

Jeffrey D. Jensen
Arizona State University
jeffrey.d.jensen@asu.edu
<http://jjensenlab.org>

EDUCATION

2002-2006 **Ph.D.** Cornell University, Genetics
Advisors: Charles Aquadro, Carlos Bustamante
1998-2002 **B.S./B.A.** Univ. of Arizona, Evol. Biology / Anthropology
Advisors: Michael Nachman, Brian Charlesworth

PROFESSIONAL EXPERIENCE

2016- **Professor**
Arizona State University, School of Life Sciences
Center for Evolution & Medicine, Center for Mechanisms of Evolution
2011-2017 **Assistant / Associate Professor**
Swiss Federal Institute of Technology (EPFL), School of Life Sciences
2009-2011 **Assistant Professor**
Univ of Massachusetts Medical School, Program in Bioinformatics
2007-2009 **NSF Biological Informatics Postdoctoral Fellow**
UC Berkeley / UC San Diego, Department of Integrative Biology
Advisors: Doris Bachtrog, Peter Andolfatto, Rasmus Nielsen

PROFESSIONAL SERVICE

Editorial:

2016- *Evolution*, Associate Editor
2014-2018 *Journal of Evolutionary Biology*, Board Member
2014-2015 *Molecular Ecology*, Associate Editor
2014-2015 *PLoS Computational Biology*, Guest Editor
2012-2015 *PLoS Genetics*, Guest Editor
2011-2015 *Frontiers*, Associate Editor

Review (funding): Austrian Science Fund, European Research Council, European Science Foundation, French National Research Agency, German Science Foundation, Human Frontier Science Program, Israeli Science Foundation, MacArthur Fellows Program, Polish National Science Centre, Swiss National Science Foundation, UK Biotechnology & Biological Sciences Research Council, UK Natural Environment Research Council, US National Institutes of Health, US National Science Foundation

Review (journal): *American Journal of Human Genetics, Annals of Human Genetics, Archives of Virology, Bioinformatics, Biological Reviews, BMC Evolutionary Biology, Cell, Evolution, Evolution Letters, Frontiers in Genetics, G3, Genetics, Genetics Research, Genetics Selection Evolution, Genome Biology, Genome Biology & Evolution, Genome Research, Heredity, Journal of Evolutionary Biology, Journal of Molecular Evolution, Molecular Biology & Evolution, Molecular Ecology, Molecular Ecology Resources, Nature, Nature Communications, Nature Ecology & Evolution, Nature Reviews Genetics, Nucleic Acids Research, Philosophical Transactions of the Royal Society B, Proceedings of the Royal Society, PNAS, PLoS Biology, PLoS Computational Biology, PLoS Genetics, PLoS One, Science, Science Advances, Scientific Reports, Statistical Physics*

Committees:

Search:

Faculty Search Committee: Mechanisms of Evolution (ASU) (2018-19)
Faculty Search Committee: Mechanisms of Evolution (ASU) (2017-18)
Faculty Search Committee: Ecology of Infectious Disease (ETH) (2013-14)
Faculty Search Committee: Integrative Biology (UMass Med School) (2010-11)

Advisory:

elected member of ASU's Graduate Faculty Mentor Academy (GFMA) (2022-present)
Research Committee: Center for Evolution & Medicine (ASU) (2016-18)
Graduate Admissions Committee: Life Sciences (EPFL) (2013-15)
German Science Foundation, Rapid Evolutionary Adaptation Grant Panel (2015-16)
Serbian Genetics Society, Scientific Advisor (2015)
National Academy of Finland, Scientific Advisor (2013)

Organizing:

Arizona PopGroup (USA, 2016-present)
'Clinically Relevant Population Genetics' workshop (USA, 2017)
'Theoretical & Empirical Evidence of Adaptation' workshop (Switzerland, 2015)
European Society for Evolutionary Biology Conference (Switzerland 2015)
'Systems Genetics & Evolution' workshop (Switzerland, 2015)
'Bridging Theoretical & Experimental Evolution' workshop (Switzerland, 2013)

Thesis:

