

Joseph Lachance, Ph.D.
Curriculum Vitae

Assistant Professor
School of Biological Sciences
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Educational Background:

- 1992-1996 A.B. in biology, University of Chicago
Thesis title: "Epistatic interactions underlie incipient speciation in Zimbabwe *Drosophila melanogaster*"
- 2005-2010 Ph.D. in genetics, Stony Brook University
Dissertation title: "Life after beanbag genetics: theoretical and empirical studies on epistasis and penetrance"

Professional Experience:

- 2015- Assistant Professor, School of Biological Sciences, Georgia Institute of Technology
- 2010-2014 NIH NRSA Postdoctoral Fellow, University of Pennsylvania

Honors and Awards:

- 1992-1996 National Merit Scholar (University of Chicago)
- 1995 Howard Hughes summer undergraduate fellowship (University of Chicago)
- 1996-1997 NIH Predoctoral training grant fellowship, Duke University
- 2005-2007 NIH Predoctoral training grant fellowship, Stony Brook University
- 2007 King-Miller Travel Award
- 2008 Research Access Project funding (Stony Brook University GSO)
- 2009 Cedar Brook Award for best student talk (Stony Brook University)
- 2009 Summer Institute in Statistical Genetics fellowship recipient
- 2011-2014 NIH Kirschstein NRSA postdoctoral fellowship
- 2016- Member of the Faculty of 1000 (Evolutionary/Comparative Genomics)

Research, Scholarship, and Creative Activities:

(members of the Lachance Lab are labeled in **bold**, * indicates corresponding author)

Book Chapters:

1. **Lachance J*** (2016). Hardy-Weinberg proportions and the mathematical population genetics of randomly mating populations. *Encyclopedia of Evolutionary Biology*, edited by Kliman RM. Academic Press. Vol. 2, pp. 208-211.

Refereed Publications:

1. **Lachance J*** (2008) A fundamental relationship between genotype frequencies and fitnesses *Genetics* 180:1087-93.
2. Yukilevich R*, **Lachance J**, Aoki F, and True JR (2008) Long-term adaptation of epistatic genetic networks. *Evolution* 62:2215-2235.
3. **Lachance J*** (2009) Detecting selection-induced departures from Hardy-Weinberg proportions. *Genetics Selection Evolution* 41:15.
4. **Lachance J*** (2009) Inbreeding, pedigree size, and the most recent common ancestor of humanity. *Journal of Theoretical Biology* 261:238-247.
5. **Lachance J*** (2010) Disease-associated alleles in genome-wide association studies are enriched for derived low frequency alleles relative to HapMap and neutral expectations. *BMC Medical Genomics* 3:57.
6. **Lachance J*** and True JR* (2010). X-autosome incompatibilities in *Drosophila melanogaster*: Tests of Haldane's rule and geographic patterns within species. *Evolution* 64:3035-3046.
7. **Lachance J***, Johnson NA, and True JR (2011). The population genetics of X-autosome synthetic lethals and steriles. *Genetics* 189:1011-1027.
8. **Lachance J**, Vernot B, Elbers CC, Ferwerda B, Froment A, Bodo JM, Lema G, Fu W, Nyambo TB, Rebbeck TR, Zhang K, Akey JM, and Tishkoff SA* (2012) Evolutionary history and adaptation from high coverage whole-genome sequences of diverse African hunter-gatherers. *Cell* 150:457-469.
9. Pickrell J*, Patterson N, Carbieri C, Berthold F, Gerlach L, Güldemann T, Kure B, Mpoloka SW, Nakagawa H, Nauman C, Lipson M, Loh PR, **Lachance J**, Mountain J, Bustamante C, Berger B, Tishkoff SA, Henn B, Stoneking M, Reich D*, and Pakendorf B* (2012). The genetic prehistory of southern Africa. *Nature Communications* doi:10.1038/ncomms2140.
10. Johnson NA* and **Lachance J** (2012) The genetics of sex chromosomes: evolution and implications for hybrid incompatibility. *Annals of the New York Academy of Natural Sciences: The Year in Evolutionary Biology* 1256:E1-E22.
11. **Lachance J*** and Tishkoff SA (2013) SNP ascertainment bias in population genetic analyses: Why it is important, and how to correct it. *BioEssays* 35:780-786
12. **Lachance J***, Jung L, and True JR (2103) Genetic background and GxE interactions modulate the penetrance of a naturally occurring wing defect in *Drosophila melanogaster*. *G3: Genes|Genomes|Genetics* 3:1893-1901.
13. Wang S, **Lachance J**, Tishkoff SA, Hey J, and Xing J* (2013) Apparent variation in Neanderthal admixture among African populations is consistent with gene flow from non-African populations. *Genome Biology and Evolution* 5:2075-2081.
14. **Lachance J*** and Tishkoff SA* (2103) Population genomics of human adaptation. *Annual Review of Ecology, Evolution, and Systematics* 44:123-143.
15. **Lachance J*** and Tishkoff SA* (2014) Biased gene conversion skews allele frequencies in human populations, increasing the disease burden of recessive alleles. *American Journal of Human Genetics* 95:408-420.

