

# Alison F. Feder

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## Contact

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## Appointments

2021- Assistant Professor, Department of Genome Sciences, *University of Washington*  
2018-2021 Miller Fellow, Department of Integrative Biology, *University of California, Berkeley*  
Hosts: Oskar Hallatschek & Monty Slatkin

## Education

2013-2018 PhD, Biology, Stanford University, Stanford, CA  
Advisor: Dmitri Petrov  
2012-2013 MSc (by Research), Statistics, University of Oxford, Oxford, UK  
Advisor: Gil McVean  
2008-2012 BA, Mathematics, *summa cum laude*, University of Pennsylvania, Philadelphia, PA  
Advisor: Joshua Plotkin

## Research Funding

2018-2021 Miller Fellowship [\[Website\]](#)  
2017-2018 Stanford Center for Computational, Evolutionary & Human Genomics Fellowship [\[Website\]](#)  
2016-2017 Gerald J. Lieberman Fellowship [\[Website\]](#)  
*Awarded yearly to twelve Stanford graduate students whose teaching, research and university service demonstrate potential for academic leadership.*  
2014 Center for Computational, Evolutionary and Human Genomics Trainee Grant  
2012-2017 National Science Foundation Graduate Research Fellowship [\[Website\]](#)  
2012-2013 Thouron Award [\[Website\]](#)

## Awards

2018 Milner Prize in Evolutionary Biology  
2018 Samuel Karlin Prize in Mathematical Biology  
*Awarded to one graduate student in the Stanford Department of Biology per year whose dissertation reaches the highest standard of mathematical biology*  
2018 James F. Crow Early Career Researcher Finalist (Genetics Society of America)  
2017 Gil Omenn Prize for the best article in evolutionary medicine published in the previous year  
*Awarded for 'More effective drugs lead to harder selective sweeps in the evolution of drug resistance in HIV-1'*  
2015 Excellence in Teaching Award (Department of Biology, Stanford)  
2012 Penn Genome Frontiers Institute Excellence in Genomics Undergraduate Award  
2012 Phi Beta Kappa (University of Pennsylvania)

## Peer-Reviewed Publications (\* denotes equal contributions)

10. **A. F. Feder**, P. S. Pennings, D. A. Petrov (2021). The clarifying role of time series data in the population genetics of HIV. *PLOS Genetics* 17(1): e1009050. [\[Link\]](#)
9. **A. F. Feder**, P. S. Pennings, J. Hermisson\*, D. A. Petrov\* (2019). Evolutionary dynamics in structured populations under strong population genetic forces. (*G3: GENES, GENOMES, GENETICS*) 9(10):3395-3407. [\[Link\]](#)  
*Selected for 2019 G3 Spotlight issue*
8. R. S. Mehta, **A. F. Feder**, S. M. Boca, N. A. Rosenberg (2019). The relationship between haplotype-based  $F_{ST}$  and haplotype length. *Genetics* 213(1):281-295. [\[Link\]](#)
7. K. Theys\*, **A. F. Feder\***, M. Gelbart\*, M. Hartl, A. Stern, and P. S. Pennings (2018). Within-patient HIV mutation frequencies reveal fitness costs of CpG dinucleotides, drastic amino acid changes and G  $\rightarrow$  A mutations. *PLoS Genetics* 14(6): e1007420. [\[Link\]](#)
6. **A. F. Feder**, C. Kline, P. Polacino, M. Cottrell, A. D. Kashuba, B. F. Keele, S.-L. Hu, D. A. Petrov, P. S. Pennings\*, and Z. Ambrose\* (2017). A spatio-temporal assessment of simian/human immunodeficiency virus (SHIV) evolution reveals a highly dynamic process within the host. *PLoS Pathogens*, 13(5): e1006358. [\[Link\]](#)
5. B. A. Wilson\*, N. R. Garud\*, **A. F. Feder\***, Z. J. Assaf\*, and P. S. Pennings (2016). The population genetics of drug resistance evolution in natural populations of viral, bacterial and eukaryotic pathogens. *Molecular Ecology*, 25(1):42–66. [\[Link\]](#)
4. **A. F. Feder**, S.-Y. Rhee, S. P. Holmes, R. W. Shafer, D. A. Petrov\*, and P. S. Pennings\* (2016). More effective drugs lead to harder selective sweeps in the evolution of drug resistance in HIV-1. *eLife*, 5:e10670. [\[Link\]](#)
3. **A. F. Feder\***, S. Kryazhimskiy\*, and J. B. Plotkin (2014). Identifying signatures of selection in genetic time series. *Genetics*, 196(2):509–522. [\[Link\]](#)
2. **A. F. Feder**, D. A. Petrov, and A. O. Bergland (2012). LDx: estimation of linkage disequilibrium from high-throughput pooled resequencing data. *PLoS One*, 7(11):e48588. [\[Link\]](#)
1. K. E. Lohmueller, A. Albrechtsen, Y. Li, S. Y. Kim, T. Korneliussen, N. Vinckenbosch, G. Tian, E. Huerta-Sanchez, **A. F. Feder**, N. Grarup, T. Jørgensen, T. Jiang, D. R. Witte, A. Sandbæk, I. Hellmann, T. Lauritzen, T. Hansen, O. Pedersen, J. Wang, R. Nielsen (2011). Natural selection affects multiple aspects of genetic variation at putatively neutral sites across the human genome. *PLoS Genetics*, 7(10):e1002326. [\[Link\]](#)