Kevin Leempoel (Golay Lab, EPFL), Pierre-Yves Helleboid (Trono Lab, EPFL), Ana Bittencourt (Fellay Lab, EPFL), Pedro Refinetti (Morgenthaler Lab, EPFL), Sebastian Waszak (Deplancke Lab, EPFL), Andreas Massouras (Deplancke Lab, EPFL), Benjamin Zoller (Naef Lab, EPFL), Dominique Monteil (Wurm Lab, EPFL), Nicee Srivastava (Fasshauer Lab, Uni Lausanne), Ryan Hietpas (Bolon Lab, UMass Med), Alex Panzierra (Bertorelle Lab, Uni Ferrara), Adele Crane (Stone Lab, ASU), Mario Apata (Wilson Lab, ASU), Gaurav Bilolikar (Geiler-Samerotte Lab, ASU), Cyril Versoza (Pfeifer Lab, ASU), Man Lin (Lynch Lab, ASU), Mark Milhaven (Pfeifer Lab, ASU), Abigail Howell (Pfeifer Lab, ASU)

TEACHING

S, 2023-current	<i>Principles of Human Genetics</i> (BIO 446/546, ASM 446), ASU
F, 2017-current	<i>Population Genetics Reading Group</i> (BIO 498/591), ASU
F, 2017-2020	<i>Research Areas of Evolution</i> (EVO 610), Guest Lecturer, ASU
S, 2018	<i>Evolution</i> (BIO 345), ASU
S, 2012-2016	<i>Statistical Population Genetics</i> (BIO 366), EPFL
F, 2014-2015	<i>Scientific Literature Analysis</i> (BIO 371), EPFL
S, 2014-2015	<i>A History of Evolutionary Thought</i> (BIO 672), EPFL
F, 2012-2014	<i>Projects in Genomics & Bioinformatics</i> (BIO 466), EPFL
F, 2010-2011	<i>Population Genetics Journal Club</i> (BBS 741), UMass Med
F, 2010-2011	<i>Molecular Evolution</i> (BBS 705), UMass Med

ADVISING

Postdoctoral	2022 -	John Terbot
	2021 -	Vivak Soni
	2018 - 2023	Parul Johri (<i>Faculty, UNC-Chapel Hill</i>)
	2019 - 2021	Susanna Sabin (<i>Government (CDC), USA</i>)
	2018 - 2020	Ana Morales-Arce (<i>Postdoc, Uni Berne</i>)
	2019 - 2020	João Santos (<i>Industry, Portugal</i>)
	2019 - 2020	Matt Jones (<i>Government (USGS), USA</i>)
	2017 - 2019	Rebecca Harris (<i>Industry, USA</i>)
	2017 - 2019	Andrew Sackman (<i>Faculty, VCU</i>)
	2015 - 2017	Sebastian Matuszewski (<i>Industry, Austria</i>)
	2014 - 2017	Stefan Laurent (<i>Faculty, Max Planck-Köln</i>)
	2015 - 2017	Severine Vuilleumier (<i>Faculty, HES-SO</i>)
	2011 - 2016	Nicholas Renzette (<i>Industry, USA</i>)
	2015 - 2016	Valeria Montano (<i>Postdoc, Uni St. Andrews</i>)
	2013 - 2015	Greg Ewing (<i>Industry, New Zealand</i>)
	2012 - 2015	Claudia Bank (<i>Faculty, Uni Berne</i>)
	2013 - 2015	Anna Ferrer Admettla (<i>Industry, Spain</i>)
	2012 - 2014	Matthieu Foll (<i>Faculty, WHO-Lyon</i>)
	2010 - 2014	Yu-Ping Poh (<i>Bioinformatician, ASU</i>)
	2013 - 2014	Cornelia Pokalyuk (<i>Faculty, Uni Magdeburg</i>)
	2012 - 2013	Lisha Mathew (<i>Industry, Germany</i>)
	2012 - 2013	Daniel Wegmann (<i>Faculty, Uni Fribourg</i>)
Graduate (Ph.D.)	2013 - 2018	Mado Kapopoulou (<i>Bioinformatician, Uni Berne</i>)
	2012 - 2017	Louise Ormond (<i>Postdoc, UCL</i>)
	2009 - 2014	Alfred Simkin (<i>Bioinformatician, UMass Med</i>)
	2009 - 2013	Jessica Crisci (<i>Industry, USA</i>)
Graduate (M.S.)	2016 - 2017	Marcel Hildebrandt (<i>Industry, Germany</i>)
	2016 - 2017	Stefano Tartini (<i>Industry, Switzerland</i>)
	2012 - 2014	Hyunjin Shim (<i>Postdoc, UC Berkeley</i>)
	2011 - 2013	Priyanka Sinha (<i>Postdoc, Otago Univ</i>)

