employ a novel computational framework to help locate (i.e. Pathfinding) and test candidate neural circuits for SEEK.
2. Understand the significance of affects, such as SEEK, in relation to the foundations of cognition, leveraging Drosophila's CNS and well-established research methodologies to investigate the neurophysiological mechanisms underlying SEEK behavior.
3. Demonstrate how Spiking Neural Network computational models support the investigation of SEEK and affective neuroscience.
4. Determine how SEEK's relation to Wilson-Cowan like motif and behavior can be applied to the Free Energy Principle (FEP), and Bayesian Inference.

In this study, we explored the seeking (SEEK) effect by identifying stable oscillatory points within pairs of neurons (NOIs) located in the fan-shaped body. This structure consists of one excitatory neuron and one inhibitory neuron. As posed by Objective 1, I created a computational framework, which employs a novel pathfinding mechanism combined with Z-score analysis. Using this framework I simulated a Wilson-Cowan model to identify these stable points in an in-silico environment. This finding is significant because it confirms the expected dynamic interactions between specific NOIs (e.g., FB1G and FB4N) within the fan-shaped body, contributing to our understanding of neural oscillations and stability in neural circuits as part of the overall Fanshaped Body internal neuronal architecture. Furthermore, this framework is relatively simple and efficient, allowing for easy reproduction of the process for other neurons in future studies.

Objective 2 focused on understanding the significance of SEEK behavior in relation to the foundations of cognition. While this study is not final proof on this matter, it provides an opportunity to investigate further the possible neurophysiological mechanisms underlying SEEK behavior and its broader role within the context of cognition.

This can be achieved by comparing the simulated stable points found as a benchmark against patch clamp recordings from live neurons in the fruit fly's fan-shaped body. By assessing whether these simulated stable points accurately represent the behavior of actual neural circuits during in vivo activity, we can bridge the gap between computational modeling and experimental evidence at the level of single neurons. This approach would enhance our understanding of the role of purported SEEK-related neurons and their underlying role in cognition.

Objective 3 was achieved using Spiking Neural Network computational models to support the investigation of SEEK and affective neuroscience. In this framework, I focused on the Wilson-Cowan motif as a potential mechanism underlying the dynamic interactions between excitatory and inhibitory neurons in the fan-shaped body. However, this simulation provides only preliminary insights into how this specific motif may contribute to SEEK. It is important to note that other brain motifs can also give rise to different oscillatory behavior, and as discussed in the Appendix section on Wilson-Cowan, studying the relationship between structural and functional connectivity is essential to understand these emergent correlation/synchronization patterns(Nazemi & Jamali, 2019). To expand on my findings, it will be possible to study other motifs within the fan-shaped body using similar computational models and compare these results with other various brain motifs and their corresponding behavior.

The thesis partially addresses Objective 4 by providing evidence for Wilson-Cowan motifs acting as control mechanisms within the FEP framework. These motifs are identified in central brain areas like the CX, raising questions about their role in arousal regulation and SEEK behavior. The FEP hypothesis suggests that biological systems minimize free energy to maintain homeostasis(Buckley et al., 2017; Friston et al., 2020), which applies to how the brain regulates emotions and behaviors. The thesis demonstrates that these motifs could serve as control mechanisms, fitting within the FEP framework. This supports the idea that biological systems minimize prediction errors to maintain stability. Additionally, this research connects to Bayesian Inference by suggesting that stable points act as posterior distributions in neural Bayesian algorithms. These points update beliefs iteratively based on sensory evidence and action costs, aligning with Bayesian principles of minimizing costs while enhancing decision accuracy. Thus, the findings suggest that Wilson-Cowan motifs could enhance Bayesian processing in neural systems, offering insights into how the brain optimizes information processing and decision-making.

## 4.2 Comparison with Existing Literature

While it is not possible to make counter arguments to every theory that tries to explain cognition or other research assertions employed by this thesis, the following sections highlight some key areas of research comparable to the goals of this thesis and how they differ from the positions taken throughout the thesis.

### 4.2.1 Orthologs and Functional Divergence

The thesis posits that the source of cognition in Drosophila is more likely found in the CX because it shares greater similarities with the mammalian central mid-brain and associated regions (i.e. ventrolateral preoptic (VLPO) and median preoptic (MnPO) nuclei, the ventral Periaqueductal Gray (vPAG), sublaterodorsal region (SLD)) rather than in higher brain areas such as the striatum in mammals and the external and internal globus pallidus (GPe, GPi). This perspective diverges from the established views presented by Strausfeld and other researchers who highlight his point of view.

### *Strausfeld's Position.*

Strausfeld's research highlights the evolutionary conservation of brain structures across species, particularly focusing on the striatum and its homologs in Drosophila, which play significant roles in cognitive functions. The deep homology between the arthropod CX (including the Fanshaped Body and Ellipsoid Body) and vertebrate basal ganglia (striatum and external and internal globus pallidus) suggests that these structures are integral to processing complex behaviors and cognitive tasks, underscoring their importance in both invertebrates and mammals(Strausfeld & Hirth, 2013). Furthermore, studies indicate that subcortical brain structures, including the striatum, are involved in regulating emotional and cognitive functions, with evidence of similar neural circuits across species(Jaak Panksepp, 2011a; Panksepp, 2016a). This cross-species analysis not only elucidates the functional parallels in brain architecture but also emphasizes the evolutionary significance of these structures in facilitating adaptive behaviors and cognitive processing(Wolff & Strausfeld, 2015).

### *Thesis Perspective*

Contrary to Strausfeld's view, the thesis highlights the role of the PAG and VLOP as comparable with the CX as the source of cognition in Drosophila. This assertion is grounded in a detailed analysis of neuroanatomical pathway analysis, supported by theoretical frameworks such as Realism, Reductionistic NCCs, and Affective Neuroscience. It is the position of this thesis that such evidence more strongly supports the comparison of CX and mid-brain regions near the PAG and VLOP, but at the same time aligns with Strausfeld in that the cortex is not a suitable homologue.

The concept of orthologs, genes that diverged due to speciation, is critical for understanding evolutionary biology and comparative genomics. Evidence suggests that orthologs are generally conserved in function across various animal taxa, particularly since the Cambrian explosion, which marked a significant diversification of life forms. This conservation is supported by studies indicating that orthologs tend to exhibit functional similarities that are statistically significant compared to paralogs, which arise from gene duplication events (Altenhoff & Dessimoz, 2012; Altenhoff et al., 2012; Rogozin, 2014). For instance, Altenhoff et al. demonstrated that orthologs are weakly but significantly more similar in function than paralogs, reinforcing the idea that orthologs maintain their functional roles over evolutionary time (None et al., 2016).

However, while many orthologs retain similar functions, there are notable exceptions where functional divergence occurs. Nehrt et al. highlighted that paralogs can sometimes serve as better predictors of function than orthologs, particularly in cases where gene duplication has led to the evolution of new functions(Nehrt et al., 2011). This suggests that while orthologs are generally reliable indicators of functional conservation, the evolutionary pressures and contexts can lead to significant functional divergence. Escorcia-Rodríguez et al. further supported this notion by showing that non-synonymous to synonymous substitution ratios indicate that orthologs tend to maintain their functions, while paralogs are often a source of functional novelty(Escorcia-Rodríguez et al., 2022). This divergence is crucial for understanding how species adapt to their environments, as it allows for the exploration of new functional roles that can arise from gene duplication events.

Moreover, the evolutionary history of orthologs can be traced back to the Cambrian period, where the emergence of complex multicellular organisms led to the establishment of diverse gene families(Erwin et al., 2011). The study of gene retention and sequence divergence across various taxa, such as vertebrates and arthropods, has provided insights into the evolutionary dynamics of orthologs and their functional roles(Waterhouse, Zdobnov, & Kriventseva, 2010; Waterhouse, Zdobnov, Tegenfeldt, et al., 2010). This historical perspective underscores the importance of orthologs in tracing evolutionary relationships and understanding the functional implications of genetic conservation and divergence.

In conclusion, while Strausfeld's perspective on orthologs and their functional divergence provides significant insights into evolutionary biology, this thesis posits that the comparative analysis of neuroanatomical pathways in Drosophila, particularly between the CX and mid-brain regions such as the PAG and VLOP, offers a more nuanced understanding of cognitive processes. By tracing the evolutionary history of orthologs from the Cambrian period and considering the instances of functional divergence, this study underscores the importance of examining both conserved and divergent functions to fully appreciate the complexity of gene evolution and its implications for cognitive neuroscience.

### 4.2.2 Cognitive Architecture Theory

Cognitive Architecture theories provide frameworks like Global Workspace Theory (GWT) for understanding the processes and structures of the human mind, often integrating principles from AI, psychology, and neuroscience.

*Community Position.*

Cognitive Architecture theories, particularly the Global Workspace Theory (GWT), present compelling arguments for understanding cognitive processes and consciousness(Baars & Franklin, 2009). One of the primary arguments in favor of GWT is its ability to explain the integration of information across various cognitive functions. GWT posits that consciousness arises from the broadcasting of information throughout the brain, allowing for the integration of disparate cognitive processes into a coherent experience. This integration is essential for higher-order cognitive functions such as decision-making and problem-solving, which require the synthesis of information from multiple sources(Baars & Franklin, 2009; Laird, 2012).

Moreover, GWT aligns with empirical findings from neuroscience that demonstrate the brain's networked nature, where different regions communicate and share information. For instance, studies have shown that event-related potentials (ERPs) provide direct evidence linking cognitive events to brain electrical activity, supporting the idea that conscious awareness is associated with widespread neural activation (Garrido et al., 2007; Penny et al., 2002). This neural connectivity is crucial for the functioning of cognitive architectures, as it allows for the dynamic interaction of specialized networks that can adapt to novel problems(Baars & Franklin, 2009).

Another significant argument in favor of GWT is its compatibility with computational models of cognition. The theory provides a framework for developing cognitive architectures that can simulate human-like reasoning and learning processes. For example, the Soar cognitive architecture, inspired by GWT, emphasizes the importance of structured yet flexible systems that can adapt to various tasks and environments (Laird, 2012; Sun, 2007). This adaptability is essential for creating artificial intelligence systems that can operate effectively in complex and changing environments, mirroring human cognitive flexibility.

Furthermore, GWT has implications for understanding consciousness itself. Integrated Information Theory (IIT), which posits that consciousness corresponds to the capacity of a system to integrate information, complements GWT by providing a mathematical framework to quantify this integration(Barrett & Seth, 2011; Oizumi, Amari, et al., 2016; Tononi, 2008). The synergy between GWT and IIT enhances our understanding of how conscious experiences emerge from neural processes, reinforcing the argument that cognitive architectures must account for both the structural and functional aspects of cognition.

In summary, the primary arguments in favor of Cognitive Architecture theories like GWT include their ability to explain the integration of information across cognitive functions, their alignment with empirical neuroscience findings, their compatibility with computational models, and their implications for understanding consciousness. These aspects collectively underscore the significance of cognitive architectures in advancing our understanding of human cognition and informing the development of artificial intelligence systems.

### *Thesis Perspective*

Global Workspace Theory (GWT) has garnered significant attention in the discourse surrounding consciousness and artificial general intelligence (AGI). Some critics argue that GWT, while providing a functionalist perspective on cognitive processes, fails to delve into the underlying mechanisms that could facilitate true cognition. This critique is rooted in the broader philosophical debates regarding the nature of consciousness and its implications for understanding cognitive architectures.

Block's assertion that "perceptual consciousness overflows cognitive access" highlights a critical distinction between the phenomenological aspects of consciousness and the cognitive processes that GWT attempts to model(Block, 2011). This overflow suggests that there are dimensions of consciousness that GWT does not adequately capture, particularly those related to subjective experience and qualitative states. The challenge lies in reconciling these subjective experiences with the computational frameworks that GWT employs, which often reduce consciousness to mere information processing(Pockett, 2014). Such reductionism is criticized for neglecting the rich qualitative aspects of conscious experience, which are essential for a comprehensive understanding of AGI(Marcus, 2018; Schurger & Graziano, 2022).

Polak and Marvan argue that contemporary consciousness research has moved beyond the philosophical dilemmas that once hindered empirical studies, suggesting that a more integrated approach could yield insights into the neural correlates of consciousness(Polák & Marvan, 2018). This perspective aligns with the critiques of GWT, which often emphasize the need for a deeper exploration of the neural mechanisms that underpin conscious experience rather than merely simulating cognitive processes.

In summary, while GWT offers a framework for understanding cognitive processes, the thesis agrees with the many criticisms of its inability to address the deeper mechanisms of consciousness that are essential for developing true AGI. The ongoing debates surrounding the nature of consciousness, as articulated by Block, Marcus and others, highlight the necessity for a more integrative approach that considers both the phenomenological and neural aspects of consciousness.

### 4.2.3 Integrated Information Theory (IIT)

Tononi's Integrated Information Theory (IIT) posits that consciousness corresponds to the capacity of a system to integrate information. This theory asserts that the degree of consciousness is quantitatively linked to the amount of integrated information $\phi$ produced by a network of interconnected elements, such as neurons (Tononi, 2008; Oizumi et al., 2016).

#### *Tononi's Position*

Tononi's Integrated Information Theory (IIT) presents a compelling framework for understanding consciousness as fundamentally linked to the capacity of a system to integrate information. According to IIT, the degree of consciousness is quantitatively associated with the amount of integrated information, denoted as \phi, produced by a network of interconnected elements such as neurons. This theory posits that consciousness is not merely a byproduct of neural activity; rather, it is intrinsically tied to the specific informational relationships within the system, which ultimately shape the quality of conscious experience (Oizumi, Amari, et al., 2016; Oizumi, Tsuchiya, et al., 2016; Tononi, 2008).

Tononi emphasizes that the integrated information generated by a complex of elements is crucial for the emergence of consciousness. Specifically, he argues that the quantity of consciousness corresponds to the amount of integrated information generated, while the quality of experience is determined by the set of informational relationships among the elements in the system(Tononi, 2008). This perspective suggests that consciousness arises from the complex interactions and dependencies among neural elements, rather than from the activity of individual neurons in isolation(Oizumi, Amari, et al., 2016; Oizumi, Tsuchiya, et al., 2016). Oizumi et al. further support this notion by providing a mathematical framework for quantifying integrated information, reinforcing the idea that the capacity to integrate information is a prerequisite for consciousness(Oizumi, Amari, et al., 2016; Oizumi, Tsuchiya, et al., 2016).

Moreover, IIT challenges traditional views of neural networks by asserting that feedforward systems, which lack recurrent connections, cannot give rise to qualia, or subjective experiences. This assertion highlights the importance of feedback loops and interconnectedness in facilitating the richness of conscious experience (Oizumi, Amari, et al., 2016; Oizumi, Tsuchiya, et al., 2016; Tononi, 2008). Oizumi et al. also note that the quality of consciousness is influenced by the specific patterns of connectivity and interaction within the neural network, underscoring the significance of these relationships in shaping conscious experience(Oizumi, Amari, et al., 2016; Oizumi, Tsuchiya, et al., 2016).

In summary, Tononi's Integrated Information Theory posits that consciousness is fundamentally linked to the integration of information within a network of interconnected elements. The degree of consciousness is quantitatively related to the amount of integrated information produced, while the quality of conscious experience is determined by the specific relationships among the elements in the system. This framework not only offers a novel perspective on the nature of consciousness but also emphasizes the critical role of information integration in the emergence of conscious experience.

### *Thesis Perspective*

Integrated Information Theory (IIT) has garnered significant attention in the field of consciousness studies. However, it faces substantial criticisms that challenge its explanatory power. One of the primary critiques is that IIT does not adequately explain why an increase in integrated information correlates with cognitive processes. Critics argue that while IIT posits that consciousness arises from the integration of information within a system, it fails to clarify the mechanisms through which this integration translates into cognitive functions(Cerullo, 2015; Oizumi et al., 2014). This gap in explanation raises questions about the theory's robustness, particularly when compared to alternative frameworks such as the Free Energy Principle (FEP) and Neural Correlates of Consciousness (NCC), which offer more comprehensive models for understanding cognition and consciousness (Friston & Penny, 2011; Parr et al., 2022).

Moreover, IIT is often positioned in opposition to computational functionalism, which emphasizes the role of computational processes in cognitive functions. Critics highlight that IIT's framework does not align with the principles of Bayesian inference, which are essential for explaining how cognitive systems update their beliefs based on new sensory information(Bogacz, 2017; Sokoloski, 2017). This lack of a Bayesian foundation is particularly problematic, as it limits IIT's ability to account for dynamic cognitive processes that require real-time updates and adaptations to changing environmental stimuli(Friston & Penny, 2011). The absence of a robust mechanism for action based on updated sensory information further underscores the limitations of IIT in providing a comprehensive account of cognitive phenomena.

Additionally, IIT is vulnerable to arguments concerning "fading" or "dancing" qualia, which suggest that the subjective experience of consciousness can vary significantly without a corresponding change in the integrated information of a system(Mørch, 2018). This criticism points to a fundamental issue within IIT: the theory's reliance on quantifying integrated information (Φ) does not necessarily correlate with the richness or stability of conscious experiences. As a result, critics argue that IIT's mathematical approach may overlook the qualitative aspects of consciousness that are crucial for understanding cognitive experiences(Oizumi, Tsuchiya, et al., 2016).

In summary, while Integrated Information Theory presents an intriguing perspective on consciousness, its explanatory power is significantly challenged by its inability to connect integrated information with cognitive processes, its divergence from computational functionalism, and its vulnerability to critiques regarding the nature of qualia. Alternative theories like the Free Energy Principle and Neural Correlates of Consciousness provide frameworks that may better account for the complexities of cognition and consciousness(Friston & Penny, 2011; Parr et al., 2022).

### 4.2.4 The Hard Problem of Consciousness

The Hard Problem of Consciousness as proposed by Chalmers is primarily a form of contemporary Dualism and posits that while physical processes can explain behavior and cognitive functions (the "easy problems"), they do not account for the qualitative aspects of experience, or qualia.

#### *Chalmer’s Position*

David Chalmers is a prominent figure in the philosophy of mind, particularly known for his articulation of the "hard problem of consciousness." This problem addresses the challenge of explaining how subjective experiences, or qualia, emerge from physical processes in the brain. Chalmers posits that while mental states are indeed natural phenomena arising from physical systems, they are also dualistic in nature, suggesting a form of "naturalistic dualism" or "dualistic naturalism"(Chalmers, 2017). This perspective asserts that mental states cannot be fully reduced to physical states, highlighting a significant ontological distinction between the two.

Central to Chalmers' argument is the notion of an "explanatory gap" that exists between the objective workings of the brain and the subjective nature of conscious experience. He argues that even with a comprehensive understanding of the brain's physical processes, this knowledge does not suffice to explain why certain physical states are accompanied by conscious experiences(Chalmers, 1998). This gap underscores the limitations of a purely physicalist approach to consciousness, suggesting that additional explanatory frameworks may be necessary to bridge the divide between the physical and the phenomenal.

Chalmers emphasizes the significance of phenomenal consciousness, which refers to the qualitative aspects of experiences that are intrinsic to the hard problem. He contends that understanding these subjective qualities is crucial for a complete account of consciousness(Chalmers, 2010). The distinction between phenomenal consciousness and access consciousness (the latter being the cognitive processes that allow us to report on our experiences) further illustrates the complexity of the issue at hand. Chalmers' work thus invites a reevaluation of how both researchers and philosophers conceptualize the relationship between mind and body, advocating for a dualistic approach that acknowledges the unique characteristics of conscious experience while still grounding them in a naturalistic framework(Chalmers, 2003).

In summary, Chalmers' contributions to the philosophy of consciousness challenge the reductionist view and highlight the intricate relationship between physical processes and subjective experiences. His advocacy for naturalistic dualism and the recognition of the explanatory gap serve as pivotal points in ongoing discussions about the nature of consciousness and the philosophical implications of our understanding of the mind(Chalmers, 2019).

### *Thesis Perspective*

Research has shown that the empirical study of consciousness is thriving, with many scholars advocating for a more integrated approach that aligns with physicalist theories. For instance, Polak and Marvan highlight that the modern brain-mind identity theory, which emerged as a response to the philosophical challenges posed by consciousness studies, has gained traction, suggesting that the obstacles Chalmers identifies may be diminishing(Polák & Marvan, 2018). This perspective is echoed by Lahav and Neemeh, who critique Chalmers' naturalistic dualism, arguing that it fails to clarify the interaction between the phenomenal and physical realms, instead perpetuating the notion of a separate existence for consciousness(Lahav & Neemeh, 2022).

Moreover, the interdisciplinary nature of consciousness research has led to significant progress in understanding its mechanisms. Blanquet notes that while challenges remain in reconciling subjective experiences with objective measures, the ongoing investigations into the neurophysiology of consciousness are yielding promising insights (Blanquet, 2011). This sentiment is reinforced by the work of Kent, who discusses how collaborative efforts between neuroscience and physics are beginning to bridge the explanatory gaps in consciousness theories, suggesting that a unified understanding is within reach(Hales & Ericson, 2022; Kent, 2021).

Chalmers' insistence on the inadequacy of materialist explanations has been met with skepticism. Dennett argues that what Chalmers labels the "hard problem" may, in fact, be a mischaracterization of the more tractable "easy problems" of consciousness, which can be addressed through empirical research without invoking dualistic frameworks(Daniel C. Dennett, 2018). This critique aligns with the views of other researchers who advocate for a more nuanced understanding of consciousness that does not rely on the dichotomy of physical versus phenomenal(Block, 2007; Schurger & Graziano, 2022).

In conclusion, Chalmers' dualistic approach has contributed to the discourse on consciousness. However, the research highlighted in this thesis along with the growing body of empirical evidence and theoretical advancements in neuroscience and psychology suggests that a comprehensive understanding of consciousness may be achievable through physicalist frameworks.

