

Kyuri Jo (조겨리)

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EDUCATION

Seoul National University, Korea

- Ph. D., Computer Science and Engineering (Advisor: Professor Sun Kim) Mar.2013 – Aug.2018
- B. S., Computer Science and Engineering (*Cum Laude*) Mar.2008 – Feb.2013

EXPERIENCE

Ewha Womans University, Korea

- Part-time lecturer, Mechanical and Biomedical Engineering Mar.2019 – present

Seoul National University, Korea

- Postdoctoral research fellow, SNU Bioinformatics Institute (Advisor: Professor Sun Kim) Sep.2018 – present

RESEARCH INTERESTS

Investigations to apply machine learning and data mining techniques for time-series analysis

RESEARCH EXPERIENCE

Graduate research in Bio & Health Informatics Lab., Seoul National University, Korea

1. Development of machine learning and data mining algorithms for biological data

〈 Network inference in high-dimensional data space 〉

- **PropaNet: finding dynamic regulator-target modules in a biological network**
 - Filtering and prioritizing regulator nodes by influence maximization and network propagation
 - Analyzed networks of plant (*Arabidopsis*) under cold and heat stress
 - Paper accepted by *Frontiers in Plant Science* (SCIE, IF=3.678) journal
- **TimeTP: detecting subnetworks with dynamic signal propagation and their regulator nodes**
 - Introduced a data mining process of 3D (time, gene, phenotype) gene expression matrix with network information
 - Incorporated cross-correlation and influence maximization techniques to detect subnetworks with dynamic signal propagation and regulator nodes of the subnetworks

- Designed a new visualization scheme (TF-Pathway map in time clock) for dynamic network
 - Paper accepted by *ISMB 2016* conference, *Bioinformatics* journal (SCI, IF=5.481)
 - **TRAP: an algorithm for prioritizing networks with dynamic signal propagation**
 - Introducing a novel statistic for measuring dynamic signal propagation in a network
 - Applied to rice RNA-seq dataset to explain different mechanism of drought-resistant rice
 - Paper accepted by *Methods* journal (SCI, IF=3.998)
- 〈 Clustering and causality inference using Gaussian process regression 〉**
- **TiCINet: an optimal clustering for time series using Gaussian process**
 - Incorporated a Gaussian process model to design an adapted gap statistic for time series
 - Generated a high-level cluster network to infer cluster-cluster relationship
 - In preparation for *Nature Machine Intelligence* journal
 - **mirTime: regulatory network inference with Gaussian process and spherical vector clustering**
 - Incorporated Gaussian process and spherical vector clustering for inference of causal relationships between two discrete vectors
 - Paper accepted by *Bioinformatics* journal (SCI, IF=5.481)

〈 Deductive reasoning on a biological knowledge-base 〉

- **Integration of deductive reasoning (Pathway Logic system) and gene expression data**
 - Used gene expression data to filter relevant rules in deductive reasoning
 - Explained different signaling paths between breast cancer subtypes

2. Application of the computational algorithms to biomedical data

- **Adipose tissue analysis in mouse**
 - Analysis of multi-conditioned gene expression data to prioritize biological pathway networks
 - Detected a potential regulator (GABA) of macrophage recruitment in adipose tissue
 - Paper accepted by *PNAS* journal (SCI, IF=9.504)
- **Time-series analysis of xenotransplantation dataset**
 - Application of time-series analysis algorithms (TRAP) to a biological data set
 - Detected dynamic change of biological pathway activation after xenotransplantation
 - Results presented at *IPITA-IXA-CTS 2015* joint congress

TEACHING EXPERIENCE

Part-time lecturer: 바이오데이터전산기초및실습, 2019 Spring, Ewha Womans University, Korea.

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Guest lecture: 생물정보학 및 실습 2, 2018 Fall, Seoul National University, Korea.

Guest lecture: 생물정보학 및 실습 2, 2016 Fall, Seoul National University, Korea.

Guest lecture: 생물정보의 이해, 2014 Spring, Konkuk University, Korea.

PUBLICATIONS

Research Highlights

1 paper in preparation for *Nature Machine Intelligence*

3 papers published in *Bioinformatics* (The flagship journal in the bioinformatics field)

1 paper presented at *Intelligent Systems for Molecular Biology (ISMB)* (한국정보과학회 선정 최우수학술대회)

International Journal (*: equal contributors)

Jo K, Lee D, Sung IY, Kim S. Time series-specific Clustering and Network inference (TiCINet) with Gaussian process and Shape-based distance. In preparation for *Nature Machine Intelligence*.

