

ROHAN MEHTA

(949)293-5566 ♦ rohan.sushrut.mehta@emory.edu

EDUCATION AND POSITIONS

Emory University	01/2019-Present
Postdoctoral Researcher (Advisor: Daniel Weissman)	
Stanford University	09/2013-01/2019
PhD in Biology (Advisor: Noah Rosenberg)	Karlin Prize
Thesis: Mathematical modeling of genetic and cultural traits	
University of California, San Diego	09/2009-06/2013
B.S. in Biology	Honors
B.S. in Mathematics	
Visiting Researcher, University of Canterbury (with Mike Steel)	09/2018-11/2018
Complex Systems Summer School, Santa Fe Institute	06/2014-07/2014

GRANTS AND FELLOWSHIPS

XSEDE Startup Allocation (\$1,157.50)	12/2020 - 12/2021
Graduate Fellowship, Center for Computational, Evolutionary, and Human Genomics, Stanford University	09/2017 - 09/2018
Eco-Evo Travel Grant, Department of Biology, Stanford University	2017, 2018
David and Lucile Packard Foundation Fellowship	09/2014 - 09/2017
EDGE (Educating and Developing Workers for the Green Economy) Internship	Spring 2012
Regents Scholarship, University of California, San Diego	09/2009-06/2013

HONORS AND ACHIEVEMENTS

Best Postdoc Talk, Southeastern Population Ecology and Evolutionary Genetics Conference	10/2020
Samuel Karlin Prize in Mathematical Biology, Stanford University	06/2019
Best Video, Complexity Challenge, Santa Fe Institute	Spring 2018
Honorable Mention, Complexity Challenge, Santa Fe Institute	Fall 2017, Spring 2018
Excellence in Teaching Award, Department of Biology, Stanford University	Spring 2015
Honorable Mention, Graduate Research Fellowship Program, National Science Foundation	02/2014
Phi Beta Kappa, University of California, San Diego	06/2012

INVITED OR SELECTED TALKS

Gordon Research Seminar, Predator-Prey Interactions: <i>Eco-evolutionary dynamics of autotomy</i> .	10/2022
Omicron Seminar Series, California State University, Chico: <i>50 Shades of Greenbeard: Robust evolution of altruism based on similarity of complex phenotypes</i> .	09/2022
Rising Stars in Genetics and Genomics, University of Utah: <i>Detecting patterns of accessory genome coevolution in bacterial species using data from thousands of bacterial genomes</i> .	05/2022
Ecology and Evolution of Infectious Disease group, University of California, Berkeley: <i>Modelling anti-vaccine sentiment as a cultural pathogen</i> .	09/2020

CONTRIBUTED PRESENTATIONS

Talk for BIRS-CMO, Online: <i>Detecting patterns of accessory genome coevolution in bacterial species using data from thousands of bacterial genomes</i> .	11/2022
Talk for Ecological Society of America, Montreal: <i>Eco-evolutionary dynamics of autotomy</i> .	08/2022
Talk for Evolution, Cleveland: <i>Eco-evolutionary dynamics of autotomy</i> .	07/2022

Talk for Workshop on Plasmids as Vehicles of Antimicrobial Resistance Spread, Abdus Salam International Centre for Theoretical Physics, Online: *Detecting Patterns of Coevolution of Gene Gains and Loss in Bacterial Species Using Data from Thousands of Bacterial Genomes*. 03/2022

Poster for Society for Molecular Biology and Evolution, Online: *Detecting genetic interactions in a large bacterial dataset*. 07/2021

Talk for Evolution, Online: *Detecting genetic interactions in a large bacterial dataset*. 06/2021

Talk for Cultural Evolution Society, Hokudai University: *Modelling anti-vaccine sentiment as a cultural pathogen*. 06/2021

Talk for Evolutionary and Ecological Systems Biology, Massachusetts Institute of Technology: *Detecting genetic interactions in a large bacterial dataset*. 04/2021

Poster for Southeast Center for Mathematics and Biology, Georgia Institute of Technology: *Eco-evolutionary dynamics of autotomy*. 12/2020

Talk for Southeastern Population Ecology and Evolutionary Genetics Conference, Auburn University: *The effect of haplotype length on haplotype-based F_{ST}* . 10/2020

Poster for Southeast Center for Mathematics and Biology, Georgia Institute of Technology: *Modeling anti-vaccine sentiment as a cultural pathogen*. 02/2020

Poster for Evolution of Complex Life, Georgia Institute of Technology: *Local context and the evolution of cooperation*. 05/2019

Talk for Phylomania, University of Tasmania : *The probability of monophyly of a sample of gene lineages on a species tree*. 11/2018

Poster for Society for Molecular Biology and Evolution, Yokohama: *Properties of haplotype-based F_{ST} computed as a function of haplotype length*. 07/2018

Poster for Feldman II Symposium, Stanford University : *Modeling anti-vaccine sentiment as a cultural parasite*. 11/2017

Talk for Evolution, Portland: *The probability of monophyly of a sample of gene lineages on a species tree*. 06/2017

Talk for Mathematical and Computational Evolutionary Biology, Hyeres: *The probability of monophyly of a sample of gene lineages on a species tree*. 06/2017

