# Chase W. Nelson
## (倪誠志)

生物多樣性研究中心
Biodiversity Research Center
中央研究院 Academia Sinica
台灣台北 Taipei, Taiwan

**Phone:** (+xxx) xxx-xxx-xxx
**Email:** cnelson@amnh.org
**ORCID:** 0000-0001-6287-1598
**Website:** www.chasewnelson.com
**GitHub:** www.github.com/chasewnelson

## Education

2011-2016 **Ph.D. Biological Sciences**, University of South Carolina. *GPA:* 4.0. *Advisor:* Austin L. Hughes.

2006-2010 **B.A. Biology (*honors*)**, Oberlin College. *GPA:* 4.0. *Advisor:* Roger Laushman.

## Expertise

**Subject Areas:** bioinformatics, cancer, computational biology, data science, $d_N/d_S$, geographic information systems, genome evolution, genomics, immunology, MHC evolution, molecular evolution, mutation, natural selection, next-generation sequencing, neutral evolution, overlapping genes, phylogenetics, population genetics, site frequency spectra, statistics, viruses

**Biological Systems:** *H. sapiens*, human immunodeficiency virus (HIV), human papillomavirus (HPV), severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), West Nile virus (WNV)

**Biological Systems Handled in Lab:** *A. thaliana, C. elegans, D. melanogaster, Z. mays*

**Programming Languages:** Eidos (SLiM), Linux/Unix, Markdown, Perl, Python, R, SAS, SQL

**Computational Skills:** AliView, ArcGIS, BEDTools, BLAST, databases, GenomicRanges, ggplot2, GitHub, IGV, liftOver, MAFFT, MEME, MEGA, motif detection, ms, OLGenie, PHYLIP, ProbCons, SAMtools, SLiM, SnpEff, SNPGenie, SWISS-MODEL, WordPress

**Molecular Biology Experience:** gel electrophoresis, DNA & RNA isolation, hemocytometry, *in vitro* cell treatment, microscopy, PCR, qRT-PCR, SDS-PAGE, TT-PCR, zymography

## Research Appointments

2019- **Postdoctoral Research Scholar** (*PI:* Wen-Hsiung Li 李文雄)
Biodiversity Research Center, Academia Sinica (Taipei, Taiwan 台灣台北)
*ChIP-seq, transcription factor binding sites,* Acinetobacter baumannii *drug resistance.*

| 2019- | **Visiting Scientist** |
| --- | --- |
| | Institute for Comparative Genomics, American Museum of Natural History (NYC, USA) |
| | *Bioinformatics tool development, human papillomavirus type 16, overlapping genes.* |

| 2017- | **Special Volunteer**, NCI-DCEG HPV Genomics Group (*PI*: Meredith Yeager) |
| --- | --- |
| | National Cancer Institute, National Institutes of Health (Rockville, MD, USA) |
| | *Human papillomavirus type 16 carcinogenesis and molecular evolution.* |

| 2016-2019 | **Gerstner Scholar in Bioinformatics and Computational Biology** |
| --- | --- |
| | Institute for Comparative Genomics, American Museum of Natural History (NYC, USA) |
| | *Bioinformatics tool development, West Nile virus, overlapping genes.* |

| 2016-2018 | **Visiting Scholar**, EvoNet Project (*PIs*: Gloria Coruzzi & Rob DeSalle) |
| --- | --- |
| | Center for Genomics and Systems Biology, New York University (NYC, USA) |
| | *PhyloGeneious pipeline for high-throughput ortholog detection.* |

| 2010-2011 | **Research Scientist** |
| --- | --- |
| | Rainbow Technologies, Inc. (Waterloo, NY, USA) |
| | *Digital evolution research examining low-impact mutations and selective neutrality.* |

# Publications

| 2021 | Jungreis I, **Nelson CW**, Ardern Z, Finkel Y, Krogan NJ, Sato K, Ziebuhr J, Stern-Ginossar N, Pavesi A, Firth AE, Gorbalenya AE, Kellis M. |
| --- | --- |
| | "Conflicting and ambiguous names of overlapping ORFs in the SARS-CoV-2 genome: a homology-based resolution." |
| | *Virology* **558**: 145-151. |

| 2021 | Yu C-P, Kuo C-H, **Nelson CW**, Chen C-A, Soh ZT, Lin J-J, Hsiao R-X, Chang C-Y, Li W-H. |
| --- | --- |
| | "Discovering unknown human and mouse transcription factor binding sites and their characteristics from ChIP-seq data." |
| | *Proceedings of the National Academy of Sciences USA* **118**(20): e2026754118. |

