# Learning developmental mode dynamics from single-cell trajectories

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*Abstract*— Recent advances in high-resolution single-cell microscopy provide unprecedented insights into collective cell motion at various stages of embryonic development. This poses the challenge of translating high-dimensional imaging data into predictive low-dimensional models that capture ordering principles governing biological development. Here, we combine mode decompositions ideas with dynamical systems inference to build a framework for learning quantitative continuum models from single-cell data. In the case of zebrafish embryogenesis, we show how cell trajectories can be represented by a characteristic hydrodynamic model which allows robust identification of developmental phases and reveals similarities between cell migration and active Brownian particle dynamics on spheres.

*Index Terms*— Embryogenesis, spectral representation, dynamical systems inference, active matter

## I. Background

Embryogenesis, the development of a multicellular organism from a single fertilized egg cell, requires coordinated collective motions of thousands of cells across a wide range of length and time scales. Understanding how a highly reproducible and robust tissue organization arises from the dynamics and interactions of individual cells presents a major interdisciplinary challenge [1]. Recent advances in high-resolution live imaging make it possible to track the internal biological states and physical movements of many individual cells on embryonic scales throughout various stages of development [2]. This unprecedented wealth of data poses two intertwined compression problems of equal practical and conceptual importance to enable a quantitative understanding of collective cell motion. The first concerns the efficient reduction of high-dimensional tracking data without loss of relevant information; the second relates to inferring predictive low-dimensional models for the developmental dynamics. We approach the first problem by formulating a coarse-grained representation of the raw data on a geometry-informed basis, and tackle the second by using data-driven sparse dynamical system equation inference [3]. Building on these ideas, we construct and demonstrate here [4] a computational framework that translates developmental single-cell trajectory data on curved surfaces into quantitative models for the dominant hydrodynamic modes.

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## II. Summary of results

Our goal is to translate experimentally measured single-cell trajectories on a curved surface into a quantitative model of collective cell migration dynamics. As a specific example, we consider published lightsheet microscopy data that captures the individual movements of thousands of cells during early zebrafish development from epiboly onset at 4 hours post-fertilization (hpf) to about 18 hpf [2]. This developmental period is characterized by a collective symmetry breaking event during which cells collectively migrate over the yolk's spherical surface.

Working with a two-dimensional (2D) sphere projection of the experimental data, we first describe a coarse-graining approach that faithfully captures cell-mass transport on a curved surface. We then construct a sparse mode representation of the resulting hydrodynamic fields in terms of scalar and vector spherical harmonic basis functions, discuss mode signatures of morphogenetic symmetry breaking events, and connect them to the dynamics of topological defects in the cellular flux. We validate this mode representation framework and the subsequent model inference using synthetic data of active Brownian Particles (ABPs) on a sphere, for which coarse-grained fields and learned models can be directly compared against analytical predictions. Finally, we infer a characteristic linear model for the mode dynamics of the experimental zebrafish data, which enables us to summarise the complex dynamics of the ensemble of cells and highlight similarities between zebrafish embryogenesis and ABPs on a sphere.

## References

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