Junghyun Jung

https://junghyunjj.github.io/

Updated: April 12, 2023
Email : junghyun.jung@usc.edu

Education

- **Dongguk University** Seoul, Korea
  Ph.D. in Life Science *Sept. 2014 – Feb. 2020*
  Mentor: Dr. Wonhee Jang
  Dissertation project: Bioinformatics-based approaches for identifying novel genetic markers

- **Dongguk University** Seoul, Korea
  M.S. in Life Science *Mar. 2012 – Aug. 2014*
  Mentor: Dr. Wonhee Jang
  Dissertation project: Studies on the *in silico* analyzing methods related to toxic effects and mechanisms of chemicals

- **Dongguk University** Seoul, Korea
  B.S. in Life Science *Mar. 2007 – Feb. 2012*

Professional and Academic Experience

- **University of Southern California** Los Angeles, CA, USA
  Postdoctoral Researcher at Center for Genetic Epidemiology, Keck School of Medicine *Aug. 2021 - present*
  Mentor: Dr. Nicholas Mancuso
  - **Large-scale integrative analysis of complex disease for new insight into its pathogenesis**
    - Perform integrative analysis using GWAS with molecular QTL (molQTL) data for TWAS analysis.
    - Perform molQTL analysis using enhancer RNAs (eRNAs) and long non-coding RNAs (lncRNAs).
    - Perform Single-cell RNA/ATAC/TCR-seq data analysis.
  - **Inference of negative selection in the evolutionary architecture**
    - Develop a novel statistical method using Variational Bayesian methods.
    - Understand the landscape of evolutionary architectures across many molecular phenotypes.

- **University of Southern California** Los Angeles, CA, USA
  Postdoctoral Researcher at Center for Genetic Epidemiology, Keck School of Medicine *Aug. 2020 - Jul. 2021*
  Mentor: Dr. Nicholas Mancuso
  - **Genome-wide association analysis of multiple phenotypes in multi-Ancestry**
    - Perform multivariate GWAS analysis by analyzing correlated cytokines phenotypes.
    - Perform multi-ancestry GWAS analysis by analyzing correlated cytokines phenotypes.
  - **Inference of negative selection in the evolutionary architecture**
    - Duties similar to above.

  Postdoctoral Researcher at Titus Family Department of Clinical Pharmacy, School of Pharmacy
  Mentor: Dr. Serghei Mangul
  - **Genome/Exome-wide association study to identify common/rare variants influencing COVID-19 outcomes using middle eastern cohort**
    - Analyze Whole-Exome seq (WES) data to identify rare variants using the Saudi Human Genome Program cohort.
    - Perform GWAS analysis to identify common variants using the Saudi Human Genome Program cohort.
  - **Rigorous benchmarking of HLA callers for RNA sequencing data**
    - Evaluate performances of multiple HLA callers using gold standard data.
    - Consensus HLA typing based on multiple HLA callers using Genotype-Tissue Expression (GTEx) data.
    - HLA typing using multiple ancestry data.

- **Dongguk University** Seoul, Korea
  Postdoctoral Researcher at Department of Computer Science and Engineering *Mar. 2020 - Jul. 2020*
  Mentor: Dr. Jong Wha J. Joo
  - **Set-based analysis to increase the power of association testing**
    - Develop a statistical method to improve statistical power using multiple causal variants.
    - Multivariate phenotype analysis by analyzing many phenotypes simultaneously.
  - **Cross-species analysis to apply animal model studies to humans**
    - Analyze biological processes and transcriptional changes of animal models.
    - Perform cross-species analysis by applying genomics animal model studies to humans.

- **Dongguk University** Seoul, Korea
  Instructor at Convergence Software Institute Dongguk *Mar. 2018 - Aug. 2020*
  (Biological Information Software Convergence)

- **Dongguk University** Seoul, Korea
  Teaching assistant at Department of Life Science *Sept. 2012 - Aug. 2013*

Research Technique

- **Computational Skills**
  - **NGS data analysis**: WES, RNA-seq, ATAC-seq, Chip-seq, scRNA/scTCR-seq data analysis
  - **Micoarray data analysis**: SNP and expression array data analysis
  - **High performance computing**: Slurm and Sun Grid Engine (SGE)
  - **Programming languages:**: R, Python, and Bash
  - **Other software applications**: Git, LaTeX, SPSS, and ImageJ

- **Experimental Skills**
  - Mammalian cell culture
  - Animal handling (mouse)

