# **Alan Ray Rogers**

April 1, 2021

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#### **Education**

1974	B.A. Dept. of Anthropology, University of Texas at Austin.
1978	M.S. Dept. of Anthropology, University of New Mexico.
1982	Ph.D. Dept. of Anthropology, University of New Mexico.

Address

## **Areas of Specialization**

Population genetics; evolutionary ecology

### **Positions and honors**

1/21–	Recommender, PCI Mathematical and Computational Biology
2/20-	Recommender, PCI Evolutionary Biology
3/16–12/20	Scientific Advisory Board, Max Planck Institute for Evolutionary Anthropology.
7/94–	Professor, Dept. of Anthropology, University of Utah.
4/98-	Adjunct Professor, Dept. of Biology, University of Utah.
3/08–4/10	Committee on the Earth System Context for Hominin Evolution, National Research Council of the National Academies.
10/96–5/98	Associate Editor, Molecular Biology and Evolution
8/96–7/97	Research Centre, King's College, Cambridge
7/94–06	Adjunct Associate Professor, Dept. of Human Genetics, University of Utah.
7/91–6/94	Associate Professor, Dept. of Anthropology, University of Utah.
1991	Superior Research Award (Junior Category), College of Social and Behavioral Science, University of Utah.
7/88–6/91	Assistant Professor, Dept. of Anthropology, University of Utah.
8/85–6/88	Research Assistant Professor, Dept. of Anthropology, University of Pittsburgh.
9/83-8/85	Assistant Professor, Dept. of Anthropology, SUNY-Albany

#### **Publications**

- [1] Jeremy S. Morris, Nala Rogers, Alan R. Rogers, and David R. Carrier. Sexual dimorphism in skeletal shape in voles (*Arvicolinae*): Disparate selection on male bodies and female heads. *Journal of Mammalogy*, 2020.
- [2] Alan R. Rogers. The deep history of human populations. *Newsletter of the Center for High-Performance Computing, University of Utah*, Spring, 2020.
- [3] Alan R. Rogers, Nathan S. Harris, and Alan A. Achenbach. Neanderthal-Denisovan ancestors interbred with a distantly-related hominin. *Science Advances*, 6(8):eaay5483, 2020.
- [4] Alan R. Rogers. Legofit: Estimating population history from genetic data. *BMC Bioinformatics*, 20: 526, 2019.
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- [6] Alan R. Rogers, Ryan J. Bohlender, and Chad D. Huff. Reply to Mafessoni and Prüfer: Inferences with and without singleton site patterns. *Proceedings of the National Academy of Sciences, USA*, 114 (48):E10258–E10260, 2017.
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- [8] Hao Hu, Nayia Petousi, Gustavo Glusman, Yao Yu, Ryan Bohlender, Tsewang Tashi, Jonathan M Downie, Jared C. Roach, Amy M. Cole, Felipe R. Lorenzo, Alan R. Rogers, Mary E. Brunkow, Gianpiero Cavalleri, Leroy Hood, Sama M. Alpatty, Josef T. Prchal, Lynn B. Jorde, Peter A. Robbins, Tatum S. Simonson, and Chad D Huff. Evolutionary history of Tibetans inferred from whole-genome sequencing. *PLoS Genetics*, 13(4):e1006675, 2017.
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- [10] Alan R. Rogers and Ryan J. Bohlender. Bias in estimators of archaic admixture. *Theoretical Population Biology*, 100:63–78, March 2015. ISSN 0040-5809.
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- [12] Alan R. Rogers. The molecular clock. In Heinrich D. Holland and Karl K. Turekian, editors, *Treatise on Geochemistry*, volume 14, pages 55–61. Elsevier, 2nd edition, 2014.
- [13] Jack M. Broughton, R. Kelly Beck, Joan B. Coltrain, Dennis H. O'Rourke, and Alan R. Rogers. A late Holocene population bottleneck in California Tule elk (*Cervus elaphus nannodes*): Provisional support from ancient DNA. *Journal of Archaeological Method and Theory*, 20(3):495–524, Sept 2013.

