Recent advances of single cell techniques catalyzed quantitative studies on the dynamics of cell phenotypic transitions (CPT) emerging as a new field. However, fixed cell-based approaches have fundamental limits on revealing temporal information, and fluorescence-based live cell imaging approaches are technically challenging for multiplex long-term imaging. To tackle the challenges, we developed an integrated experimental/computational platform for reconstructing single cell phenotypic transition dynamics. Experimentally, we developed a live-cell imaging platform to record the phenotypic transition path of A549 VIM-RFP reporter cell line and unveil parallel paths of epithelial-to-mesenchymal transition (EMT). Computationally, we modified a finite temperature string method to reconstruct the reaction coordinate from the paths, and reconstruct a corresponding quasi-potential, which reveals that the EMT process resembles a barrier-less relaxation process. Our work demonstrates the necessity of extracting dynamical information of phenotypic transitions and the existence of a unified theoretical framework describing transition and relaxation dynamics in systems with and without detailed balance.

About the speaker:

Dr. Weikang Wang is currently a postdoctoral research fellow in Dept. of Computational and Systems Biology, University of Pittsburgh, working with Dr. Jianhua Xing. Dr. Wang’s research is focusing on the dynamics of cell phenotype transition (epithelial-mesenchymal transition as example system) by using live cell imaging, machine learning and modeling.

Dr. Wang received his bachelor’s degree and doctor’s degree from school of physics, Peking University. During his Ph.D., his research was studying cancer stem cell via methods of quantitative biology, radiation biology and microfabrication. As a visiting scholar, Dr. Wang worked on microfluidic devices in Dr. Yong Chen’s lab, Ecole Normale Superieure (ENS) in Paris when he was a PhD student.