

NOOR YOUSSEF

Harvard Medical School ◊ Broad Institute of Harvard and MIT

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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: 5, Second author: 4, Corresponding author: 4

Equal contribution*, Corresponding^c

12. **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. (2025). Computationally designed proteins mimic antibody immune evasion in viral evolution. *Immunity*, 58: 1–11.

11. 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.

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.

MACHINE LEARNING WORKSHOP PAPERS

4. Gurev S^{*c}, **Youssef N**^{*c}, Marks DS^c (2024). Alignment-based and protein foundation models for viral evolution, vaccines and vectors. *NeurIPS Workshop Artificial Intelligence for New Drug Modalities (AI4Drug)*.
3. **Youssef N**^{*c}, Gurev S^{*c}, Marks DS^c (2024). Tradeoffs of alignment-based and protein language models for predicting viral mutation effects. *NeurIPS Workshop Machine Learning for Structural Biology (MLSB)*.
2. **Youssef N**^{*c}, Gurev S^{*c}, Pierce-Hoffman H, Cohen AA, Caldera LF, Bjorkman PJ, Marks DS^c (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 (ML4LMS)*.
1. Gurev S^{*c}, **Youssef N**^{*c}, Pierce-Hoffman H, Marks DS^c (2024). Future-proof vaccine design with a generative model of antibody cross-reactivity. *ICLR Workshop on Generative and Experimental Perspectives for Biomolecular Design (GenBio)*.

INVITED NATIONAL AND INTERNATIONAL SEMINARS

Future-proof vaccines using generative AI models Co-sponsored Dept. Biochemistry & Molecular Biology and Dept. Microbiology & Immunology at Dalhousie University NS, Canada. Oct, 2024.

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

Unsupervised generative model of viral antibody escape for the design and testing of variant-proof vaccines *Virus Genomics, Evolution and Bioinformatics*. Cambridge, UK. Nov, 2024.

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 <i>Institute of Comparative Genomics (ICG)</i>	2022
Award for Best Presentation in Symposium <i>12th Annual Dr. Patrick Lett Research Symposium.</i>	2019
Award for Best Session Presentation <i>12th Annual Dr. Patrick Lett Research Symposium.</i>	2019
Featured Scientist <i>Center for Comparative Genomics and Evolutionary Bioinformatics</i>	2018 - 2019
Featured Scientist in-lecture interview <i>Cell Biology</i>	2019

TEACHING EXPERIENCE

Co-Creator and Instructor Course: Calling Baloney - The Art of Questioning Data <i>Sufflock County Jail, The Educational Justice Institute (TEJI), MIT.</i>	Oct 2022 - Present
Co-Creator and Instructor Course: Summer Antibody and Viral Initiative (SAVI) Workshop <i>Harvard Medical School</i>	July 2024 - Sept 2024
Teaching Assistant Course: Introduction to Computation and Programming Using Python <i>The Educational Justice Institute (TEJI), MIT.</i>	April 2022 - May 2022
Tutorial Instructor Course: Genetics <i>Second Year Undergraduate Course, Dalhousie University.</i>	Sept 2016 - May 2020
Guest Lecturer Course: Genetics <i>Second Year Undergraduate Course, Dalhousie University.</i>	Sept 2017 - May 2019
Creator and Instructor Course: Inference of natural selection pressure in protein coding DNA sequences <i>Graduate-Level Course, Dalhousie University.</i>	Jan 2018 - May 2018
Guest Lecturer Course: Molecular Evolution <i>Third Year Undergraduate Course, Dalhousie University.</i>	Sept 2017 - Dec 2017
Lab Teaching Assistant Course: Genetics <i>Second Year Undergraduate Course, Dalhousie University.</i>	Sept 2015 - May 2016
Lab Teaching Assistant Course: General Chemistry <i>First Year Undergraduate Course, Saint Mary's University.</i>	Sept 2012 - May 2013

ACADEMIC SERVICE

Journal Reviews PNAS, 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	2018 - 2020

Dalhousie University

Search Committee for the Jarislowsky Chair in Marine Ecosystem Forecasting

2019

Dalhousie University

Vice-President

2019 - 2020

Biology Organization of Graduate Students, Dalhousie University

Social Coordinator

2019 - 2020

Biology Organization of Graduate Students, Dalhousie University

Volunteer, Lett Symposium

2016- 2018

Dalhousie University

Treasurer

2016 - 2017

Biology Organization of Graduate Students, Dalhousie University

MENTORSHIP

PhD Students

Tomas Lio Grudny, Massachusetts Institute of Technology (MIT)

2024 - Present

Fiona Qu, Harvard Medical School

2024 - Present

Abigail Jackson, Harvard Medical School

2023 - Present

Sarah Gurev, Massachusetts Institute of Technology (MIT)

2022 - Present

Ralph Estantbouli (MD-PhD), Harvard Medical School

2022 - 2023

Masters Students

Hannah Pierce-Hoffman, Harvard Medical School

2023 - 2024

Research Associates

Daniel Ritter, Harvard Medical School

2022 - 2024

Ben Kotzen, Massachusetts General Hospital

2022 - Present

Undergraduate Students

Aarushi Mehrotra, Massachusetts Institute of Technology (MIT)

2024 - Present

Seojean Kim, Wellesley College

2024 - Present

Hailey Pan, Massachusetts Institute of Technology (MIT)

2024

Sahil Sood, Harvard University

2024

Omolvie Eboreime, Harvard University

2024

Sage Widder, Wellesley College

2024

Steven Nguyen, Dalhousie University

2018

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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Dr. Debora Marks

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