### 4.2.5 Orchestrated Objective Reduction (OOR)

OOR theories of consciousness posit that the collapse of quantum states somehow manifest cognition within the brain. These theories remain highly speculative and are characterized by a lack of consensus and a multitude of competing hypotheses.

*Hameroff and Penrose Position*

The theory of consciousness proposed by Stuart Hameroff and Roger Penrose, known as Orchestrated Objective Reduction (Orch OR), posits that consciousness arises from quantum processes occurring within neuronal microtubules. This theory diverges from traditional views that regard consciousness as a mere product of neural connections and interactions. Instead, Orch OR suggests that discrete moments of consciousness are linked to quantum computations orchestrated by the microtubules, which are structural components of the cytoskeleton in neurons. These quantum processes are theorized to correlate with neuronal activity and influence synaptic and membrane functions, thereby playing a crucial role in the emergence of conscious experience(Hameroff, 2012, 2020; Hameroff & Penrose, 2014).

Hameroff and Penrose argue that the Orch OR model provides a framework for understanding how consciousness can be both a biological and a quantum phenomenon. They propose that the continuous evolution of quantum states within microtubules culminates in an objective reduction, a process influenced by the specific Diósi-Penrose scheme of objective reduction (OR)(Hameroff & Penrose, 2007, 2014). This perspective challenges the classical view of consciousness as purely computational, suggesting instead that consciousness involves non-computable elements that arise from quantum mechanics(Hameroff, 2020; Hameroff, 2007). The implications of this theory extend to discussions about free will and determinism, as it suggests that conscious experiences are not merely epiphenomenal but are rooted in fundamental quantum processes(Hameroff, 2012, 2020).

Critics of Orch OR often highlight the challenges of empirical validation and the philosophical implications of linking consciousness to quantum mechanics, but proponents of Orch OR maintain that it is a falsifiable theory, which is a significant advantage in the scientific discourse surrounding consciousness(Hameroff, 2012, 2020). The theory's reliance on quantum mechanics also invites interdisciplinary collaboration between neuroscience and physics, potentially leading to new insights into the nature of consciousness (Hales & Ericson, 2022).

In summary, Orch OR presents a provocative and controversial framework for understanding consciousness, suggesting that it is fundamentally linked to quantum processes within the brain's microtubules. This theory not only challenges conventional views of consciousness but also opens new avenues for research that integrate insights from both neuroscience and quantum physics.

*Thesis Perspective*

The theory of orchestrated objective reduction (Orch OR) proposed by Hameroff and Penrose has garnered significant attention in the field of consciousness studies. However, it faces substantial criticism, particularly regarding its reliance on quantum mechanics as a foundational principle for understanding consciousness. Critics argue that Orch OR lacks empirical support and is overly complex compared to alternative models grounded in biological and neurophysiological evidence. This response synthesizes the critiques of Orch OR and presents a simpler model based on evidence from biology, neurophysiology, and Bayesian inference.

Critics of Orch OR highlight the absence of direct empirical evidence linking quantum processes in microtubules to conscious experience. For instance, Oizumi et al. discuss the limitations of Integrated Information Theory (IIT), which, like Orch OR, attempts to explain consciousness through complex theoretical frameworks but often lacks direct biological validation(Oizumi et al., 2014). Furthermore, Hameroff's assertions regarding quantum computations in microtubules have been met with skepticism, particularly because the cerebellum, a brain region rich in microtubules, is known not to contribute to conscious experience(Oizumi et al., 2014). This suggests that the mechanisms proposed by Orch OR may not be necessary for consciousness, as simpler biological processes could suffice.

In contrast, models grounded in neurophysiology and Bayesian inference offer a more parsimonious explanation of consciousness. Bayesian models, which are inherently simpler and more aligned with biological processes, have been shown to effectively account for decision-making and perception in the brain. For example, Ji emphasizes the utility of Bayesian decision models in understanding neural firing patterns and their implications for cognitive processes(Ma, 2019). This approach aligns with the principles of active inference, which posits that the brain continuously updates its beliefs about the world based on sensory input and prior knowledge(Friston & Frith, 2015). Such models not only simplify the understanding of consciousness but also provide a robust framework for integrating empirical findings from neuroscience.

Moreover, the predictive coding framework, which is closely related to Bayesian inference, posits that the brain functions as a predictive machine, constantly generating and updating predictions about sensory input(Yon et al., 2019). This model has gained traction in explaining various cognitive phenomena, including perception and attention, without invoking the complexities of quantum mechanics. The predictive brain model suggests that consciousness arises from the brain's ability to minimize prediction errors, thereby providing a more biologically plausible account of conscious experience(Yon et al., 2019).

In summary, while Orch OR presents an intriguing perspective on consciousness, its reliance on quantum mechanics and lack of empirical support renders it less favorable compared to simpler, evidence-based models grounded in neurophysiology and Bayesian inference. These alternative frameworks not only align more closely with biological realities but also offer a more coherent understanding of the mechanisms underlying consciousness.

### 4.3 Implications for Behavior and Affective Cognitive Processes

The result shown here raises intriguing questions, namely, that loosely coupled oscillators form a natural construct that acts as the basis of fundamental control within the brain of Drosophila. This hypothesis is not beyond scientific reasoning. Similar ideas are seen in the field of PI Controllers used as error correction systems. For instance, PI Controllers are employed by biological systems such as homeostatic regulation of body temperature, where the error (difference between actual and desired temperature) is minimized over time. The question then is, how ubiquitous are these control mechanisms and how do they relate to cognition?

Within the theoretical space about cognition and control, one intriguing possibility is that loosely coupled oscillators offer a necessary control mechanism, and further that this mechanism offers a solution to understanding foundational cognition across species, as well as a mechanism that can explain the neuromechanical mechanism for affective systems. This is more than mere speculation. Both Almada, Damasio and Solms (Almada et al., 2013; A. Damasio, 2001; Damasio, 2003; A. R. Damasio, 2001; Parvizi & Damasio, 2001) theorize that affective systems play a foundational role in cognition, along with Fabbro and Panksepp's work(Fabbro et al., 2015) that suggests affective systems give rise to self-awareness and perception of the external world. If affective systems are essential for cognition, their presence in the CX aligns with theories locating such systems in the basal ganglia, analogous to the CX in higher organisms (Strausfeld & Hirth, 2013). Strausfeld strengthens this view by showing links between the CX and basal ganglia via an evolutionarily conserved genetic program, suggesting shared developmental and functional principles across species(Strausfeld & Hirth, 2013). While human comparisons are challenging, they're not impossible. Solms, Panksepp, and Northoff propose that the periaqueductal grey (PAG) within the human basal ganglia is a crucial hub for affective/emotional-motor integration(Alcaro et al., 2010; Panksepp, 2016b; Solms, 2021).

This study demonstrates that loosely coupled oscillators could be a mechanism in the CX to regulate previously identified basic affective behaviors. If similar motifs and circuits are conserved across species, simulations testable against experimental data could illuminate traditionally challenging subjects.

### 4.4 Implications for Bayesian Brain Theories

Given the findings here, the implication for Bayesian-based algorithms is that the stable points can be used to provide the result of $p(s \mid x_{\text{trial}})$ (see equation 2) because they act as a posterior to drive activity that is then fed back into the Bayesian Inference equation once the costs of the action have been calculated. This iterative process of updating beliefs and minimizing costs aligns with the principles of Bayesian decision-making, highlighting the potential for stable points to enhance the accuracy and efficiency of Bayesian inference in neural systems. In decision-making processes, Bayesian inference plays a pivotal role, particularly through the formulation of cost functions that quantify the consequences of various actions. Remember that the cost function as explained earlier with equation 3:

$$\mathbb{E}C(a) = \sum_s p(s \mid x_{\text{trial}})C(s,a) \tag{14}$$

where $C(s,a)$ denotes the cost associated with state $s$ and action $a$, serves as a tool for decision-makers aiming to minimize potential losses associated with their choices. This framework is essential in Bayesian decision models, which emphasize that optimal behavior is inherently Bayesian, allowing for the accommodation of suboptimal behaviors through various candidate models(Ma, 2019).

As shown by equation 29 in the appendix, the Free Energy Principle (FEP) can be mathematically expressed as:

$$F = D[Q(x) \parallel P(x \mid \tilde{o})] - \ln P(\tilde{o}) \tag{15}$$

See the appendix for details of each term. This equation highlights the goal of minimizing the difference between the predicted and actual sensory inputs, thereby reducing surprise or uncertainty. With equation 29 one can then draw a parallel between the Bayesian cost function and the FEP. The FEP equation can then be rewritten in a form that resembles the Bayesian framework using the following steps:

1. Start with an approximate posterior distribution $Q(x)$ that is easier to compute than the true posterior $P(x \mid \tilde{o})$ .
2. Minimize the free energy $F$, which involves minimizing the KL divergence term $D[Q(x) \parallel P(x \mid \tilde{o})]$.
3. The log evidence term $\ln P(\tilde{o})$ is treated as a constant because its value does not change significantly during the optimization process. This allows us to focus on the KL divergence term. In other words, this term is simply ignored.

The three steps above thus start with:

$$F = D[Q(x) \parallel P(x \mid \tilde{o})] - \ln P(\tilde{o}) \tag{16}$$

Then using equation 31 one can replace the Divergence of Q and P and expand to:

$$\mathrm{F} = \sum_x P(x) \ln \frac{P(x)}{Q(x)} - \ln P(\tilde{o}) \tag{17}$$

Focusing on the KL Divergence term one simply drops the log evidence term which thus ends up with:

$$F = \sum_x P(x) ln \frac{P(x)}{Q(x)} \tag{18}$$

This simplification highlights the importance of the KL divergence term in aligning the approximate posterior with the true posterior, which is essential for reducing uncertainty and maintaining stability in neural syastems. Further, with equation 18 in hand, it is now possible to simply replace the $P(x)$ term with $p(s \mid x_{\text{trial}})$ and reveal that in effect, all the following are roughly the equivalent:

$$\mathrm{F} \approx \mathrm{EC(a)} \approx \sum_s p(s \mid x_{\text{trial}})\mathrm{C(s,a)} \tag{19}$$

Research has shown that the self-organization of neurons during learning adheres to the mathematical principles of free energy minimization. This self-organization can be seen as the neural basis for the stable points observed in my simulations. These stable points, acting as attractors, could facilitate the brain's ability to predict and adapt to environmental changes, thereby optimizing decision-making processes. Furthermore, the Free Energy Principle has been used to explain how the brain processes perceptual information, learns about the environment, and selects actions to maintain a stable preferred state. This aligns with my hypothesis that stable points within the fan-shaped body of Drosophila contribute to the SEEK effect by providing a stable neural basis for decision-making and behavior. By minimizing free energy, these stable points help the neural system maintain homeostasis and adapt to new information, which is crucial for survival.

In summary, the integration of stable points into Bayesian inference and the Free Energy Principle provides a rich framework for the exploration and understanding of neural decision-making processes. The stable points of found here not only serve as posteriors in Bayesian algorithms but also act as attractors that minimize free energy, thereby enhancing the brain's ability to predict, learn, and adapt. This dual role underscores the significance of stable points in both theoretical and practical applications, offering new insights into the neural mechanisms underlying decision-making and behavior.

# Chapter 5 Conclusion

## 5.0 Contributions to the Field

My thesis makes significant contributions to computational affective neuroscience by advancing our understanding of dynamic neural interactions within the fan-shaped body (FSB) of Drosophila melanogaster . Through the exploration of oscillator stable points using the Wilson-Cowan model, this work provides valuable insights into neural oscillations and stability, which are crucial for understanding complex brain control mechanisms. While these findings offer supportive evidence rather than definitive conclusions, they lay a foundation for future experimental studies and theoretical explorations.

A key contribution lies in its emphasis on proto-feelings, exemplified by the identification of specific affective states such as "seek" within Drosophila . This work not only narrows the explanatory gap concerning consciousness but also proposes a natural construct for fundamental control mechanisms in the brain. These findings are particularly relevant to theories related to the Free Energy Principle, which suggests that oscillator coupling may play a role in maintaining homeostasis and minimizing prediction error.

This research has developed a novel computational framework and method for neuronal Pathfinding based on neural weighted Z-score analysis, offering a promising approach to identifying understandable pathways within the fruit fly neural systems. By applying this technique, I have identified several significant candidate neuron pairs through Pathfinding analysis, which hold substantial promise for future research endeavors.

Additionally, statistical analysis revealed that acetylcholine and GLUT neurons within the FSB of Drosophila melanogaster are relatively uncommon. This finding underscores the importance of identifying specific significant candidate neuron pairs using P-score analysis, which provides valuable insights into potential targets for further study.

By integrating these elements, this thesis not only advances our understanding of consciousness but also establishes a robust framework for future investigations into the neural basis of affective experience and behavior. The emphasis on acetylcholine and GLUT neurons, coupled with the identification of significant candidate neuron pairs through both Pathfinding and statistical analysis methods, highlights the importance of these findings in guiding subsequent research directions.

### 5.1 Limitations of the Study

Before presenting the extended discussion of methodological constraints in this section, the following bullet-point summary highlights the key limitations arising from dataset constraints, modelling assumptions, and simulation-dependent parameters.

- The α values derived from normalized Z-scores require empirical validation, as they function only as approximations until biological ground-truth data are available.
- Enforcing $\alpha \geq 1$ ensures model stability but may not reflect true neuronal gain and may require future refinement.
- Graph-based models sacrifice biological fidelity due to simplification and removal of neuron-specific connectivity details.
- Circuit diagrams are manually assembled, which limits completeness and may omit important neuropil interactions.
- Transformation weights between neuron types are estimated due to a lack of available computational datasets defining neurotransmitter-specific synaptic strengths.
- Neurotransmitter data from Flywire is incomplete relative to the Hemibrain dataset, creating uncertainty in how neurotransmitter identity influences model behaviour.
- Priors embedded in the Nengo simulation framework constrain the model and may need revision when more precise data become available.
- Reducing the network to a two-population EI motif omits finer interneuron variability that may influence oscillatory behaviour in more detailed models.

While simulations and phase plane analysis offer valuable insights, they also identify areas for further exploration and refinement, it seems clear at this point that several aspects and or assumptions used in the study warrant further investigation to enhance the robustness and applicability of these results. For instance: a deeper look at the values for α can be investigated to better quantify the strength of synaptic innervation between neurons based on biological ground truths; graph models constructed from general neuron types help with readability but do not take into account more complex network motifs with higher biological fidelity and complexity; developing more rigorous code-driven methods for circuit diagram would encompass broader neuropil innervation; developing improved transformation weights used between neurons based on their neurotransmitter types; and integrating these findings into a Bayesian framework, such as the free energy principle.

In this study, the thesis introduced a novel approach to calculating the alpha value within the FI curve transfer function, utilizing normalized Z scores derived from synaptic distributions between neurons. This method appears reasonable for alpha values greater than one. However, an intriguing aspect of our methodology is the adjustment made to ensure that the alpha value is always larger than one. This modification is necessitated by the fact that the same alpha values are employed when conducting phase plane analysis. It raises the question of whether all alpha values need to be adjusted in a symmetrical manner or adjusted via other methods. While it is conceivable that a theoretically improved version of alpha could be found, it seems more likely that further comparisons to experimental ground truths will provide significant insights on this topic. Our approach underscores the importance of empirical validation in refining our understanding of neural dynamics and improving the accuracy of our simulations.

In the process of generating graph models, a potential concern is the loss of fidelity during the simplification of data to create bidirectional graphs based on basic neuron types. While excluding edges related to the unique names of neurons does enhance the readability of the hierarchical graph layouts, it may result in the omission of pertinent information. One potential solution to this challenge could be to refine the algorithm used to handle the compactification of unique neurons down to a lower number of dimensions, thereby retaining more information. In this context, artificial intelligence (AI) could prove to be a valuable tool. By leveraging AI training algorithms, one could in the future make the simplification of neuronal topology more objective and standardized, ensuring that information is preserved while still maintaining the readability and interpretability of the graph models.

The creation of the circuit diagram in our study is not driven by code generation. Instead, it involves manual efforts to render the circuit comprehensible for readers and to incorporate necessary context within the biological hierarchy of the Drosophila brain. This practice, while necessary in the field of neuroscience, it is not sufficient(Briggman & Bock, 2012) and further work to expand the current version of the diagram will be needed. Specifically, there is a need to include more details about neurons outside the Fan-shaped Body (FB) that provide key insights into incoming signals from sensory inputs. In reality, the circuit diagram serves as a simplified roadmap, offering a general direction for conducting simulations. However, striking a balance between information density and readability is crucial. If the diagram becomes overloaded with information, its readability may be compromised and fail to offer insights. However, the thesis suggests that the right balance has been achieved. If meaningful NOI can be identified, the simplicity of the diagram does not adversely degrade the complexity of the simulation, an acceptable outcome as our simulator will still generate all possible connections based on the full set of data within the Hemibrain dataset, ensuring a comprehensive representation of neuronal dynamics.

Another point regarding the simulation is in regard to priors that constrain the model used by Nengo. The most significant of these are the transformation weights used between neurons based on their neurotransmitter types. In more precise terms, when FB1G and FB4N have their ensembles connected, the choice of neurotransmitter comes from querying the Flywire Dataset provided by the Janelia Research Campus. Although the number of neurons available and their morphological data is less robust than the Hemibrain dataset, Flywire incorporates neurotransmitter data not otherwise available. The benefit here is that it allows the code to programmatically choose a neurotransmitter and then decide on the combination of pre and post-synaptic connections and their associated transfer weights. It’s important to note that these transfer weights are used not only in the simulation but also during the calculation of the nullclines phase plane analysis. At this point in time, the weights (i.e. $W_{ee}, W_{ei}, W_{ie}, W_{ii}$) must be estimated as there are no computational datasets (to our knowledge) that makes this clear for specific neuron combinations. However, even though estimated, there is still value in the simulation. This is because the output of the simulation and its associated phase plane analysis can be compared to future studies where patch clamp recordings can provide a corrective ground truth. With repetitive simulations and correctives reiterations of interneuron weights, it is conceivable that a path toward true interneuron weights can be found. In fact, with the ability to simulate a larger number of neuron types, it is rather-straight forward to generate a significant amount of simulated data from which to promote the creation of new experiments. Over time, a back and forth between simulation and experiment should allow these transfer weights to be objectively defined.

There is also a need to explain error minimization functions hypothesized within the Free Energy Principle, that posits that biological systems, like the brain, minimize free energy - a measure of surprise or prediction error - to maintain homeostasis (Friston et al., 2021; Solms, 2019; Solms, 2021). This principle has been used to explain a wide range of biological phenomena, from perception and learning to action control and behavior.

As this study helps support the hypothesis that loosely coupled oscillators act as the type of mechanism of SEEK used by Drosophila for basic cognition, it makes sense to see if similar motifs and circuits are conserved across species. If so, testable simulations against experimental data can shed light on what has traditionally been a difficult subject to explore and test.

## 5.2 Future Experimental Validation Plan

Future experimental validation will be essential for assessing the plausibility of the computational results presented here. As outlined in Section 5.3, empirical approaches such as patch-clamp recordings, analysis of local field potentials, and targeted investigations of sleep and arousal mechanisms in Drosophila provide promising avenues for comparing model-derived predictions with biological measurements. These methods offer a path toward testing the stability patterns and oscillatory regimes identified in the FB1G–FB4N motif. Incorporating such experimental data in future work will enable iterative refinement of the modelling framework and help determine whether the proposed computational mechanisms reflect underlying neural dynamics in vivo.

## 5.3 Future Experimental Approaches

The following methods are considered as methods to further investigate the findings presented here in the thesis.

### 5.3.1 Sleep And Arousal Mechanisms

The exploration of neural oscillatory interactions (NOIs) within the fan-shaped body (FB) of Drosophila melanogaster is crucial for understanding the neural circuits that govern sleep and arousal mechanisms. Recent studies have identified various NOIs, particularly in the sixth layer of the FB, which are associated with sleep and arousal states. For instance, the work by Kottler et al. highlights a sleep/wake circuit that modulates sleep duration and sensitivity to anesthetics, indicating a significant role of the FB in these processes(Kottler et al., 2013). Additionally, the findings of Kirszenblat and Swinderen emphasize the interplay between sleep and attention, suggesting that sleep functions such as stimulus suppression and synaptic plasticity are essential for maintaining cognitive functions(Kirszenblat et al., 2018; Kirszenblat & van Swinderen, 2019). This interplay underscores the necessity of understanding how NOIs can influence behavioral states.

Moreover, the innervation of the FB from key neuropils like the superior medial protocerebrum (SMP) and lateral horn (LH) adds another layer of complexity to these interactions. The study by Swinderen and Kottler discusses the synaptic release machinery's role in sleep circuits, which may be influenced by inputs from these neuropils (van Swinderen & Kottler, 2014). This suggests that the FB's connections with the SMP and LH could be pivotal in modulating the neural circuits responsible for sleep and arousal, potentially through mechanisms involving neurotransmitter dynamics and synaptic plasticity.

In terms of methodological approaches, integrating simulation studies with patch clamp recordings is essential for validating the findings related to NOIs. The research by Yap et al. demonstrates the utility of local field potentials (LFPs) in characterizing sleep stages in Drosophila, providing a framework for comparing simulation data with empirical recordings(Yap et al., 2017). This approach can enhance our understanding of the oscillatory patterns associated with different sleep states and their underlying neural mechanisms.

The ongoing identification of new NOIs and their functional implications in sleep and arousal highlights the need for further exploration in this field. By targeting these interactions and employing advanced methodologies, researchers can unravel the intricate neural circuits that influence sleep and arousal mechanisms, ultimately contributing to a more comprehensive understanding of these critical biological processes.