Staff	2019 - 2021	Kellen Riall (<i>PhD student, Univ. of Chicago</i>)
	2014 - 2017	Kristen Irwin (<i>Grants Administration, EPFL</i>)
	2012 - 2013	Shivani Mahajan (<i>Industry, USA</i>)

Bachelor Projects:

UMass (2009-11): Aslihan Dincer, Daniel Virgil, Guang Xu
EPFL (2011-17): Luc Aeberli, Laurent Alter, Laure Cetre, Edouard Deckersberg, Anna Dussuet, Philippe Fabrice, Christopher Finelli, Anais Haget, Roger Kung, Marie Malier, Dariush Mollet, Mathieu Quinodoz, Pauline Reiff, Tamara Rossy, Stefano Tartini, Gaelle Thurre, Florian Widmer
ASU (2017-current): Kellen Riall, Emma Howell, Andrew Hopkins

Sabbatical & Study Abroad Visitors

2016 Matt Jones (PhD Student, Univ of Montana), Study Abroad
2014 Derek Setter (PhD Student, Univ Vienna), Study Abroad
2012 Daniel Bolon, (Professor, UMass Medical School), Sabbatical

FUNDING & AWARDS

2022 Outstanding Postdoctoral Mentor of the Year Award
- Awarded annually by ASU in recognition of outstanding mentorship

2022-2023 U.S. National Institutes of Health, NIGMS, P30
Funded Consultant (PIs: B. Bowler, J. Good, B. Cooper)
Surveillance genome resequencing to detect SARS-CoV-2 variants

2021-2026 U.S. National Institutes of Health, NIGMS, R35
'Established Investigator MIRA'
PI
On differentiating selective and neutral evolutionary processes

2019-2024 U.S. National Institutes of Health, NIAID, P01
co-I (with: S. Permar, T. Kowalik, A. Kaur, P. Barry, S. Pfeifer)
Immunologic and virologic determinants of CMV transmission

2019-2022 U.S. National Institutes of Health, NIGMS/DMS, R01
PI
Novel coalescent approaches for the study of virus evolution

2015-2020 U.S. Department of the Army, DARPA
co-I (with: R. Finberg, C. Schiffer, D. Bolon, T. Kowalik, J. Wang)
Anticipating influenza resistance evolution

- 2017-2018 Illumina Innovative Investigators program
co-I (with: T. Kowalik, S. Pfeifer, B. Trumble)
Characterizing HCMV infections in native Bolivian populations
- 2017-2018 Center for Evolution & Medicine, Venture Fund
co-I (with: S. Pfeifer, B. Trumble)
The evolutionary history of HCMV in native Americans
- 2015-2018 Swiss National Science Foundation
PI
The population genetics of adaptation (renewal)
- 2013-2018 European Research Council
PI
Theoretical, empirical, & computational tools in evolution
- 2012-2015 Swiss National Science Foundation
PI
The population genetics of adaptation
- 2012-2015 Swiss National Science Foundation
co-I (with: H. Hoekstra, L. Excoffier)
Genetic basis of adaptive change in camouflaged deer mice
- 2011-2014 DARPA
co-I (with: R. Finberg, J. Wang, T. Kowalik, D. Bolon, C. Schiffer)
Algorithms to limit viral epidemics
- 2011 AAAS Newcomb Cleveland Prize
- Awarded for Outstanding Paper of the Year in *Science*
- 2010-2011 U.S. National Science Foundation
PI
The population genetics of adaptation
- 2010-2011 Worcester Foundation for Biomedical Research
PI
Method developments: searching for selection
- 2006-2008 U.S. National Science Foundation
Biological Informatics Postdoc Fellowship
Identifying cis-acting binding sites for dosage compensation