16. Karmin M*, Saag L, Vicente M, Wilson-Sayres MA, ... **Lachance J** (author 33 of 100) ... Kivisild T* (2015) A recent bottleneck of Y chromosome diversity coincides with a global change in culture. *Genome Research* 25:459-466.
17. Hsieh PH, Veeramah KR, **Lachance J**, Tishkoff SA, Wall JD, Hammer MF, Gutenkunst RN* (2016) Whole genome sequence analyses of Western Central African Pygmy hunter-gatherers reveal a complex demographic history and identify candidate genes under positive natural selection. *Genome Research* 26:279-290.
18. Hsieh PH, Woerner AE, Wall JD, **Lachance J**, Tishkoff SA, Gutenkunst RN, Hammer MF* (2016) Model-based analyses of whole genome data reveal a complex evolutionary involving archaic introgression in Central African Pygmies. *Genome Research* 26:291-300.
19. Pagani L, Lawson D, Jagoda E, Mörseburg A, Eriksson A... **Lachance J** (author 41 of 98) ... Metspalu M* (2016) Genomic analyses inform on migration events during the peopling of Eurasia. *Nature* 538:238-242.
20. **Berens AJ, Cooper TL, and Lachance J*** (2017) The genomic health of ancient hominins. *Human Biology*. *Accepted*.

Submitted Journal Articles and Articles in Preparation:

1. **Lachance J*, Quiver MH**, Mullen K, Hansen MEB, **Berens AJ**, Chen MA, Hsieh PH, Veeramah KR, and Tishkoff SA* (2017) Genomic evidence of male-biased migration out-of-Africa and the effects of different modes of subsistence. *Submitted*.
2. **Lachance J*, Berens AJ**, Hansen MEB, **Teng AK**, Tishkoff SA, and Rebbeck TR (2017) Population and evolutionary genomics of prostate cancer associated variants: implications for health disparities in men of African descent. *Submitted*.
3. Rishishwar L, Wang L, Wang J, Yi S, **Lachance J**, Jordan K* (2017) Population-specific positive selection on human transposable element insertions. *Submitted*.
4. Hansen MEB, **Lachance J**, Soi S, Scheinfeldt L, Thompson S, Ranciaro A, Hirbo J, and Tishkoff SA* (2017) Anthropometric and cardiovascular trait variation among sub-Saharan African populations: the role of gender, subsistence, and genetic ancestry. *In preparation*.
5. **Kim M, Patel K, Teng AK, Berens AJ, and Lachance J*** (2017) Ascertainment creates the illusion of genetic health disparities. *In preparation*.
6. **Lachance J*** (2017) Adaptive introgression and the evolutionary genetics of hybrid fitness effects. *In preparation*.
7. **Quiver MH and Lachance J*** (2017) Adaptive eQTLs in human populations. *In preparation*.

Other Publications:

1. **Lachance J*** (2007) Book Review: Compositional Evolution by Watson. *Quarterly Review of Biology* 82:148-149.
2. **Lachance J*** (2008) Book Review: Modelling for Field Biologists and other Interesting People by Kokko. *Quarterly Review of Biology* 83:296.
3. **Lachance J*** (2008) Subject to Change. *Nature* 454:916.