### 5.3.2 Linear Control Matrix Analysis

The proposed utilization of Linear Control Matrix analysis to enhance our understanding of the neural organization within the fan-shaped body of Drosophila melanogaster is a promising approach. This method leverages Z-score analysis to quantify the connectivity and strength between neurons, thereby creating a robust strength matrix that can elucidate the complex interactions within this neural structure.

The foundational dynamics equation, expressed as:

$$\dot{x}(t) = Ax(t) + Bu(t) \tag{20}$$

This equation serves as a critical starting point for this analysis. Here, $x(t)$ represents the state vector that encapsulates the activity of various brain regions, while $A$ denotes the system matrix that characterizes the connections among neuropils. The binary control matrix $B$ indicates the basic connectivity through a matrix of 0s and 1s, and $u(t)$ is the control input vector that modulates these interactions. The integration of a new strength matrix $S$, derived from Z-score calculations, allows for a more nuanced understanding of the connectivity patterns among different neuron types, such as FB1G and FB4N, by normalizing values between 0 and 1.

The proposed method combines matrices $A, B$ and $S$ into the new dynamic equation:

$$\dot{x}(t) = Ax(t) + B \cdot S \cdot u(t) \tag{21}$$

This facilitates a comprehensive exploration of neural interactions. This formulation allows for the investigation of how varying levels of connectivity influence the overall neural dynamics and behavior of the organism. The application of Z-score analysis to derive the strength matrix is particularly advantageous, as it provides a standardized measure of connectivity that can be compared across different neuron types and conditions.

Moreover, the integration of Z-score metrics into the control matrix aligns with contemporary approaches in neuroscience that emphasize the importance of statistical measures in understanding neural networks. For instance, Sokoloski et al. discuss modeling neural codes in large populations of correlated neurons, highlighting the significance of correlation patterns in deciphering neural interactions(Sokoloski et al., 2020). This perspective supports the notion that a strength matrix informed by Z-scores can yield valuable insights into the functional architecture of the fan-shaped body.

In conclusion, the proposed Linear Control Matrix analysis, augmented by Z-score strength calculations, presents a sophisticated framework for investigating the connectivity and strength of neural interactions within the fan-shaped body of Drosophila. By integrating established findings on the role of this neural structure in sleep and sensory processing, this method not only enhances our understanding of neural dynamics but also paves the way for future research into the intricate workings of the fly brain.

#### 5.3.3 Hypergraphs and Poisson Distributions

The exploration of neural dynamics and the complexity of neuronal interactions necessitates advanced modeling techniques that extend beyond traditional frameworks such as the Wilson-Cowan model. As the identification of novel neural oscillatory interactions (NOIs) progresses, the need for sophisticated analytical tools becomes paramount. The HypergraphX package developed by Federico Battiston and the neural-mixtures framework proposed by Sacha Sokoloski are pivotal in this regard, as they facilitate the analysis of higher-order interactions within hypergraphs, which are essential for understanding complex neural networks.

The Wilson-Cowan model has been foundational in computational neuroscience, providing insights into the dynamics of neural populations through its representation of excitatory and inhibitory interactions. However, as research evolves, it becomes increasingly clear that the simplistic pairwise interactions modeled by Wilson and Cowan do not capture the intricate relationships observed in biological systems. Battiston et al. emphasize the importance of higher-order interactions in complex systems, arguing that many real-world phenomena cannot be adequately described by pairwise interactions alone(Battiston et al., 2020). This perspective is crucial for advancing our understanding of neural dynamics, as it allows for a more nuanced view of how neurons interact within larger networks.

Sokoloski et al. further contribute to this discourse by introducing mixtures of Poisson distributions to model the neural code in large populations of correlated neurons. Their work demonstrates that these statistical approaches can effectively capture the over-dispersion and complex spike-count distributions observed in cortical activity, which are often overlooked in simpler models(Sokoloski et al., 2021). The integration of such advanced statistical tools is essential for accurately modeling the behavior of neural populations, particularly in the context of oscillatory dynamics and synchronization phenomena.

Moreover, the application of hypergraph theory in neuroscience, as discussed by Battiston et al., provides a framework for understanding the multi-dimensional interactions that characterize neural networks(Battiston et al., 2021). This approach aligns with the findings of Nazemi and Jamali, who explore the influence of structural connectivity on correlation patterns and network synchronization, highlighting the critical role of network architecture in shaping neural dynamics(Nazemi & Jamali, 2019). By employing these advanced analytical tools, researchers can better elucidate the complex interplay between neurons and their oscillatory behaviors, ultimately enhancing our ability to model the dynamic processes within the brain.

In conclusion, the integration of advanced analytical frameworks such as HypergraphX and neural-mixtures is essential for progressing beyond the limitations of traditional models like Wilson-Cowan. These tools not only facilitate the exploration of higher-order interactions but also provide a more comprehensive understanding of the complex dynamics inherent in neural networks. As the field continues to evolve, leveraging these sophisticated methodologies will be crucial for unraveling the intricacies of neuronal interactions and their implications for cognitive processes.

## Appendices, Detailed Methodologies And References

A. Free Energy Principal**.**

The Free Energy Principle aims to minimize the free energy F, which balances the complexity of the model and its accuracy in predicting observed data. By minimizing free energy, an organism can maintain a good approximation of the true posterior distribution, leading to better predictions and actions. This principle extends Bayesian inference by incorporating both perception and action, allowing organisms to actively minimize their uncertainty about the world.

The free energy $F$ can be defined as an expected value with respect to distribution $Q$:

$$\mathrm{F} = \mathrm{E}_Q[\ln Q(\mathrm{x}) - \ln P(\mathrm{x}, \tilde{o})] \tag{22}$$

Here, $\mathrm{E}_Q$ denotes the expectation with respect to the variational (ensemble) distribution $Q(x)$, which is a variational distribution approximation to the true posterior distribution $P(x, \tilde{o})$, and where $\tilde{o}$ represents the observed incoming sensory data. The variational (ensemble) density refers to the distribution of possible states that a system can occupy, capturing the uncertainty associated with these states. It is a probabilistic representation that informs how likely different configurations are, given the generative model and the observed data The variable $x$ denotes hidden states and parameters where $x = (\tilde{s}, \pi, \eta)$, with $\tilde{s}$ as a sequence of hidden states until the end of all trials, $\pi$ as policies that result in action sequences, and $\eta$ represents a large set of parameters used by the generative model that are not directly observable and will not be covered by this document. For details on $\eta$ it is best to refer to Friston's paper entitled Active inference and learning. Nonetheless, this equation measures the difference between the variational distribution $Q(x)$ and the true joint distribution $P(x, \tilde{o})$. Equation 22 above can further be expressed in terms of the conditional probability $P(x, \tilde{o})$ and the marginal probability $P(\tilde{o})$. Using the definition of conditional probability, the following is true:

$$P(x, \tilde{o}) = P(x|\tilde{o})\, P(\tilde{o}) \tag{23}$$

Using the above, one can take the natural logarithm of both sides of the equation:

$$\ln\, P(x, \tilde{o}) = \ln\, [P(x \mid \tilde{o}) P(\tilde{o})] \tag{24}$$

Using the distributive property of logarithms that $\ln(\mathrm{ab}) = \ln(\mathrm{a}) + \ln(\mathrm{b})$, one can rewrite 24 above as:

$$\ln P(x, \tilde{o}) = \ln P(\, x \mid \tilde{o}\, ) + \ln P(\tilde{o}) \tag{25}$$

At this point we substitute equation 25 into the original free energy equation, $F = \mathrm{E}_Q[\ln\ Q(x) - \ln\ P(x, \tilde{o})]$, which then allows the following transformations. Note that in the third transformation below $\mathrm{E}_Q[\ln\ P(\tilde{o})]$, the distribution of $\tilde{o}$ is invariant to $Q$and therefore it is considered a constant:

$$\begin{aligned} F &= \mathrm{E}_Q[\ln\ Q(x) - \ln P(\, x \mid \tilde{o}\,) + \ln P(\tilde{o})] \\ F &= \mathrm{E}_Q[\ln\ Q(x)] - \mathrm{E}_Q[\ln\ P(x \mid \tilde{o})] - \mathrm{E}_Q[\ln\ P(\tilde{o})] \qquad (26) \\ F &= \mathrm{E}_Q[\ln Q(x)] - \mathrm{E}_Q[\ln P(\, x \mid \tilde{o}\,)] - \ln P(\tilde{o}) \end{aligned}$$

This now allows us to simplify the Equality of Q and P into the following and then further simplified using power rules:

$$F = \mathrm{E}_Q[\ln Q(x) - \ln P(\, x \mid \tilde{o}\,)] - \ln P(\tilde{o}) \qquad (27)$$

$$F\ = \mathrm{E}_Q\left[\ln \frac{Q(x)}{P(\, x|\tilde{o}\,)}\right] - \ln P(\tilde{o}) \qquad (28)$$

And at this point, it is revealed that the expected value E with respect to Q is mathematically equivalent to Kullback-Leibler (KL) Divergence (see equation supplementary material below). Replacing the $\mathrm{E}_Q$ term, one can represent the Free Energy as:

$$F =\ D[Q(x) \parallel P(\, x \mid \tilde{o}\,)] - \ln P(\tilde{o}) \qquad (29)$$

In simpler terms, the equation 29 can be understood as follows. The term $-\ln P(\tilde{o})$ represents the negative logarithm of the probability of the observed sensory information. This can be thought of as a measure of how surprising or unexpected the sensory input is. The second term $D[Q(x) \parallel P(\, x \mid \tilde{o}\,)]$ is the Kullback-Leibler (KL) divergence, which measures the relative entropy or 'surprise' when comparing the expected distribution $Q(x)$ to the actual distribution $P(\, x \mid \tilde{o}\,)$. Together, these terms quantify the overall surprise or uncertainty an organism experiences when comparing its expected sensory input to the actual observed input.

## B. Kullback-Leibler (KL) Divergence.

KL-Divergence is a measure of how one probability distribution diverges from a second, reference probability distribution. It is a fundamental concept in information theory and statistics, often used to quantify the difference between two probability distributions. Mathematically, the KL Divergence from distribution (P) to distribution (Q) is defined as:

$$D_{KL}(P \parallel Q) = \textstyle\sum_x P(x) \log \frac{P(x)}{Q(x)} \qquad (30)$$

For continuous distributions, the KL Divergence is given by:

$$D_{KL}(P \parallel Q) = \int_{-\infty}^{\infty} p(x) \log \frac{p(x)}{q(x)} dx \tag{31}$$

Here, $P$ and $Q$ are the two probability distributions, $P(x)$ and $Q(x)$ are their respective probability density functions, and (x) represents the random variable. Also note that the integral is weighted by the value $p(x)$. While this is one way to consider KL Divergence, one must take note that it can also be written as an expected value with respect to $Q$. In this latter form, it takes on the following form:

$$D[Q(x) \parallel P(x \mid \delta)] = \mathrm{E}_Q \left[ \ln \frac{Q(x)}{P(x|\delta)} \right] \tag{32}$$

KL Divergence is always non-negative and is zero if and only if the two distributions are identical. It is not symmetric, meaning $D_{KL}(P|Q) \neq D_{KL}(Q|P)$, and thus it is not a true metric. Despite this, it is widely used in various fields due to its ability to measure the "distance" between distributions.

KL Divergence is a versatile tool that provides a quantitative measure of how one probability distribution diverges from another. Its applications span a wide range of fields, making it an essential concept in both theoretical and applied statistics.

### C. The Hodgkin-Huxley Model.

The Hodgkin-Huxley model is a set of nonlinear differential equations that describe how action potentials in neurons are initiated and propagated. The basic equations is the Membrane Current $I$ which sums up the membrane values given by:

$$I = C_m \frac{dV_m}{dt} + I_{\mathrm{Na}} + I_{\mathrm{K}} + I_{\mathrm{L}} \tag{33}$$

where:
$C_m$ is the membrane capacitance.
$V_m$ is the membrane potential.
$\mathrm{I}_{\mathrm{Na}}$, $I_{\mathrm{k}}$ , and $I_{\mathrm{L}}$ are the maximum conductances for sodium, potassium, and leak channels respectively. The ionic currents in the above equation are calculated by using the following formulas:

$$\begin{aligned} I_{\mathrm{Na}} &= g_{\mathrm{Na}} m^3 h (V_m - E_{\mathrm{Na}}) \\ I_{\mathrm{K}} &= g_{\mathrm{K}} n^4 (V_m - E_{\mathrm{K}}) \\ I_{\mathrm{L}} &= g_{\mathrm{L}} (V_m - E_{\mathrm{L}}) \end{aligned} \tag{34}$$

where:
$g_{\mathrm{Na}}$, $g_{\mathrm{K}}$, and $g_{\mathrm{L}}$ are the maximum conductance for sodium, potassium, and leak channels. $\mathrm{E}_{\mathrm{Na}}$, $\mathrm{E}_{\mathrm{K}}$, and $\mathrm{E}_{\mathrm{L}}$ are the reversal potentials for sodium, potassium, and leak channels, and $m$, $h$, and $n$ are gating variables that represent the probability of ion channels being open.

The gating variables $m$, $h$, and $n$ follow first-order kinetics ( or the rate of change of a variable is proportional to the difference between its current value and its equilibrium value ) for the probabilities of ion channels being open. These variables follow first-order differential equations:

$$\begin{aligned} \frac{dm}{dt} &= \alpha_m(1-m) - \beta_m m \\ \frac{dh}{dt} &= \alpha_h(1-h) - \beta_h h \\ \frac{dn}{dt} &= \alpha_n(1-n) - \beta_n n \end{aligned} \tag{35}$$

where $\alpha$ and β are voltage-dependent rate constants that determine how quickly the gating variables approach their equilibrium values. The equations are called first-order because the rate of change of each gating variable depends linearly on the variable itself. This linear dependence is characteristic of first-order kinetics. Note that the gating variables represent probabilities, and their dynamics are governed by the rates at which channels open and close. These rates are described by the first-order kinetic equations, which capture the probabilistic nature of ion channel behavior. The rate constants in the above first order kinetic equations are finally calculated by the following equations:

For m sodium activation:

$$\begin{aligned} \alpha_m &= \frac{0.1(V_m+40)}{1-e^{-(V_m+40)/10}} \\ \beta_m &= 4e^{-(V_m+65)/18} \end{aligned} \tag{36}$$

For h Sodium Inactivation:

$$\begin{aligned} \alpha_h &= 0.07e^{-(V_m+65)/20} \\ \beta_h &= \frac{1}{1+e^{-(V_m+35)/10}} \end{aligned} \tag{37}$$

For n Potassium Activation:

$$\begin{aligned} \alpha_n &= \frac{0.01(V_m+55)}{1-e^{-(V_m+55)/10}} \\ \beta_n &= 0.125e^{-(V_m+65)/80} \end{aligned} \tag{38}$$

The rate constants alpha and beta above depend on the membrane potential $V_m$, making the gating dynamics voltage-dependent. This allows the model to capture the complex behavior of ion channels as they respond to changes in membrane potential. The exponential terms in the rate constants bring nonlinearity into the system, which is needed for accurately modeling the rapid changes in ion channel states during action potentials. These rate constants were derived from experimental data on the squid giant axon, providing a biophysically realistic description of ion channel kinetics.

A special note is required for the alpha and beta rate constants above. Because they were calculated based on experiments with the giant squid axon, any use for Drosophila (the model organism chosen for the thesis) need to be recalibrated based on experimental data from Drosophila neurons. Researchers typically conduct voltage-clamp experiments on Drosophila neurons to obtain the necessary data. These experiments help determine the specific rate constants and other parameters that accurately reflect the ion channel kinetics in Drosophila.

The alpha and beta rate constants in the Hodgkin-Huxley model were indeed derived from experiments on the squid giant axon. While these constants provide a foundational understanding of ion channel dynamics, they are specific to the biophysical properties of squid neurons. When applying the Hodgkin-Huxley model to other organisms, such as Drosophila, it is essential to consider species-specific differences in ion channel properties.

## D. Wilson-Cowan

The modeling of excitatory (E) and inhibitory (I) neural populations through differential equations is a fundamental aspect of understanding neural dynamics. The Wilson-Cowan model, which is a prominent framework in computational neuroscience, describes how the activity of these populations evolves over time based on their interactions and external inputs. This model utilizes a set of differential equations to capture the dynamics of excitatory and inhibitory neurons, providing insights into how these populations synchronize and influence each other (Nazemi & Jamali, 2019).

$$\frac{dE}{dt} = -E + S(w_{EE}E - w_{EI}I + P_E) \tag{39}$$

$$\frac{dI}{dt} = -I + S(w_{IE}E - w_{II}I + P_I) \tag{40}$$

Where in equations 39 and 40 above, $E$ is the average activity level of the excitatory neuron population, and $I$ is the average activity level of the inhibitory neuron population. Further, the -$E$ terms and $-I$ represent the natural decay of the activity levels of the excitatory and inhibitory populations, respectively. This means that in the absence of any input, the activity levels will decrease over time.

Also note that between the inhibitory and excitatory weights are applied such that:

$w_{EE}$ is the strength of the excitatory connections within the excitatory population.
$w_{EI}$ is the strength of the inhibitory connections from the inhibitory population to the excitatory population.
$w_{IE}$ is the strength of the excitatory connections from the excitatory population to the inhibitory population.
$w_{II}$ is the strength of the inhibitory connections within the inhibitory population.

External inputs to the model are shown as:

$P_E$ is the external input to the excitatory population.
$P_I$ is the external input to the inhibitory population.

And finally, S is a sigmoid function that represents the response function of the neurons, typically of the form:

$$\mathrm{S(x)} = \frac{1}{1+\mathrm{e}^{-\alpha(\mathrm{x}-\theta)}} \tag{41}$$

where α is the gain and θ is the threshold. The following diagram makes these values meaningful within the context of the sigmoid function.

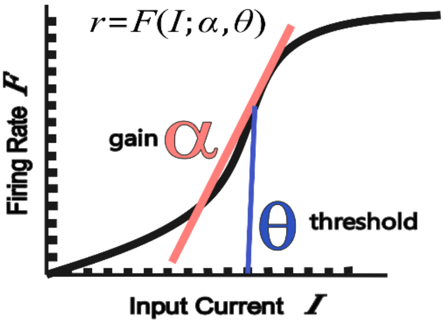


**Fig. 22.** Sigmoid Function used in the Wilson-Cowan model.

Here α determines how sharply (i.e. slope-like) the sigmoid function transitions from 0 to 1. A higher α value means a steeper transition, making the neuron's response more binary-like (either firing or not firing).

θ sets the threshold at which the neuron's response starts to increase significantly. It shifts the sigmoid curve along the x-axis, affecting the point at which the neuron starts to respond to the input.

Replacing the x variable in equations 39 and 40 above thus gives us the following more detailed equations for the sigmoid:

$$S(w_{EE}E - w_{EI}I + P_E) = \frac{1}{1+e^{-\alpha(w_{EE}E - w_{EI}I + P_E - \theta)}} \tag{42}$$

and

$$S(w_{IE}E - w_{II}I + P_I) = \frac{1}{1+e^{-\alpha(w_{IE}E - w_{II}I + P_I - \theta)}} \tag{43}$$

In the context of neural mass models, the interactions between nodes can be represented through a system of differential equations. Specifically, demonstrate that the dynamics of each node can be expressed using a combination of second-order and first-order differential equations, highlighting the complexity of neural interactions within a network (Kazemi & Jamali, 2022). This approach allows for the exploration of various behaviors arising from the coupling strength and synchronization patterns among the excitatory and inhibitory populations, which are critical for understanding phenomena such as oscillations and collective dynamics in neural circuits(Kazemi & Jamali, 2022).

Moreover, the integration of stochastic elements into these models can enhance their realism by accounting for the inherent variability in neural responses. For instance, conditional mixtures of Poisson distributions can be employed to model the correlations in neural responses, which are often influenced by both excitatory and inhibitory inputs(Sokoloski & Coen-Cagli, 2019). This stochastic framework captures the nuanced behaviors of large populations of neurons, as it reflects the probabilistic nature of neural firing and the complex interactions that occur within neural networks(Sokoloski & Coen-Cagli, 2019).

Classical Wilson–Cowan (WC) systems exhibit a range of dynamical regimes depending on coupling strengths and gain parameters. In this thesis, the WC equations are *not* used for broad parameter exploration. Instead, a single biologically constrained parameter set is derived from the FB1G–FB4N circuit structure and used consistently throughout the analysis.

A key feature of the present modelling framework is that the gain parameters $\alpha_E$and $\alpha_I$are not hard-coded constants. Rather, they are computed dynamically at simulation runtime from the synaptic Z-scores of the Hemibrain connectome. Specifically, for each pre–post pair, α is calculated inline as the ratio of the normalized post-synaptic Z-value to the normalized pre-synaptic Z-value (that is, $\alpha = Z_{\text{post}}/Z_{\text{pre}}$), with a minimum enforced value of 1.0 to ensure a meaningful sigmoid slope during phase-plane analysis. This novel, biologically motivated approach ensures that gain values directly reflect connectomic structure without requiring arbitrary tuning.

Importantly, this dynamic α-calculation does not disrupt or alter any expected qualitative behavior of standard WC models. The nullclines, vector fields, and fixed-point behavior that arise under these α values remain fully consistent with the established theory of excitatory–inhibitory Wilson–Cowan dynamics.

Because there is no experimentally validated ground truth for the synaptic weights or gain functions of FB1G and FB4N, sweeping these parameters across wide ranges would only reproduce the well-known generic WC bifurcation landscape and would not provide meaningful biological insight. For this reason, the WC analysis in this thesis focuses on demonstrating the possible existence of a stable operating point within a parameter regime that is both structurally grounded and mathematically coherent. This does not assert that the biological system *does* operate in that regime, but it does rigorously establish that such a regime is not impossible given the constraints of current connectomic data. A full empirical characterization of bifurcation boundaries awaits future electrophysiological measurement.

