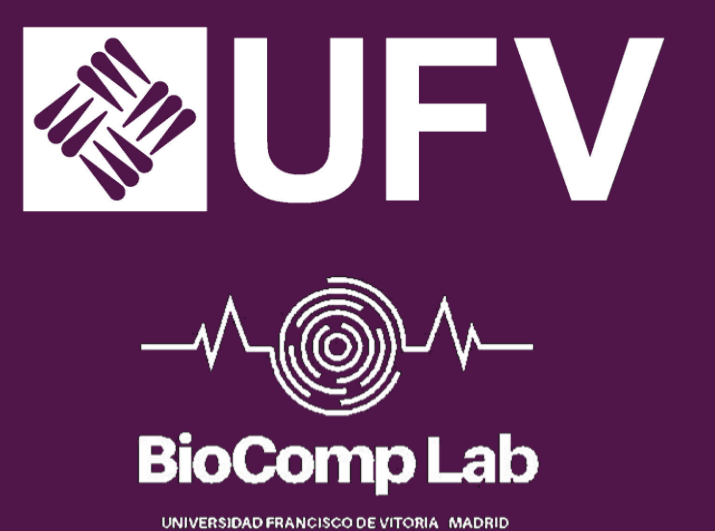


Planar Horizontal Visibility Graphs for Chromatin Dynamics Analysis: Applications to Cellular Metabolic States

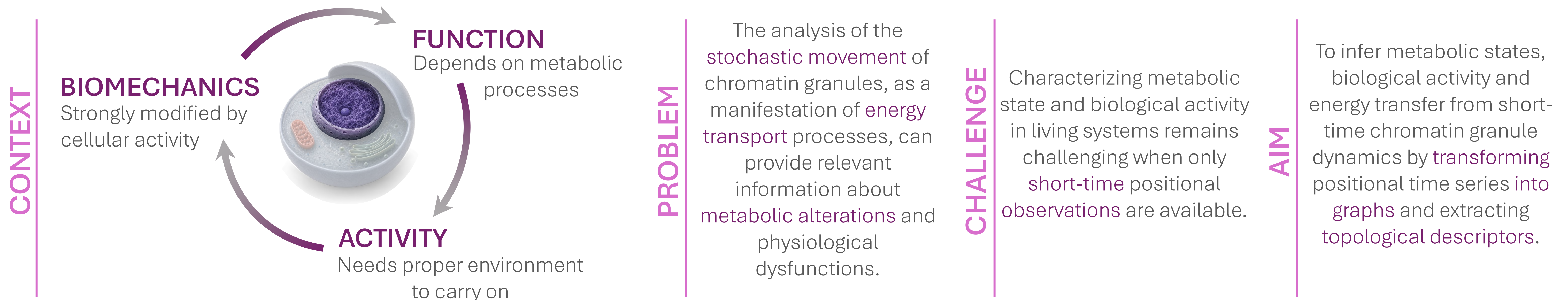


Lucía Benito-Barca^{1,2}, Diego Herráez-Aguilar¹

¹ Faculty of Experimental Sciences, Francisco de Vitoria University (UFV), 28223, Pozuelo de Alarcón, Madrid, Spain.
² Higher Technical School of Engineering, Francisco de Vitoria University (UFV), 28223, Pozuelo de Alarcón, Madrid, Spain.

