

Chase W. Nelson

Sackler Institute for Comparative Genomics
American Museum of Natural History
Central Park West at 79th St.
New York, NY 10024

Phone: (616) 283-7294

Email: cnelson@amnh.org

Website: www.chasewnelson.com

GitHub: www.github.com/chasewnelson

Education

- 2011-2016 **Ph.D. Biological Sciences**, University of South Carolina
2006-2010 **B.A. Biology (*honors*)**, Oberlin College

Expertise

Subject Areas: bioinformatics, computational biology, data analysis, evolution, geographic information systems (GIS), genomics, immunogenetics, molecular evolution, mutation, next-generation sequencing (NGS), phylogenetics, population genetics, statistics, virology

Model Organisms Handled: *A. thaliana*, *C. elegans*, *D. melanogaster*, *Z. mays*

Computational Skills: ArcGIS, BLAST, Clustal, databases, Excel, GitHub, IGV, MEGA, motif detection, Perl, PHYLIP, PowerPoint, Python, R, SAMtools, SAS, SQL, SWISS-MODEL, Unix & Linux, Word

Molecular Biology Skills: gel electrophoresis, DNA & RNA isolation, hemocytometer use, in vitro cell treatment, microscopes, PCR, qRT-PCR, SDS-PAGE, TT-PCR, zymography

Research Appointments

- 2016- **Gerstner Scholar in Bioinformatics and Computational Biology**
Sackler Institute for Comparative Genomics, American Museum of Natural History (NYC)
Bioinformatics tool development and research on West Nile virus, overlapping genes, etc.
- 2017- **Special Volunteer**, NCI-DCEG HPV Genomics Group (PI: Lisa Mirabello)
National Cancer Institute, National Institutes of Health (Rockville, MD)
Evolutionary bioinformatics research on human papillomavirus and cervical cancer.
- 2016- **Visiting Scholar**, EvoNet Project (PIs: Gloria Coruzzi & Rob DeSalle)
Center for Genomics and Systems Biology, New York University (NYC)
Development of molecular evolution methods for the PhyloGeneious pipeline.

2010-2011

Research Scientist

Rainbow Technologies, Inc. (Waterloo, NY)

Digital evolution research examining the role of low-impact mutations and selective neutrality.

Publications

- 2017 Hücker SM, Ardern Z, Goldberg T, Schafferhans A, Bernhofer M, Vestergaard G, **Nelson CW**, Schlöter M, Rost B, Scherer S, Neuhaus K. Discovery of numerous novel small genes in the intergenic regions of the Escherichia coli O157:H7 Sakai genome. *PLoS One* **12**(9): e0184119.
- 2017 Mirabello L, Yeager M, Yu K, Clifford GM, Xiao Y, Zhu B, Cullen M, Boland JF, Wentzensen N, **Nelson CW**, Raine-Bennett T, Chen Z, Bass S, Song L, Yang Q, Steinberg M, Burdett L, Dean M, Roberson D, Mitchell J, Lorey T, Franceschi S, Castle PE, Walker J, Zuna R, Kreimer AR, Beachler DC, Hildesheim A, Gonzalez P, Porras C, Burk RD, Schiffman M. HPV16 E7 genetic conservation is critical to carcinogenesis. *Cell* **170**(6): 1164-74.
- 2017 Moncla LH, Weiler AM, Barry G, Weinfurter JT, Dinis JM, Charlier O, Lauck M, Bailey AL, Wahl-Jensen V, **Nelson CW**, Johnson JC, Cai Y, Goldberg TL, O'Connor DH, Jahrling PB, Kuhn JH, Friedrich TC. Within-host evolution of simian arteriviruses in crab-eating macaques. *Journal of Virology* **91**(4): e02231-16.
- 2017 **Nelson C**. The obstetrical dilemma. *Inference: International Review of Science* **2**(4).
- 2016 Bailey AL, Lauck M, Ghai RR, **Nelson CW**, Heimbruch K, Hughes AL, Goldberg TL, Kuhn JH, Jasinska AJ, Freimer NB, Apetrei C, O'Connor DH. Arteriviruses, pegiviruses, and lentiviruses are common among wild African monkeys. *Journal of Virology* **90**(15): 6724-6737.
- 2016 **Nelson C**. Austin L. Hughes: the neutral theory of evolution. *Inference: International Review of Science* **2**(2).
- 2016 **Nelson CW**. Remembering Austin L. Hughes. *Infection, Genetics and Evolution* **40**: 262-5.
- 2016 Moncla LH, Zhong G, **Nelson CW**, Dinis JM, Mutschler J, Hughes AL, Watanabe T, Kawaoka Y, Friedrich TC. Selective bottlenecks shape evolutionary pathways taken during mammalian adaptation of a 1918-like avian influenza virus. *Cell Host & Microbe* **19**(2): 169-80.
- 2016 **Nelson CW**. The humble scientist. *The New Atlantis* **47**: 98-102.
- 2015 Gellerup D, Balgeman A, **Nelson CW**, Ericson A, Scarlotta M, Hughes AL, O'Connor S (2015) Conditional immune escape during chronic SIV infection. *Journal of Virology* **90**(1): 545-52.

