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## EDUCATION

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### 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

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### Chungbuk National University, Korea

- **Assistant professor**, Department of Computer Engineering Sep.2019 – present

### Ewha Womans University, Korea

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

### Seoul National University, Korea

- **Postdoctoral researcher**, SNU Bioinformatics Institute (Advisor: Professor Sun Kim) Sep.2018 – Aug.2019

## RESEARCH INTERESTS

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**Machine learning, Artificial Intelligence (AI)** and data mining techniques

**Integration of BT and IT (Bioinformatics)** for bio big data, especially time-series & network analysis

## RESEARCH EXPERIENCE

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### 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 (SCIE, 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 (SCIE, IF=3.998)

#### 〈 Clustering and causality inference using Gaussian process regression 〉

- **TRACS: a time series clustering framework for inferring TRANscriptomic Cellular States**
  - 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 *Bioinformatics* 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 (SCIE, 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
  - Paper accepted by *Methods* journal (SCIE, IF=3.998)

## 2. Application of 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 (SCIE, IF=9.504)
- **Time-series analysis of xenotransplantation dataset**
  - Detected dynamic change of biological pathway activation after xenotransplantation
  - Results presented at *IPITA-IXA-CTS 2015* joint congress
  - Paper accepted by *Scientific Reports* journal (SCIE, IF=4.011)

## PUBLICATIONS

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### Research Highlights

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**, Sung IY, Lee D, Jang H, Kim S. Inferring transcriptomic cell states and transitions from time series transcriptome data, *Scientific Reports*, 2021 Jun 15; 11:12566.

Kim S\*, Bae S\*, Piao Y, **Jo K**. Graph Convolutional Network for Drug Response Prediction Using Gene Expression Data. *Mathematics*, 2021 Apr 2; 9(7):772.

Oh M, Park S, Lee S, Lee D, Lim S, Jeong D, **Jo K**, Jung I, Kim S. DRIM: A web-based system for investigating drug response at the molecular level by condition-specific multi-omics data integration. *Frontiers in Genetics* (SCIE, IF=), 2020 Nov 12; 11:1-14.

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. *Methods* (SCIE, IF=3.998), 2020 Jul 1; 179:89-100.

Kim HJ, Moon JH, Chung H, Shin JS, Kim B, Kim JM, Kim JS, Yoon IH, Min BH, Kang SJ, Kim YH, **Jo K**, Choi J, Chae H, Lee WW, Kim S, Park CG. Bioinformatic analysis of peripheral blood RNA-sequencing sensitively detects the cause of late graft loss following overt hyperglycemia in pig-to-nonhuman primate islet xenotransplantation. *Scientific Reports* (SCIE, IF=4.122), 2019 Dec 11; 9(1):1-11.

Kim JI, Park J, Ji Y, **Jo K**, Han SM, Sohn JH, Shin KC, Han JS, Jeon YG, Goong HN, Han KH, Kim J, Kim S, Choe SS, Kim JB. During adipocyte remodeling, lipid droplet configurations regulate insulin sensitivity through F-actin and G-actin reorganization. *Molecular and Cellular Biology* (SCIE, IF=3.813), 2019 Sep 27; 39(20):e00210-19.

Ahn H\*, **Jo K\***, Jeong D, Pak 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), 2019 June 14; 10:698.

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* (SCIE, IF=9.504), 2019 June 11; 116(24):11936-11945.

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* (SCIE, IF=5.481), 2019 May 9 [online advanced article].

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* (SCIE, 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* (SCIE, 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.

**Jo K**, Jung I, Moon JH, Kim S. Influence maximization in time bounded network identifies transcription factors regulating perturbed pathways. **Bioinformatics** (SCIE, 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** (SCIE, 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**

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**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.

### **SERVICE**

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**Publication Chair**, The Asia Pacific Bioinformatics Conference (APBC), 2020.

### **TEACHING EXPERIENCE (highlights)**

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**Instructor**: 인공지능, 2020 Fall, Chungbuk National University, Korea.

**Instructor**: 머신러닝, 2020/2021 Spring, Chungbuk National University, Korea.

**Instructor**: 선형대수학, 2019 Fall, Chungbuk National University, Korea.

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

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

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

**Guest lecturer**: 생물정보의 이해, 2014 Spring, Konkuk University, Korea.