

Reporting Summary

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Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a Confirmed

- ☐ ☒ The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
- ☐ ☒ A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- ☒ ☐ The statistical test(s) used AND whether they are one- or two-sided
Only common tests should be described solely by name; describe more complex techniques in the Methods section.
- ☒ ☐ A description of all covariates tested
- ☒ ☐ A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
- ☐ ☒ A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
- ☒ ☐ For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
Give P values as exact values whenever suitable.
- ☒ ☐ For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
- ☒ ☐ For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
- ☒ ☐ Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated

Our web collection on [statistics for biologists](#) contains articles on many of the points above.

Software and code

Policy information about [availability of computer code](#)

Data collection

Large-scale Atomic/Molecular Massively Parallel Simulator (LAMMPS, 16 Mar 2018 version) was used to generate simulated packing configurations.

Data analysis

Cluster analysis of simulated data was performed using the scikit-learn toolkit (version 0.19.1).
3D Confocal microscopy images were analyzed using Imaris (Bitplane, version 7.6.2) and visualized using ZEN software (Carl Zeiss, version 2.3, blue edition).
MATLAB and Python codes used to analyze the data, in addition to the 42 experimental datasets, are available publicly on GitHub (<https://github.com/xianshine/cJamming>).

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research [guidelines for submitting code & software](#) for further information.

Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

The datasets generated and analyzed within this study are available publicly on GitHub (<https://github.com/xianshine/cJamming>) or from the corresponding authors upon request.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☒ Life sciences ☐ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see [nature.com/documents/nr-reporting-summary-flat.pdf](https://www.nature.com/documents/nr-reporting-summary-flat.pdf)

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	34 planarians were imaged and analyzed for quantification of neuronal packing in the brain (Fig 1-3, Supplementary Fig 1), in addition to 8 planarians analyzed for heterotypic neuronal pairs (Supplementary Fig 2). These numbers were sufficient for generating the probability distributions for model comparison.
Data exclusions	No data were excluded from this study.
Replication	Experimental data were collected in 3 separate sessions, each of which reproduced results successfully. All data was collected using the same microscopy settings and experimental conditions, then analyzed with the same software and code, with no issues and full reproducibility between each.
Randomization	Not applicable to our study. Data were collected by localizing cells in the brains of wild-type planarians, with no group comparison or randomization necessary.
Blinding	Not applicable to our study.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☐	☒ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology
☐	☒ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used	Primary antibodies: mouse anti-SYNORF1 (3C11, Developmental Studies Hybridoma Bank (DSHB)), 1:75 sheep anti-digoxigenin-POD, Fab fragments (11207733910, Roche), 1:1000 anti-DNP-HRP (FP1129, Perkin-Elmer), 1:300 anti-DNP-HRP (ZC0330, Vector Labs), 1:5000 Secondary antibody: goat anti-mouse IgG+IgM, peroxidase conjugated (115-035-044, Jackson ImmunoResearch), 1:250
Validation	All primary antibodies were verified in separate independent studies or prior co-localization experiments.

Animals and other organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research

Laboratory animals	Asexual Schmidtea mediterranea (CIW4 strain) flatworms were used as the model organism of this study.
Wild animals	No wild animals were used in this study.

Field-collected samples

No field-collected samples were used in this study.

Ethics oversight

No Stanford IACUC protocol review or approval is required for studies involving planarian flatworms.

Note that full information on the approval of the study protocol must also be provided in the manuscript.