

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 (<i>n</i>) 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 <i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>
☒	☐ 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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable.</i>
☒	☐ 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 <i>d</i> , Pearson's <i>r</i>), 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	All data used in this study are derived from existing literature and are publicly accessible through the links provided in Supplementary Table 1-4. No software was used for data collection.
Data analysis	The models was trained and tested using Python (3.11.9) and Pytorch (2.6.0). All the quantitative evaluation were performed with Python (version 3.11.9). PSNR was calculated using scikit-image package (version 0.22.0). MS-SSIM was calculated using pytorch-MS-SSIM package (version 1.0.0). SQUIRREL analysis was performed with NanoPyx framework (version 1.3.1). CCP diameter measurements were performed using in-house MATLAB (R2023b) code, the length of filaments in MT network were quantified using SIFNE package, the detection of nodes in ER network was performed using Nellie (version 0.4.1) Statistical analyses were performed using SciPy package (version 1.12.0).

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](#)

All the datasets used in this study are derived from existing literature and are publicly accessible through the corresponding links provided in Supplementary Table 1-4. Example data for training and testing are available on Zenodo repository (<https://doi.org/10.5281/zenodo.18382702>). Source data are provided with this paper.

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	Sex and gender were not considered in study design and no finds were sex- or gender-dependent.
Reporting on race, ethnicity, or other socially relevant groupings	No socially constructed or socially relevant categorization variable(s) were used.
Population characteristics	No human research participants.
Recruitment	No human research participants.
Ethics oversight	No human research participants.

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](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	No formal sample size calculation was performed. The sample size for each experiment was determined by the number of publicly available image datasets used in our study. Our study focused on evaluating models across various publicly available datasets, which were sufficiently large and diverse to provide meaningful performance evaluation. The sample size was chosen to ensure that the models were tested on a wide range of image types, structures and image conditions.
Data exclusions	There is no data excluded from the analysis.
Replication	Since our study is based on computational methods and uses publicly available image datasets, no traditional biological or experimental replications were performed. To ensure robustness, the models were evaluated across multiple publicly available datasets, covering diverse image types and conditions. All the experiments were completed with computer, ensuring reproducibility.
Randomization	The data is randomly divided into train and test sets.
Blinding	No investigator blinding is necessary since our experiments are based on software analysis.

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

Eukaryotic cell lines

Policy information about [cell lines and Sex and Gender in Research](#)

Cell line source(s)

Images of the COS-7 cell line (Cercopithecus aethiops kidney, ATCC CRL-1651) were obtained exclusively from publicly available fluorescence microscopy image datasets, as reported in (Qiao, C. et al. Evaluation and development of deep neural networks for image super-resolution in optical microscopy. Nat Methods 18, 194–202 (2021).) No cell culture was performed by the authors.

Authentication

Cell line authentication was not reported in the original dataset publication.

Mycoplasma contamination

The COS-7 cell line was reported to be negative for mycoplasma contamination in the original dataset publication

Commonly misidentified lines
(See [ICLAC](#) register)

No commonly misidentified cell lines were reported.

Plants

Seed stocks

No plants were used in this study.

Novel plant genotypes

No plants were used in this study.

Authentication

No plants were used in this study.