- 2015 **Nelson CW**, Moncla LH, Hughes AL. SNPGenie: estimating evolutionary parameters to detect natural selection using pooled next-generation sequencing data.
Bioinformatics **31**(22): 3709-11.
- 2015 **Nelson C**. Haldane's dilemma.
Inference: International Review of Science **1**(3).
- 2015 **Nelson CW**, Hughes AL (2015) Within-host nucleotide diversity of virus populations: Insights from next-generation sequencing.
Infection, Genetics and Evolution **30**: 1-7.
- 2014 Bailey AL, Lauck A, Weiler A, Sibley SD, Dinis JM, Bergman Z, **Nelson CW**, Correll M, Gleicher M, Hyeroba D, Tumukunde A, Weny G, Chapman C, Kuhn JH, Hughes AL, Friedrich TC, Goldberg TL, O'Connor DH. High genetic diversity and adaptive potential of two simian hemorrhagic fever viruses in a wild primate population.
PLoS ONE **9**(3): e90714.
- 2013 Wilker PR, Dinis JM, Starrett G, Imai M, Hatta M, **Nelson CW**, O'Connor DH, Hughes AL, Neumann G, Kawaoka Y, Friedrich TC. Selection on haemagglutinin imposes a bottleneck during mammalian transmission of reassortant H5N1 influenza viruses.
Nature Communications **4**: 2636.
- 2013 **Nelson CW**, Sanford JC. Computational evolution experiments reveal a net loss of genetic information despite selection.
Biological Information: New Perspectives, World Scientific, pp. 338-368.
- 2013 Gryder BE, **Nelson CW**, Shepard SS. Biosemiotic entropy of the genome: mutations and epigenetic imbalances resulting in cancer.
Entropy **15**: 234-261.
- 2012 Sanford JC, **Nelson CW**. The next step in understanding population dynamics: comprehensive numerical simulation.
Studies in Population Genetics, InTech, pp. 117-136.
- 2011 **Nelson CW**, Sanford JC. The effects of low-impact mutations in digital organisms.
Theoretical Biology and Medical Modeling **8**: 9.
- 2011 Lichtenberg J, Yilmaz A, Kurz K, Liang X, **Nelson C**, Bitterman T, Stockinger E, Grotewold, Welch LR. Encyclopedias of DNA elements for plant genomes.
Science, Engineering, and Biology Informatics – Vol. 7: Advances in Genomic Sequence Analysis and Pattern Discovery, World Scientific, pp. 159-178.
- 2009 Lichtenberg J, Alam M, Bitterman T, Drews F, Ecker K, Elnitski L, Evans S, Grotewold E, Gu D, Jacox E, Kurz K, Lee SS, Liang X, Majmudar PM, Morris P, **Nelson C**, Stockinger E, Welch JD, Wyatt S, Yilmaz A, Welch LR. Construction of genomic regulatory encyclopedias: strategies and case studies.
IEEE: Proceedings of the Ohio Collaborative Conference on Bioinformatics, pp. 65-70.

