

MAGIK - Microscopic motion analysis through graph inductive knowledge



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1 Introduction

In the past two decades, optical microscopy has undergone significant developments, enabling us to study the motion of cells, organelles, and individual molecules with unprecedented detail at various scales in space and time. However, analysing the dynamic processes that occur in complex and crowded environments remains a challenge [1].

Here, we present **MAGIK** [2], a versatile framework for the characterization of dynamic properties from time-lapse microscopy. Harnessing the power of deep learning, MAGIK captures the full spatiotemporal complexity of biological experiments.

Take-home message

MAGIK provides a key enabling technology to estimate dynamic parameters in a complete linking-free fashion.

As such, **MAGIK** represents a powerful solution for those experiments where trajectory linking cannot be reliably performed, for example, as a consequence of high object density or probe blinking.

2 MAGIK

MAGIK models the objects' motion and physical interactions using a graph representation

Why a graph?

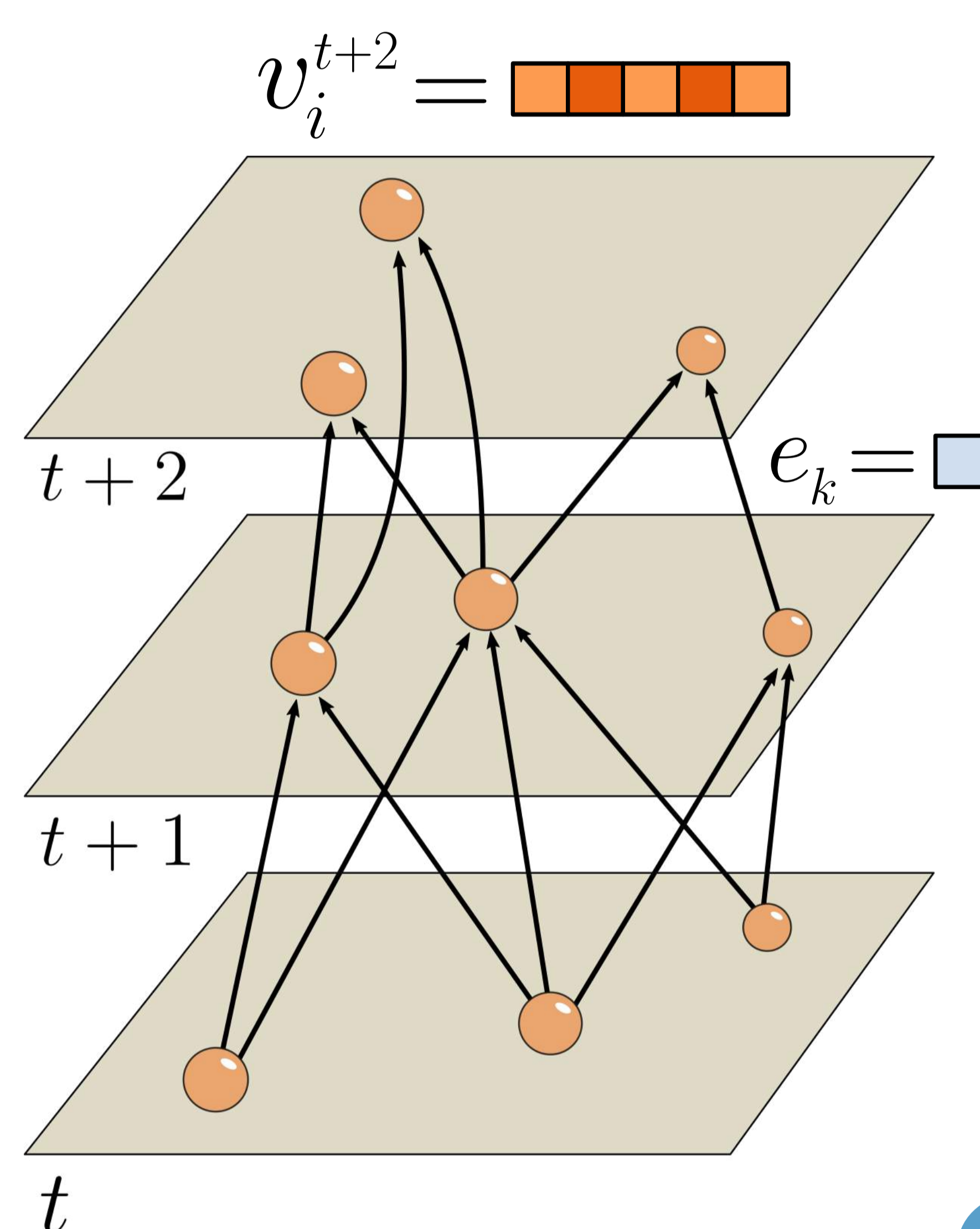
Graphs unveil complex dependencies between objects or entities involved in the motion.

