

FlyWire: online community for whole-brain connectomics

2025-5-29

- **Introduction to Brain Connectomics and Applications in Model Organisms——王姣**
- **Foundational Principles and Operational Guidelines of the FlyWire——李畅**
- **Current Advances in Drosophila Research Using FlyWire——邢丽敏**

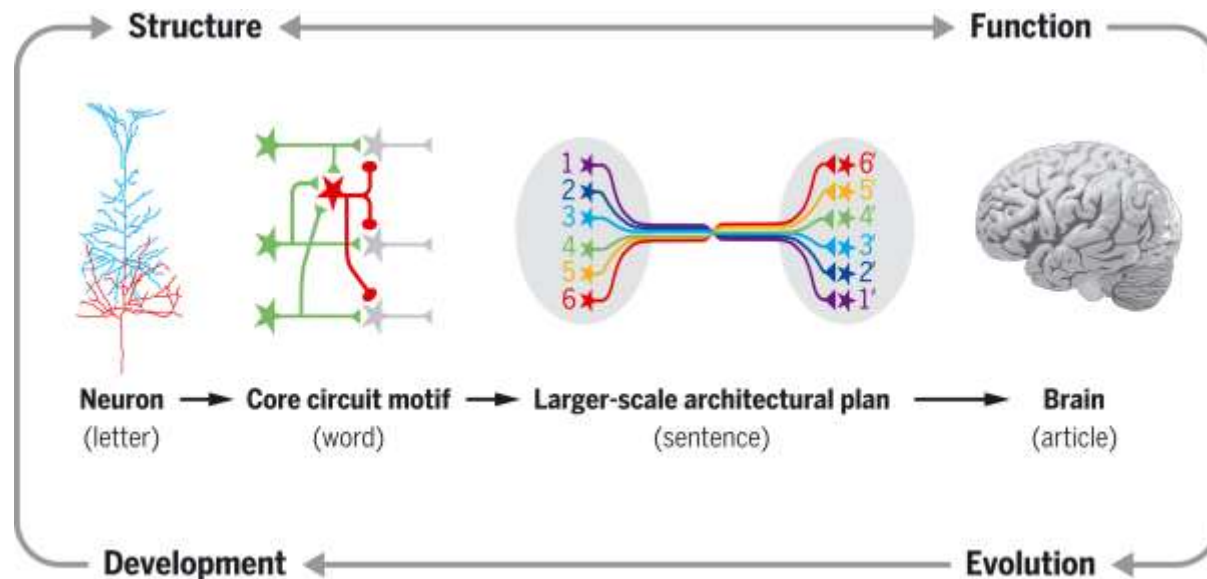
连接组学概述

1. Connectome & Connectomics
2. 连接组学中的常用技术
3. 连接组学中的突破性进展

What is the Connectomics

Connectomics: a branch of biotechnology concerned with applying the techniques of computer-assisted image acquisition and analysis to the structural mapping of sets of neural circuits or to the complete nervous system of selected organisms using high-speed methods, with organizing the results in databases, and with applications of the data.

——Jeff W. Lichtman



- 对大脑进行大范围的观察，明确特定功能与特定区域之间的联系。
- 描述单个神经细胞的特性以及它们如何使用电和化学信号进行通信。

How to get a Neural Connection Diagram

连接组映射依赖于获取和分析大视场（large-field-of-view）高分辨率（high-resolution）大脑图像的方法。

神经环路示踪技术：

传统神经示踪工具：

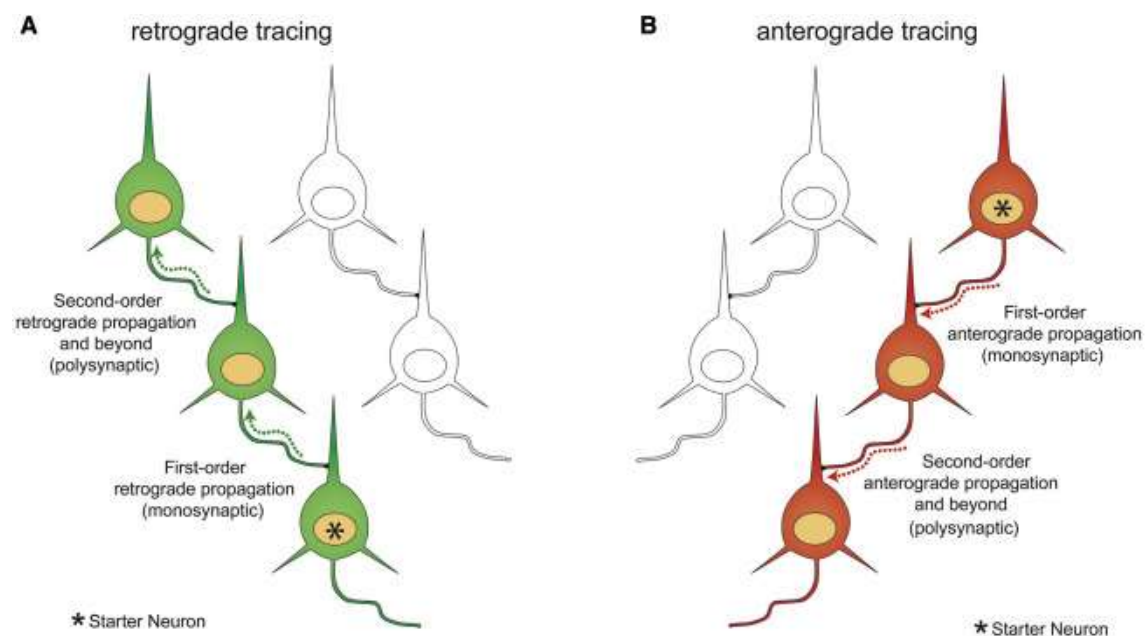
常用的示踪剂有：HRP（horse radish peroxidase，辣根过氧化物酶），快蓝（fast blue），荧光金

（fluorogold），核黄（nuclear yellow），神经生物素

（neurobiotin），生物素化葡聚糖胺（biotinylated dextran amine, BDA）等

①无法特异性标记细胞类型；②几乎没有跨突触能力；
难以用于多个脑区、多种类型神经元通过突触连接形成的复杂神经网络研究。

跨突触示踪（病毒转导）：



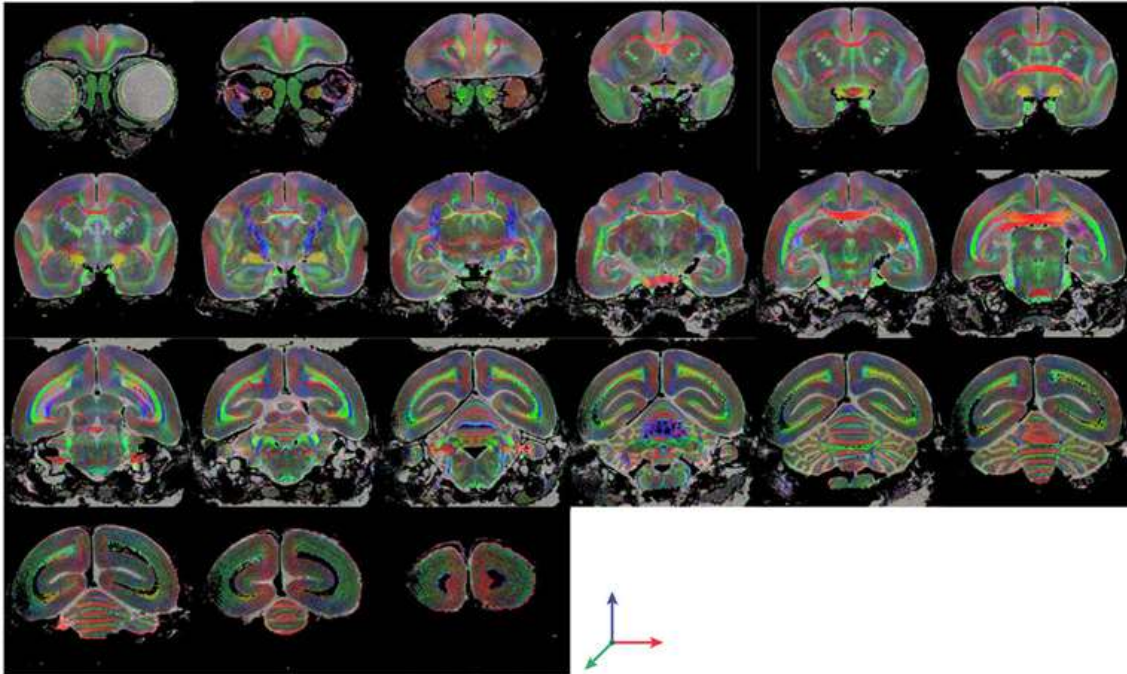
How to get a Neural Connection Diagram

神经影像技术：

	Light/fluorescence microscopy	Magnetic resonance imaging	Electron microscopy
Imaging performed using	Light (fluorescence)	Magnetic resonance	Electron
Resolution	High	Low	Extremely high
Skill level required for imaging	Low	High	High
Expense	Moderate	High	High
Whole-brain imaging	Difficult	Easy	Very difficult
Live imaging	Easy	Easy	Difficult

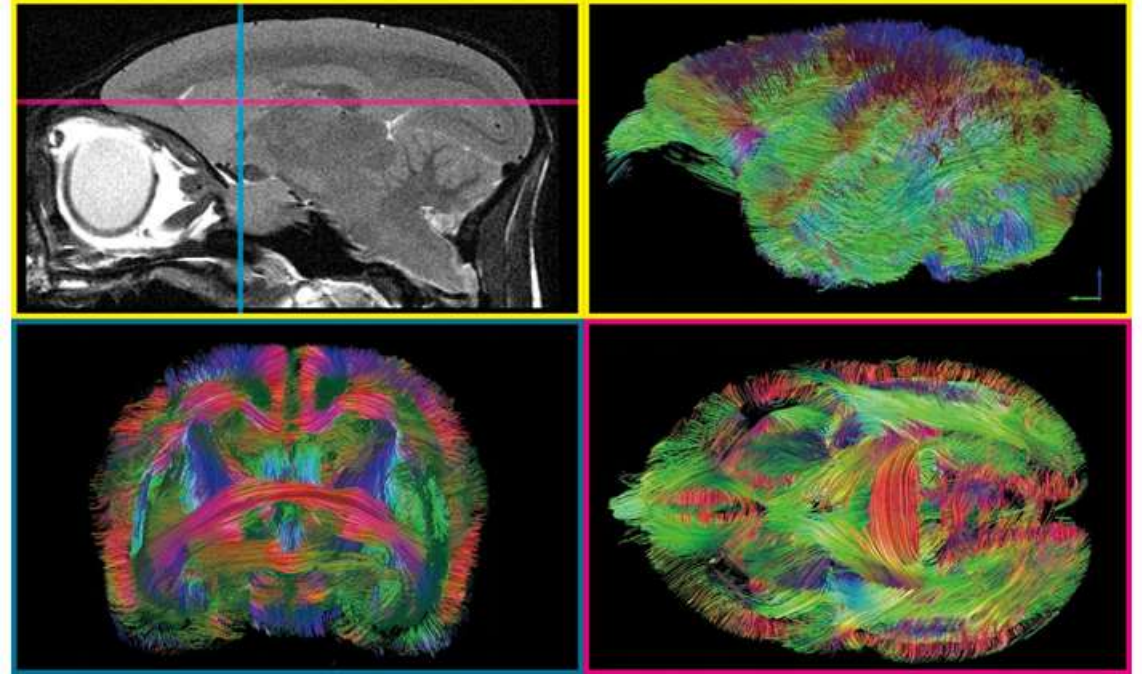
The three major technologies used for connectomics analysis

Macroscale connectomics with MRI



Images from MRI connectomics analysis

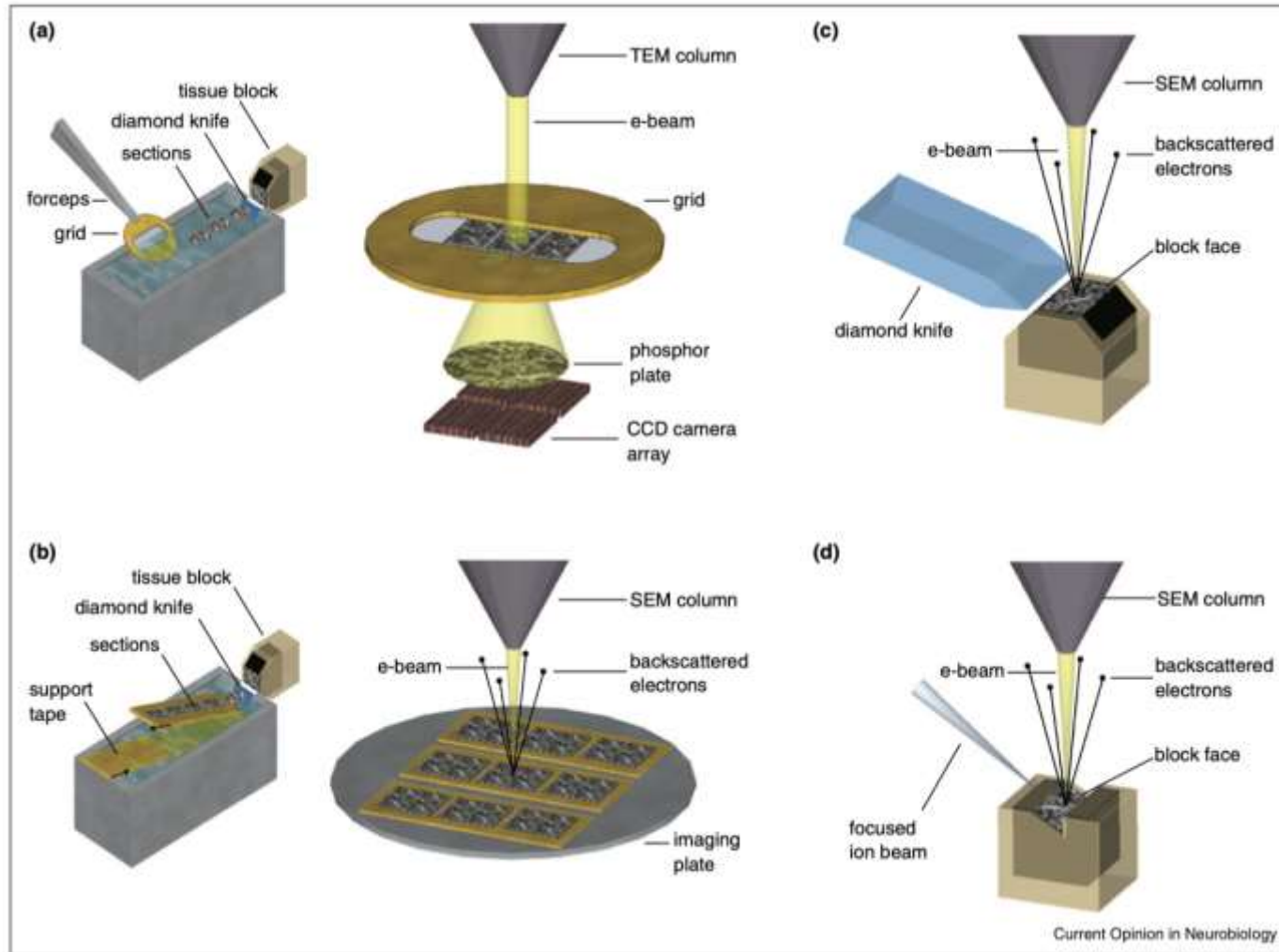
Colors indicate the fiber direction: green, antero-posterior; red, medio-lateral and blue, cranio-caudal.



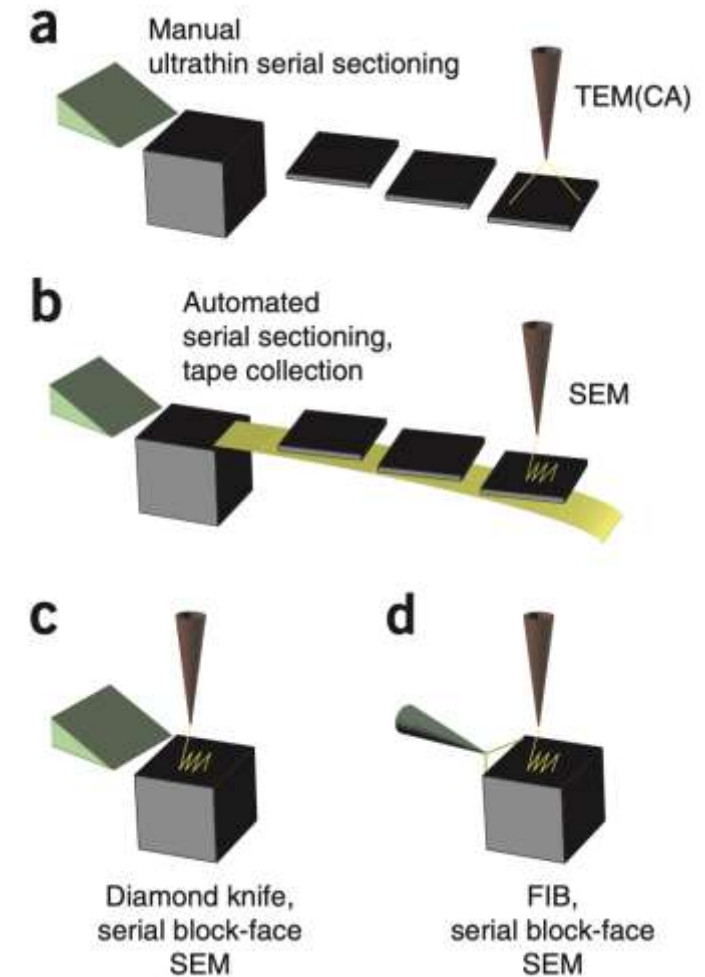
The macroscale fiber connections of the whole brain identified using tractography.

整个大脑的宏观纤维连接

Microscale connectomics with EM



(a)ssTEM. (b)ATUM-SEM. (c)SBEM. (d)FIB-SEM.




(a)TEM或TEMCA.(b)ATUM-SEM.(c)SBEM.(d)FIB-SEM

Mesoscale connectomics with LM

nature

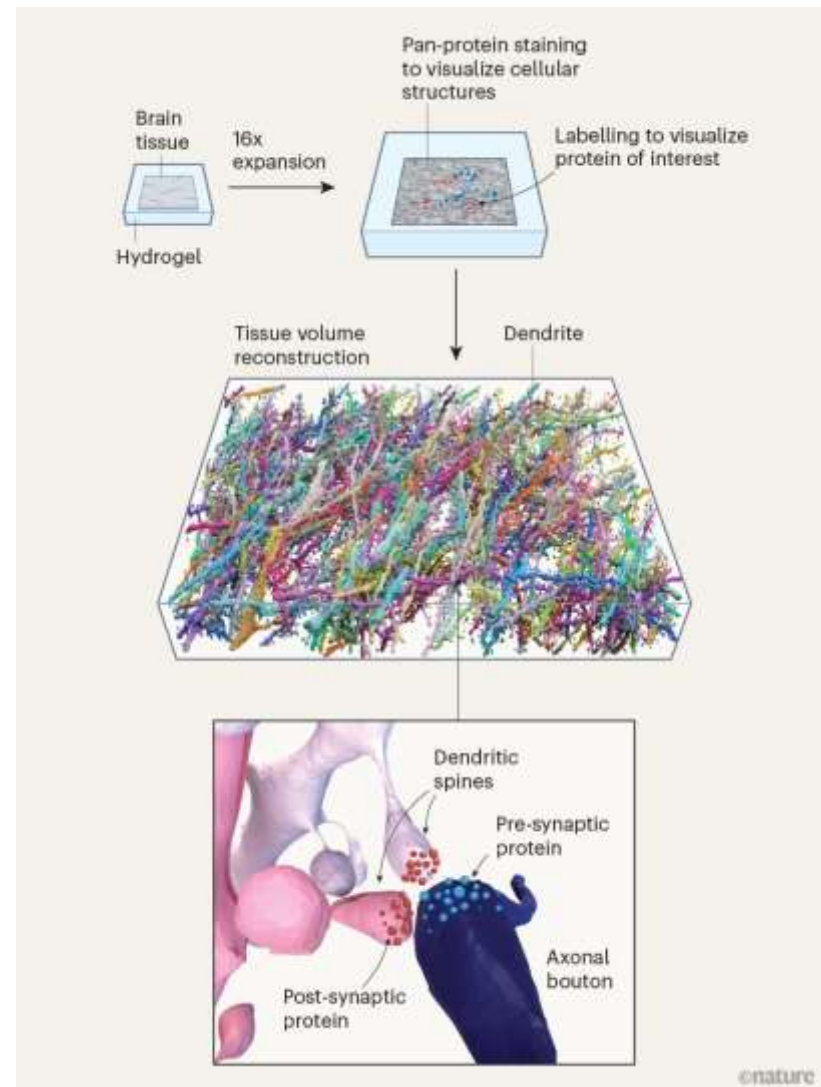
Light-microscopy-based connectomic reconstruction of mammalian brain tissue

[Mojtaba R. Tavakoli](#), [Julia Lyudchik](#), [Michał Januszewski](#), [Vitali Vistunou](#), [Nathalie Agudelo Dueñas](#), [Jakob Vorlauffer](#), [Christoph Sommer](#), [Caroline Kreuzinger](#), [Bárbara Oliveira](#), [Alban Cenameri](#), [Gaia Novarino](#), [Virer Jain](#) & [Johann G. Danzl](#) 

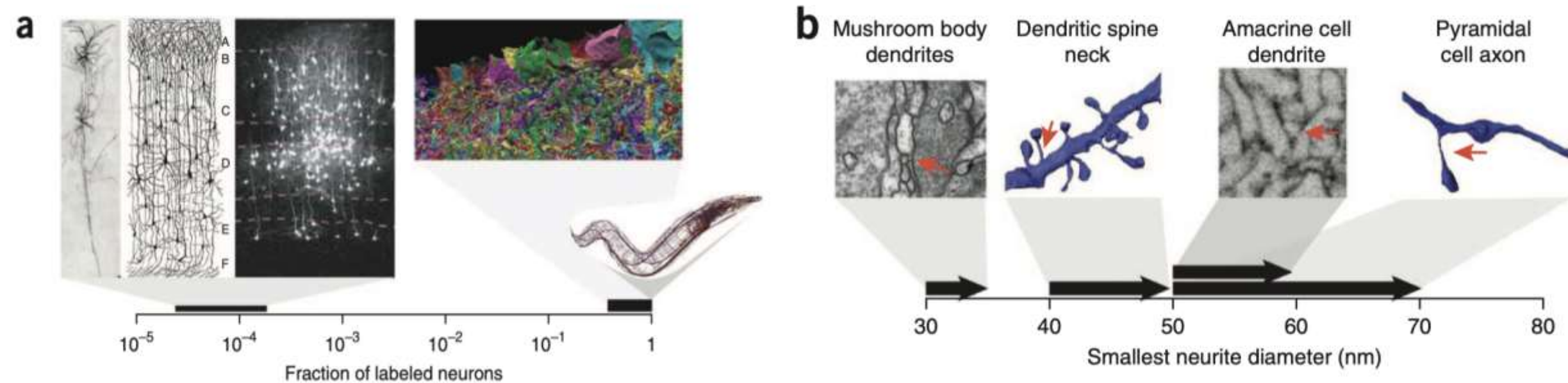
[Nature](#) (2025) | [Cite this article](#)

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LICONN——利用传统光学显微镜实现类似电子显微镜分辨率的连接组重建，并且还能获得有价值的分子信息。

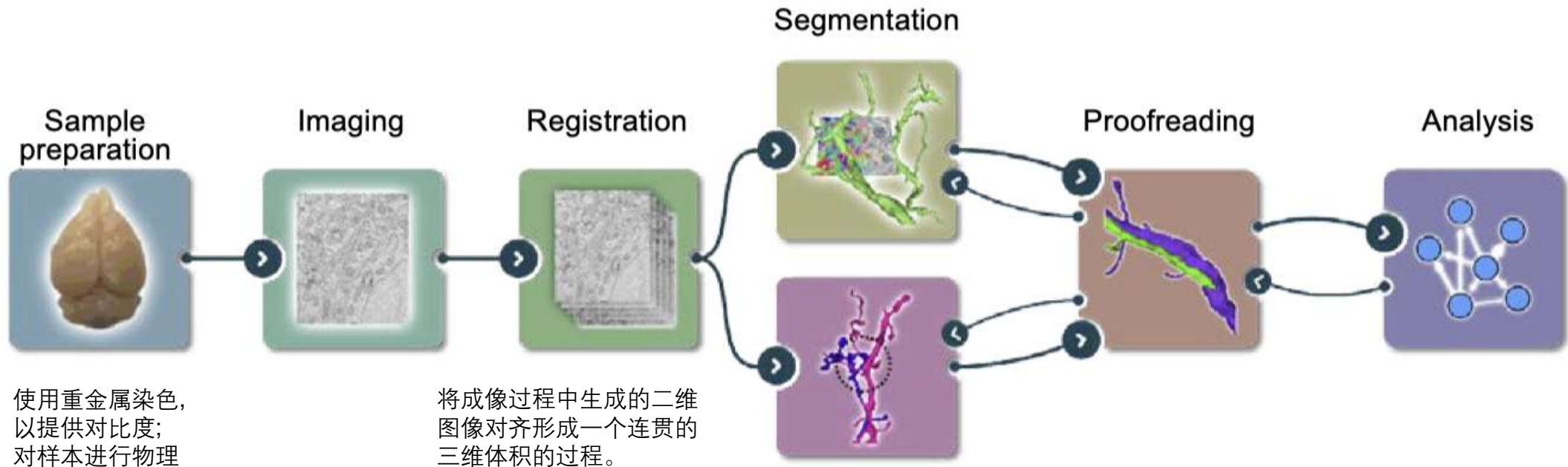


Microscale connectomics with EM, comparing to the mesoscale

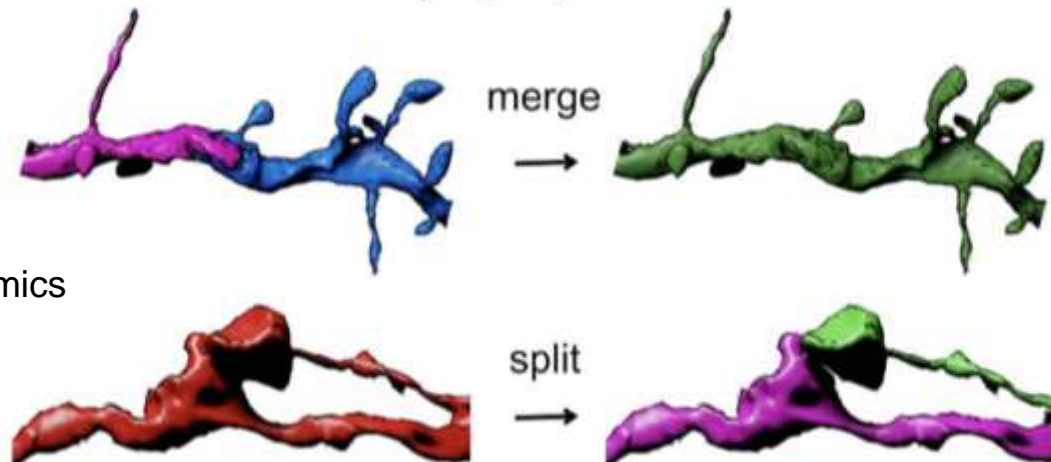


EM 的分辨率比 LM 高，是实现转录组研究的主要方法

Schematic pipeline for whole-brain connectomics

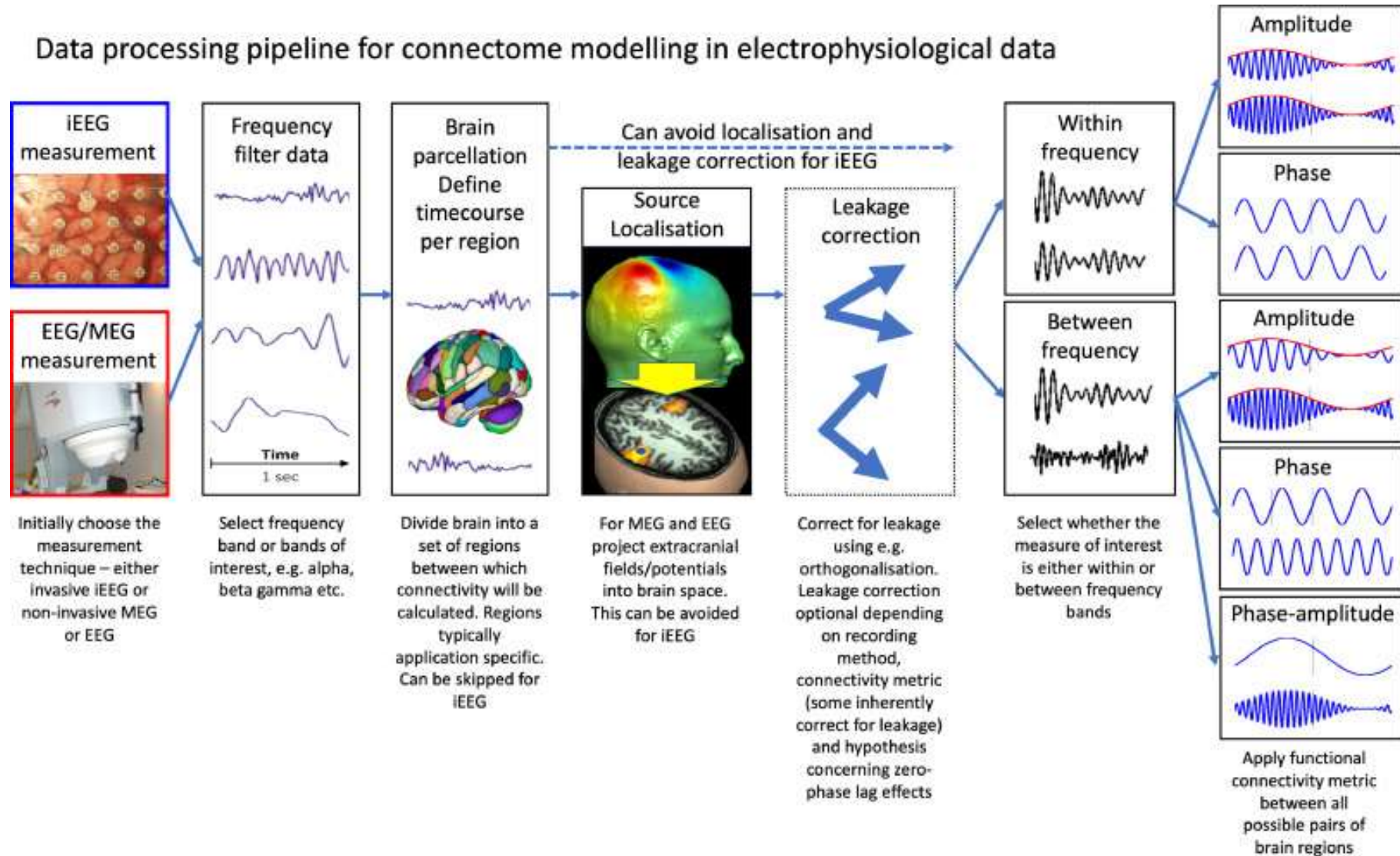


Synapse prediction



Connectomics of electrophysiology

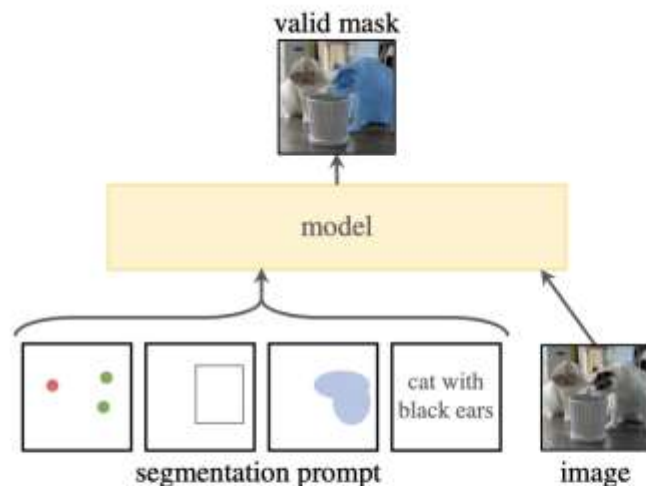
Data processing pipeline for connectome modelling in electrophysiological data