| 2021 | Yeager M, Machiela MJ, Kothiyal P, Dean M, Bodelon C, Suman S, Wang M, Mirabello L, **Nelson CW**, Zhou W, Palmer C, Ballew B, Colli LM, Freedman ND, Dagnall C, Hutchinson A, Vij V, Maruvka Y, Hatch M, Illienko I, Belayev Y, Nakamura N, Chumak V, Bakhanova E, Belyi D, Kryuchkov V, Golovanov I, Gudzenko N, Cahoon EK, Albert P, Drozdovitch V, Little MP, Mabuchi K, Stewart C, Getz G, Bazyka D, de Gonzalez AB, Chanock SJ. |
| --- | --- |
| | "Lack of transgenerational effects of ionizing radiation exposure from the Chernobyl accident." |
| | *Science* **372**(6543): 725-729. |

- ▪ PRESS: Ars Technica, BBC News, Black Tech Daily, CNN, CNN Philippines, Daily Mail, EurekAlert!, GenomeWeb, Gizmodo, The Guardian, Live Science, MedicalXPress, The National Cancer Institute, National Geographic, Psych News Daily, Science, ScienceDaily, The Scientist, U.S. News & World Report, Yahoo!News

2021    San JE, Ngcapu S , Kanzi AM, Tegally H, Fonseca V, Giandhari J, Wilkinson E, **Nelson CW**, Smidt W, Kiran AM, Chimukangara B , Pillay S , Singh L , Fish M , Gazy I , Martin DP, Khanyile K , Lessells R , de Oliveira T.
"Transmission dynamics of SARS-CoV-2 within-host diversity in two major hospital outbreaks in South Africa."
*Virus Evolution* **7**(1): veab041.

2021    Perelman SS, James DBA, Boguslawski KM, **Nelson CW**, Ilmain JK, Zwack EE, Prescott RA, Mohamed A , Tam K, Chan R, Narechania A, Pawline MB, Vozhilla N, Moustafa AM, Kim SY, Dittmann M, Ekiert DC, Bhabha G, Shopsin B, Planet PJ, Koralov SB, Torres VJ.
"Genetic variation of staphylococcal LukAB toxin determines receptor tropism."
*Nature Microbiology* **6**(6): 731-745.

2020    **Nelson CW**, Ardern Z, Goldberg TL, Meng C, Kuo C-H, Ludwig C, Kolokotronis S-O, Wei X.
"Dynamically evolving novel overlapping gene as a factor in the SARS-CoV-2 pandemic."
*eLife* **9**: e59633.
- PRESS: BBC Brasil, BBC Mundo, CNN Español, CNN Indonesia, Current Science Daily, EurekAlert!, Kreiszeitung, Live Science, ScienceAlert, ScienceDaily, The Telegraph, Yahoo!News, 自由時報 (Liberty Times Net Taiwan)

2020    **Nelson CW**, Ardern Z, Wei X.
"OLGenie: estimating natural selection to predict functional overlapping genes."
*Molecular Biology and Evolution* **37**(8): 2440-2449.

2020    **Nelson CW**
"COVID-19: time for WHO to reconsider its stance towards Taiwan."
*Nature* **579**(7798): 193.
- PRESS: 中央廣播電臺 (Radio Taiwan International), 中央通訊社 (Central News Agency Taiwan), 自由時報 (Liberty Times Net Taiwan)

2020    Zhu B, Xiao Y, Yeager M, Clifford G, Wentzensen N, Cullen M, Boland JF, Bass S, Steinberg MK, Raine-Bennett T, Lee D, Burk RD, Pinheiro M, Song L, Dean M, **Nelson CW**, Burdett L, Yu K, Roberson D, Lorey T, Franceschi S, Castle PE, Walker J, Zuna R, Schiffman M, Mirabello L.
"Mutations in the HPV16 genome induced by APOBEC3 are associated with viral clearance."
*Nature Communications* **11**: 886.

2018    **Nelson CW**, Sibley SD, Kolokotronis S-O, Hamer GL, Newman CM, Anderson TK, Walker ED, Kitron UD, Brawn JD, Ruiz MO, Goldberg TL.
"Selective constraint and adaptive potential of West Nile virus within and among naturally infected avian hosts and mosquito vectors."
*Virus Evolution* **4**(1): vey013.

2018    Mirabello L, Clarke MA, **Nelson CW**, Dean M, Wentzensen N, Yeager M, Cullen M, Boland JF, NCI HPV Workshop, Schiffman M, Burk RD.
"The intersection of HPV epidemiology, genomics and mechanistic studies of HPV-mediated carcinogenesis."
*Viruses* **10**(2): 80.