- [14] Alan R. Rogers. Genetic relatedness to sisters' children has been underestimated. *Proceedings of the Royal Society of London, Series B*, 280, 2012.
- [15] Alan R. Rogers. The Evidence for Evolution. University of Chicago Press, 2011.
- [16] NRC Committee on the Earth Systems Context for Hominin Evolution. *Understanding Climate's Influence on Human Evolution*. The National Academies Press, Washington, D. C., 2010.
- [17] Chad D. Huff, Henry C. Harpending, and Alan R. Rogers. Detecting positive selection from genome scans of linkage disequilibrium. *BMC Genomics*, 11(1):8, 2010.
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- [19] Alan R. Rogers and Chad Huff. Linkage disequilibrium between loci of unknown phase. *Genetics*, 182(3):839–844, July 2009.
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### **Research Funding**

NSF BCS 1945782. "Genetic evidence on the deep history of human populations." (AR Rogers, PI; T Webster, Co-PI) Amount: \$267,670.
NSF BCS 1638840. "Effect of archaic admixture on modern human adaptations." (AR Rogers, PI) Amount: \$175,000.
NSF BCS 1321412. "Did hunting or climate change cause a Late Holocene bottleneck in California Tule Elk? An integrated test using ancient DNA and stable isotopes." (J Broughton, PI; AR Rogers & JB Coltrain, Co-PIs) Amount: \$203,716.
NSF 0343198. Demography of the Tchimba of Northwest Namibia (AR Rogers, PI). Funded Steven Josephson's field work. Amount: \$30,314.
NSF SBR-0218338. Collaborative research: mobile elements and primate evolution (LB Jorde, PI). Provides summer salary for 5 years, and paid for a computer programmer.
NIH GM59290 Population genetics of mobile elements. (LB Jorde, PI) provides $50\%$ release from teaching for 4 years.
NSF 9512178. "Acquisition of Equipment for Automated DNA Sequencing." (LB Jorde, PI) Amount: \$112,932.
Supplement to NSF grant DBS-9310105 for purchase of PCR machine. Amount: \$5,400. [The University of Utah contributed an additional \$5,400.]
NSF DBS–9310105. 2-year continuation of "Molecular Genetic Studies of Human Evolutionary History." Amount: \$192,522.
NSF DBS-9211255 1-year project "Molecular Genetic Studies of Human Evolutionary History." Amount: \$90,709.
Grant from the College of Social and Behavioral Sciences, University of Utah, for a study of age-differences in rates of time preference. Amount: \$1,200.
NIH grant MGN 1 R29 GM39593: Structured emigration and genetic population differences. Funding for first year: \$57,805.

# **Presentations**

Oct 2014	How population growth affects linkage disequilibrium. American Society of Human Genetics. San Diego, CA. (poster)
Nov 2014	Bias in estimates of archaic admixture. Utah Molecular Evolution Retreat. Deer Valley, UT.
Oct 2015	The recent history of human population size. American Society of Human Genetics. Baltimore, MD. (poster)
Apr 2016	Allele sharing between archaic and modern humans. American Association of Physical Anthropologists. Atlanta, GA.
May 2016	Bias in estimates of archaic admixture. Society of Molecular Biology and Evolution Satellite Meeting on the Genetics of Admixed Populations. San Antonio, TX. (poster)
Nov 2016	Legofit: a new estimator of the history of population size and admixture. Southwest Association of Biological Anthropologists. Arizona State University. (poster)
April 2017	Genetic evidence for an archaic human diaspora. American Association of Physical Anthropologists. New Orleans, LA.
July 2017	The origin of Neanderthals and Denisovans. Society for Molecular Biology and Evolution. Austin, TX.
Feb 2018	Hyperarchaic admixture into Denisovans. Invited lecture, University of Utah.
Feb 2018	Hyperarchaic admixture into Denisovans. Invited lecture, Rutgers University.
Feb 2018	Hyperarchaic admixture into Denisovans. Invited lecture, University of Utah.
April 2018	Genetic evidence for early separation of Neanderthals and Denisovans and an early archaic bottleneck. American Association of Physical Anthropologists. Austin, TX.
Sept 2018	The early history of Neanderthals and Denisovans. International Symposium on Biomolecular Archaeology. Jena, Germany.
Mar 2019	Superarchaic admixture confirms a deep separation of Neanderthals and Denisovans. American Association of Physical Anthropologists. Cleveland, OH.
Nov 2019	Neanderthal-Denisovan ancestors interbred with a distantly-related hominin. Southwest Association of Biological Anthropologists, Arizona State University.
Apr 2019	Neanderthal-Denisovan ancestors interbred with a distantly-related hominin. American Association of Physical Anthropologists. Los Angeles; moved online at https://meeting.physanth.org/registration/286033.
Mar 2021	Neanderthal-Denisovan ancestors interbred with a distantly-related hominin. Dept. of Bioinformatics and genomics, UNC-Charlotte. Invited lecture.