A Nodes (\mathcal{V}) represent detections. Each node contains the object's centroid and other relevant features, such as morphological and intensity attributes.

B Edges (e) connect spatiotemporally close nodes and encode the Euclidean distance between connected objects.

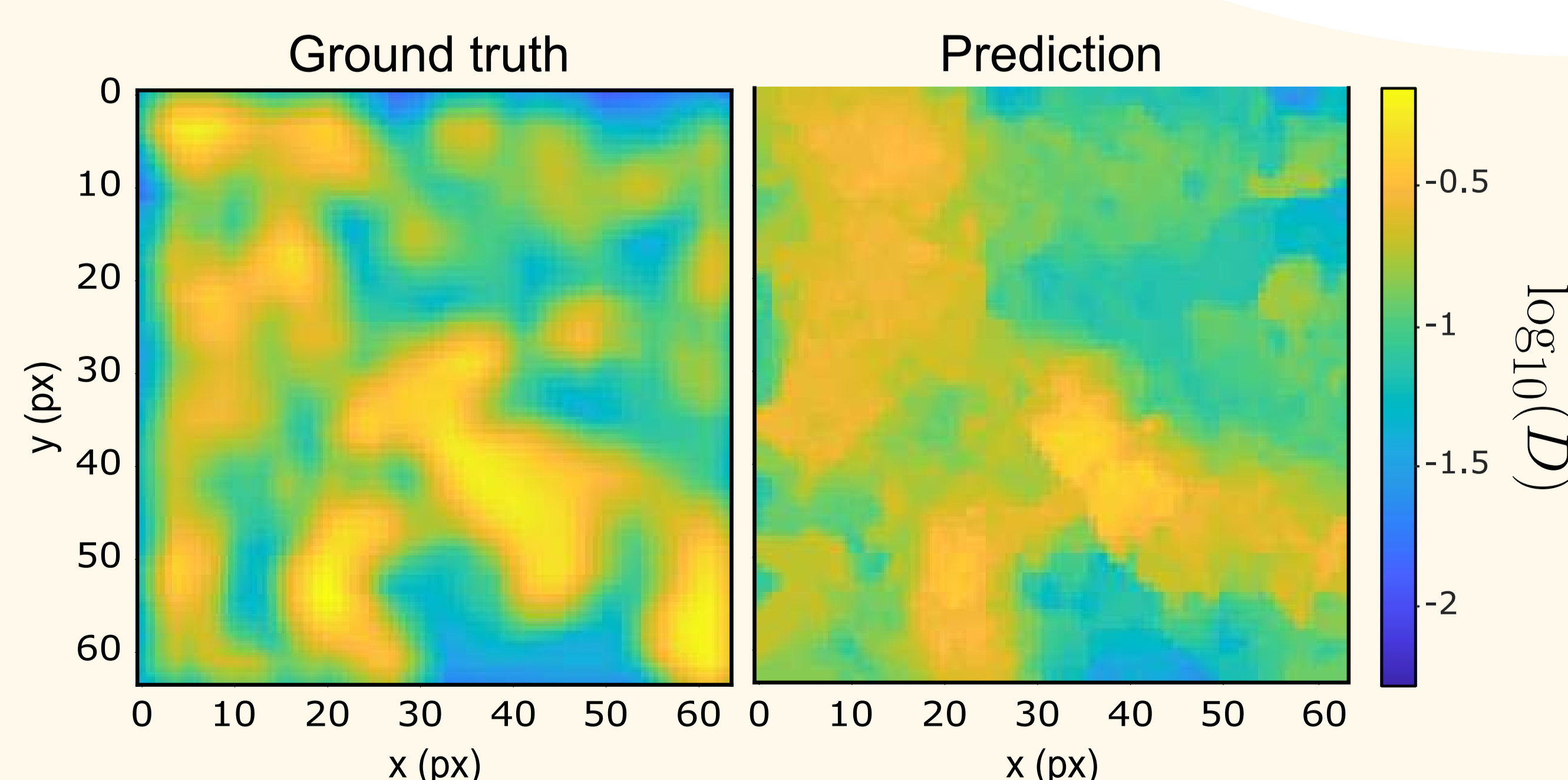
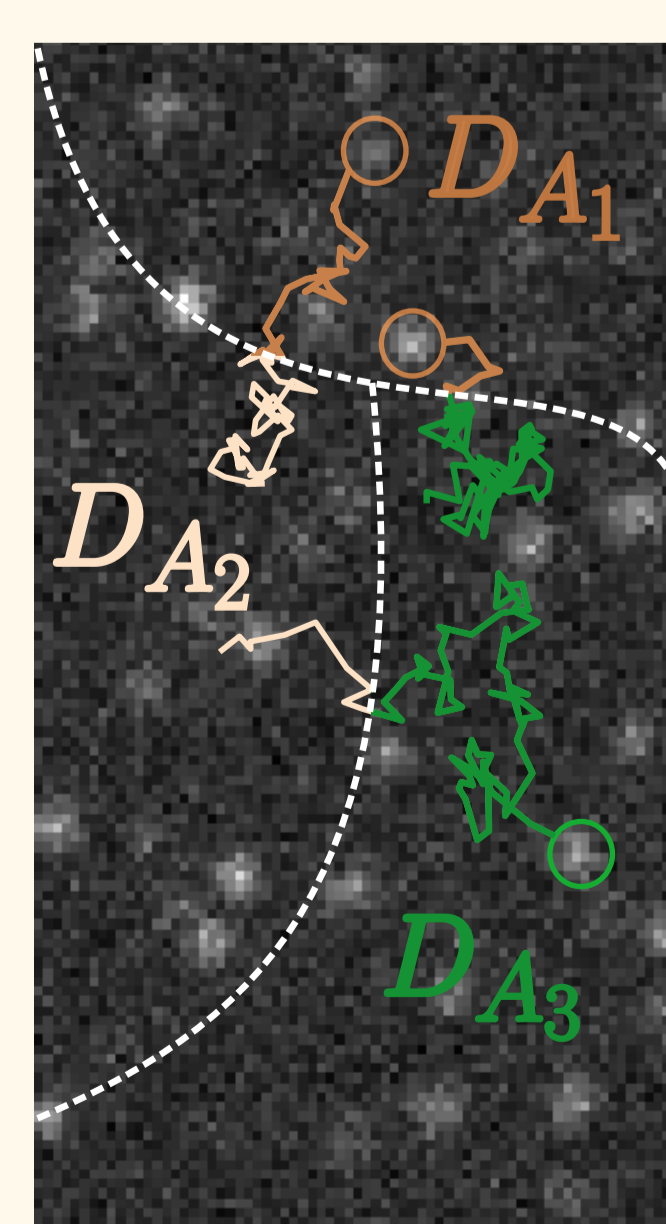
C **MAGIK** modulates the association strength between nodes using message-passing neural networks.

D **MAGIK** incorporates global object relationships using self-attention.

