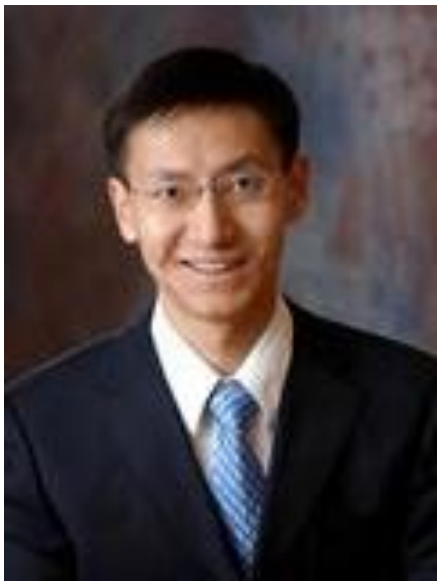
BIOSTATISTICS SEMINAR



Sheng Zhong, PhD

Professor, Bioengineering
Jacobs School of Engineering
University of California San Diego

Rainbow-seq: combining cell lineage tracking with single-cell RNA sequencing in preimplantation embryos

We developed the Rainbow-seq technology to trace cell division history and reveal single-cell transcriptomes. With distinct fluorescent protein genes as lineage markers, Rainbow-seq enables each single-cell RNA-seq experiment to simultaneously decode the lineage marker genes and read single-cell transcriptomes. We triggered lineage tracking in each blastomere at 2-cell stage, observed microscopically inequivalent contributions of the progeny to the two embryonic poles at the blastocyst stage, and analyzed every single cell at either 4- or 8-cell stage with deep paired-end sequencing of full-length transcripts. Although lineage difference was not marked unequivocally at a single-gene level, the lineage difference became clear when the transcriptome was analyzed as a whole. Moreover, several groups of novel transcript isoforms with embedded repeat sequences exhibited lineage difference, suggesting a possible link between DNA demethylation and cell fate decision. Rainbow-seq bridged a critical gap between division history and single-cell RNA-seq assays.

Thursday September 6, 2018 **3:30 pm - 4:30 pm**
Blue Cross and Blue Shield of North Carolina Foundation Auditorium

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