

Seojin Bang

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RESEARCH INTEREST

My research interest is in the interpretability of black-box machine learning models. I develop interpretable machine learning approaches and investigate the relationship between interpretability and robustness in machine learning algorithms. I also develop multimodal/multiview machine learning approaches for combining different data modalities.

EDUCATION

Aug 2020 (expected)	The School of Computer Science, Carnegie Mellon University PhD candidate in Computational Biology	Advisor: Wei Wu
2013	Seoul National University, Korea MS in Statistics	Advisor: Taesung Park
2010	Sungkyunkwan University, Korea BS in Mathematical Education · BE in Statistics (double major)	

PUBLICATIONS/PREPRINTS

- [1] **Explaining a black-box using deep variational information bottleneck approach.**
preprint arXiv:1902.06918, submitted, 2020.
Bang, Seojin and Xie, Pengtao and Lee, Heewook and Wu, Wei and Xing, Eric.
- [2] **Robust multiple kernel k-means clustering using min-max optimization.**
preprint arXiv:1803.02458, submitted, 2020.
Bang, Seojin and Yu, Yaoliang and Wu, Wei.
- [3] **Kw-han: Knowledge infused hierarchical attention network for enhancing interpretability.**
preprint, under review, 2020.
Jang, Hyeju and Bang, Seojin.
- [4] **Detecting attackable sentences in arguments.**
preprint, under review, 2020.
Jo, Yohan and Bang, Seojin.
- [5] **Dropout prediction over weeks in moocs via interpretable multi-layer representation learning.**
AAAI AI4EDU, 2020.
Jeon, Byungsoo* and Park, Namyong* and Bang, Seojin* (co-first).
- [6] **Phased-lstm based predictive model for ehers with complex missing patterns.**
preprint, <https://www.cs.cmu.edu/~epxing/Class/10708-17/project-reports/project8.pdf>, 2019.
Bang, Seojin and Yang, Yang and Wang, Yuchuan.
- [7] **A mixture model to detect edges in sparse co-expression graphs.**
Statistics in Medicine, under review, preprint arXiv:1804.01185, 2019.
Bar, Haim and Bang, Seojin.
- [8] **Multiview cluster analysis identifies variable corticosteroid response phenotypes in severe asthma.**
American Journal of Respiratory and Critical Care Medicine, (IF 16.49) Highlighted Articles, 2019.

Wu*, Wei and **Bang*** (co-first), **Seojin** and Bleecker, Eugene and Castro, Mario and Denlinger, Loren and Erzurum, Serpil and Fahy, John and Fitzpatrick, Anne and Gaston, Ben and Hastie, Annette and Israel, Elliot and Jarjour, Nizar and Kerr, Sheena and Levy, Bruce Meyers, Deborah and Moore, Wendy and Peters, Michael and Phipatanakul, Wanda and Sorkness, Ronald and Wenzel, Sally.

- [9] **Phosphoproteomic analysis of the amygdala response to adolescent glucocorticoid exposure reveals g-protein coupled receptor kinase 2 as a target for reducing motivation for alcohol.**
Proteomes, 6(4), 2018.
Bertholomey, Megan L. and Stone, Kathryn and Lam, TuKiet T. and **Bang, Seojin** and Wu, Wei and Nairn, Angus C. and Taylor, Jane R. and Torregrossa, Mary M.
- [10] **Naïve bayes ensemble: A new approach to classifying unlabeled multi-class asthma subjects.**
In *IEEE International Conference on Bioinformatics and Biomedicine*, 2016.
Bang, Seojin and Wu, Wei.
- [11] **Joint selection of snps for improving prediction in genome-wide association studies.**
In *IEEE International Conference on Bioinformatics and Biomedicine. Workshops*, 2012.
Bang, Seojin and Kim, Yong-Gang and Park, Taesung.
- [12] **Ethnic variability in the allelic distribution of pharmacogenes between korean and other populations.**
Pharmacogenetics and genomics, 22(12), 2012.
Kim, In-Wha and Im Kim, Kyung and Chang, Hyeu-jin and Yeon, Bora and **Bang, Seojin** and Park, Taesung and Kwon, Ji-sun and Kim, Sangsoo and Oh, Jung Mi.

RESEARCH EXPERIENCE

Multimodal/Multiview Machine Learning for Asthma Subtype Identification 2015 – 2020
Research Assistant advised by Dr. Wei Wu *Carnegie Mellon University, Pittsburgh, PA, USA*

- Developed a robust multiple kernel clustering approach.
- Identified asthma subtypes showing differential responses to corticosteroid by combining multiview clinical data.
- Developed an R-package: **MKKC** (github.com/SeojinBang/MKKC)
- Three papers published in *AJRCCM*, *IEEE BIBM* and *Proteomes*, and a paper submitted to *[blinded]*.

