Curriculum Vitae
Natalia Rincon

Position: PhD Candidate
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EDUCATION

09/2020 - Present
Ph.D. in Biomedical Engineering, Johns Hopkins University, Baltimore, MD.
Thesis Advisor: Professor Jeffrey Gray
Relevant course work: Learning, Estimation and Control; Machine Learning; Immunology; Immunology/Infectious Disease

09/2014 - 05/2019
Bachelors of Science in Chemical and Biomolecular Engineering from Johns Hopkins University, Baltimore, MD.
Relevant course work: Calculus III; Differential Equations; Linear Algebra; Dynamic Modeling and Control; Probability and statistics; Transport I and II; Thermodynamics; Data Structures; Computer Graphics; Parallel Programming

HONORS AND SERVICES

Honors

- 2020-2021 NIH/NIGMS Pre-Doctoral Training Program in Computational Medicine, CMT32
- 2018 Vredenburg Travel Grant Recipient

Services

- 2023-2024 Executive Board member, Women of Whiting, Johns Hopkins University
- 2023-2024 Young Women in Biology Ambassador, Women in Bio National Organization
- 2022-2024 Passport to Future Technology Leadership (PTFL) program, Johns Hopkins University
- 2021-2023 Biomedical Engineering Graduate Student Mentor, Johns Hopkins Medicine
- 2021-2023 Second Look PhD Recruit volunteer, Johns Hopkins University
- 2020-2023 Science in Action program volunteer, Johns Hopkins Medicine

PUBLICATIONS

FIRST AUTHORED, PEER-REVIEWED PUBLICATIONS

N. Rincon, J. Lu, D. E. Wood, F. P. Breitwieser, C. Pockrandt, B. Langmead, S. L. Salzberg, M. Steinegger. (2022) "Metagenome analysis using the Kraken software suite" *Nature Protocols.* https://doi.org/10.1038/s41596-022-00738-y

CO-AUTHORED, PEER-REVIEWED PUBLICATIONS

A Varabyou, M.J. Sommer, B. Ergdogdu, I. Shinder, I. Minkin, K. Chao,S. Park, J. Heinz, C. Pockrandt, A. Shumate, **N. Rincon** et al. (2023) "CHESS 3: an improved, comprehensive catalog of human genes and transcripts based on large-scale expression data, phylogenetic analysis, and protein structure" *Genome Biol,* https://doi.org/10.1186/s13059-023-03088-4

M.J. Sommer, S. Cha, A. Varabyou, **N. Rincon**, S Park, et al. (2022) "Highly accurate isoform identification for the human transcriptome" *eLife,* https://doi.org/10.7554/eLife.82556

A.S. Shifera, C. Pockrandt, **N. Rincon**, Y. Ge, J. Lu, A. Varabyou, et al. (2021) "Identification of microbial agents in tissue specimens of ocular and periocular sarcoidosis using a metagenomics approach" *F1000Research*, https://doi.org/10.12688/f1000research.55090.1

K. Fujikura, W. Hosoda, M. Felsenstein, Q. Song, J.G. Reiter, L. Zheng, V.B. Guthrie, **N. Rincon**, M.D. Molin, et al. (2021) "Multiregion whole-exome sequencing of intraductal papillary mucinous neoplasms reveals frequent somatic KLF4 mutations predominantly in low-grade regions" *Gut*, 70:928-939.

RESEARCH EXPERIENCE

05/2024 – Present
PhD Researcher in the Data Science and Artificial Intelligence Institute for Dr. Jeffrey Gray at Johns Hopkins University, Baltimore, MD.
- Benchmarking antibody language models by comparing synthetic sequences to natural ones to assess biological realism. Characterized gene usage discrepancies between natural and IgLM-generated antibody sequences, identifying key areas for model improvement (manuscript underway).
- Developing an annotated dataset to support the generation of task-specific antibody sequences with the aim of enabling tissue-, disease-, and isotype-specific design. Find more details in the submitted personal statement.

07/2023 — 05/2024
PhD Researcher in the Infectious Disease Dynamics Group for Dr. Alison Hill at Johns Hopkins University, Baltimore, MD.
- Developed a viral dynamics model incorporating the pharmacokinetics/pharmacodynamics of the trispecific antibody SAR441236, capturing infection set points, treatment response, viral rebound, and latent cell dynamics.

09/2020 – 07/2023
PhD Researcher in the Center for Computational Biology for Dr. Steven Salzberg at Johns Hopkins University, Baltimore, MD.
- Using evolutionary conservation (dn/ds ratio) as way to improve bacterial gene annotation by removing hypothetical genes, moving annotated start codons and removing short genes that are not conserved within a genus.
- Identified potential microbial pathogens for a cohort of human tissue samples isolated from patients with ocular sarcoidosis leading to improved understanding of the disease.
- Executed and designed the microbiome analysis protocol and implemented the alpha diversity script as part of the KrakenTools suite for post-analysis of Kraken/KrakenUniq/Kraken2/Bracken results.
- Folded, visualized and annotated protein structures using ColabFold and PyMol to show how protein structure can provide additional insight when determining if a transcript is functional.

09/2019 — 05/2020
Student Researcher in the Institute for Computational Medicine for Dr. Rachel Karchin at Johns Hopkins University, Baltimore, MD.
- Worked on a pilot study using the Facets copy number analysis tool on pancreatic intraepithelial neoplasia whole-exome sequencing data to identify differences in loss of heterozygosity between samples at varying degrees of neoplasia.

05/2018 — 08/2018
Student Intern for Dr. Peter Neri's Laboratoire des Systemes Perseptifs at Ecole Normale Superieure, Paris, France.
- Conducted 30,000+ static visual trials to analyze stimulus-based responses, modeling how participants weighted probe orientations after a brief 0.01-second exposure.
- Implemented a vision experiment using the CamVid dataset, placing a Gabor wavelet in frames with object edges or high-motion edges to assess their impact on participants' ability to distinguish probe orientation.
- Implemented a motion energy detector in Python to find the max/min motion and direction of motion in each video for probe insertion