INVITED LECTURES

- 2023 Virginia Tech (USA); Florida State University (USA)
- 2022 University of Chicago (USA)
- 2021 University of Berne (Switzerland); 'Precision Medicine 2.0' symposium (USA)
- 2020 Ohio State University (USA), University of Edinburgh (UK)
- 2019 University of Wisconsin - Madison (USA); 'Evolutionary Genetics of Infectious Disease' symposium (Canada); Midwestern University, College of Veterinary Medicine (USA)
- 2018 Cornell University (USA); Max Planck Institute for Plant Breeding Research (Germany)
- 2017 University of Arizona, Quantitative Biology Colloquium (USA); University of Montana (USA); Arizona PopGroup (USA); 'Clinically Relevant Population Genetics' workshop (USA)
- 2016 Swiss Institute of Bioinformatics Symposium (Switzerland); University of Basel (Switzerland); Max Planck Institute for the Science of Human History (Germany); Mathematical and Computational Evolutionary Biology Conference (France); EMBO Conference (Germany); Max Planck Institute for Plant Breeding Research (Germany)
- 2015 University of Southern California (USA); Arizona State University (USA); Society for the Study of Evolution Conference (Brazil); 'Theoretical & Empirical Evidence of Adaptation' workshop (Switzerland); Univ of Zurich Next Generation Sequencing Retreat (Switzerland); Swiss Federal Institute of Aquatic Sciences (Switzerland); Max Planck Institute for Plant Breeding Research (Germany); University of Munich (Germany); University of Veterinary Medicine (Austria); Institute of Science & Technology (Austria); 'Population Genomics: the Footprint of Wolfgang Stephan' workshop (Germany)
- 2014 Systems Genetics & Evolution Conference (Switzerland); University of Arizona (USA)
- 2013 National Academy of Finland (Finland); Society for Molecular Biology & Evolution Conference (USA); Instituto Gulbenkian Ciencia (Portugal); 'Population Genetics Models Including Selection' workshop (Germany); University of Konstanz (Germany); Makerere University (Uganda)

- 2012 ‘Landscape Genomics’ workshop (Switzerland); University of Edinburgh (UK); Konrad Lorenz Institute for Evolution & Cognition Research (Austria); University of Vienna (Austria); Heidelberg Institute for Theoretical Studies (Germany); SIB Population Genetics Summer School (Switzerland); Lausanne Genomics Day (Switzerland); University of Basel (Switzerland); University of Lausanne (Switzerland)
- 2011 ‘Evolutionary Innovations’ workshop (Germany); Society for Molecular Biology & Evolution Conference (Japan); European Society for Evolutionary Biology Conference (Germany); Harvard University (USA); Oxford University (UK); University of Southern California (USA); Swiss Federal Institute of Technology (Switzerland); University of Idaho (USA)
- 2010 Brandeis University (USA)
- 2009 ‘Mathematical Challenges from Genetics’ workshop (Canada); Neandertal Genome Consortium Conference (USA); Neandertal Genome Consortium Conference (Croatia)
- 2008 Harvard University (USA); NC State University (USA); University of North Carolina (USA); University of Munich (Germany); Max Planck Institute for Evolutionary Anthropology (Germany); Sanger Institute (UK)
- 2007 ‘Statistical Inference of Selection’ workshop (Austria); Cornell University Probability Symposium (USA); Monod Conference in Evolutionary Genetics (France); University of Arizona (USA)
- 2006 University of Vienna (Austria); University of Maryland (USA); University of California, San Diego (USA); Society for Molecular Biology & Evolution Conference (Spain); University of Chicago (USA)
- 2005 Society for Molecular Biology & Evolution Conference (USA)

PUBLICATIONS

lab members indicated; * authors contributed equally; # co-corresponding authors

GoogleScholar metrics: citations: 13,600 h-index: 52 i10-index: 103

In review / In revision

- 132) Mostrom, M., S. Yu, D. Tran, F. Saccoccio, C. Versoza, D. Malouli, A. Mirza, S. Valencia, M. Gilbert, R. Blair, S. Hansen, P. Barry, K. Fruh, J.D. Jensen, S.P. Pfeifer, T. Kowalik, S. Permar, and A. Kaur. 2023. Protective effect of pre-existing natural immunity in a nonhuman primate reinfection model of congenital cytomegalovirus infection. In review.
- 131) Soni, V., P. Johri, and J.D. Jensen. 2023. Evaluating power to detect recurrent selective sweeps under increasingly realistic evolutionary null models. In review.
- 130) Johri, P., S.P. Pfeifer, and J.D. Jensen. 2023. Developing an evolutionary baseline model for humans: jointly inferring purifying selection with population history. Accepted pending revision, *Molecular Biology & Evolution*.
- 129) Howell, A.A., J. Terbot, V. Soni, P. Johri, J.D. Jensen, and S.P. Pfeifer. 2023. Developing an appropriate evolutionary baseline model for the study of human cytomegalovirus. Accepted pending revision, *Genome Biology & Evolution*.