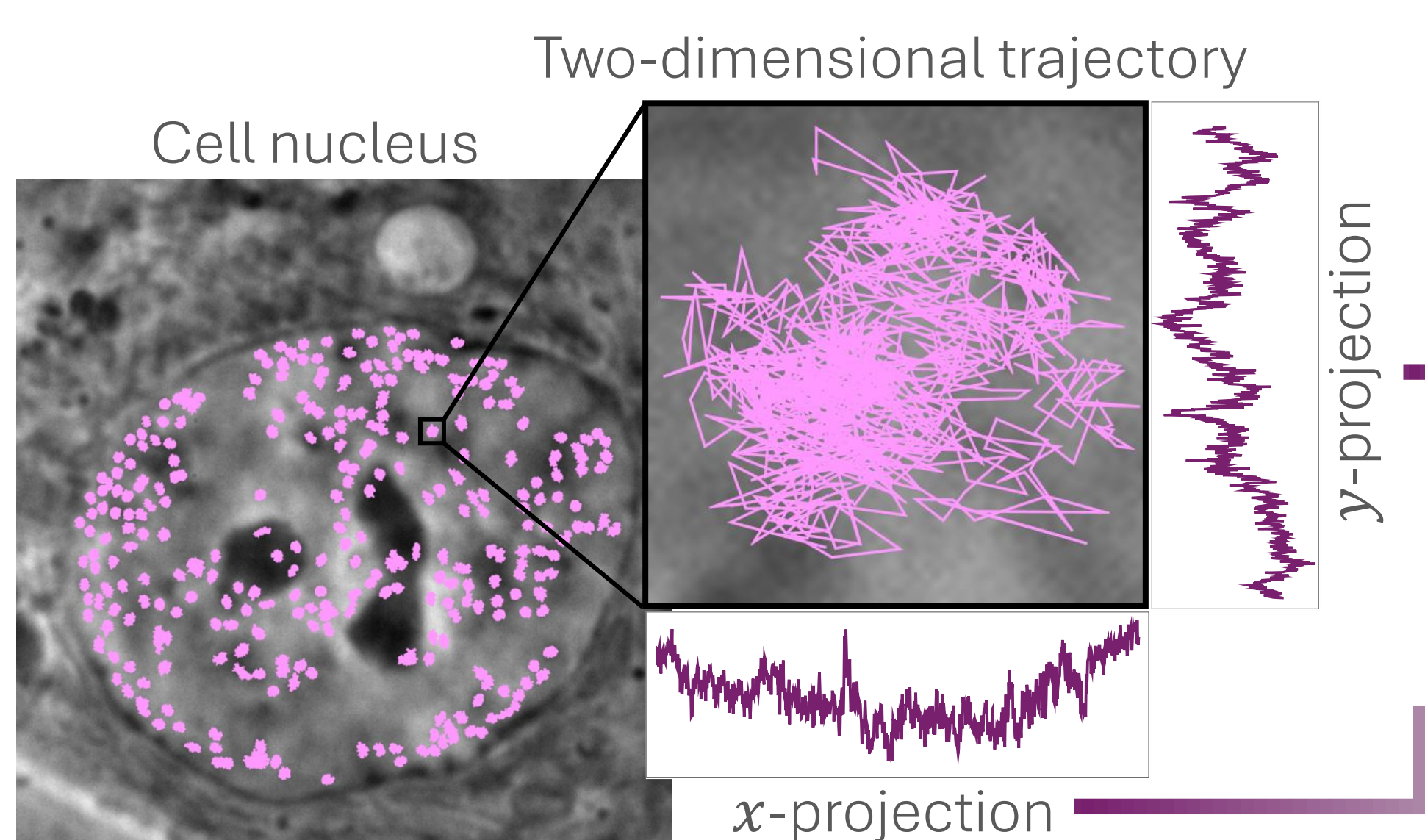


INTRODUCTION



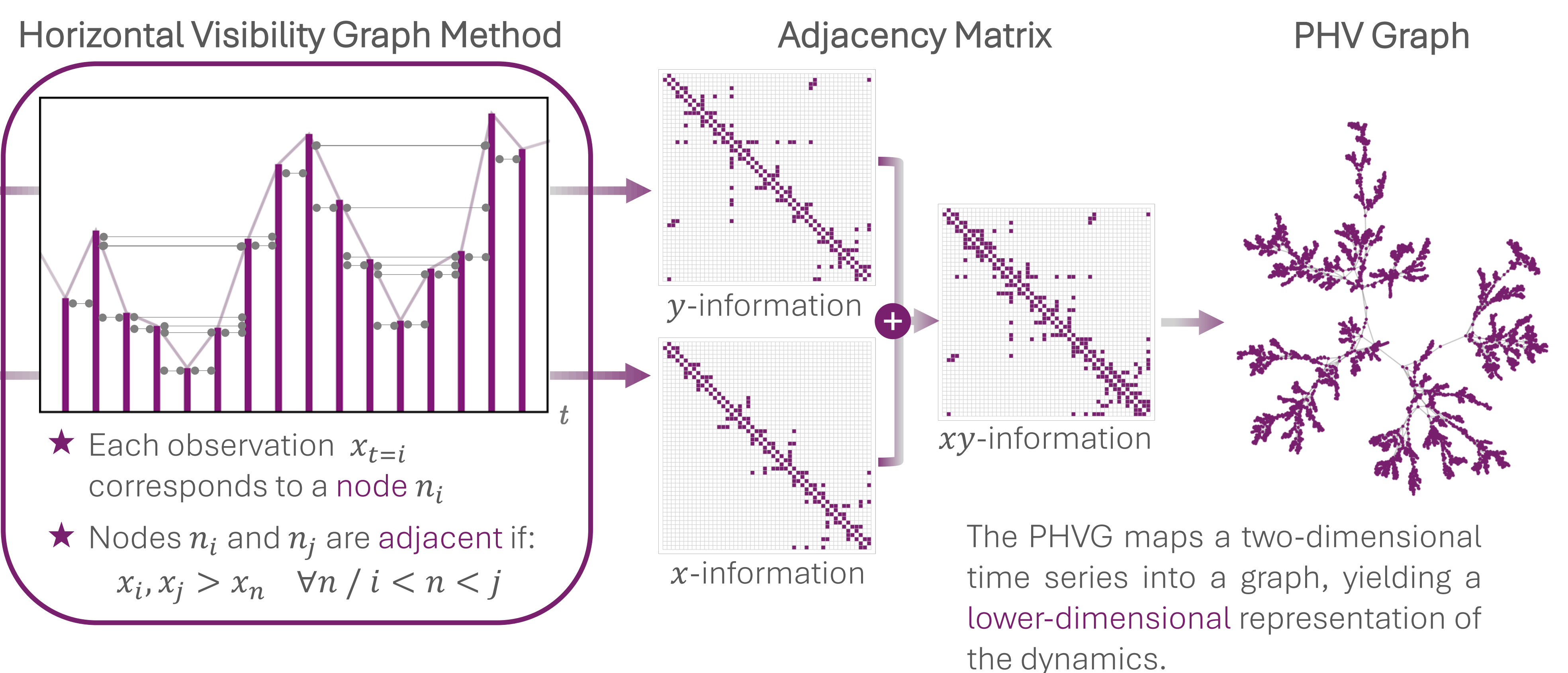
METHODS

PARTICLE TRACKING



Chromatin domains were identified as high-contrast regions in high-resolution microscopy images, and their two-dimensional trajectories were obtained by maximizing cross-correlation between pixel windows in consecutive frames.

