## Measuring the functional complexity of nanoscale connectomes: polarity matters Qingyang Wang<sup>1\*</sup>, Nadine Randel<sup>2</sup>, Yijie Yin<sup>2</sup>, Cameron Shand<sup>3</sup>, Amy Strange<sup>3</sup>, Michael Winding<sup>2</sup>, Albert Cardona<sup>3</sup>, Marta Zlatic<sup>3</sup>, Joshua Vogelstein<sup>1</sup>, Carey Priebe<sup>1</sup> I Johns Hopkins University, 2 University of Cambridge, 3 The Francis Crick Institute, \* correspondence: qwang88@jhu.edu

#### Summarv

learning-independent to answer.

### Motivation

How does a network's Excitatory-Inhibitory connectivity structure affect its functional complexity?

### **Functional Complexity**

Functional complexity = fraction of 'XORable' subnetworks Functional Complexity



The two XOR type tasks on the right are *not* linearly-separable, thus more complex than the two on the left.



Illustration on the procedure of experimentally determining whether a subnetwork, defined by  $\{I_1, I_2, O\}$ , is XORable or not.

# EM connectome constrained mode

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----- Postsynaptic neurons

(Winding et al., 2023) (Dorkenwald et al., 2024)

#### Whole-brain RNNs

$\mathbf{I}(l)$	$- MeLO(\mathbf{vv})$

# neurons

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functional complexity measurement that is task-agnostic and of Exc. neurons lead to higher functional complexity, but only when Inhib. neurons are highly connected.





Sven Dorkenwald et al. "Neuronal wiring diagram of an adult brain". In: Nature 634.8032 (2024), pp. 124–138.

🔿 Class A 🔅 Class B

$$\nabla^T \mathbf{r}(t-1) + \mathbf{E}^{(t)})$$

 $n_{\text{Larva }Drosophila} = 2952,$  $n_{\text{Adult Drosophila}} = 132,490$ Weight matrix  $\mathbf{W} = \boldsymbol{lpha}_{\mathsf{sign}} \odot \mathbf{M}_{\mathsf{EM}}$ 

> Michael Winding et al. "The connectome of an insect brain". In: Science 379.6636 (2023).

• Why do we have so many excitatory neurons? We propose a • Leveraging EM connectomes, we show that over-abundance • The predicted E-I properties of highest functional complexity • These insights learnt from whole-brain nanoscale match the real brains, providing a normative explanation to connectomes are further leveraged to provide clues to guide the development of deep neural networks. these highly conserved E-I connectivity properties.

Marc Corrales et al. "A single-cell transcriptomic atlas Kristofer Davie et al. "A Single-Cell of complete insect nervous systems across multiple life Transcriptome Atlas of the Aging Drosophila Brain". In: Cell 174.4 (2018). stages". In: Neural Development 17.1 (2022).

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