4. **Lachance J*** (2009) Book Review: *Evolving Pathways: Key Themes in Evolutionary Developmental Biology* by Minelli and Fusco. *Quarterly Review of Biology* 84:102-103.
5. **Lachance J*** and Bourdeau P* (2010) *Evolution by Futuyma: online supplements*, 2nd ed. Sinauer Associates, Sunderland MA.
6. **Lachance J*** (2011) Book Review: *How Many Friends Does One Person Need?* by Dunbar. *Quarterly Review of Biology* 86:104.
7. **Lachance J*** (2012) The genomics of African hunter-gatherers: what cutting-edge technology can tell us about human history. *Huffington Post* (invited guest blog).
8. **Lachance J*** (2013) Book Review: *An Introduction to Population Genetics: Theory and Applications* by Nielsen and Slatkin. *Quarterly Review of Biology* 88:353.
9. **Lachance J*** (2014) Book Review: *Human Evolutionary Genetics*, 2nd ed. by Jobling, Hollox, Hurles, Kivisild, and Tyler-Smith. *Quarterly Review of Biology* 89:176-177.
10. **Lachance J*** (2016) Book Review: *Population in the Human Sciences: Concepts, Models, Evidence* by Kreager, Winney, Uliaszek, and Capelli. *Quarterly Review of Biology* 91:234-235.

Presentations:

Invited Seminars:

1. Inbreeding, Fibonacci constants, and the most recent common ancestor of humanity. *Provost's Graduate Student Lecture Series* (Stony Brook University - 2010)
2. Synthetic incompatibilities and incomplete penetrance in *Drosophila melanogaster* / Inbreeding, the MRCA of humanity, and alleles that are associated with genetic disease. *Invited seminar* (University of Pennsylvania - 2010).
3. Evolutionary history and adaptation inferred from whole genome sequences of diverse African hunter-gatherers. *Annual Meeting of the American Society of Human Genetics - session chair* (San Francisco, CA - 2012).
4. Evolutionary history and adaptation inferred from whole genome sequences of diverse African hunter-gatherers. *Department of Biology invited seminar* (Union College - 2012).
5. Evolutionary medicine and the population genetics of diverse African hunter-gatherers. *Department of Pathology invited seminar* (Philadelphia VA Medical Center - 2012).
6. Evolutionary genomics of diverse African hunter-gatherers. *College of Biological Sciences invited seminar* (University of Minnesota - 2013).
7. Evolutionary genomics of diverse African hunter-gatherers. *Department of Biology invited seminar* (Temple University - 2013).
8. Evolutionary genomics of diverse African hunter-gatherers. *School of Biology invited seminar* (Georgia Institute of Technology - 2013).
9. "Spatializing" research on genetic diversity. *Relocating Human Conference invited panel discussant* (University of Cambridge - 2013).

10. Evolutionary genomics of diverse African hunter-gatherers. *Department of Biology invited seminar* (University of Illinois at Urbana-Champaign - 2014).
11. Population and evolutionary genomics of prostate cancer-associated variants: Implications for health disparities in men of African descent. *Satellite meeting of the African Organization for Research and Training in Cancer* (Marrakech, Morocco - 2015).
12. Evolutionary history, cancer, and the population genetics of health disparities. *Integrated BioSystems Institute Chalk Talk* (Georgia Institute of Technology - 2015).
13. Ancient introgression in Africa and the evolutionary genetics of hybrid fitness effects. *American Association of Anthropological Genetics* (Atlanta, GA - 2016).
14. Population and evolutionary genomics of prostate cancer-associated variants: Implications for health disparities in men of African descent. *Annual meeting of the International Society for Evolution, Medicine, and Public Health* (Durham, NC - 2016).
15. Evolutionary genomics of prostate cancer in African men. *Integrated Cancer Research Center seminar series* (Georgia Institute of Technology - 2016).
16. Evolutionary genomics of prostate cancer in African men. *4th Biennial Science of Global Prostate Cancer Disparities Conference* (Orlando, FL - 2016).
17. Genetic ancestry and computational genomics of African populations. *MADCaP Investigator's Meeting* (Cape Town, South Africa - 2017).
18. Evolutionary history and the genomic health of ancient and modern humans. (Cedar Crest College - 2017).
19. Evolutionary history and the genomic health of ancient and modern humans. (Vanderbilt University - 2017).

