

NOOR YOUSSEF

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Harvard Medical School ◊ Broad Institute of Harvard and MIT

nooryoussef.github.io

I develop statistical and machine learning models, grounded in biological insight, to (1) *Forecast* immune evasion in high-pandemic risk viruses to inform public health strategies, (2) *Design* vaccines and therapeutics to enhance protection and minimize viral escape, and (3) *Discover* patterns and processes in viral evolution that drive long-term immune evasion, aiding the development of more robust interventions.

EMPLOYMENT

Scientific lead, Predictive Modeling for Vaccine Design

March 2023 - Present

Harvard Medical School

Advisor: Debora Marks, Dept. Systems Biology

Machine Learning Postdoctoral Fellow

Sept 2021 - March 2023

Harvard Medical School

Advisor: Debora Marks, Dept. Systems Biology

EDUCATION

PhD, Computational Biology

2015 - 2021

Dalhousie University

Title: Evolutionary dynamics under a stability-constrained model

Advisor: Dr. Joseph Bielawski, Dept. Biology and Dept. Mathematics & Statistics

Advisor: Dr. Edward Susko, Dept. Mathematics & Statistics

BSc, Combined Honours in Mathematics & Biology

2011 - 2015

Dalhousie University

Title: Addressing the Impacts of Non-stationary Evolution on Selection Pressure Inference.

First Class Honours

PUBLICATIONS

First author: 7, Second author: 4, Corresponding author: 4

Equal contribution*, Corresponding^c

14. **Youssef N**, Gurev S, Ghantous F, Brock K, Jaimes JA, Dauphin A, Yurkovetskiy L, Soto D, Estanboulieh R, Kotzen B, Bosso M, Lemieux J^c, Luban J^c, Seaman MS^c, Marks DS^c. (2023). Protein design for evaluating vaccines against future viral variation *bioRxiv*. 10.08.561389. Under review in *Cell*.

13. Yu Y, Kass MA, Zhang M, **Youssef N**, Freije CA, Brock KP, Seifert LL, Venkittu S, Hong X, Shlomai A, de Jong YP, Marks DS, Rice CM^c, Schneider WM^c (2024). Deep mutational scanning of HBV reveals a mechanism for *cis*-preferential reverse transcription. *Cell*, 187: 2735-2745.

12. **Youssef N***, Gurev S*, Pierce-Hoffman H, Cohen AA, Caldera LF, Bjorkman PJ, Marks DS (2024). Future-proof vaccine design with a generative model of antibody cross-reactivity. *ICML Workshop Machine Learning for Life and Material Science: From Theory to Industry Applications*.