Interpretable Machine Learning 2018 – 2020
Research Intern advised by Dr. Pengtao Xie *AI/ML Solution Team at Petuum, Pittsburgh, PA, USA*

- (Worked as an intern at Petuum between May and Dec 2018. Worked as a student at Carnegie Mellon University from 2019.)
- Developed a system-agnostic interpretable ML approach using neural networks using information bottleneck principle.
- Improved an out-of-sample prediction of epitope-TCR binding using an interpretable model.
- Developed a pytorch based software: **VIBI** (github.com/SeojinBang/VIBI) and **TCR** (github.com/SeojinBang/TCR)
- A paper submitted to *[blinded]*

Machine Learning for Natural Language Processing 2018 – 2020
Graduate Student *Carnegie Mellon University, Pittsburgh, PA, USA*

- Developed an ontology-based neural network model for patient need detection from an online ovarian cancer discussion forum. A paper submitted to *[blinded]*.
- Analyzed to detect attackable sentences in arguments for successful persuasion using online discussions from the Change-MyView (CMV) subreddit. A paper submitted to *[blinded]*.

Interpretability and Robustness in Machine Learning 2019
Visiting Graduate Student advised by Dr. Adrian Weller *ML Group at University of Cambridge, UK*

- Investigated the relationship between interpretability and robustness of machine learning and deep learning models.
- Developing a knowledge guided interpretable ML model using the posterior regularization.

Statistical Modeling of Sparse Gene Networks

2013 – 2015

Research Assistant advised by Dr. Haim Bar

University of Connecticut, Storrs, CT, USA

- Developed a statistical mixture model for better estimating sparse gene network.
- Helped to develop an R-package: **edfinder**
- A paper under review in *Statistics in Medicine*.

Statistical Approaches for Biomedical Problems

2012 – 2013

Research Assistant and Scientist advised by Dr. Taesung Park

Seoul National University, Korea

- Developed a joint feature selection method using the elastic-net regularization to high-dimensional data.
- Deployed a time-dependent survival model to identify subtypes of intraductal papillary mucinous neoplasm.
- Two papers published in *IEEE BIBM* and *Pharmacogenetics and genomics*.

PROFESSIONAL SERVICE

2020	Reviewer of <i>ACM CHIL</i> , <i>ISMB</i>
2019	Reviewer , <i>NeurIPS ML4H Workshop</i> , <i>IEEE Access</i> , <i>IEEE TNNLS</i>
2018	Reviewer , <i>ACM BCB</i>
2018	Admission Committee , <i>Computational Biology Department</i> , <i>Carnegie Mellon University</i>
2012	Program Committee , <i>International Symposium on Statistical Genetics</i> , Korea
2012	Program Committee , <i>Microarray Analysis Workshop: Statistical Analysis using R language</i> , Korea
2011	Program Committee , <i>The Spring Conference of the Korean Statistical Society</i> , Korea

HONORS AND AWARDS

2018	The Center for Machine Learning and Health Fellowships in Digital Health full tuition and stipend for 12 months and research-related expenses (total \$75,200)	
2013	The Korean Statistical Society Paper Awards (3st Place)	
2012	The Korean Statistical Society Poster Awards (1st Place)	
2006 – 2010	National Science and Engineering Undergraduate Scholarship full tuition for 8 semesters an additional \$500 grant for a high GPA an additional \$500 grant for a high GPA	2006 – 2010 2009 2008

SOFTWARE

Python	VIBI : pytorch implementation of VIBI https://github.com/SeojinBang/VIBI
Python	TCR : TCR to epitope binding prediction approach using VIBI https://github.com/SeojinBang/TCR
R-package	MKKC : multiple kernel k -means clustering on a multi-view data https://github.com/SeojinBang/MKKC
LaTeX template	TidyCV : simple and tidy LaTeX template for your curriculum vitae https://github.com/SeojinBang/TidyCV

TECHNICAL STRENGTHS

Computer Languages	Python, R, C/C++, MATLAB, Bash, HTML
Library & Others	Pytorch, Tensorflow, Caffe, Keras, Git, LaTeX

TEACHING EXPERIENCE

Carnegie Mellon University

Teaching Assistant

2018 Quantitative Cell and Molecular Biology Lab

2017 Computational Methods for Proteogenomics and Metabolomics

University of Connecticut

Teaching Assistant

2014 Mathematical Statistics

2014 Introduction to Mathematical Statistics

2013 Elementary Concepts of Statistics

2013 Introduction to Statistics I and II

2013 Statistical Methods

Seoul National University, Korea

Teaching Assistant

2012 Statistics Laboratory

2012 Regression and Analysis and Laboratory

2011 Statistics

Bongyoung Girls' Middle School, Korea

Student Teacher

2009 Middle School Mathematics

Sungkyunkwan University, Korea

Teacher

2006 Alternative Elementary/Middle School Mathematics