Preprint

- D. Kim, J. Song, S. Mangul, N. Mancuso, C.W. Ahn, **J. Jung**, and W. Jang, Large-scale integrative analysis of juvenile idiopathic arthritis for new insight into its pathogenesis, *medRxiv*, pp. 2023–04, 2023.
- **J. Jung**, Z. Lu, A. J. de Smith, and N. Mancuso, Novel insight into the etiology of ischemic stroke gained by integrative transcriptome-wide association study, *medRxiv*, pp. 2023–03, 2023.
- Z. Zhang, **J. Jung**, A. Kim, N. Suboc, S. Gazal, and N. Mancuso, A scalable variational approach to characterize pleiotropic components across thousands of human diseases and complex traits using gwas summary statistics, *medRxiv*, pp. 2023–03, 2023

Publications

[1] G. Butler-Laporte, G. Povysil, J. A. Kosmicki, E. T. Cirulli, T. Drivas, S. Furini, C. Saad, A. Schmidt, P. Olszewski, U. Korotko, **J. Jung**, *et al.*, "Exome-wide association study to identify rare variants influencing COVID-19 outcomes: Results from the Host Genetics Initiative," *PLoS Genetics*, vol. 18, no. 11, p. e1010367, 2022.

[2] Y. Shim, M. Shin, **J. Jung**, B. Koo, and W. Jang, "An in-silico approach to studying a very rare neurodegenerative disease using a disease with higher prevalence with shared pathways and genes: Cerebral adrenoleukodystrophy and Alzheimer's disease," *Frontiers in molecular neuroscience*, vol. 15, 2022.

[3] J. Song, D. Kim, S. Lee, **J. Jung**, J. W. J. Joo, and W. Jang, "Integrative transcriptome-wide analysis of atopic dermatitis for drug repositioning," *Communications biology*, vol. 5, no. 1, pp. 1–13, 2022.

[4] J. L. Wiemels, R. Wang, M. Zhou, H. Hansen, R. Gallant, **J. Jung**, N. Mancuso, A. J. De Smith, C. Metayer, S. C. Kogan, *et al.*, "Cytomegalovirus proteins, maternal pregnancy cytokines, and their impact on neonatal immune cytokine profiles and acute lymphoblastic leukemogenesis in children," *Haematologica*, 2022.

[5] A. Kousathanas, E. Pairo-Castineira, K. Rawlik, A. Stuckey, C. A. Odhams, S. Walker, C. D. Russell, T. Malinauskas, Y. Wu, J. Millar, **J. Jung**, *et al.*, "Whole genome sequencing reveals host factors underlying critical Covid-19," *Nature*, pp. 1–10, 2022.

[6] C. Fallerini, N. Picchiotti, M. Baldassarri, K. Zguro, S. Daga, F. Fava, E. Benetti, S. Amitrano, M. Bruttini, M. Palmieri, **J. Jung**, *et al.*, "Common, low-frequency, rare, and ultra-rare coding variants contribute to COVID-19 severity," *Human genetics*, pp. 1–27, 2021.

[7] M. D'Antonio, J. P. Nguyen, T. D. Arthur, H. Matsui, B. M. Neale, M. Daly, A. Ganna, C. Stevens, G. A. Pathak, S. J. Andrews, **J. Jung**, *et al.*, "SARS-CoV-2 susceptibility and COVID-19 disease severity are associated with genetic variants affecting gene expression in a variety of tissues," *Cell reports*, vol. 37, no. 7, p. 110020, 2021.

[8] B. Lee, M. K. Shin, I.-W. Hwang, **J. Jung**, Y. J. Shim, G. W. Kim, S. T. Kim, W. Jang, and J.-S. Sung, "A Deep Learning Approach with Data Augmentation to Predict Novel Spider Neurotoxic Peptides," *International Journal of Molecular Sciences*, vol. 22, no. 22, p. 12291, 2021.

[9] G. Povysil, G. Butler-Laporte, N. Shang, C. Wang, A. Khan, M. Alaamery, T. Nakanishi, S. Zhou, V. Forgetta, R. J. Eveleigh, **J. Jung**, *et al.*, "Rare loss-of-function variants in type I IFN immunity genes are not associated with severe COVID-19," *The Journal of Clinical Investigation*, vol. 131, no. 14, 2021.

[10] F. Hormozdiari†, **J. Jung**†, E. Eskin, and J. W. J. Joo, "MARS: leveraging allelic heterogeneity to increase power of association testing," *Genome biology*, vol. 22, pp. 1–26, April 2021.

