**강의개요**

Bayesian interpretation in the context of large biological data collections

The advance of biotechnology has enabled the democratization of massive bio-data generation at the level of individual laboratories, thus providing a multi-faceted view of the complexity of living systems. Yet, much of this data is left under-utilized or sometimes even misinterpreted owing to the lack of appropriate computational tools and bioinformatic algorithms. In this course, we will cover the theorical basis of one computational technique called the Bayesian methodology and its success in interpreting large biological data collections. We will start by introducing the difference between Frequentist and Bayesian, and then build up to probabilistic graphical models and specialized bioinformatic algorithms for reconstructing biological networks from public data, quantifying gene expression by expectation maximization, and more. It is not required but recommended to read the following materials before this class:

1. Li, B., & Dewey, C. N. (2011). RSEM: accurate transcript quantification from RNA-Seq data with or without a reference genome. BMC bioinformatics, 12(1), 1-16.
2. Lee YS, Krishnan A, Zhu Q and Troyanskaya OG (2013) "Ontology-aware classification of tissue and cell-type signals in gene expression profiles across platforms and technologies." Bioinformatics 29 (23), 3036-3044

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**Curriculum Vitae**

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**Educational Experience**

2010 B.S. Computer Science and B.S. Mathematics, The University of Texas at Austin

2014 M.S. Computer Science, Princeton University

2016 Ph.D. Computer Science, Princeton University

**Professional Experience**

2016-2020 Research fellow, Seoul National University and Institute for Basic Science

2020- Assistant Professor, Department of Bio and Brain Engineering, Korea Advanced Institute of Science and Technology

**Selected Publications (5 maximum)**

1. Lee S\*, **Lee YS\***, Choi Y, Son A, Park Y, Lee KM, Kim J, Kim JS, Kim VN (2021) “The SARS-CoV-2 RNA interactome.” *Molecular Cell* \*equal contributions
2. Kim D\*, **Lee YS\***, Jung SJ\*, Yeo J\*, Seo JJ, Lee YY, Lim J, Chang H, Song J, Yang J, Jung G, Ahn K and Kim VN (2020) “Viral hijacking of the TENT4-ZCCHC14 complex protects viral RNAs via mixed tailing.” *Nature structural & molecular biology* \*equal contributions
3. **Lee YS**, Krishnan A, Oughtred R, Rust R, Chang CS, Ryu J, Kristensen VN, Dolinski K, Theesfeld CL and Troyanskaya OG (2019) "A Computational Framework for Genome-wide Characterization of the Human Disease Landscape." *Cell systems* 8 (2), 152-162. e6
4. **Lee YS**, Wong AK, Tadych A, Hartmann BM, Park CY, DeJesus VA, Ramos I, Zaslavsky E, Sealfon SC and Troyanskaya OG (2018) "Interpretation of an individual functional genomics experiment guided by massive public data." *Nature methods* 15 (12), 1049
5. Lim J\*, Kim D\*, **Lee YS\***, Ha M, Lee M, Yeo J, Chang H, Song J, Ahn K and Kim VN (2018) "Mixed tailing by TENT4A and TENT4B shields mRNA from rapid deadenylation." *Science* 361 (6403), 701-704, \*equal contributions