Software

- 2017- **overlapgenie**. <https://github.com/chasewnelson/overlapgenie>
Perl implementation of d_N/d_S methods for overlapping genes.
- 2016- **PhyloGeneious**. https://bitbucket.org/bigplant/bigplant_v4
Perl implementations of d_N/d_S likelihood and counting (within- and between-group) methods.
- 2014- **SNPGenie**. Nelson *et al.* (2015). <https://github.com/chasewnelson/snpgenie>
Perl software for estimation of d_N/d_S and diversity measures for next-generation sequence data.
Used and cited in 10 peer-reviewed studies.
- 2014- **CHASeq**. <https://github.com/chasewnelson/CHASeq>
Perl scripts providing Computational Help for the Analysis of SEquence data.

Awards & Honors

- 2013-2016 **Graduate Research Fellowship**, National Science Foundation
Support for doctoral research under Austin L. Hughes at the University of South Carolina.
- 2015 **F1000 Poster Prize**, Great Lakes Bioinformatics Conference
Awarded by the International Society for Computational Biology.
- 2015 **Kathryn Hinnant-Johnson, M.D. Memorial Fellowship**, University of South Carolina
Department of Biological Science award providing a one-time \$3,500 stipend supplement.
- 2015 **Department of Biological Sciences STEM Award**, University of South Carolina
Department of Biological Science award providing a one-time \$6,000 stipend supplement.
- 2011-2015 **Presidential Fellowship**, University of South Carolina
The Graduate School's premier merit-based fellowship, awarded annually to ≤ 30 Ph.D. students, providing a stipend supplement totaling \$16,000 over 4 years.
- 2013 **East Asian and Pacific Summer Institutes Fellowship**, National Science Foundation
Support for summer research under Wen-Hsiung Li at Academia Sinica (中央研究院) in Taiwan, providing round-trip airfare, a US\$5,000 stipend, and a ~US\$1,366 living allowance.
- 2011-2012 **ESPCoR Middleware Training Program Scholarship**, National Science Foundation
Awarded to graduate students pursuing computational research, offering specialized courses.
- 2010 **High Honors in Biology**, Oberlin College
Awarded for high GPA (4.01) and honors thesis work on Arabidopsis thaliana gene expression.
- 2010 **Society of Sigma Xi, The Oberlin Chapter**, Oberlin College
Selected by faculty for membership.
- 2010 **Joshua Levitt Memorial Prize in Biology**, Oberlin College
Academic achievement award given annually to a Junior and Senior Biology major.

- 2009-2010 **S-STEM Scholarship in Computation and Modeling**, National Science Foundation
Scholarship awarded to 4 Seniors pursuing careers in computational and modeling.
- 2006-2010 **John F. Oberlin Scholarship**, Oberlin College
Oberlin's premier academic scholarship, providing \$100,000 over 4 years.
- 2009 **IDeA Networks of Biomedical Research Excellence Fellowship**, National Institutes of Health
REU under David A. Liberles at the University of Wyoming providing a \$1,000 stipend.
- 2009 **Norman H. Wright Prize in Biology**, Oberlin College
Academic achievement awarded given annually to a rising to 2 Junior Biology majors.
- 2009 **Third Place Paper Award**, Ohio Collaborative Conference on Bioinformatics
Awarded for Lichtenberg et al. (2009).

Research Experience

- 2016- **Research Consulting**
HistoGenetics, LLC (Ossining, NY)
Comparative sequence analysis of whole-gene human leukocyte antigen (HLA) PacBio data.
- 2011-2016 **Doctoral Research**, Austin L. Hughes Lab
Department of Biological Sciences, University of South Carolina (Columbia, SC)
Dissertation: "Studying Within-Host Viral Evolution Using Pooled Next-Generation Sequencing Data"
- 2013, 2014 **Research Assistant**, Wen-Hsiung Li Lab
Biodiversity Research Center, Academia Sinica (中央研究院) (Taipei, Taiwan)
TNG67 rice genomics; production of in-house Perl scripts for Illumina data processing
- 2009-2010 **Honors Research**, Angela J. Roles Lab
Biology Department, Oberlin College (Oberlin, OH)
Thesis: "Differential Gene Expression in Arabidopsis thaliana Mutation Accumulation Lines".
- 2009 **REU**, Anne W. Sylvester & David A. Liberles Labs
Department of Molecular Biology, University of Wyoming (Laramie, WY)
Zea mays RAB2A molecular biology, homology modeling, and phylogenetics.
- 2007, 2008 **REU**, Lonnie R. Welch Lab
Electrical Engineering and Computer Science, Ohio University (Athens, OH)
Development and testing of the DNA motif-discovery tool, WordSeeker.

