

ARBEL HARPAK

Curriculum Vitae

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## CURRENT POSITION

**SIMONS FOUNDATION FELLOW**, Simons Society of Fellows, New York, NY, USA

and

**POSTDOCTORAL RESEARCHER** advised by Dr. Molly Przeworski at the Department of Biological Sciences, **COLUMBIA UNIVERSITY**, New York, NY, USA

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## EDUCATION

### **PH.D. BIOLOGY, STANFORD UNIVERSITY**

(2013-2018) Advisor: Jonathan K. Pritchard

- Thesis: "Statistical Inference of Mutational Mechanisms"
- Stanford Center of Evolutionary and Human Genomics Fellow

### **M.S. STATISTICS, STANFORD UNIVERSITY**

(2016-2017)

- Focus on machine learning

### **M.SC. ECOLOGY & EVOLUTION, THE HEBREW UNIVERSITY OF JERUSALEM**

(2011-2013) Advisor: Guy Sella

- Thesis: "Genetic Diversity in an Evolutionary Experiment Setting"
- Summa Cum Laude

### **B.SC. DUAL DEGREE: MATHEMATICS AND PHYSICS, THE HEBREW UNIVERSITY OF JERUSALEM**

(2007-2011) Undergrad thesis advisor: Nathalie Q. Balaban

- Thesis: "Probabilistic Modeling of Bacterial Colony Growth"
- Dean's list
- Additional coursework in Computer Science

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## SCIENTIFIC PUBLICATIONS

(8 as first author, 5 as corresponding author)

\* contributed equally, + corresponding author

### Pre-print:

1. **A. Harpak**<sup>+</sup>, N.R. Garud, N.A. Rosenberg, D.A. Petrov, Matthew Combs, P.S. Pennings, J. Munshi-South<sup>+</sup>. Genetic Adaptation in New York City Rats. *bioRxiv* 2020; (featured in [Nature](#), [The Guardian](#), [The Independent](#), [New York Post](#), [Newsweek](#), [The Sun](#) and [more](#))
2. S. Mohammadi<sup>\*</sup>, L. Yang<sup>\*</sup>, **A. Harpak**<sup>\*</sup>, M. Rodríguez-Ordoñez, S.H. Alvarez, J. Storz, S. Dobler, A., Crawford, P. Andolfatto. Selection maintains co-adapted amino acid substitutions in toxin resistant toad-eating frogs. *bioRxiv* 2020.
3. **A. Harpak**, J.J. Berg, H. Mostafavi, G. Coop, M.D. Edge. Estimating of the proportion of variance in polygenic scores due to direct genetic effects. *In preparation*.
4. Q. Yu, M. Gralka, M. Duvernoy, M. Sousa, **A. Harpak**, O. Hallatschek. The local mutational landscape of demographic noise in microbial range expansions. *In preparation*.

### Peer-reviewed:

5. H. Mostafavi<sup>\*,+</sup>, **A. Harpak**<sup>\*,+</sup>, I. Agarwal, D. Conley, J.K. Pritchard, M. Przeworski<sup>+</sup>. Variable Prediction Accuracy of Polygenic Scores Within an Ancestry Group. *eLife* 2020 (featured in [VICE article](#) and [eLife Digest](#))
6. J.J. Berg<sup>\*</sup>, **A. Harpak**<sup>\*</sup>, N. Sinnott-Armstrong<sup>\*</sup>, A.M. Jørgensen, H. Mostafavi, Y. Field, E.A. Boyle, X. Zhang, F. Racimo, J.K. Pritchard, G. Coop. Reduced signal for polygenic adaptation of height in UK Biobank. *eLife*, 2019 (cited over 50 times, less than six months post publication; featured in an [eLife editorial](#) and in [Quanta magazine](#))