2023

- 128) Charlesworth, B., and J.D. Jensen. 2023. Population genetics. Forthcoming in the *Encyclopedia of Biodiversity, 3rd ed.* Elsevier Ltd.
- 127) Terbot, J., P. Johri, S. Liphardt, V. Soni, S.P. Pfeifer, B.S. Cooper[#], J.M. Good[#], and J.D. Jensen[#]. 2023. Developing an appropriate evolutionary baseline model for the study of SARS-CoV-2 patient samples. In press, *PLoS Pathogens*.
- 126) Freund, F., E. Kerdoncuff, S. Matuszewski, M. Lapierre, M. Hildebrandt, J.D. Jensen, L. Ferretti, A. Lambert, T. Sackton, and G. Achaz. 2023. Interpreting the pervasive observation of U-shaped site frequency spectra. In press, *PLoS Genetics*.
- 125) Ghafoor, S., J. Santos, C.J. Versoza, J.D. Jensen, and S.P. Pfeifer. 2023. The impact of sample size and population history on observed mutational spectra: a case study in human and chimpanzee populations. In press, *Genome Biology & Evolution*.
- 124) Charlesworth, B., and J.D. Jensen. 2023. Population genetic considerations regarding evidence of biased mutation rates in *Arabidopsis thaliana*. *Molecular Biology & Evolution* 40: msac275.

- 123) Jensen, J.D. 2023. Population genetic concerns related to the interpretation of empirical outliers and the neglect of common evolutionary processes. *Heredity* 130: 109-110.

2022

- 122) Charlesworth, B., and J.D. Jensen. 2022. Some complexities in interpreting apparent effects of hitchhiking: a commentary on Gompert *et al.* 2022. *Molecular Ecology* 31: 4440-4443.
- 121) Hager, E.R., O. Harringmeyer, T.B. Wooldridge, S. Theingi, J. Gable, S. McFadden, B. Neugeboren, K. Turner, J.D. Jensen, and H.E. Hoekstra. 2022. A chromosomal inversion contributes to divergence in multiple traits between deer mouse ecotypes. *Science* 377: 399-405.
- 120) Charlesworth, B., and J.D. Jensen. 2022. How can we resolve Lewontin's paradox? *Genome Biology & Evolution* 14(7): evac096.
- 119) Johri, P., A. Eyre-Walker, R. Gutenkunst, K. Lohmueller, and J.D. Jensen. 2022. On the prospect of achieving accurate joint estimation of selection with population history. *Genome Biology & Evolution* 14(7): evac088.
- 118) Johri, P., C.F. Aquadro, M. Beaumont, B. Charlesworth, L. Excoffier, A. Eyre-Walker, P. Keightley, M. Lynch, G. McVean, B.A. Payseur, S.P. Pfeifer, W. Stephan, and J.D. Jensen. 2022. Recommendations for improving statistical inference in population genomics. *PLoS Biology* 20(5): e3001669.
- 117) Sabin, S., A. Morales-Arce, S.P. Pfeifer, and J.D. Jensen. 2022. The impact of frequently neglected model violations on bacterial recombination rate estimation: a case study in *Mycobacterium canettii* and *Mycobacterium tuberculosis*. *G3: Genes, Genomes, Genetics* 12(5): jkac055.
- 116) Jiang, L., N. Samant, P. Liu, M. Somasundaran, J.D. Jensen, W. Marasco, C. Schiffer, R. Finberg, J. Wang, T.F. Kowalik, and D.N. Bolon. 2022. Identification of a permissive secondary mutation that restores the enzymatic activity of oseltamivir resistance mutation H275Y. *Journal of Virology* 96: e0198221.
- 115) Morales-Arce, A.*, P. Johri*, and J.D. Jensen. 2022. Inferring the distribution of fitness effects in patient-sampled and experimental virus populations: two case studies. *Heredity* 128: 79-87.
- 114) Johri, P., W. Stephan, and J.D. Jensen. 2022. Soft selective sweeps: addressing new definitions, evaluating competing models, and interpreting empirical outliers. *PLoS Genetics* 18(2): e1010022.

