

Presenter: Martin Tran

Title: Lineage motifs: recurrent patterns of cell differentiation during development

Author(s): Martin Tran, Amjad Askary, Michael B. Elowitz

Abstract: Lineage trees provide an accurate record of the relationships between a group of related cells throughout development. However, it is clear that developmental lineage trees are highly variant across individuals (even within an individual for paired or bilaterally symmetric organs), especially for vertebrates. Therefore, in order to understand defining features about the overall developmental process, we need new methods for identifying significant patterns from a set of variable lineage trees. Here, I will develop a novel strategy termed Lineage Motif Analysis, an algorithm that systematically processes a set of lineage trees to identify all over- or under-represented cellular subtrees and provides a quantitative measure for their relative abundance without requiring any user input or assumptions about the underlying developmental process. Similar motif strategies have been used to find the defining features of complex networks such as transcriptional networks and ecological food webs but have not been applied to developmental lineage trees yet. The lineage motif approach is general and will serve as a widely available resource in the scientific community to analyze any lineage tree dataset, including all other fields of developmental biology, stem cell biology, regeneration, and cancer biology. When applied to many lineage tree datasets from diverse developmental contexts, such as in different areas of the central nervous system (spinal cord, retina, hippocampus) or within the same organ but across different species (fish, mouse, human), Lineage Motif Analysis will provide new insight into the universal building blocks of developmental lineage that may be evolutionarily conserved across divergent systems.