## E Kuramoto Model

The Kuramoto model is a mathematical framework developed by Yoshiki Kuramoto in the 1970s to describe synchronization phenomena in large populations of coupled oscillators. This model is useful in understanding how individual oscillators, each with its own natural frequency, can synchronize their phases when coupled together. The Kuramoto model has applications in various fields, including neuroscience, physics, and engineering.

The Kuramoto model considers a population of N oscillators, each characterized by its phase $\theta_i$(t) and natural frequency $\omega_i$. The key idea is that the oscillators interact with each other through a coupling mechanism that depends on the phase differences between them. The strength of this coupling is denoted by a constant K.

In research involving the Drosophila model organism, the coupling strength K can vary depending on the specific experimental setup and the nature of the oscillators being studied. However, there are some general trends and typical values observed in related studies.

When studying neural oscillations in Drosophila, K values are often chosen based on the strength of synaptic connections or other forms of neural coupling. These values can range from small to moderate, typically around 0.1 to 10, depending on the specific neural circuits and the degree of synchronization observed.

The dynamics of the i-th oscillator in the Kuramoto model are described by the following differential equation:

$$\frac{d\theta_i}{dt} = \omega_i + \frac{K}{N}\sum_{j=1}^{N} \sin\left(\theta_j - \theta_i\right) \tag{44}$$

Where $\theta_i$(t) is the phase of the i -th oscillator at time t is the natural frequency of the i-th oscillator. $K$ is the coupling strength, and the right-side term $\frac{K}{N}\sum_{j=1}^{N} \sin\left(\theta_j - \theta_i\right)$ represents the interaction between oscillators.

To quantify the degree of synchronization, the Kuramoto model introduces an order parameter r, defined as:

$$re^{i\psi} = \frac{1}{N}\sum_{j=1}^{N} e^{i\theta_j} \tag{45}$$

Where r takes a value of $0 \leq r \leq 1$ and measures the coherence of the oscillators. A value of $r = 1$ indicates perfect synchronization, while r = 0 indicates complete incoherence. The value ψ is the average phase of the oscillators.

As the coupling strength K increases, the system undergoes a phase transition from incoherence to partial or full synchronization. When K exceeds a critical threshold, a significant fraction of the oscillators begin to synchronize, leading to a non-zero value of $r$.

The Kuramoto model provides a powerful theoretical framework for understanding synchronization in large populations of coupled oscillators. By analyzing the interactions between oscillators and the resulting phase transitions, the model offers insights into the collective behavior of large neuronal systems.

## F Stochastic Neural Network Models

Stochastic neural networks introduce randomness into a network's architecture or its learning process. This randomness can come from various sources, such as random weights, biases, or noise added to the inputs or activations, and are particularly useful for capturing the variability observed in biological neural systems and for improving the robustness and generalization of artificial neural networks.

### *Neural Networks with Additive Noise*

Here noise is added to the activations or inputs of the network. The general form of the equations for such a network can be written as:

$$X_n + 1 = F(X_n, W_n) + \eta_n \qquad (46)$$

where $X_n$ is the state of the network at layer n, $W_n$ represents the weights, and $\eta_n$ is the noise term.

### *Neural Networks with Random Weights and Biases.*

Here, the weights and biases themselves are treated as random variables. The equations for such a network can be expressed as:

$$X_n + 1 = \phi\big(W_n(\omega)Xn + b_n(\omega)\big) \qquad (47)$$

where $W_n(\omega)$ and $b_n(\omega)$ are random weight matrices and bias vectors, respectively, and (\phi) is the activation function.

### *Stochastic Differential Equation (SDE) Models*

These models use SDEs to describe the evolution of the network's state over time. A common form of such an equation is:

$$dX_t = f(X_t, t)dt + g(X_t, t)dW_t \qquad (48)$$

where $X_t$ is the state of the network at time t, $f$ and $g$ are functions describing the deterministic and stochastic parts of the system, respectively. $W_t$ is a Wiener process (Brownian motion), which is a continuous-time stochastic process named after Norbert Wiener. It is characterized by the following properties:

It begins with an Initial Condition $\mathrm{W}_0 = 0$, with increments of the process that are independent. For any $0 \ \leq \mathrm{s} < \ \mathrm{t}$, the increment $W_t - W_s$ is independent of the past values $W_u$ for $\mathrm{u} \ \leq s$.

*Gaussian Increments*

Gaussian increments refer to the fact that the changes in the Wiener process over any time interval follow a normal (Gaussian) distribution even though the increments are independent of each other. A normal distribution, also known as a Gaussian distribution, is a probability distribution that is symmetric about the mean. It is characterized by its mean and variance. For a Wiener process W(t), an increment is the change in the process over a time interval [s, t]. This increment is denoted as $W_t - W_s$ and is normally distributed with a mean of 0 and a variance of t – s, and is written as:

$$W_t - W_s \sim \mathcal{N}(0, t - s) \qquad (49)$$

In the above equation, the increment has a mean of 0 and indicates that, on average, the increment $W_t - W_s$ is centered around 0. This signifies that there is no systematic drift in the process; it is equally likely to move up or down over any interval. The variance of t-s indicates how much the increments can vary. The longer the time interval t - s, the larger the variance, meaning the potential change in the process increases with time. The characteristics of the mean and variance thus take a random system that at the same time offers some level of predictability.

*Continuous Paths.*

Here the statement is made that the paths of the Wiener process are “almost surely continuous”. This means that, with a probability 1, the function $t \mapsto W_t$ is continuous for all t. This is a crucial property of the Wiener process and distinguishes it from other types of stochastic processes that might have jumps or discontinuities.

Within this model, Continuity is defined as a function $f(t)$ is continuous if, for any small change in $t$, the change in $f(t)$ is also small. Formally, $f(t)$ is continuous at $t = t_0$ if:

$$\lim_{t \to t_0} f(t) = f(t_0) \quad (50)$$

For the Wiener process $W_t$, this means that as $t$ changes, $W_t$ changes smoothly without any abrupt jumps. The term "almost surely" in probability theory means that an event happens with probability 1. So, when one says the paths of the Wiener process are almost surely continuous, it mean that the paths are continuous for all practical purposes, though there might be a set of paths with discontinuities that has probability 0.

## G Detailed Methodology Software Setup

Code associated with this research is available on the GitHub repository at `https://github.com/sgarnell/THESIS`. The code relies on several Python packages for mathematical computations, data visualization, graph analysis, and neural simulation. The primary python packages include: `math`, `re`,`numpy`, `scipy`, `IPython`, `matplotlib`, `graphviz`, `pydot`, `networkx`, `neuroarch`, `nengo`, `tensorflow`, `nengo_dl`, `nengo_extras`.

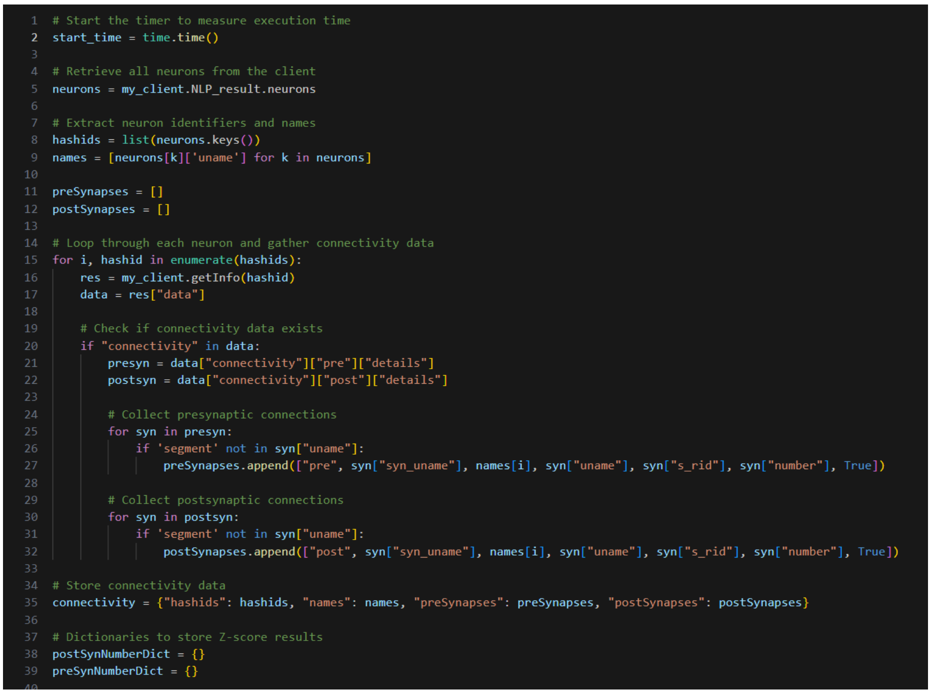
The code also utilizes the FlybrainLab software package available at `https://github.com/FlyBrainLab.`

FlyBrainLab is an adaptive computing platform for examining the function of executable circuits derived from fruit fly brain data. The platform offers three primary capabilities: (i) 3D exploration and visualization of fruit fly brain data, (ii) construction of executable circuits directly from examined and visualized fly brain data, and (iii) interactive investigation of the functional logic of developed executable circuits.

The research is based on the Hemibrain 1.1 and Flywire 1.2 datasets, including raw, processed, and intermediate data. Contact the corresponding author for access to the code and data. Consistent package versions are recommended for reproducibility.

## H Detailed Methodology Implementation Code Highlights

The code provided below (**Fig. 23**) accomplishes the Z-score analysis by first collecting connectivity data for each neuron (lines 5-35). Specifically, it retrieves the details of pre- and post-synaptic connections (lines 14-33), then organizes this information into lists that hold the number of synapses associated with each connection.



```
1  # Start the timer to measure execution time
2  start_time = time.time()
3
4  # Retrieve all neurons from the client
5  neurons = my_client.NLP_result.neurons
6
7  # Extract neuron identifiers and names
8  hashids = list(neurons.keys())
9  names = [neurons[k]['uname'] for k in neurons]
10
11 preSynapses = []
12 postSynapses = []
13
14 # Loop through each neuron and gather connectivity data
15 for i, hashid in enumerate(hashids):
16     res = my_client.getInfo(hashid)
17     data = res["data"]
18
19     # Check if connectivity data exists
20     if "connectivity" in data:
21         presyn = data["connectivity"]["pre"]["details"]
22         postsyn = data["connectivity"]["post"]["details"]
23
24         # Collect presynaptic connections
25         for syn in presyn:
26             if 'segment' not in syn["uname"]:
27                 preSynapses.append(["pre", syn["syn_uname"], names[i], syn["uname"], syn["s_rid"], syn["number"], True])
28
29         # Collect postsynaptic connections
30         for syn in postsyn:
31             if 'segment' not in syn["uname"]:
32                 postSynapses.append(["post", syn["syn_uname"], names[i], syn["uname"], syn["s_rid"], syn["number"], True])
33
34 # Store connectivity data
35 connectivity = {"hashids": hashids, "names": names, "preSynapses": preSynapses, "postSynapses": postSynapses}
36
37 # Dictionaries to store Z-score results
38 postSynNumberDict = {}
39 preSynNumberDict = {}
```

**Fig. 23.** Python Notebook Demonstrating Z-score Analysis Lines 1-40

In the `process_synapses` function (**Fig. 24**), for each neuron in the dataset, the code compiles the synaptic connections and calculates the Z-score for the number of synapses each partner neuron has (lines 42-49). The Z-score, which measures how many standard deviations a data point is from the mean, helps identify connections that have significantly more synapses compared to others, signaling stronger signal propagation (lines 51-53). The `process_synapses` function plays a crucial role by iterating through the synapse lists, calculating the Z-scores, and normalizing these scores to highlight the most meaningful connections (lines 65-71). This normalization step converts the raw Z-scores into a range that indicates the relative strength of each connection.

```
40
41 # Function to process synaptic data and calculate Z-scores
42 def process_synapses(synapses, synNumberDict, synType):
43     for neuronName in connectivity['names']:
44         singleNeuron_synNumber = []
45         singleNeuron_synData = []
46         for syn in synapses:
47             if neuronName == syn[2]:
48                 singleNeuron_synNumber.append(syn[5])
49                 singleNeuron_synData.append([syn[3], syn[4], syn[5]])
50
51         # Calculate the Z-score for the number of synapses
52         synZscore = stats.zscore(singleNeuron_synNumber)
53         isnan = np.isnan(synZscore)
54
55         if not np.any(isnan):
56             synZmax = max(synZscore)
57             print(f'\033[92m{neuronName}: {synType}SynZmax= {synZmax}\033[0m')
58         else:
59             for syn in synapses:
60                 if neuronName == syn[2]:
61                     syn[6] = False
62             print(f'\033[93m{neuronName} Error: Nan Value Found in array\033[0m')
63             continue
64
65         for r in range(len(singleNeuron_synData)):
66             syn_uname = singleNeuron_synData[r][0]
67             if 'segment' not in syn_uname:
68                 syn_rid = singleNeuron_synData[r][1]
69                 # Normalize the Z-score to highlight the most meaningful connections
70                 normSynZ = 1 - ((synZmax - synZscore[r]) / synZmax)
71                 synNumberDict[syn_rid] = [syn_uname, synZscore[r], normSynZ]
72
```

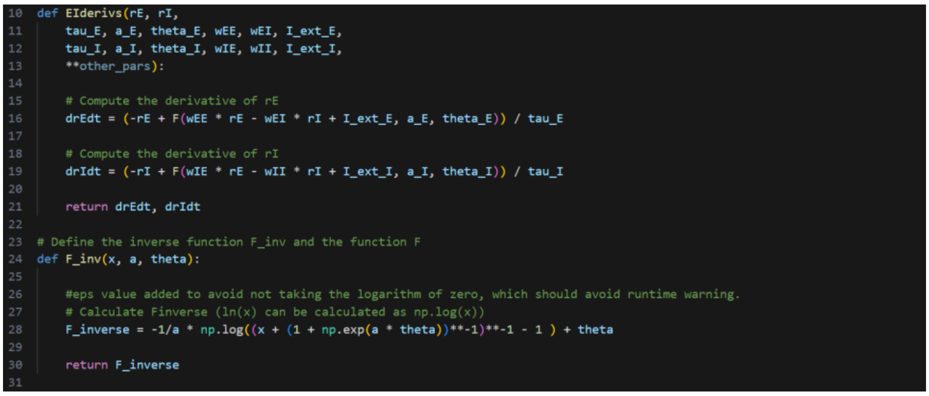
**Fig. 24.** Python Notebook Demonstrating Z-score Analysis Lines 41-72

Throughout the process, the code also ensures that any neurons with undefined (NaN) Z-scores are flagged and excluded from further analysis, maintaining the accuracy and reliability of the results (lines 58-62). By focusing on larger synaptic connectivity and using statistical analysis, this approach identifies key NOIs within the neural circuit, supporting the study's hypothesis regarding the role of synaptic connections in neural signal propagation.

It is important to acknowledge that the code used for the Phase Plane analysis in this thesis is based significantly on code provided by the neuromatch Academy(Kording, 2021; Viegen et al., 2021). As a result, the structure, logic, and even some comments in the code may closely resemble those found in the original neuromatch Academy materials. This similarity is intentional, as the neuromatch Academy's resources were fundamental in guiding the development and implementation of the analysis presented here.

In this section, the focus is on the Phase Plane analysis for understanding the dynamic behaviors of excitatory (E) and inhibitory (I) neurons in a neural network. The analysis primarily involves calculating the nullclines for these neurons and plotting them to observe the equilibrium points and their interactions.

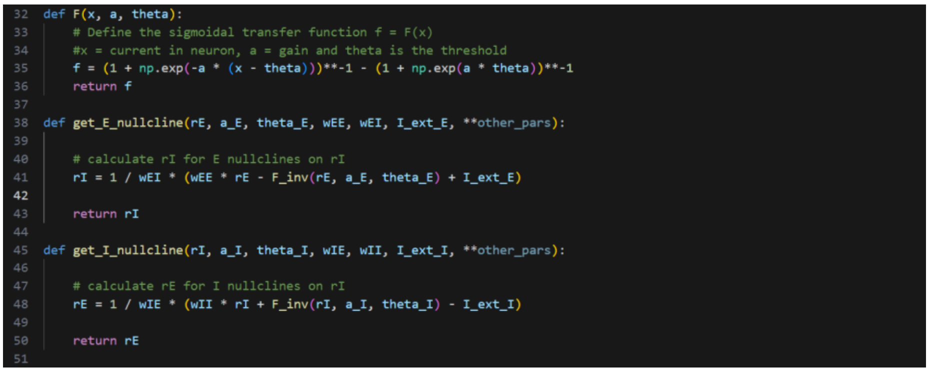
The nullclines calculation begins by defining functions and parameters. The functions F and F_inv (**Fig. 25** lines 23-34) represent the sigmoidal transfer function and its inverse, respectively. These functions help in determining the firing rates of neurons based on their inputs. The excitatory (rE) and inhibitory (rI) firing rates are derived using the function EIderivs (**Fig. 25** lines 10-21).



```
10  def EIderivs(rE, rI,
11      tau_E, a_E, theta_E, wEE, wEI, I_ext_E,
12      tau_I, a_I, theta_I, wIE, wII, I_ext_I,
13      **other_pars):
14
15      # Compute the derivative of rE
16      drEdt = (-rE + F(wEE * rE - wEI * rI + I_ext_E, a_E, theta_E)) / tau_E
17
18      # Compute the derivative of rI
19      drIdt = (-rI + F(wIE * rE - wII * rI + I_ext_I, a_I, theta_I)) / tau_I
20
21      return drEdt, drIdt
22
23  # Define the inverse function F_inv and the function F
24  def F_inv(x, a, theta):
25
26      #eps value added to avoid not taking the logarithm of zero, which should avoid runtime warning.
27      # Calculate Finverse (ln(x) can be calculated as np.log(x))
28      F_inverse = -1/a * np.log((x + (1 + np.exp(a * theta))**-1)**-1 - 1 ) + theta
29
30      return F_inverse
31
```

**Fig. 25.** Phase plane analysis – nullcline calculations

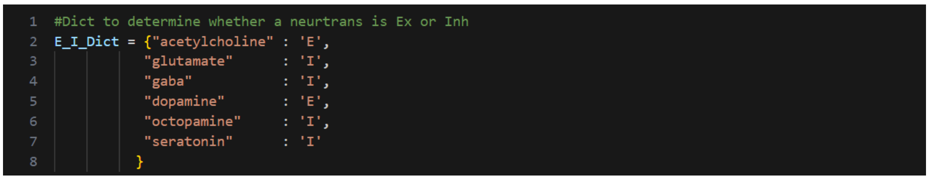
The nullclines represent the set of points where the rate of change (derivative) of a variable is zero. For the E and I neurons, nullclines are calculated using the functions `get_E_nullcline` (**Fig. 26** lines 38-43) and `get_I_nullcline` (**Fig. 26** lines 45-50). The E nullcline is determined by calculating the inhibitory rate rI for a given excitatory rate rE. Similarly, the I nullcline is calculated by computing the excitatory rate rE for a given inhibitory rate rI.



```
32  def F(x, a, theta):
33      # Define the sigmoidal transfer function f = F(x)
34      #x = current in neuron, a = gain and theta is the threshold
35      f = (1 + np.exp(-a * (x - theta)))**-1 - (1 + np.exp(a * theta))**-1
36      return f
37
38  def get_E_nullcline(rE, a_E, theta_E, wEE, wEI, I_ext_E, **other_pars):
39
40      # calculate rI for E nullclines on rI
41      rI = 1 / wEI * (wEE * rE - F_inv(rE, a_E, theta_E) + I_ext_E)
42
43      return rI
44
45  def get_I_nullcline(rI, a_I, theta_I, wIE, wII, I_ext_I, **other_pars):
46
47      # calculate rE for I nullclines on rI
48      rE = 1 / wIE * (wII * rI + F_inv(rI, a_I, theta_I) - I_ext_I)
49
50      return rE
51
```

**Fig. 26.** Phase plane analysis – nullclines for excitatory and inhibitory derivatives

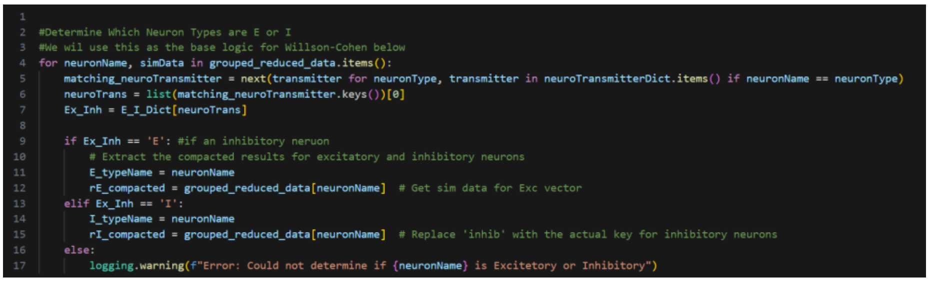
Neurons are then classified as excitatory or inhibitory based on the type of neurotransmitter using the dictionary `E_I_Dict` (**Fig. 27** lines 1-8).



```
#Dict to determine whether a neurtrans is Ex or Inh
E_I_Dict = {"acetylcholine" : 'E',
            "glutamate"     : 'I',
            "gaba"          : 'I',
            "dopamine"      : 'E',
            "octopamine"    : 'I',
            "seratonin"     : 'I'
            }
```