2021

- 113) Johri, P. *, B. Charlesworth*, E. Howell, M. Lynch, and J.D. Jensen. 2021. Revisiting the notion of deleterious sweeps. *Genetics* 219: iyab094.
- 112) Charlesworth, B., and J.D. Jensen. 2021. Effects of selection at linked sites on patterns of genetic variability. *Annual Review of Ecology, Evolution, and Systematics* 52: 177-197.
- 111) Johri, P., K. Riall, H. Becher, L. Excoffier, B. Charlesworth, and J.D. Jensen. 2021. The impact of purifying and background selection on the inference of population history: problems and prospects. *Molecular Biology & Evolution* 38: 2986-3003.
- 110) Wang, H.-Y., S. Valencia, S.P. Pfeifer, J.D. Jensen, T.F. Kowalik, and S.R. Permar. 2021. Common polymorphisms in the glycoproteins of human cytomegalovirus and associated strain-specific immunity. *Viruses* 13: 1106.
- 109) Jensen, J.D. 2021. Studying population genetic processes in viruses: from drug-resistance evolution to patient infection dynamics. In the *Encyclopedia of Virology, 4th ed.* Elsevier Ltd., Vol. 5: pgs. 227-232.
- 108) Clemente, F., M. Unterlander, O. Dolgova, C. Amorim, F. Coroado-Santos, S. Neunschwander, E. Ganiatsou, D. Cruz Davalos, L. Anchieri, F. Michaud, L. Winkelbach, J. Blocher, Y. Cardenas, B. Sousa de Mota, E. Kalliga, A. Souleles, I. Kontopoulos, G. Karamitrou-Mendessidi, O. Philaniotou, A. Sampson, D. Theodorou, M. Tsipopoulou, I. Akamatis, P. Halstead, K. Kotsakis, D. Urem-Kotsou, D. Panagiopoulous, C. Ziota, S. Triantaphyllou, O. Delaneau, J.D. Jensen, J. Moreno-Mayar, J. Burger, V.C. Sousa, O. Lao, A-S. Malaspinas, and C. Papageorgopoulou. 2021. The genomic history of the Aegean palatial civilizations. *Cell* 184: 2565-2586.
- 107) Morales-Arce, A., S. Sabin, A. Stone, and J.D. Jensen. 2021. Recent insights in to the population genomics of within-host tuberculosis. *Heredity* 126: 1-9.

2020

- 106) Jensen, J.D., R.A. Stikeleather, T.F. Kowalik, and M. Lynch. 2020. Imposed mutational meltdown as an antiviral strategy. *Evolution* 74: 2549-59.
- 105) Jones, M., L.S. Mills, J.D. Jensen, and J.M. Good. 2020. Convergent evolution of seasonal camouflage in response to reduced snow cover across the snowshoe hare range. *Evolution* 74: 2033-45.
- 104) Jones, M., L.S. Mills, J.D. Jensen, and J.M. Good. 2020. The origin and spread of locally adaptive seasonal camouflage in snowshoe hares. *The American Naturalist* 196: 316-32.

- 103) Harris, R. and J.D. Jensen. 2020. Considering genomic scans for selection as coalescent model choice. *Genome Biology & Evolution* 12: 871-877.
- 102) Morales-Arce, A.Y., R. Harris, A.C. Stone, and J.D. Jensen. 2020. Evaluating the contributions of purifying selection and progeny-skew in dictating within-host *Mycobacterium tuberculosis* evolution. *Evolution* 74: 992-1001.
- 101) Johri, P., B. Charlesworth, and J.D. Jensen. 2020. Towards an evolutionarily appropriate null model: jointly inferring demography and purifying selection. *Genetics* 215: 173-92.
- 100) Jensen, J.D., and M. Lynch. 2020. Considering mutational meltdown as a potential SARS-CoV-2 treatment strategy. *Heredity* 124: 619-20.
- 99) Harris, R., K. Irwin, M. Jones, S. Laurent, R. Barrett, M. Nachman, J. Good, C. Linnen, J.D. Jensen, and S.P. Pfeifer. 2020. The population genetics of crypsis in vertebrates: recent insights from mice, hares, and lizards. *Heredity* 124: 1-14.
- 98) Jensen, J.D., and T.F. Kowalik. 2020. A consideration of within-host human cytomegalovirus (HCMV) genetic diversity. *PNAS* 117: 816-7.