Conference Talks:

1. Inbreeding, the pruning of family trees, and the most recent common ancestor of humanity. *Annual Meeting of the Society for the Study of Evolution* (Christchurch, New Zealand - 2007).
2. A fundamental relationship between genotype frequencies and fitnesses. *Annual Meeting of the Society for the Study of Evolution* (University of Minnesota - 2008).
3. X-autosome interactions in *Drosophila melanogaster*: phenotypes, incompatibilities, and geography. *Department of Ecology and Evolution Retreat* (Stony Brook University - 2009).
4. X-autosome interactions in *Drosophila melanogaster*: phenotypes, Incompatibilities, and geography. *Annual Meeting of the Society for the Study of Evolution – session chair* (University of Idaho - 2009).
5. Genotype-phenotype maps and the population genetics of incomplete penetrance. *Annual Meeting of the Society for the Study of Evolution* (Portland State University - 2010).
6. The population genetics of X-autosome incompatibilities and the origins of Haldane's rule. *Annual Meeting of the Society for the Study of Evolution* (University of Oklahoma - 2011).

7. Evolutionary history and adaptation inferred from whole genome sequences of diverse African hunter-gatherers. *Annual Meeting of the Society for the Study of Evolution* (Ottawa, Canada - 2012).
8. Scans of selection using whole genome sequences of diverse African hunter-gatherers reveal associations between pituitary loci and Pygmy stature. *Annual Meeting of the Society for the Study of Evolution - session chair* (Snowbird, Utah - 2013).
9. Scans of selection using whole genome sequences of diverse African hunter-gatherers reveal associations between pituitary loci and Pygmy stature. *Annual Meeting of the Society for Molecular Biology and Evolution* (Chicago, IL - 2013).
10. GC-biased gene conversion and the curse of the converted. *Annual Meeting of the Society for the Study of Evolution - session chair* (Raleigh, NC - 2014).
11. GC-biased gene conversion and the curse of the converted. *School of Biology retreat* (Georgia Institute of Technology - 2014).
12. Population and evolutionary genomics of prostate cancer-associated variants: Implications for health disparities in men of African descent. *The Science of Cancer at Georgia Tech* (Georgia Institute of Technology - 2015).
13. Population and evolutionary genomics of prostate cancer-associated variants: Implications for health disparities in men of African descent. *Annual Meeting of the American Society of Human Genetics* (Baltimore, MD - 2015).
14. Simulating human history many genomes at a time. *High Performance Computing Science Day* (Georgia Institute of Technology - 2015).
15. Adaptive introgression and the evolutionary genetics of hybrid fitness effects. *SMBE/AAAG Satellite Meeting on the Genetics of Admixed Populations* (San Antonio, TX - 2016).
16. Adaptive introgression and the evolutionary genetics of hybrid fitness effects. *Annual Meeting of the Society for the Study of Evolution* (Austin, TX - 2016).
17. Ascertainment bias in predicting disease risks. *Annual Meeting of the American Society of Human Genetics* (Vancouver, BC - 2016). Chaired a platform session on ancestry, admixture, and migration.
18. Health disparities and biased predictions of genetic disease risks. *4th Biennial Science of Global Prostate Cancer Disparities Conference* (Orlando, FL - 2016).
19. The genomic health of ancient hominins. *Annual Meeting of the Society for Molecular Biology and Evolution* (Austin, TX - 2016).
[presented by Lachance Lab postdoc: **Ali Berens**]
20. Ascertainment bias can create the illusion of genetic health disparities. *Annual Meeting of the Society for Molecular Biology and Evolution* (Austin, TX - 2016).
[presented by Lachance Lab Ph.D. student: **Michelle Kim**]

Conference Posters:

1. Inference of post-selection genotype frequencies. *Stony Brook University Genetics Program Retreat* (Brookhaven National Laboratory - 2006).
2. Inbreeding, the pruning of family trees, and the most recent common ancestor of humanity. *Stony Brook University Genetics Program Retreat* (Cold Spring Harbor

