Jeffrey D. Jensen

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EDUCATION

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

PROFESSIONAL EXPERIENCE

2016-present	**Professor** Arizona State University, School of Life Sciences Center for Evolution & Medicine, Center for Mechanisms of Evolution
2024	**Sabbatical Fellow** University of Oxford, Merton College
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
2001	**BRAVO Undergraduate Research Abroad Fellow** University of Edinburgh, Institute of Evolutionary Biology Advisor: Brian Charlesworth

PROFESSIONAL INTERESTS

population genetics, evolutionary genomics

FUNDING & AWARDS

2021-2026	U.S. National Institutes of Health, NIGMS, R35 PI *On differentiating selective and neutral evolutionary processes*
2022	Outstanding Postdoctoral Mentor of the Year Award - Awarded annually by ASU in recognition of contributions to mentorship
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*
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*
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*

PROFESSIONAL SERVICE

Societies:

Genetics Society of America (GSA); Society for the Study of Evolution (SSE); Society for Molecular Biology and Evolution (SMBE); American Association for the Advancement of Science (AAAS)

Editorial:

2016-2023	*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, Cell Genomics, Ecology and Evolution, 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:
SOLS Research Initiatives (RI) Committee (ASU) (2023-present)
elected member of ASU's Graduate Faculty Mentor Academy (GFMA) (2022-present)
AZPopGroup organizer (USA, 2016-present)
Faculty Search Committee: Mechanisms of Evolution (ASU) (2018-19)
Faculty Search Committee: Mechanisms of Evolution (ASU) (2017-18)
Research Committee: Center for Evolution & Medicine (ASU) (2016-18)
‘Clinically Relevant Population Genetics’ workshop organizer (USA, 2017)
German Science Foundation, Rapid Evolutionary Adaptation Grant Panel (2015-16)
‘Theoretical & Empirical Evidence of Adaptation’ workshop organizer (CH, 2015)
European Society for Evolutionary Biology Conference organizer (CH, 2015)
‘Systems Genetics & Evolution’ workshop organizer (CH, 2015)
Serbian Genetics Society, Scientific Advisor (2015)
Graduate Admissions Committee: Life Sciences (EPFL) (2013-15)
Faculty Search Committee: Ecology of Infectious Disease (ETH) (2013-14)
National Academy of Finland, Scientific Advisor (2013)
‘Bridging Theoretical & Experimental Evolution’ workshop organizer (CH, 2013)
Faculty Search Committee: Integrative Biology (UMass Med School) (2010-11)

TEACHING

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

ADVISING

Postdoctoral Scholars

2024-present	Adriana Calahorra-Oliart
2022-present	John Terbot II
2021-present	Vivak Soni

2018-2023	Parul Johri *Asst Professor, Dept of Genetics, UNC-Chapel Hill, USA*
2019-2021	Susanna Sabin *Staff Biologist, CDC, USA*
2018-2020	Ana Morales-Arce *Research Fellow, IZSVe, IT*
2019-2020	João Santos *Research Consultant, INSA, PT*
2019-2020	Matt Jones *Research Biologist, USGS, USA*
2017-2019	Rebecca Harris *Senior Manager of Comp Bio, Adaptive Biotech, USA*
2017-2019	Andrew Sackman *Asst Professor, Virginia Commonwealth Univ, USA*
2015-2017	Sebastian Matuszewski *Data Engineering Manager, Accenture, AT*
2014-2017	Stefan Laurent *Associate Director of Bioinformatics, BioNTech, DE*
2015-2017	Severine Vuilleumier *Professor & Vice-Dean of Research, La Source (HES-SO), CH*
2011-2016	Nicholas Renzette *Director of Bioinformatics, Essex Management, USA*
2015-2016	Valeria Montano *Statistical Geneticist, James Hutton Institute (BioSS), UK*
2013-2015	Greg Ewing *Test Engineer, Rocket Lab, NZ*
2012-2015	Claudia Bank *Professor & Director of Inst of Ecol & Evol, Univ of Bern, CH*
2013-2015	Anna Ferrer Admettla *General Director, Naccari Ravà Foundation, ES*
2012-2014	Matthieu Foll *Bioinformatics Scientist, IARC-WHO, FR*
2010-2014	Yu-Ping Poh *Research Scientist, ASU Center for Mechanisms of Evol, USA*
2013-2014	Cornelia Pokalyuk *Professor, Institute of Mathematics, Univ of Lübeck, DE*
2012-2013	Lisha Mathew *Bioinformatician, CeGaT, DE*
2012-2013	Daniel Wegmann *Professor, Dept of Biology, Univ of Fribourg, CH*

Graduate Students (Ph.D.)