2019

- 97) Sackman, A., R. Harris, and J.D. Jensen. 2019. Inferring demography and selection in organisms characterized by skewed offspring distributions. *Genetics* 211: 1019-28.
- 96) Barrett, R. *, S. Laurent*, R. Mallorino*, S.P. Pfeifer, C. Xu, M. Foll, K. Wakamatsu, J. Duke-Cohan, J.D. Jensen, and H.E. Hoekstra. 2019. Linking a mutation to survival in wild mice. *Science* 363: 499-504.
- 95) Jensen, J.D., B. Payseur, W. Stephan, C. Aquadro, M. Lynch, D. Charlesworth, and B. Charlesworth. 2019. The importance of the Neutral Theory in 1968 and 50 years on: a reply to Kern & Hahn 2018. *Evolution* 73: 111-14.
- 94) Prachanronarong, K., A.S. Canale, P. Liu, M. Somasundaran, S. Hou, Y.-P. Poh, T. Han, Q. Zhu, N. Renzette, K. Zeldovich, T.F. Kowalik, N. Kurt-Yilmaz, J.D. Jensen, D.N. Bolon, W.A. Marasco, R.W. Finberg, C.A. Schiffer, and J.P. Wang. 2019. Mutations in influenza A virus neuraminidase and hemagglutinin confer resistance against a broadly neutralizing hemagglutinin stem antibody. *Journal of Virology* 93(2): e01639.

2018

- 93) Harris, R. *, A. Sackman*, and J.D. Jensen. 2018. On the unfounded enthusiasm for soft selective sweeps II: examining recent evidence from humans, flies and viruses. *PLoS Genetics* 14(12): e1007859.

- 92) Fragata, I. *, S. Matuszewski*, M. Schmitz, T. Bataillon, J.D. Jensen, and C. Bank. 2018. The fitness landscape of the codon table across environments. *Heredity* 121: 422-37.
- 91) Kapopoulou, A., S.P. Pfeifer, J.D. Jensen, and S. Laurent. 2018. The demographic history of African *Drosophila melanogaster*. *Genome Biology & Evolution* 10(9): 2338-42.
- 90) Jones, M.R., L. S. Mills, P.C. Alves, C.M. Callahan, J. Alves, D.J.R. Lafferty, F.M. Jiggins, J.D. Jensen, J. Melo-Ferreira, and J.M. Good. 2018. Adaptive introgression underlies polymorphic seasonal camouflage in Snowshoe Hares. *Science* 360(6395): 1355-58.
- 89) Canale, A., S. Venev, T. Whitfield, D. Caffrey, W. Marasco, C. Schiffer, T. Kowalik, J.D. Jensen, R. Finberg, K. Zeldovich, J. Wang, and D. Bolon. 2018. Synonymous mutations at the beginning of the influenza A virus hemagglutinin gene impact experimental fitness. *Journal of Molecular Biology* 430: 1098-1115.
- 88) Pfeifer, S.*, S. Laurent*, V. Sousa*, C. Linnen*, M. Foll, L. Excoffier#, H.E. Hoekstra#, and J.D. Jensen#. 2018. The evolutionary history of Nebraska deer mice: local adaptation in the face of strong gene flow. *Molecular Biology & Evolution* 35: 792-806.
- 87) Sackman, A.M., S.P. Pfeifer, T.F. Kowalik, and J.D. Jensen. 2018. On the demographic and selective forces shaping patterns of human cytomegalovirus variation within hosts. *Pathogens* 7: 16.
- 86) Matuszewski, M., M. Hildebrandt, G. Achaz, and J.D. Jensen. 2018. Coalescent processes with skewed offspring distributions and non-equilibrium demography. *Genetics* 208: 323-38.
- 2017**
- 85) Avnir, Y., K. Prachanronarong, Z. Zhang, S. Hou, E. Peterson, J. Sui, H. Zayed, V. Kurella, A. McGuire, L. Stamatatos, B. Hilbert, M. Bohn, K. Zeldovich, T. Kowalik, J.D. Jensen, D. Bolon, R. Finberg, J. Wang, R. Jefferis, Q. Zhu, N. Yilmaz, C. Schiffer, and W. Marasco. 2017. Structural determination of the broadly reactive anti-IGHV1-69 anti-idiotypic antibody G6 and its idiotope. *Cell Reports* 21: 3243-3255.
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