[11] D. Kim, J. Song, S. Lee, **J. Jung**, and W. Jang, "An Integrative Transcriptomic Analysis of Systemic Juvenile Idiopathic Arthritis for Identifying Potential Genetic Markers and Drug Candidates," *International Journal of Molecular Sciences*, vol. 22, no. 2, p. 712, 2021.

[12] J. H. Choi, T. Kim, **J. Jung**, and J. W. J. Joo, "Fully automated web-based tool for identifying regulatory hotspots," *BMC genomics*, vol. 21, no. 10, pp. 1–7, 2020.

[13] G. J. Lee, S. M. Park, **J. Jung**, and J. W. J. Joo, "A Fully Automated Parallel-Processing R Package for High-Dimensional Multiple-Phenotype Analysis Considering Population Structure," *International Journal of Fuzzy Logic and Intelligent Systems*, vol. 20, no. 3, pp. 219–226, 2020.

[14] J. Song, D. Kim, J. Hong, G. W. Kim, **J. Jung**, S. Park, H. J. Park, J. W. J. Joo, and W. Jang, "Meta-analysis of polymyositis and dermatomyositis microarray data reveals novel genetic biomarkers," *Genes*, vol. 10, no. 11, p. 864, 2019.

[15] **J. Jung**, G. W. Kim, B. Lee, J. W. J. Joo, and W. Jang, "Integrative genomic and transcriptomic analysis of genetic markers in Dupuytren's disease," *BMC medical genomics*, vol. 12, no. 5, pp. 1–10, 2019.

[16] E. Lee, H. Jeon, M. Lee, J. Ryu, C. Kang, S. Kim, **J. Jung**, and Y. Kwon, "Molecular origin of AuNPs-induced cytotoxicity and mechanistic study," *Scientific reports*, vol. 9, no. 1, pp. 1–13, 2019.

[17] **J. Jung**, G. W. Kim, W. Lee, C. Mok, S. H. Chung, and W. Jang, "Meta-and cross-species analyses of insulin resistance based on gene expression datasets in human white adipose tissues," *Scientific reports*, vol. 8, no. 1, pp. 1–13, 2018.

[18] H. Kim, J. Yoo, J. Shin, Y. Chang, **J. Jung**, D.-G. Jo, J. Kim, W. Jang, C. J. Lengner, B.-S. Kim, *et al.*, "Modelling APOE 3/4 allele-associated sporadic Alzheimer's disease in an induced neuron," *Brain*, vol. 140, no. 8, pp. 2193–2209, 2017.

[19] J. Yoo, E. Lee, H. Y. Kim, D.-H. Youn, **J. Jung**, H. Kim, Y. Chang, W. Lee, J. Shin, S. Baek, *et al.*, "Electromagnetized gold nanoparticles mediate direct lineage reprogramming into induced dopamine neurons in vivo for Parkinson's disease therapy," *Nature nanotechnology*, vol. 12, no. 10, pp. 1006–1014, 2017.

[20] **J. Jung**, K. Hah, W. Lee, and W. Jang, "Meta-analysis of microarray datasets for the risk assessment of coplanar polychlorinated biphenyl 77 (PCB77) on human health," *Toxicology and Environmental Health Sciences*, vol. 9, no. 2, pp. 161–168, 2017.

[21] **J. Jung**, C. Mok, W. Lee, and W. Jang, "Meta-analysis of microarray and RNA-Seq gene expression datasets for carcinogenic risk: An assessment of Bisphenol A," *Molecular & Cellular Toxicology*, vol. 13, no. 2, pp. 239–249, 2017.

[22] E. Lee, **J. Jung**, D. Jung, C. S. Mok, H. Jeon, C.-S. Park, W. Jang, and Y. Kwon, "Inhibitory effects of novel SphK2 inhibitors on migration of cancer cells," *Anti-Cancer Agents in Medicinal Chemistry (Formerly Current Medicinal Chemistry-Anti-Cancer Agents)*, vol. 17, no. 12, pp. 1689–1697, 2017.

[23] H. G. Kang, D.-H. Kim, S.-J. Kim, Y. Cho, **J. Jung**, W. Jang, and K.-H. Chun, "Galectin-3 supports stemness in ovarian cancer stem cells by activation of the Notch1 intracellular domain," *Oncotarget*, vol. 7, no. 42, p. 68229, 2016.