**Fig. 27.** Phase Plane analysis – neuron classification.

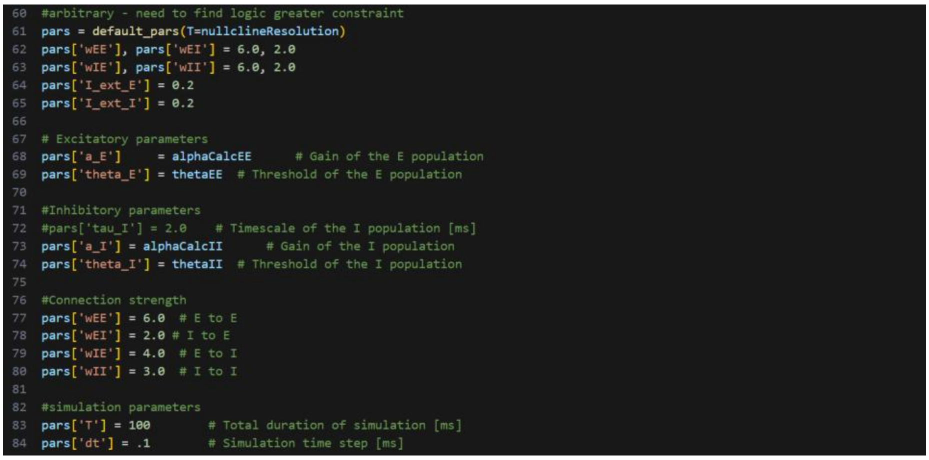
This process involves identifying whether each neuron is excitatory or inhibitory (**Fig. 28** lines 2-17).



```
1
2  #Determine Which Neuron Types are E or I
3  #We wil use this as the base logic for Willson-Cohen below
4  for neuronName, simData in grouped_reduced_data.items():
5      matching_neuroTransmitter = next(transmitter for neuronType, transmitter in neuroTransmitterDict.items() if neuronName == neuronType)
6      neuroTrans = list(matching_neuroTransmitter.keys())[0]
7      Ex_Inh = E_I_Dict[neuroTrans]
8
9      if Ex_Inh == 'E': #if an inhibitory neruon
10         # Extract the compacted results for excitatory and inhibitory neurons
11         E_typeName = neuronName
12         rE_compacted = grouped_reduced_data[neuronName]  # Get sim data for Exc vector
13     elif Ex_Inh == 'I':
14         I_typeName = neuronName
15         rI_compacted = grouped_reduced_data[neuronName]  # Replace 'inhib' with the actual key for inhibitory neurons
16     else:
17         logging.warning(f"Error: Could not determine if {neuronName} is Excitetory or Inhibitory")
```

**Fig. 28.** Phase Plan analysis – neuron identification.

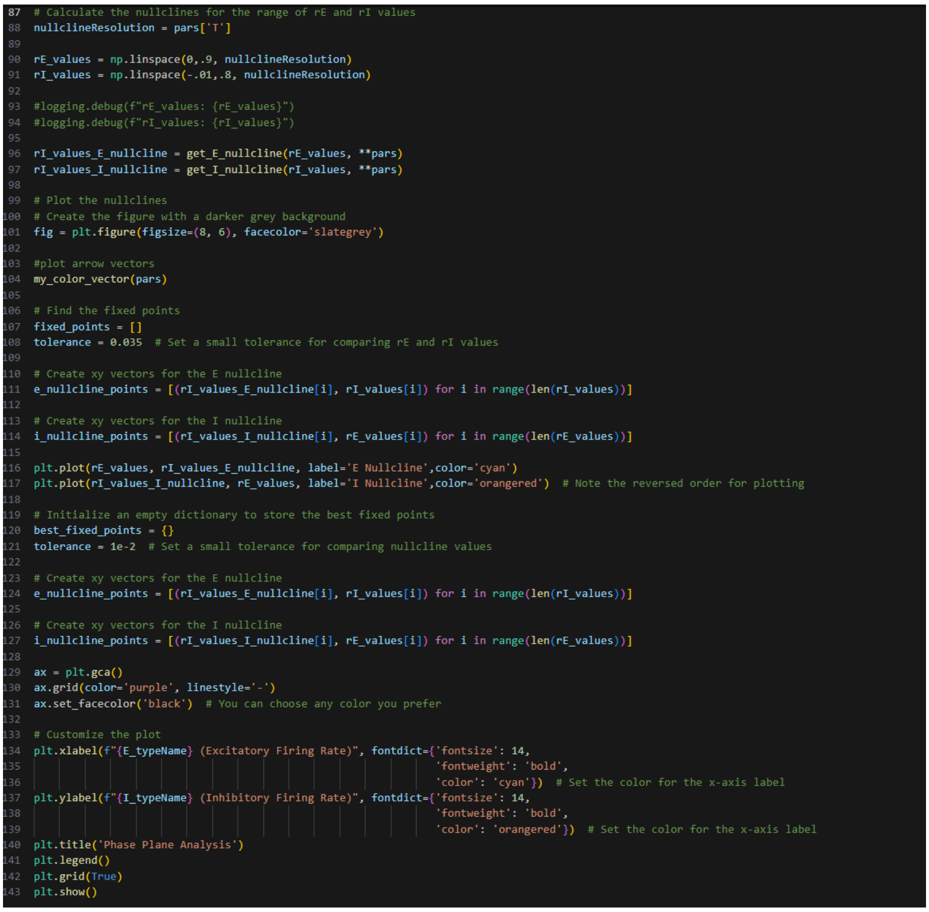
Subsequently, parameters such as connection weights (e.g. *Wee, Wei, Wie, Wii*), gain (a_E, a_I), and threshold (theta_E, theta_I) are established. These parameters (**Fig. 29** lines 60-84) influence the interactions and behaviors of the neurons.



```
60  #arbitrary - need to find logic greater constraint
61  pars = default_pars(T=nullclineResolution)
62  pars['wEE'], pars['wEI'] = 6.0, 2.0
63  pars['wIE'], pars['wII'] = 6.0, 2.0
64  pars['I_ext_E'] = 0.2
65  pars['I_ext_I'] = 0.2
66
67  # Excitatory parameters
68  pars['a_E']     = alphaCalcEE      # Gain of the E population
69  pars['theta_E'] = thetaEE  # Threshold of the E population
70
71  #Inhibitory parameters
72  #pars['tau_I'] = 2.0    # Timescale of the I population [ms]
73  pars['a_I'] = alphaCalcII      # Gain of the I population
74  pars['theta_I'] = thetaII  # Threshold of the I population
75
76  #Connection strength
77  pars['wEE'] = 6.0  # E to E
78  pars['wEI'] = 2.0 # I to E
79  pars['wIE'] = 4.0  # E to I
80  pars['wII'] = 3.0  # I to I
81
82  #simulation parameters
83  pars['T'] = 100        # Total duration of simulation [ms]
84  pars['dt'] = .1        # Simulation time step [ms]
```

**Fig. 29.** Phase plane analysis – gain and threshold parameters.

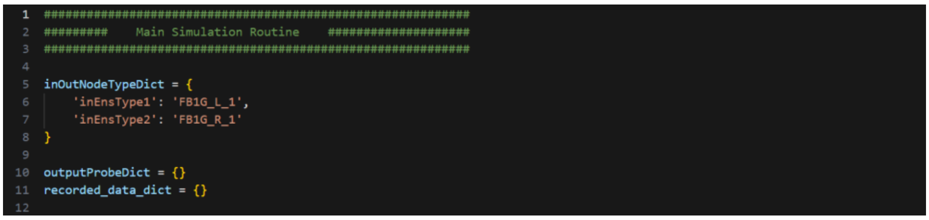
The graph generation involves plotting the nullclines using a range of rE and rI values (**Fig. 30** lines 117-121). The Phase Plane graph visualizes the E and I nullclines, showing where the neurons' firing rates intersect and highlighting potential equilibrium points. The nullclines are color-coded (`cyan` for E nullcline, `orangered` for I nullcline) and plotted on a dark background to enhance visibility (**Fig. 30** lines 123-154). The plot includes labels and a legend to help interpret the results.



```
 87 # Calculate the nullclines for the range of rE and rI values
 88 nullclineResolution = pars['T']
 89 
 90 rE_values = np.linspace(0,.9, nullclineResolution)
 91 rI_values = np.linspace(-.01,.8, nullclineResolution)
 92 
 93 #logging.debug(f"rE_values: {rE_values}")
 94 #logging.debug(f"rI_values: {rI_values}")
 95 
 96 rI_values_E_nullcline = get_E_nullcline(rE_values, **pars)
 97 rI_values_I_nullcline = get_I_nullcline(rI_values, **pars)
 98 
 99 # Plot the nullclines
100 # Create the figure with a darker grey background
101 fig = plt.figure(figsize=(8, 6), facecolor='slategrey')
102 
103 #plot arrow vectors
104 my_color_vector(pars)
105 
106 # Find the fixed points
107 fixed_points = []
108 tolerance = 0.035  # Set a small tolerance for comparing rE and rI values
109 
110 # Create xy vectors for the E nullcline
111 e_nullcline_points = [(rI_values_E_nullcline[i], rI_values[i]) for i in range(len(rI_values))]
112 
113 # Create xy vectors for the I nullcline
114 i_nullcline_points = [(rI_values_I_nullcline[i], rE_values[i]) for i in range(len(rE_values))]
115 
116 plt.plot(rE_values, rI_values_E_nullcline, label='E Nullcline',color='cyan')
117 plt.plot(rI_values_I_nullcline, rE_values, label='I Nullcline',color='orangered')  # Note the reversed order for plotting
118 
119 # Initialize an empty dictionary to store the best fixed points
120 best_fixed_points = {}
121 tolerance = 1e-2  # Set a small tolerance for comparing nullcline values
122 
123 # Create xy vectors for the E nullcline
124 e_nullcline_points = [(rI_values_E_nullcline[i], rI_values[i]) for i in range(len(rI_values))]
125 
126 # Create xy vectors for the I nullcline
127 i_nullcline_points = [(rI_values_I_nullcline[i], rE_values[i]) for i in range(len(rE_values))]
128 
129 ax = plt.gca()
130 ax.grid(color='purple', linestyle='-')
131 ax.set_facecolor('black')  # You can choose any color you prefer
132 
133 # Customize the plot
134 plt.xlabel(f"{E_typeName} (Excitatory Firing Rate)", fontdict={'fontsize': 14,
135                                                                'fontweight': 'bold',
136                                                                'color': 'cyan'})  # Set the color for the x-axis label
137 plt.ylabel(f"{I_typeName} (Inhibitory Firing Rate)", fontdict={'fontsize': 14,
138                                                                'fontweight': 'bold',
139                                                                'color': 'orangered'})  # Set the color for the x-axis label
140 plt.title('Phase Plane Analysis')
141 plt.legend()
142 plt.grid(True)
143 plt.show()
```

**Fig. 30.** Phase plane analysis – graph generation

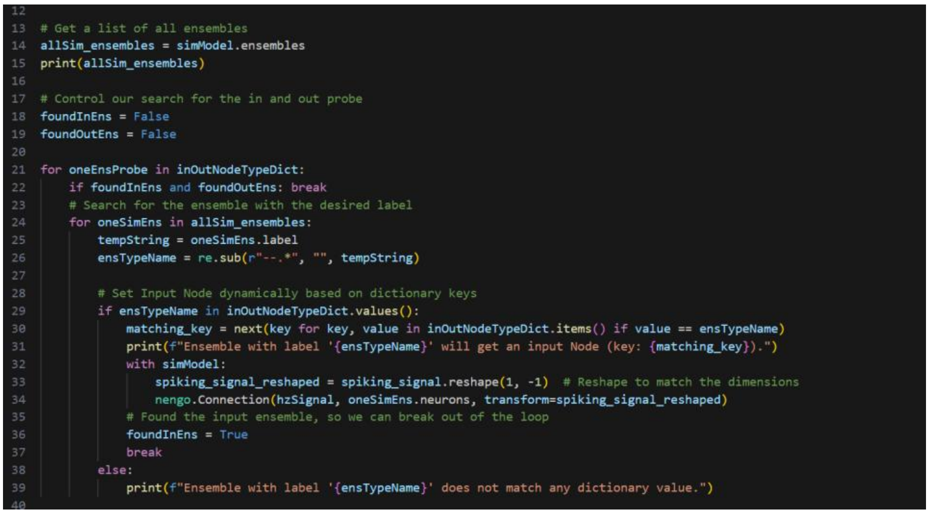
The provided code (**Fig. 31**) achieves the simulation results by first setting up the simulation environment and defining the input and output nodes for the neuron ensembles. The dictionary `inOutNodeTypeDict` (lines 5-8) maps input ensemble types to their respective labels.



```
 1  ############################################################
 2  #########    Main Simulation Routine    ####################
 3  ############################################################
 4
 5  inOutNodeTypeDict = {
 6      'inEnsType1': 'FB1G_L_1',
 7      'inEnsType2': 'FB1G_R_1'
 8  }
 9
10  outputProbeDict = {}
11  recorded_data_dict = {}
12
```

**Fig. 31.** Main Simulation Routine

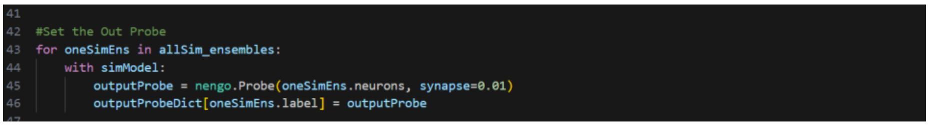
The next lines of code () then retrieves all ensembles in the simulation model (lines 13-15) and searches for the ensembles that match the specified input node types (lines 21-39). Once an input ensemble is found (line 29), it dynamically sets the input node and connects it to the neuron ensemble using the `nengo.Connection` function (lines 32-34).



```
12
13  # Get a list of all ensembles
14  allSim_ensembles = simModel.ensembles
15  print(allSim_ensembles)
16
17  # Control our search for the in and out probe
18  foundInEns = False
19  foundOutEns = False
20
21  for oneEnsProbe in inOutNodeTypeDict:
22      if foundInEns and foundOutEns: break
23      # Search for the ensemble with the desired label
24      for oneSimEns in allSim_ensembles:
25          tempString = oneSimEns.label
26          ensTypeName = re.sub(r"--.*", "", tempString)
27
28          # Set Input Node dynamically based on dictionary keys
29          if ensTypeName in inOutNodeTypeDict.values():
30              matching_key = next(key for key, value in inOutNodeTypeDict.items() if value == ensTypeName)
31              print(f"Ensemble with label '{ensTypeName}' will get an input Node (key: {matching_key}).")
32              with simModel:
33                  spiking_signal_reshaped = spiking_signal.reshape(1, -1)  # Reshape to match the dimensions
34                  nengo.Connection(hzSignal, oneSimEns.neurons, transform=spiking_signal_reshaped)
35              # Found the input ensemble, so we can break out of the loop
36              foundInEns = True
37              break
38          else:
39              print(f"Ensemble with label '{ensTypeName}' does not match any dictionary value.")
40
```

**Fig. 32.** Simulation routine - setting up input ensemble neurons

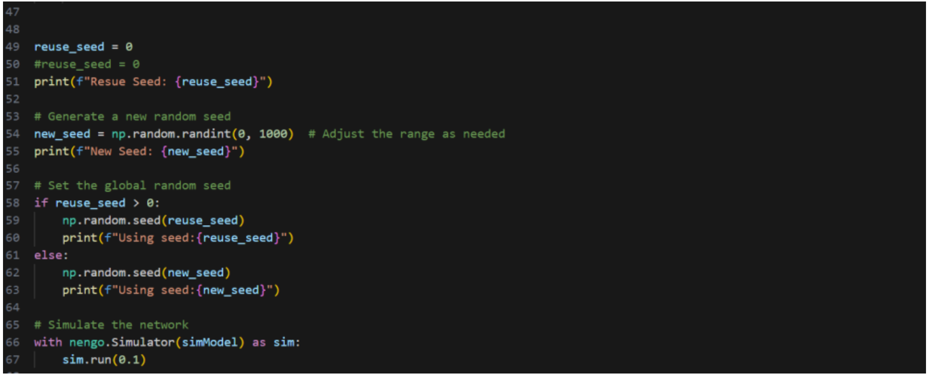
Next, the code (**Fig. 33**) sets up output probes for each ensemble in the simulation model (lines 41-45) to record the neuron firing rates during the simulation.



```
41
42  #Set the Out Probe
43  for oneSimEns in allSim_ensembles:
44      with simModel:
45          outputProbe = nengo.Probe(oneSimEns.neurons, synapse=0.01)
46          outputProbeDict[oneSimEns.label] = outputProbe
```

**Fig. 33.** Simulation routine - setting up Out Probes

A random seed is generated or reused (**Fig. 34**) to ensure reproducibility of the simulation results (lines 47-61). The network simulation is then run for a specified duration (0.1 seconds) using the `nengo.Simulator` (lines 63-65).



```
47
48
49  reuse_seed = 0
50  #reuse_seed = 0
51  print(f"Resue Seed: {reuse_seed}")
52
53  # Generate a new random seed
54  new_seed = np.random.randint(0, 1000)  # Adjust the range as needed
55  print(f"New Seed: {new_seed}")
56
57  # Set the global random seed
58  if reuse_seed > 0:
59      np.random.seed(reuse_seed)
60      print(f"Using seed:{reuse_seed}")
61  else:
62      np.random.seed(new_seed)
63      print(f"Using seed:{new_seed}")
64
65  # Simulate the network
66  with nengo.Simulator(simModel) as sim:
67      sim.run(0.1)
```

**Fig. 34.** Simulation routing – set random seed and run simulation

After the simulation, the code (**Fig. 35**) initializes a dictionary to store the recorded data (lines 67-68) and plots the firing rates of the neuron ensembles over time (lines 70-79). Each neuron's firing rate is plotted with a distinct color, showing the Hz frequency firing rate and demonstrating the consistent rise and steady maintenance of firing rates in accordance with the Wilson-Cowan theory.

```
68
69  # Initialize an empty dictionary to store probe names and recorded data
70  recorded_data_dict = {}
71
72
73  # Plot the results
74  plt.figure()
75  for probeKey, probeInstance in outputProbeDict.items():
76      recorded_data_dict[probeKey] = sim.data[probeInstance] #Store the data for later use in Phase Plane Analysis
77      plt.plot(sim.trange(), sim.data[probeInstance], label=probeKey)
78  plt.xlabel("Time (s)")
79  plt.ylabel("Firing Rate")
80  plt.title("Wilson-Cowan Model with Sigmoid Transfer Function")
81  plt.legend()
82  plt.show()
```

**Fig. 35.** Simulation routine – record and plot output

By following these steps, the code effectively simulates the neural network and visualizes the results, highlighting the stabilization of neuron firing rates within an excitatory-inhibitory network, as expected by the theory. The graph (Fig. 20) shows the simulated firing rates of four ensembles, with Y values representing an abstract Hz rate that can be converted into biologically relevant values.

