# Spatial-Stochastic Model of Cell Fate Decisions in Early Mouse Development

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***Abstract*— The delicate balance necessary for ensuring reliable specification of cell lineages is an intriguing problem in developmental biology. As an important paradigm in tissue development, the early mouse embryo cell fate decisions have been extensively researched, but the underlying mechanisms remain poorly understood. Current approaches to this problem still primarily rely on deterministic modeling techniques, although stochasticity is an inherent feature of this biological process. As such, we are developing a multi-scale event-driven spatial-stochastic simulator for emerging-tissue development. We build new simulation schemes for incorporating suitable tissue-scale phenomena, and we fix important parameters by using experimental values or numerical optimization to infer biophysically-feasible regimes. We first explore the characteristics of this system in a single-cell setting. We then extend the study to a multi-cellular setting in order to understand how positional information is robustly achieved and preserved.**

***Index Terms*— Systems Biology, Gene Expression, Stochastic Processes, Stochastic Simulation Algorithm, Cellular Signalling.**

## I. Introduction

The aim of our project is to elucidate different strategies of biological cell decision making and signal processing in fundamentally noisy environments. We focus first on understanding noise control mechanisms at intracellular level, with the overarching goal of unraveling how these processes are orchestrated at tissue level. Our efforts will converge toward a new framework for performing realistic-yet-efficient simulations of intracellular biochemical dynamics, tissue-scale biomechanical interactions, and intercellular communication, for a wide variety of systems.

Sustaining cell plasticity and protecting steady specification of cell lineages is an important paradigm in early tissue development. How can multicellular organisms robustly form a plethora of cell types from one single cell, despite the intrinsically stochastic nature of the processes driving this development?

As keys to answering this core question for mammals, signaling dynamics and fate specification during the preimplantation period in the early mouse embryo have been extensively researched; [1], [2]. This complex system exhibits dynamic cross regulation between gene expression and molecular signaling, plus mechanical cues for tissue remodeling, which from a theoretical view are difficult to capture with deterministic mathematical techniques.

Although stochasticity is an immanent characteristic of gene expression and many other biological processes, the current approaches to this problem still generally treat noise as an ad hoc property; [3], [4]. For this reason, we are establishing a multi-scale event-driven spatial-stochastic simulator for emerging-tissue development, based on biophysical principles.

Departing from well-known event-driven algorithms, we construct new schemes for simulating phenomena at tissue scale. Whenever possible, important biophysical and morphological parameters are fixed by values provided by experimental collaborators or adopted from recent literature.

Numerical optimization algorithms will be implemented to infer biologically-feasible regimes for relevant parameters leveraging the experimental data available to us, as a complete characterization of the underlying parameter values in this system is practically impossible from the experimental standpoint. Here we envision a combined approach, where a smooth mixing between a model-free data-driven inference method and a data-free biophysics-inspired optimization technique is possible thanks to a recently developed framework unifying both regimes from the Bayesian perspective; [5].

## II. Discussion

Our latest results indicate a potential mechanism for reliable patterning emergence, despite strong constraints imposed by cell cycles. We are closely exploring how this information redefines cell fates through the action of auto- and paracrine signalling feedbacks.

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