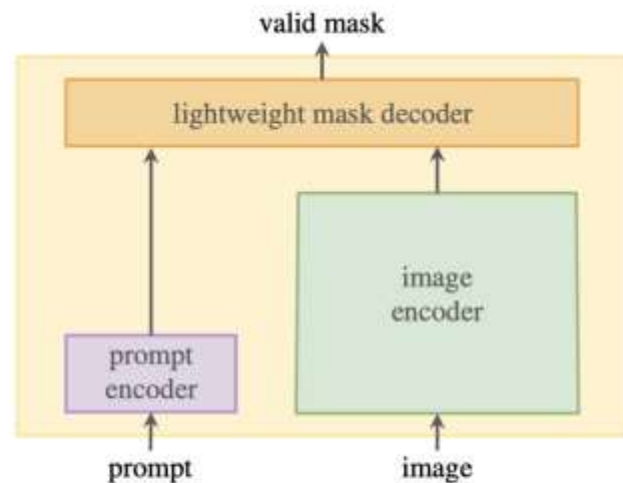
AI for Connectomics

限制连接组重建的主要计算问题是图像分割，其目标是识别图像中属于各个对象的特定像素集。

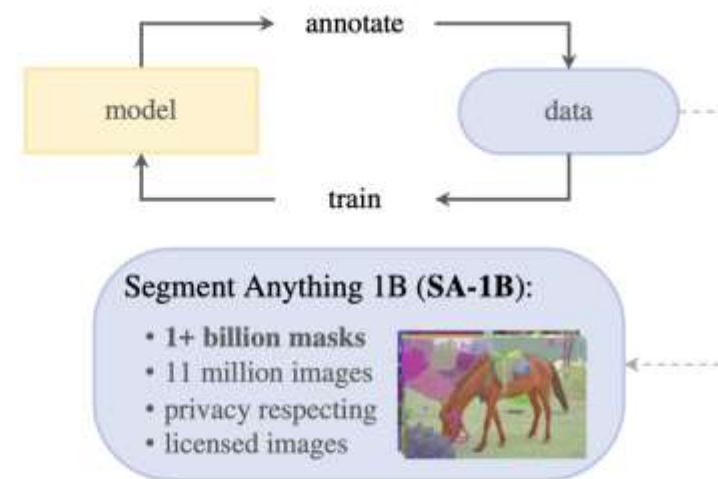
“segment anything model” (SAM)



(a) **Task:** promptable segmentation



(b) **Model:** Segment Anything Model (SAM)



(c) **Data:** data engine (top) & dataset (bottom)

Figure 1: We aim to build a foundation model for segmentation by introducing three interconnected components: a promptable segmentation *task*, a segmentation *model* (SAM) that powers data annotation and enables zero-shot transfer to a range of tasks via prompt engineering, and a *data* engine for collecting SA-1B, our dataset of over 1 billion masks.

The Landmark studies in connectomics

1. Whole-animal connectomes of *Caenorhabditis elegans*

The Structure of the Nervous System of the Nematode *Caenorhabditis elegans* ***(The Mind of a Worm)***

J.G. White, E. Southgate, J.N. Thomson, and S. Brenner

Sydney Brenner Facts



Sydney Brenner
The Nobel Prize in Physiology or Medicine 2002

Born: 13 January 1927, Germiston, South Africa

Died: 5 April 2019, Singapore

Affiliation at the time of the award: The Molecular Sciences
Institute, Berkeley, CA, USA

Prize motivation: "for their discoveries concerning genetic
regulation of organ development and programmed cell
death"

Prize share: 1/3

Photo from the Nobel
Foundation archive.

1986年，Brenner等人首次构建了线虫的大脑连接组。

线虫脑内包含大约300个神经元（共302个），他们的工作使人类第一次在神经元水平上看到了脑连接的全貌。

在这项工作中，共计302个神经元，被划分为118个类别，建立了5,000个化学突触、2,000个神经肌肉接头和600个电隙连接。

The Landmark studies in connectomics

1. Whole-animal connectomes of *Caenorhabditis elegans*

Circuit diagrams of nervous system:

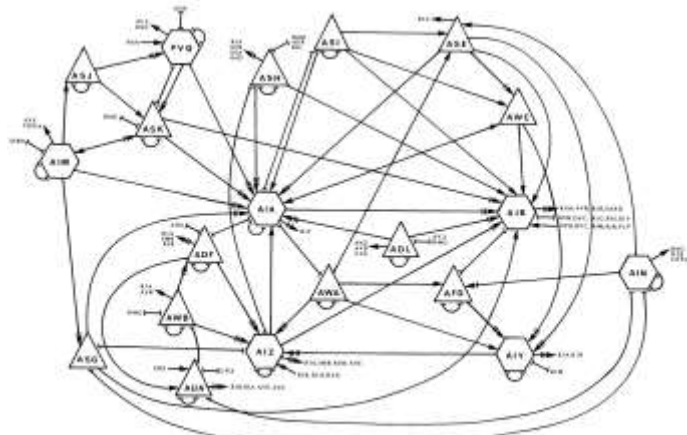


FIGURE 21. (a) Circuitry associated with amphids.

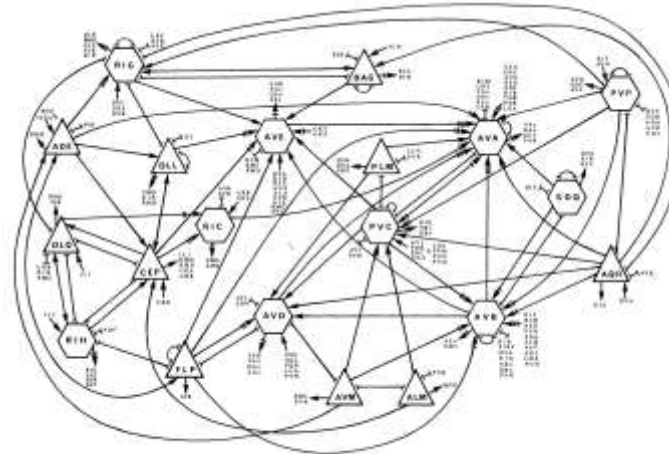


FIGURE 21. (b) Circuitry associated with other sensory receptors in the head.

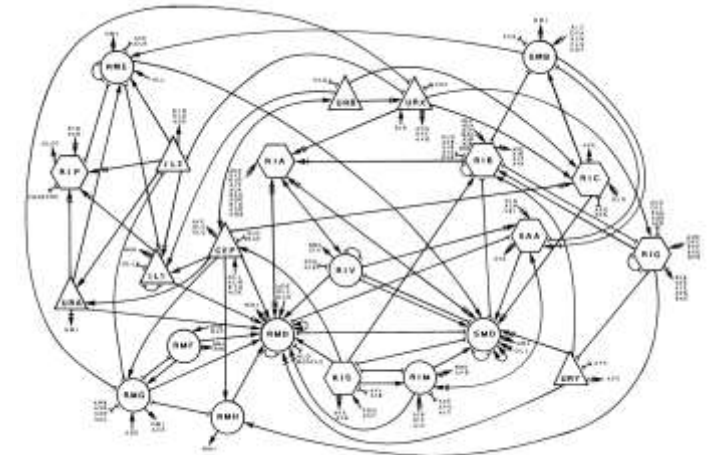


FIGURE 21. (c) Circuitry associated with the motoneurons in the nerve ring.

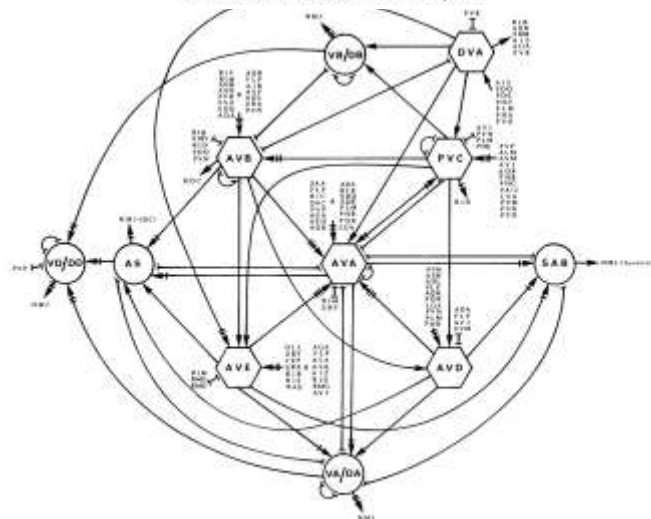


FIGURE 21. (d) Circuitry associated with the motoneurons of the ventral cord.

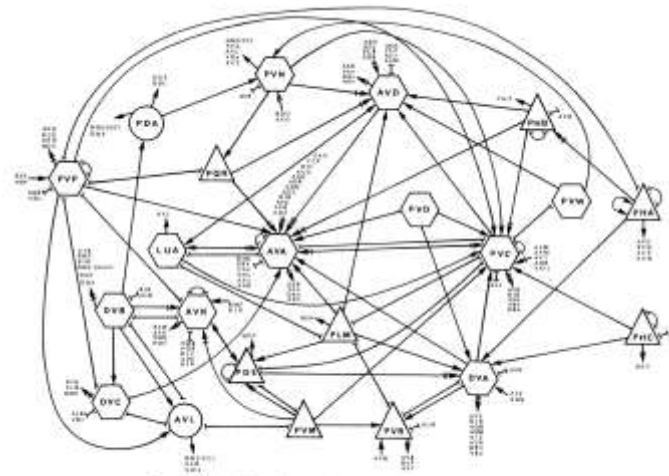


FIGURE 21. (e) Circuitry associated with neurons in the tail ganglia.

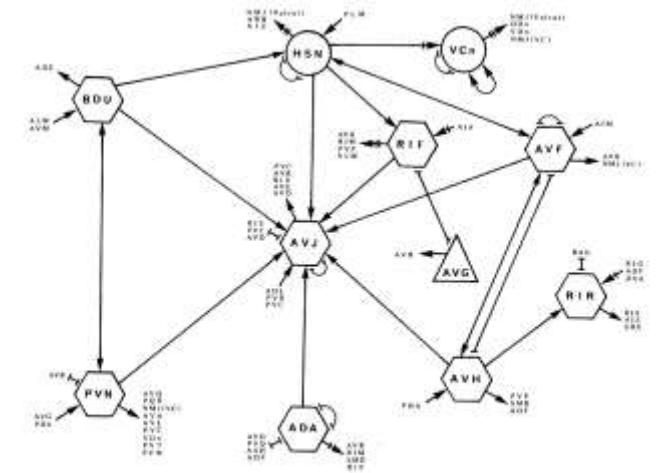
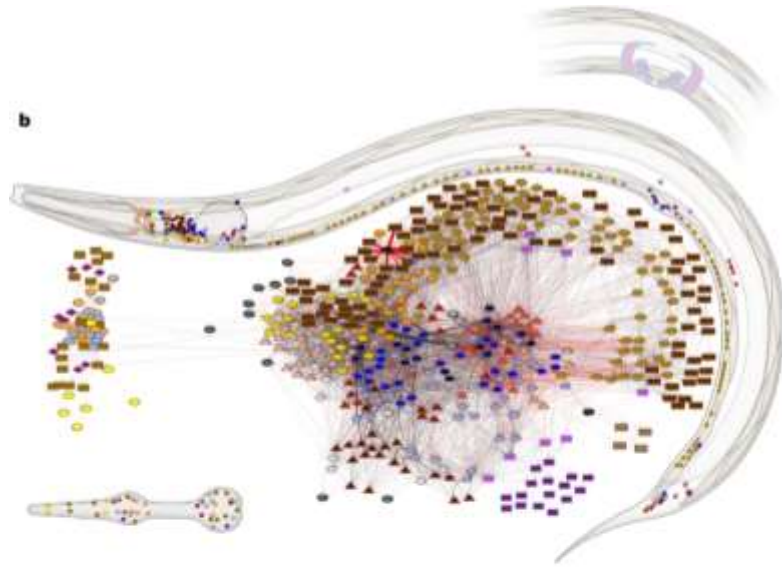


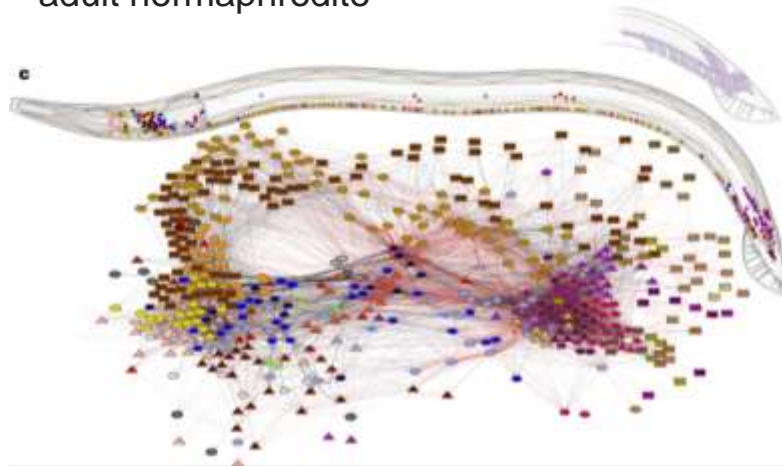
FIGURE 21. (f) Egg-laying circuitry.

The Landmark studies in connectomics

1. Whole-animal connectomes of *Caenorhabditis elegans*



adult hermaphrodite




adult male

[nature](#) > [articles](#) > [article](#)

Article | Published: 03 July 2019

Whole-animal connectomes of both *Caenorhabditis elegans* sexes

[Steven J. Cook](#), [Travis A. Jarrell](#), [Christopher A. Brittin](#), [Yi Wang](#), [Adam E. Bloniarz](#), [Maksim A. Yakovlev](#), [Ken C. Q. Nguyen](#), [Leo T.-H. Tang](#), [Emily A. Bayer](#), [Janet S. Duerr](#), [Hannes E. Bülow](#), [Oliver Hobert](#), [David H. Hall](#) & [Scott W. Emmons](#) 

[Nature](#) **571**, 63–71 (2019) | [Cite this article](#)

- 利用EM绘制了线虫的两性（雌雄同体和雄性）的完整神经系统
- 对神经系统进行分层排列
- 性别差异

The Landmark studies in connectomics

2. The FlyWire connectome: neuronal wiring diagram of a complete fly brain(2024)

[nature](#) > [articles](#) > [article](#)

Article | Published: 20 April 2015


A multilevel multimodal circuit enhances action selection in *Drosophila*

[Tomoko Ohyama](#), [Casey M. Schneider-Mizell](#), [Richard D. Fetter](#), [Javier Valdes Aleman](#), [Romain Franconville](#), [Marta Rivera-Alba](#), [Brett D. Mensh](#), [Kristin M. Branson](#), [Julie H. Simpson](#), [James W. Truman](#), [Albert Cardona](#)  & [Marta Zlatic](#) 

[Nature](#) **520**, 633–639 (2015) | [Cite this article](#)

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对果蝇幼虫中枢神经系统完整的电子显微镜体积成像和组装。

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Research Advance
[Neuroscience](#)

Conserved neural circuit structure across *Drosophila* larval development revealed by comparative connectomics

[Stephan Gerhard](#), [Ingrid Andrade](#), [Richard D Fetter](#), [Albert Cardona](#) , [Casey M Schneider-Mizell](#) 

Howard Hughes Medical Institute, United States; University of Cambridge, United Kingdom

Oct 23, 2017 • <https://doi.org/10.7554/eLife.29089>  

使用基于网络的协作工具逐步重建了第一龄幼虫大脑中2,500个神经元的形态和连接性。

The Landmark studies in connectomics

2. The FlyWire connectome: neuronal wiring diagram of a complete fly brain(2024)

Research Article
Computational and Systems Biology, Neuroscience

A connectome and analysis of the adult *Drosophila* central brain

Louis K Scheffer¹, C Shan Xu, Michal Januszewski, Zhiyuan Lu, Shin-ya Takemura, Kenneth J Hayworth, Gary B Huang, Kazunori Shinomiya, Jeremy Maitlin-Shepard ... Stephen M Plaza² [see all](#)

Janelia Research Campus, Howard Hughes Medical Institute, United States; Google Research, United States; Life Sciences Centre, Dalhousie University, Canada; Google Research, Google LLC, Switzerland; Institute for Quantitative Biosciences, University of Tokyo, Japan; MRC Laboratory of Molecular Biology, United States; Institute of Zoology, Biocenter Cologne, University of Cologne, Germany; Department of Zoology, University of Cambridge, United Kingdom

Sep 3, 2020 • <https://doi.org/10.7554/eLife.57443>  

[nature](#) > [articles](#) > article

Article | [Open access](#) | Published: 02 October 2024

Neuronal wiring diagram of an adult brain

[Sven Dorkenwald](#), [Arie Matsliah](#), [Amy R. Sterling](#), [Philipp Schlegel](#), [Szi-chieh Yu](#), [Claire E. McKellar](#), [Albert Lin](#), [Marta Costa](#), [Katharina Eichler](#), [Yijie Yin](#), [Will Silversmith](#), [Casey Schneider-Mizell](#), [Chris S. Jordan](#), [Derrick Brittain](#), [Akhilesh Halageri](#), [Kai Kuehner](#), [Oluwaseun Ogedengbe](#), [Ryan Morey](#), [Jay Gager](#), [Krzysztof Kruk](#), [Eric Perlman](#), [Runzhe Yang](#), [David Deutsch](#), [Doug Bland](#), [The FlyWire Consortium](#) [+ Show authors](#)

[Nature](#) **634**, 124–138 (2024) | [Cite this article](#)

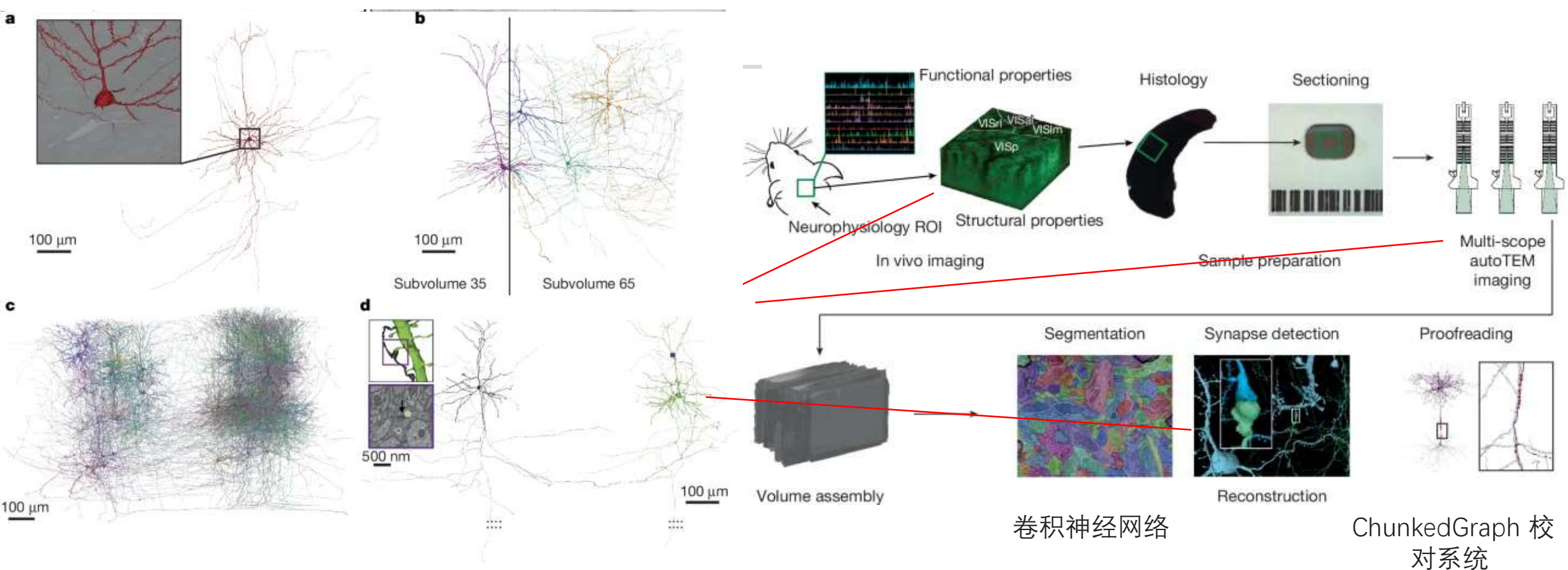
162k Accesses | **1135** Altmetric | [Metrics](#)

果蝇半脑连接组图

首个雌性果蝇大脑的完整神经元连接组

The Landmark studies in connectomics

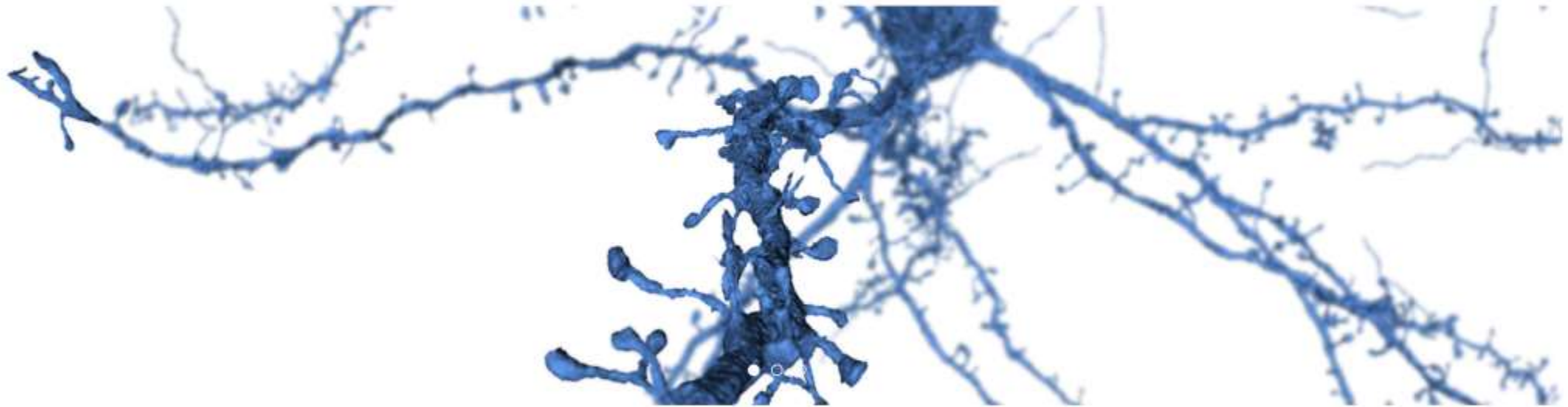
3. MICrONS (Machine Intelligence from Cortical Networks) (2025)



The Landmark studies in connectomics

3. MICrONS (Machine Intelligence from Cortical Networks) (2025)

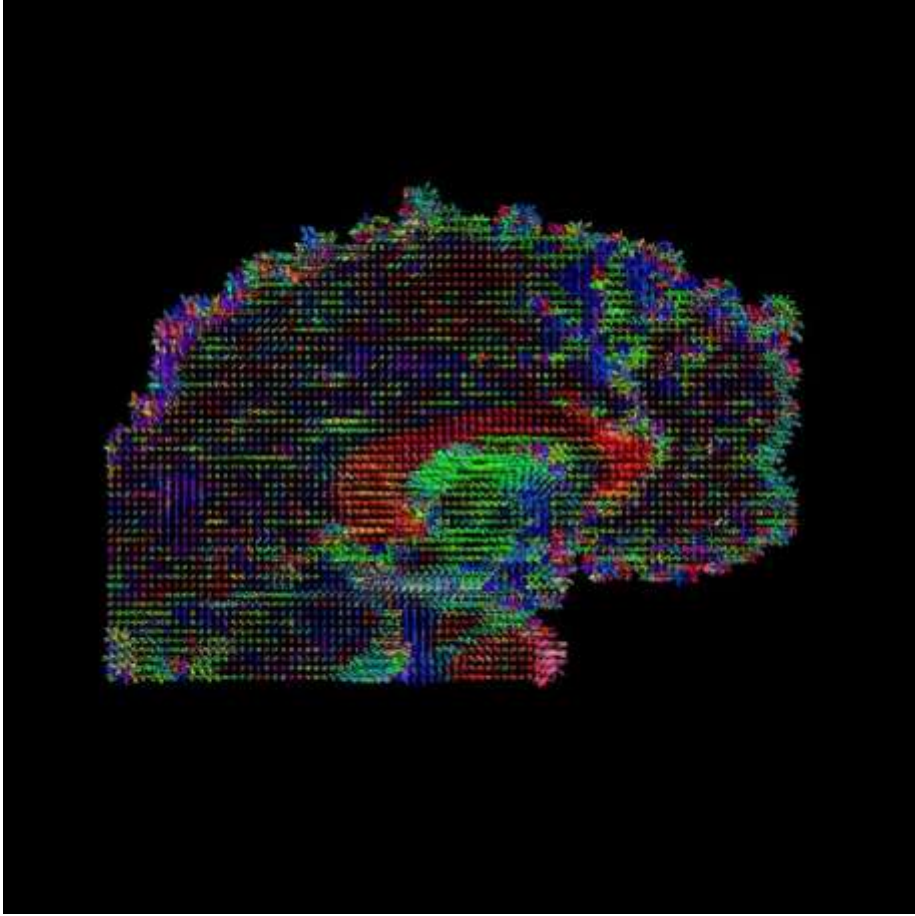
MICrONS Explorer [Home](#) [Data](#) [Requests](#) [Tools](#) [Gallery](#) [About](#)



MICrONS Explorer: A virtual observatory of the cortex

The Landmark studies in connectomics

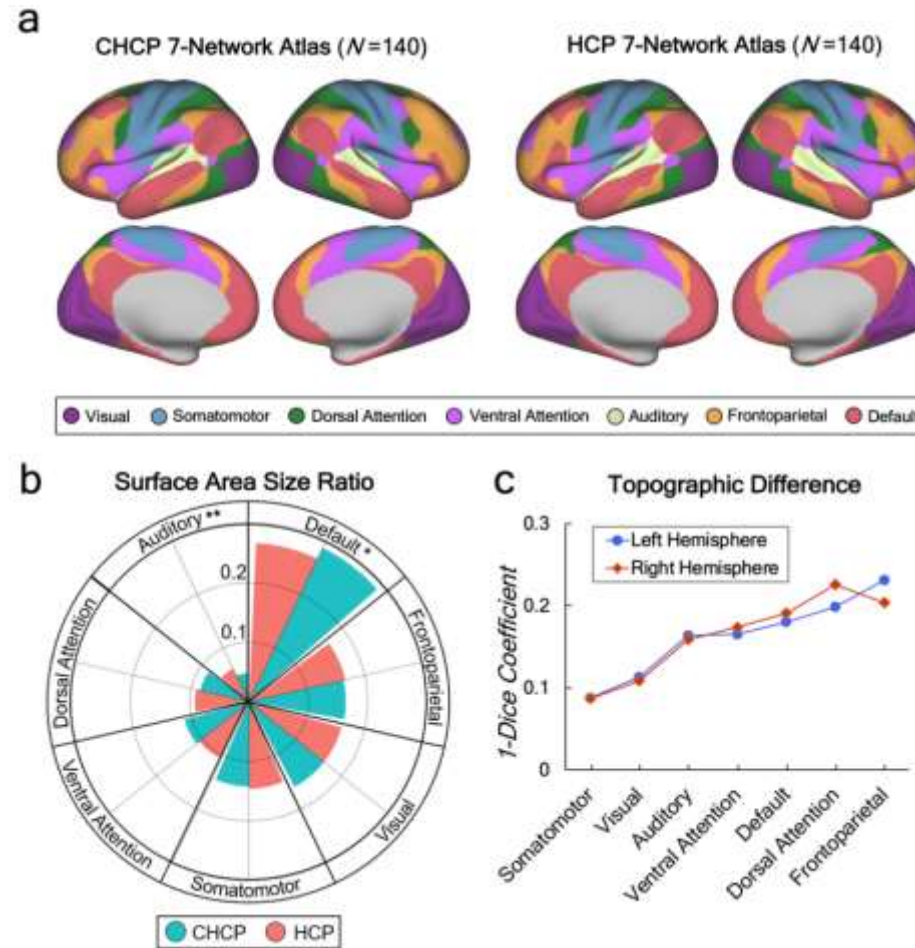
4. The Human Connectome Project (2010)



The Human Connectome Project (HCP) is a project to construct a map of the complete structural and functional neural connections in vivo within and across individuals. The HCP represents the first large-scale attempt to collect and share data of a scope and detail sufficient to begin the process of addressing deeply fundamental questions about human connective anatomy and variation.

