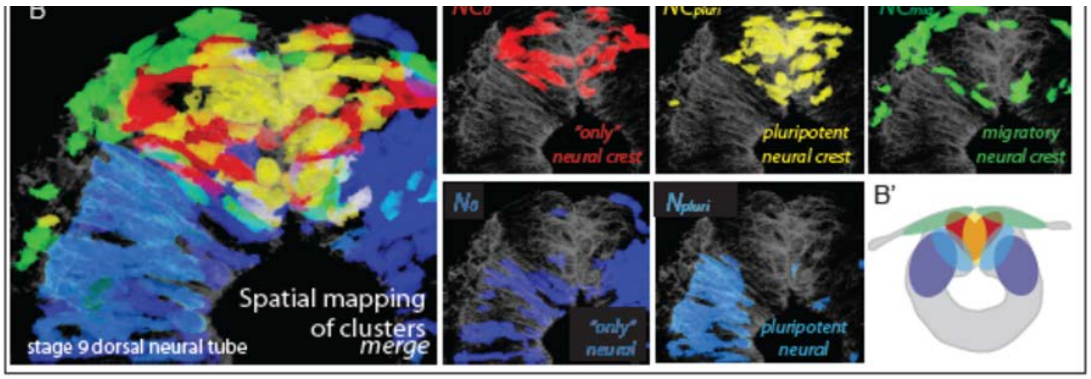
GUEST SPEAKER SEMINAR

Molecular Genetics
UNIVERSITY OF TORONTO

Spatial genomics and single cell lineage dynamics by seqFISH and MEMOIR



Identifying the spatial organization of tissues at cellular resolution from single cellgene expression profiles is essential to understanding many biological systems. We have developed an in situ 3D multiplexed imaging method to quantify hundreds of genes with single cell resolution via Sequential barcodedFluorescence in situ hybridization (seqFISH) (Lubeck et al., 2014). We used seqFISH to identifyunique transcriptional states by quantifying and clustering up to 249 genes in 16,958 cells. By visualizing these clustered cells in situ, we identified regions within distinct composition of cells in different transcriptional states. Together, these resultsdemonstrate the power of seqFISH in transcriptional profiling of complex tissues. Lastly, I will discuss our work in writing lineages and cell event history into genome of cells by CRISPR/Cas9 genome editing and reading out the stored information in single cells by seqFISH.

Dr. Long Cai

Department of Biology and Biological Engineering
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Host: Dr. Julie Lefebvre

Date: Monday September 25, 2017
Time: 4PM
Place: Room 103, Fitzgerald Building, 150 College Street