nature portfolio

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Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our Editorial Policies and the Editorial Policy Checklist.

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	We use previously published datasets in this manuscript.
Data analysis	In this manuscript, we present our custom software TubULAR, which is available at https://github.com/npmitchell/tubular. We also built upon ImSAnE available at https://github.com/npmitchell/imsane and used the ImSAnE software for comparison with TubULAR's performance. We ran these tools on MATLAB version 2023a for analysis.

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 and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio 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 description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our policy

The data generated in this work are available at https://doi.org/10.6084/m9.figshare.c.6178351.

The datasets analyzed here were collected on a collected on a custom multiview light sheet microscope as described in Mitchell et al, eLife (2022) for the embryonic Drosophila midgut dataset and as described in Chan et al, IEEE Transactions on Computational Imaging (2016) for the zebrafish heart dataset from Sebastian Streichan and Michael Liebling.

Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](). See also policy information about [sex, gender (identity/presentation), and sexual orientation]() and [race, ethnicity and racism]().

Reporting on sex and gender	N/A
Reporting on race, ethnicity, or other socially relevant groupings	N/A
Population characteristics	N/A
Recruitment	N/A
Ethics oversight	N/A

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

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]()

Life sciences study design

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

Sample size	No sample size calculation was performed. Our sample sizes were chosen based on the availability of published datasets. The sample sizes are sufficient because they had previously been validated to reflect wildtype behavior of the respective developmental programs in previous publications. Our study applies an analysis technique to these data, demonstrating a method to facilitate analysis of complex, dynamic tissues. Comparison of phenotypes across groups was not part of the study design.
Data exclusions	No data were excluded from the analyses.
Replication	The analysis of tissue motion in the Drosophila midgut was found to be highly stereotyped across three different fluorescent markers and two different frame rates in Mitchell et al, eLife (2022). For the zebrafish heart analysis, we obtained one dataset at this developmental stage from Sebastian Streichan and thus did not replicate this analysis.
Randomization	This is not relevant to our study, as we did not compare characteristics across groups.
Blinding	No blinding was performed. The study analyses previously published datasets to obtain objective measures of tissue deformation. No methodological cross comparisons between groups were part of the study design. No subjective assessments by raters that would make blinding desirable were part of the study design.

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 and archaeology
☐ ☒	Animals and other organisms
☒ ☐	Clinical data
☒ ☐	Dual use research of concern
☒ ☐	Plants

Methods

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

Animals and other research organisms

Policy information about <u>studies involving animals</u>; <u>ARRIVE guidelines</u> recommended for reporting animal research, and <u>Sex and Gender in Research</u>

Laboratory animals	This study reports example analysis in an embryo from a cross of female w;48Y-GAL4;klar Drosophila melanogaster with male w;UAS-CAAX:mCherry Drosophila melanogaster. The embryo was analyzed during embryonic stage 15-16. This study also reports analysis of a Tg(cmlc2:eGFP) zebrafish early on the second day of embryonic development.
Wild animals	The study did not involve wild animals.
Reporting on sex	Sex information has not been collected. The dynamics of the systems studied here are insensitive to sex.
Field-collected samples	The study did not involves samples collected from the field.
Ethics oversight	No ethical approval or guidance was required for the analysis presented here.

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