The Landmark studies in connectomics

4. The Chinese Human Connectome Project (2017)



CHCP 与 HCP 在功能网络上表现出的差异，可能受到人类认知、情感和动机中与文化相关的影响。

Differences in the seven-network atlases between the CHCP and HCP.

Foundational Principles and Operational Guidelines of the FlyWire

- Data Sources and Foundational Principles of Flywire
- FlyWire Platform Overview and Operational Guidelines

LC
25.5.29

1

Data Sources and Foundational Principles of Flywire

● Murthy Lab



image: Mary Sym

Mala Murthy	
Born	1975 (age 49–50)
Nationality	American
Alma mater	Massachusetts Institute of Technology Stanford University
Scientific career	
Institutions	California Institute of Technology Princeton University
Doctoral advisor	Thomas Schwarz Richard Scheller
Website	https://mala-murthy.square-space.com

Mala Murthy (b. 1975) is an American neuroscientist and Professor of **Neuroscience** at Princeton University and leads the Murthy lab in the **Princeton Neuroscience Institute** – their work focuses on the **neural mechanisms that underlie social communication**, using the fruit fly *Drosophila* as a model system. In July 2022, she was named Director of the Princeton Neuroscience Institute.

● Seung Lab



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RESEARCH AREAS

- **Machine Learning**
- **Computational Biology**

Sebastian Seung

Professor of Computer Science and **Princeton Neuroscience Institute**

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- sseung@cs.princeton.edu
- (609) 258-7713
- Ph.D., Harvard University, 1990

● Murthy Lab



image: Mary Sym

Mala Murthy (b. 1975) is an American neuroscientist and Professor of **Neuroscience** at Princeton University and leads the Murthy lab in the **Princeton Neuroscience Institute** – their work focuses on the **neural mechanisms that underlie social communication**, using the fruit fly *Drosophila* as a model system. In July 2022, she was named Director of the Princeton Neuroscience Institute.

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- Arthur, BJ, Sunayama-Morita, T, Coen, P, Murthy, M* and Stern, DL*. *Multi-channel acoustic recording and automated analysis of Drosophila courtship songs*. **BMC Biology**. 2013. January vol. 11(1): 11. *co-corresponding authors [BMC Biology website](#)
- Calhoun, AJ, Pillow, JW, and Murthy, M. *Unsupervised identification of the internal states that shape natural behavior*. **Nature Neuroscience** 2019. Nov 25. #
 - News&Views: [Opening the black box of social behavior](#)
 - Princeton Discovery Magazine: [Neuroscientists develop models to identify internal states of the brain](#)
 - Nature: [Inside the Mind of an Animal](#)
- Pereira, TD, Tabris, N, Matsliah, A, Turner, DM, Li, J, Ravindranath, S, Papadoyannis, ES, Normand, E, Deutsch, DS, Wang, ZY, McKenzie-Smith, GC, Mitelut, CC, Castro, MD, D'Uva, J, Kislin, M, Sanes, DH, Kocher, SD, Wang, SSH, Falkner, AL, Shaevitz, JW, Murthy, M. *SLEAP: A deep learning system for multi-animal pose tracking*. **Nature Methods** 2022. Vol 19 April 486–495. doi.org/10.1038/s41592-022-01426-1.
- News&Views: [Tracking together: estimating social poses](#)
- Cowley, BR, Calhoun, AJ, Rangarajan, N, Turner, M, Pillow, JW, Murthy, M. *Mapping model units to visual neurons reveals population code for social behaviour*. **Nature** 2024 629, 1100–1108. <https://doi.org/10.1038/s41586-024-07451-8>

Our Research

Interpretation of connectomes

We are devising concepts and methods for interpreting neuronal wiring diagrams. The fly connectome includes as a corollary the first wiring diagram of a visual system. By studying this wiring diagram, we have discovered a new circuit for [form vision](#) in the fly brain. We have also discovered that many inhibitory interneuron types function as a highly diverse set of normalization mechanisms in fly vision. Both of these discoveries draw on the striking analogy between the fly visual system and convolutional nets.

Scaling up to mammalian brains

Today's connectomic technologies are sufficient for reconstructing an entire fly brain, and are also being applied to [millimeter-scale chunks of mammalian brains](#). A mouse brain is 1000× larger, and a human brain 1000× larger still. *There is plenty of room at the top*. We are participating in a ["transformative project"](#) of the NIH BRAIN Initiative that aims to scale up connectomics to a whole mouse brain. The Princeton Neuroscience Institute is the only site in the world with both of the EM image acquisition technologies that are being scaled up to the mouse connectome, [beam-deflection transmission electron microscopy](#) and [multi-beam scanning electron microscopy](#).

Reconstructing neural circuits

In ongoing collaborations, we are applying and refining connectomic technologies to reconstruct more fly connectomes (Mala Murthy), as well as a patch of mouse retina (Thomas Euler). We are reconstructing mouse neural circuits for memory (David Tank), decision making (Adrian Wanner and Jeff Lichtman), and reinforcement learning (Ilana Witten). These collaborations make use of the [high throughput EM facility](#) at the Princeton Neuroscience Institute. In many of the projects, neural circuit reconstruction is preceded by calcium imaging of neural activity *in vivo*.

Scaling down to molecules

The fly connectome was reconstructed from [EM images](#) with $4 \times 4 \times 40 \text{ nm}^3$ voxels, which is sufficient for detecting chemical synapses and tracing the "wires" of the brain. This resolution might seem very fine, but is actually coarse compared to the 0.1 nm theoretical limit of EM. *There is plenty of room at the bottom*. Serial section EM tomography can improve resolution; the challenge is to deliver this improvement over much larger volumes than before. One can imagine, for example, imaging an entire fly brain at $4 \times 4 \times 4 \text{ nm}^3$ or $2 \times 2 \times 2 \text{ nm}^3$ resolution. This would reveal brain cell biology in fantastic detail, within the full context of neurons and their connections.

●Seung Lab



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- [Computational Biology](#)

Sebastian Seung

Professor of Computer Science and [Princeton Neurosciences Institute](#)

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- ☎ (609) 258-7713
- 🎓 Ph.D., Harvard University, 1990

Technical Support Required to Establish Flywire

Data Sources

- Cell segments were auto-generated from **electron-microscopy images** with AI
- Cell reconstructions were assembled from segments (proofread) by the FlyWire community (see [FlyWire](#))
- **Synaptic connections** were automatically detected using the **Buhmann et al.** method and refined with synapse segmentations from [Heinrich et al.](#)
- Free-form labels (cell identification tags) were provided by the FlyWire community - see the [labeling leaderboard](#) and detailed credits in each cell info page
- Hierarchical annotations (side, flow, super class, cell class, cell type, Hemibrain type, nerve and hemi-lineage) were provided by Schlegel et al. (Jefferis lab)
- **Neurotransmitter types** were predicted by **Eckstein, Bates et al.**
- Morphological similarity scores (NBLAST based) were computed for the central brain cells by Philipp Schlegel
- Links from FlyWire neurons and cell types to Virtual Fly Brain and FlyBase were curated by Clare Pilgrim
- Repository of known functions for cell types is curated by Yijie Yin and synced periodically; see [source spreadsheet](#) for credits (corrections/contributions welcome)
- Refer to the table below or contact flywire@princeton.edu for additional info / questions on data credits

When using the FlyWire resource, please co-cite the Dorkenwald et al. and Schlegel et al. manuscripts. To give credit for specific aspects of data creation (=columns) please select the appropriate citations based on this table.

citation	doi	reconstruction	Data						hemibrain matching	connectivity tags	synapses & connectivity	neurotransmitter information
			community	hierarchical	nerves	hemilineages	gene	cell_type				
Dorkenwald et al., 2024	https://doi.org/10.1038/s41586-024-07558-y	x	x	x	x	x		x	x		x	x
Schlegel et al., 2024	https://doi.org/10.1038/s41586-024-07686-5	x		x	x	x		x	x			
Zheng et al., 2018	https://doi.org/10.1016/j.cell.2018.06.019	x	x	x	x	x		x	x		x	x
Buhmann et al., 2021	https://doi.org/10.1038/s41592-021-01183-7										x	
Heinrich et al., 2018	https://doi.org/10.1007/978-3-030-00934-2_36										x	
Eckstein, Bates et al., 2024	https://doi.org/10.1016/j.cell.2024.03.016											x
Matsliah, Yu et al., 2024	https://doi.org/10.1038/s41586-024-07981-1							x				
Lin et al., 2024	https://doi.org/10.1038/s41586-024-07968-y									x		
Deutsch et al., 202X	TBD						x	x				

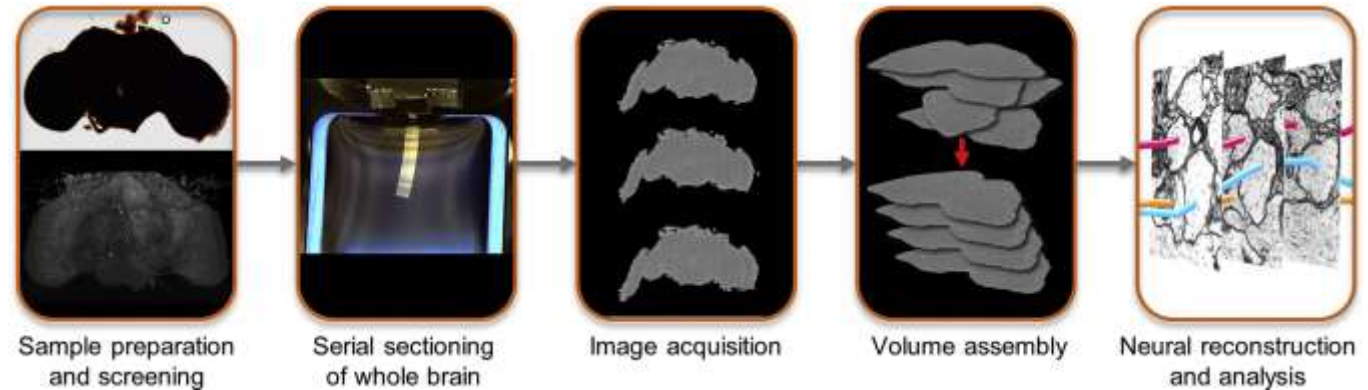
A complete adult Drosophila brain was imaged with EM and has been made publicly available

> Cell. IF: 45.5 Q1 2018 Jul 26;174(3):730-743.e22. doi: 10.1016/j.cell.2018.06.019. Epub 2018 Jul 19.

A Complete Electron Microscopy Volume of the Brain of Adult *Drosophila melanogaster*

Zhihao Zheng¹, J Scott Lauritzen¹, Eric Perlman¹, Camenzind G Robinson¹, Matthew Nichols¹, Daniel Milkie², Omar Torrens², John Price³, Corey B Fisher¹, Nadiya Sharifi¹, Steven A Calle-Schuler¹, Lucia Kmecova¹, Iqbal J Ali¹, Bill Karsh¹, Eric T Trautman¹, John A Bogovic¹, Philipp Hanslovsky¹, Gregory S X E Jefferis⁴, Michael Kazhdan⁵, Khaled Khairy¹, Stephan Saalfeld¹, Richard D Fetter¹, David D Bock⁶

PMID: 30033368 PMCID: PMC6063995 DOI: 10.1016/j.cell.2018.06.019

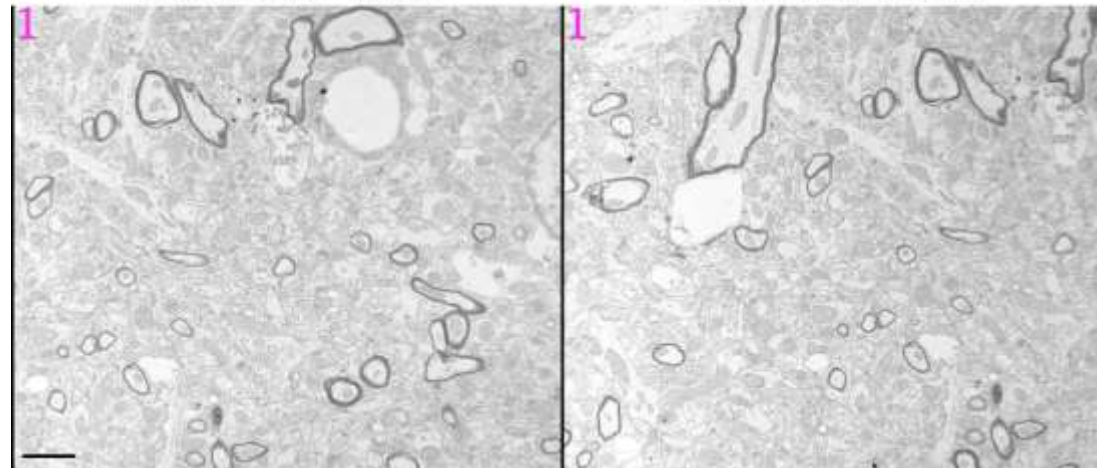


Fast Stage

elongated vacuum chamber

2 × 2 camera array

Standard stage, 1 move



Custom stage, 16 moves



Automatic detection of synaptic partners in a whole-brain Drosophila electron microscopy data set

> Nat Methods. IF: 36.1 Q1 2021 Jul;18(7):771-774. doi: 10.1038/s41592-021-01183-7.
Epub 2021 Jun 24.

Automatic detection of synaptic partners in a whole-brain Drosophila electron microscopy data set

Julia Buhmann^{1,2}, Arlo Sheridan¹, Caroline Malin-Mayor¹, Philipp Schlegel³,
Stephan Gerhard^{4,5}, Tom Kazimiers¹, Renate Krause^{1,2}, Tri M Nguyen⁴, Larissa Heinrich¹,
Wei-Chung Allen Lee⁶, Rachel Wilson⁴, Stephan Saalfeld¹, Gregory S X E Jefferis³, Davi D Bock⁷,
Srinivas C Turaga¹, Matthew Cook², Jan Funke⁸

PMID: 34168373 PMCID: PMC7611460 DOI: 10.1038/s41592-021-01183-7

Funke Lab

Our lab at HHMI Janelia develops machine learning methods for the life sciences, with a focus on microscopy image analysis.

We are particularly interested in:

1. Identification of Structures of Interest in Large Datasets

In the field of connectomics, we develop methods to segment neurons, detect synapses, and to classify synapses in very large electron microscopy datasets.

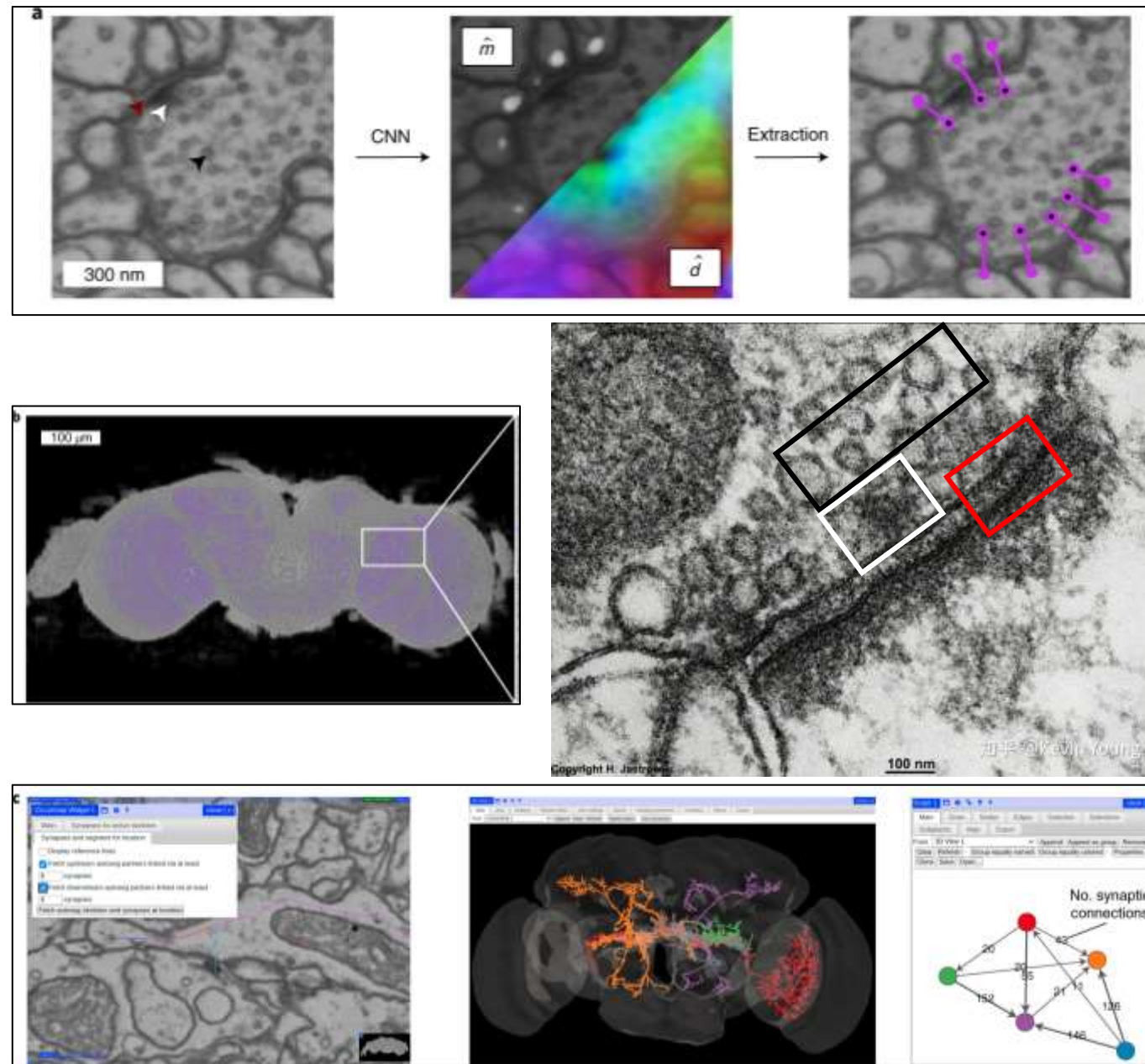
We also work on the segmentation and tracking of cells in live-cell imaging datasets.

2. Explainable Machine Learning Methods

We develop methods that use machine learning to identify and visualize subtle patterns in biological datasets. Those methods can reveal previously unknown phenotypical differences, e.g., in image data.

3. Mechanistic Machine Learning

To increase the utility and interpretability of machine learning methods, we design models that directly incorporate biophysical constraints and domain knowledge. So far, our models have been used to count fluorophores beyond the diffraction limit and to infer synaptic plasticity rules from behavioral measurements.



Artificial neural networks can predict transmitter types for presynapses from electron micrographs (acetylcholine, glutamate, GABA, serotonin, dopamine, octopamine)

> Cell. IF: 45.5 Q1 2024 May 9;187(10):2574-2594.e23. doi: 10.1016/j.cell.2024.03.016.

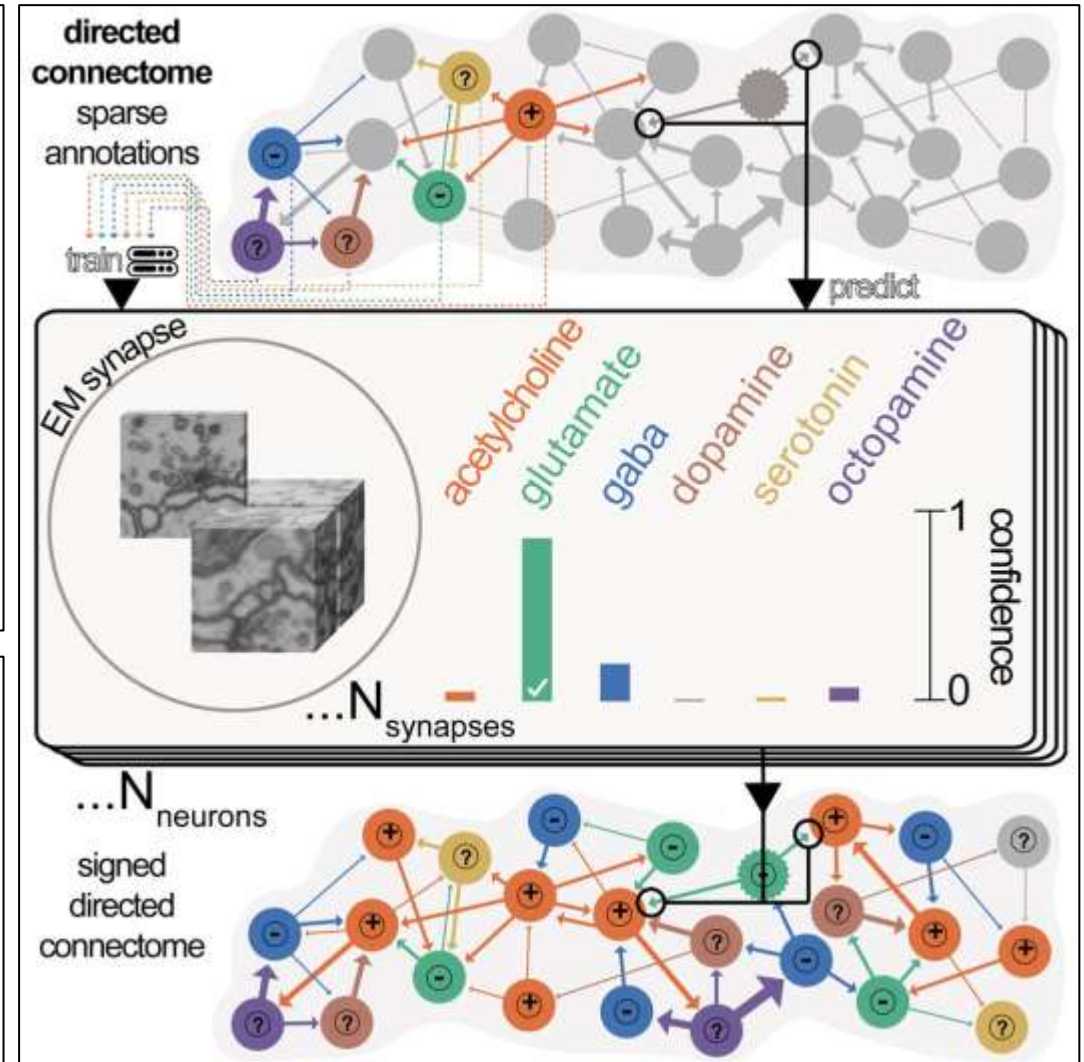
Neurotransmitter classification from electron microscopy images at synaptic sites in *Drosophila melanogaster*

Nils Eckstein¹, Alexander Shakeel Bates², Andrew Champion³, Michelle Du⁴, Yijie Yin³, Philipp Schlegel⁵, Alicia Kun-Yang Lu⁴, Thomson Rymer⁴, Samantha Finley-May⁴, Tyler Paterson⁴, Ruchi Parekh⁴, Sven Dorkenwald⁶, Arie Matsliah⁶, Szi-Chieh Yu⁶, Claire McKellar⁶, Amy Sterling⁶, Katharina Eichler³, Marta Costa³, Sebastian Seung⁶, Mala Murthy⁶, Volker Hartenstein⁷, Gregory S X E Jefferis⁸, Jan Funke⁹

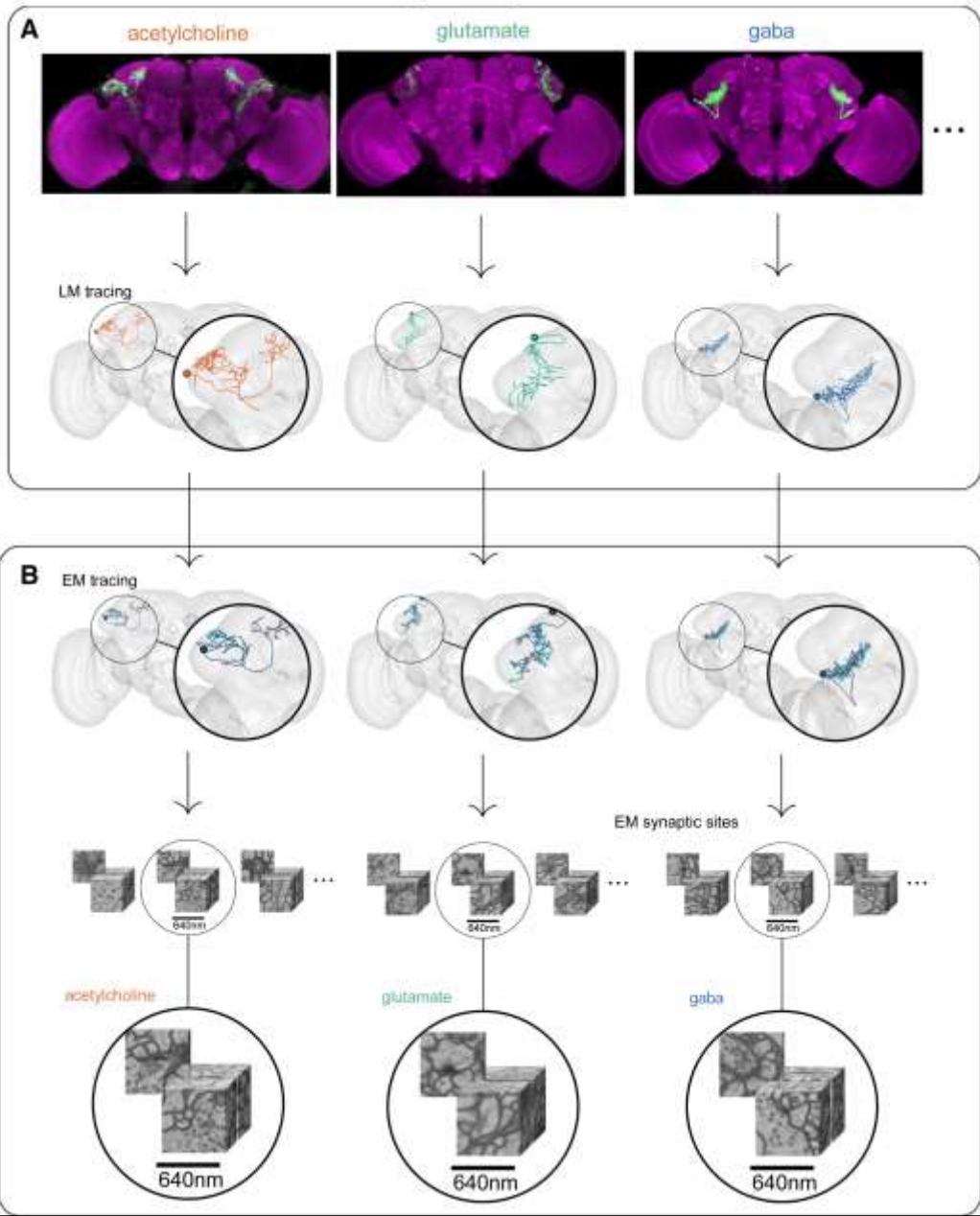
PMID: 38729112 PMCID: PMC11106717 DOI: 10.1016/j.cell.2024.03.016

Highlights

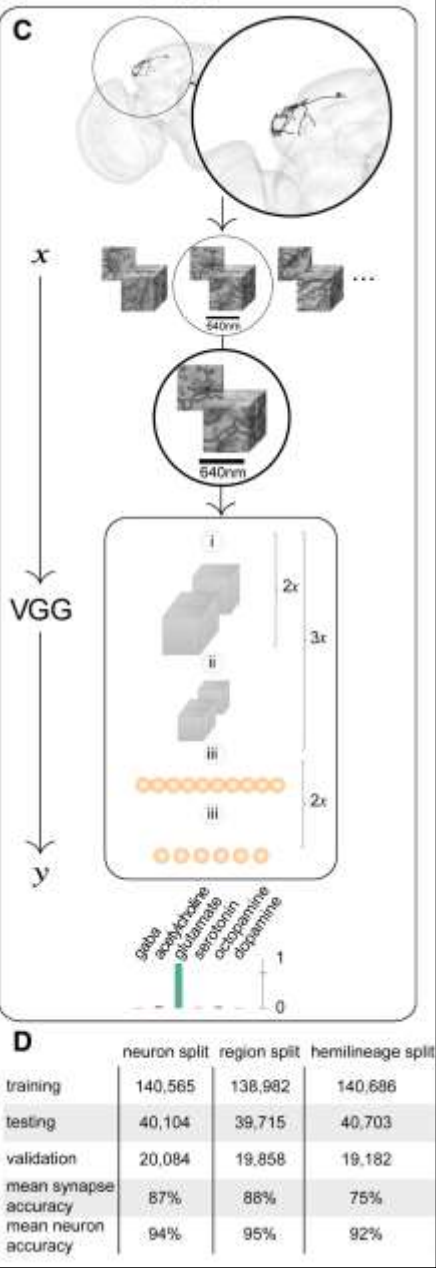
- Machine learning identifies synaptic transmitters from electron micrographs
- Six transmitters predicted across the whole fly brain connectome
- Explainable AI reveals ultrastructural differences between transmitter identities
- Fly brain hemilineages predominantly express one fast-acting transmitter



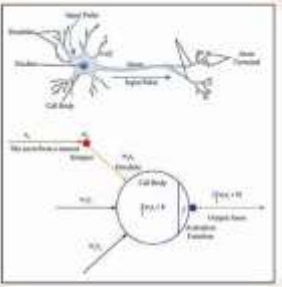
training data generation



training/application



Dale's law, also known as **Dale's principle**, states that a neuron releases the same neurotransmitter or group of neurotransmitters at all its synaptic connections. However, this principle has been shown to be incorrect for many neurons, as research indicates that some neurons can release multiple types of neurotransmitters. Current neuroscience suggests that Dale's law has been partially or totally disproven, reflecting a more complex understanding of neurotransmitter release. [Oxford Reference](#) +2



Lacin's law: In the ventral nerve cord Lacin et al. comprehensively showed that only one of acetylcholine, glutamate, or GABA is expressed per hemilineage. By analogy with Dale's law, we call this observation Lacin's law.