2017      Hücker SM, Ardern Z, Goldberg T, Schafferhans A, Bernhofer M, Vestergaard G, **Nelson CW**, Schloter 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): 1164-11 74.
- PRESS: GenomeWeb, MedicalXpress

2017      Moncla LH, Weiler AM, Barry G, Weinfurter JT, Dinis JM, Charlier O, Lauck M, Bailey AL, Wahl-Jensen V, **Nelson CW**, Johnson JC, Caì 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.

2016      **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      Gellerup D, Balgeman A, **Nelson CW**, Ericsen A, Scarlotta M, Hughes AL, O'Connor S.
"Conditional immune escape during chronic SIV infection."
*Journal of Virology* **90**(1): 545-552.

2015        **Nelson C.**
"Haldane's dilemma."
*Inference: International Review of Science* **1**(3).

2015        **Nelson CW.**
"The humble scientist."
*The New Atlantis* **47**: 98-102.

2015        **Nelson CW**, Moncla LH, Hughes AL.
"SNPGenie: estimating evolutionary parameters to detect natural selection using pooled next-generation sequencing data."
*Bioinformatics* **31**(22): 3709-3711.

2015        **Nelson CW**, Hughes AL.
"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.

## Peer-Review Service

2021  *Molecular Biology and Evolution* (1)

2016  *Molecular Phylogenetics and Evolution* (1)

2019  *Papillomavirus Research* (1)

2021  *PLoS One* (1)

2019  *Virus Evolution* (1)

## Software

2019  **Trevolver.** https://github.com/chasewnelson/trevolver
     Program for simulating non-reversible DNA sequence evolution on a fixed bifurcating tree using trinucleotide context.

2017  **OLGenie.** https://github.com/chasewnelson/OLGenie
     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.

2014  **Evolutionary Bioinformatics Toolkit.** https://github.com/chasewnelson/EBT
     A smorgasbord of scripts providing computational help for the analysis of sequence data.

# Awards & Honors

**2020**  **Best Poster Award**, International Symposium on Evolutionary Genomics and Bioinformatics
*Taiwan Society of Evolution and Computational Biology.*

**2016-2019**  **Gerstner Scholars Fellowship**, Gerstner Family Foundation
*Support for independent research in molecular evolution and bioinformatics at the Institute for Comparative Genomics, American Museum of Natural History.*

**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 (4.0) 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).* |

## Additional Research Experience

| 2016-2017 | **Consulting** |
|---|---|
| | HistoGenetics, LLC (Ossining, NY, USA) |
| | *Comparative sequence analysis of whole-gene human leukocute antigen (HLA) PacBio data.* |

| 2011-2016 | **Ph.D. Research**, Austin L. Hughes Lab |
|---|---|
| | Department of Biological Sciences, University of South Carolina (Columbia, SC, USA) |
| | *Dissertation: "Studying Within-Host Viral Evolution Using Pooled Next-Generation Sequencing Data"* |

| 2013, 2014 | **Research Intern**, 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, USA) |
| | *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, USA) |
| | *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, USA) |
| | *Development and testing of the DNA motif-discovery tool, WordSeeker.* |

## Teaching & Leadership

| 2019 | **Coordinator**, Institute for Comparative Genomics Workgroup Biweekly Meeting |
|---|---|
| | SICG, American Museum of Natural History (NYC, USA) |

| 2019 | **Instructor**, "Bioinformatics Data Analysis with R Workshop" |
|---|---|
| | Richard Gilder Graduate School, American Museum of Natural History (NYC, USA) |

| 2018 | **Guest Lecturer**, "Introduction to Molecular Evolution and Detecting Selection" |
|---|---|
| | Richard Gilder Graduate School, American Museum of Natural History (NYC, USA) |

| 2018 | **Instructor**, "R Workshop: Basic Data Manipulation and Visualization Using `ggplot2`" |
|---|---|
| | Richard Gilder Graduate School, American Museum of Natural History (NYC, USA) |

| | |
|---|---|
| 2017 | **Instructor**, "Bioinformatics Bootcamp" <br> Richard Gilder Graduate School, American Museum of Natural History (NYC, USA) |
| 2017 | **Guest Lecturer**, "Variant Analysis and Signatures of Selection, $d_N/d_S$" <br> Richard Gilder Graduate School, American Museum of Natural History (NYC, USA) |
| 2012-2014 | **BioInvestigations Lab Coordinator** <br> EdVenture Children's Museum (Columbia, SC, USA) |
| 2014 | **BioDetectives Program Instructor** <br> C.A. Johnson High School (Columbia, SC, USA) |
| 2012-2013 | **Lab Instructor**, Cell & Molecular Biology <br> Department of Biological Sciences, University of South Carolina (Columbia, SC, USA) |
| 2011-2012 | **Lab Instructor**, Biological Principles I <br> Department of Biological Sciences, University of South Carolina (Columbia, SC, USA) |
| 2011 | **Teaching Assistant**, Organismal Biology Lab <br> Biology Department, Oberlin College (Oberlin, OH, USA) |