2013-2018	Mado Kapopoulou *Senior Bioinformatician, Inst of Ecol & Evol, Univ of Bern, CH*
2012-2017	Louise Ormond *Research Scientist, Univ of Lausanne Hospital (CHUV), CH*
2009-2014	Alfred Simkin *Asst Research Professor, Dept of Pathology, Brown Univ, USA*
2009-2013	Jessica Crisci *freelance artist, USA*

Graduate Students (M.S.)

2016-2017	Marcel Hildebrandt *Research Scientist, Siemens, DE*
2016-2017	Stefano Tartini *Project Manager, SBB CFF FFS, CH*
2012-2014	Hyunjin Shim *Asst Professor, College of Science, Cal State Univ - Fresno, USA*
2011-2013	Priyanka Sinha *Lead Consultant for Data Science, Capgemeni, NZ*

Staff Members

2019-2021	Kellen Riall *PhD student, Berg Lab, Univ of Chicago, USA*
2014-2017	Kristen Irwin *Head of International Funding, EPFL, CH*
2012-2013	Shivani Mahajan *Head of Computational Science, Helio Genomics, USA*

Sabbatical & Study Abroad Visitors

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

Thesis Committees

Kevin Leempoel (Golay Lab, EPFL), Pierre Helleboid (Trono Lab, EPFL), Ana Bittencourt (Fellay Lab, EPFL), Piedro 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, Univ. of Lausanne), Ryan Hietpas (Bolon Lab, UMass Med School), Alex Panzierra (Bertorelle Lab, Univ. of Ferrara), Adele Crane (Stone Lab, ASU), Gaurav Bilolikar (Geiler-Samerotte Lab, ASU), Abigail Howell (Pfeifer Lab, ASU), Mario Apata (Wilson Lab, ASU), Cyril Versoza (Pfeifer Lab, ASU), Man Lin (Lynch Lab, ASU), Mark Milhaven (Pfeifer Lab, ASU)

Undergraduate Research 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, Anaïs Haget, Roger Kung, Marie Malier, Dariush Mollet, Mathieu Quinodoz, Pauline Reiff, Tamara Rossy, Stefano Tartini, Gaelle Thurre, Florian Widmer
ASU (2017-present): Kellen Riall, Emma Howell, Devangana Shah

INVITED LECTURES

2020-current	Cornell (USA); U.Pittsburgh (USA); Virginia Tech (USA); FSU (USA); U.Chicago (USA); U.Berne (CH); 'Precision Medicine 2.0' symposium (USA); OSU (USA), U.Edinburgh (UK)
2015-2019	UW-Madison (USA); 'Evolutionary Genetics of Infectious Disease' symposium (CA); MidwesternU. (USA); Cornell (USA); MPI Plant Breeding (DE); U.Arizona (USA); U.Montana (USA); AZPopGroup (USA); ‘Clinically Relevant Population Genetics’ workshop (USA); SIB symposium (CH); U.Basel (CH); MPI Human History (DE); Mathematical Evolutionary Biology Conf (FR); EMBO Conf (DE); MPI Plant Breeding (DE); USC (USA); ASU (USA); SSE Conf (BR); ‘Theoretical & Empirical Evidence of Adaptation’ workshop (CH); U.Zurich (CH); EAWAG (CH); MPI Plant Breeding (DE); LMU-Munich (DE); VetMedUni (AT); IST (AT); PopGenomics workshop (DE)
2010-2014	Systems Genetics & Evolution Conf (CH); U.Arizona (USA); National Academy of Finland (FI); SMBE Conf (USA); Instituto Gulbenkian Ciencia (PT); ‘Population Genetics Models Including Selection’ workshop (DE); U.Konstanz (DE); MakerereU. (UG); ‘Landscape Genomics’ workshop (CH); U.Edinburgh (UK); Konrad Lorenz Institute (AT); U.Vienna (AT); Heidelberg Institute for Theoretical Studies (DE); SIB Population Genetics Summer School (CH); Lausanne Genomics Day (CH); U.Basel (CH); U.Lausanne (CH); ‘Evolutionary Innovations’ workshop (DE); SMBE Conf (JP); ESEB Conf (DE); Harvard (USA); Oxford (UK); USC (USA); EPFL (CH); U.Idaho (USA)
2005-2009	Brandeis (USA); ‘Mathematical Challenges from Genetics’ workshop (CA); Neandertal Genome Consortium Conf (USA); Neandertal Genome Consortium Conf (HR); Harvard (USA); NCSU (USA); UNC (USA); LMU-Munich (DE); MPI Evolutionary Anthropology (DE); Sanger Institute (UK); ‘Statistical Inference of Selection’ workshop (AT); Cornell (USA); Monod Conf in Evolutionary Genetics (FR); U.Arizona (USA); U.Vienna (AT); U.Maryland (USA); UCSD (USA); SMBE Conf (ES); U.Chicago (USA); SMBE Conf (USA)