7. E. Glassberg, Z. Gao, **A. Harpak**, X. Lan, J.K. Pritchard. Measurement of selective constraint on human gene expression. *Genetics*, 2019 (Chosen as [GSA Genetics Spotlight](#) publication for 2019)
8. V. Garcia, E.C. Glassberg, **A. Harpak**, M.W. Feldman. Finite-sites multiple mutations interference gives rise to wavelet-like oscillations of multilocus linkage disequilibrium. *Journal of the Royal Society Interface*, 2018
9. **A. Harpak**<sup>+</sup>, X. Lan<sup>\*</sup>, Z. Gao, J.K. Pritchard<sup>+</sup>. Frequent nonallelic gene conversion on the human lineage and its effect on the divergence of gene duplicates. *Proceedings of the National Academy of Sciences (PNAS)*, 2017
10. R. Sun, Z. Hu, A. Sottoriva, T.A. Graham, **A. Harpak**, Z. Ma, J.M. Fischer, D. Shibata, C. Curtis. Genetic Diversity in Multi-Region Sequencing Data Reflects the Mode and Tempo of Tumor Evolution. *Nature Genetics*, 2017
11. **A. Harpak**<sup>+</sup>, A. Bhaskar<sup>\*</sup>, J.K. Pritchard. Effects of mutation rate variation on the distribution of allele frequencies in humans. *PLoS Genetics*, 2016 (award for 1/10 best abstracts by the American Society of Human Genetics (ASHG); [F1000Prime recommended paper](#))
12. A. Raj, S. Wang, H. Shim, **A. Harpak**, Y.I. Li, B. Engelmann, M. Stephens, Y. Gilad, J. K. Pritchard. Thousands of novel translated open reading frames in humans inferred by ribosome footprint profiling. *eLife*, 2016
13. **A. Harpak**<sup>+</sup> and G. Sella<sup>+</sup>. Neutral null models for diversity in serial transfer evolution experiments. *Evolution*, 2014

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## ACADEMIC SERVICE

- **Symposium co-chair:**
  - SMBE 2017 - "Mutational Mechanisms"
  - ICHG 2016 - "Population and Evolutionary Genetics"
- **Panelist:** Columbia Data Science Institute Workshop on Diversity in Healthcare and Health Research, 2019
- **Statistical Consultant** for Stanford Statistics Department (service to all Stanford affiliates) 2016-2017
- **Reviewer:** *PLoS Genetics*; *eLife*; *Proceedings of the National Academy of Sciences (PNAS)*; *Nature Ecology and Evolution*; *Molecular Biology and Evolution (MBE)*; *Frontiers in Zoology*; *Heredity*; *Genetics*; *Evolution, Medicine and Public Health (EMPH)*,

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## AWARDS AND FUNDING

- 2019-2023 [Simons Foundation Society of Fellows Junior Fellowship #633313](#)
- 2020 NIH NHGRI Keystone Symposia Award to present in "[Beyond a Million Genomes: From Discovery to Precision Health](#)", Grant #1R13HG010827-01
- 2019 Chan-Zuckerberg Initiative award to present in "[Reaching Diverse and Understudied Groups in Multimodal Studies](#)" meeting in Aurora, Colorado
- 2017-2018 Stanford Center for Computational, Evolutionary and Human Genomics (Stanford CEHG) Fellow
- 2017 "Quest for Orthologs" award to present work on genetic exchange between gene duplicates at annual meeting in Los Angeles, California
- 2017 Young Investigator award, SMBE 2017 in Austin, Texas
- 2016 American Society of Human Genetics (ASHG) [Best Abstract Award](#) (10 recipients in the US) included travel award to Kyoto, Japan for the International Congress of Human Genetics
- 2015 Co-wrote the successful [National Science Foundation \(NSF\) DEB 1457523 grant](#) to collect and sequence brown rat samples for my work on "Genetic Adaptation in New York City Rats"
- 2013-2017 Howard B. Kerzner Graduate Fellowship

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## SELECTED CONFERENCE TALKS