- Laboratory - 2007).
3. Long-term adaptation of epistatic genetic networks. *Laufer Center for Computational Biology and Genome Sciences* (Stony Brook University - 2009).
 4. Long-term adaptation of epistatic genetic networks. *Stony Brook University Genetics Program Retreat* (Brookhaven National Laboratory - 2010).
 5. Evolutionary history and adaptation inferred from whole genome sequences of diverse African hunter-gatherers. *Annual Meeting of the Society for Molecular Biology and Evolution* (Dublin, Ireland - 2012).
 6. GC-biased gene conversion and the curse of the converted. *Annual Meeting of the American Society of Human Genetics* (Boston, MA - 2013).
 7. GC-biased gene conversion and the curse of the converted. *Annual Meeting of the Society for Molecular Biology and Evolution* (San Juan, Puerto Rico - 2014).
 8. Selective constraint and sex-biased demography of human populations from X chromosome-autosome comparisons. *Annual Meeting of the Society for Molecular Biology and Evolution* (Vienna, Austria - 2015).
 9. Selective constraint and sex-biased demography of human populations from X chromosome-autosome comparisons. *Annual Meeting of the American Society of Human Genetics* (Baltimore, MD - 2015).
[presented by Lachance Lab PhD. student: **Melanie Quiver**]
 10. Selective constraint and sex-biased demography of human populations from X chromosome-autosome comparisons. *Annual Meeting of American Indian Society Science and Engineering Society* (Phoenix, AZ - 2015).
[presented by Lachance Lab Ph.D. student: **Melanie Quiver**]
 11. Population and evolutionary genomics of prostate cancer-associated variants: Implications for health disparities in men of African descent. *South Big Data Hub Workshop: High Impact Applications of Data Science in Precision Medicine, Health Analytics, and Health Disparities* (Atlanta, GA - 2016).
 12. Painting by evolutionary history: inference of local ancestry in admixed genomes. *SMBE/AAAG Satellite Meeting on the Genetics of Admixed Populations* (San Antonio, TX - 2016).
[presented by Lachance Lab postdoc: **Ali Berens**]
 13. Evidence of sex-biased migration and selection against recessive alleles from X chromosome-autosome comparisons. *SMBE/AAAG Satellite Meeting on the Genetics of Admixed Populations* (San Antonio, TX - 2016).
[presented by Lachance Lab Ph.D. student: **Melanie Quiver**]
 14. Painting by evolutionary history: inference of local ancestry in admixed genomes. *Annual Meeting of the American Society of Human Genetics* (Vancouver, BC - 2016).
[presented by Lachance Lab postdoc: **Ali Berens**]
 15. Population and evolutionary genomics of prostate cancer-associated variants: Implications for health disparities in men of African descent. *AACR International Conference on New Frontiers in Cancer Research* (Cape Town, South Africa - 2017).
 16. The genomic health of ancient hominins. *Annual Meeting of the Society for the*

Study of Evolution (Portland, OR - 2017).
[presented by Lachance Lab undergraduate: **Taylor Cooper**]

Grants and Contracts:

Currently Funded:

2015-2020 Genetic Epidemiology of Prostate Cancer in Africa
NIH U01CA184374
Role: Subcontractor (one of nine)
Collaborator: Timothy Rebbeck (PI)
Direct and indirect funding: \$8,890,000 total (\$267,000 to Georgia Tech)

Previously Funded:

2011-2014 Population Genomics of Geographically and Ethnically Diverse Africans
NIH F32HG006648
Role: PI
Direct and indirect funding: \$154,000 total

Societal and Policy Impacts:

Media coverage of hunter-gatherer genomes and ancient introgression:

New York Times (front page), Washington Post (front page), Philadelphia Inquirer, Veja, Science, Nature, Nature Genetics, Scientific American, Chronicle of Higher Education, ScienceNews, io9, GenomeWeb, PBS, and others

One of 139 professors to sign a letter criticizing Nicholas Wade's book: *A Troublesome Inheritance*. Media coverage of this letter:

New York Times, Wall Street Journal, Huffington Post, Daily Mail, Scientific American, Science, and Nature

Media coverage of Y chromosomes, mtDNA, and the invention of agriculture:

Ars Technica, Phys.Org, Pacific Standard, and Science Daily

Media coverage of how evolution has shaped the genomes of African Pygmies:

New York Times, Smithsonian, and Nature

Lachance Lab Ph.D. student Melanie Quiver featured in Georgia Tech's *Research Horizons* magazine