## Pre-prints (\* denotes equal contributions)

**A. F. Feder**, K. Harper, P. S. Pennings, Challenging conventional wisdom on the evolution of resistance to multi-drug HIV treatment: Lessons from data and modeling. *bioRxiv*, 807560. [\[Link\]](#)

## Invited Presentations

2021	[Scheduled] Quantitative Evolution, Phylogeny and Ecology: from models to data and back, IHP Workshop, Paris, France ( <i>virtual</i> )
2021	Institute of Ecology & Evolution, University of Oregon, Eugene, USA ( <i>virtual</i> )
2020	Ecology & Evolution Seminar, University of California, Davis, USA ( <i>virtual</i> )
2020	Department of Genome Sciences, University of Washington, Seattle, USA
2019	Department of Ecology & Evolutionary Biology, University of Chicago, Chicago, USA
2019	Department of Computational Biology, Cornell University, Ithaca, USA
2019	Science & Mathematics Seminar, University of Puget Sound, Tacoma, USA
2019	European Society of Evolutionary Biology, Turku, Finland
2019	Society of Molecular Biology & Evolution, Manchester, UK
2019	Trainee Invited Speaker Series, Arjun Raj Lab at Penn, Philadelphia, USA
2019	Science & Technology Seminar, Joint Genome Institute, Walnut Creek, USA
2019	Departmental seminar, University of San Francisco, San Francisco, USA
2018	Palo Alto Research Center, Palo Alto, USA
2018	Milner Prize Lecture, University of Bath, Bath, UK
2018	Systems Biology Seminar, Cancer Research UK Cambridge Institute, UK
2018	Ad hoc seminar, University of California, Davis, USA
2018	Institute for Disease Modeling Annual Symposium, Seattle, USA
2017	Center for Theoretical Evolutionary Genomics, University of California, Berkeley, USA
2017	Institute for Disease Modeling, Bellevue, USA
2017	Center for Inference and Dynamics of Infectious Disease, Fred Hutchinson Cancer Research Institute, Seattle, USA
2017	Omenn Prize talk at the International Society of Evolution, Medicine and Public Health, Groningen, Netherlands
2017	Program for Evolutionary Dynamics, Harvard University, Cambridge, USA
2016	“Darwin’s Weekly” Seminar, University of Chicago, Chicago, USA