## References

Aaronson, S. (2014 ). Why I Am Not An Integrated Information Theorist (or, The Unconscious Expander). *Shtetl-Optimized*. https://scottaaronson.blog/?p=1799

Alcaro, A., & Panksepp, J. (2011). The SEEKING mind: primal neuro-affective substrates for appetitive incentive states and their pathological dynamics in addictions and depression. *Neurosci Biobehav Rev*, *35*(9), 1805-1820. https://doi.org/10.1016/j.neubiorev.2011.03.002

Alcaro, A., Panksepp, J., Witczak, J., Hayes, D. J., & Northoff, G. (2010). Is Subcortical–cortical Midline Activity in Depression Mediated by Glutamate and GABA? A Cross-Species Translational Approach. *34*(4), 592-605. https://doi.org/10.1016/j.neubiorev.2009.11.023

Almada, L. F., Pereira, A., & Carrara-Augustenborg, C. (2013). What Affective Neuroscience Means for Science of Consciousness. *Mens Sana Monographs*, *11*(1), 253. https://doi.org/10.4103/0973-1229.100409

Altenhoff, A. M., & Dessimoz, C. (2012). Inferring Orthology and Paralogy. 259-279. https://doi.org/10.1007/978-1-61779-582-4_9

Altenhoff, A. M., Studer, R. A., Robinson-Rechavi, M., & Dessimoz, C. (2012). Resolving the Ortholog Conjecture: Orthologs Tend to Be Weakly, but Significantly, More Similar in Function Than Paralogs. *8*(5), e1002514. https://doi.org/10.1371/journal.pcbi.1002514

Anderson, D. J. (2022). *The Nature of the Beast: How Emotions Guide Us*. Basic Books. https://books.google.com/books?id=u4h_zgEACAAJ

Andretic, R., Swinderen, B. v., & Greenspan, R. J. (2005). Dopaminergic Modulation of Arousal in Drosophila. *Current Biology*, *15*(13), 1165-1175. https://doi.org/10.1016/j.cub.2005.05.025

Anthoney, N., Tainton-Heap, L. A. L., Luong, H., Notaras, E., Kewin, A. B., Zhao, Q., Perry, T., Batterham, P., Shaw, P. J., & van Swinderen, B. (2023). Experimentally induced active and quiet sleep engage non-overlapping transcriptional programs in Drosophila. *bioRxiv*. https://doi.org/10.1101/2023.04.03.535331

Aranyi, C., Képes, Z., Nagy, M., Opposits, G., Garai, I., Káplár, M., & Emri, M. (2022). Topological Dissimilarities of Hierarchical Resting Networks in Type 2 Diabetes Mellitus and Obesity. *Journal of Computational Neuroscience*, *51*(1), 71-86. https://doi.org/10.1007/s10827-022-00833-9

Armstrong, P. B. (2017). *The Phenomenology of Henry James*. University of North Carolina Press. https://books.google.com/books?id=IYU6DwAAQBAJ

Ashwin, P., Coombes, S., & Nicks, R. (2016). Mathematical Frameworks for Oscillatory Network Dynamics in Neuroscience. *The Journal of Mathematical Neuroscience*, *6*(1). https://doi.org/10.1186/s13408-015-0033-6

Audi, R. (1998). *Epistemology: A Contemporary Introduction to the Theory of Knowledge*. Routledge. https://books.google.com/books?id=6VqgtQEACAAJ

Baars, B. J., & Franklin, S. (2009). Consciousness Is Computational: The Lida Model of Global Workspace Theory. *01*(01), 23-32. https://doi.org/10.1142/s1793843009000050

Bahri, Y., Kadmon, J., Pennington, J., Schoenholz, S. S., Sohl-Dickstein, J., & Ganguli, S. (2020). Statistical Mechanics of Deep Learning. *11*(1), 501-528. https://doi.org/10.1146/annurev-conmatphys-031119-050745

Barrett, A. B., & Seth, A. K. (2011). Practical Measures of Integrated Information for Time-Series Data. *7*(1), e1001052. https://doi.org/10.1371/journal.pcbi.1001052

Barrett, L. F., & Bliss-Moreau, E. (2009). Chapter 4 Affect as a Psychological Primitive [Review]. *Advances in Experimental Social Psychology*, *41*, 167-218. https://doi.org/10.1016/S0065-2601(08)00404-8

Barron, A. B., Gurney, K. N., Meah, L. F. S., Vasilaki, E., & Marshall, J. A. R. (2015). Decision-making and action selection in insects: inspiration from vertebrate-based theories. *Frontiers in Behavioral Neuroscience*, *9*, 216. https://doi.org/10.3389/fnbeh.2015.00216

Barron, A. B., & Klein, C. (2016). What insects can tell us about the origins of consciousness. *Proceedings of the National Academy of Sciences of the United States of America*, *113*(18), 4900-4908. https://doi.org/10.1073/pnas.1520084113

Barron, A. B., & Plath, J. A. (2017). The evolution of honey bee dance communication: a mechanistic perspective. *The Journal of experimental biology*, *220*(Pt 23), 4339-4346. https://doi.org/10.1242/jeb.142778

Bates, A. S., Schlegel, P., Roberts, R. J. V., Drummond, N., Tamimi, I. F. M., Turnbull, R., Zhao, X., Marin, E. C., Popovici, P. D., Dhawan, S., Jamasb, A., Javier, A., Serratosa Capdevila, L., Li, F., Rubin, G. M., Waddell, S., Bock, D. D., Costa, M., & Jefferis, G. S. X. E. (2020). Complete Connectomic Reconstruction of Olfactory Projection Neurons in the Fly Brain. *Current Biology*, *30*(16), 3183-3199.e3186. https://doi.org/10.1016/j.cub.2020.06.042

Battiston, F., Amico, E., Barrat, A., Bianconi, G., Ferraz de Arruda, G., Franceschiello, B., Iacopini, I., Kéfi, S., Latora, V., Moreno, Y., Murray, M. M., Peixoto, T. P., Vaccarino, F., & Petri, G. (2021). The Physics of Higher-Order Interactions in Complex Systems. *17*(10), 1093-1098. https://doi.org/10.1038/s41567-021-01371-4

Battiston, F., Cencetti, G., Iacopini, I., Latora, V., Lucas, M., Patania, A., Young, J.-G., & Petri, G. (2020). Networks Beyond Pairwise Interactions: Structure and Dynamics. *874*, 1-92. https://doi.org/10.1016/j.physrep.2020.05.004

Bayraktar, O. A., Boone, J. Q., Drummond, M. L., & Doe, C. Q. (2010). Drosophilatype II Neuroblast Lineages Keep Prospero Levels Low to Generate Large Clones That Contribute to the Adult Brain Central Complex. *Neural Development*, *5*(1). https://doi.org/10.1186/1749-8104-5-26

Berry, J. A., Cervantes-Sandoval, I., Chakraborty, M., & Davis, R. L. (2015). Sleep Facilitates Memory by Blocking Dopamine Neuron-Mediated Forgetting. *Cell*, *161*(7), 1656-1667. https://doi.org/10.1016/j.cell.2015.05.027

Blanquet, P. R. (2011). Advances InInterdisciplinary Researches to Construct a Theory of Consciousness. *01*(04), 242-261. https://doi.org/10.4236/jbbs.2011.14031

Block, N. (2007). Consciousness, Accessibility, and the Mesh Between Psychology and Neuroscience. *30*(5-6), 481-499. https://doi.org/10.1017/s0140525x07002786

Block, N. (2011). Perceptual Consciousness Overflows Cognitive Access. *15*(12), 567-575. https://doi.org/10.1016/j.tics.2011.11.001

Bogacz, R. (2017). A Tutorial on the Free-Energy Framework for Modelling Perception and Learning. *76*, 198-211. https://doi.org/10.1016/j.jmp.2015.11.003

Borst, J. P., & Anderson, J. R. (2015). Using the ACT-R Cognitive Architecture in Combination With fMRI Data. 339-352. https://doi.org/10.1007/978-1-4939-2236-9_17

Briggman, K. L., & Bock, D. D. (2012). Volume Electron Microscopy for Neuronal Circuit Reconstruction. *Current Opinion in Neurobiology*, *22*(1), 154-161. https://doi.org/10.1016/j.conb.2011.10.022

Brouillet, D., & Friston, K. (2023). Relative Fluency (Unfelt vs Felt) in Active Inference. *115*, 103579. https://doi.org/10.1016/j.concog.2023.103579

Buckley, C. L., Kim, C. S., McGregor, S., & Seth, A. K. (2017). The Free Energy Principle for Action and Perception: A Mathematical Review. *Journal of Mathematical Psychology*, *81*, 55-79. https://doi.org/10.1016/j.jmp.2017.09.004

Burkitt, N. (2006). A Review of the Integrate-and-Fire Neuron Model: I. Homogeneous Synaptic Input. *Biological Cybernetics*, *95*(1), 1-19. https://doi.org/10.1007/s00422-006-0068-6

Casalegno, F., Cremonesi, F., Yates, S., Hines, M. L., Schürmann, F., & Delalondre, F. (2016). Error analysis and quantification in NEURON simulations. ECCOMAS Congress 2016 - Proceedings of the 7th European Congress on Computational Methods in Applied Sciences and Engineering,

Catterall, W. A., Raman, I. M., Robinson, H. P. C., Sejnowski, T. J., & Paulsen, O. (2012). The Hodgkin-Huxley Heritage: From Channels to Circuits. *Journal of Neuroscience*, *32*(41), 14064-14073. https://doi.org/10.1523/jneurosci.3403-12.2012

Cerullo, M. A. (2015). The Problem With Phi: A Critique of Integrated Information Theory. *11*(9), e1004286. https://doi.org/10.1371/journal.pcbi.1004286

Chakravartty, A. (2017). *Scientific Realism*. Metaphysics Research Lab, Stanford University. https://plato.stanford.edu/archives/sum2017/entries/scientific-realism

Chalmers, D. (2007). The Hard Problem of Consciousness. In *The Blackwell Companion to Consciousness* (pp. 223-235). https://doi.org/10.1002/9780470751466.ch18

Chalmers, D. (2017). The Hard Problem of Consciousness. 32-42. https://doi.org/10.1002/9781119132363.ch3

Chalmers, D. J. (1998). Facing Up to the Problem of Consciousness. 207-228. https://doi.org/10.4324/9780203826430-11

Chalmers, D. J. (2003). Consciousness and Its Place in Nature. 102-142. https://doi.org/10.1002/9780470998762.ch5

Chalmers, D. J. (2010). The Character of Consciousness. https://doi.org/10.1093/acprof:oso/9780195311105.001.0001

Chalmers, D. J. (2019). Extended Cognition and Extended Consciousness. 9-C1.P67. https://doi.org/10.1093/oso/9780190662813.003.0002

Chen, C.-C., Kilner, J. M., Friston, K. J., Kiebel, S. J., Jolly, R. K., & Ward, N. (2010). Nonlinear Coupling in the Human Motor System. *Journal of Neuroscience*, *30*(25), 8393-8399. https://doi.org/10.1523/jneurosci.1194-09.2010

Chen, K.-F., Lowe, S., Lamaze, A., Krätschmer, P., & Jepson, J. (2019). Neurocalcin regulates nighttime sleep and arousal in Drosophila. *Elife*, *8*, e38114. https://doi.org/10.7554/eLife.38114

Choi, E. Y., Ding, S. L., & Haber, S. N. (2017). Combinatorial Inputs to the Ventral Striatum From the Temporal Cortex, Frontal Cortex, and Amygdala: Implications for Segmenting the Striatum. *eNeuro*, *4*(6), ENEURO.0392-0317.2017. https://doi.org/10.1523/eneuro.0392-17.2017

Coenen, V. A., Schlaepfer, T. E., Maedler, B., & Panksepp, J. (2011). Cross-Species Affective Functions of the Medial Forebrain Bundle—Implications for the Treatment of Affective Pain and Depression in Humans. *35*(9), 1971-1981. https://doi.org/10.1016/j.neubiorev.2010.12.009

Collette, S., Pauli, W. M., Bossaerts, P., & O'Doherty, J. P. (2017). Neural Computations Underlying Inverse Reinforcement Learning in the Human Brain. *Elife*, *6*. https://doi.org/10.7554/elife.29718

Damasio, A. (2001). Fundamental feelings [Short Survey]. *Nature*, *413*(6858), 781. https://doi.org/10.1038/35101669

Damasio, A. (2003). Feelings of emotion and the self. *Ann N Y Acad Sci*, *1001*, 253-261. https://doi.org/10.1196/annals.1279.014

Damasio, A., Damasio, H., & Tranel, D. (2013). Persistence of feelings and sentience after bilateral damage of the insula. *Cereb Cortex*, *23*(4), 833-846. https://doi.org/10.1093/cercor/bhs077

Damasio, A. R. (2001). Emotion and the human brain. In *Annals of the New York Academy of Sciences* (Vol. 935, pp. 101-106).

Davis, E., & Marcus, G. (2015). Commonsense Reasoning and Commonsense Knowledge in Artificial Intelligence. *Communications of the Acm*, *58*(9), 92-103. https://doi.org/10.1145/2701413

Davis, K. L., Panksepp, J., & Normansell, L. (2003). The Affective Neuroscience Personality Scales: Normative Data and Implications. *Neuropsychoanalysis*, *5*(1), 57-69. https://doi.org/10.1080/15294145.2003.10773410

Dennett, D. (2003). Explaining the "Magic" of Consciousness. *1*(1), 7-19. https://doi.org/10.1556/jcep.1.2003.1.2

Dennett, D. C. (2018). *Consciousness Explained*. Little, Brown. https://books.google.com/books?id=BKQjEQAAQBAJ

Dennett, D. C. (2018). Facing Up to the Hard Question of Consciousness. *373*(1755), 20170342. https://doi.org/10.1098/rstb.2017.0342

Dissel, S., Angadi, V., Kirszenblat, L., Suzuki, Y., Donlea, J., Klose, M., Koch, Z., English, D., Winsky-Sommerer, R., van Swinderen, B., & Shaw, Paul J. (2015). Sleep Restores Behavioral Plasticity to Drosophila Mutants. *25*(10), 1270-1281. https://doi.org/10.1016/j.cub.2015.03.027

Dissel, S., Klose, M. K., van Swinderen, B., Cao, L., Ford, M., Periandri, E. M., Jones, J. D., Li, Z., & Shaw, P. J. (2022). Sleep-promoting neurons remodel their response properties to calibrate sleep drive with environmental demands. *PLoS Biol*, *20*(9), e3001797. https://doi.org/10.1371/journal.pbio.3001797

Dodig-Crnkovic, G. (2023). How GPT Realizes Leibniz's Dream and Passes the Turing Test without Being Conscious. *Computer Sciences &amp; Mathematics Forum*, *8*(1).

Dreyfus, H., Dreyfus, S. E., & Athanasiou, T. (1986). *Mind Over Machine*. Simon & Schuster. https://books.google.com/books?id=e9W9m_4q4pYC

Dreyfus, H. L. (2007). Why Heideggerian AI Failed and How Fixing It Would Require Making It More Heideggerian. *Philosophical Psychology*, *20*(2), 247-268. https://doi.org/10.1080/09515080701239510

Dreyfus, H. L. (2016). 20. What Computers Can't Do: A Critique of Artificial Reason. 90-100. https://doi.org/10.1515/9781400848393-021

Einstein, E. B., Asaka, Y., Yeckel, M. F., Higley, M. J., & Picciotto, M. R. (2013). Galanin-induced Decreases in Nucleus Accumbens/Striatum Excitatory Postsynaptic Potentials and Morphine Conditioned Place Preference Require Both Galanin Receptor 1 and Galanin Receptor 2. *European Journal of Neuroscience*, *37*(9), 1541-1549. https://doi.org/10.1111/ejn.12151

Enochson, A., Ewert, D., Mitar, D., Striker, R., Cleveland, J., Wolf, H., Gieser, A., Braaten, B., Allen, J., & Allen, M. (2022). MODELING THE HODGKIN-HUXLEY NEURON TO DETERMINE NEURONAL ENERGY CONSUMPTION EFFICIENCY AND OXYGEN CONSUMPTION VALUES [Article]. *Biomedical Sciences Instrumentation*, *58*(2), 50-58. https://doi.org/10.34107/NSJX733550

Erwin, D. H., Laflamme, M., Tweedt, S. M., Sperling, E. A., Pisani, D., & Peterson, K. J. (2011). The Cambrian Conundrum: Early Divergence and Later Ecological Success in the Early History of Animals. *334*(6059), 1091-1097. https://doi.org/10.1126/science.1206375

Escorcia-Rodríguez, J. M., Esposito, M., Freyre-González, J. A., & Moreno-Hagelsieb, G. (2022). Non-Synonymous to Synonymous Substitutions Suggest That Orthologs Tend to Keep Their Functions, While Paralogs Are a Source of Functional Novelty. *10*, e13843. https://doi.org/10.7717/peerj.13843

Fabbro, F., Aglioti, S. M., Bergamasco, M., Clarici, A., & Panksepp, J. (2015). Evolutionary aspects of self- and world consciousness in vertebrates [Article]. *Frontiers in Human Neuroscience*, *9*(MAR), Article 157. https://doi.org/10.3389/fnhum.2015.00157

Faville, R., Kottler, B., Goodhill, G. J., Shaw, P. J., & van Swinderen, B. (2015). How deeply does your mutant sleep? Probing arousal to better understand sleep defects in Drosophila. *Scientific Reports*, *5*(1), 8454. https://doi.org/10.1038/srep08454

Feldman Barrett, L., & Lida, T. (2024). Constructionist Theories of Emotions in Psychology and Neuroscience. 350-387. https://doi.org/10.4324/9781315559940-20

Fiser, J., Berkes, P., Orbán, G., & Lengyel, M. (2010). Statistically Optimal Perception and Learning: From Behavior to Neural Representations. *Trends in Cognitive Sciences*, *14*(3), 119-130. https://doi.org/10.1016/j.tics.2010.01.003

Fisher, Y. E., Lu, J., D'Alessandro, I., & Wilson, R. I. (2019). Sensorimotor experience remaps visual input to a heading-direction network. *Nature*, *576*(7785), 121-125. https://doi.org/10.1038/s41586-019-1772-4

Florensa, C., Duan, Y., & Abbeel, P. (2017). Stochastic Neural Networks for Hierarchical Reinforcement Learning. https://doi.org/10.48550/arxiv.1704.03012

Fornito, A., Zalesky, A., & Breakspear, M. (2013). Graph Analysis of the Human Connectome: Promise, Progress, and Pitfalls. *Neuroimage*, *80*, 426-444. https://doi.org/10.1016/j.neuroimage.2013.04.087

Franconville, R., Beron, C., & Jayaraman, V. (2018). Building a functional connectome of the Drosophila central complex. *Elife*, *7*, e37017. https://doi.org/10.7554/eLife.37017

Fridman, L. (2019, Oct 3, 2019 ). *Gary Marcus: Toward a Hybrid of Deep Learning and Symbolic AI*, YouTube. https://www.youtube.com/watch?v=vNOTDn3D_RI

Frighetto, G., Zordan, M. A., Castiello, U., Megighian, A., & Martin, J.-R. (2022). Dopamine Modulation of Drosophila Ellipsoid Body Neurons, a Nod to the Mammalian Basal Ganglia [Original Research]. *Frontiers in physiology*, *13*. https://doi.org/10.3389/fphys.2022.849142

Friston, K. (2024). *Davos 2024: A Conversation With Karl Friston & Gary Marcus* YouTube. https://www.youtube.com/watch?v=CJSEZj3zxZ4

Friston, K., Da Costa, L., & Parr, T. (2020). Some Interesting Observations on the Free Energy Principle. https://doi.org/10.48550/arxiv.2002.04501

Friston, K., & Penny, W. (2011). Post hoc Bayesian model selection. *Neuroimage*, *56*(4), 2089-2099. https://doi.org/10.1016/j.neuroimage.2011.03.062

Friston, K. J., Da Costa, L., & Parr, T. (2021). Some Interesting Observations on the Free Energy Principle. *Entropy (Basel)*, *23*(8). https://doi.org/10.3390/e23081076

Friston, K. J., FitzGerald, T. H. B., Rigoli, F., Schwartenbeck, P., & Pezzulo, G. (2017). Active Inference: A Process Theory. *Neural Computation*, *29*(1), 1-49. https://doi.org/10.1162/neco_a_00912

Friston, K. J., & Frith, C. D. (2015). Active Inference, Communication and Hermeneutics. *Cortex*, *68*, 129-143. https://doi.org/10.1016/j.cortex.2015.03.025

Friston, K. J., & Kiebel, S. J. (2009). Predictive Coding Under the Free-Energy Principle. *Philosophical Transactions of the Royal Society B Biological Sciences*, *364*(1521), 1211-1221. https://doi.org/10.1098/rstb.2008.0300

Frith, C. D. (2019). The Neural Basis of Consciousness. *Psychological Medicine*, *51*(4), 550-562. https://doi.org/10.1017/s0033291719002204

Frye, M. A., & Dickinson, M. H. (2004). Motor Output Reflects the Linear Superposition of Visual and Olfactory Inputs In Drosophila. *Journal of Experimental Biology*, *207*(1), 123-131. https://doi.org/10.1242/jeb.00725

Garrido, M. I., Kilner, J. M., Kiebel, S. J., & Friston, K. J. (2007). Evoked Brain Responses Are Generated by Feedback Loops. *Proceedings of the National Academy of Sciences*, *104*(52), 20961-20966. https://doi.org/10.1073/pnas.0706274105

Gerstner, W., & Kistler, W. M. (2002). Spiking Neuron Models. https://doi.org/10.1017/cbo9780511815706

Gonze, D., Halloy, J., & Goldbeter, A. (2004). Stochastic Models for Circadian Oscillations: Emergence of a Biological Rhythm. *98*(2), 228-238. https://doi.org/10.1002/qua.10875

Grabowska, M. J., Jeans, R., Steeves, J., & van Swinderen, B. (2020). Oscillations in the central brain of Drosophila are phase locked to attended visual features. *Proc Natl Acad Sci U S A*, *117*(47), 29925-29936. https://doi.org/10.1073/pnas.2010749117

Gray, C. M. (1994). Synchronous Oscillations in Neuronal Systems: Mechanisms and Functions. *Journal of Computational Neuroscience*, *1*(1-2), 11-38. https://doi.org/10.1007/bf00962716

Guerguiev, J., Lillicrap, T. P., & Richards, B. A. (2017). Towards Deep Learning With Segregated Dendrites. *Elife*, *6*. https://doi.org/10.7554/elife.22901

Hafez, O. A., Escribano, B., Ziegler, R. L., Hirtz, J. J., Niebur, E., & Pielage, J. (2023). The Cellular Architecture of Memory Modules in Drosophila Supports Stochastic Input Integration. *12*. https://doi.org/10.7554/elife.77578

Haikonen, P. O. (2020). On Artificial Intelligence and Consciousness. *Journal of Artificial Intelligence and Consciousness*, *07*(01), 73-82. https://doi.org/10.1142/s2705078520500046

Hales, C. G., & Ericson, M. (2022). Electromagnetism's Bridge Across the Explanatory Gap: How a Neuroscience/Physics Collaboration Delivers Explanation Into All Theories of Consciousness. *16*. https://doi.org/10.3389/fnhum.2022.836046

Hameroff, S. (2012). How Quantum Brain Biology Can Rescue Conscious Free Will. *6*. https://doi.org/10.3389/fnint.2012.00093

Hameroff, S. (2020). 'Orch OR' Is the Most Complete, and Most Easily Falsifiable Theory of Consciousness. *12*(2), 74-76. https://doi.org/10.1080/17588928.2020.1839037

Hameroff, S., & Penrose, R. (2007). Conscious Events as Orchestrated Space-Time Selections. *1*(1). https://doi.org/10.14704/nq.2003.1.1.3

Hameroff, S., & Penrose, R. (2014). Consciousness in the Universe. *11*(1), 39-78. https://doi.org/10.1016/j.plrev.2013.08.002

Hameroff, S. R. (2007). The Brain Is Both Neurocomputer and Quantum Computer. *31*(6), 1035-1045. https://doi.org/10.1080/03640210701704004

Hameroff, S. R., & Penrose, R. (2016). Consciousness in the Universe an Updated Review of the "Orch Or" Theory. 517-599. https://doi.org/10.1142/9789814644266_0014

Han, B., McCarren, H. S., O'Neill, D. G., & Kelz, M. B. (2014). Distinctive Recruitment of Endogenous Sleep-Promoting Neurons by Volatile Anesthetics and a Nonimmobilizer. *Anesthesiology*, *121*(5), 999-1009. https://doi.org/10.1097/aln.0000000000000383

