CDB SEMINAR

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16:00~17:00 Auditorium C1F

Development of novel single-cell RNA sequencing technologies

Summary

Single-cell transcriptome analysis allows us to know non-genetic cellular heterogeneity, which includes a difference of cell type originated from differentiation and cell state within a cell population. Our research group aims to develop novel single-cell omics technologies to reveal development and aging of various organs. Especially, we focus on the development of the experimental methods and bioinformatics techniques for analysis single-cell transcriptome. In our unit, we developed two novel single-cell RNA-sequencing methods (scRNA-seq), a high throughput scRNA-seq (Quartz-Seq2) and full-length total scRNA-seq (RamDA-seq). In the presentation, I will present a reaction principle of each method and its applications.

Quartz-Seq2 is a number of cells can be pooled into one tube was up to 1,536. The method allows us to effectively utilize initial sequence read from next generation sequencer, led to increasing resulted in gene expression counts. To improve a performance of single-cell capture, we also introduced Drop-seq which capture a thousand of single cells and barcoded beads in water-in-oil droplets using droplet-generation microfluidics devices. We compared a performance of Quartz-Seq2 and Drop-seq.

To show that the high throughput scRNA-seq contribute to understand developmental phenomenon, I will discuss a novel computational algorithm of prediction for spatial information from scRNA-seq. By combining high throughput scRAN-seq data with whole-mount in situ hybridization images of several genes, we were able us to computationally infer the spatial position of the analyzed cells and the spatial expression pattern of hundreds of genes. Using these, we will be able to construct a model of regionalization the neuroectoderm of frog embryo.

Finally, I will mention that RamDA-seq can observe hundreds of dynamically regulated non-poly(A) transcripts including histone transcripts and the long non-coding RNA in single-cell level. I also showed that RamDA-seq could profile recursive splicing in >300-kb introns in pre-mRNA. Furthermore, RamDA-seq detected enhancer RNAs and their cell type-specific activity in single cells.

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