C

acetylcholine	→	glutamate	dimmer cleft, darker t-bar
acetylcholine	→	gaba	dimmer cleft
acetylcholine	→	serotonin	thinner cleft, more dense core vesicles (DCVs)
acetylcholine	→	dopamine	filled vesicles, fewer PSDs, fewer synaptic partners
acetylcholine	→	octopamine	thinner cleft, larger vesicles, less circular vesicles
glutamate	→	gaba	smaller vesicles
glutamate	→	serotonin	thinner cleft, more DCVs
glutamate	→	dopamine	thinner cleft, larger vesicles, fewer PSDs

> Nat Methods. IF: 36.1 Q1 2022 Jan;19(1):119-128. doi: 10.1038/s41592-021-01330-0.
Epub 2021 Dec 23.

FlyWire: online community for whole-brain connectomics

Sven Dorkenwald ^{# 1 2}, Claire E McKellar ^{# 1}, Thomas Macrina ^{# 1 2}, Nico Kemnitz ^{# 1},
Kisuk Lee ^{# 1 3}, Ran Lu ^{# 1}, Jingpeng Wu ^{# 1}, Sergiy Popovych ^{1 2}, Eric Mitchell ¹,
Barak Nehoran ^{1 2}, Zhen Jia ^{1 2}, J Alexander Bae ^{1 4}, Shang Mu ¹, Dodam Ih ¹, Manuel Castro ¹,
Oluwaseun Ogedengbe ¹, Akhilesh Halageri ¹, Kai Kuehner ¹, Amy R Sterling ¹, Zoe Ashwood ^{1 2},
Jonathan Zung ^{1 2}, Derrick Brittain ⁵, Forrest Collman ⁵, Casey Schneider-Mizell ⁵, Chris Jordan ¹,
William Silversmith ¹, Christa Baker ¹, David Deutsch ¹, Lucas Encarnacion-Rivera ¹,
Sandeep Kumar ¹, Austin Burke ¹, Doug Bland ¹, Jay Gager ¹, James Hebditch ¹, Selden Koolman ¹,
Merlin Moore ¹, Sarah Morejohn ¹, Ben Silverman ¹, Kyle Willie ¹, Ryan Willie ¹, Szi-Chieh Yu ¹,
Mala Murthy ⁶, H Sebastian Seung ^{7 8}

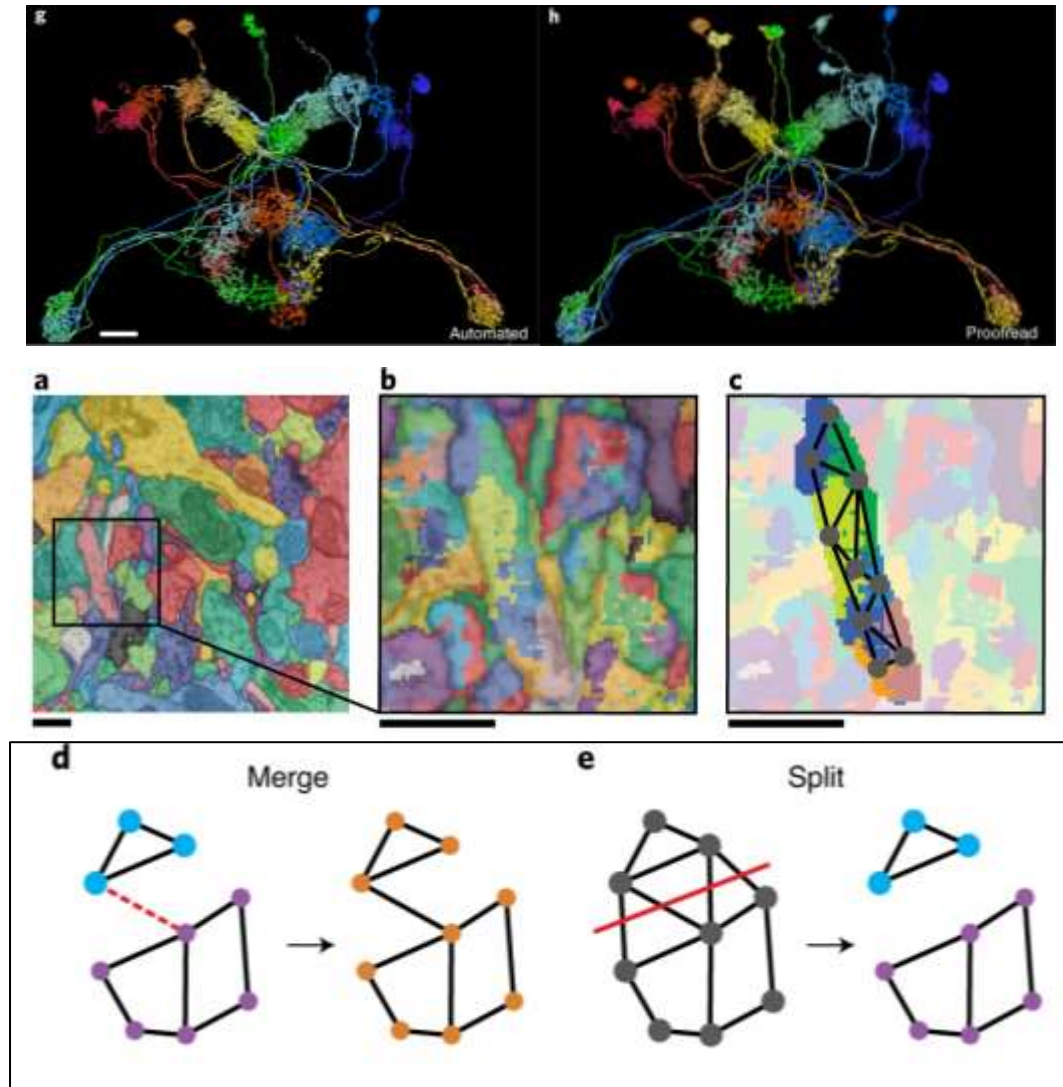
PMID: 34949809 PMCID: PMC8903166 DOI: 10.1038/s41592-021-01330-0

Proofreading time calculation for a full fly brain

We based our estimate of the proofreading time for an entire fly brain on the measured mean proofreading time of 19.1 min multiplied by an estimated 116,000 neurons in the fly brain⁵⁸. We assumed 2,000 h of work per year per person.



FlyWire: online community for whole-brain connectomics



Dorkenwald, Sven et al. Nature methods vol. 19,1 (2022): 119-128.




A whole-brain connectome of the fruit fly, including ~130k annotated neurons and tens of millions of typed synapses!

FlyWire @FlyWireNews · Jul 1, 2023
 4 years. 250 people. 2.7 million edits to proofread 127,000 neurons. The fly connectome is here!

Preprint: Neuronal wiring diagram of an adult brain
[biorxiv.org/content/10.1101/2023.07.01.548111](https://www.biorxiv.org/content/10.1101/2023.07.01.548111)

Explore it in Codex: codex.flywire.ai



> Nature. [IP: 50.5](#) [Q1](#) 2024 Oct;634(8032):124-138. doi: 10.1038/s41586-024-07558-y. Epub 2024 Oct 2.

Neuronal wiring diagram of an adult brain

Sven Dorkenwald^{1,2}, Arie Matsliah¹, Amy R Sterling^{1,3,4}, Philipp Schlegel^{4,5}, Szi-Chieh Yu¹, Claire E McKellar¹, Albert Lin^{1,6}, Marta Costa⁵, Katharina Eichler⁵, Yijie Yin⁵, Will Silverman¹, Casey Schneider-Mizell², Chris S Jordan¹, Derrick Brittain², Akhilesh Halageni¹, Kai Kuehner¹, Oluwaseun Ogedengbe¹, Ryan Morey¹, Jay Gager¹, Krzysztof Kruk³, Eric Perlman⁸, Runzhe Yang^{1,2}, David Deutsch^{1,9}, Doug Bland¹, Marissa Sorek^{1,3}, Ran Lu¹, Thomas Macrina^{1,2}, Klsuk Lee^{1,10}, J Alexander Bae^{1,11}, Shang Mu¹, Barak Nehoran^{1,2}, Eric Mitchell¹, Sergiy Popovych^{1,2}, Jingpeng Wu^{1,2}, Zhen Jia¹, Manuel A Castro¹, Nico Kemnitz¹, Dodam Ih¹, Alexander Shakeel Bates^{4,12,13}, Nils Eckstein¹⁴, Jan Funke¹⁴, Forrest Collman², Davi D Bock¹⁵, Gregory S X E Jefferis^{4,5}, H Sebastian Seung^{16,17}, Mala Murthy¹⁸; FlyWire Consortium

PMID: 39358518 PMCID: PMC11446842 DOI: 10.1038/s41586-024-07558-y

> Nature. [IP: 50.5](#) [Q1](#) 2024 Oct;634(8032):139-152. doi: 10.1038/s41586-024-07686-5. Epub 2024 Oct 2.

Whole-brain annotation and multi-connectome cell typing of *Drosophila*

Philipp Schlegel^{1,2}, Yijie Yin², Alexander S Bates^{1,3,4}, Sven Dorkenwald^{5,6}, Katharina Eichler², Paul Brooks², Daniel S Han^{1,7}, Marina Gkantia², Marcia Dos Santos², Eva J Munnely², Griffin Badalamente², Laia Serratos Capdevila², Varun A Sane², Alexandra M C Fragniere², Ladann Kiasat², Markus W Pleijzier¹, Tomke Stülmer^{1,2}, Imaan F M Tamimi², Christopher R Dunne², Irene Salgarella², Alexandre Javier², Siqi Fang², Eric Perlman⁸, Tom Kazimiers⁹, Sridhar R Jogannathan², Arie Matsliah⁶, Amy R Sterling^{6,10}, Szi-Chieh Yu⁶, Claire E McKellar⁶; FlyWire Consortium; Marta Costa², H Sebastian Seung^{5,6}, Mala Murthy⁶, Volker Hartenstein¹¹, Davi D Bock¹², Gregory S X E Jefferis^{13,14}

PMID: 39358521 PMCID: PMC11446831 DOI: 10.1038/s41586-024-07686-5



Dorkenwald, Sven et al. Nature vol. 634,8032 (2024): 124-138.
 Schlegel, Philipp et al. Nature vol. 634,8032 (2024): 139-152.

Take home message

- FlyWire is created at Princeton University



Data Sources

- Cell segments were auto-generated from [electron-microscopy images](#) with AI
- Cell reconstructions were assembled from segments (proofread) by the FlyWire community (see [FlyWire](#))
- [Synaptic connections](#) were automatically detected using the [Buhmann et al.](#) method and refined with synapse segmentations from [Heinrich et al.](#)
- Free-form labels (cell identification tags) were provided by the FlyWire community - see the [labeling leaderboard](#) and detailed credits in each cell info page
- Hierarchical annotations (side, flow, super class, cell class, cell type, Hemibrain type, nerve and hemi-lineage) were provided by Schlegel et al. (Jefferis lab)
- [Neurotransmitter types](#) were predicted by [Eckstein, Bates et al.](#)
- Morphological similarity scores (NBLAST based) were computed for the central brain cells by Philipp Schlegel
- Links from FlyWire neurons and cell types to Virtual Fly Brain and FlyBase were curated by Clare Pilgrim
- Repository of known functions for cell types is curated by Yijie Yin and synced periodically; see [source spreadsheet](#) for credits (corrections/contributions welcome)
- Refer to the table below or contact flywire@princeton.edu for additional info / questions on data credits

2

FlyWire Platform Overview and Operational Guidelines

WEB APP

**Codex**

The Connectome Data Explorer provides access to the FlyWire connectome, including over 120K+ proofread neurons, 150K+ annotations, and 30M+ synapses. Users can traverse connections, gather snapshots of individual and groups of cells, visualize connectivity networks, paths, and more.

#Search Engine

#Annotation

#Network Vis

PYTHON PACKAGE

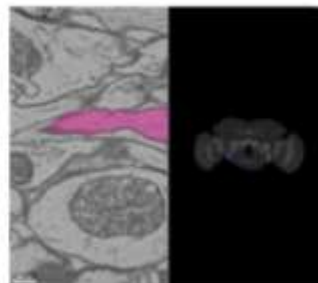
**CAVE**

CAVE is the underlying infrastructure developed by the Seung Lab and the Allen Institute that powers FlyWire's technology. It includes a distributed framework of API services that support large scale proofreading and annotation in a number of connectomics datasets, including the MICRONS project and FANC. You can use Python to access these APIs using the CAVEclient python repository.

#Data API

#Queries

WEB APP

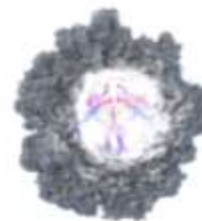
**FlyWire Proofreading**

FlyWire is a game-like platform for proofreading, annotation and interactive visualization. Thanks to the combined efforts of hundreds of people editing the automatic segmentation of *Drosophila melanogaster* over several years, the first centralized brain Connectome will become openly available in 2023.

#Proofreading

#Annotation

WEB APP

**FlyWire Gateway**

Find cells from FlyWire in other datasets. Transform and visualize neuron skeletons in FlyWire.

#Transformations

#Brain Templates

WEB APP

**Catmaid Spaces**

Use CATMID for in-depth interactive analysis of FlyWire data. Includes connectomics, skeletons and annotations.

#analysis

#visualisation

#graphs

WEB APP

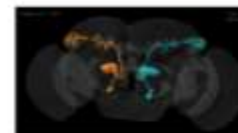
**BrainCircuits.io Tools**

A collection of tools and resources for connectomics.

#Analysis

#Genetic Lines

WEB APP

**cocoglancer**

Visualize FlyWire and hemibrain neurons. Query and display cell type annotations in the viewer.

#flywire + hemibrain

#annotation queries

R PACKAGE

**coconatfly**

R package for comparative connectomics for the fly, including connectivity clustering between flywire and hemibrain datasets to help identify cell types.

#Comparative connectomics

#Metadata queries

#Connectivity queries

#Cosine clustering

#Network

PYTHON PACKAGE

FAFBseg**fafbseg-py**

Python package to query and analyze FlyWire data. Integrated with cox.

#Neurons

#Analysis

#Visualisation

Codex

Connectome Data Explorer : [tutorials](#)

Developed at [Princeton Neuroscience Institute](#)

FlyWire Brain Dataset (FAFB v783)

Connectome of a female adult fly brain (see [FlyWire Brain homepage](#) for details). Exploring version v783 that includes:

139,255

proofread cells

138,059 (99%)

typed or labeled cells

2,700,513

connections [?]

34,153,566

synapses [?]

See [About FlyWire](#) and [FAQs](#) pages for more details.

Switch datasets from the drop-down menu in the top-right corner.

search cells and annotations



Datasets in Codex (May 2025)

- FlyWire FAFB - female brain
- BANC - female brain and nerve cord (requires access token)
- MANC - male nerve cord
- Optic Lobe - male optic lobe (coming soon)
- Mouse datasets (coming later)

manc v1.2.1

fafb v783

banc v554

manc v1.2.1

hhmi janelia

Research Campus

RESEARCH GROUPS

MORE IN THIS PAGE

FlyEM / Research

The strategic objective of the FlyEM project team is to develop a fully detailed, cellular- and synaptic-resolution map of the central nervous system of *Drosophila melanogaster*, at both larval and adult stages. Simply having this “wiring-diagram” is necessary but not sufficient to understand how the fly’s nervous system functions. We are, however, confident that the wiring diagram will be a foundational tool necessary to develop that greater understanding, in much the same way that genomic sequence information has proved essential in enabling and accelerating studies of genetics, development and molecular and cellular biology.

In addition to their shorter-term applications to the neurobiology of *Drosophila*, in the longer term we expect that the imaging and computational techniques developed by this team will become applicable to ever larger problems in functional neurobiology, such as those posed by vertebrate nervous systems. Towards this end, our project complements and cooperates with other projects at Janelia.

For information on FlyEM’s sample preparation and imaging technology, please refer to [Data Acquisition](#). For information on FlyEM’s software and algorithms to reconstruct a connectome from a stack of EM images, please refer to [Reconstruction Technology](#).

● MANC

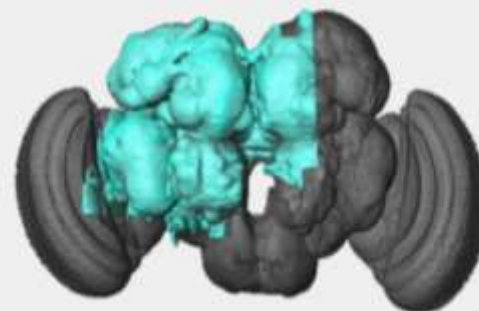
Male Adult Nerve Cord

MANC dataset



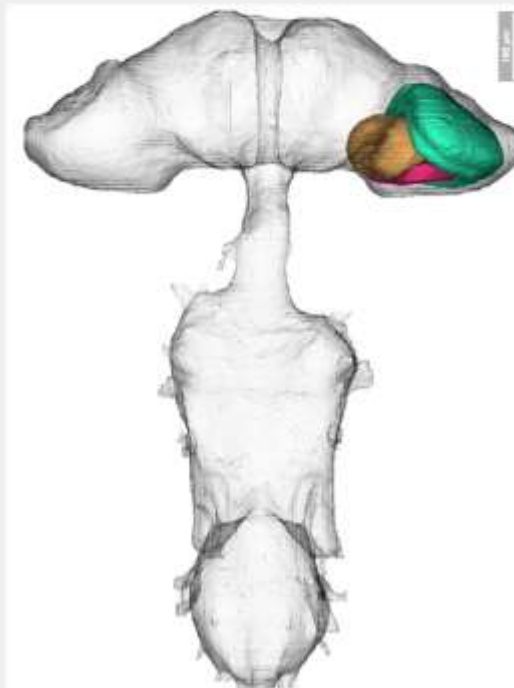
The MANC dataset covers the entirety of the a male fly ventral nerve cord (VNC), about 25% of the fly’s overall central nervous system. The VNC integrates descending signals from the brain and sensory inputs from the body to influence control over motor neurons controlling the wings and legs.

The hemibrain dataset



The hemibrain dataset encompasses the part of the fly brain highlighted here in blue. This region includes neurons involved in learning, navigation, smell, vision, and many other functions.

Optic Lobe dataset



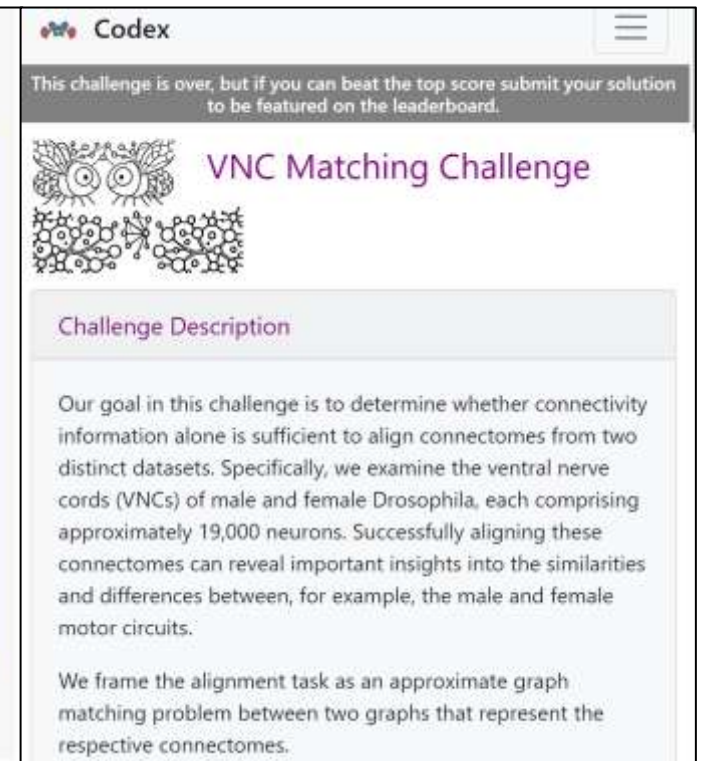
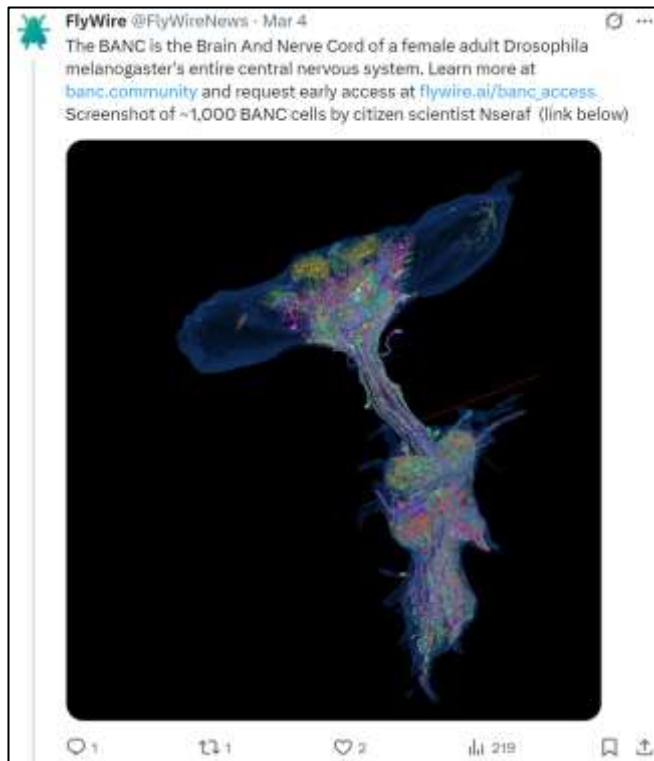
The Optic Lobe dataset covers the right optic lobe of a male fruit fly. More than half the neurons in the adult fly brain are found in the optic lobes, the portion of the brain devoted to processing visual information.

This image shows the full male fly central nervous system with the right optic lobe highlighted. The medulla is in green, the lobula plate is in purple and the lobula is in yellow-green. Scale bar is 100 μm .



● BANC

The Brain And Nerve Cord of a female adult *Drosophila melanogaster*



● The connectome of an insect brain

> Science. IF: 44.7 Q1 2023 Mar 10;379(6636):eadd9330. doi: 10.1126/science.add9330.
Epub 2023 Mar 10.

The connectome of an insect brain

Michael Winding^{1,2,3}, Benjamin D Pedigo⁴, Christopher L Barnes^{2,5}, Heather G Patsolic^{6,7},
Youngser Park⁸, Tom Kazimiers^{3,9}, Akira Fushiki^{3,10}, Ingrid V Andrade¹¹, Avinash Khandelwal³,
Javier Valdes-Aleman^{1,3}, Feng Li³, Nadine Randel^{1,2}, Elizabeth Barsotti^{2,5}, Ana Correia^{2,5},
Richard D Fetter^{3,12}, Volker Hartenstein¹¹, Carey E Priebe^{6,8}, Joshua T Vogelstein^{4,8},
Albert Cardona^{2,3,5}, Marta Zlatic^{1,2,3}

PMID: 36893230 PMCID: PMC7614541 DOI: 10.1126/science.add9330

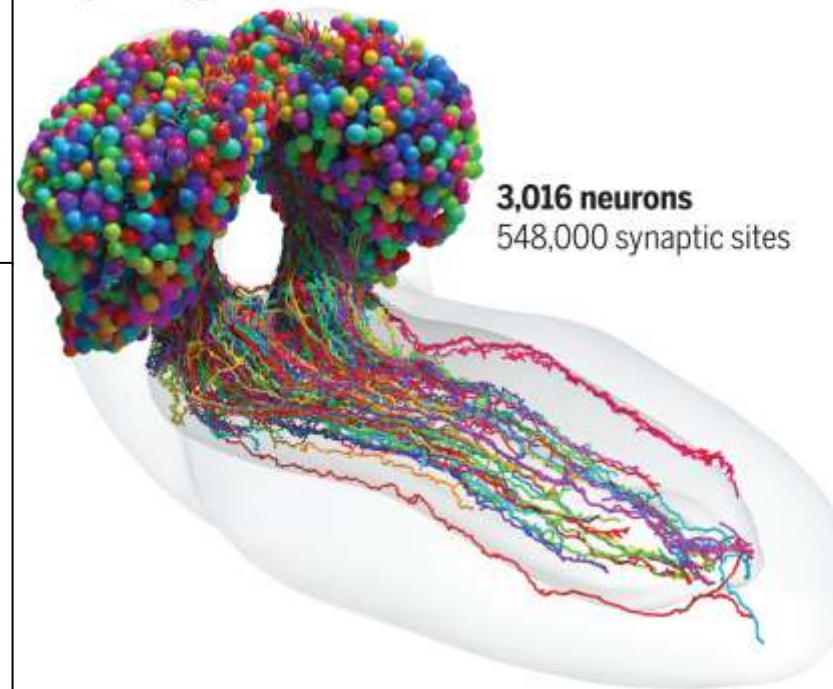


Marta Zlatic

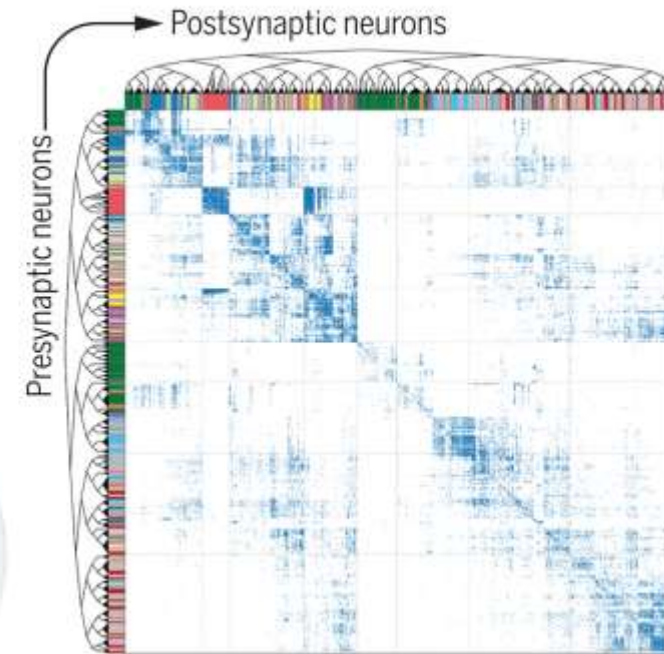
Circuit mechanisms of learning and action-selection

mzlatic@mrc-lmb.cam.ac.uk

Morphology



Connectivity



3

Codex 常用功能

红色标注的功能是最常使用的。

神经元检索



Search

Find neurons using free-form or structured queries

检索结果统计



Stats

See statistics and charts for various attributes of all or subset of neurons in the dataset

神经元注释



Annotations

Browse cell types, labels, and groupings of the neurons in the dataset

目标神经元的详细信息



Cell Details

Information about individual cells, their connectivity, similar/twin cells, 3D rendering and annotations

脑区结构检索



Neuropils

Visualize and query connections in specific brain regions

神经元3D结构显示



3D Viewer

Visualize queried neurons and synapses in annotated Neuroglancer scenes

目标神经元的连接网络



Network Graphs

Visualize connectivity of neurons and their synaptic links

神经元通路检索



Pathways

Analyse shortest-paths between pairs of neurons

源数据

{DATA}

Download Data

Export raw data for analysis with other tools / programs

By GC

Search: Find neurons using free-form or structured queries

Codex

Search

Stats

Cell Info

3D

Explore

Connectivity

cell_type == pC1a

2 matches

List

Stats

Taxonomy

Network

3D view

Copy IDs

Pathways

Connections

CSV

Cell IDs

Name/ID

SMP.SIP.8 / 720575940625792698

FAFB

SMP.SIP.9 / 720575940646310947

FAFB

Taxonomy

Annotation Taxonomy

Context : flow : super_class : class : sub_class : resolved_type : side : number of cells

query : intrinsic : central : [class] : [sub_class] : pC1a :

right : 1 cells

left : 1 cells

Connections

From	To	Neuropil	Synapses	Neuro Transmitter
720575940625792698	720575940646310947	SMP_R	11	ACH
720575940625792698	720575940646310947	SIP_L	7	ACH
720575940625792698	720575940646310947	SIP_R	5	ACH
720575940625792698	720575940646310947	MB_VL_R	1	ACH
720575940625792698	720575940646310947	SMP_L	10	ACH
720575940646310947	720575940625792698	SIP_L	4	ACH
720575940646310947	720575940625792698	SMP_L	3	ACH
720575940646310947	720575940625792698	SMP_R	6	ACH
720575940646310947	720575940625792698	SIP_R	10	ACH







PN




dorsal











57363

Schlegel, Philipp et al. Nature vol. 634,8032 (2024): 139-152.