PUBLICATIONS

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

in review / revision

145) Soni, V., C. Versoza, S.P. Pfeifer#, and J.D. Jensen#. 2025. Estimating the distribution of mutational fitness effects in aye-ayes (*Daubentonia madagascariensis*), accounting for the confounding effects of population history, background selection, and mutation and recombination rate variation. in review.

144) Soni, V. *, C. Versoza*, J. Terbot, J.D. Jensen#, and S.P. Pfeifer#. 2025. Inferring fine-scale mutation and recombination rate maps in aye-ayes (*Daubentonia madagascariensis*). in review.

143) Versoza, C. *, Lloret-Villas, A. *, J.D. Jensen, and S.P. Pfeifer. 2025. A pedigree-based map of crossovers and non-crossovers in aye-ayes (*Daubentonia madagascariensis*). in review.

142) Versoza, C., E. Ehmke, J.D. Jensen, and S.P. Pfeifer. 2025. Characterizing the rates and patterns of *de novo* germline mutations in the aye-aye (*Daubentonia madagascariensis*). in review.

141) Soni, V., J. Terbot, C. Versoza, S.P. Pfeifer#, and J.D. Jensen#. 2025. A whole-genome scan for evidence of recent positive and balancing selection in aye-ayes (*Daubentonia madagascariensis*) utilizing a well-fit evolutionary baseline model. in review.

140) Versoza, C., J.D. Jensen, and S.P. Pfeifer. 2025. The landscape of structural variation in aye-ayes (*Daubentonia madagascariensis*). in review.

139) Soni, V., and J.D. Jensen. 2025. Inferring demographic and selective histories from population genomic data using a two-step approach in species with coding-sparse genomes: an application to human data. in review.

138) Terbot, J., V. Soni, C. Versoza, S.P. Pfeifer#, and J.D. Jensen#. 2025. Inferring the demographic history of aye-ayes (*Daubentonia madagascariensis*) from high-quality, whole-genome, population-level data. in revision.

2024

137) Soni, V., and J.D. Jensen. 2024. Temporal challenges in detecting balancing selection from population genomic data. *G3* 14: jkae069.

136) Soni, V., J. Terbot, and J.D. Jensen. 2024. Population genetic considerations regarding the interpretation of within-patient SARS-CoV-2 polymorphism data. *Nature Communications* 15: 3240.

135) Soni, V., S.P. Pfeifer, and J.D. Jensen. 2024. The effects of mutation and recombination rate heterogeneity on the inference of demography and the distribution of fitness effects. *Genome Biology & Evolution* 16: evae004.

134) Versoza, C., S. Weiss, R. Johal, B. La Rosa, J.D. Jensen, and S.P. Pfeifer. 2024. Novel insights into the landscape of crossover and non-crossover events in rhesus macaques. *Genome Biology & Evolution* 16: evad223.

133) Charlesworth, B., and J.D. Jensen. 2024. Population genetics. *Encyclopedia of Biodiversity, 3rd ed.* Elsevier Ltd. Vol. 7: 467-483.

2023

132) Terbot, J., B. Cooper, J. Good, and J.D. Jensen. 2023. A simulation framework for modeling the within-patient evolutionary dynamics of SARS-CoV-2. *Genome Biology & Evolution* 15: evad204.

131) Moström, 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. *PLoS Pathogens* 19: e1011646.

130) Soni, V., P. Johri, and J.D. Jensen. 2023. Evaluating power to detect recurrent selective sweeps under increasingly realistic evolutionary null models. *Evolution* 77: 2113-2127.

129) Johri, P., S.P. Pfeifer, and J.D. Jensen. 2023. Developing an evolutionary baseline model for humans: jointly inferring purifying selection with population history. *Molecular Biology & Evolution* 40: msad100.

128) 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. *Genome Biology & Evolution* 15: evad059.

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. *PLoS Pathogens* 19: e1011265.

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. *PLoS Genetics* 19: e1010677.

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. *Genome Biology & Evolution* 15: evad019.

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. Panagiotopoulous, 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.

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