Hanesch, U., Fischbach, K. F., & Heisenberg, M. (1989). Neuronal Architecture of the Central Complex in Drosophila Melanogaster. *Cell and Tissue Research*, *257*(2), 343-366. https://doi.org/10.1007/bf00261838

Hatfield, G. (2024). *René Descartes*. Metaphysics Research Lab, Stanford University. https://plato.stanford.edu/archives/sum2024/entries/descartes

He, K., Zhang, X., Ren, S., & Sun, J. (2016). Deep Residual Learning for Image Recognition. https://doi.org/10.1109/cvpr.2016.90

Heidegger, M., & Stambaugh, J. (1996). *Being and Time : A Translation of Sein Und Zeit* [Book]. SUNY Press. https://search.ebscohost.com/login.aspx?direct=true&db=nlebk&AN=7751&site=ehost-live&scope=site

Heinze, S., & Homberg, U. (2007). Maplike Representation of Celestial <i>E</I> -Vector Orientations in the Brain of an Insect. *Science*, *315*(5814), 995-997. https://doi.org/10.1126/science.1135531

Hepburn, R. W., Heidegger, M., Macquarrie, J., & Robinson, E. L. (1964). Being and Time. *The Philosophical Quarterly*, *14*(56), 276. https://doi.org/10.2307/2955477

Hiley, B. J., & Pylkkänen, P. (2022). Can Quantum Mechanics Solve the Hard Problem of Consciousness? , 415-459. https://doi.org/10.1093/oso/9780197501665.003.0016

Hodgkin, A. L., & Huxley, A. (1952). A Quantitative Description of Membrane Current and Its Application to Conduction and Excitation in Nerve. *The Journal of Physiology*, *117*(4), 500-544. https://doi.org/10.1113/jphysiol.1952.sp004764

Honkanen, A., Hensgen, R., Kannan, K., Adden, A., Warrant, E., Wcislo, W., & Heinze, S. (2023). Parallel Motion Vision Pathways in the Brain of a Tropical Bee. *209*(4), 563-591. https://doi.org/10.1007/s00359-023-01625-x

Hossenfelder, S. (2022, YouTube). *Consciousness and Quantum Mechanics: How are they related?* YouTube. https://www.youtube.com/watch?v=v1wqUCATYUA

Hossenfelder, S. (2024, Jun 13, 2024). *Is the Intelligence-Explosion Near? A Reality Check.* YouTube. https://www.youtube.com/watch?v=xm1B3Y3ypoE&t=540s

Hulse, B. K., Haberkern, H., Franconville, R., Turner-Evans, D., Takemura, S.-y., Wolff, T., Noorman, M., Dreher, M., Dan, C., Parekh, R., Hermundstad, A. M., Rubin, G. M., & Jayaraman, V. (2021). A connectome of the Drosophila central complex reveals network motifs suitable for flexible navigation and context-dependent action selection. *Elife*, *10*, e66039. https://doi.org/10.7554/eLife.66039

Huoviala, P., Dolan, M. J., Love, F. M., Myers, P., Frechter, S., Namiki, S., Pettersson, L., Roberts, R. J., Turnbull, R., Mitrevica, Z., Breads, P., Schlegel, P., Bates, A. S., Rodrigues, T. M., Aso, Y., Bock, D. D., Rubin, G. M., Stensmyr, M. C., Card, G. M., . . . Jefferis, G. S. (2018). Neural Circuit Basis of Aversive Odour Processing in <i>Drosophila</I> From Sensory Input to Descending Output. https://doi.org/10.1101/394403

Huston, S. J., & Jayaraman, V. (2011). Studying Sensorimotor Integration in Insects. *Current Opinion in Neurobiology*, *21*(4), 527-534. https://doi.org/10.1016/j.conb.2011.05.030

Ikemoto, S., & Panksepp, J. (1999). The Role of Nucleus Accumbens Dopamine in Motivated Behavior: A Unifying Interpretation With Special Reference to Reward-Seeking. *Brain Research Reviews*, *31*(1), 6-41. https://doi.org/10.1016/s0165-0173(99)00023-5

Jung, C. G., Baynes, H. G., & Beebe, J. (2016). *Psychological types* [Book]. https://doi.org/10.4324/9781315512334

Kasabov, N. K., Bahrami, H., Doborjeh, M., & Wang, A. (2023). Brain-Inspired Spatio-Temporal Associative Memories for Neuroimaging Data Classification: EEG and fMRI. *Bioengineering*, *10*(12).

Kato, Y., Tomita, J., & Kume, K. (2022). Interneurons of Fan-Shaped Body Promote Arousal in Drosophila. *PLoS One*, *17*(11), e0277918. https://doi.org/10.1371/journal.pone.0277918

Kazemi, S., & Jamali, Y. (2022). Phase Synchronization and Measure of Criticality in a Network of Neural Mass Models. *12*(1). https://doi.org/10.1038/s41598-022-05285-w

Keating, B. (2024, May 21, 2024). *Dan Dennett: Sir Roger Penrose Is WRONG About Human Consciousness!* [Interview]. YouTube. https://www.youtube.com/watch?v=fZejt_F1sX8

Kent, A. (2021). Collapse and Measures of Consciousness. *51*(3). https://doi.org/10.1007/s10701-021-00467-4

Keny, V., Vanlalnghaka, C., Hakim, S. S., Barnabas, R. J., & Joshi, D. S. (2007). Two Oscillators Might Control the Locomotor Activity Rhythm of the High-Altitude Himalayan Strain Of<i>Drosophila Helvetica</I>. *24*(5), 821-834. https://doi.org/10.1080/07420520701649463

Kerr, B. J., Cafferty, W. B. J., Gupta, Y., Bacon, A., Wynick, D., McMahon, S. B., & Thompson, S. W. N. (2000). Galanin Knockout Mice Reveal Nociceptive Deficits Following

Peripheral Nerve Injury. *European Journal of Neuroscience*, *12*(3), 793-802. https://doi.org/10.1046/j.1460-9568.2000.00967.x

Keshishian, M., Akbari, H., Khalighinejad, B., Herrero, J. L., Mehta, A. D., & Mesgarani, N. (2020). Estimating and Interpreting Nonlinear Receptive Field of Sensory Neural Responses With Deep Neural Network Models. *Elife*, *9*. https://doi.org/10.7554/elife.53445

Kieras, D. E., Meyer, D. E., Mueller, S., & Seymour, T. (1999). Insights Into Working Memory From the Perspective of the EPIC Architecture for Modeling Skilled Perceptual-Motor and Cognitive Human Performance. 183-223. https://doi.org/10.1017/cbo9781139174909.009

Kieras, D. E., Wood, S. D., & Meyer, D. E. (1995). Predictive Engineering Models Using the EPIC Architecture for a High-Performance Task. 11-18. https://doi.org/10.1145/223904.223906

Kietzmann, T. C., Spoerer, C. J., Sörensen, L. K. A., Cichy, R. M., Hauk, O., & Kriegeskorte, N. (2019). Recurrence Is Required to Capture the Representational Dynamics of the Human Visual System. *116*(43), 21854-21863. https://doi.org/10.1073/pnas.1905544116

Kirszenblat, L., Ertekin, D., Goodsell, J., Zhou, Y., Shaw, P. J., & van Swinderen, B. (2018). Sleep Regulates Visual Selective Attention in <i>Drosophila</I>. https://doi.org/10.1242/jeb.191429

Kirszenblat, L., & van Swinderen, B. (2019). Sleep in Drosophila. 333-347. https://doi.org/10.1016/b978-0-12-813743-7.00022-0

Ko, J. S., Koh, H., Park, N., & Jhe, W. (2022). Homotopy-Based Training of NeuralODEs for Accurate Dynamics Discovery. https://doi.org/10.48550/arxiv.2210.01407

Koch, C. (2018). What Is Consciousness? [Article]. *Scientific American*, *318*(6), 60-64. https://doi.org/10.1038/scientificamerican0618-60

Koch, C. (2021). Reflections of a natural scientist on panpsychism [Article]. *Journal of Consciousness Studies*, *28*(9-10), 65-75. https://doi.org/10.5376/20512201.28.9.065

Kording, K. P. (2021). For love of neuroscience: The Neuromatch movement. *Neuron*, *109*(19), 3034-3035. https://doi.org/10.1016/j.neuron.2021.07.021

Kottler, B., Bao, H., Zalucki, O., Imlach, W., Troup, M., van Alphen, B., Paulk, A., Zhang, B., & van Swinderen, B. (2013). A Sleep/Wake Circuit Controls Isoflurane Sensitivity in Drosophila. *23*(7), 594-598. https://doi.org/10.1016/j.cub.2013.02.021

Krizhevsky, A., Sutskever, I., & Hinton, G. E. (2017). ImageNet Classification With Deep Convolutional Neural Networks. *60*(6), 84-90. https://doi.org/10.1145/3065386

Kroeger, D., Absi, G., Gagliardi, C., Bandaru, S. S., Madara, J. C., Ferrari, L. L., Arrigoni, E., Münzberg, H., Scammell, T. E., Saper, C. B., & Vetrivelan, R. (2018). Galanin Neurons in the Ventrolateral Preoptic Area Promote Sleep and Heat Loss in Mice. *9*(1). https://doi.org/10.1038/s41467-018-06590-7

Kulkarni, S. R., Parsa, M., Mitchell, J. P., & Schuman, C. D. (2021). Benchmarking the performance of neuromorphic and spiking neural network simulators [Article]. *Neurocomputing*, *447*, 145-160. https://doi.org/10.1016/j.neucom.2021.03.028

Kuramoto, Y. (1984). *Chemical Oscillations, Waves, and Turbulence*. https://doi.org/10.1007/978-3-642-69689-3

Lahav, N., & Neemeh, Z. A. (2022). A Relativistic Theory of Consciousness. *12*. https://doi.org/10.3389/fpsyg.2021.704270

Laird, J. E. (2012). The Soar Cognitive Architecture. https://doi.org/10.7551/mitpress/7688.001.0001

Långsjö, J., Alkire, M. T., Kaskinoro, K., Hayama, H., Maksimow, A., Kaisti, K. K., Aalto, S., Aantaa, R., Jääskeläinen, S. K., Revonsuo, A., & Scheinin, H. (2012). Returning From Oblivion: Imaging the Neural Core of Consciousness. *Journal of Neuroscience*, *32*(14), 4935-4943. https://doi.org/10.1523/jneurosci.4962-11.2012

Larkin, A., Chen, M. Y., Kirszenblat, L., Reinhard, J., van Swinderen, B., & Claudianos, C. (2015). Neurexin-1 Regulates Sleep and Synaptic Plasticity In Drosophila Melanogaster. *42*(7), 2455-2466. https://doi.org/10.1111/ejn.13023

Lawrence Kuhn, R. ( 2022, Jun 5, 2022). *Max Tegmark - Quantum Physics of Consciousness* YouTube. https://www.youtube.com/watch?v=R04USRugo90

Lazar, A. A., Liu, T., Turkcan, M. K., & Zhou, Y. (2021). Accelerating With FlyBrainLab the Discovery of the Functional Logic of the Drosophila Brain in the Connectomic and Synaptomic Era. *Elife*, *10*. https://doi.org/10.7554/elife.62362

Lazar, A. A., Turkcan, M. K., & Zhou, Y. (2021). A Programmable Ontology Encompassing the Functional Logic of the <i>Drosophila</I> Brain. https://doi.org/10.1101/2021.12.28.474399

Lazopulo, S., Lopez, J. A., Levy, P., & Syed, S. (2015). A Stochastic Burst Follows the Periodic Morning Peak in Individual Drosophila Locomotion. *10*(11), e0140481. https://doi.org/10.1371/journal.pone.0140481

LeDoux, J. E. (2023). *The Four Realms of Existence: A New Theory of Being Human*. Belknap Press.

Li, Z., Wang, S. H., Fan, R. R., Cao, G., Zhang, Y. D., & Guo, T. (2019). Teeth Category Classification via Seven-layer Deep Convolutional Neural Network With Max Pooling and Global Average Pooling. *29*(4), 577-583. https://doi.org/10.1002/ima.22337

Linkenkaer-Hansen, K., Nikouline, V. V., Palva, J. M., & Ilmoniemi, R. J. (2001). Long-Range Temporal Correlations and Scaling Behavior in Human Brain Oscillations. *21*(4), 1370-1377. https://doi.org/10.1523/jneurosci.21-04-01370.2001

Linnman, C., Moulton, E. A., Barmettler, G., Becerra, L., & Borsook, D. (2012). Neuroimaging of the Periaqueductal Gray: State of the Field. *Neuroimage*, *60*(1), 505-522. https://doi.org/10.1016/j.neuroimage.2011.11.095

Litt, A., Eliasmith, C., Kroon, F., Weinstein, S. J., & Thagard, P. (2006). Is the Brain a Quantum Computer? *Cognitive Science*, *30*(3), 593-603. https://doi.org/10.1207/s15516709cog0000_59

Liu, Q., Bell, B. J., Kim, D. W., Lee, S. S., Keles, M. F., Liu, Q., Blum, I. D., Wang, A. A., Blank, E. J., Xiong, J., Bedont, J. L., Chang, A. J., Issa, H., Cohen, J. Y., Blackshaw, S., & Wu, M. N. (2023). A clock-dependent brake for rhythmic arousal in the dorsomedial hypothalamus. *Nature Communications*, *14*(1), 6381. https://doi.org/10.1038/s41467-023-41877-4

Liu, Q., Li, S., Kodama, L., Driscoll, M. R., & Wu, M. N. (2012). Two Dopaminergic Neurons Signal to the Dorsal Fan-Shaped Body to Promote Wakefulness in Drosophila. *Current Biology*, *22*(22), 2114-2123. https://doi.org/10.1016/j.cub.2012.09.008

Ma, C. (2022). Generated Artificial General Intelligence. https://doi.org/10.14293/s2199-1006.1.sor-.pph6xzb.v2

Ma, W. J. (2019). Bayesian Decision Models: A Primer. *104*(1), 164-175. https://doi.org/10.1016/j.neuron.2019.09.037

Marcus, G. (2008). Language as Kluge. https://doi.org/10.1142/9789812776129_0084

Marcus, G. (2018). Deep Learning: A Critical Appraisal. https://doi.org/10.48550/arxiv.1801.00631

Mazzoni, A., Lindén, H., Cuntz, H., Lansner, A., Panzeri, S., & Einevoll, G. T. (2015). Computing the Local Field Potential (LFP) From Integrate-and-Fire Network Models. *PLoS Computational Biology*, *11*(12), e1004584. https://doi.org/10.1371/journal.pcbi.1004584

McGee, M. J., & Grill, W. M. (2016). Modeling the Spinal Pudendo-Vesical Reflex for Bladder Control by Pudendal Afferent Stimulation. *Journal of Computational Neuroscience*, *40*(3), 283-296. https://doi.org/10.1007/s10827-016-0597-5

Mehta, K., Goldin, R., & Ascoli, G. A. (2022). Circuit Analysis of the Drosophila Brain Using Connectivity-Based Neuronal Classification Reveals Organization of Key Communication Pathways. https://doi.org/10.1101/2022.03.11.484039

Merker, B. (2007). Consciousness without a cerebral cortex: a challenge for neuroscience and medicine. *Behav Brain Sci*, *30*(1), 63-81; discussion 81-134. https://doi.org/10.1017/s0140525x07000891

Merleau-Ponty, M., & Landes, D. (2013). *Phenomenology of Perception*. Taylor & Francis. https://books.google.com/books?id=Lh_e0_y1YjgC

Meyer, D. E., & Kieras, D. E. (1997). A Computational Theory of Executive Cognitive Processes and Multiple-Task Performance: Part I. Basic Mechanisms. *Psychological Review*, *104*(1), 3-65. https://doi.org/10.1037/0033-295x.104.1.3

Michel, M., & Morales, J. (2019). Minority Reports: Consciousness and the Prefrontal Cortex. *Mind & Language*, *35*(4), 493-513. https://doi.org/10.1111/mila.12264

Millidge, B. (2019a). Combining Active Inference and Hierarchical Predictive Coding: A Tutorial Introduction and Case Study. https://doi.org/10.31234/osf.io/kf6wc

Millidge, B. (2019b). Implementing Predictive Processing and Active Inference: Preliminary Steps and Results. https://doi.org/10.31234/osf.io/4hb58

Mitchell, H. A., & Weinshenker, D. (2010). Good Night and Good Luck: Norepinephrine in Sleep Pharmacology. *Biochemical Pharmacology*, *79*(6), 801-809. https://doi.org/10.1016/j.bcp.2009.10.004

Mørch, H. H. (2018). Is the Integrated Information Theory of Consciousness Compatible With Russellian Panpsychism? , *84*(5), 1065-1085. https://doi.org/10.1007/s10670-018-9995-6

Motta, S. C., Carobrez, A. P., & Canteras, N. S. (2017). The Periaqueductal Gray and Primal Emotional Processing Critical to Influence Complex Defensive Responses, Fear Learning and Reward Seeking. *Neuroscience & Biobehavioral Reviews*, *76*, 39-47. https://doi.org/10.1016/j.neubiorev.2016.10.012

Müller, V. C. (2009). Symbol Grounding in Computational Systems: A Paradox of Intentions. *Minds and Machines*, *19*(4), 529-541. https://doi.org/10.1007/s11023-009-9175-1

Nazemi, P. S., & Jamali, Y. (2019). On the Influence of Structural Connectivity on the Correlation Patterns and Network Synchronization. *12*. https://doi.org/10.3389/fncom.2018.00105

Nehrt, N. L., Clark, W. T., Radivojac, P., & Hahn, M. W. (2011). Testing the Ortholog Conjecture With Comparative Functional Genomic Data From Mammals. *7*(6), e1002073. https://doi.org/10.1371/journal.pcbi.1002073

None, N., Altenhoff, A. M., Boeckmann, B., Capella-Gutierrez, S., Dalquen, D. A., DeLuca, T., Forslund, K., Huerta-Cepas, J., Linard, B., Pereira, C., Pryszcz, L. P., Schreiber, F., da Silva, A. S., Szklarczyk, D., Train, C.-M., Bork, P., Lecompte, O., von Mering, C., Xenarios, I., . . . Dessimoz, C. (2016). Standardized Benchmarking in the Quest for Orthologs. *13*(5), 425-430. https://doi.org/10.1038/nmeth.3830

Oesterle, J., Behrens, C., Schröder, C., Hermann, T., Euler, T., Franke, K., Smith, R. G., Zeck, G., & Berens, P. (2020). Bayesian Inference for Biophysical Neuron Models Enables Stimulus Optimization for Retinal Neuroprosthetics. *Elife*, *9*. https://doi.org/10.7554/elife.54997

Oizumi, M., Albantakis, L., & Tononi, G. (2014). From the Phenomenology to the Mechanisms of Consciousness: Integrated Information Theory 3.0. *PLoS Computational Biology*, *10*(5), e1003588. https://doi.org/10.1371/journal.pcbi.1003588

Oizumi, M., Amari, S.-i., Yanagawa, T., Fujii, N., & Tsuchiya, N. (2016). Measuring Integrated Information From the Decoding Perspective. *12*(1), e1004654. https://doi.org/10.1371/journal.pcbi.1004654

Oizumi, M., Tsuchiya, N., & Amari, S. (2016). Unified Framework for Information Integration Based on Information Geometry. *Proceedings of the National Academy of Sciences*, *113*(51), 14817-14822. https://doi.org/10.1073/pnas.1603583113

Okubo, T., Patella, P., D'Alessandro, I., & Wilson, R. I. (2020). A Neural Network for Wind-Guided Compass Navigation. *Neuron*, *107*(5), 924-940.e918. https://doi.org/10.1016/j.neuron.2020.06.022

Olsen, S. R., & Wilson, R. I. (2008). Cracking Neural Circuits in a Tiny Brain: New Approaches for Understanding the Neural Circuitry of Drosophila. *31*(10), 512-520. https://doi.org/10.1016/j.tins.2008.07.006

Panksepp, J. (1998). *Affective neuroscience : the foundations of human and animal emotions*. Oxford University Press.

Panksepp, J. (2007). Affective Consciousness. 114-129. https://doi.org/10.1002/9780470751466.ch9

Panksepp, J. (2010). Evolutionary Substrates of Addiction: The Neurochemistries of Pleasure Seeking and Social Bonding in the Mammalian Brain. 137-167. https://doi.org/10.1037/12067-006

Panksepp, J. (2011). Cross-Species affective neuroscience decoding of the primal affective experiences of humans and related animals [Article]. *PLoS One*, *6*(9), Article e21236. https://doi.org/10.1371/journal.pone.0021236

Panksepp, J. (2011a). Toward a Cross-species Neuroscientific Understanding of the Affective Mind: Do Animals Have Emotional Feelings? , *73*(6), 545-561. https://doi.org/10.1002/ajp.20929

Panksepp, J. (2011b). What Is an Emotional Feeling? Lessons About Affective Origins From Cross-Species Neuroscience. *36*(1), 4-15. https://doi.org/10.1007/s11031-011-9232-y

Panksepp, J. (2013). Cross-species neuroaffective parsing of primal emotional desires and aversions in mammals [Article]. *Emotion Review*, *5*(3), 235-240. https://doi.org/10.1177/1754073913477515

Panksepp, J. (2016a). The Cross-mammalian Neurophenomenology of Primal Emotional Affects: From Animal Feelings to Human Therapeutics. *524*(8), 1624-1635. https://doi.org/10.1002/cne.23969

Panksepp, J. (2016b). The Psycho-Neurology of Cross-Species Affective/Social Neuroscience: Understanding Animal Affective States as a Guide to Development of Novel Psychiatric Treatments. 109-125. https://doi.org/10.1007/7854_2016_458

Panksepp, J., & Biven, L. (2012). *The archaeology of mind : neuroevolutionary origins of human emotions* (1st ed.). W. W Norton.