## Invited Talks

| | |
|---|---|
| 2020 | **"A new gene in SARS-CoV-2"** <br> American Museum of Natural History Board Meeting <br> Institute for Comparative Genomics, American Museum of Natural History (NYC, USA) |
| 2020 | **"A novel overlapping gene in SARS-CoV-2 and the origins of the COVID-19 pandemic"** <br> Seminar Series, Office of the VP for Research and Graduate Studies <br> Universidad Católica del Cibao (La Vega, Dominican Republic) |
| 2017 | **"Virus-host coevolution and carcinogenicity through the lens of human papillomavirus"** <br> International Symposium for Molecular Evolution & Medicine <br> SMBE, Temple University (Philadelphia, USA) |
| 2015 | **"SNPGenie: a software platform for detecting natural selection in pooled next-generation sequencing samples"** <br> ENCODE Research Applications and Users Meeting <br> NHGRI, Bolger Center (Potomac, MD, USA) |

## Oral Presentations

| | |
|---|---|
| 2019 | **"Mutation and GC-biased gene conversion are the main drivers of human genome evolution"** <br> Molecular Evolution Symposium, Evolution 2019 (Providence, RI, USA) |

| | |
|---|---|
| 2016 | "Characterizing the molecular evolution of new viruses with comparative sequence analysis: a case study with simian arteriviruses" <br> Comparative Biology Seminar Series, American Museum of Natural History (NYC, USA) |
| 2013 | "The spatial distribution of genetic variation in classical human leukocyte antigen contact residues" <br> GIS Institute, Center for Digital Humanities (Columbia, SC, USA) |
| 2013 | "Using GIS to analyze genetic variation in pathogen populations: a case study with Plasmodium falciparum" <br> SCARC: Consuming GIS, South Carolina Arc GIS Users Group (Columbia, SC, USA) |

## Posters

| | |
|---|---|
| 2020 | "Dynamically evolving novel overlapping gene as a factor in the SARS-CoV-2 pandemic" <br> International Symposium on Evolutionary Genomics and Bioinformatics (Taipei, Taiwan) |
| 2018 | "Naturally occurring West Nile virus infections display no evidence for heightened selective constraint in avian hosts over mosquito vectors" <br> Annual Meeting of the Society for Molecular Biology and Evolution (Yokohama, Japan) |
| 2017 | "Divergence of HPV16 variants reflects loci undergoing inter-host positive selection, potentially immunologic selection" <br> Annual Meeting of the Society for Molecular Biology and Evolution (Austin, TX, USA) |
| 2015 | "SNPGenie: A software platform for detecting natural selection in pooled next-generation sequencing samples" <br> ENCODE Research Applications and Users Meeting (NHGRI, Potomac, MD, USA) |
| 2015 | "SNPGenie: A software platform for detecting natural selection in pooled next-generation sequencing samples" <br> Great Lakes Bioinformatics Conference, Purdue University (West Lafayette, IN, USA) |
| 2011 | "Selection threshold constrains adaptive evolution in computational evolution experiments" <br> Great Lakes Bioinformatics Conference, Ohio University (Athens, OH, USA) |
| 2010 | "Differential gene expression in Arabidopsis thaliana mutation accumulation lines" <br> Evolution, Portland State University (Portland, OR, USA) |
| 2007 | "Using WordSeeker to identify regulatory elements in CBF genes from the Triticeae" <br> Ohio Collaborative Conference on Bioinformatics, Miami University (Oxford, OH, USA) |