11. Gurev S*, **Youssef N*** Pierce-Hoffman H, Marks DS (2024). Future-proof vaccine design with a generative model of antibody cross-reactivity. *ICLR Workshop on Generative and Experimental Perspectives for Biomolecular Design*.
10. Thadani NT*, Gurev S*, Notin P*, **Youssef N**, Rollins NJ, Sander C A, Gal Y, and Marks D^c (2023). Learning from pre-pandemic data to forecast viral antibody escape. *Nature*, 622: 818–825.
9. **Youssef N^c**, Susko E, Roger A, and Bielawski JP (2022). Evolution of amino acid propensities under stability-mediated epistasis. *Molecular Biology and Evolution*, 39(3): msac030.
8. **Youssef N^c**, Susko E, Roger A, and Bielawski JP (2021). Shifts in amino acid preferences as proteins evolve: a synthesis of experimental and theoretical work. *Protein Science*, 30(10): 2009–2028.
7. Stewart DT, Robicheau BM, **Youssef N**, Garrido-Ramos MA, Chase EE, and Breton S^c (2021). Expanding the search for sperm transmission elements in the mitochondrial genomes of bivalve mollusks. *Genes*, 12(8): 1211.
6. **Youssef N^c**, Susko E, and Bielawski JP (2020). Consequences of stability-induced epistasis for substitution rates. *Molecular Biology and Evolution*. 37(11): 3131–3148.
5. Jones CT^c, **Youssef N**, Susko E, and Bielawski JP (2020). A Phenotype–Genotype Codon Model for Detecting Adaptive Evolution. *Systematic Biology*, 69(4): 722–738.
4. Stewart DT^c, Breton S, Chase EE, Robicheau BM, Bettinazzi S, Pante E, **Youssef N**, and Garrido-Ramos MA (2020). An unusual evolutionary strategy: the origins, genetic repertoire, and implications of doubly uniparental inheritance of mitochondrial DNA in bivalves. In: Pontarotti P (eds) Evolutionary Biology—A Transdisciplinary Approach. *Springer, Cham*.
3. **Youssef N^c**, Budd A, and Bielawski JP (2019). Introduction to genome biology and diversity. In: Anisimova M. (eds) Evolutionary Genomics. Methods in Molecular Biology, vol 1910. *Humana, New York, NY*.
2. Jones CT^c, **Youssef N**, Susko E, and Bielawski JP (2018). Phenomenological load on model parameters can lead to false biological conclusions. *Molecular Biology and Evolution*, 35: 1473–1488.
1. Jones CT^c, **Youssef N**, Susko E, and Bielawski JP (2017). Shifting balance on a static mutation-selection landscape: a novel scenario of positive selection. *Molecular Biology and Evolution*, 34: 391–407.

INVITED SEMINARS

Learning from evolution to future-proof vaccines *Institute of Comparative Genomics (ICG)*. NS, Canada. Aug, 2024.

Protein design for future proof vaccines. *Centre for Genomic Regulation (CRG)*. Barcelona, Spain. Mar, 2024.

Unsupervised viral antibody escape prediction for future proof vaccines. *Models, Inference and Algorithms (MIA)*. MA, USA. Feb, 2024. [Video](#).

Sequence models for fitness effect predictions. *Andean School on host-pathogen dynamics*. Bogotá, Colombia. Jan, 2024.

Using the past to predict the future: Deep learning for early warning, design and test future-proof therapeutics. *Andean School on host-pathogen dynamics*. Bogotá, Colombia. Jan, 2024.

Unsupervised early warning of viral antibody escape to design and test variant-proof therapeutics. *Boston Protein Design and Modeling Club*. MA, USA. Jan, 2024. [Video](#).

Predicting viral antibody escape: An integrated computational and experimental approach. *Dept. Systems Biology, Harvard Medical School.* MA, USA. Mar, 2023.

FUNDING

Learning to predict and design proteins with deep generative models 2024-2025

Award: \$100,000 USD

Contribution: Co-principal Investigator.

Funder: Dean's Innovation Award, Harvard Medical School

AI-aided Immunogen Design of H5N1 Virus for Pandemic Preparedness 2024-2025

Award: \$942,145 USD

Contribution: Co-author and named senior personnel.

Funder: Coalition for Epidemic Preparedness Innovations (CEPI)

Iterative computational modeling and assays for infectivity and antibody neutralization to predict SARS-CoV-2 potential for vaccine escape 2023-2027

Award: \$8,072,687 USD

Contribution: Co-author and named senior personnel.

Funder: Coalition for Epidemic Preparedness Innovations (CEPI)

Computational predictive modelling for the assessment of vaccine escape potential of SARS-CoV-2 variants 2022-2023

Contribution: Co-author and named senior personnel.

