

Hanan I. Salim

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Education

Pennsylvania State University

B.S. in Mathematics

University Park, PA

August 2015 - May 2019

University of Cincinnati

Non-degree seeking student

Cincinnati, OH

August 2020 - December 2021

Research

Cincinnati Children's Hospital Medical Center

Research Assistant, Drs. John Harley & Ken Kaufman

Cincinnati, OH

January 2020 -

- Led the development and implementation of VirScan statistical pipeline
- Performed topological data analysis on VirScan data consisting of ~400k peptides across ~5k proteins and experimented with statistical inference
- Developed pipeline to perform permutation tests on whole exome sequencing data with over 200k samples to determine rare variants among systemic lupus erythematosus patients
- Performed quantitative trait locus(QTL) analysis on ~180k variants to determine loci associated with the number of nephrons in mice
- Contributed to writing grants and manuscripts
- Supported the planning and analysis of Regulatory Element Locus Intersection(RELI) projects, created visualizations
- Collaborated with an interdisciplinary group of researchers and provided computational support
- Conducted differential expression analysis of Affymetrix microarray data
- Performed quality control and clustering of scRNA-seq data
- Performed large scale genomics analysis on WGS, WES, scRNA-seq, Microarray, and VirScan data; including quality control, downstream analysis and result visualization
- Wrote scripts in bash and R; delegated jobs to high performance computing cluster via LSF

Pennsylvania State University

Research Assistant, Dr. Jasna Kovac

University Park, PA

September 2018 - May 2019

- Analyzed microbiome data to detect pathogens in water supply
- Wrote R scripts to extrapolate rarefaction curves and visualize results

Pennsylvania State University

Research Assistant, Dr. Katerina Makova

University Park, PA

June 2018 - Aug 2018

- Developed pipelines to compute codon indices, calculate percentage of GC-content, and create visualizations
- Applied statistical models using Python to determine whether codon bias exists in the human mitochondrial genome
- Performed quality control on sequence data
- Aligned sequences to detect mutations and conducted path analysis

Teaching and Outreach

Huntington Learning Center

Math and Science Tutor

Cincinnati, OH

March 2020 -

- Teacher of the Month: November 2020
- Tutored students in Calculus, Algebra, Statistics, Physics, and standardized tests such as SAT, ACT, HSCPT, and IOWA exam

Mathematical Masti

- o Developed a static website using HTML/CSS
- o Wrote expository notes to explore ideas in mathematics and their connections to computational biology

Huntington Learning Center

Math and Science Tutor

- o Tutored students in the SAT and ACT

Harrisburg, PA

October 2019 - December 2019

Publications

- [1] Viktoryia Laurynenka, Sreeja Parameswaran, Craig Slusher, **Hanan Salim**, Baldwin Liu, Xiaoting Chen, Jonh Harley, Kenneth Kaufman1, Matthew T. Weirauch, and Leah Kottyan. “Interaction of EBV-encoded transcription factors with chronic lymphocytic leukemia risk loci as a possible genetic mechanism in pathogenesis of the disease”. *In Preparation*.
- [2] Hillarey K. Stone, **Hanan Salim**, Xiaoming Lu, Matthew T. Weirauch, Leah Kottyan, and Russell P. Sawyer. “Frontotemporal Degeneration Genetic Risk Loci and Transcription Regulation as a Possible Mechanistic Link to Disease Risk”. *In Preparation*.
- [3] Hillarey K. Stone, **Hanan Salim**, Sreeja Parameswaran, Xiaoting Chen, Mario Pujato, Prasad Devarajan, Matthew T. Weirauch, and Leah Kottyan. “Altered transcription factor binding in IgA nephropathy: The missing link between genetic variant and disease pathogenesis?” *In Preparation*.
- [4] Xianyong Yin, Kwangwoo Kim, Hiroyuki Suetsugu, So-Young Bang, Leilei Wen, Masaru Koido, Eunji Ha, Lu Liu, Yuma Sakamoto, Sungsin Jo, Rui-Xue Leng, Nao Otomo, Viktoryia Laurynenka, Young-Chang Kwon, Yujun Sheng, Nobuhiko Sugano, Mi Yeong Hwang, Weiran Li, Masaya Mukai, Kyunghoon Yoon, Minglong Cai, Kazuyoshi Ishigaki, Won Tae Chung, He Huang, Daisuke Takahashi, Shin-Seok Lee, Mengwei Wang, Kohei Karino, Seung-Cheol Shim, Xiaodong Zheng, Tomoya Miyamura, Young Mo Kang, Dongqing Ye, Junichi Nakamura, Chang-Hee Suh, Yuanjia Tang, Goro Motomura, Yong-Beom Park, Huihua Ding, Takeshi Kuroda, Jung-Yoon Choe, Chengxu Li, Hiroaki Niuro, Youngho Park, Changbing Shen, Takeshi Miyamoto, Ga-Young Ahn, Wenmin Fei, Tsutomu Takeuchi, Jung-Min Shin, Keke Li, Yasushi Kawaguchi, Yeon-Kyung Lee, Yongfei Wang, Koichi Amano, Dae Jin Park, Wanling Yang, Yoshifumi Tada, Ken Yamaji, Masato Shimizu, Takashi Atsumi, Akari Suzuki, Takayuki Sumida, Yukinori Okada, Koichi Matsuda, Keitaro Matsuo, Yuta Kochi, Leah C Kottyan, Matthew T Weirauch, Sreeja Parameswaran, Shruti Eswar, **Hanan Salim**, Xiaoting Chen, Kazuhiko Yamamoto, John B Harley, Koichiro Ohmura, Tae-Hwan Kim, Sen Yang, Takuaki Yamamoto, Bong-Jo Kim, Nan Shen, Shiro Ikegawa, Hye-Soon Lee, Xuejun Zhang, Chikashi Terao, Yong Cui, and Sang-Cheol Bae. “Meta-analysis of 208370 East Asians identifies 113 susceptibility loci for systemic lupus erythematosus”. In: *Annals of the Rheumatic Diseases* 80.5 (2021), pp. 632–640. ISSN: 0003-4967. DOI: 10.1136/annrheumdis-2020-219209. eprint: <https://ard.bmj.com/content/80/5/632.full.pdf>. URL: <https://ard.bmj.com/content/80/5/632>.

Additional

- Programming Languages & Tools: Python, R, Julia, Bash, Excel, L^AT_EX, HTML/CSS, Unix
- Bioinformatics Tools: Bamtools, Samtools, VCFtools, Plink, Bedtools, BWA, Cutadapt
- Graduate Coursework:
 - **Mathematics:** Algebraic Number Theory, Topology
 - **Computational Biology:** Computational Systems Biology, Statistical Genetics
- Undergraduate Coursework:
 - **Mathematics** - Linear Algebra, Combinatorics, Real Analysis, Mathematical Coding Theory, Calculus, Differential Equations
 - **Computer Science** - Numerical Analysis, Data Structures and Algorithms, Linear Programming
 - **Biology** - Molecular Biology, Molecular Evolution, Physiology
- Languages: English, Punjabi, and Urdu