

Wiring the Fly Brain into a World Model

Piaget Team



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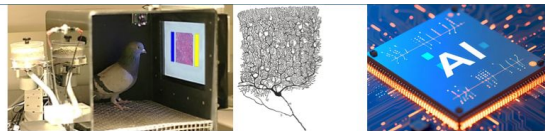


NOWAK-ASSIS Daniel



THIL Lucas

Pigeon vs Modern ML-trained AI model



Neurons	≈ 70,000,000	> 175,000,000,000
Power usage (inference)	0.01 W	1-10 W (single query)
Power usage (training)	14 Wh	1,400,000,000 Wh
	0.1 kg CO ₂	20,000 tonnes CO ₂
Ability to diagnose cancer	✓	✓
Distinguish human identities/emotions	✓	✓
Distinguish Monet vs Picasso	✓	✓
Produce human-like text	✗	✓
Make human-like artwork	✗	✓
Understanding of abstract math	~	✓
High-performance navigation system	✓	✗
Autonomous Agent	✓	✗
Adapt to new environment	✓	✗

The message is: we are not 'there' yet.



The Dataset: FlyWire (FAFB)

First complete wiring diagram of an adult brain — the **Female Adult Fly Brain (FAFB) of Drosophila**. One of the openly explorable connectomes in Codex (v783).

Built from electron-microscopy imaging, AI-segmented, then **expert- and community-proofread** (2019–2024)

The numbers: **~138,639 neurons** · ~3.73M connections · ~50.7M synapses · 99% of neurons typed.

A total of **96 scenarios**, where a scenario = one trial with a specific task (find sugar, avoid a smell, escape a spider...)

Perceive a stimulus → **Triggers** the fly brain → **Acts** in the environment (walk forward, or turn left/right). A closed loop that is repeated every 50 ms.

[2] Zheng et al., "A Complete Electron Microscopy Volume of the Brain of Adult *Drosophila melanogaster*", *eLife* (2018).

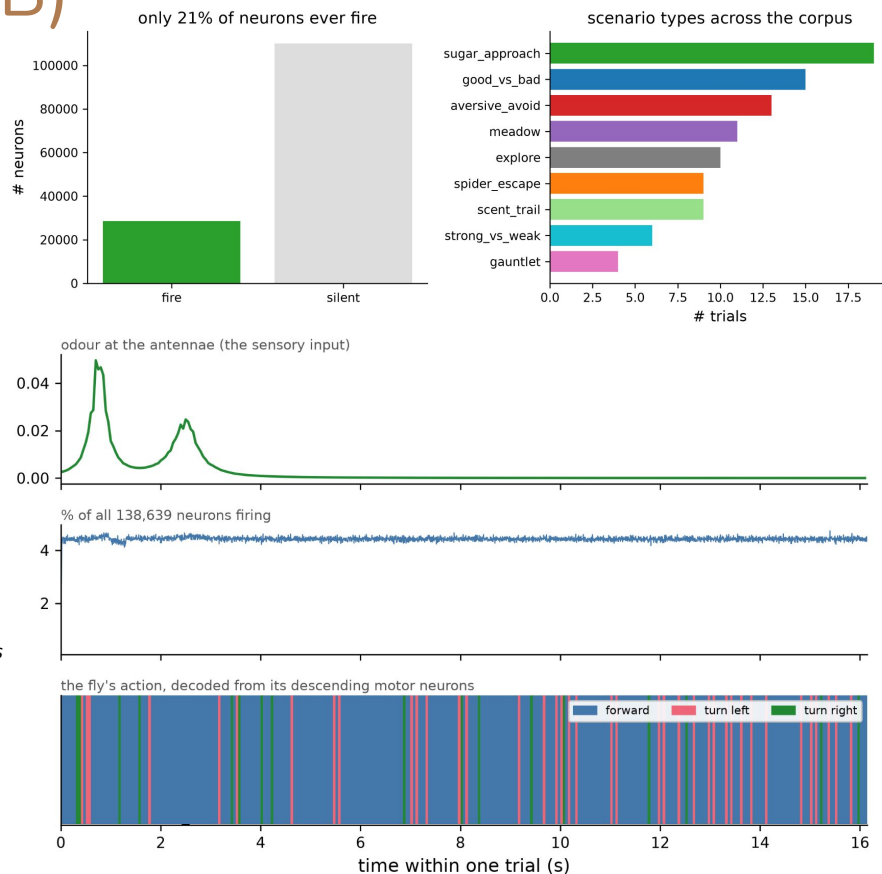
[3] Dorkenwald et al., "FlyWire: Online Community for Whole-Brain Connectomics", *Nature Methods* (2022).