## Workshops & Meetings

| | |
|---|---|
| 2020 | International Symposium on Evolutionary Genomics and Bioinformatics 2020 <br> Taiwan Society for Evolution and Computational Biology (Taipei, Taiwan) |

| 2020 | **SLiM Workshop (Ben Haller)**<br>University of Iceland (Reykjavík, Iceland) |
|---|---|
| 2019 | **International Symposium on Evolutionary Genomics and Bioinformatics 2019**<br>Taiwan Society for Evolution and Computational Biology (Miaoli, Taiwan) |
| 2019 | **Galaxy Training Workshop (Anton Nekrutenko)**<br>Taiwan Society for Evolution and Computational Biology (Miaoli, Taiwan) |
| 2019 | **SMBE 2019**<br>Society for Molecular Biology and Evolution (Manchester, UK) |
| 2019 | **Evolution 2019**<br>ASN, SSB, and SSE (Providence, RI, USA) |
| 2018 | **SMBE 2018**<br>Society for Molecular Biology and Evolution (Yokohama, Japan) |
| 2017 | **SMBE 2017**<br>Society for Molecular Biology and Evolution (Austin, TX, USA) |
| 2016 | **New Trends in Evolutionary Biology**<br>The Royal Society (London, UK) |
| 2016 | **HPV Workshop: Mechanistic Understanding of Cervical Carcinogenesis**<br>National Cancer Institute-National Institutes of Health (Rockville, MD, USA) |
| 2016 | **Genomics and Bioinformatics Workshop** (University of Maryland Institute for Genome Sci.)<br>Richard Gilder Graduate School, American Museum of Natural History (New York, USA) |
| 2015 | **RNASeq Workshop**<br>Great Lakes Bioinformatics Conference, Purdue University (West Lafayette, IN, USA) |
| 2014 | **Workshop in Next Generation Science**<br>Dept. of Bioinformatics and Genetics, University of North Carolina (Charlotte, NC, USA) |
| 2012 | **Workshop in Next Generation Sequence Analysis**<br>Dept. of Bioinformatics and Genetics, University of North Carolina (Charlotte, NC, USA) |
| 2009 | **Introductory Bioinformatics Workshop**<br>Ohio Collaborative Conference on Bioinformatics, Miami University (Oxford, OH, USA) |

## Other Skills

Alto saxophone, dance (ballet, jazz-funk, swing), improvisation, live performance, Chinese (elementary conversational), music theory, piano, podcasting, public speaking, theatre, teaching, visualization, voice (singing) technique, writing

# References

**Tony L. Goldberg**

INSTITUTION: University of Wisconsin-Madison (Madison, WI, USA)
DEPARTMENT: Department of Pathobiological Sciences, School of Vet. Medicine
POSITION: John D. MacArthur Research Chair & Professor of Epidemiology
EMAIL/PHONE: tony.goldberg@wisc.edu / (608) 890-2618

**John J. Flynn**

INSTITUTION: American Museum of Natural History (NYC, USA)
DEPARTMENT: Richard Gilder Grad School & Institute for Comparative Genomics
POSITION: Dean, Frick Curator of Fossil Mammals, and Principal Investigator
EMAIL/PHONE: jflynn@amnh.org / (212) 769-5806

**Meredith Yeager**

INSTITUTION: National Cancer Institute-NIH; Leidos Biomedical Research (USA)
DEPARTMENT: Division of Cancer Epidemiology and Genetics; Cancer Genomics
POSITION: Scientific Director, Cancer Genomics Research Laboratory
EMAIL/PHONE: yeagerm@mail.nih.gov / (240) 760-6561

**Apurva Narechania**

INSTITUTION: American Museum of Natural History (NYC, USA)
DEPARTMENT: Institute for Comparative Genomics
POSITION: Senior Bioinformaticist & Manager of the Gerstner Bioinformatics Program
EMAIL/PHONE: anarechania@amnh.org / (646) 522-8888

**Wen-Hsiung Li**
(李文雄)

INSTITUTION: University of Chicago (Chicago, USA) & 中央研究院 (Taipei, Taiwan)
DEPARTMENT: Department of Ecology and Evolution; Biodiversity Research Center
POSITION: Emeritus Professor & Distinguished Research Fellow
EMAIL/PHONE: whli@gate.sinica.edu.tw / 886-2-2789-9930

**Michael Dean**

INSTITUTION: National Cancer Institute-NIH (Rockville, MD, USA)
DEPARTMENT: Division of Cancer Epidemiology and Genetics
POSITION: Senior Investigator
EMAIL/PHONE: deanm@mail.nih.gov / (240) 760-6484

**Lisa Mirabello**

INSTITUTION: National Cancer Institute-NIH (Rockville, MD, USA)
DEPARTMENT: Division of Cancer Epidemiology and Genetics
POSITION: Earl Stadtman Investigator
EMAIL/PHONE: mirabellol@mail.nih.gov / (240) 276-7258