PLANAR HORIZONTAL VISIBILITY GRAPH



RESULTS

Cell-Averaged Analysis

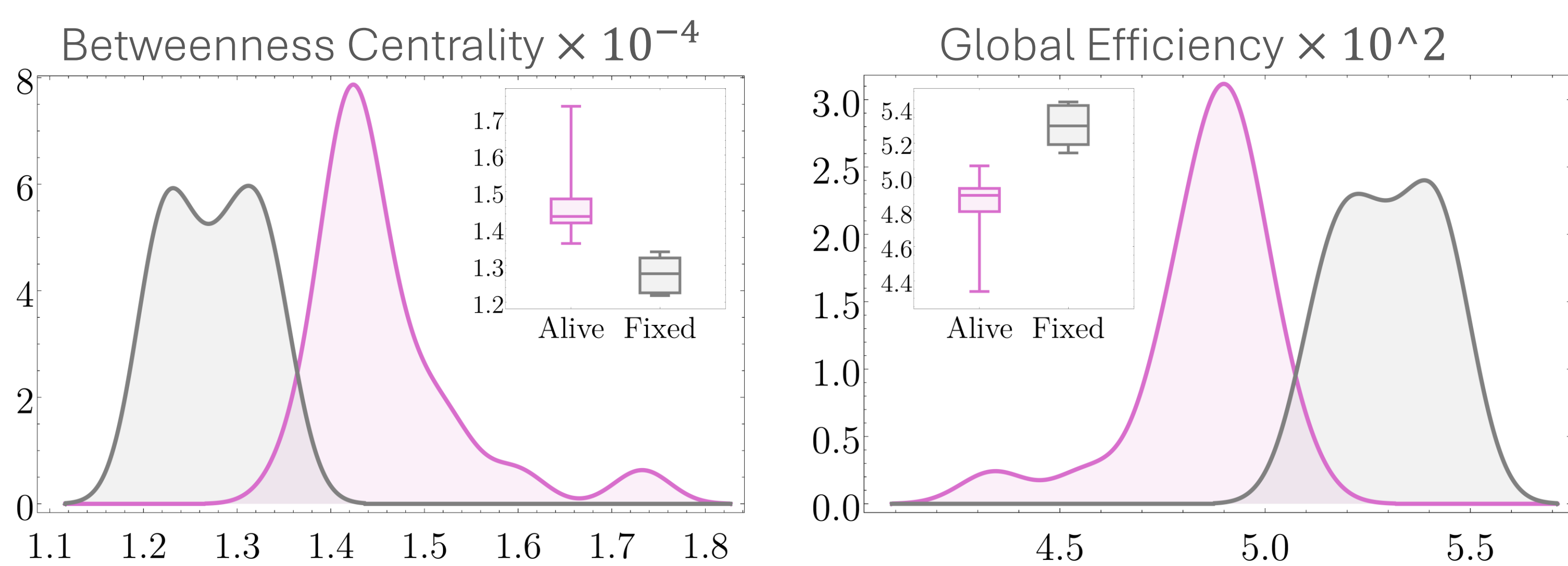


Figure 1. Betweenness centrality and global efficiency distributions across nuclear domains. Kernel density estimates with boxplots show graph-level measures at nuclear sampling sites, pooled by experimental group (alive, pink; fixed, gray).