Teaching

- 2017 **Workshop Leader**, "Bioinformatics Bootcamp"
Richard Gilder Graduate School, American Museum of Natural History (New York)

- 2017 **Guest Lecturer**, “Variant Analysis and Signatures of Selection, d_N/d_S ”
Richard Gilder Graduate School, American Museum of Natural History (New York)
- 2012-2014 **BioInvestigations Lab Coordinator**
EdVenture Children’s Museum (Columbia, SC)
- 2014 **BioDetectives Program Instructor**
C.A. Johnson High School (Columbia, SC)
- 2012-2013 **Lab Instructor**, Cell & Molecular Biology
Department of Biological Sciences, University of South Carolina (Columbia, SC)
- 2011-2012 **Lab Instructor**, Biological Principles I
Department of Biological Sciences, University of South Carolina (Columbia, SC)
- 2011-2011 **Teaching Assistant**, Organismal Biology Lab
Biology Department, Oberlin College (Oberlin, OH)

Presentations

- 2017 **“Virus-host coevolution and carcinogenicity through the lens of human papillomavirus”**
Presentation, International Symposium for Molecular Evolution & Medicine (Philadelphia)
- 2017 **“Divergence of HPV16 variants reflects loci undergoing inter-host positive selection, potentially immunologic selection”**
Poster, Annual Meeting of the Society for Molecular Biology and Evolution (Austin, TX)
- 2016 **“Characterizing the molecular evolution of new viruses with comparative sequence analysis: a case study with simian arteriviruses”**
Comparative Biology Seminar, American Museum of Natural History (NYC)
- 2015 **“SNPGenie: A software platform for detecting natural selection in pooled next-generation sequencing samples”**
Presentation, ENCODE Research Applications and Users Meeting (Potomac, MD)
- 2015 **“SNPGenie: A software platform for detecting natural selection in pooled next-generation sequencing samples”**
Poster, Great Lakes Bioinformatics Conference, Purdue University (West Lafayette, IN)
- 2013 **“The spatial distribution of genetic variation in classical human leukocyte antigen contact residues”**
Presentation, GIS Institute, Center for Digital Humanities (Columbia, SC)
- 2013 **“Using GIS to analyze genetic variation in pathogen populations: a case study with Plasmodium falciparum”**
Presentation, SCARC: Consuming GIS, South Carolina Arc GIS Users Group (Columbia, SC)
- 2011 **“Selection threshold constrains adaptive evolution in computational evolution experiments”**
Poster, Great Lakes Bioinformatics Conference, Ohio University (Athens, OH)

- 2010 **“Differential gene expression in Arabidopsis thaliana mutation accumulation lines”**
Poster, Evolution, Portland State University (Portland, OR)
- 2007 **“Using WordSeeker to identify regulatory elements in CBF genes from the Triticeae”**
Abstract, Ohio Collaborative Conference on Bioinformatics, Miami University (Oxford, OH)

Workshops & Meetings

- 2016 **New Trends in Evolutionary Biology**
The Royal Society (London)
- 2016 **HPV Workshop: Mechanistic Understanding of Cervical Carcinogenesis**
National Cancer Institute-National Institutes of Health (Rockville, MD)
- 2016 **Genomics and Bioinformatics Workshop**, University of Maryland Institute for Genome Sci.
Richard Gilder Graduate School, American Museum of Natural History (New York)
- 2015 **RNASeq Workshop**
Great Lakes Bioinformatics Conference, Purdue University (West Lafayette, IN)
- 2014 **Workshop in Next Generation Science**
Department of Bioinformatics and Genetics, University of North Carolina (Charlotte, NC)
- 2012 **Workshop in Next Generation Sequence Analysis**
Department of Bioinformatics and Genetics, University of North Carolina (Charlotte, NC)
- 2009 **Introductory Bioinformatics Workshop**
Ohio Collaborative Conference on Bioinformatics, Miami University (Oxford, OH)

Other Skills

Alto saxophone, ballet, hip-hop, improvisation, live performance, Mandarin Chinese (conversational), music theory, piano, public speaking, swing dancing, theatre, teaching, voice (singing), writing