

# Kyuri Jo (조겨리)

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## EDUCATION

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### Seoul National University, Korea

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

## EXPERIENCE

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### Seoul National University, Korea

- Postdoctoral fellowship, Computer Science and Engineering Sep.2018 – present  
(Advisor: Professor Sun Kim)

## RESEARCH INTERESTS

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

## RESEARCH EXPERIENCE

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

#### 1. Development of machine learning and data mining algorithms for time-series

- **Inference of a cluster network from unevenly spaced time-series** Jan.2017 - present  
- Improving clustering results for time-series considering time dependency  
- Generation of a cluster network to infer cluster-cluster relationship
- **Integration of Pathway Logic system and gene expression data** Sep.2017-Mar.2018  
- Using gene expression data to filter relevant rules in deductive reasoning  
- Explained different signaling paths between breast cancer subtypes  
- Submitted to *ECCB 2018* conference
- **Applying influence maximization technique in time bounded network to identify transcription factors regulating perturbed pathways** Jun. 2015-Jan.2016  
- Introduced a data mining process of the biological network for time-series gene expression data  
- Provided a new information visualization scheme (TF-Pathway map in time clock) for dynamic network  
- Paper accepted by *ISMB 2016* conference, *Bioinformatics* journal
- **Development of Time-series RNA-seq Analysis Package (TRAP) and its web service** Aug.2013-Jan.2014  
- Introduced a novel pathway-level statistics for time-series gene expression data

- Applied to rice RNA-seq dataset to explain different mechanism of drought-resistant rice
- Paper accepted by *Methods* journal

## 2. Application of the algorithms on biomedical data

- **Fat-depot of mouse** **Jan.2016 - present**
  - Analysis of multi-conditioned gene expression data to prioritize biological pathways
  - Participated in monthly discussions with biological scientists
  - Detected a potential regulator of macrophage recruitment in adipose tissue
  - Subsequent experiments in progress
- **Time-series analysis of xenotransplantation dataset** **Jun.2014-Dec.2014**
  - Application of time-series analysis algorithms (TRAP) to the biological dataset
  - Participated in monthly discussions with medical scientists
  - Detected dynamic change of biological pathway activation after xenotransplantation
  - Results presented at *IPITA-IXA-CTS 2015* joint congress

## TEACHING EXPERIENCE

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**Guest lecture: Understanding Bioinformatics**, 2014 Spring, Konkuk University, Korea.

## PUBLICATIONS

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### International Journal

**Jo K**, Jung I, Kim S. Time series-specific Clustering and Network inference (TiCINet) with Gaussian process and Shape-based distance. In preparation.

**Jo K**, Buitrago B, Kim M, Rhee S, Talcott C, Kim S. Logic-based analysis of gene expression identifies potential pathway crosstalk between TNF, TGFB1 and EGF in basal-like breast cancer. In review.

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*, 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*, 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*, 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*. 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*, 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**

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**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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Naver PhD Fellowship, Jan 20, 2017

Best Paper Award, BIOINFO 2016, Aug 19, 2016

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

Best Poster Award, BIOINFO 2015, Oct 23, 2015