

# Deepree

Automated Deep Lineage Tree

Analysis via Single-Cell Tracking Pipeline



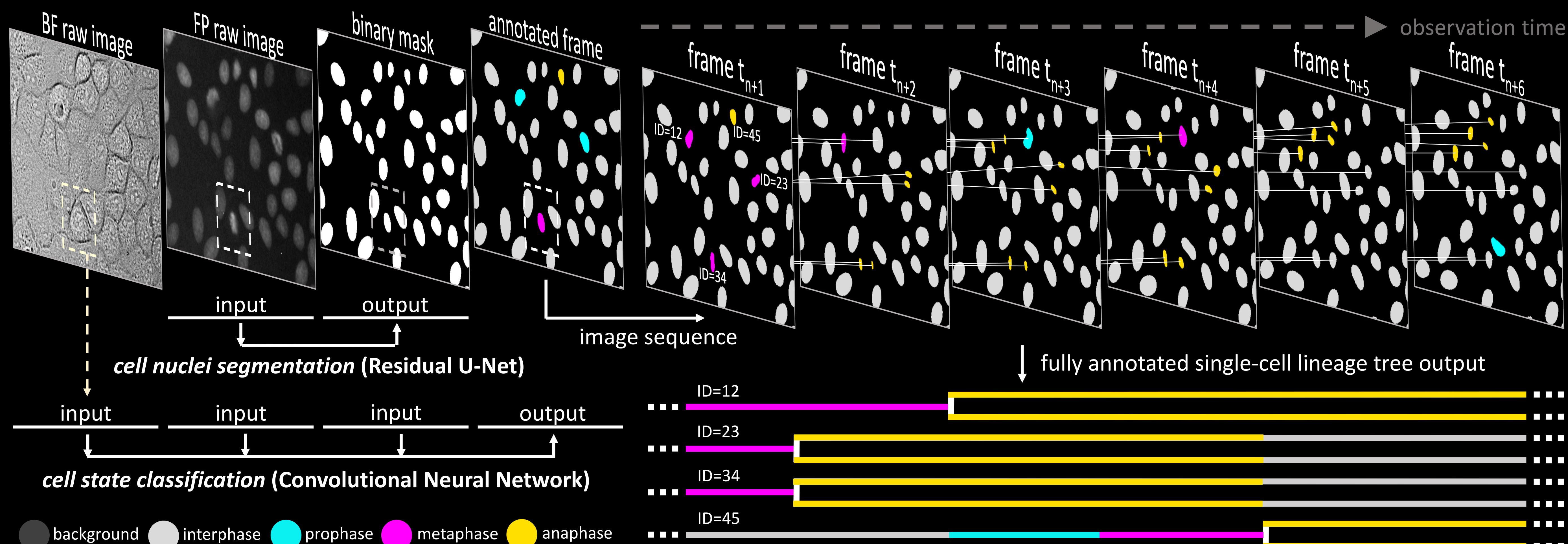
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[BioRxiv preprint](#)