Poster for Society for Molecular Biology and Evolution, Gold Coast: *The probability of monophyly of a sample of gene lineages given a species tree: an application to maize domestication*. 07/2016

Poster for Biological Sciences Research Showcase, University of California, San Diego: *Using Cell-Profiler as an alternative to other methods in collecting data related to the study of bacterial aging*. 06/2013

PUBLICATIONS

1. RS Mehta, D Bryant, and NA Rosenberg. "The probability of monophyly of a sample of gene lineages on a species tree." *Proc Natl Acad Sci USA* 113.29 (2016): 8002-8009.
2. RS Mehta and NA Rosenberg. "The probability of reciprocal monophyly of gene lineages in three and four species." *Theor Popul Biol* 129 (2019): 133-147.
3. DE LaScala-Gruenewald, RS Mehta, Y Liu, and MW Denny. "Sensory perception plays a larger role in foraging efficiency than heavy-tailed movement strategies." *Ecol Mod* 404 (2019): 69-82.
4. RS Mehta, AF Feder, SM Boca, and NA Rosenberg. "The relationship between haplotype-based F_{ST} and haplotype length." *Genetics* 213.1 (2019):281-295.
5. RS Mehta and NA Rosenberg. "Modelling anti-vaccine sentiment as a cultural pathogen." *Evol Hum Sci* 2 (2020): E21.
6. RS Mehta and JA Kraus. "Eco-evolutionary dynamics of autotomy." *Theor Ecol* (2021) 14(3): 445-465.
7. RS Mehta, MA Steel, and NA Rosenberg. "The probability of joint monophyly of all species in an arbitrary species tree." *J Comp Biol* (2022) 29(7):679-703.

8. V Talla, RS Mehta, and JC de Roode. "Temporal genomics in monarch butterflies: increasing genetic diversity suggests stable population size or modest decline." Under revision.
9. RS Mehta, RA Petit III, TD Read, DB Weissman. "Detecting patterns of accessory genome coevolution in bacterial species using data from thousands of bacterial genomes." Under revision. <https://doi.org/10.1101/2022.03.14.484367v1>.
10. LM Bavik*, RS Mehta*, DB Weissman. "50 Shades of Greenbeard: Robust evolution of altruism based on similarity of complex phenotypes." Under revision. <https://doi.org/10.1101/2022.05.26.493612v1>.

TEACHING

Undergraduate Teaching Assistant for BILD 3 at the University of California, San Diego. Instructors: Carolyn Kurler, Krystal Rypien Fall 2012, Spring 2013
 Graduate Teaching Assistant for BIO 143 at Stanford University. Instructors: Noah Rosenberg, Dmitri Petrov Spring 2015
 Graduate Teaching Assistant for BIO 43 at Stanford University. Instructors: Hunter Fraser, Mary Beth Mudgett, Peter Vitousek, Waheeda Khalfan. Spring 2016
 Instructor for Stanford SPLASH:

1. Introduction to Sabermetrics Spring, Fall 2014; Spring 2015; Spring, Fall 2017
2. A Brief Introduction to Population Genetics Spring 2015
3. Mathemagical Puzzles Fall 2015
4. Continued Fractions Fall 2015
5. Sneaky Statistics, Perplexing Probability Spring, Fall 2016
6. Evolutionary Game Theory Spring 2016
7. The $3n + 1$ Problem Spring 2018

Mentor for Figure Workshops, BIO 499R, at Emory University. Instructor: Nicole Gerardo. Fall 2019
 Instructor for BIO 131 at Stanford University. Winter 2017

OUTREACH

Associate Editor and Reviewer for Journal of Emerging Investigators 2020-2021
 Stanford Speaker Panel, Monta Vista High School 05/2018
 Judge, Synopsys Silicon Valley Science and Technology Championship 2017, 2018
 Volunteer, Sea Lion Bowl, Stanford University 2015, 2016

NON-ACADEMIC PUBLICATIONS

- The Dish on Science (online science magazine produced by Stanford graduate students)
1. Quantifying the Effects of Anti-vaccine Sentiment on the Spread of Disease. 03/2016
 2. Linguistic Whodunits 11/2017
 3. The Supreme Court Through the Eyes of Statistical Mechanics 03/2019

UNDERGRADUATE RESEARCH

Developed techniques for measuring bacterial cell fluorescence from images of bacterial colonies (Advisor: Lin Chao) 2012-2013
 Performed experiments and collected diversity data for algal competition studies (Advisor: Jonathan

Shurin)	2011-2012
Analyzed stable isotope data of rat diets in the Aleutian islands (Advisor: Carolyn Kurle)	2011

REFERENCES

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| 1. Daniel Weissman | dbweissman@gmail.com |
| 2. Noah Rosenberg | noahr@stanford.edu |
| 3. Marc Feldman | mfeldman@stanford.edu |

Referee for: Journal of the Royal Society Interface, IEEE Transactions on Network Science and Engineering, Ecological Modeling, Theoretical Population Biology, Bioinformatics, IEEE/ACM Transactions on Computational Biology and Bioinformatics, Acta Biotheoretica, Journal of Emerging Investigators, Systematic Biology, PNAS, and PNAS Nexus.