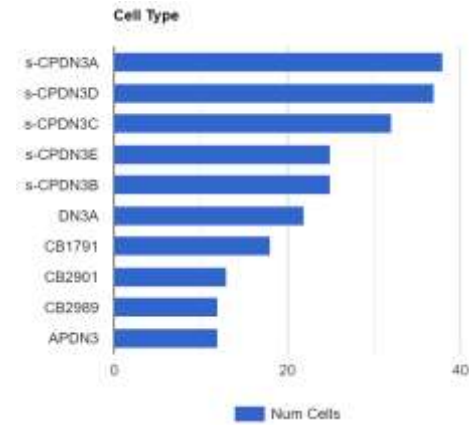
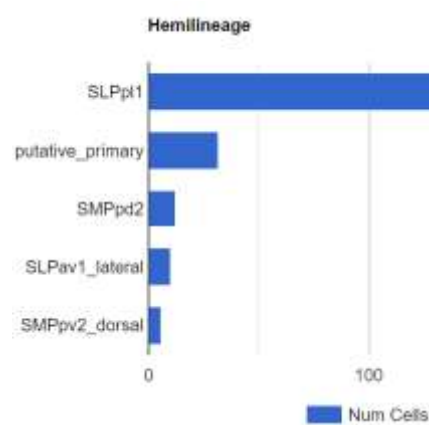
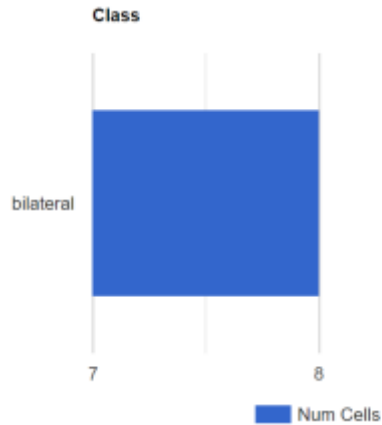
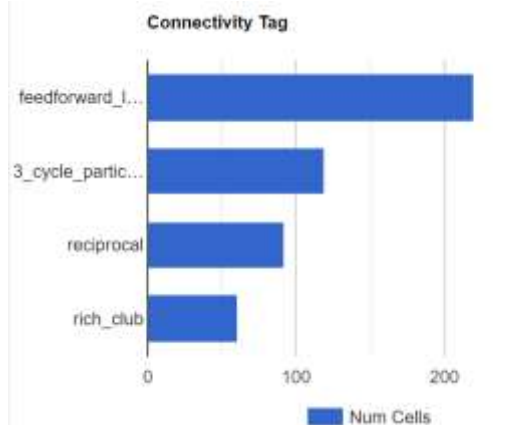
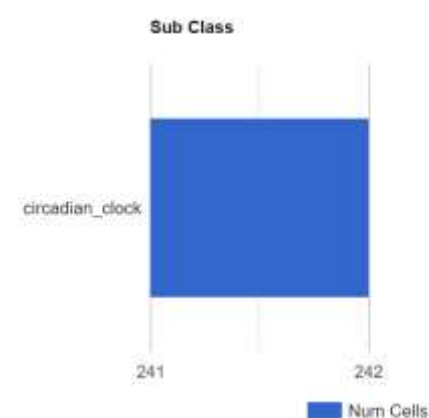
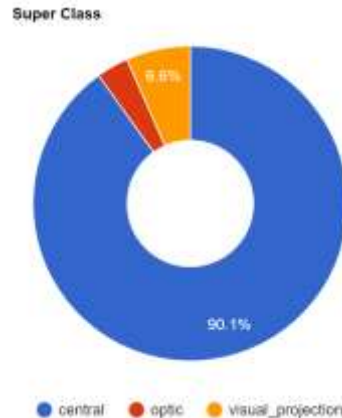
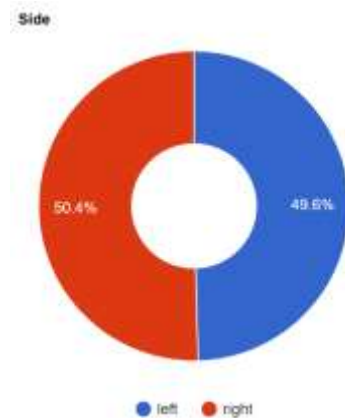
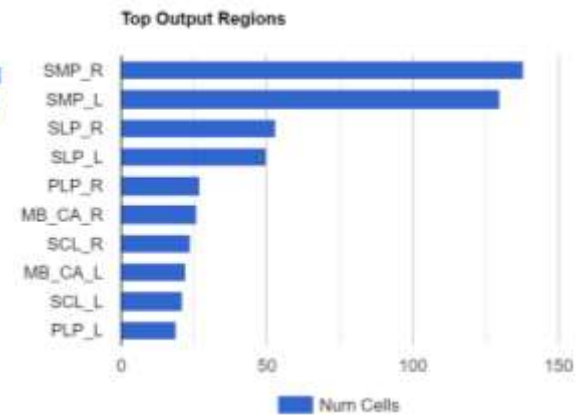
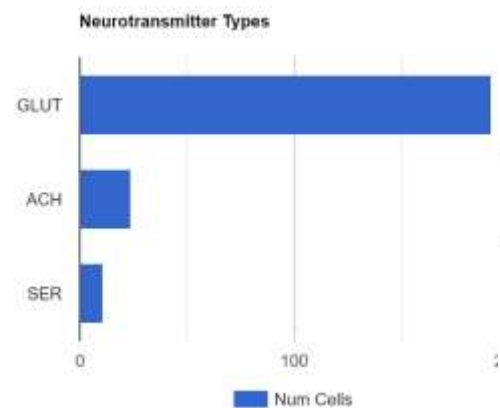
Stats: See statistics and charts for various attributes of all or subset of neurons in the dataset

Codex Search **Stats** Cell Info 3D Explore Connectivity      

clock ×   Cc W 

242 matches  List  Stats  Taxonomy  Network  3D view  Copy IDs  Pathways  Synapse table  CSV  Cell IDs

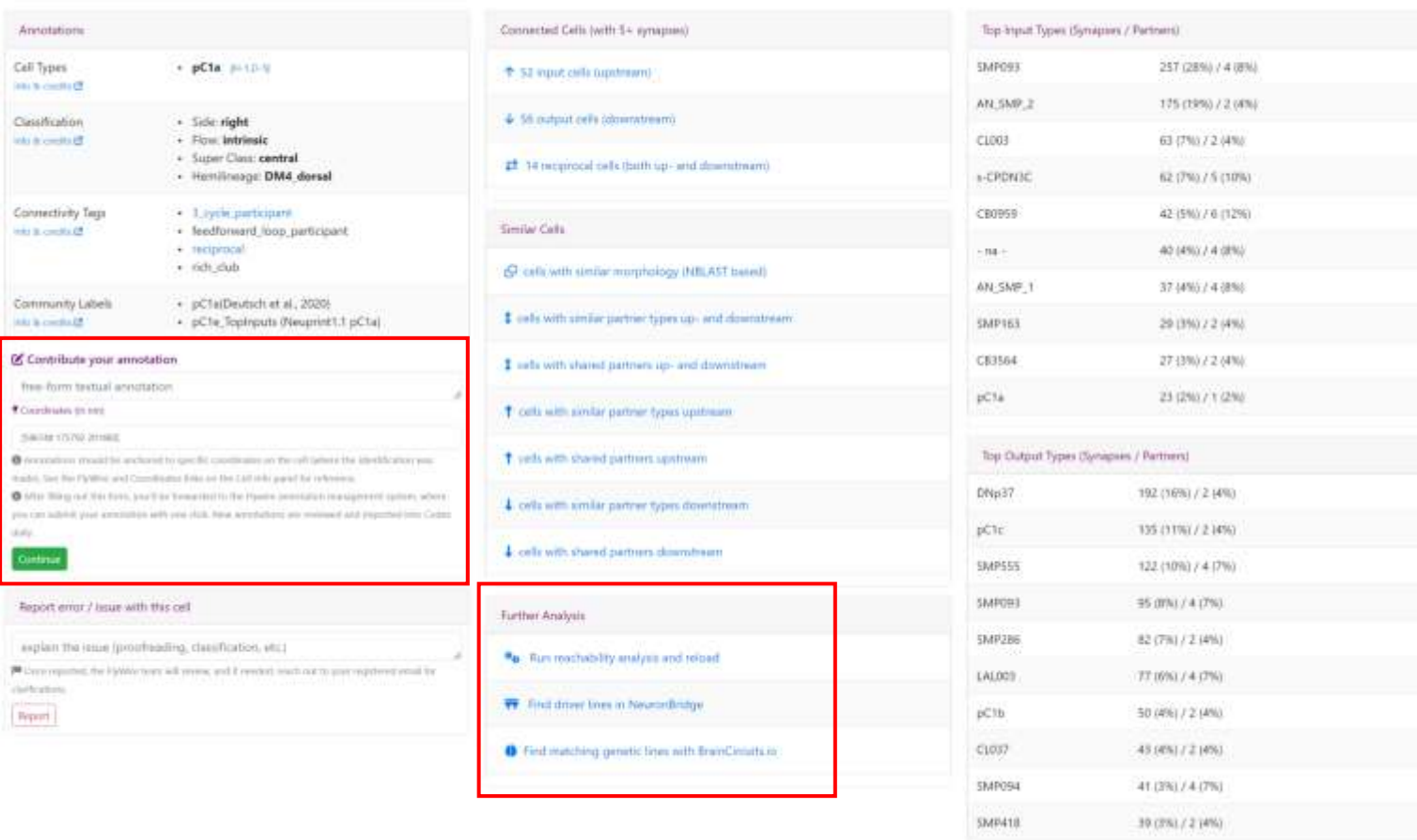
Cells	242	Top Types	Top Input Types (Synapses / Partners)	Top Output Types (Synapses / Partners)
- Cell Types	21	s-CPDN3A 38	s-CPDN3D 1,734 (5%) / 26 (3%)	DN1pD 1,210 (3%) / 8 (1%)
- Typed cells	242	s-CPDN3D 37	aMe3 1,577 (4%) / 2 (0%)	CL086_a 1,185 (3%) / 10 (1%)
- Internal connections / syns	711 / 7,166	s-CPDN3C 32	DN1pA 1,507 (4%) / 8 (1%)	s-CPDN3D 964 (2%) / 34 (3%)
- Ext. upstream partners / syns	866 / 29,300	s-CPDN3E 25	aMe8 1,195 (3%) / 4 (0%)	SMP234 830 (2%) / 2 (0%)
- Ext. downstream partners / syns	1,182 / 32,940	s-CPDN3B 25	SMP517 1,059 (3%) / 9 (1%)	DN1pC 805 (2%) / 4 (0%)
- Combined length	359,664 μm	APDN3 12	CB0710 737 (2%) / 4 (0%)	SMP285 801 (2%) / 2 (0%)
- Combined area	774,900 μm^2	I-LNv 8	aMe1 725 (2%) / 4 (0%)	DNd01 705 (2%) / 4 (0%)
- Combined volume	64,771 μm^3	DN1pA 8	SMP202 725 (2%) / 2 (0%)	LNd_CRY+_ITP+ 672 (2%) / 2 (0%)
		DN1pD 8	cM04 694 (2%) / 6 (1%)	- na - 616 (2%) / 26 (2%)
		s-LNv 8	SLP270 644 (2%) / 2 (0%)	SMP335 597 (1%) / 2 (0%)





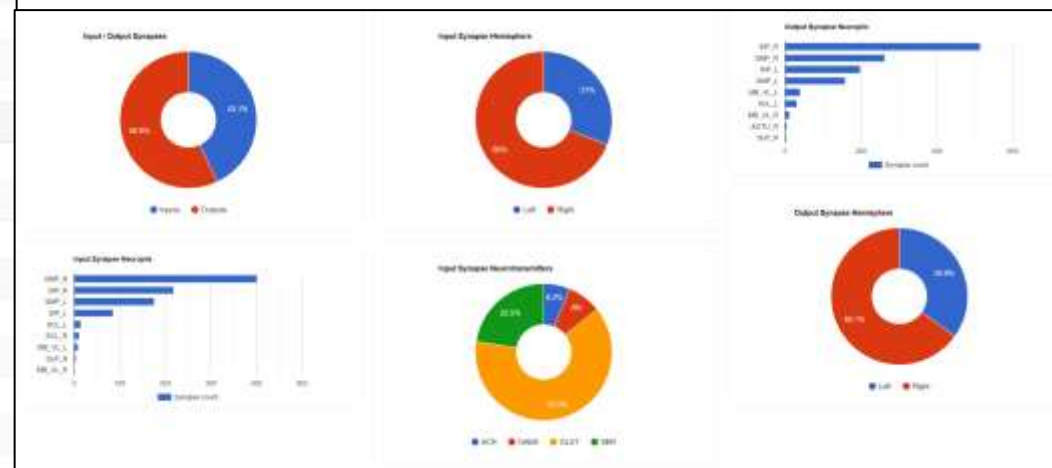
Cell Details:

Information about individual cells, their connectivity, similar/twin cells, 3D rendering and annotations



References and external links

- Neuron bridge (matching driver lines)
- [BrainCircuits.io](https://braincircuits.io) (genetic lines)
- Virtual Fly Brain and FlyBase (neuron and cell type information)
- Automated summary and literature citations (not very useful yet)
- Coming soon: known function of certain cell types



3D Viewer: Visualize queried neurons and synapses in annotated Neuroglancer scenes

← ↻ https://codex.flywire.ai/app/view_3d?dataset=fafb&query=clock&action=

Codex Search Stats Cell Info **3D** Explore Connectivity 🏆 📄 ✂️ ⬇️ 👤 ?

clock 🔍 Color by 3D only NGL

Color by

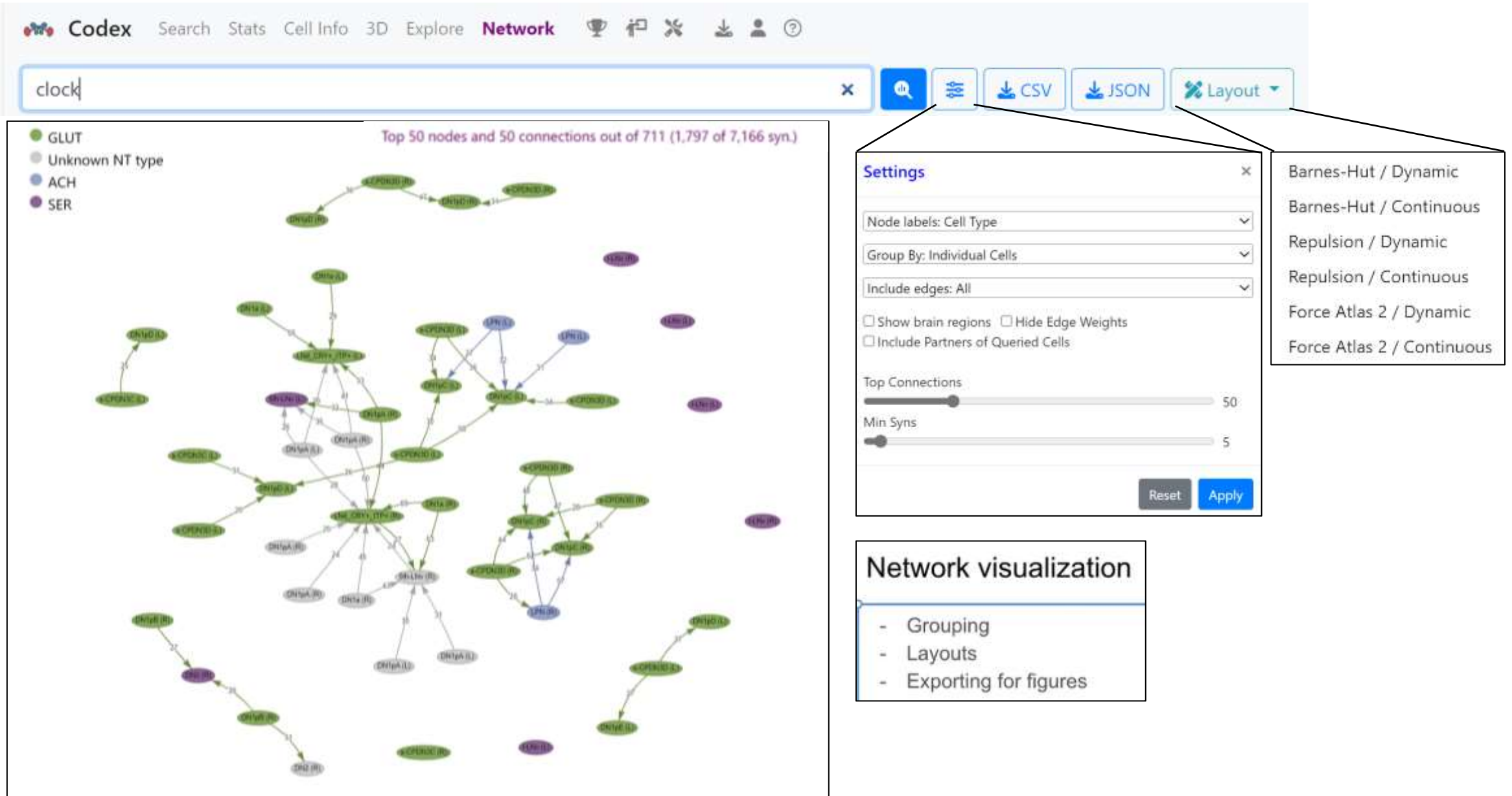
- Color by Neurotransmitter
- Color by Type
- Color by Class
- Color by Super Class
- Color by Flow
- Color by Top Neuropils
- Color by Soma Side
- Color by Visual Orbit
- Color by Visual axis P
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- Color by Visual axis X
- Color by Visual axis Y
- Color by Visual column ID

3D only

With EM



Network Graphs: Visualize connectivity of neurons and their synaptic links



Pathways: Analyse shortest-paths between pairs of neurons

Codex

Search

Stats

Cell Info

3D

Explore

Pathways

pC1a

DN1a

min syn5

Group byIndividual Cells

	DN1a	DN1a	DN1a	DN1a
from \ to	MB_CA.PLP.3	MB_CA.PLP.4	MB_CA.PLP.1	MB_CA.PLP.2
	720575940624155416	7205759406172266A1	720575940626715673	720575940617864961
pC1a	4 hops	4 hops	4 hops	4 hops
SNP.SRP.8	View Pathways chart	View Pathways chart	View Pathways chart	View Pathways chart
720575940625792698				
pC1a	4 hops	4 hops	4 hops	4 hops
SNP.SRP.9	View Pathways chart	View Pathways chart	View Pathways chart	View Pathways chart
720575940646310947				

Download CSV

ACH

GABA

GLUT

Unknown NT type

PLPSLP16 (connected cell)

720575940635228335

• new clone_1

Individual Cells

Type

Class

Super Class

Flow

Side

Nt Type

Type & side

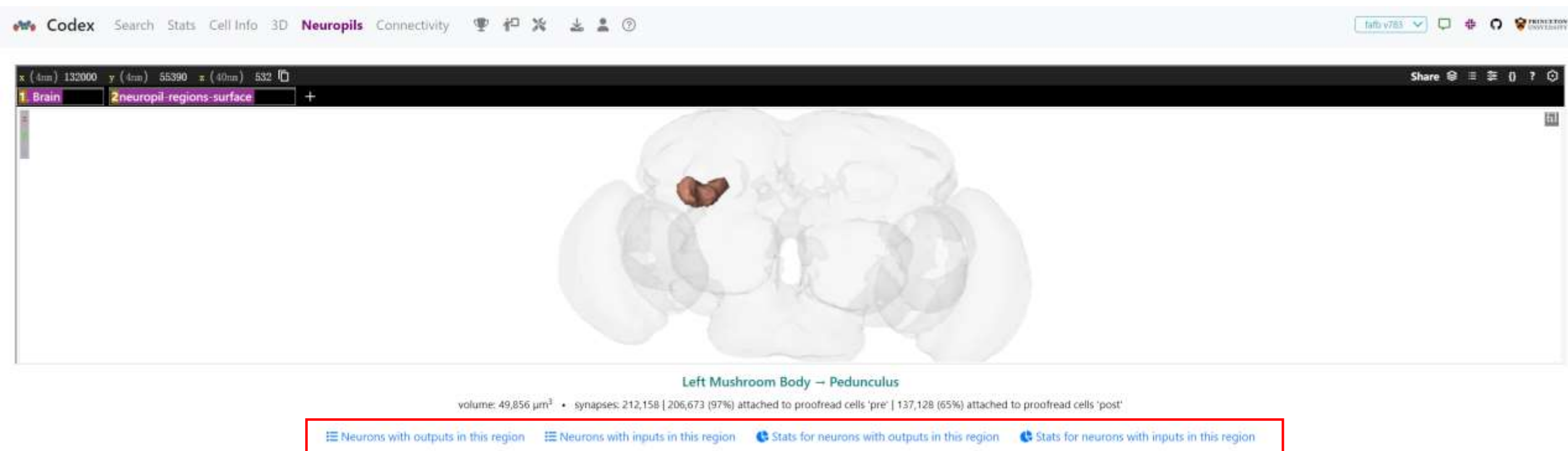
Class & side

Super Class & side

Flow & side

Nt Type & side

Neuropils: Visualize and query connections in specific brain regions



Take home message

Datasets in Codex (May 2025)

- FlyWire FAFB - female brain
- BANC - female brain and nerve cord (requires access token)
- MANC - male nerve cord
- Optic Lobe - male optic lobe (coming soon)
- Mouse datasets (coming later)

Codex 常用功能

神经元检索



Search

Find neurons using fish names or anatomical queries

检索结果统计



Stats

See statistics and checks for common attributes of all or subset of neurons in the dataset

神经元注释



Annotations

Browse cell types, labels, and groupings of the neurons in the dataset

目标神经元的详细信息



Cell Details

Information about individual cells, their connecting synapses, and 3D rendering and annotations

脑区结构检索



Neuropils

Visualize and query connections in specific brain regions

神经元3D结构显示



3D Viewer

Visualize queried neurons and synapses in a 3D environment

目标神经元的连接网络



Network Graphs

Visualize connectivity of neurons and their synaptic links

神经元通路检索



Pathways

Visualize synaptic paths between pairs of neurons

源数据



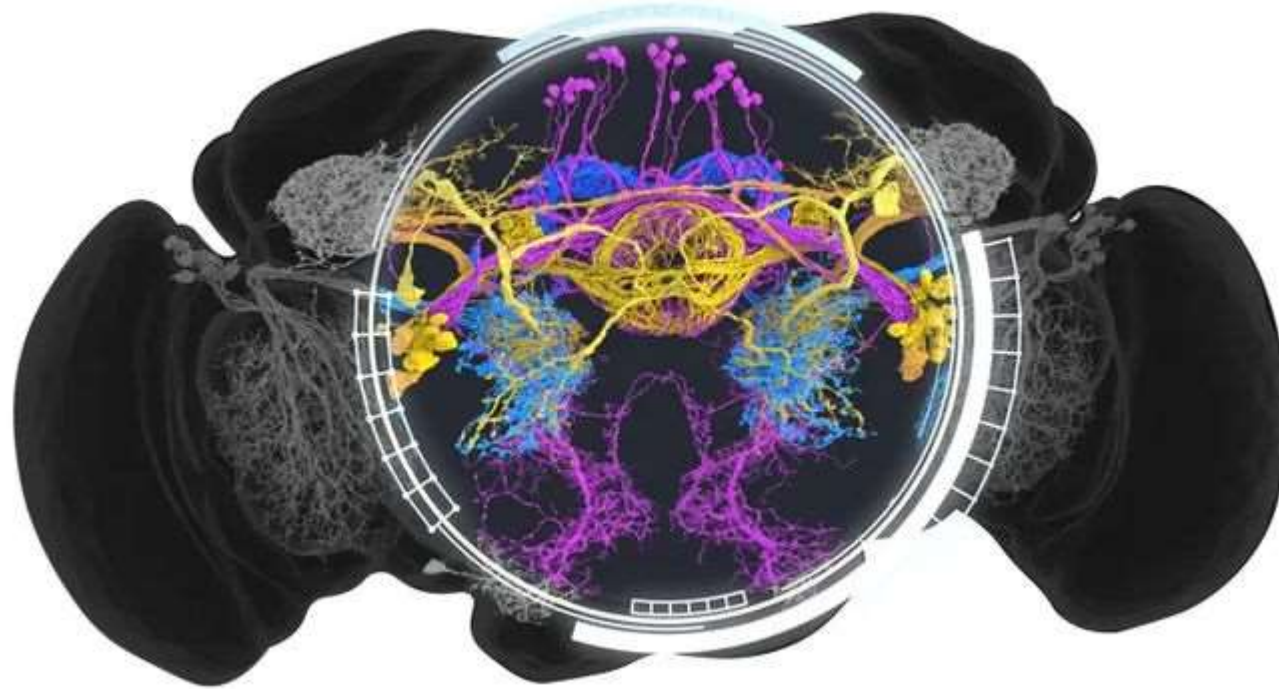
Download Data

Export raw data for analysis with other tools / programs

By GC

PART 3:

Current Advances in *Drosophila* Research Using FlyWire
XLM



From the Flywire to scientific researches:


What research areas are covered by FlyWire's applications?

What can we inspire from these researches using FlyWire?

Development and application of flywire

Author Manuscript

Author Manuscript

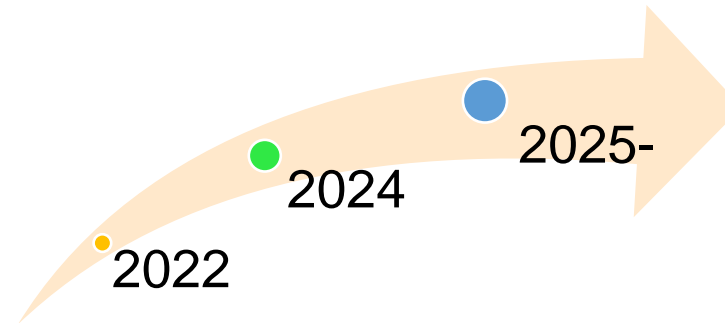
**HHS Public Access**
Author manuscript
Nat Methods. Author manuscript; available in PMC 2022 June 23.

Published in final edited form as:
Nat Methods. 2022 January ; 19(1): 119–128. doi:10.1038/s41592-021-01330-0.

FlyWire: Online community for whole-brain connectomics

Sven Dorkenwald^{1,2,*}, Claire E. McKellar^{1,*}, Thomas Macrina^{1,2,*}, Nico Kemnitz^{1,*}, Kisuk Lee^{1,5,*}, Ran Lu^{1,*}, Jingpeng Wu^{1,*}, Sergiy Popovych^{1,2}, Eric Mitchell¹, Barak Nehoran^{1,2}, Zhen Jia^{1,2}, J. Alexander Bae^{1,3}, Shang Mu¹, Dodam Ih¹, Manuel Castro¹, Oluwaseun Ogedengbe¹, Akhilesh Halageri¹, Kai Kuehner¹, Amy R. Sterling¹, Zoe Ashwood^{1,2}, Jonathan Zung^{1,2}, Derrick Brittain⁴, Forrest Collman⁴, Casey Schneider-Mizell⁴, Chris Jordan¹, William Silversmith¹, Christa Baker¹, David Deutsch¹, Lucas Encarnacion-Rivera¹, Sandeep Kumar¹, Austin Burke¹, Doug Bland¹, Jay Gager¹, James Hebditch¹, Selden Koolman¹, Merlin Moore¹, Sarah Morejohn¹, Ben Silverman¹, Kyle Willie¹, Ryan Willie¹, Szi-chieh Yu¹, Mala Murthy^{1,†}, H. Sebastian Seung^{1,2,†}

¹Princeton Neuroscience Institute, Princeton University, Princeton, NJ, USA
²Computer Science Department, Princeton University, Princeton, NJ, USA
³Electrical Engineering Department, Princeton University, Princeton, NJ, USA
⁴Allen Institute for Brain Science, Seattle, WA, USA
⁵Brain & Cognitive Sciences Department, Massachusetts Institute of Technology, Cambridge, MA, USA



Establishment of FlyWire
The auditory pathway relating to courtship

Whole-brain connectome
The connectome of sensory system
Circadian rhythm

Clock neurons

Codex
Connectome Data Explorer [Tutorials](#)
Developed at Princeton Neuroscience Institute

FlyWire Brain Dataset (FAFB v783)
Connectome of a female adult fly brain (see [FlyWire Brain homepage](#) for details). Exploring version v783 that includes:

139,255 proofread cells	138,059 (99%) typed or labeled cells
2,700,513 connections [T]	34,153,566 synapses [T]

See [About FlyWire](#) and [FAQs](#) pages for more details.
Switch datasets from the drop-down menu in the top-right corner.

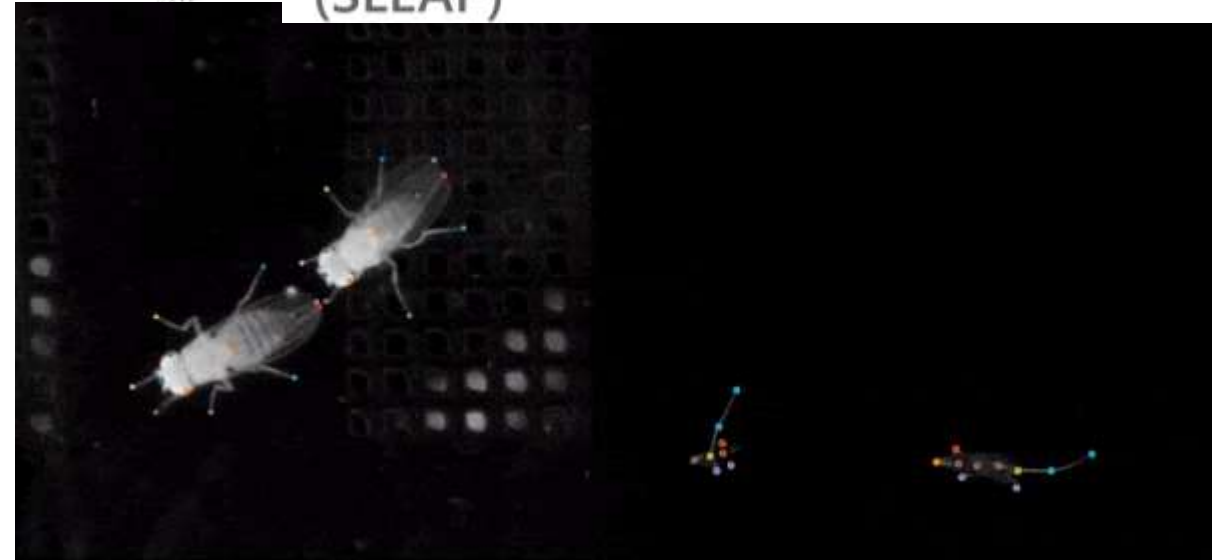


Mala Murthy (b. 1975) is an American neuroscientist and Professor of Neuroscience at Princeton University and leads the Murthy lab in the Princeton Neuroscience Institute – their work focuses on **the neural mechanisms that underlie social communication**, using the fruit fly *Drosophila* as a model system.

