Hannah Kim

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Research	Interest	
DISEASE DY	NAMICS VIRAL EVOLUTION ALGORITHM DEVELOPMENT	
Educatio	n	
Temple University		Philadelphia, PA
• Advisor: Dr	RMATICS : Sergei L Kosakovsky Pond	08/2019 - 05/2024
Carnegie Mellon University		Pittsburgh, PA
MS COMPUTATIONAL BIOLOGY		08/2015 - 12/2016
Carnegie Me BS CHEMISTR	ellon University Y	Pittsburgh, PA 08/2010 - 05/2013
Relevant	Experience	
2017-2019	Bioinformatics Analyst / Software Engineer, Children's Hospital of Ph	iladelphia
2017	Research Programmer, Computational Biology Department, Carnegie	Mellon University
2016	Graduate Researcher, Computational Biology Department, Carnegie M	ellon University
2016	Course Developer, Computational Biology Department, Carnegie Mello	on University
2013-2014	Post-Baccalaureate Researcher, Department of Biological Sciences, Ca	9
2012-2013	Undergraduate Student Researcher , Department of Chemistry, Carnes	9
2011	Student Intern, Summer Research Institute, Department of Biologica	l Sciences, Carnegie Mellon University
Publicati	ons	
Dunieus		

PUBLISHED

- Ding, Y., Kim, H., Madden, K., Loftus, J., Chen, G., Allen, D., Zhang, R., Xu, J., Chen, C., Xu, Y., Tasian, S., Tan, K. (2021). Network Analysis Reveals Synergistic Genetic Dependencies for Rational Combination Therapy in Philadelphia Chromosomelike Acute Lymphoblastic Leukemia. Clinical Cancer Research. doi:10.1158/1078-0432.CCR-21-0553
- Tarca, A. L., Pataki, B. Á., Romero, R., Sirota, M., Guan, Y., Kutum, R., Gomez-Lopez, N., Done, B., Bhatti, G., Yu, T., Andreoletti, G., Chaiworapongsa, T., The DREAM Preterm Birth Prediction Challenge Consortium, Hassan, S. S., Hsu, C., Aghaeepour, N., Stolovitzky, G., Csabai, I., Costello, J. C. (2021). Crowdsourcing assessment of maternal blood multiomics for predicting gestational age and preterm birth. Cell Reports Medicine, 2(6). doi:10.1016/j.xcrm.2021.100323
- Ichikawa, Y., Bruno, V. M., Woolford, C. A., Kim, H., Do, E., Brewer, G., Mitchell, A. P. (2021). Environmentally contingent control of Candida albicans cell wall integrity by transcriptional regulator Cup9. Genetics. doi: 10.1093/genetics/iyab075
- Tao, Y., Rajaraman, A., Cui, X., Cui, Z., Chen, H., Zhao, Y., Eaton, J., Kim, H., Ma, J., Schwartz, R. (2021). Assessing the Contribution of Tumor Mutational Phenotypes to Cancer Progression Risk. PLOS Computational Biology, 17(3). doi:10.1371/journal.pcbi.1008777
- He, B., Gao, P., Ding, Y., Chen, C., Chen, G., Chen, C., Kim, H., Tasian, S. K., Hunger, S. P., Tan, K. (2020). Diverse noncoding mutations contribute to deregulation of cis-regulatory landscape in pediatric cancers. Science Advances, 6(30). doi:10.1126/sciadv.aba3064

Lin, C., Jain, S., **Kim, H.**, Bar-Joseph, Z. (2017). Using neural networks for reducing the dimensions of single-cell RNA-Seq data. *Nucleic Acids Research*, 45(17). doi:10.1093/nar/gkx681

PREPRINT

Tao, Y., Rajaraman, A., Cui, X., Cui, Z., Eaton, J., **Kim, H.**, Ma, J., Schwartz, R. (2019). Improving personalized prediction of cancer prognoses with clonal evolution models. *bioRxiv*. doi:10.1101/761510

Presentations _____

CONTRIBUTED PRESENTATIONS

Hu, Y., Chen, C., Ding, Y.*, **Kim, H.**, Tan, K. (2019). Synergistic Control Genes in Cancer Gene Networks as Targets for Combination Therapy. Poster: Children's Hospital of Philadelphia Research Poster day and Scientific Symposium, Philadelphia, PA.

Awards, Fellowships, & Grants _____

2015	Departmental Merit Fellowship, Carnegie Mellon University	\$ 3000
2015	Departmental Merit Fellowship, Carnegie Mellon University	\$ 3000

2013 Mellon College of Science Research Honors, Carnegie Mellon University

2012 Summer Undergraduate Research Fellowship, Carnegie Mellon University \$ 3500

Teaching Experience _____

^{*} awarded Research Assistantship unless otherwise noted

F2020 BIOL-3111/5111 Genomics in Medicine, Teaching Assistar	F2020	BIOL-3111	/5111 Genor	nics in Me	dicine. 1	Teaching Assistan
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S2020 BIOL-1012 General Biology II, Teaching Assistant

F2019 BIOL-2112 Introduction to Cellular and Molecular Biology, Teaching Assistant

Doctoral Coursework _____

F2020	BIOI -5128 Genomics and Infectious Disease Dynamics
トノロノロ	BIOL-5178 Genomics and Intectious Disease Dynamics

F2020 BIOL-8210 Seminar: "Ecoevo discuss"

Coding Languages _____

PYTHON, R, MATLAB, BASH, JAVASCRIPT, GOLANG

^{*} presenting author

F2020 STAT-8109 Applied Statistics and Data Science

S2020 BIOL-5241 Genomics and Evolutionary Biology of Parasites

S2020 CIS-5517 Data-Intensive and Cloud Computing

S2020 CIS-5523 Knowledge Discovery and Data Mining

F2019 BIOL-5111 Genomics in Medicine

F2019 BIOL-5466 Topics in Bioinformatics

F2019 BIOL-8210 Seminar Biol 8210 at Center for Computational Genetics and Genomics