## Contributed/selected presentations      \* *talk*      † *poster*

2018	[*] Society for Molecular Biology & Evolution, Yokohama, Japan
2018	[*] James F. Crow Award finalist session at PEQG, Madison, USA
2018	[*] HIV Dynamics & Evolution, Leavenworth, USA
2017	[†] Gordon Research Conference: Microbial Population Biology, Andover, USA
2017	[*] Gordon Research Seminar: Microbial Population Biology, Andover, USA
2017	[*] Society for Molecular Biology & Evolution Annual Meeting, Austin, USA
2016	[*] International Society of Evolution, Medicine and Public Health, Raleigh, USA
2016	[*] International HIV Drug Resistance Workshop, Boston, USA
2016	[† †] Conference on Retroviruses and Opportunistic Infections (CROI), Boston, USA
2015	[†] Bio-X Interdisciplinary Initiatives Symposium, Stanford, USA
2015	[*] Society for Molecular Biology & Evolution Annual Meeting, Vienna, Austria
2015	[†] “Forecasting Evolution?” SFB 680 Conference, Lisbon, Portugal
2011	[*] NIMBioS Undergraduate Research Conference at the Interface of Biology and Mathematics, Knoxville, USA
2011	[††] Society for Molecular Biology & Evolution Annual Meeting, Kyoto, Japan

## Research Supervision

2020-        Maya Lewinsohn, Genome Sciences PhD student, *U. Washington* (joint with T. Bedford)  
2020        Helen Sakharova, Center for Computational Biology rotation student, *UC Berkeley*  
2016        Michael Herschl, undergraduate, *Stanford University*

## Teaching

### *University:*

Fall 2015    Co-teacher for BioCore Exploration (3 hour course), ‘Are we still evolving?’ with L. Uricchio  
Spring 2015 TA for Bio 143, *Evolution*  
Spring 2014 TA for Bio 43, *Evolution, Ecology & Plant Biology*

### *High School:*

2016        Guest lecturer, *Evolutionary genomics theory, application and you!*  
              Stanford Pre-Collegiate Institute  
2014-2016   Stanford Splash! Teacher  
              Taught 6 one-session mini-courses to high school students (two each on mathematical/logical thinking, population genetics and statistics/probability).

## Public Outreach

2019        Invited speaker at Nerd Nite East Bay, a general audience seminar series  
2017        Finalist in Evolution Film Festival for “Intra-patient Simian-HIV drug resistance evolution: does blood tell the whole story?”  
2016        Finalist in Evolution Film Festival for “Better drugs lead to harder sweeps in HIV-1”

## Competitive travel support

2018        Young Investigator Travel Award from SMBE (Yokohama, Japan)  
2016        International Society for Evolutionary Medicine and Public Health Travel Award (Durham, USA)  
2016        CROI Young Investigator Scholarship (Boston, USA)  
2015        Wellcome Trust Travel Award (for “Forecasting Evolution?” meeting, Lisbon, Portugal)  
2013        Cargese Summer School in Quantitative Genetics Grant (Cargese, France)  
2011        NiMBioS Undergraduate Conference Grant (Knoxville, USA)

## Academic, Community & University Service

2019-2021   Miller Symposium Planning Committee  
2018        Co-organizer of SMBE 2018 symposium on ‘Intra-host evolutionary dynamics’ with K. Xue  
2017        Co-organizer of ‘Petrino’ joint lab retreat between D. Petrov and R. Andino (UCSF) labs  
2016-2017   Department of Biology TA Mentorship Program mentor and program organizer  
2014-2017   Stanford Bioscience Students Association new student Mentor  
2014-2015   Mentored student writing NSF Graduate Research Fellowship application

Referee for *Evolution*, *Genetics*, *Journal of Theoretical Biology*, *Molecular Biology and Evolution*, *PCI Evolutionary Biology*, *PLOS Computational Biology* (with mentor), *PLOS Genetics*, *PNAS*