2024

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correspondi
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Social LEAP Estimates Animal Poses (SLEAP)

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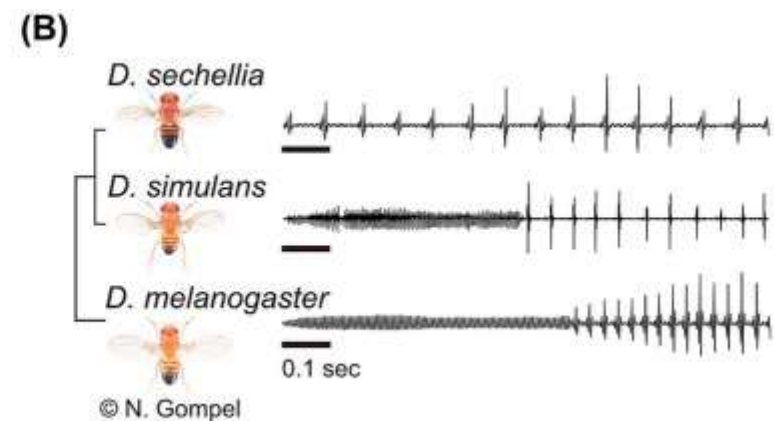
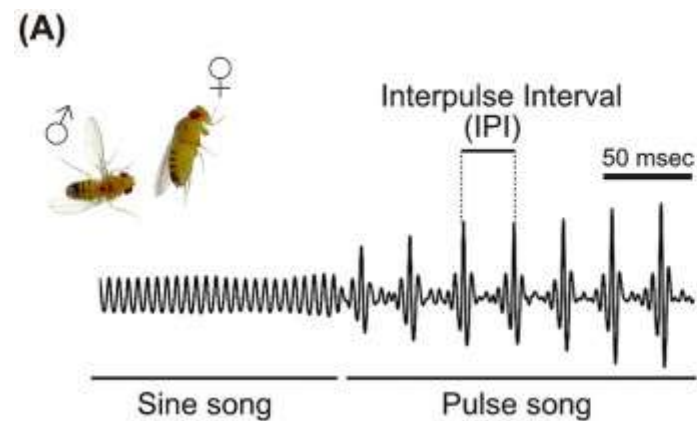
Munnelly, EJ,
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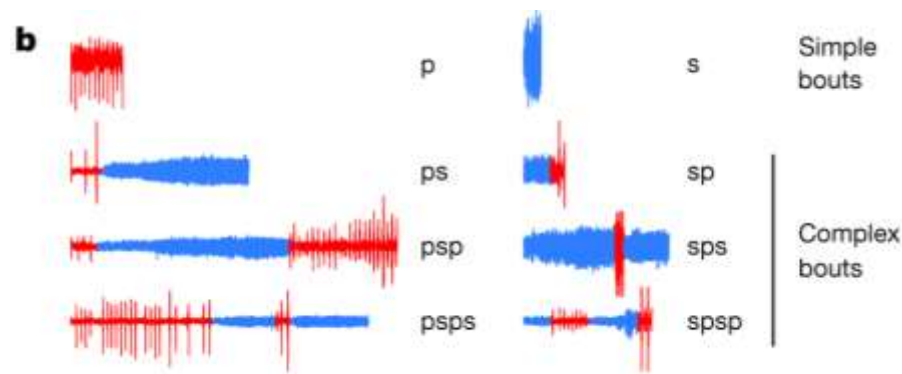
AS, Eckstein, N, Funke, J, Jefferis, GSXE, and Murthy, M. *Network Statistics of the Whole-Brain Connectome of Drosophila*. **Nature** 2024. 634, 153–165. doi.org/10.1038/s41586-024-07968-y #

- Matsliah A, Yu SC, Kruk K, Bland D, Burke A, Gager J, Hebditch J, Silverman B, Willie K, Willie R, Sorek M, Sterling AR, Kind E, Garner D, Sancer G, Wernet M, Kim SS, Murthy M, Seung HS, and the FlyWire Consortium. *Neuronal "parts list" and wiring diagram for a visual system*. **Nature** 2024. 634, 166–180. doi.org/10.1038/s41586-024-07981-1 #
- Shiu, PK, Sterne, GR, Spiller, N, Franconville, R, Sandoval, A, Zhou, J, Simha, N, Kang, CH, Yu, S, Kim, J, Dorkenwald, S, Matsliah, A, Sterling, AR, Yu, S-C, McKellar, CE, Schlegel, P, Costa, M, Eichler, K, Jefferis, GSXE, Murthy, M, Bates, AS, Eckstein, N, Funke, J, Bidaye, SS, Hampel, S, Seeds, AM, and Scott, K. *A leaky integrate-and-fire computational model based on the connectome of the entire adult Drosophila brain reveals insights into sensorimotor processing*. **Nature** 2024. 634, 210–219. doi.org/10.1038/s41586-024-07763-9 #

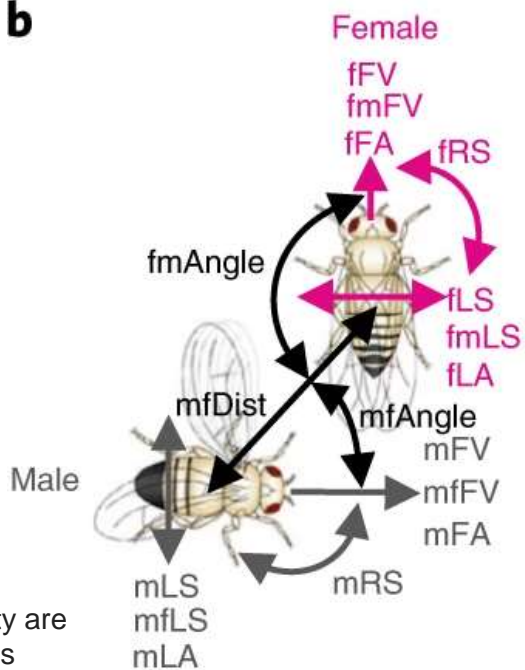
Courtship song is an important factor for the successful mating



b

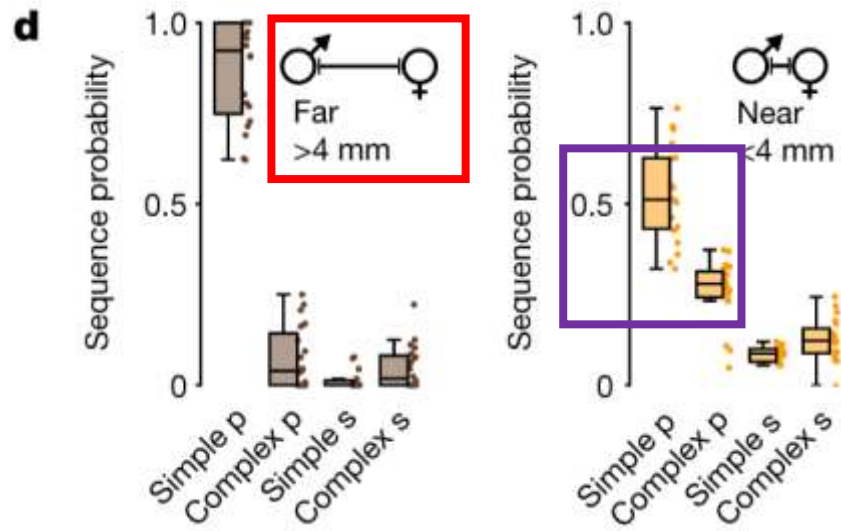


Male song patterning, timing and intensity are known to be modulated by feedback cues stemming from the female

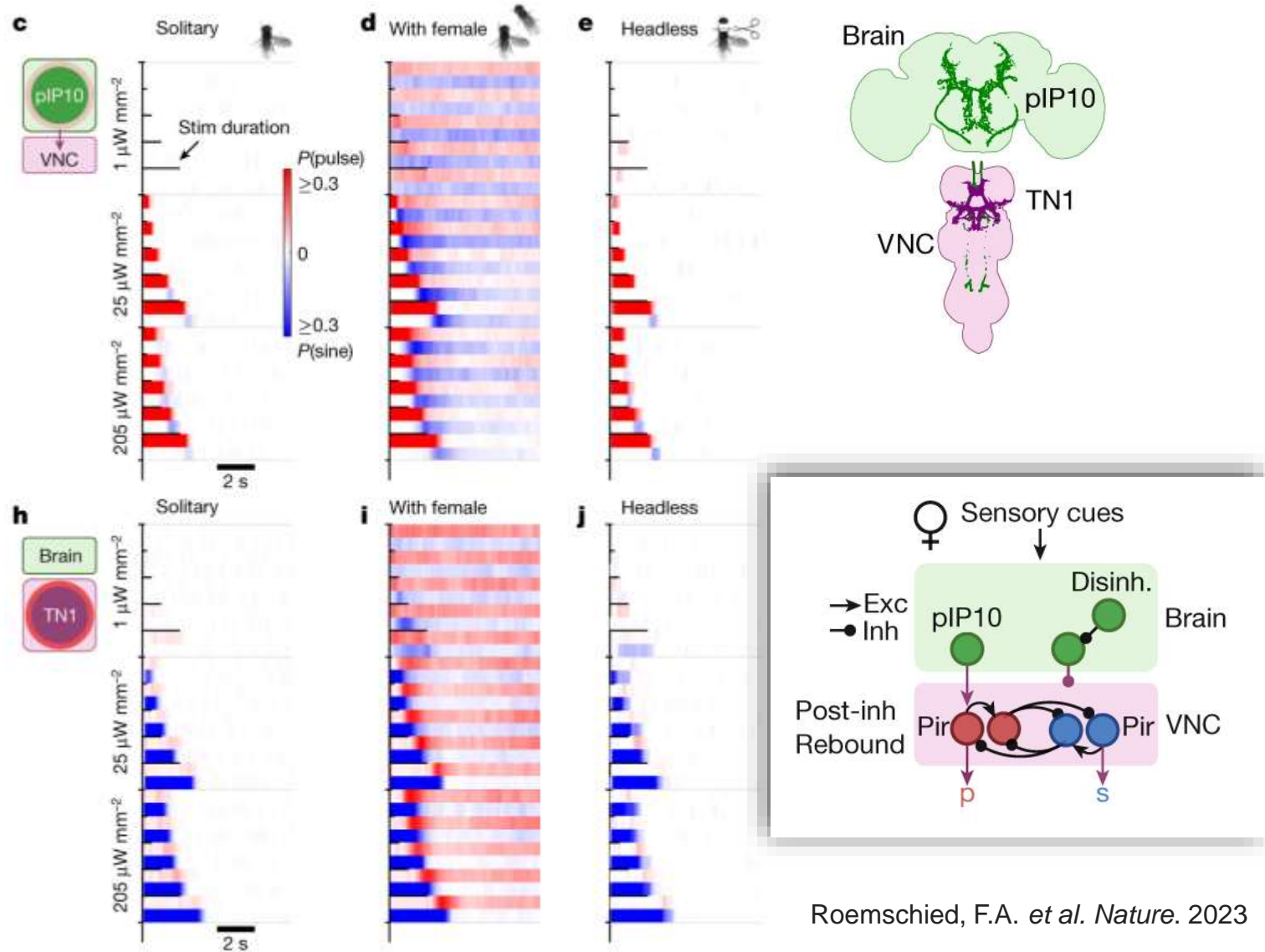


Receptive females reduce locomotor speed in response to multiple features within conspecific song.

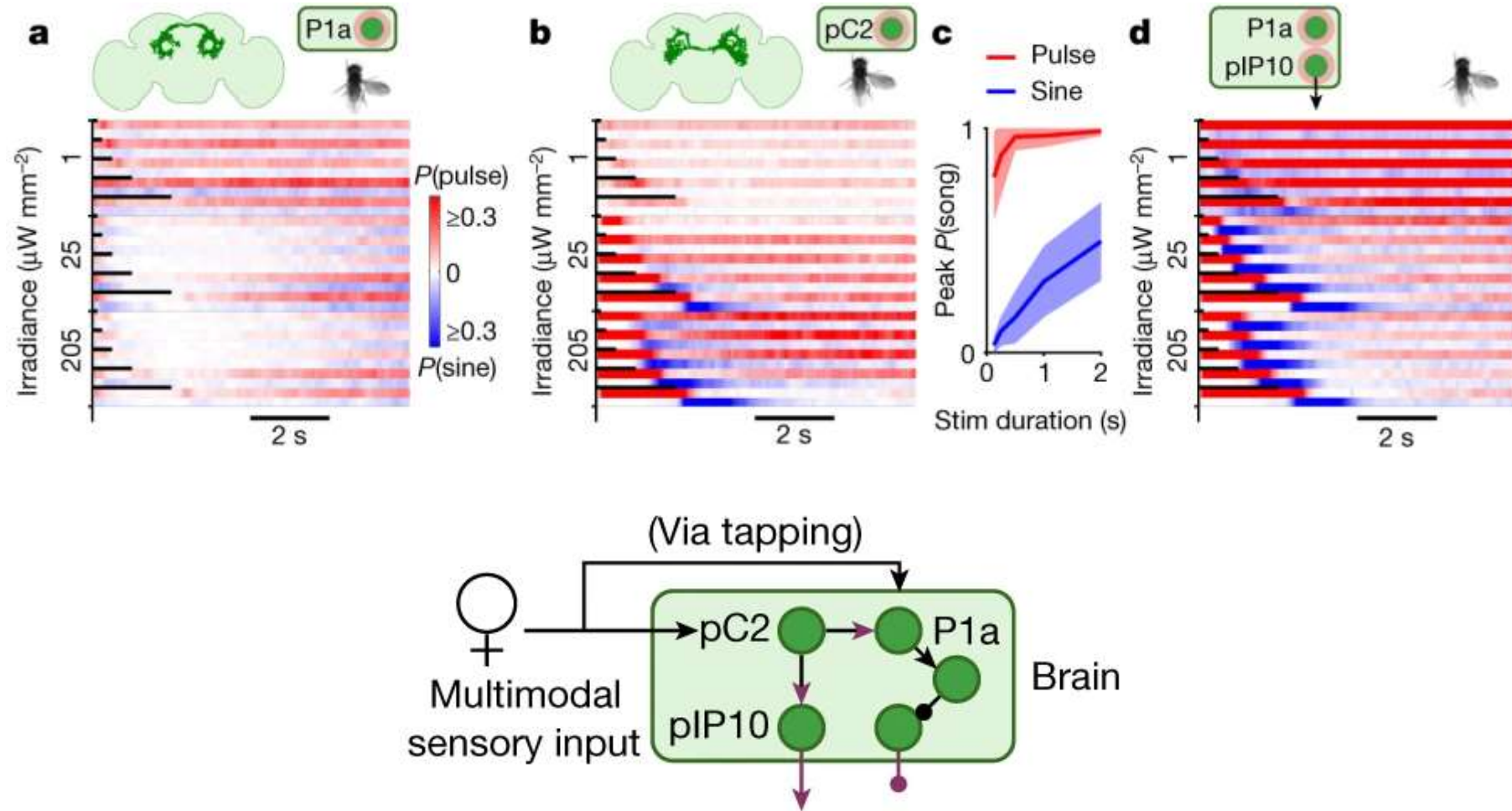
Reciprocal interactions between pulse-producing and sine-producing neurons in the presence of a female



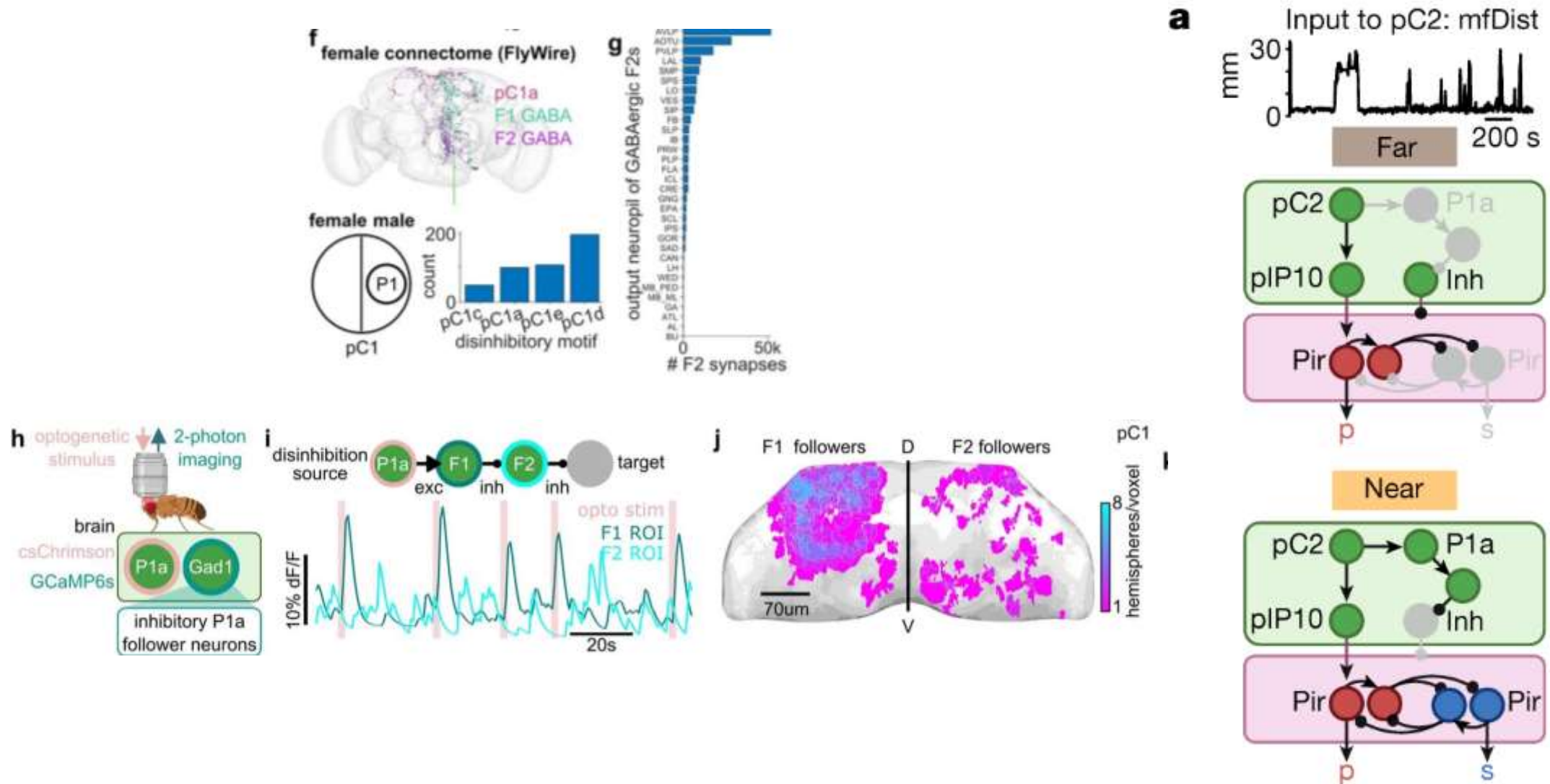
Context alters sequencing of male song
Pulse-neurons are activated initially



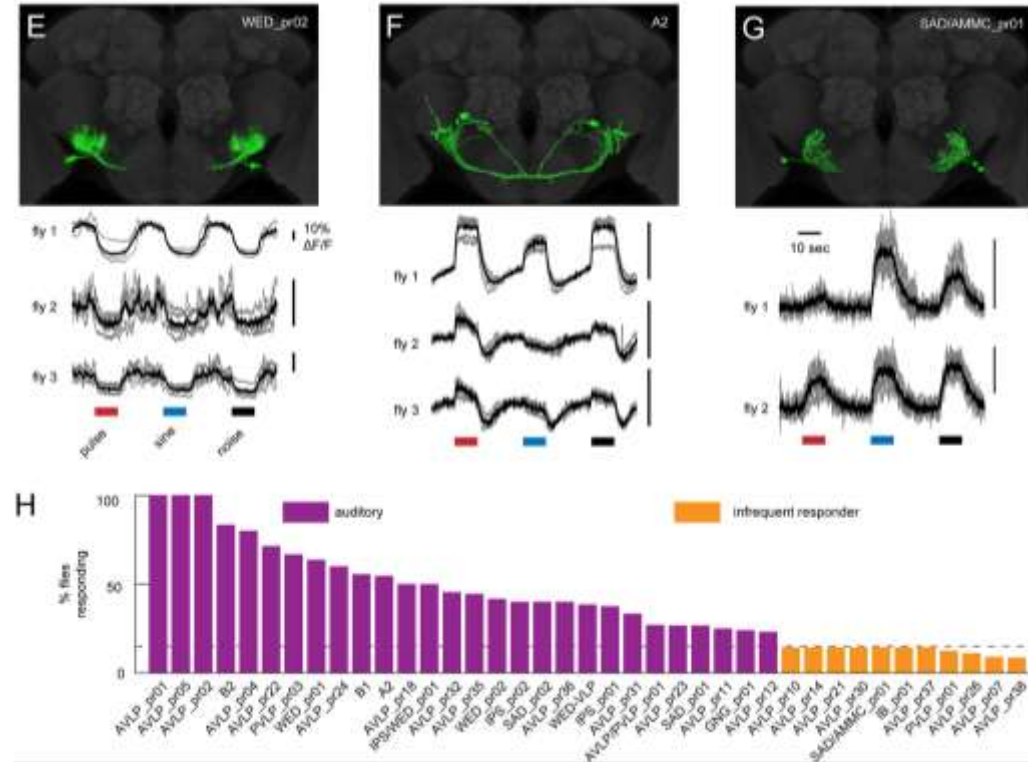
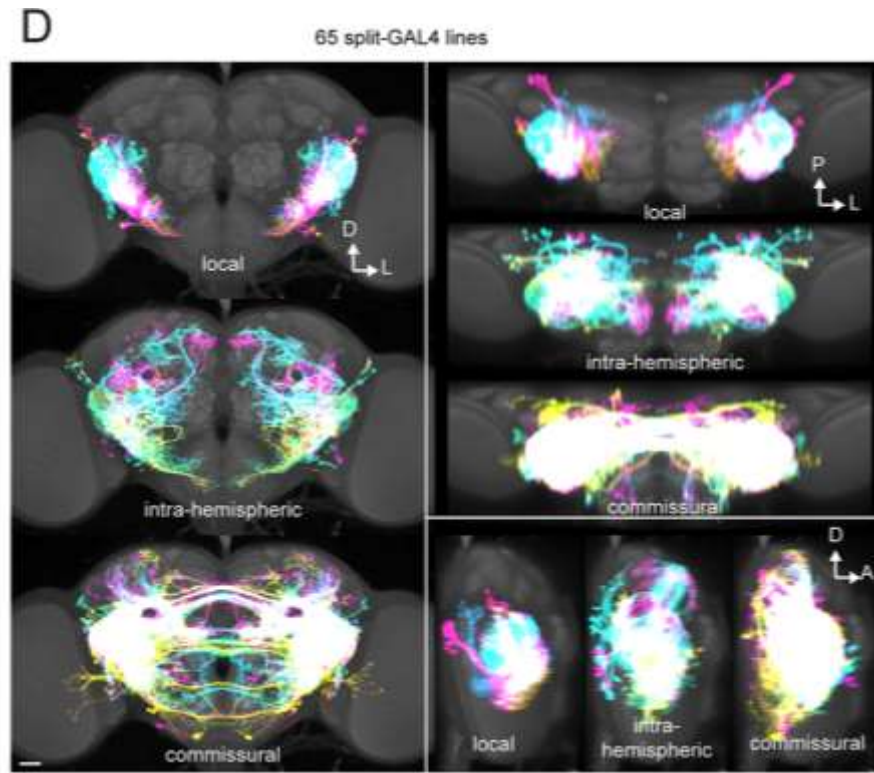
Female sensory cues promote complex song bout generation



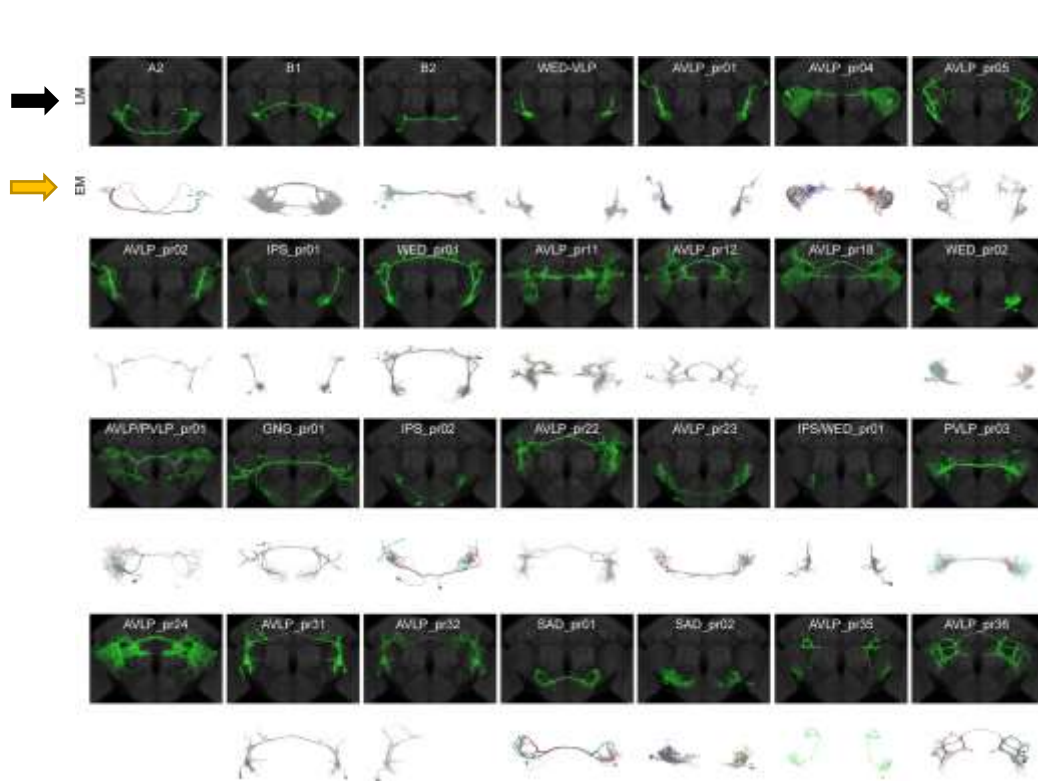
Neural circuit model of context-dependent song patterning



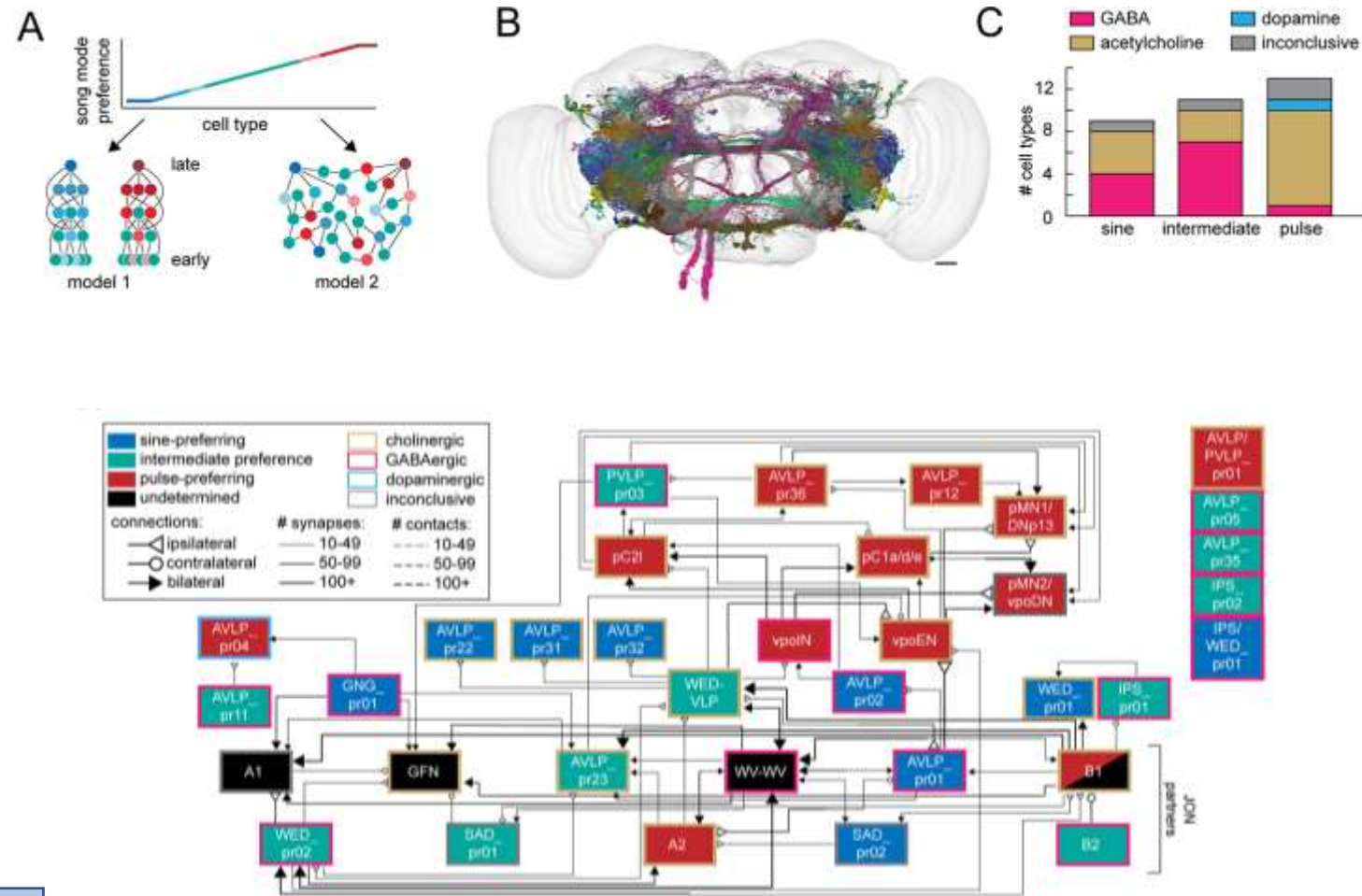
Anatomic and functional screen for auditory neurons