[4] Buhmann et al., "Automatic Detection of Synaptic Partners in a Whole-Brain *Drosophila* Electron Microscopy Dataset", *Nature Methods* (2021).

[5] Eckstein et al., "Neurotransmitter Classification from Electron Microscopy Images at Synaptic Resolution in *Drosophila*", *Nature Methods* (2024).

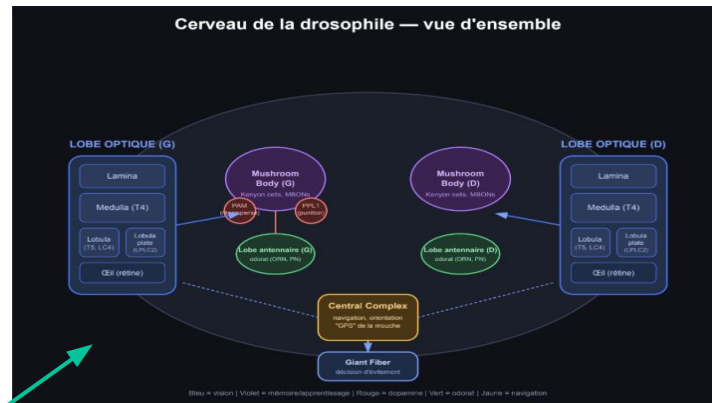
[6] Dorkenwald, S., Matsliah, A., Sterling, A.R., et al. (2024). "Neuronal wiring diagram of an adult brain." *Nature*, 634(8032), 124–138.

[7] Schlegel, P., Yin, Y., Bates, A.S., et al. (2024). "Whole-brain annotation and multi-connectome cell typing of *Drosophila*." *Nature*, 634(8032), 139–152.

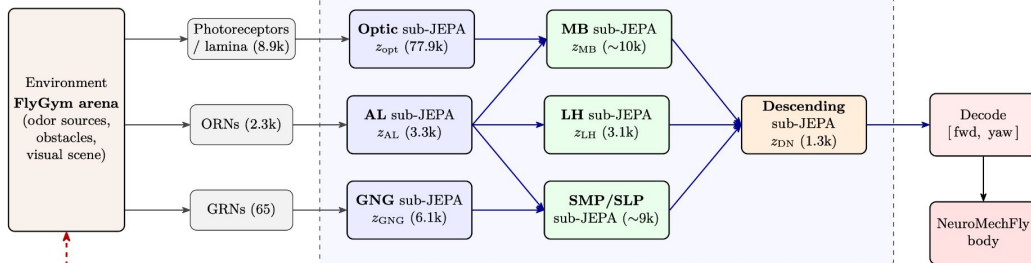


Our focus: hierarchical, brain-region EB-JEPAs

- Sub-EB-JEPAs for each region / neuron-types
- World Model from Spike Activations
- Biology-inspired



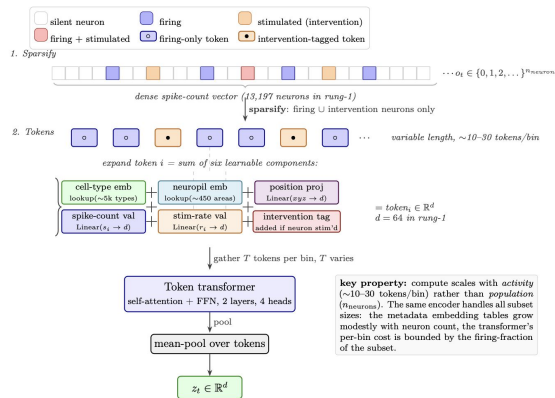
Hierarchical world model — region sub-JEPAs, self-supervised (JEPA)