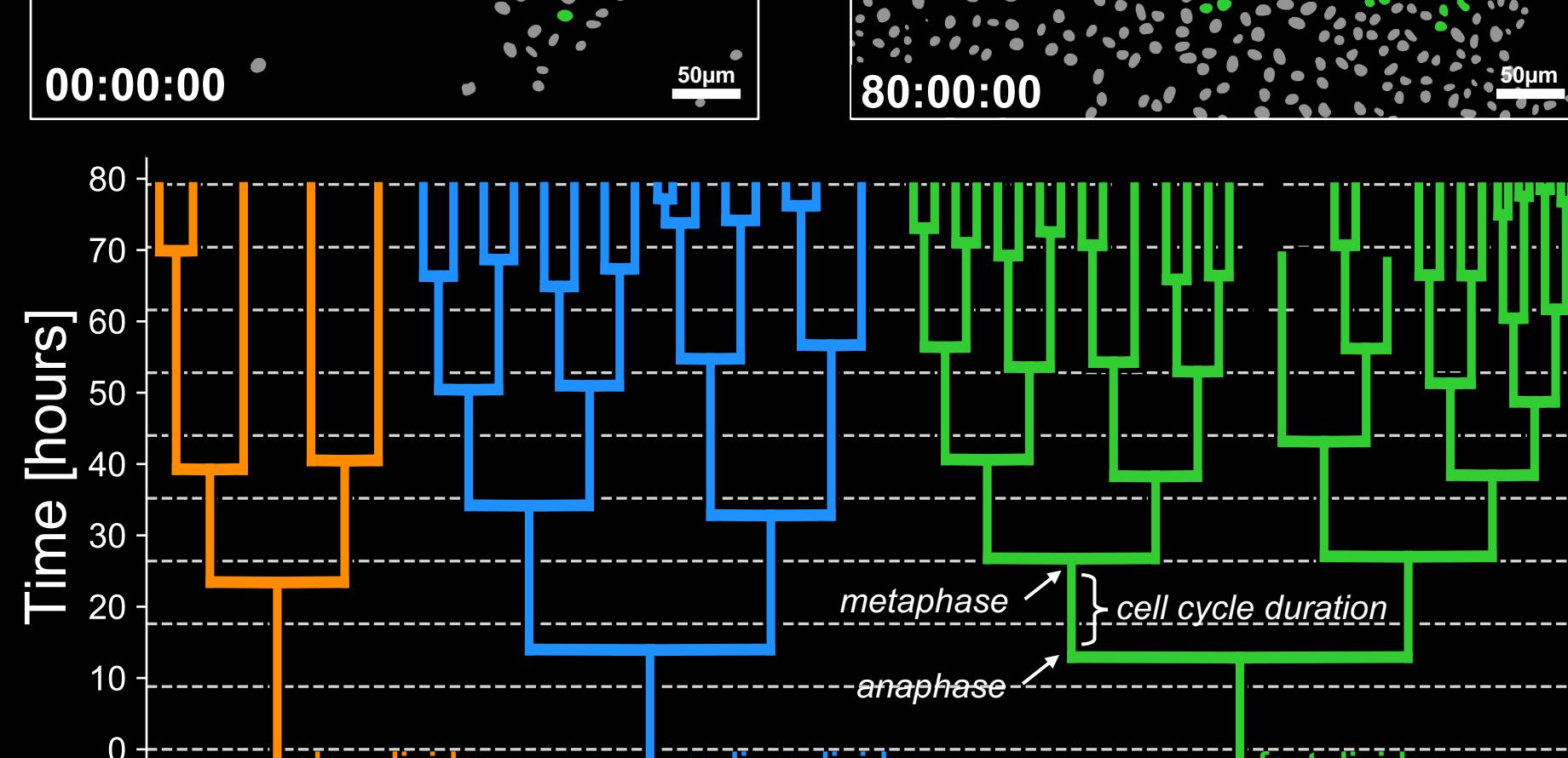
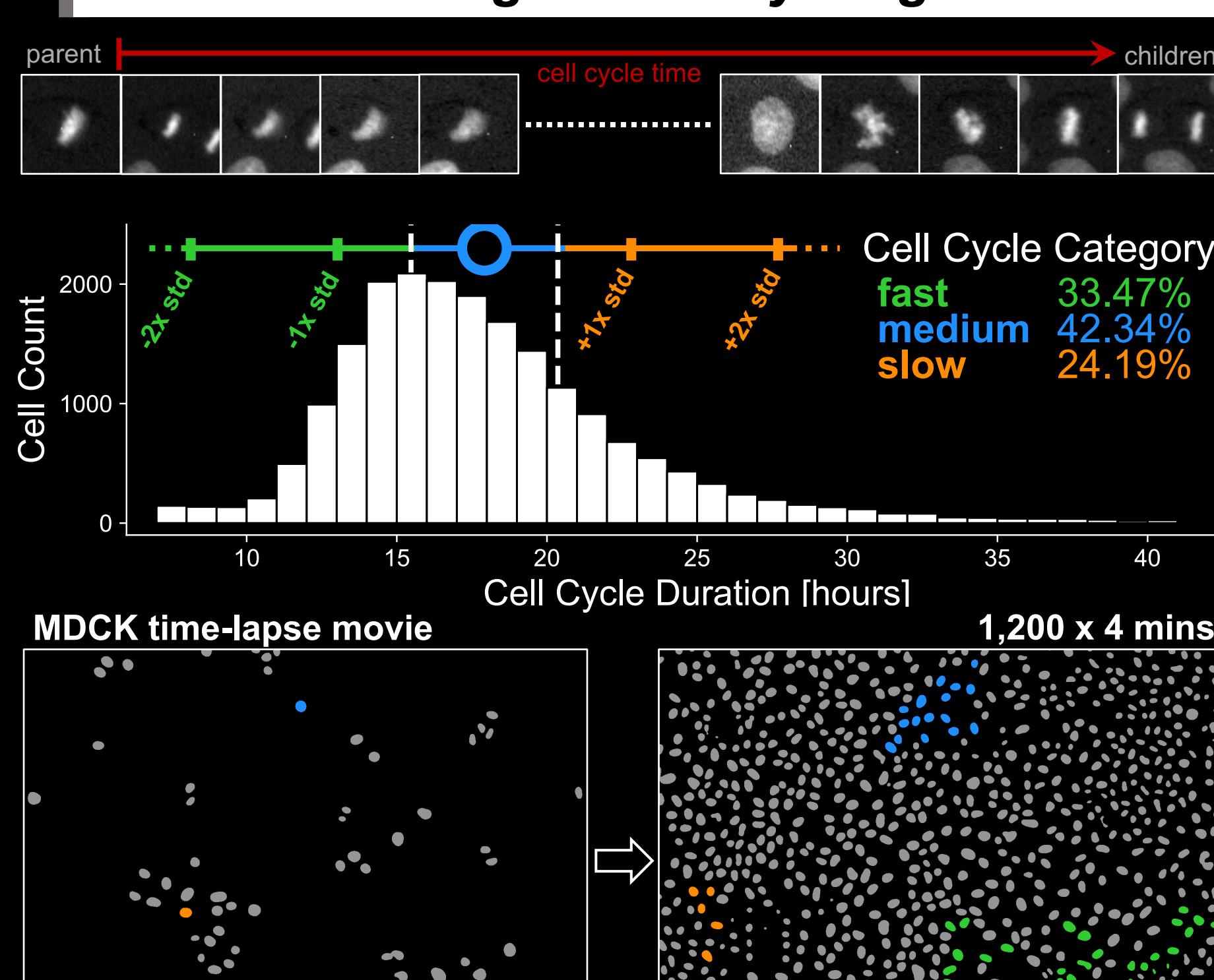
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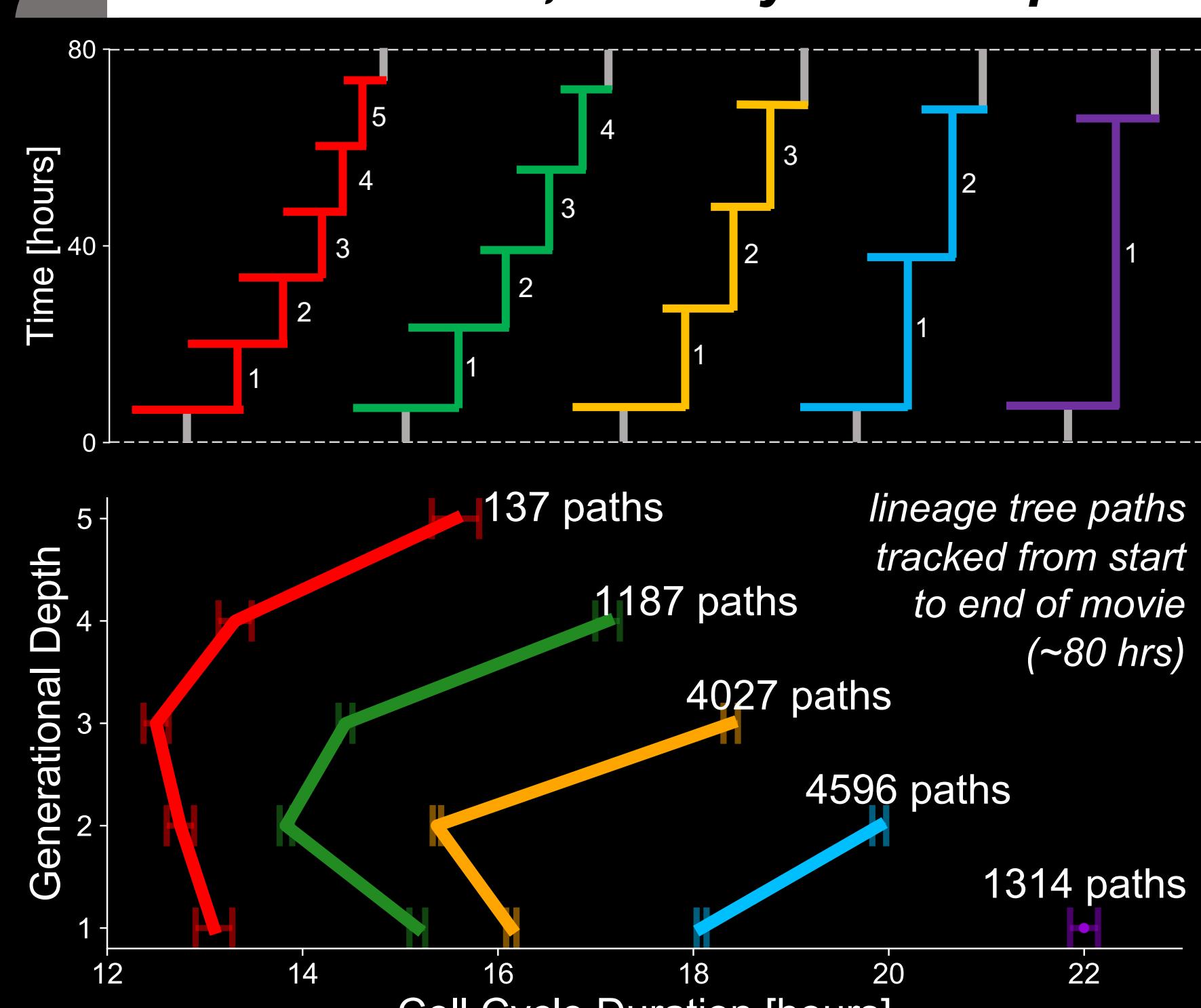
**ABSTRACT** | To study the stochastic or deterministic nature of cell population heterogeneity, we developed a **deep learning and computer vision-based single-cell tracking workflow** for fully unsupervised analysis of large automated time-lapse live-cell microscopy datasets. We retrieved **cell cycle durations** in >20,000 mammalian MDCK cells organised into >5,000 multigenerational, **automatically reconstructed**, fully annotated **deep lineage trees** spanning up to 8 generations, without the demand for manual curation of computer-generated lineage trajectories.



**1** >20,000 automatically tracked single cells exhibit heterogeneous cycling duration



**2** Cell cycle duration is generationally heritable in >11,000 fully tracked paths



**CONCLUSIONS** | Our user-friendly, open-source software implementation to **single-cell analysis** of non-cancer cell lines recovered **previously observed trends** from manual annotation-dependent studies <sup>A,B,C</sup> and extended the analysis with orders of magnitude **more experimental data**, enabled by our fully automated approach.

**3** Cell cycle duration remains correlated in >5,000 extended family lineage trees