Award: \$1,266,693 USD

Funder: Coalition for Epidemic Preparedness Innovations (CEPI)

Graduate Student Conference Travel Grant 2017

Award: \$500 CAD

Funder: Center for Comparative Genomics and Evolutionary Bioinformatics

Graduate Student Conference Travel Grant 2017

Award: \$100 CAD

Funder: Dalhousie Association of Graduate Students, Dalhousie University

Graduate Student Fellowship 2015-2019

Award: \$6,000 CAD

Funder: Dept. of Biology, Dalhousie University

Entrance Scholarship for Academic Excellence 2011 - 2015

Award: \$20,000 CAD

Funder: Faculty of Science, Dalhousie University

CONFERENCE TALKS

Deep generative model foreshadows SARS-CoV-2 evolution and facilitates early vaccine evaluation. *American Society for Virology.* OH, USA. June, 2024.

Forecasting viral escape from neutralizing antibodies using machine learning, *World Vaccine Congress.* DC, USA. Nov, 2023.

Implications of Epistasis on Protein Evolution: A Thermodynamically Guided Walk Through Sequence Space. *Lett Research Symposium.* NS, Canada. March, 2019.

The implied differences in evolutionary dynamics between intragenic epistasis and site-independence modelling *Lett Research Symposium.* NS, Canada. March, 2018.

Assessing methods for detecting adaptive peak shifts from comparative codon data. *Lett Research Symposium*. NS, Canada. March, 2016.

Codon Substitution Models are ill-equipped to deal with non-stationary evolution. *Lett Research Symposium*. NS, Canada. March, 2015.

Analysis of the *Prochlorococcus* *cpeβ* gene to determine the effects of non-stationary evolution on the inference of selection pressure. *Cameron Conference*. NS, Canada. Feb, 2015.

CONFERENCE POSTERS

Deep generative model for forecasting antibody escape and proactive assessment of vaccines and therapeutics *Broad Institute of MIT and Harvard*. MA, USA. Dec, 2023.

Design and testing of variant-proof vaccines from machine learning models on pre-pandemic data *Vaccine Summit*. MA, USA. Nov, 2023.

Learning from pre-pandemic data to design and test variant-proof vaccines *Molecular Machine Learning Conference* MA, USA. Nov, 2023.

Consequences of stability-induced epistasis on theoretical and inferred substitution rates. *SMBE*. QC, Canada. June, 2020.

AWARDS

Gray-Doolittle Award for Research Excellence 2022
Institute of Comparative Genomics (ICG)

Award for Best Presentation in Symposium 2019
12th Annual Dr. Patrick Lett Research Symposium.

Award for Best Session Presentation 2019
12th Annual Dr. Patrick Lett Research Symposium.

Featured Scientist 2018 - 2019
Center for Comparative Genomics and Evolutionary Bioinformatics

Featured Scientist in-lecture interview 2019
Cell Biology

TEACHING EXPERIENCE

Co-Creator and Instructor Oct 2022 - Sept 2023
Course: Calling Baloney - The Art of Questioning Data
Nashua Street Jail, The Educational Justice Institute, MIT.

Teaching Assistant April 2022 - May 2022
Course: Introduction to Computation and Programming Using Python
The Educational Justice Institute, MIT.

Tutorial Instructor Sept 2016 - May 2020
Course: Genetics
Second Year Undergraduate Course, Dalhousie University.

Guest Lecturer Sept 2017 - May 2019
Course: Genetics
Second Year Undergraduate Course, Dalhousie University.

Creator and Instructor	<i>Jan 2018 - May 2018</i>
Course: Inference of natural selection pressure in protein coding DNA sequences <i>Graduate-Level Course, Dalhousie University.</i>	
Guest Lecturer	<i>Sept 2017 - Dec 2017</i>
Course: Molecular Evolution <i>Third Year Undergraduate Course, Dalhousie University.</i>	
Lab Teaching Assistant	<i>Sept 2015 - May 2016</i>
Course: Genetics <i>Second Year Undergraduate Course, Dalhousie University.</i>	
Lab Teaching Assistant	<i>Sept 2012 - May 2013</i>
Course: General Chemistry <i>First Year Undergraduate Course, Saint Mary's University.</i>	