Conference Presentations - Oral presentation

- **J. Jung**, G.W. Kim, B. Lee, J.W.J. Joo., W. Jang. Integrative genomic and transcriptomic analysis for genetic markers in Dupuytren's disease. TBC/BIOINFO 2018. Seoul, Korea, 2018
- **J. Jung**, G.W. Kim, J.H. Park, S.H. Chung, W. Jang . Meta-analysis of insulin resistance based on gene expression datasets in human adipose tissues. The 13th international congress on obesity (ICO). Vancouver, Canada, 2016.
- G.W. Kim, **J. Jung**, H.K. Jo, K.J. Jeong, W. Jang, S.H. Chung. Elucidation of suppressive mechanism of betulinic acid on adipogenesis using global gene expression profiling. The 13th international congress on obesity (ICO). Vancouver, Canada, 2016.

Conference Presentations - Poster presentation

- Z. Zhang, **J. Jung**, N. Suboc, S. Gazal, N. Mancuso. A variational Bayesian approach to characterize pleiotropic components across thousands of human diseases and complex traits using GWAS summary statistics. ASHG, Los Angeles, CA, USA, 2022
- **J. Jung**, Z. Lu, N. Mancuso. Novel insight into the etiology of ischemic stroke gained by integrating human transcriptome-wide association study with rodent expression data. ASHG, Virtual, 2021
- Z. Zhang, **J. Jung**, N. Suboc, S. Gazal, N. Mancuso. A variational Bayesian approach to characterize latent genetic components using GWAS summary statistics. ASHG, Virtual, 2021
- Z. Lu, **J. Jung**, S. Gazal, N. Mancuso. Residual proteome-wide association study identifies genes for blood-related traits. ASHG, Virtual, 2021
- **J. Jung**, R. Brown, W. Jang, B. Pasaniuc, J.W.J. Joo and E. Eskin. GGmend: A Mendelian randomization method for finding gene-on-gene regulatory effects in the presence of unobserved confounders. 23th RECOMB, Washington, D.C., USA, 2019.
- F. Hormozdiari, **J. Jung**, E. Eskin and J.W.J. Joo. Leveraging allelic heterogeneity to increase power of association testing. 23th RECOMB, Washington, D.C., USA, 2019.

- J. Song, W. Jang, J. Jung, D.E. Kim and J.Y. Hong W. Jang. Meta-analysis of polymyositis and dermatomyositis microarray data sets. 23th RECOMB, Washington, D.C., USA, 2019.
- **J. Jung**, G.W. Kim, J.H. Park, S.H. Chung, W. Jang. Cross-species analysis reveals molecular mechanisms of insulin resistance in white adipose tissues. 12th International Conference on Toxicogenomics (ICT), Seoul, Korea, 2016.
- **J. Jung**, G.W. Kim, J.H. Park, S.H. Chung, W. Jang. Integrative cross-species analysis of insulin resistance expression profile in white adipose tissues. 9th International Conference on Environmental Health Sciences (ICoEHS), Incheon, Korea, 2016.
- **J. Jung**, J.H. Park, W. Jang. Meta-analysis of microarray gene expression datasets for silver nanoparticles. 11th International Conference on Toxicogenomics (ICT), Seoul, Korea, 2015.
- **J. Jung**, J.H. Park, W. Jang. Meta-analysis of microarray and RNA-Seq gene expression datasets for carcinogenic risk assessment of Bisphenol A. 8th International Conference on Environmental Health Sciences (ICoEHS), Incheon, Korea, 2015.
- **J. Jung**, J.H. Park, W. Jang. Meta-analysis of microarray gene expression datasets for in silico risk assessment of Bisphenol A. 6th International Conference on Environmental Health Sciences (ICoEHS), Incheon, Korea, 2013.

Patents

- Composition for diagnosing Insulin Resistance and its uses. 2018.03.21. (1020180032865)
- Diagnostic kit comprising biomarkers for bisphenol A exposure diagnosis. 2018.12.21 (1019336950000)
- Diagnostic kit comprising biomarkers for genistein exposure diagnosis. 2018.12.21 (1019336940000)
- Diagnostic kit comprising biomarkers for polychlorinated biphenyl 77 exposure diagnosis. 2018.12.21 (1019336920000)
- Genetic markers for diagnosing juvenile idiopathic arthritis and diagnosis method using these markers. 2021.09.02 (1020210116775)

Honors and Awards

- 2014 Dongguk Global Researcher Scholarship
- 13th International Conference on Toxicogenomics (ICT), Best poster, The Korea Society of Toxicogenomics and Toxicoproteomics, 2016
- 9th International Conference on Environmental Health Sciences (ICoEHS), Best poster, Society of Environmenatal Risk Assessment and Health Science, 2016
- 6th International Conference on Environmental Health Sciences (ICoEHS), Best poster, Society of Environmenatal Risk Assessment and Health Science, 2013