Buitrago B*, **Jo K***, Kim M*, Rhee S, Talcott C, Kim S. Logic-based Analysis of Gene Expression Data Predicts Pathway Crosstalk between TNF, TGFB1 and EGF in Basal-like Breast Cancer. In preparation.

Kim HJ, Moon JH, Shin JS, Kim B, Kim JS, Yoon IH, Min BH, Kim JM, Kang SJ, Kim YH, **Jo K**, Choi J, Chae H, Lee WW, Kim S, Park CG. Bioinformatics analyses with peripheral blood RNA-sequencing unveiled the cause of the graft loss after pig-to-nonhuman primate islet xenotransplantation model. *Scientific Reports* (SCI, IF=4.122), in review.

Kim JI, Park J, Ji Y, **Jo K**, Sohn JH, Shin KC, Han JS, Jeon YG, Hahn NG, Han KH, Kim J, Kim S, Choe SS, Kim JB. During adipocyte remodeling, lipid droplet shape determines insulin sensitivity via actin dynamics. *Molecular and Cellular Biology* (SCI, IF=3.813), in review.

Hwang I, **Jo K**, Shin KC, Kim JI, Ji Y, Park YJ, Park J, Jeon YG, Ka S, Suk S, Noh HL, Choe SS, Alfadda AA, Kim JK, Kim S, Kim JB. GABA-stimulated adipose-derived stem cells suppress subcutaneous adipose inflammation in obesity. *Proceedings of the National Academy of Sciences* (SCI, IF=9.504), in press.

Ahn H*, **Jo K***, Jung D, Park M, Hur J, Jung W, Kim S. PropaNet: Time-varying condition-specific transcriptional network construction by network propagation. *Frontiers in Plant Science* (SCIE, IF=3.678), in press.

Kang H*, Ahn H*, **Jo K**, Oh M, Kim S. mirTime: Identifying Condition-Specific Targets of MicroRNA in Time-series Transcript Data using Gaussian Process Model and Spherical Vector Clustering. *Bioinformatics* (SCI, IF=5.481), in press.

Jung I, **Jo K**, Kang H, Ahn H, Yu Y, Kim S. TimesVector: A vectorized clustering approach to the analysis of time series transcriptome data from multiple phenotypes. *Bioinformatics* (SCI, IF=5.481), 2017 Dec 1;33(23):3827-3835.

Moon JH, Lim S, **Jo K**, Lee S, Seo S, Kim S. PINTnet: construction of condition-specific pathway interaction network by computing shortest paths on weighted PPI. *BMC Systems Biology* (SCI, IF=2.050), 2017 Mar 14; 11(Suppl 2): 15.

Lee J, **Jo K**, Lee S, Kang J, Kim S. Prioritizing biological pathways by recognizing context in time-series gene expression data. *BMC Bioinformatics* (SCIE, IF=2.213), 2016 Dec 23;17(17):477.

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Jo K, Jung I, Moon JH, Kim S. Influence maximization in time bounded network identifies transcription factors regulating perturbed pathways. **Bioinformatics** (SCI, IF=5.481). 2016 Jun 15;32(12):i128-i136.

Jo K, Kwon HB, Kim S. Time-series RNA-seq analysis package (TRAP) and its application to the analysis of rice, *Oryza sativa* L. ssp. Japonica, upon drought stress. **Methods** (SCI, IF=3.998), 2014 Jun 1;67(3):364-72.

International Conference

Jo K, Jung I, Moon JH, Kim S. Influence maximization in time bounded network identifies transcription factors regulating perturbed pathways. **Intelligent Systems for Molecular Biology (ISMB)** 2016, Jul 8-12, Orlando, FL.

Kim HJ, Moon JH, Shin JS, Kim JS, Min BH, Kim JM, Kim YH, Lee WW, Kang BC, Kang SJ, Kim SJ, **Jo K**, Kim S, Park CG. A new bioinformatics analysis reveals intestinal infection as a possible cause of intrahepatic graft rejection in non-human primate porcine islet xenotransplantation. **IPITA-IXA-CTS 2015**, Nov 15-19, Melbourne, Australia.

GRANTS / AWARDS

Institutional participant (서울대학교 공과대학 대표 5인), Asian Deans' Forum 2018 - The Rising Stars: Women in Engineering Workshop, Oct 4-7, 2018.

Naver PhD Fellowship, 네이버(주), Jan 20, 2017

Best Paper Award, 한국생물정보시스템생물학회 학술대회 BIOINFO 2016, Aug 19, 2016

ISMB Travel Fellowship, Intelligent Systems in Molecular Biology (ISMB) 2016, Jul 12, 2016

Best Poster Award, 한국생물정보시스템생물학회 학술대회 BIOINFO 2015, Oct 23, 2015