CDB SEMINAR

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Thursday, August 10, 2017
11:00 – 12:00 Auditorium C1F

Computational modeling of cellular fate and wound healing: probability landscape of stochastic networks, chromosome folding, and large-scale migration of proliferating cells

Summary

Genome sequences provide the overall genetic blueprint of cells, but cells possessing the same genome can exhibit diverse phenotypes.

There is a multitude of mechanisms controlling cellular epigenetic states and the behavior of cells. Among these, networks of interacting molecules, often under stochastic control, can exhibit different landscapes of phenotypic states. In addition, chromosome folding in three-dimensional space provides another important control mechanism for selective activation and repression of gene expression.

Fully differentiated cells with different properties grow, divide, and interact through mechanical forces and communicate through signal transduction, resulting in the formation of complex tissue patterns that are important for wound healing. We discuss recent results of theoretical models, algorithms, and computational tools, including the exact ACME method for computing time-evolving probability landscape, the nC-SAC model of 3D chromosome folding, and the DyCelFEM dynamic finite element method of cells with large scale migration for investigating these multi-scale problems.

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