BK21 Plus Seminar

"Building Human Developmental Cell Atlas using Fast Batch Alignment across Multiple Single Cell RNA-seq Datasets"

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Increasing numbers of large-scale single cell RNA-Seq projects are leading to a data explosion, which can only be fully exploited through integrated data analysis. To overcome the challenge of enormous datasets, we have developed BBKNN, an extremely fast graph-based data integration method for exploratory analysis. BBKNN successfully experimentally populations connects cell across single cell RNA-seg datasets, revealing heterogenous underlying global structure of cell population based on RNA expression profile. We have applied BBKNN to recently time course obtained human developmental dataset. especially focusing on thymus development. This analysis unveils T cell differentiation trajectory into multiple lineages and novel dendritic cell type required for negative T cell selection.

Date: 4:30 PM/Oct. 30(Tue.)/2018

Place: Auditorium(1F), Postech Biotech Center

■ Inquiry: Prof. Yoontae Lee (279-2354)

* This seminar will be given in English.

Please refrain from taking photos during seminars. *