Media coverage of human genomics, introgression, and migration out-of-Africa:

New York Times (front page), Seattle Times, The Conversation, Daily Mail, Washington Post, Christian Science Monitor, Economic Times, Ars Technica, New Scientist, TIME, Discover Magazine, GenomeWeb, Sinc, Science Daily, The Verge, ABC, BBC, Science, Nature, and others

Guest speaker for "Your Health Connection" on Clark Atlanta University's radio station: WCLK, FM 91.9. This show was hosted by Pattie Walden and the Center for Cancer Research and Therapeutic Development

Teaching:

Courses Taught at Georgia Institute of Technology:

Scores shown are interpolated medians

- Spring 2015 Mathematical Models in Biology (BIOL 2400)
1.5 credit hours, 24 students
Overall teaching effectiveness: 4.64
- Spring 2016 Human Evolutionary Genomics (BIOL 4803/8803)
3 credit hours, 16 students
Overall teaching effectiveness: 5.00 undergraduate, 4.79 graduate
- Fall 2016 Frontiers in Molecular Cell Biology (BIOL 8803)
0.5 credit hours, 9 students
Overall teaching effectiveness: 5.00
- Spring 2017 Mathematical Models in Biology (BIOL 2400)
1.5 credit hours, 21 students
Overall teaching effectiveness: 4.91

Individual Student Guidance:

Postdoctoral Researchers:

- 2015-2017 Ali Berens
Placed into a private-sector data scientist job at Monsanto

Ph.D. Students:

- 2015- Melanie Quiver (biology)
NIH T32 training grant fellowship
2nd place poster award at the 2015 AISES Conference
Jackson Lab short course on the genetics of addiction - travel award
Summer internship for indigenous peoples in genomics fellowship
- 2016- Michelle Kim (bioinformatics)

Rotating Ph.D. Students:

- 2015 Maxine Harlemon (bioinformatics, Clark Atlanta University)
- 2016 Annachiara Korchmaros (bioinformatics)

M.S. Students:

- 2015-2016 Binbin Huang (bioinformatics)
Placed into a Ph.D. program at Michigan State University
- 2015-2016 Andrew Teng (bioinformatics)
NIH/NCI summer intern
Placed into a Ph.D. program at the University of Washington
- 2016- Venna Wang (bioinformatics)

Undergraduate Students:

- 2015 Anna Paulino (biochemistry)
- 2015 Imon Ghosh (biochemistry)

- 2015 Claire Hanson (biology)
Obtained PURA summer salary award
- 2015-2016 Kane Patel (biology)
Obtained PURA travel award
Georgia Tech research symposium: 2nd place poster award
Placed into a job at the CDC
- 2016- Taylor Cooper (biology)
School of Biological Sciences Fast-Track to Research Scholar
SSE/BEACON Undergraduate Diversity in Evolution travel award
- 2016- Collin Spencer (biology)
School of Biological Sciences Fast-Track to Research Scholar
- 2017- Greg Johnston (computer science)
- 2017 Nigel Blackwood (computational biology, University of Pennsylvania)

Service on Thesis or Dissertation Committees:

- 2015 Jing Zhao (biology)
- 2015- Diana Williams (biology)
- 2015- Dan Sun (biology)
- 2015- Maxine Harlemon (bioinformatics, Clark Atlanta University)
- 2015- Biao Zeng (bioinformatics)
- 2016- Zuehui Zhao (biology)
- 2016- Emily Norris (bioinformatics)

Other Teaching Activities:

- 1996 Teaching assistant: University of Chicago
Genetics (undergraduate level - BIOS 143)
- 2006 Teaching assistant: Stony Brook University
Genetics (undergraduate level - BIO 320)
- 2006 Teaching assistant: Stony Brook University
Molecular and cell biology techniques (undergraduate level - BIO 311)
- 2008 Instructor: Stony Brook University
Population genetics and evo-devo (Ph.D. level - BGE 510)
- 2006-2010 Research Mentor: Stony Brook University
Mentored three undergraduates (JoAnn Lenci, Jamal Hyder, Lawrence Jung) and five high school students (Marek Solomianko, Michael Casper, Sangmi Ahn, Michael Luke, Manny Vivekanandan)
- 2012-2014: Research Mentor: University of Pennsylvania
Mentored two undergraduates (Kristen Mullen and Michael Chen)
- 2007-2009 Guest instructor: Stony Brook University
Molecular diversity laboratory (undergraduate level - BIO 367)
- 2011 Guest instructor: Perelman School of Medicine
Population genetics (M.D. level - Core Principles Module 1)
- 2012 Guest instructor: University of Pennsylvania
Population genetics (Ph.D. level - CAMB 550)
- 2012 Instructor: University of Pennsylvania
Human evolutionary genomics (undergraduate level - BIOL 522)