Inside each sub-JEPA (region r):
 spikes $s_t^r \rightarrow$ **encoder** \rightarrow latent z_t^r
 (z_t^r , drive/context) \rightarrow **predictor** \rightarrow \hat{z}_{t+1}^r
 loss = $\|\hat{z}_{t+1}^r - z_{t+1}^r\|^2 + \lambda VC/SIGReg$
 coupling: upstream z 's are part of the context



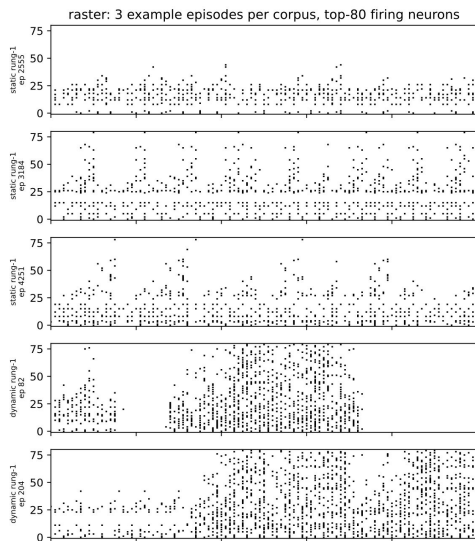
Architecture: The Winding Paths of the Mind... of a Fly



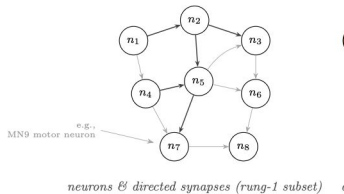
- ~4.43% brain usage (human ~10%)
- **→ COLLAPSE**

Solutions:

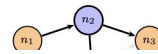
- SpikeEncoder
- Spike K-Hops (ours): spike encoder mixing each neuron with its synaptic neighbors at k-th depth.



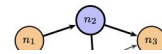
A. Connectome subgraph



B. $K=1$ from query n_2



C. $K=2$ from query n_2



encoder	skill h2	skill h4	skill h8	PR (64)	$z \rightarrow \text{motor } R^2$	$z \rightarrow \text{spikes } R^2$
MLP (no connectome)	+0.36	+0.38	+0.05	43.7	0.38	0.65
graph · replace · K1	+0.36	+0.39	+0.36	36.0	0.33	0.83
graph · concat · K1	+0.46	+0.39	+0.39	41.0	0.36	0.60

Effect of the graph K-Hop approach on predictive performance.

Sub-JEPAs Performances

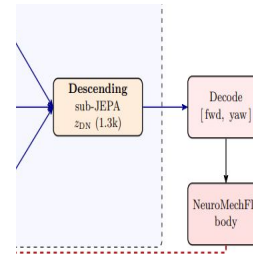
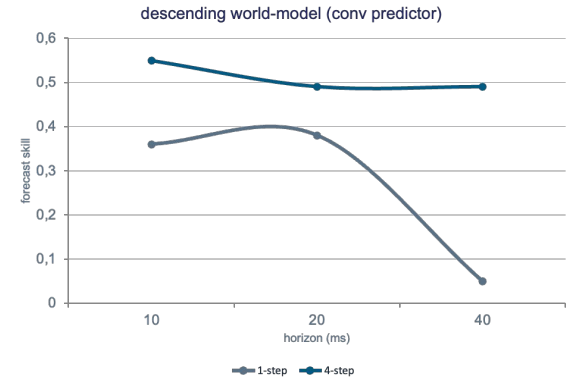


Hierarchical Architecture

region	neurons	z→spikes R ²
descending	1,301	0.65
AL	3,335	0.27
MB_CA	4,827	0.50
LH	3,110	0.44
optic	77,867	0.24