- “Variable prediction accuracy of polygenic scores within an ancestry group”, Keynote Symposia: Beyond a Million Genomes, Beckridge, Colorado, January 2020
- “Variable prediction accuracy of polygenic scores within an ancestry group”, Reaching Diverse and Understudied Groups in Multimodal Studies, Aurora, Colorado, September 2019
- “Poor portability of polygenic scores even within an ancestry group”, The Biology of Genomes, Cold Spring Harbor Labs, May 2019
- “How brown rats adapted to NYC’s concrete jungle”, Population, Evolutionary and Quantitative Genetics, Maddison WI, May 2018
- “The adaptation of brown rats to urban environments”, Center for Evolutionary and Human Genetics Annual Conference, Stanford University, February 2018
- “How brown rats adapted to NYC’s concrete jungle”, Society for Molecular Biology and Evolution (SMBE), Austin, Texas, July 2017
- “Estimating the rate of genetic exchange between gene duplicates”, Quest for Orthologs meeting, Los Angeles, California, June 2017
- “Non-allelic gene conversion rate is ten times higher than point mutation rate in humans”, Society for Molecular Biology and Evolution (SMBE), Gold Coast Australia, July 2016
- “Effects of mutation rate variation on allele frequencies in humans”, International Congress of Human Genetics (ICHG), Kyoto, Japan, April 2016
- “Variable mutation rate and epistasis affect the distribution of allele frequencies in humans”, Center for Evolutionary and Human Genetics Annual Conference, Stanford University, February 2016

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## **INVITED SEMINAR TALKS**

- “Interpreting and Decomposing Polygenic Scores”, Weizmann Institute of Science, Department of Molecular Genetics, January 2020
- “Predicting Complex Human Traits: Why so Complex?”, Hebrew University of Jerusalem, Computer Science Department, January 2020
- “Interpreting and Decomposing Polygenic Scores”, Tel Aviv University, Statistics Departmental Seminar, December 2019
- “Variable prediction accuracy of polygenic scores within an ancestry group”, New York Genome Center Population Genetics Working Group, September 2019
- “How brown rats adapted to NYC’s concrete jungle”, Invited Biological Sciences Departmental Seminar Speaker, Fordham University in New York, December 2018
- “Effects of epistasis and mutation rate variation on allele frequencies in humans”, Graduate University for Advanced Studies, Sokendai, Japan, April 2016

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## **TEACHING EXPERIENCE**

### ***TEACHING ASSISTANT***

- Biology department, Stanford University, 2013-2015
  - Fundamentals of Molecular Evolution (Bio 113/244)
  - Ethical Issues in Biology
- Statistics department, Stanford University, 2016-2017
  - Statistical Consultant in the department’s drop-in consulting service
- Mathematics department, The Hebrew University of Jerusalem, 2010-2011
  - Calculus for Engineering and Physics Students (80177)
  - Mathematical Methods I (80114)

### ***HIGH SCHOOL MATH TEACHER***

Sudbury School, Jerusalem, 2009-2010

### ***VOLUNTEER TUTOR***

- Tutoring first-year math courses to first-generation Arab undergraduates, The Social Equality Unit at HUJI, 2010-2011
- Secondary school Mathematics and English, Social outreach Unit and "Perach" outreach program for transitional youth, HUJI 2007-2009

### ***NETWORK INTELLIGENCE INSTRUCTOR***

Intelligence Corps Elite Unit, Israel Defense Forces, 2005-2006  
Commanding and instructing a unit of 20.

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## **OTHER WORK EXPERIENCE**

### ***TEAM LEAD***

Castlogic LTD., Netanya, Israel, 2006-2007

- Managing the Data Analysis and QA four-person team
- Developing fraud-detection algorithms based on data from user logs

### ***DIRECTOR OF INTELLIGENCE TEAM***

Israel Defense Forces (IDF), Israel, 2002-2005

- Managing a team of 50 soldiers
- Commendation for excellence in performance (sole receiver) 2005

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## **Languages**

***Spoken:*** Hebrew, English (fluent), Spanish and Arabic (very basic)

***Programming:*** R, Python, MATLAB, Bash (fluent). JAVA, Assembly, C++ (very basic)