- 2013 Instructor: University of Pennsylvania
Human population genetics (Ph.D. level - CAMB 550)
- 2014 Guest instructor: Georgia Institute of Technology
Human evolutionary genetics (undergraduate level - BIOL 3600)
- 2015 Guest instructor: Georgia Institute of Technology
Human evolutionary genetics (undergraduate level - BIOL 3600)
- 2015 Guest instructor: Georgia Institute of Technology
African genetic variation (undergraduate level - BIOL 4545)
- 2016 Instructor: Summer Institute in Statistical Genetics
Introduction to genetics and genomics (Ph.D. level - Module 2)
Teaching ratings: 16/19 excellent/very good, 3/19 good
- 2017 Instructor: Summer Institute in Statistical Genetics
Introduction to genetics and genomics (Ph.D. level - Module 2)

Service:

Professional Contributions:

Reviewed Publications:

BMC Genomics, Evolution, Genes and Genetic Systems, Genetica, Genetics, Genome Biology, Genome Biology and Evolution, Heredity, Journal of Theoretical Biology, Molecular Biology and Evolution, Molecular Ecology, Oxford University Press, Physical Biology, PLoS Genetics, PLoS One, Proceedings of the National Academy of Sciences, Quarterly Review of Biology, Sinauer Associates, Theoretical Population Biology, Trends in Genetics

Guest editor:

2015-16 PLoS Genetics

Reviewed Grants:

2008 King Miller Fellowship
2015 Leakey Foundation

Society Memberships:

2002- Society for the Study of Evolution (attended eleven meetings)
2006- Genetics Society of America
2009- Society for Molecular Biology and Evolution (attended six meetings)
2010- American Society of Human Genetics (attended five meetings)
2015- American Association of Anthropological Genetics (attended one meeting)
2016- International Society for Evolution, Medicine, and Public Health (attended one meeting)
2016- American Association for Cancer Research (attended one meeting)

Institute Contributions:

2015 Evolution@Tech seminar series organizer
2015- Active participant in the College of Sciences New Faculty Mentoring

Workshop
2015 Science Olympiad judge (CEISMC)
2015 Commencement alignment volunteer
2015 Organized the School of Biology holiday party
2016 Participated in the Best Practices Forum on Mentoring
2016 Assisted in the Research Bound in STEM workshop
2016 Faculty-staff advisory committee for the Engineered Biosystems Building
2016- School of Biological Sciences graduate committee
2016 Petit Scholars review committee

Other Service:

2005-2009 Organized a philosophy of biology discussion (Stony Brook University)
2006 Assisted in organizing SSE's Evolution 2006 conference
2007-2009 Led Darwin Day discussions (Stony Brook University)
2007-2009 New teaching assistant workshop (Stony Brook University)
2009-2010 Student representative on the executive committee of the Graduate Program in Genetics (Stony Brook University)
2012-2014 Organized journal club for the Department of Genetics (University of Pennsylvania)
2015 Represented Georgia Institute of Technology at the National Science Foundation South Big Data Hub and Spokes meeting (Atlanta, GA)
2015- Member of the Petit Institute for Bioengineering and Bioscience (Georgia Institute of Technology)
2015- Member of the Integrated Cancer Research Center (Georgia Institute of Technology)
2015- Member of the Center for Integrated Genomics (Georgia Institute of Technology)
2016 Represented Georgia Institute of Technology at the Atlanta area Quantitative Biology Workshop (Spelman College)
2016 Organized a networking event for members of Georgia Tech's School of Biology and global experts in Neanderthal and Denisovan genomics
2016- Men of African Descent and Carcinoma of the Prostate (MADCaP) network: co-chair of the array development working group