Identifying the connectome of *Drosophila* auditory neurons



To identify the preferred responses of different neurons to sine song and pulse song



The first circuit-level map of the auditory pathway



► Nat Commun. 2024 Dec 5;15:10392. doi: [10.1038/s41467-024-54694-0](https://doi.org/10.1038/s41467-024-54694-0)

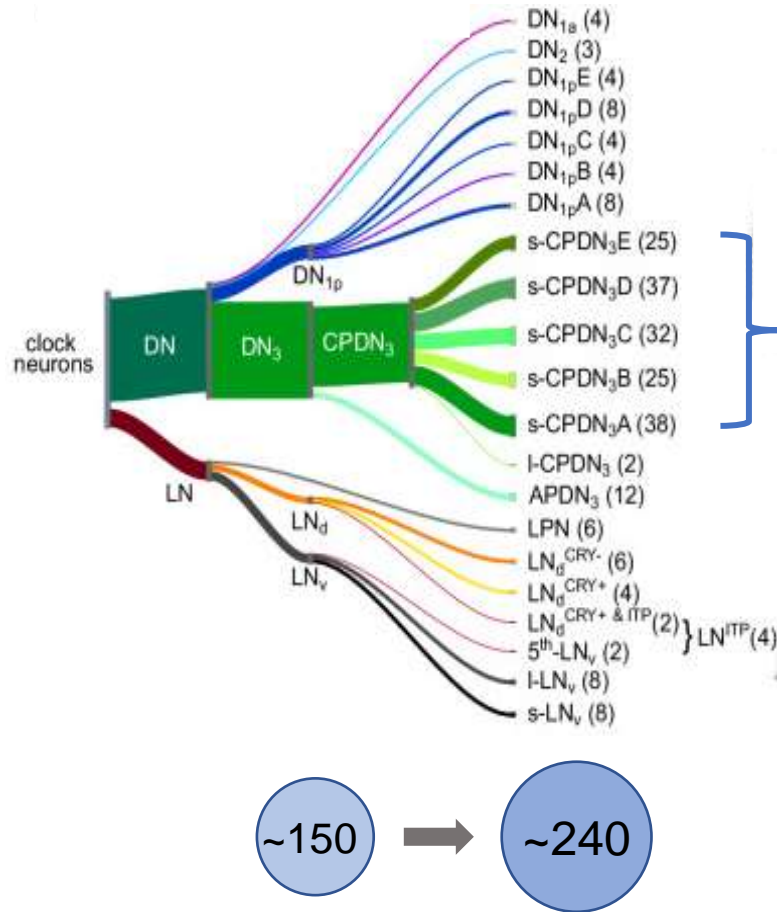
Synaptic connectome of the *Drosophila* circadian clock

[Nils Reinhard](#)^{1,#}, [Ayumi Fukuda](#)^{2,#}, [Giulia Manoli](#)¹, [Emilia Derksen](#)¹, [Aika Saito](#)², [Gabriel Möller](#)¹, [Manabu Sekiguchi](#)², [Dirk Rieger](#)¹, [Charlotte Helfrich-Förster](#)^{1,✉}, [Taishi Yoshii](#)², [Meet Zandawala](#)^{1,3,✉}

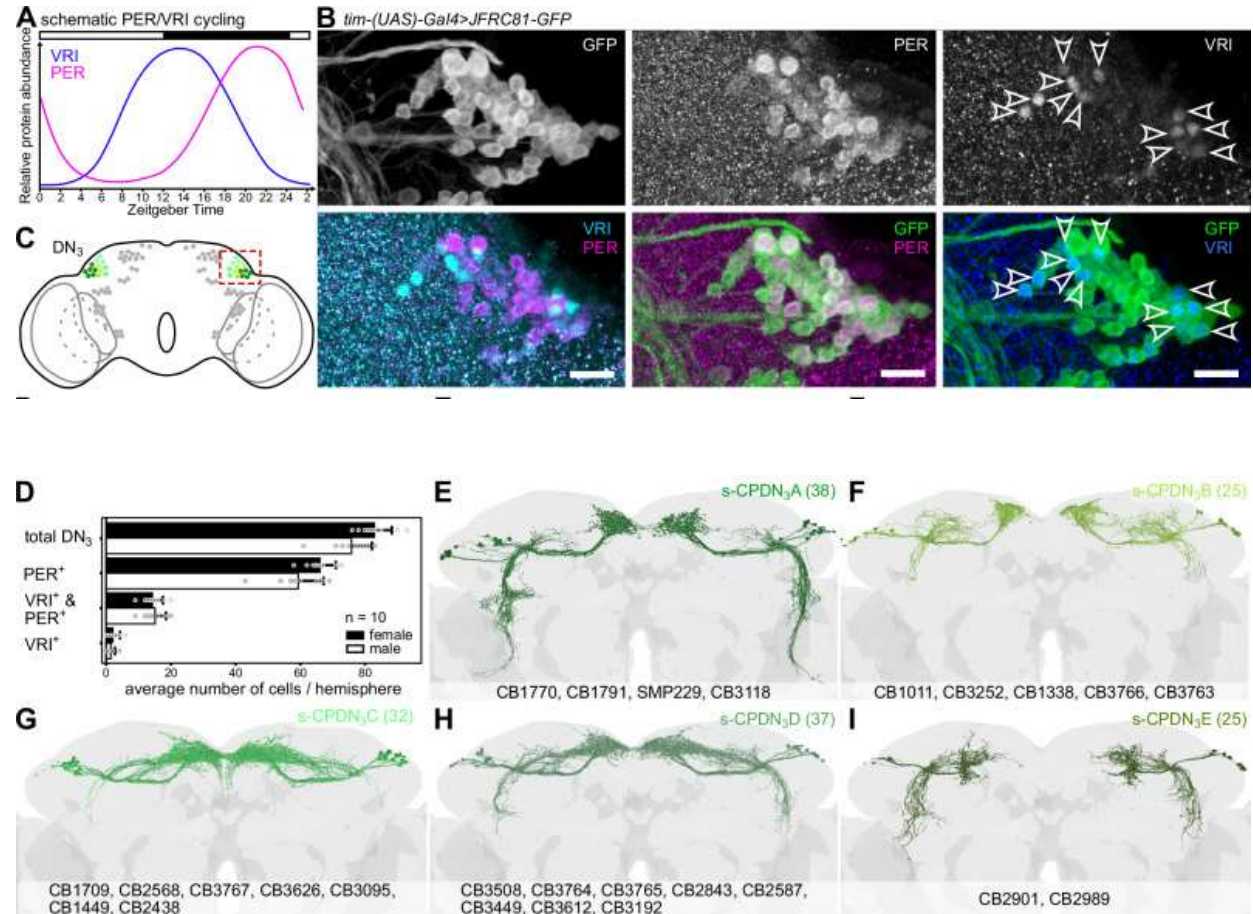
► [Author information](#) ► [Article notes](#) ► [Copyright and License information](#)

PMCID: PMC11621569 PMID: [39638801](https://pubmed.ncbi.nlm.nih.gov/39638801/)

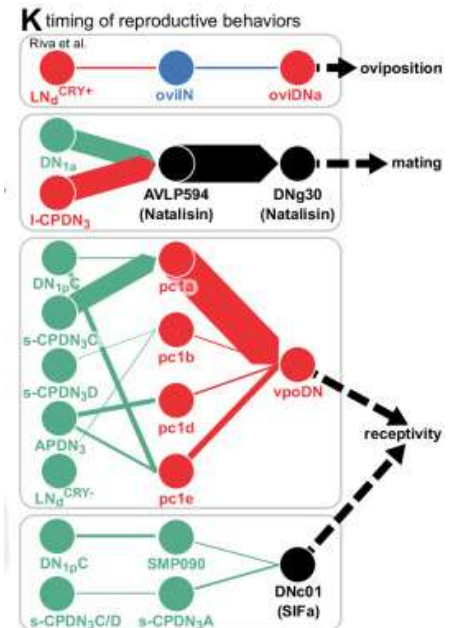
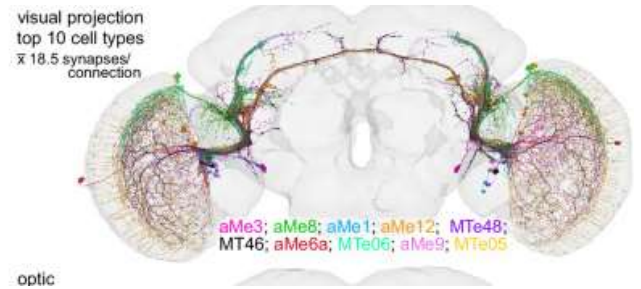
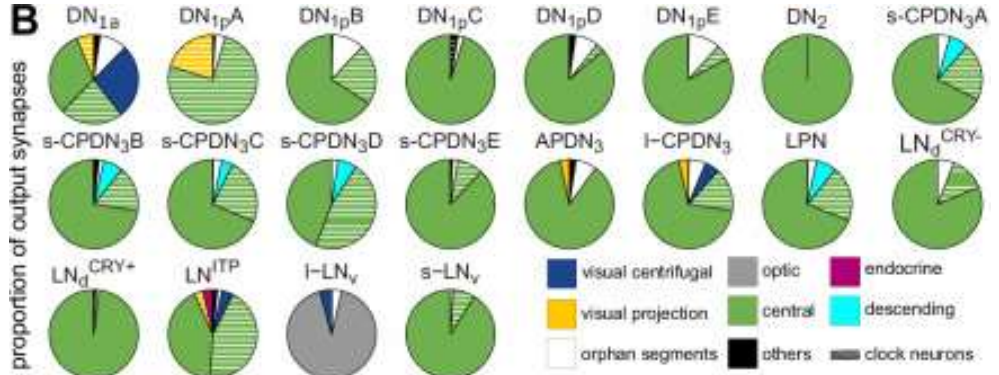
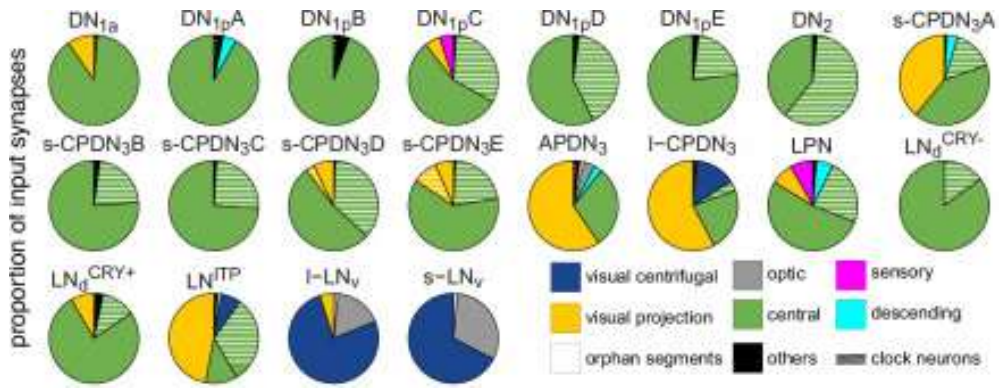
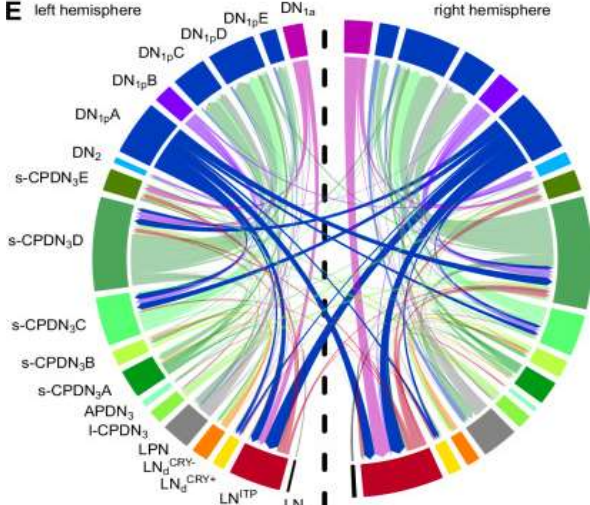
Additional dorsal clock neurons are identified, by using FlyWire

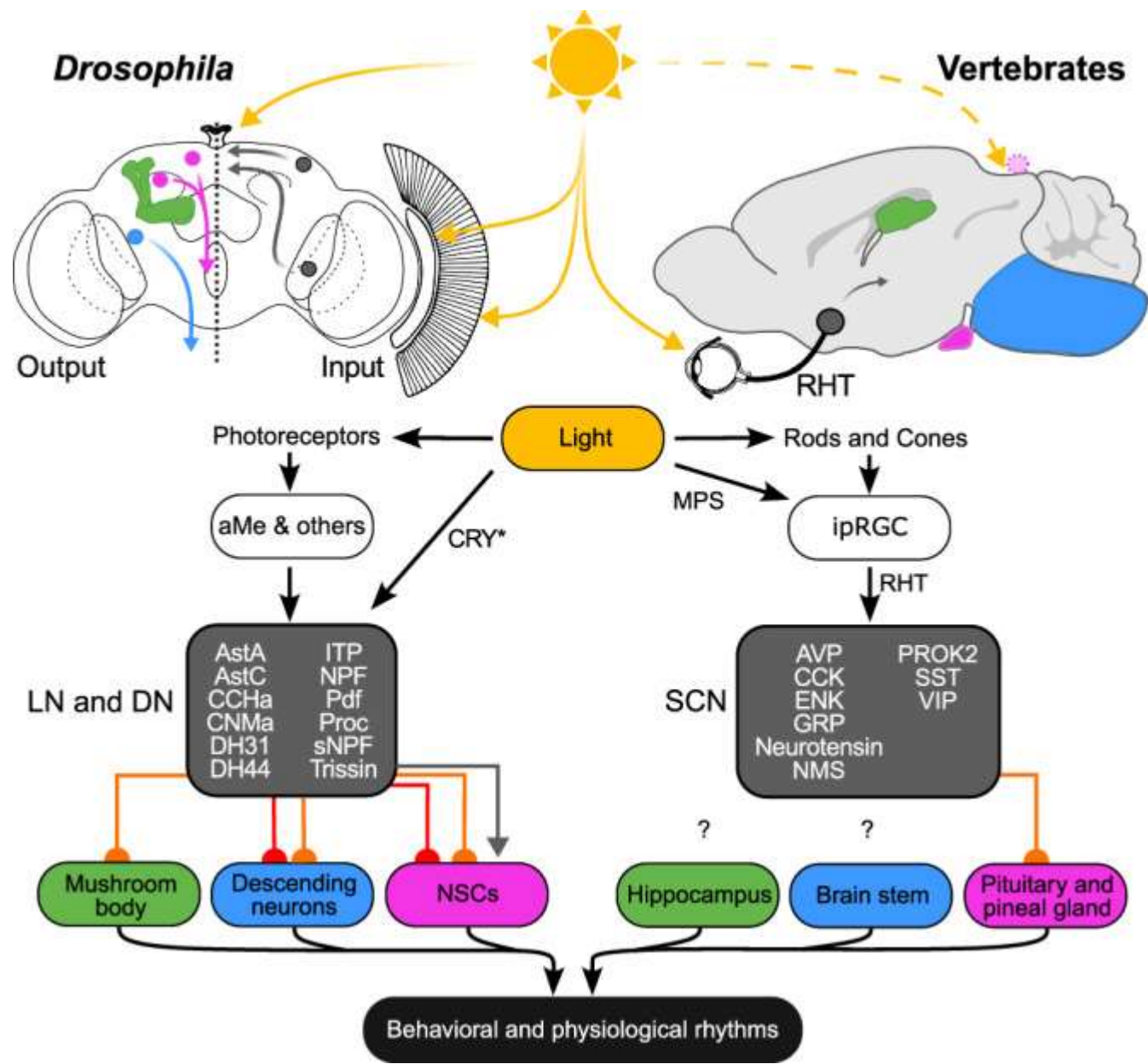
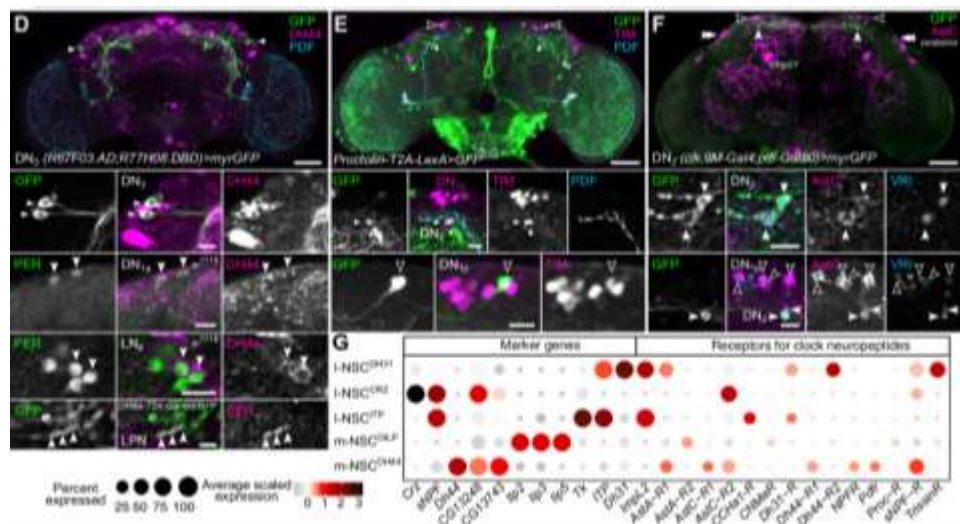


根据形态学、先前确定的连通性及其胞体位置的组合鉴定了 242 个时钟神经元



The upstream and downstream neural networks centered on rhythmic neurons are described in more detail





Current Biology

Regulation of pre-dawn arousal in *Drosophila* by a pair of trissinergic descending neurons of the visual and circadian networks

Highlights

- DNP27 neurons integrate circadian and visual signals
- Calcium oscillations in DNP27 peak at night and decline at day
- Activating trissinergic DNP27 reduces activity, and silencing advances the morning peak
- DNP27 inhibits light-responsive activity, promoting sleep stability before dawn

Authors

Ruihan Jiang, Yue Tian, Xin Yuan, Fang Guo

Correspondence

gfang@zju.edu.cn

In brief

Jiang et al. investigate two trissinergic DNP27 neurons in the *Drosophila* brain, which exhibit extensive innervation and integrate circadian and visual inputs. These neurons modulate the onset of the morning anticipation peak through Trissin-TrissinR signaling, inhibiting activity in downstream brain regions to regulate arousal thresholds.

郭方

教授、博士生导师

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实验室网站：https://person.zju.edu.cn/guofang#

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研究方向：生物节律调控行为的分子和神经机制

PLOS BIOLOGY

RESEARCH ARTICLE

Temperature cues are integrated in a flexible circadian neuropeptidergic feedback circuit to remodel sleep-wake patterns in flies

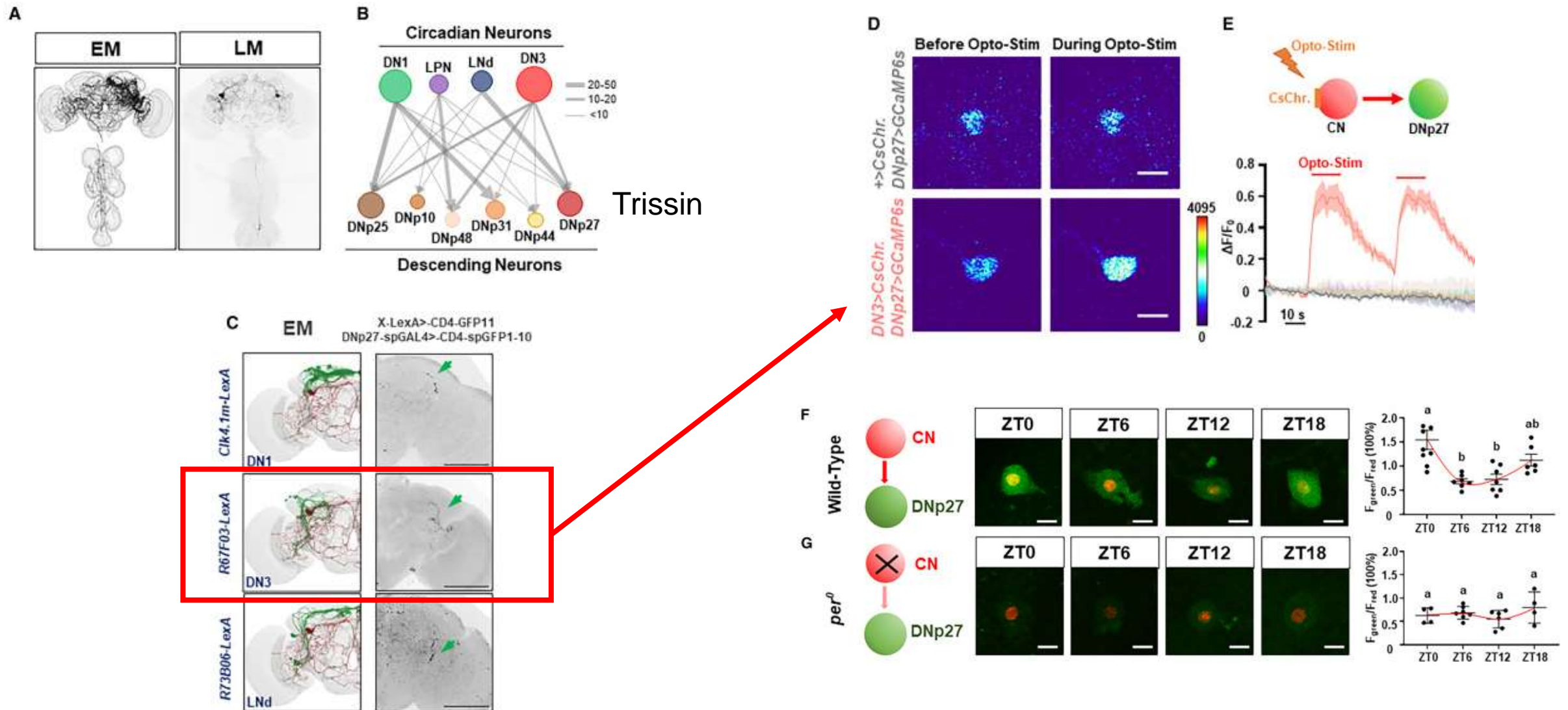
Xin Yuan^{1,2,3}, Hailiang Li^{2,3,4}, Fang Guo^{1,2,3,4*}

1 Department of Neurology of Children's Hospital and School of Brain Science and Brain Medicine, Zhejiang University School of Medicine, Hangzhou, China, **2** MCE Frontier Science Center for Brain Research and Brain-Machine Integration, State Key Laboratory of Brain-machine Intelligence, Zhejiang University, Hangzhou, China, **3** NHC and CAMS Key Laboratory of Medical Neurobiology, Zhejiang University, Hangzhou, China, **4** Department of Neurobiology, Department of Neurology of Sir Run Run Shaw Hospital and School of Brain Science and Brain Medicine, Zhejiang University School of Medicine, Hangzhou, China

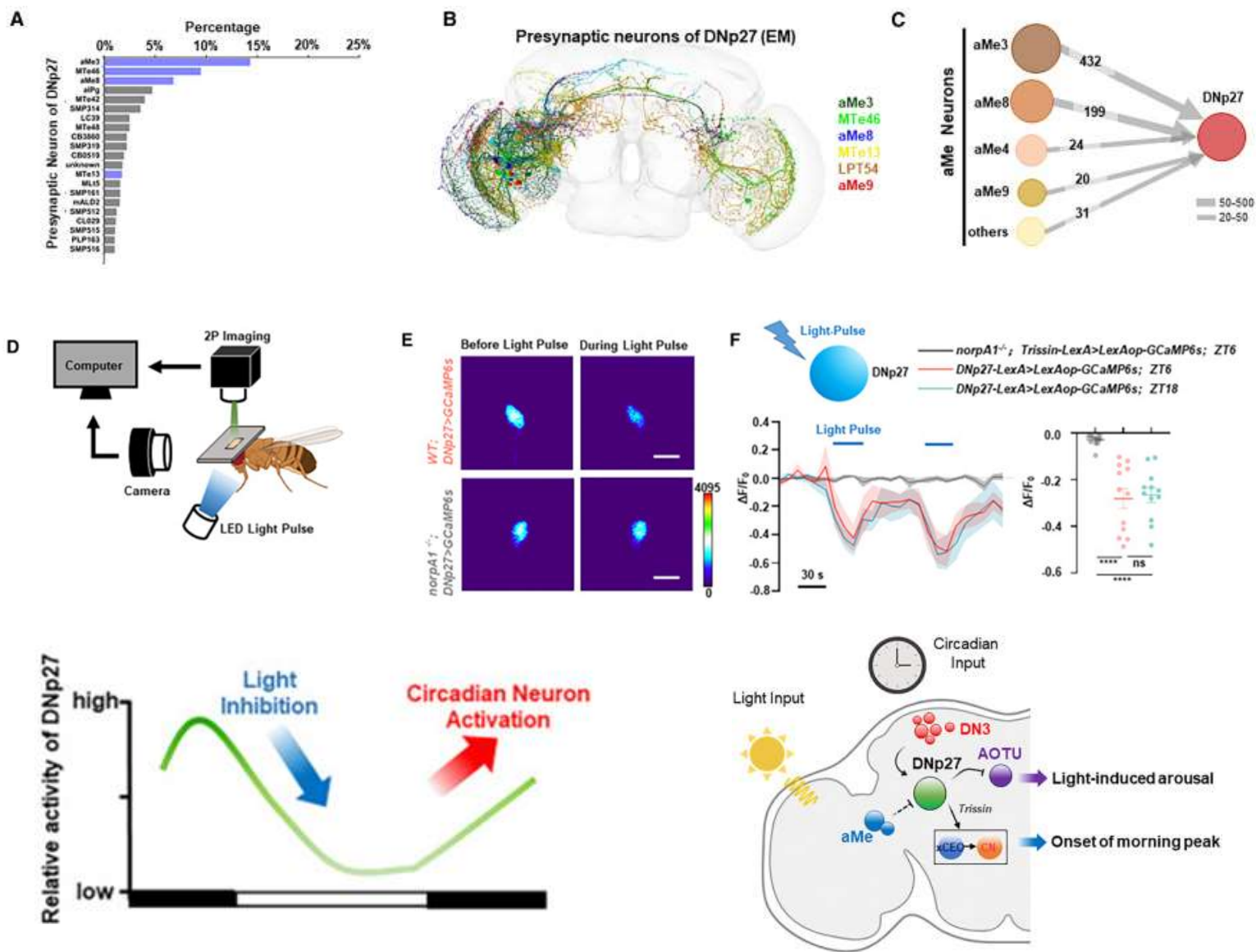
* gfang@zju.edu.cn



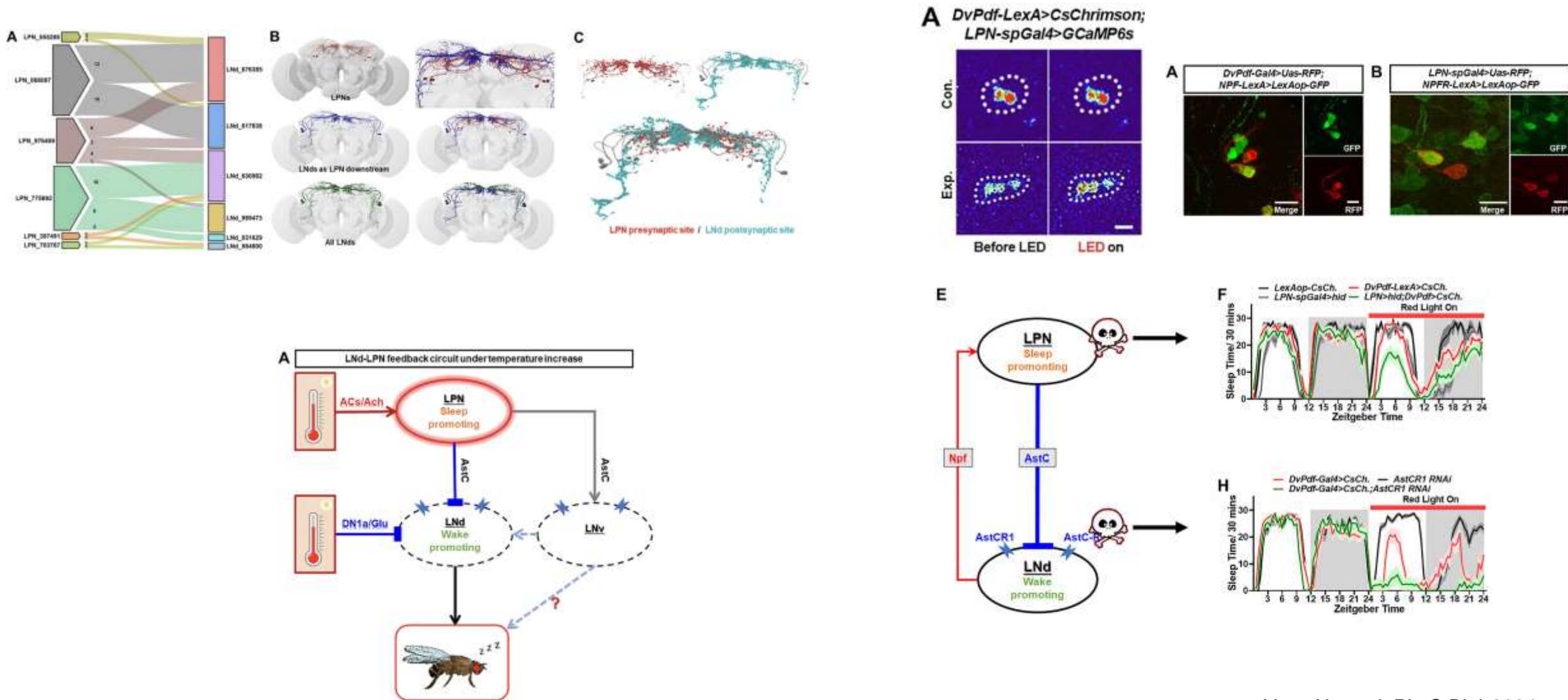
Searching in Flywire: DNp27 receives excitatory input from circadian neurons DN3