Single-Cell Analysis

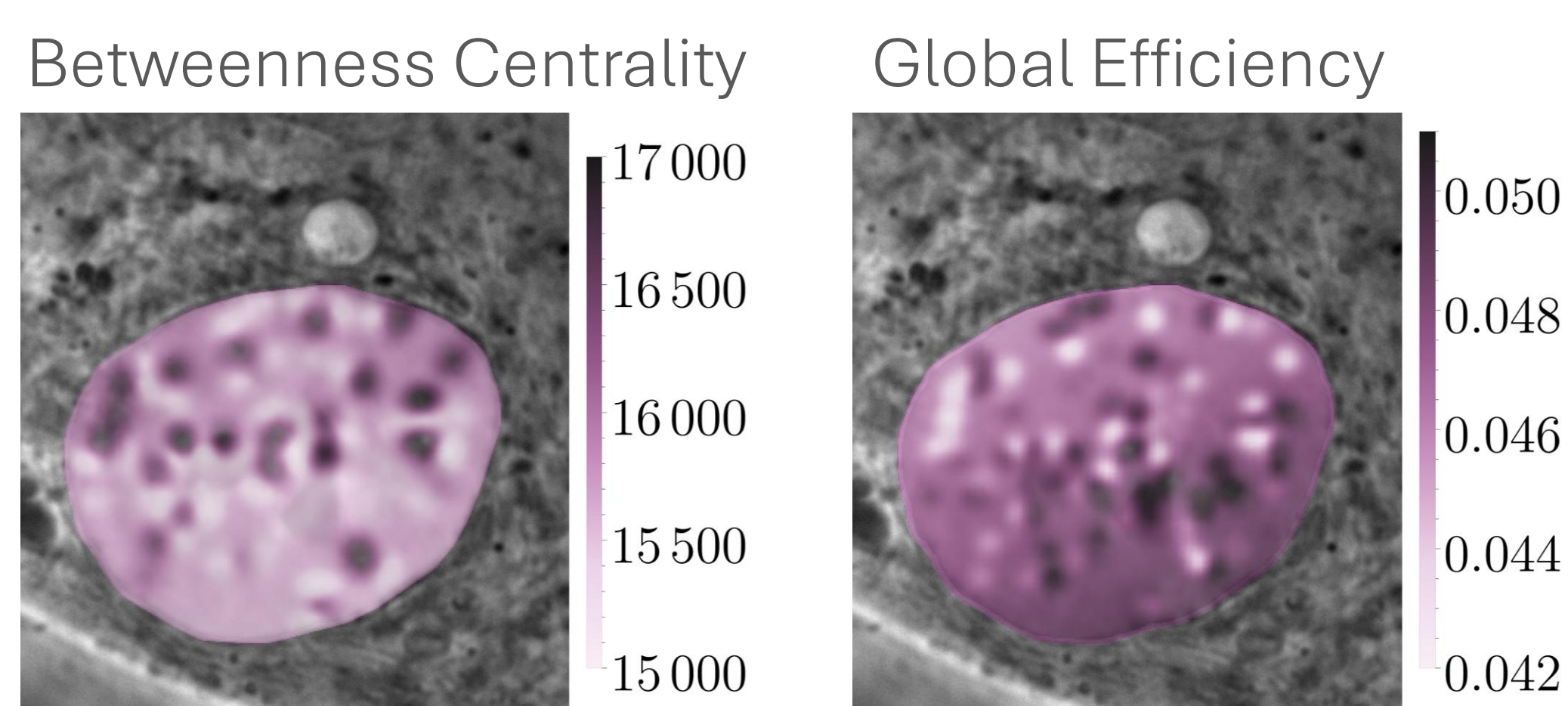


Figure 2. Spatial maps of betweenness centrality and global efficiency in a representative live cell nucleus, revealing spatial heterogeneity in nuclear dynamics.