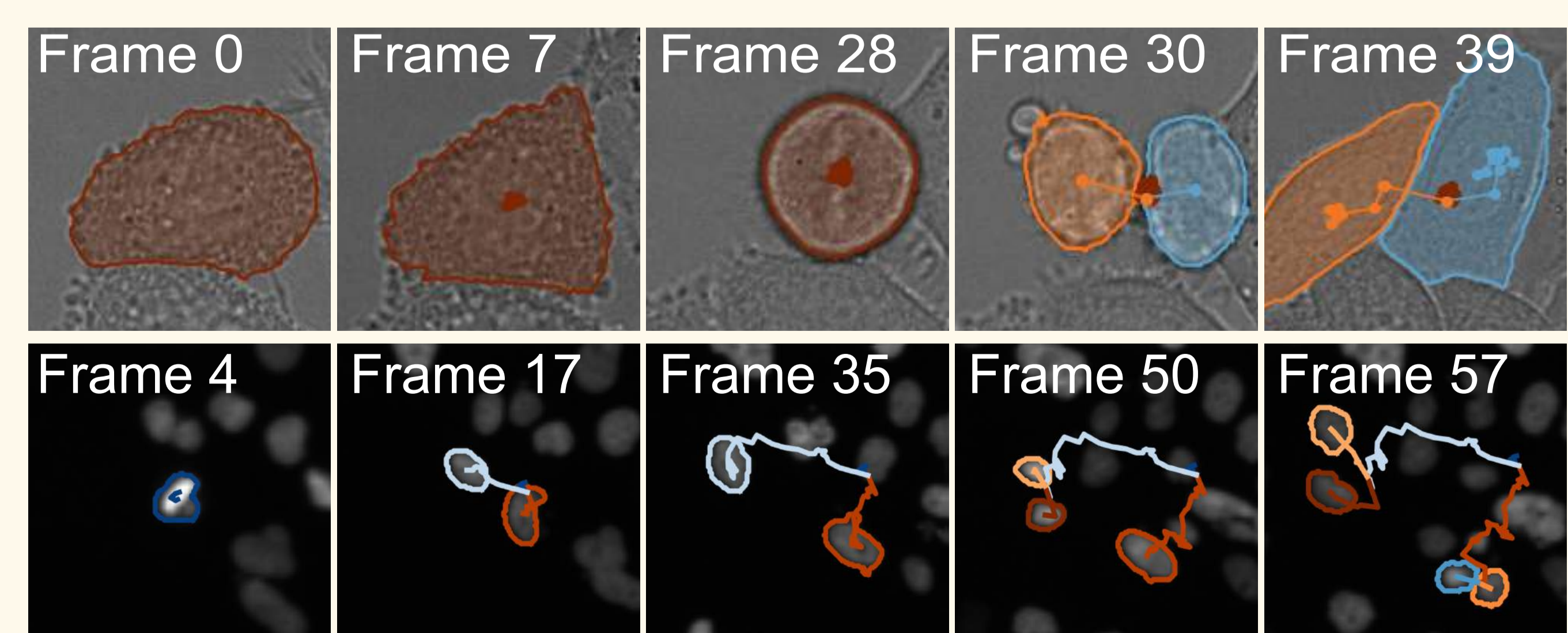


3 Results

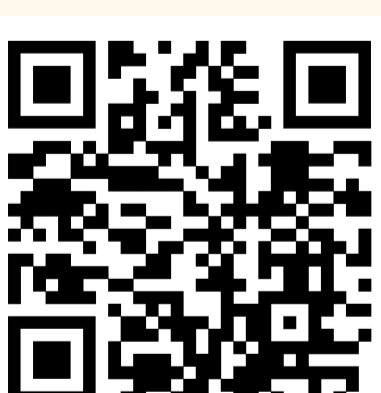
MAGIK resolves a spatially modulated landscape without trajectory linking



MAGIK reliably links cell trajectories in various experimental scenarios



Videos



References

- [1] Maška, Martin, et al. Nature Methods (2023): 1-11.
- [2] Pineda, J., et al. Nature Machine Intelligence 5, 71-82