

박주영 (Jooyoung Park)

Undergraduate

Bioinformatics & Bioengineering major

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Personal Data

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About

I am an undergraduate student majoring Bioinformatics and Bioengineering. Taking lectures during undergraduate course and working as a research intern, I got interested in *in silico* genomic data analysis, next generation sequencing (NGS), Genetic features and diseases association, Immunology and Cancer genomics.

Through graduate course, I am expecting to study association between genetic features and diseases via *in silico* genomic data analysis, and contribute to developing novel immunotherapy by relating it with immunology.

Field of Interest

Bioinformatics > *in silico* analyses of biological data, NGS

Genomics > Discovering genetic features related to diseases (Cancer, Autoimmune disease)

Immunotherapy > Relating aberrant genetic features with human immune system to find novel therapy

Personal Projects

Practice of Biostatistics > Expression quantitative loci for TLR6 which leads cytokine secretion important in pathogenesis of Atopic Dermatitis (AD)

Computational Biology > Discovering Novel ligand for CBG (Corticosteroid Binding Globulin) using Smina Docking

GPA & English Score

GPA: 3.87/4.5 , Percentage equivalent : 91.00/100

IBT TOEFL : 102/120 (Reading : 26, Listening : 29, Speaking : 25, Writing : 22) available until 2021.08.03

Abilities

Software language : R Python

Computer OS (except Window) : Linux

Experience

Insilicogen, 人CoINTERNSHIP

2020.01.06 ~ 2020.02.14

SIG (Samsung Genome Institute) Research Intern (Advisor : 정제균 박사님)

Multi-regional Prostate cancer data analysis with WTS, WES data

> Multi-region mutation clonal analysis (phylip, R clonevol), CNV , Gene mutation analysis , signature analysis (TCGA), immune profiling

Small intestine cancer TCR analysis with RNA-seq data case : 8 normal : 5

> TCR clonotyping (Mixcr, VDJ tools), TCR analysis (R immunarch), CDR3 region (R sq1f, WebLogo), DEG analysis (R edgeR)

Prostate cancer intra-heterogeneity 국문 review 논문 작성 (Submit 예정. 다듬는 작업 중)

Single-cell data machine learning with Published lung cancer single-cell data (doi:10.1038/s41467-020-16164-1)

> DEG analysis (R Seurat), WEKA (machine learning tool)

2020.07.01 ~ 2021.01.31