Precision-Efficiency Trade-Off

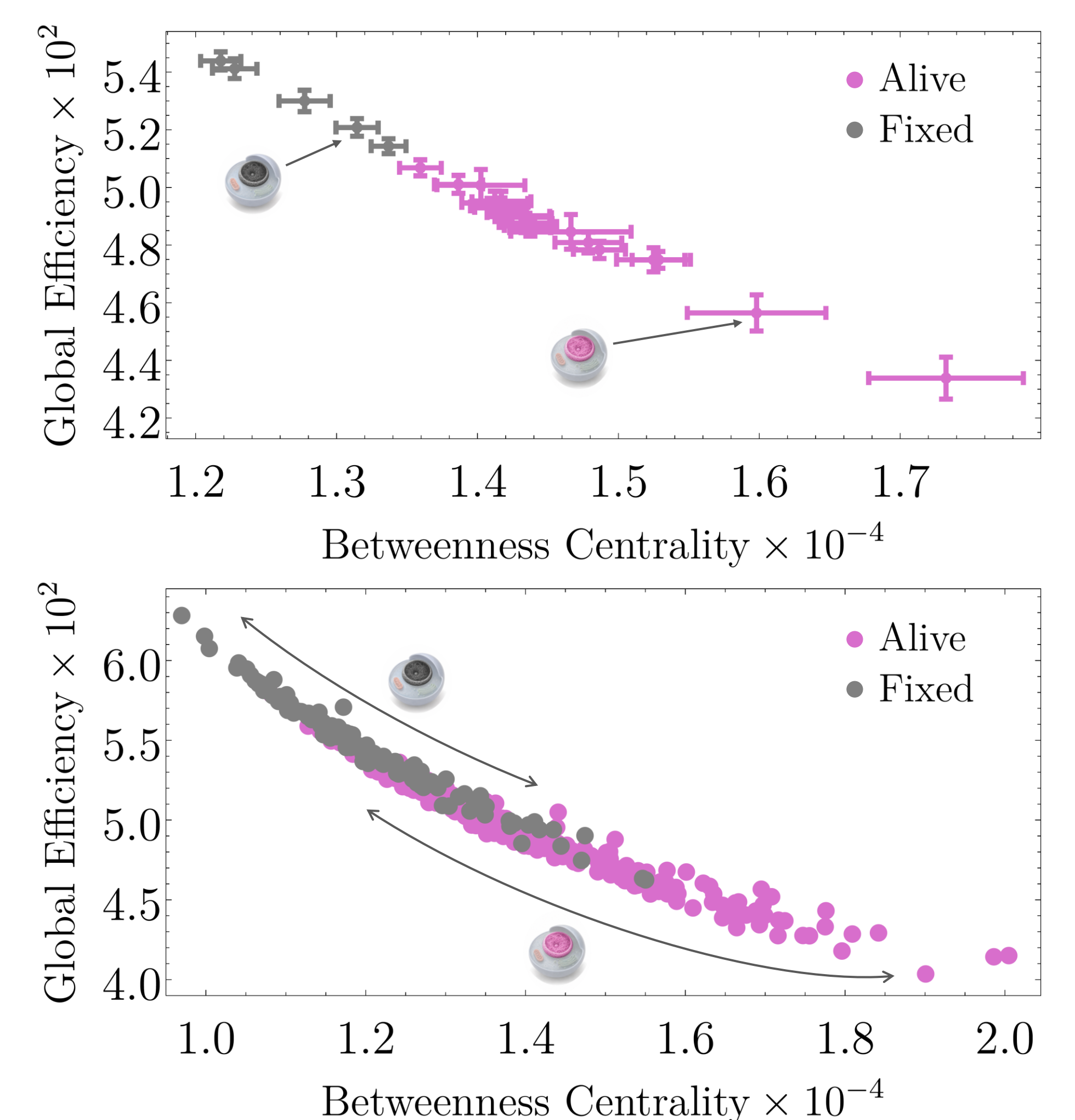


Figure 3. Betweenness centrality–global efficiency correlations at the cell-averaged (top) and single-cell (bottom) levels for live (pink) and fixed (gray) cells, revealing signatures of the Thermodynamic Uncertainty Relation.

CONCLUSIONS

The topological properties of PHVGs capture key features of living systems:

- **Metabolic dependence:** PHVG topological metrics distinguish between the two metabolic states under study.
- **Spatial heterogeneity:** PHVG properties vary across the cell nucleus, reflecting heterogeneous nuclear dynamics.
- **Non-equilibrium behavior and entropy production:** PHVG topology reveals signatures consistent with the Thermodynamic Uncertainty Relation, whereby increased process precision is associated with reduced efficiency and higher entropy production.

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