Nighttime circadian excitatory input and daytime photo-inhibitory input induce the daily fluctuating calcium pattern of DNp27

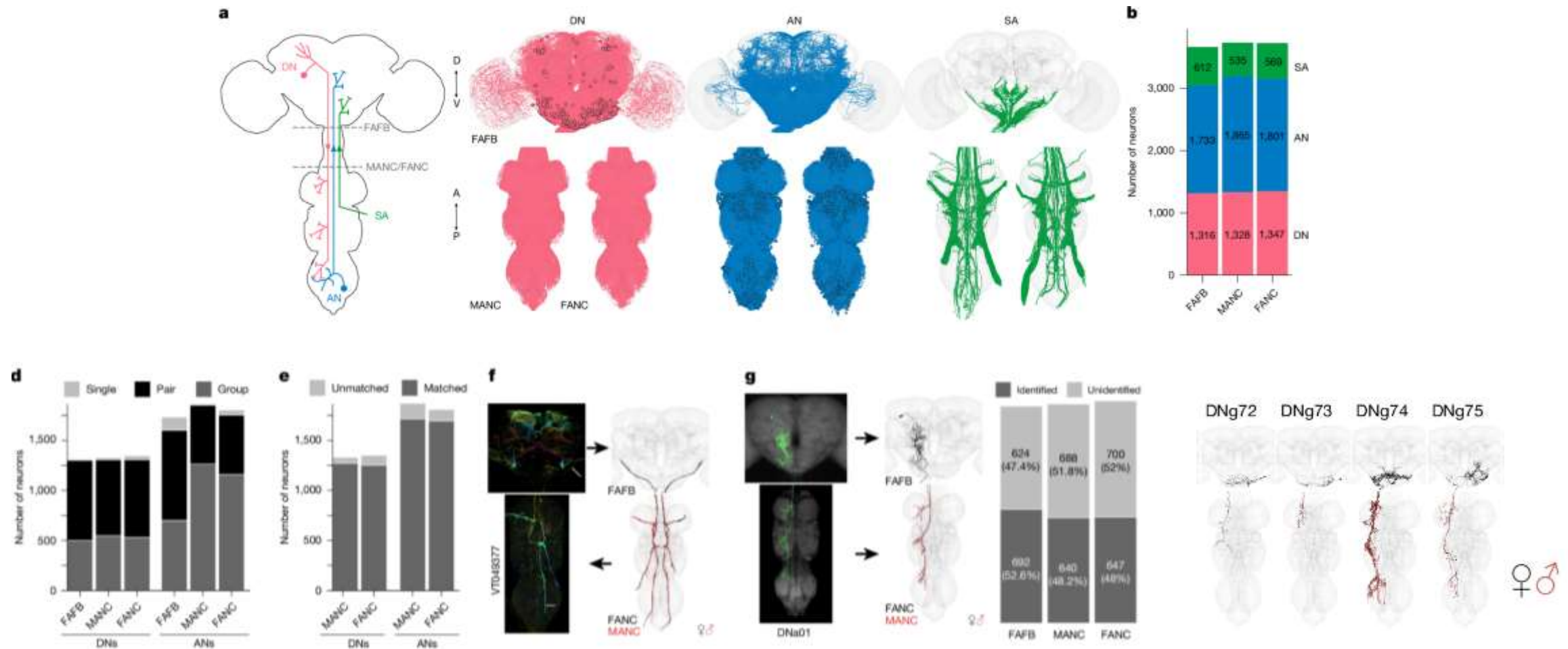


Temperature cues are integrated in a flexible circadian neuropeptidergic feedback circuit to remodel sleep-wake patterns in flies

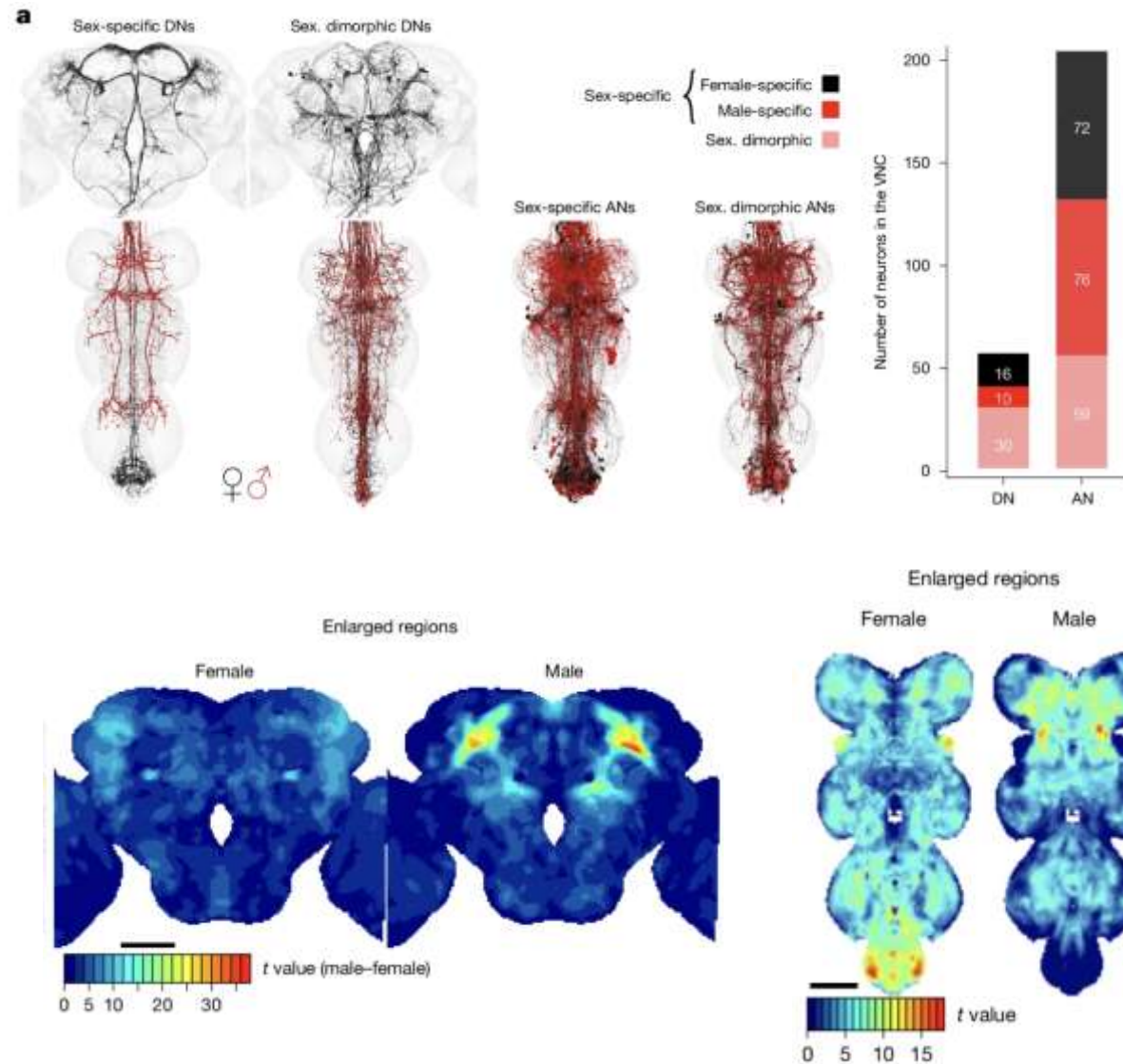


Matching neurons across three datasets

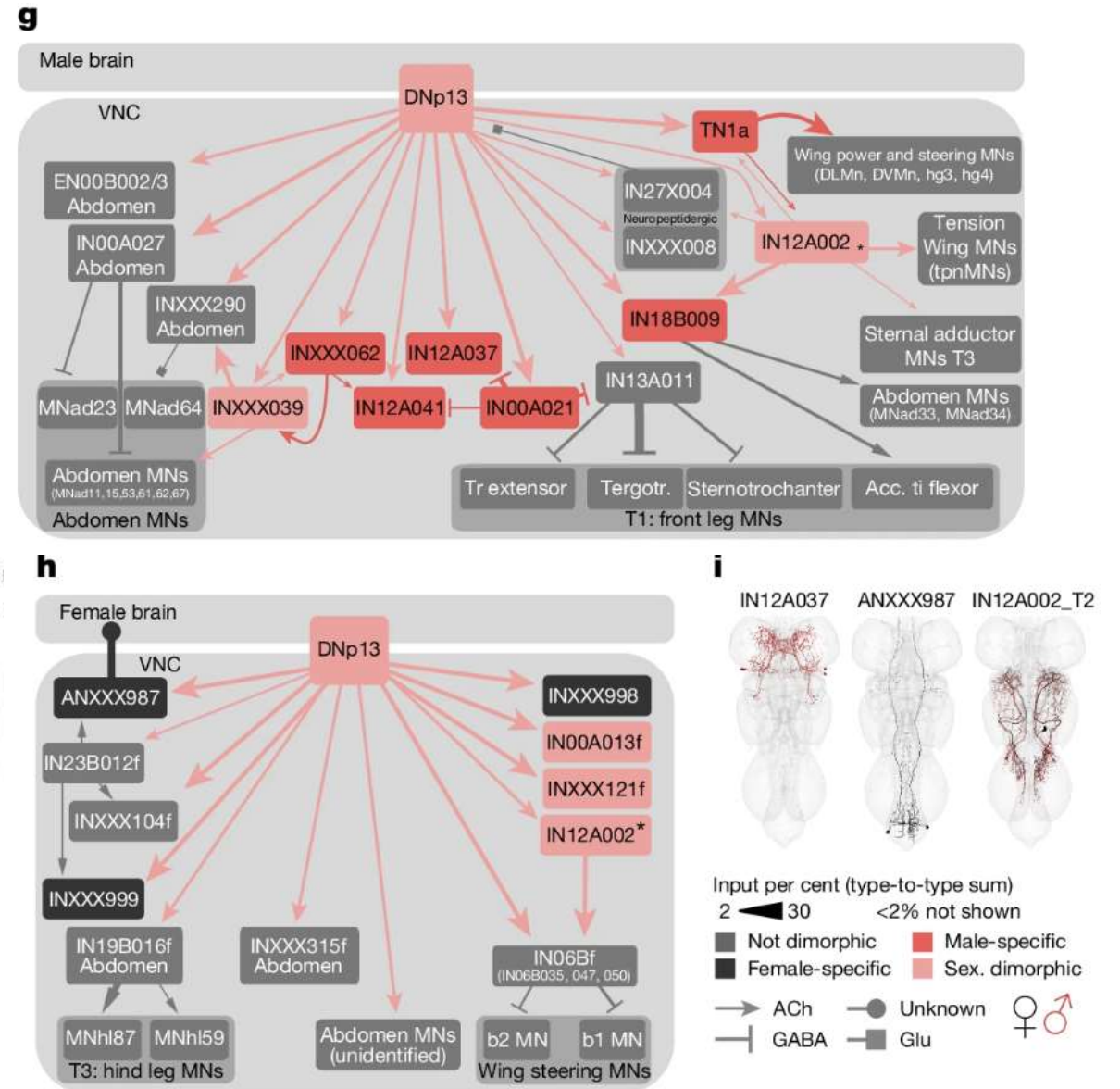
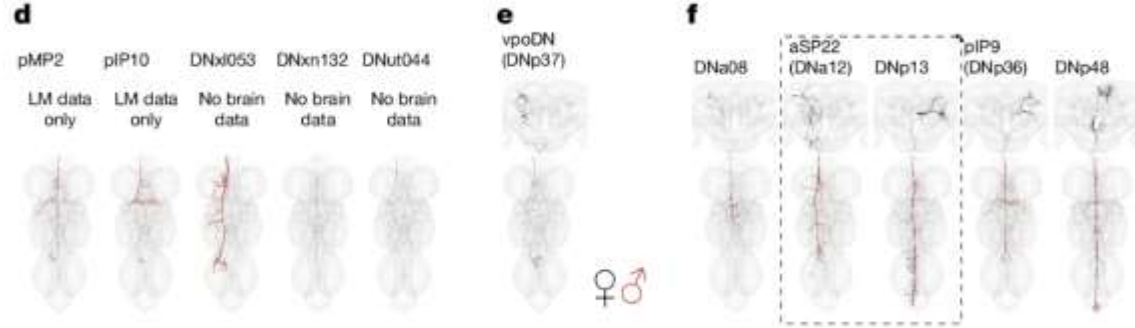
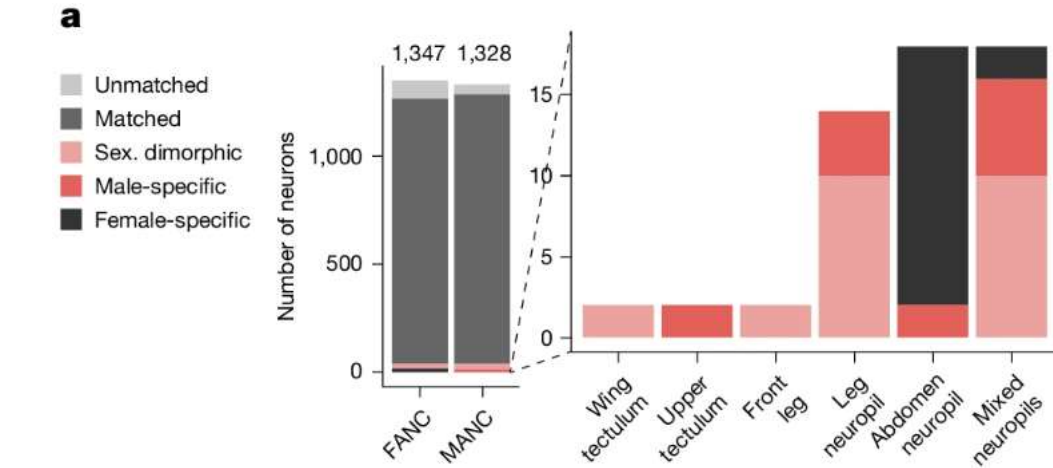
female adult fly brain (FAFB-FlyWire), female adult nerve cord (FANC), MANC



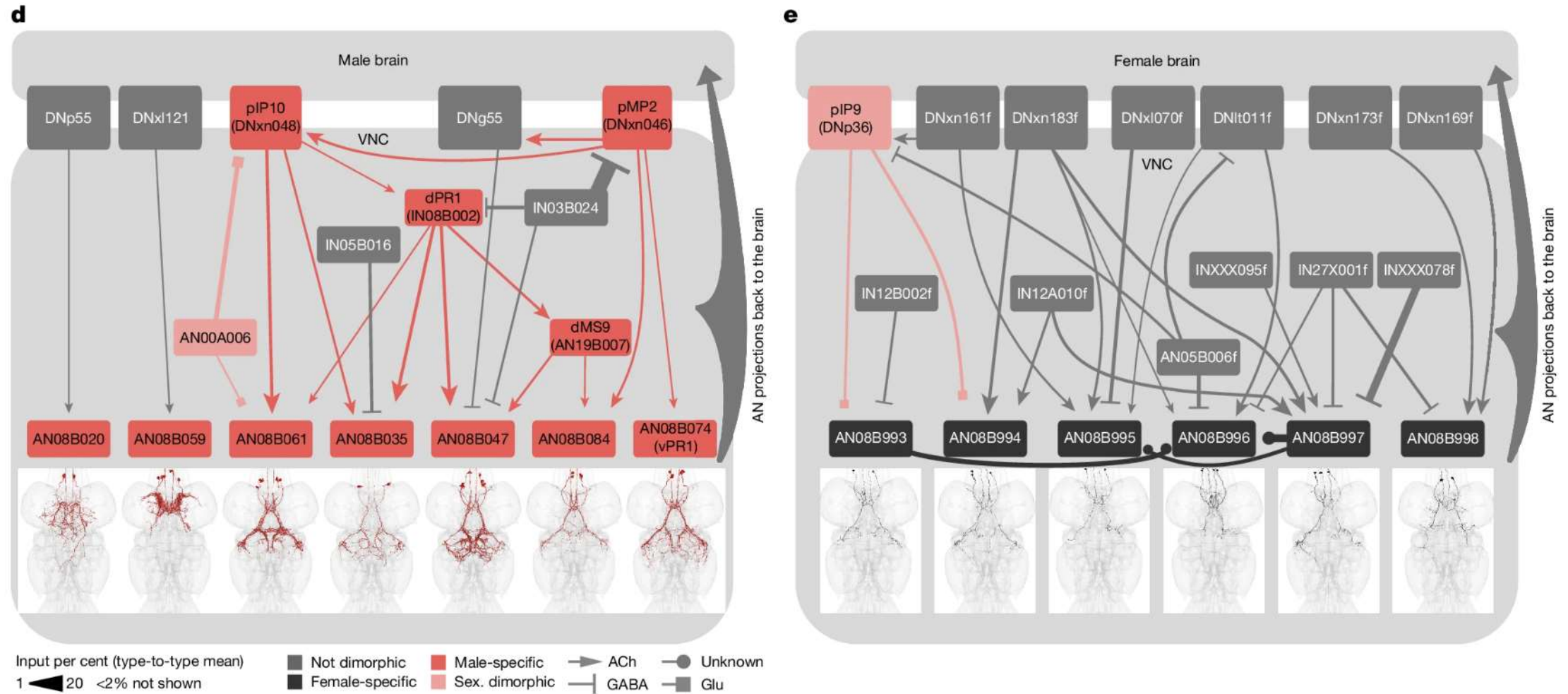
Sex-specific or sexually dimorphic neurons



Sexually dimorphic and sex-specific DNs.



Sexually dimorphic and sex-specific ANs



A *Drosophila* computational brain model reveals sensorimotor processing

<https://doi.org/10.1038/s41586-024-07763-9>

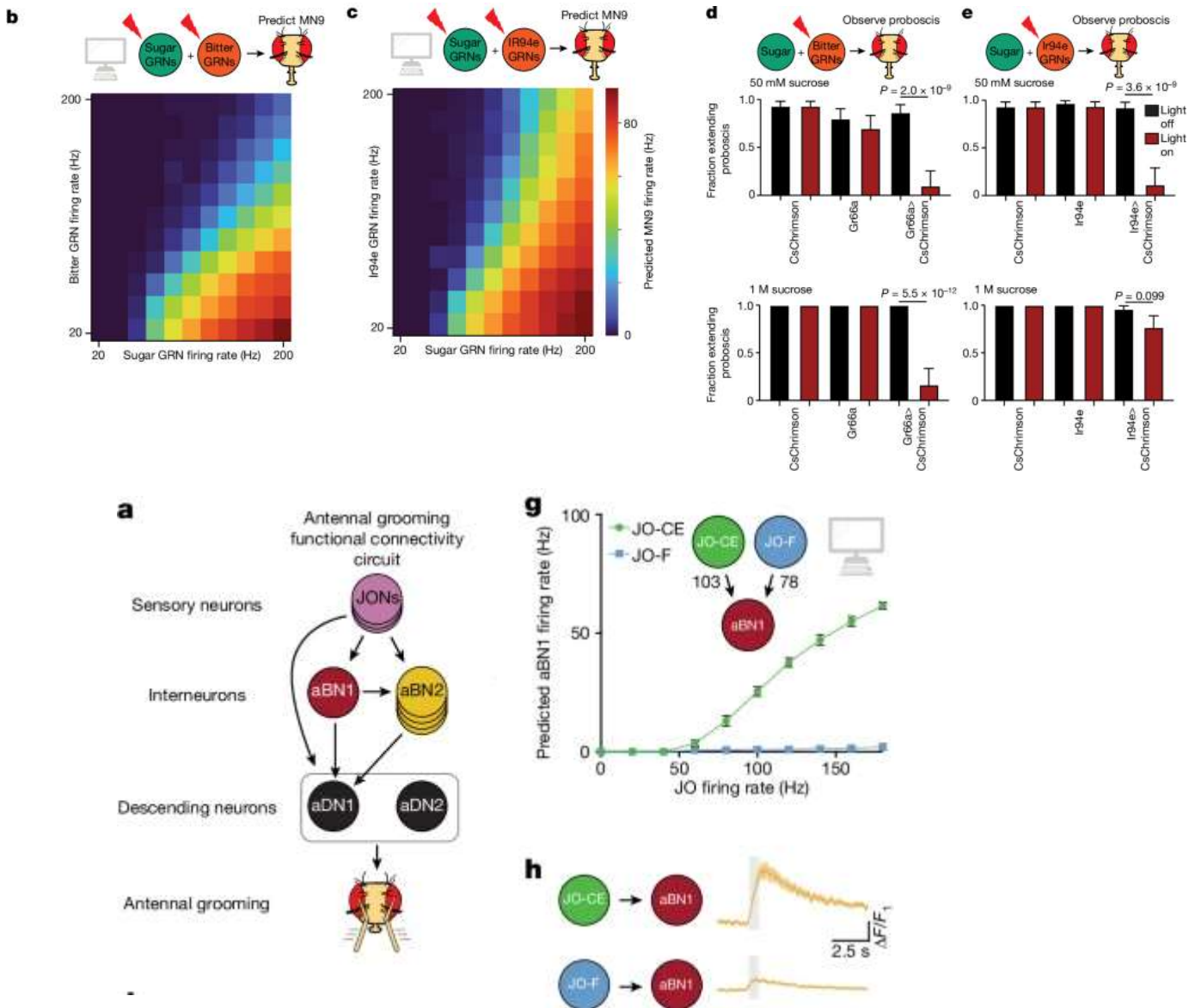
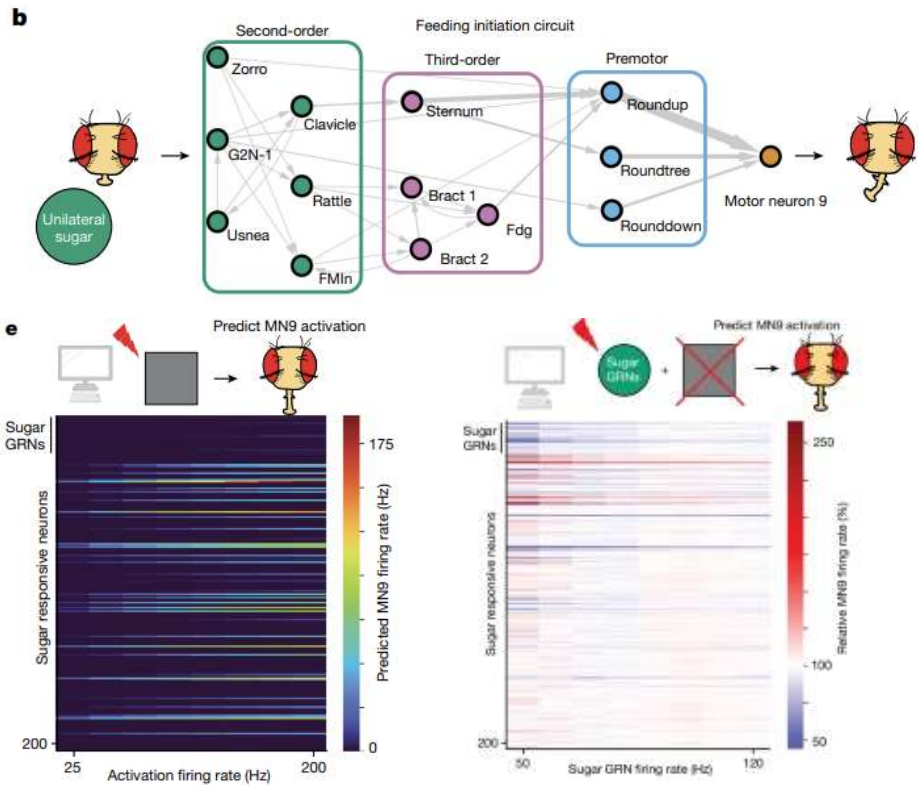
Received: 26 July 2023

Accepted: 27 June 2024

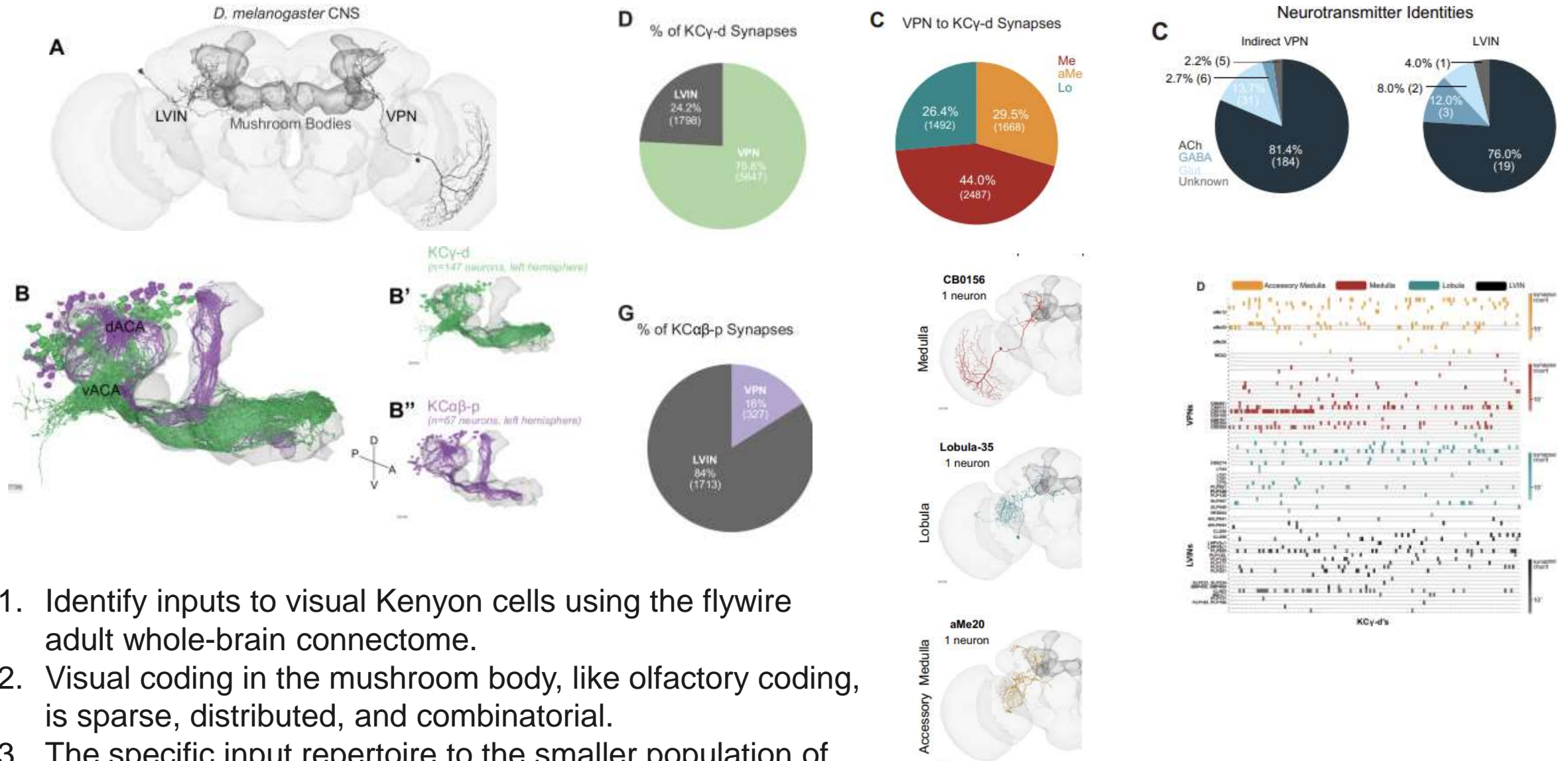
Published online: 2 October 2024

Open access

Philip K. Shiu^{1,2,3,4}, Gabriella R. Sterne^{1,2}, Nico Spiller³, Romain Franconville⁴,
Andrea Sandoval¹, Joie Zhou¹, Neha Simha¹, Chan Hyuk Kang¹, Seongbong Yu⁵,
Jinseop S. Kim⁶, Sven Dorkenwald^{6,7}, Arie Matsliah⁶, Philipp Schlegel^{8,9}, Szi-chieh Yu⁶,
Claire E. McKellar⁶, Amy Sterling⁶, Marta Costa⁶, Katharina Eichler⁷,
Alexander Shakeel Bates^{6,10,11}, Nils Eckstein⁴, Jan Funke⁴, Gregory S. X. E. Jefferis^{6,9},
Mala Murthy⁴, Saill S. Bidaye³, Stefanie Hampel¹³, Andrew M. Seeds¹² & Kristin Scott⁴



Diversity of visual inputs to Kenyon cells of the *Drosophila* mushroom body



1. Identify inputs to visual Kenyon cells using the flywire adult whole-brain connectome.
2. Visual coding in the mushroom body, like olfactory coding, is sparse, distributed, and combinatorial.
3. The specific input repertoire to the smaller population of visual Kenyon cells

Conclusions:

- FlyWire has been well applied in various research fields, such as courtship, sleep rhythms, etc.
- The application of FlyWire has largely facilitated the search for potential neurons and the exploration of the connections in neural circuits.
- The use of FlyWire should be rational, as it is based on neural connection mechanisms and the brain structure of female.



Thanks

25.5.29