ACADEMIC SERVICE

Journal Reviews

Nature Communications, Nature Machine Intelligence, Molecular Biology and Evolution, Royal Society, Genome Biology and Evolution, Journal of Molecular Evolution, BMC Evolutionary Biology

Organiser, Evolution and Philosophy Discussion Group	<i>2018 - 2020</i>
<i>Dalhousie University</i>	

Search Committee for the Jarislowsky Chair in Marine Ecosystem Forecasting	<i>2019</i>
<i>Dalhousie University</i>	

Vice-President	<i>2019 - 2020</i>
<i>Biology Organization of Graduate Students, Dalhousie University</i>	

Social Coordinator	<i>2019 - 2020</i>
<i>Biology Organization of Graduate Students, Dalhousie University</i>	

Volunteer, Lett Symposium	<i>2016- 2018</i>
<i>Dalhousie University</i>	

Treasurer	<i>2016 - 2017</i>
<i>Biology Organization of Graduate Students, Dalhousie University</i>	

MENTORSHIP

PhD Students

Sarah Gurev, Massachusetts Institute of Technology (MIT)
Tomas Lio Grudny, Massachusetts Institute of Technology (MIT)
Ralph Estantboulieh (MD-PhD), Harvard Medical School
Abigail Jackson, Harvard Medical School

Masters Students

Hannah Pierce-Hoffman, Harvard Medical School

Research Associates

Daniel Ritter, Harvard Medical School
Ben Kotzen, Massachusetts General Hospital

Undergraduate Students

Sahil Sood, Harvard University
Omolivie Eboreime, Harvard University

Sage Widder, Wellesley College
Seojean Kim, Wellesley College
Steven Nguyen, Dalhousie University

WORKSHOPS AND RELEVANT COURSEWORK

Workshops:

Parallel Computing Summer Workshop. Compute Canada. 2020.
Programming Numerical Methods in Python. Udemy. 2020.
Synchronous Teaching workshop. The Centre for Learning and Teaching, Dalhousie University. 2020.
Darwinizing Gaia. Institute of Comparative Genomics (ICG), Dalhousie University. 2019.
Philosophy of Biology Workshop. Dalhousie University. 2018.
Evolutionary Roles of Transposable Elements and ‘non-coding’ DNA: the Science and the Philosophy. Dalhousie University. 2018.

Graduate Courses:

Stochastic Processes. Bioinformatics. Algorithms in Bioinformatics. Communication Skills-Scientist.

Biology Undergraduate Courses:

Evolution. Genetics. Molecular Evolution.

Mathematics Undergraduate Courses:

Matrix Theory/Linear Algebra (I and II). Cryptography. Theory of Numbers. Game Theory.

PROGRAMMING SKILLS

◦ Python ◦ R ◦ Matlab ◦ Shell ◦ L^AT_EX

STUDENT COMMENTS

Teaching Evaluations from 2nd-year Genetics Tutorial

2016 - 2020

“The best TA I have had in university. She explained things extremely clearly and offered different approaches to problems. Attending this tutorial with Noor was a critical part of doing well in this course and grasping material.”

“Noor was amazing! So knowledgeable on the subject, amazing at explaining everything. I can really tell that the subject matter really resonates with Noor. Great at answering questions and checking in if we all understand. Very personable and approachable”

“Noor was clearly very well prepared for each genetics tutorial. She would make a really great professor or lab instructor one day!”

“Noor was very knowledgeable and I was impressed with how prepared she was for tutorial every week and really taught the material well. I did a lot better on the quizzes because of how well Noor could explain the subject.”

“I was lucky to have such an awesome and helpful TA!”

REFERENCES

Dr. Joseph Bielawski

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Department of Biology

Department of Mathematics & Statistics

Dalhousie University

Dr. Edward Susko

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Department of Mathematics & Statistics

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Harvard Medical School

Broad Institute of Harvard and MIT

Dr. Andrew Roger

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Department of Biochemistry & Molecular Biology

Dalhousie University