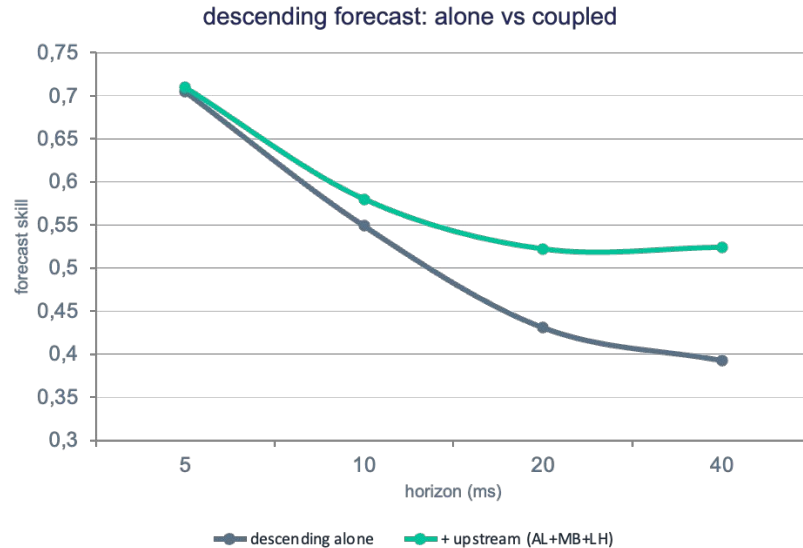
Sub-JEPA R² performance

Recurrence or Convolution?



En fin de modèle oui: la représentation se conditionne vers l'espace moteur (actions)

Should we use a hierarchy? Yes!



+0.131

skill gain at 40 ms (0.39 → 0.52, +33% relative)

The coupling delay ranges from approximately 0 to 5 ms to +0.131 to 40 ms: upstream integration regions provide a longer-time-scale context for changes in dynamics.

The forward transmission flow of the connectome (sensory → integration → motor) measurably improves the motor model of the world: the central architectural hypothesis is thus validated.

Key Takeaway: Hierarchical coupling is playing an increasingly significant role over time (+0.131 at 40 ms), and the brain's forward-projection structure enhances the model of the world.

0.07s (1.0x)

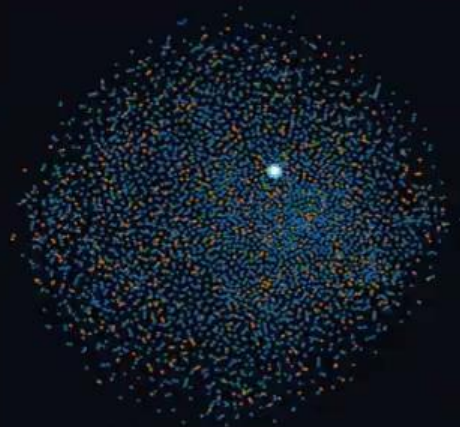


FlyWire connectome - live activation



P9 L/R = 140 / 160 Hz win 1/80

sub-JEPA latent 1-SME - live fly = white



live descending latent win 1/80

forward turn_left turn_right

The connectome as a *frontier* for JEPA

- **Analysis.** The latent variable linearly encodes the motor command (dna02 $R^2 = 0.26$), located in the motor region.
- **Prediction.** Multi-step rollout learning provides stable predictions up to 80 ms.
- **Hierarchy.** Coupling with upstream regions improves the motor model, particularly at longer time horizons (+0.131 at 40 ms).

First application of JEPA to a complete brain: decodable and anatomically accurate, but with challenges.

Limits and perspectives

- **Learning Underlying States.** in complex systems: industry, robotics, safety
- **Geometrical Representations.** Harness topological representations in the fly's brain
- Nature has many **intelligent systems we still can't replicate:** a good reference

“Intelligence organizes the world by organizing itself”

- Jean Piaget, The Construction of Reality in the Child 1937, (EN 1957).

Thank you for your attention !

Any questions ?

References

- [1] Jesse Read adapting “Drawing (1890s) by Santiago Ramon y Cajal of Pigeon brain section; Levenson et al., Pigeons
- [2] Zheng et al., "A Complete Electron Microscopy Volume of the Brain of Adult *Drosophila melanogaster*", *eLife* (2018).
- [3] Dorkenwald et al., "FlyWire: Online Community for Whole-Brain Connectomics", *Nature Methods* (2022).
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