Panksepp, J., Knutson, B., & Burgdorf, J. (2002). The Role of Brain Emotional Systems in Addictions: A Neuro-evolutionary Perspective and New 'Self-report' Animal Model. *97*(4), 459-469. https://doi.org/10.1046/j.1360-0443.2002.00025.x

Panksepp, J., Lane, R. D., Solms, M., & Smith, R. (2017). Reconciling cognitive and affective neuroscience perspectives on the brain basis of emotional experience [Review]. *Neuroscience and Biobehavioral Reviews*, *76*, 187-215. https://doi.org/10.1016/j.neubiorev.2016.09.010

Parr, T., Pezzulo, G., & Friston, K. J. (2022). Active Inference. https://doi.org/10.7551/mitpress/12441.001.0001

Parvizi, J., & Damasio, A. (2001). Consciousness and the brainstem [Article]. *Cognition*, *79*(1-2), 135-160. https://doi.org/10.1016/S0010-0277(00)00127-X

Pennington, J., & Worah, P. (2019). Nonlinear Random Matrix Theory for Deep Learning. *2019*(12), 124005. https://doi.org/10.1088/1742-5468/ab3bc3

Penny, W. D., Kiebel, S. J., Kilner, J. M., & Rugg, M. D. (2002). Event-Related Brain Dynamics. *25*(8), 387-389. https://doi.org/10.1016/s0166-2236(02)02202-6

Perry, C. J., & Barron, A. B. (2013). Neural mechanisms of reward in insects. *Annual review of entomology*, *58*, 543-562. https://doi.org/10.1146/annurev-ento-120811-153631

Pezzulo, G., Parr, T., & Friston, K. (2022). The evolution of brain architectures for predictive coding and active inference. *Philos Trans R Soc Lond B Biol Sci*, *377*(1844), 20200531. https://doi.org/10.1098/rstb.2020.0531

Pfaff, D. (2019). *How Brain Arousal Mechanisms Work: Paths Toward Consciousness*. Cambridge University Press. https://books.google.com/books?id=8VN-DwAAQBAJ

Pfaff, D. W. (2019). *How Brain Arousal Mechanisms Work*. Cambridge University Pres.

Pfeiffer, M., & Pfeil, T. (2018). Deep Learning With Spiking Neurons: Opportunities and Challenges. *Frontiers in Neuroscience*, *12*. https://doi.org/10.3389/fnins.2018.00774

Pockett, S. (2014). Problems With Theories That Equate Consciousness With Information or Information Processing. *8*. https://doi.org/10.3389/fnsys.2014.00225

Polák, M., & Marvan, T. (2018). Neural Correlates of Consciousness Meet the Theory of Identity. *9*. https://doi.org/10.3389/fpsyg.2018.01269

Polger, T. W. (2004). Natural Minds. https://doi.org/10.7551/mitpress/4863.001.0001

Raji, J. I., & Potter, C. J. (2021). The Number of Neurons in Drosophila and Mosquito Brains. *PLoS One*, *16*(5), e0250381. https://doi.org/10.1371/journal.pone.0250381

Rashid, M. M., & Kurata, H. (2020). Coupling Protocol of Interlocked Feedback Oscillators in Circadian Clocks. *17*(167), 20200287. https://doi.org/10.1098/rsif.2020.0287

Razetti, A., Medioni, C., Malandain, G., Besse, F., & Descombes, X. (2018). A Stochastic Framework to Model Axon Interactions Within Growing Neuronal Populations. *14*(12), e1006627. https://doi.org/10.1371/journal.pcbi.1006627

Rich, D., Cazettes, F., Wang, Y., Peña, J. L., & Fischer, B. J. (2015). Neural Representation of Probabilities for Bayesian Inference. *Journal of Computational Neuroscience*, *38*(2), 315-323. https://doi.org/10.1007/s10827-014-0545-1

Rogozin, I. B. (2014). Complexity of Gene Expression Evolution After Duplication: Protein Dosage Rebalancing. *2014*, 1-8. https://doi.org/10.1155/2014/516508

Rozin, P., & Haidt, J. (2013). The domains of disgust and their origins: contrasting biological and cultural evolutionary accounts. *Trends in Cognitive Sciences*, *17*(8), 367-368. https://doi.org/https://doi.org/10.1016/j.tics.2013.06.001

Saper, C. B., Fuller, P. M., Pedersen, N. P., Lu, J., & Scammell, T. E. (2010). Sleep state switching. *Neuron*, *68*(6), 1023-1042. https://doi.org/10.1016/j.neuron.2010.11.032

Sartre, J. P., & Richmond, S. (2022). *Being and Nothingness: An Essay in Phenomenological Ontology*. Taylor & Francis. https://books.google.com/books?id=bglsEAAAQBAJ

Scheffer, L. K., Xu, C. S., Januszewski, M., Lu, Z., Takemura, S.-y., Hayworth, K. J., Huang, G. B., Shinomiya, K., Maitlin-Shepard, J., Berg, S., Clements, J., Hubbard, P. M., Katz, W. T., Umayam, L., Zhao, T., Ackerman, D., Blakely, T., Bogovic, J., Dolafi, T., . . . Plaza, S. M. (2020). A connectome and analysis of the adult Drosophila central brain. *Elife*, *9*, e57443. https://doi.org/10.7554/eLife.57443

Schurger, A., & Graziano, M. (2022). Consciousness Explained or Described? , *2022*(1). https://doi.org/10.1093/nc/niac001

Searle, J. R. (2004). *Mind: A Brief Introduction*. Oxford University Press. https://books.google.com/books?id=oSm8JUHJXqcC

Seelig, J. D., & Jayaraman, V. (2013). Feature Detection and Orientation Tuning in the Drosophila Central Complex. *Nature*, *503*(7475), 262-266. https://doi.org/10.1038/nature12601

Shanahan, M. (2006). A Cognitive Architecture That Combines Internal Simulation With a Global Workspace. *Consciousness and Cognition*, *15*(2), 433-449. https://doi.org/10.1016/j.concog.2005.11.005

Singh, R. B., Singh, V., & Ramaswamy, R. (2010). Stochastic Synchronization of Circadian Rhythms. *23*(5), 978-988. https://doi.org/10.1007/s11424-010-0208-x

Smith, R., & Lane, R. D. (2016). Unconscious emotion: A cognitive neuroscientific perspective. *Neuroscience & Biobehavioral Reviews*, *69*, 216-238. https://doi.org/https://doi.org/10.1016/j.neubiorev.2016.08.013

Sokoloski, S. (2017). Implementing a Bayes Filter in a Neural Circuit: The Case of Unknown Stimulus Dynamics. *29*(9), 2450-2490. https://doi.org/10.1162/neco_a_00991

Sokoloski, S., Aschner, A., & Coen-Cagli, R. (2020). Modelling the Neural Code in Large Populations of Correlated Neurons. https://doi.org/10.1101/2020.11.05.369827

Sokoloski, S., Aschner, A., & Coen-Cagli, R. (2021). Modelling the Neural Code in Large Populations of Correlated Neurons. *10*. https://doi.org/10.7554/elife.64615

Sokoloski, S., & Coen-Cagli, R. (2019). Conditional Finite Mixtures of Poisson Distributions for Context-Dependent Neural Correlations. https://doi.org/10.48550/arxiv.1908.00637

Solms, M. (1996). What are affects? *Psyche (Stuttg)*, *50*(6), 485-522. (Was sind Affekte?)

Solms, M. (2017a). Some innate predictions are social in nature: Commentary on “mentalizing homeostasis” by Fotopoulou and Tsakiris [Note]. *Neuropsychoanalysis*, *19*(1), 55-57. https://doi.org/10.1080/15294145.2017.1309622

Solms, M. (2017b). What is “the unconscious,” and where is it located in the brain? A neuropsychoanalytic perspective. In *Annals of the New York Academy of Sciences* (Vol. 1406, pp. 90-97).

Solms, M. (2019). The Hard Problem of Consciousness and the Free Energy Principle. *Frontiers in Psychology*, *9*. https://doi.org/10.3389/fpsyg.2018.02714

Solms, M. (2021). *The Hidden Spring: A Journey to the Source of Consciousness*. W. W. Norton & Company.

Solms, M., & Turnbull, O. (2007). To Sleep, Perchance to REM? The Rediscovered Role of Emotion and Meaning in Dreams. 478-500. https://doi.org/10.1093/acprof:oso/9780198568773.003.0030

Song, Z., Postma, M., Billings, Stephen A., Coca, D., Hardie, Roger C., & Juusola, M. (2012). Stochastic, Adaptive Sampling of Information by Microvilli in Fly Photoreceptors. *22*(15), 1371-1380. https://doi.org/10.1016/j.cub.2012.05.047

Steup, M. a. N., Ram. (2024). *Epistemology*. Metaphysics Research Lab, Stanford University. https://plato.stanford.edu/archives/win2024/entries/epistemology

Stoleru, D., Peng, Y., Agosto, J., & Rosbash, M. (2004). Coupled Oscillators Control Morning and Evening Locomotor Behaviour of Drosophila. *431*(7010), 862-868. https://doi.org/10.1038/nature02926

Stoljar, D. (2024). *Physicalism*. Metaphysics Research Lab, Stanford University. https://plato.stanford.edu/archives/spr2024/entries/physicalism/

Strausfeld, N. J., & Hirth, F. (2013). Deep Homology of Arthropod Central Complex and Vertebrate Basal Ganglia. *Science*, *340*(6129), 157-161. https://doi.org/10.1126/science.1231828

Strogatz, S. H. (2000). From Kuramoto to Crawford: Exploring the Onset of Synchronization in Populations of Coupled Oscillators. *143*(1-4), 1-20. https://doi.org/10.1016/s0167-2789(00)00094-4

Stubbs, G., & Friston, K. (2024). The Police Hunch: The Bayesian Brain, Active Inference, and the Free Energy Principle in Action. *15*. https://doi.org/10.3389/fpsyg.2024.1368265

Suckow, S., Deichsel, E., Ingram, S., Morgan, M. M., & Aicher, S. A. (2012). Columnar Distribution of Catecholaminergic Neurons in the Ventrolateral Periaqueductal Gray and Their Relationship to Efferent Pathways. *Synapse*, *67*(2), 94-108. https://doi.org/10.1002/syn.21624

Sullivan, L. F. (2019). Rewiring the Drosophila Brain With Genetic Manipulations in Neural Lineages [Mini Review]. *Frontiers in Molecular Neuroscience*, *12*. https://doi.org/10.3389/fnmol.2019.00082

Sun, R. (2005). The CLARION Cognitive Architecture: Extending Cognitive Modeling to Social Simulation. 79-100. https://doi.org/10.1017/cbo9780511610721.005

Sun, R. (2007). The Importance of Cognitive Architectures: An Analysis Based on CLARION. *19*(2), 159-193. https://doi.org/10.1080/09528130701191560

Sytsma, J. (2009). Phenomenological Obviousness and the New Science of Consciousness. *76*(5), 958-969. https://doi.org/10.1086/605821

Taatgen, N., Lebiere, C., & Anderson, J. (2005). Modeling Paradigms in ACT-R. 29-52. https://doi.org/10.1017/cbo9780511610721.003

Taherkhani, A., Belatreche, A., Li, Y., Cosma, G., Maguire, L. P., & McGinnity, T. M. (2020). A Review of Learning in Biologically Plausible Spiking Neural Networks. *122*, 253-272. https://doi.org/10.1016/j.neunet.2019.09.036

Tainton-Heap, L. A. L., Kirszenblat, L. C., Notaras, E. T., Grabowska, M. J., Jeans, R., Feng, K., Shaw, P. J., & van Swinderen, B. (2021). A Paradoxical Kind of Sleep in Drosophila melanogaster [Article]. *Current Biology*, *31*(3), 578-590.e576. https://doi.org/10.1016/j.cub.2020.10.081

Takemura, S.-y., Bharioke, A., Lů, Z., Nern, A., Vitaladevuni, S., Rivlin, P. K., Katz, W. T., Olbris, D. J., Plaza, S. M., Winston, P., Zhao, T., Horne, J. A., Fetter, R. D., Takemura, S., Blazek, K., Chang, L.-A., Ogundeyi, O., Saunders, M. A., Shapiro, V. L., . . . Chklovskii, D. B. (2013). A Visual Motion Detection Circuit Suggested by Drosophila Connectomics. *Nature*, *500*(7461), 175-181. https://doi.org/10.1038/nature12450

Tavanaei, A., Ghodrati, M., Kheradpisheh, S. R., Masquelier, T., & Maida, A. (2019). Deep Learning in Spiking Neural Networks. *111*, 47-63. https://doi.org/10.1016/j.neunet.2018.12.002

Thummerer, T., Stoljar, J., & Mikelsons, L. (2022). NeuralFMU: Presenting a Workflow for Integrating Hybrid NeuralODEs Into Real-World Applications. *11*(19), 3202. https://doi.org/10.3390/electronics11193202

Tobias Thummerer, N., Lars Mikelsons, N., & Josef Kircher, N. (2021). NeuralFMU: Towards Structural Integration of FMUs Into Neural Networks. https://doi.org/10.3384/ecp21181297

Tononi, G. (2008). Consciousness as Integrated Information: A Provisional Manifesto. *Biological Bulletin*, *215*(3), 216-242. https://doi.org/10.2307/25470707

Troup, M., Yap, M. H., Rohrscheib, C., Grabowska, M. J., Ertekin, D., Randeniya, R., Kottler, B., Larkin, A., Munro, K., Shaw, P. J., & van Swinderen, B. (2018). Acute control of the sleep switch in Drosophila reveals a role for gap junctions in regulating behavioral responsiveness. *Elife*, *7*. https://doi.org/10.7554/eLife.37105

Tsai, J. W., Hannibal, J., Hagiwara, G., Colas, D., Ruppert, É., Ruby, N. F., Heller, H. C., Franken, P., & Bourgin, P. (2009). Melanopsin as a Sleep Modulator: Circadian Gating of the Direct Effects of Light on Sleep and Altered Sleep Homeostasis in Opn4−/− Mice. *PLoS Biology*, *7*(6), e1000125. https://doi.org/10.1371/journal.pbio.1000125

van Alphen, B., Semenza, E. R., Yap, M., van Swinderen, B., & Allada, R. (2021). A deep sleep stage in Drosophila with a functional role in waste clearance. *Sci Adv*, *7*(4). https://doi.org/10.1126/sciadv.abc2999

van Alphen, B., Yap, M. H., Kirszenblat, L., Kottler, B., & van Swinderen, B. (2013). A dynamic deep sleep stage in Drosophila. *J Neurosci*, *33*(16), 6917-6927. https://doi.org/10.1523/JNEUROSCI.0061-13.2013

Van De Poll, M., Tainton-Heap, L., Troup, M., & van Swinderen, B. (2023). Whole-Brain Electrophysiology and Calcium Imaging in Drosophila during Sleep and Wake. *Cold Spring Harb Protoc*. https://doi.org/10.1101/pdb.top108394

Van De Poll, M. N., & van Swinderen, B. (2021). Balancing Prediction and Surprise: A Role for Active Sleep at the Dawn of Consciousness? *Front Syst Neurosci*, *15*, 768762. https://doi.org/10.3389/fnsys.2021.768762 van Swinderen, B. (2007). Sleep in Invertebrates. 451-456. https://doi.org/10.1016/b0-12-370878-8/00185-3

van Swinderen, B., & Kottler, B. (2014). Explaining General Anesthesia: A Two-step Hypothesis Linking Sleep Circuits and the Synaptic Release Machinery. *36*(4), 372-381. https://doi.org/10.1002/bies.201300154

Viegen, T. v., Akrami, A., Bonnen, K., DeWitt, E., Hyafil, A., Ledmyr, H., Lindsay, G. W., Mineault, P. J., Murray, J. D., Pitkow, X., Puce, A., Sedigh-Sarvestani, M., Stringer, C., Achakulvisut, T., Alikarami, E., Atay, M. S., Batty, E., Erlich, J. C., Galbraith, B. V., . . . Peters, M. A. K. (2021). Neuromatch Academy: Teaching Computational Neuroscience With Global Accessibility. *Trends in Cognitive Sciences*, *25*(7), 535-538. https://doi.org/10.1016/j.tics.2021.03.018

Vilas, M. G., Auksztulewicz, R., & Melloni, L. (2021). Active Inference as a Computational Framework for Consciousness [Article]. *Review of Philosophy and Psychology*. https://doi.org/10.1007/s13164-021-00579-w

Wang, D., & Li, M. (2017). Stochastic Configuration Networks: Fundamentals and Algorithms. *47*(10), 3466-3479. https://doi.org/10.1109/tcyb.2017.2734043

Wang, L., Fu, F., & Chen, X. (2024). Mathematics of multi-agent learning systems at the interface of game theory and artificial intelligence. *Science China Information Sciences*, *67*(6), 166201. https://doi.org/10.1007/s11432-024-3997-0

Wang, X.-J. (2010). Neurophysiological and Computational Principles of Cortical Rhythms in Cognition. *90*(3), 1195-1268. https://doi.org/10.1152/physrev.00035.2008

Wang, X. J. (2010). Neurophysiological and Computational Principles of Cortical Rhythms in Cognition. *Physiological Reviews*, *90*(3), 1195-1268. https://doi.org/10.1152/physrev.00035.2008

Waterhouse, R. M., Zdobnov, E. M., & Kriventseva, E. V. (2010). Correlating Traits of Gene Retention, Sequence Divergence, Duplicability and Essentiality in Vertebrates, Arthropods, and Fungi. *3*, 75-86. https://doi.org/10.1093/gbe/evq083

Waterhouse, R. M., Zdobnov, E. M., Tegenfeldt, F., Li, J., & Kriventseva, E. V. (2010). OrthoDB: The Hierarchical Catalog of Eukaryotic Orthologs in 2011. *39*(suppl_1), D283-D288. https://doi.org/10.1093/nar/gkq930

Weir, P., Schnell, B., & Dickinson, M. H. (2014). Central Complex Neurons Exhibit Behaviorally Gated Responses to Visual Motion In<i>Drosophila</I>. *Journal of Neurophysiology*, *111*(1), 62-71. https://doi.org/10.1152/jn.00593.2013

Whyte, C., & Smith, R. (2020). The Predictive Global Neuronal Workspace: A Formal Active Inference Model of Visual Consciousness. https://doi.org/10.1101/2020.02.11.944611

Wilson, H. R., & Cowan, J. D. (1972). Excitatory and inhibitory interactions in localized populations of model neurons. *Biophys J*, *12*(1), 1-24. https://doi.org/10.1016/s0006-3495(72)86068-5

Wilson, H. R., & Cowan, J. D. (2021). Evolution of the Wilson–Cowan Equations. *Biological Cybernetics*, *115*(6), 643-653. https://doi.org/10.1007/s00422-021-00912-7

Wilson, R. I. (2023). Neural Networks for Navigation: From Connections to Computations. *Annual Review of Neuroscience*, *46*(1), 403-423. https://doi.org/10.1146/annurev-neuro-110920-032645

Wilson, R. I., Turner, G., & Laurent, G. (2004). Transformation of Olfactory Representations in The <i>Drosophila</I> Antennal Lobe. *Science*, *303*(5656), 366-370. https://doi.org/10.1126/science.1090782

Wolff, Gabriella H., & Strausfeld, Nicholas J. (2015). Genealogical Correspondence of Mushroom Bodies Across Invertebrate Phyla. *25*(1), 38-44. https://doi.org/10.1016/j.cub.2014.10.049

Xie, H., Li, J., Zhang, Q., & Wang, Y. (2016). Comparison among dimensionality reduction techniques based on Random Projection for cancer classification. *Computational Biology and Chemistry*, *65*, 165-172. https://doi.org/https://doi.org/10.1016/j.compbiolchem.2016.09.010

Xu, Z., & Cai, X. (2009). Stochastic Simulation of Delay-Induced Circadian Rhythms in Drosophila. *2009*, 1-14. https://doi.org/10.1155/2009/386853

Yamins, D. L. K., Hong, H., Cadieu, C. F., Solomon, E. A., Seibert, D., & DiCarlo, J. J. (2014). Performance-Optimized Hierarchical Models Predict Neural Responses in Higher Visual Cortex. *111*(23), 8619-8624. https://doi.org/10.1073/pnas.1403112111

Yap, M., Grabowska, M., Rohrscheib, C., Jeans, R., Troup, M., Paulk, A. C., Alphen, B. v., Shaw, P. J., & Swinderen, B. v. (2017). Oscillatory Brain Activity in Spontaneous and Induced Sleep Stages in Flies. *Nature Communications*, *8*(1). https://doi.org/10.1038/s41467-017-02024-y

Yon, D., de Lange, F. P., & Press, C. (2019). The Predictive Brain as a Stubborn Scientist. *23*(1), 6-8. https://doi.org/10.1016/j.tics.2018.10.003

Young, J. M., & Armstrong, J. D. (2010). Structure of the Adult Central Complex in Drosophila: Organization of Distinct Neuronal Subsets. *The Journal of Comparative Neurology*, *518*(9), 1500-1524. https://doi.org/10.1002/cne.22284

Yu, T., Yang, Y., Li, D., Hospedales, T., & Xiang, T. (2021). Simple and Effective Stochastic Neural Networks. *35*(4), 3252-3260. https://doi.org/10.1609/aaai.v35i4.16436

Zahavi, D. (2003). *Husserl's Phenomenology*. Stanford University Press. https://books.google.com/books?id=kdVqnnJXVoMC

Zhang, J., Zhou, J., Wu, J., & Yang, S. (2019). SDChannelNets: Extremely Small and Efficient Convolutional Neural Networks. *E102.D*(12), 2646-2650. https://doi.org/10.1587/transinf.2019edl8120