CURRICULUM VITAE AND TABLE OF CONTENTS

JOSEPH LACHANCE, PH.D.
ASSOCIATE PROFESSOR
SCHOOL OF BIOLOGICAL SCIENCES

JOSEPH LACHANCE PH.D.
ASSOCIATE PROFESSOR
SCHOOL OF BIOLOGICAL SCIENCES

I. EARNED DEGREES

1992-1996 B.A. 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"
Ph.D. advisor: John True

II. EMPLOYMENT HISTORY

2021- Associate Professor, School of Biological Sciences, Georgia Institute of Technology

2015-2021 Assistant Professor, School of Biological Sciences, Georgia Institute of Technology

2010-2014 NIH NRSA Postdoctoral Fellow, University of Pennsylvania
Postdoctoral advisor: Sarah Tishkoff

III. HONORS AND AWARDS

1992-1996 National Merit Scholar (University of Chicago)
1995 HHMI 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)
2009 Cedar Brook Award for best student talk (Stony Brook University)
2011-2014 NIH Kirschstein NRSA postdoctoral fellowship
2016- Member of the Faculty of 1000, expertise: evolutionary & comparative genetics
2017-2018 Class of 1969 Teaching Fellow (Georgia Tech)
2019 CTL/BP Junior Faculty Teaching Excellence Award (Georgia Tech)
2019 Elected to the Executive Council of the of the AAAG
2019 NIH MIRA Award
2020 Selected as one of Georgia Tech's Faces of Inclusive Excellence

IV. RESEARCH, SCHOLARSHIP, AND CREATIVE ACTIVITIES

Bold *text indicates members of the Lachance Lab*
Underlined text indicates corresponding author
** indicates work done at Georgia Tech*
PD *indicates Lachance Lab postdoc author*
G *indicates Lachance Lab graduate student author*
UG *indicates Lachance Lab undergraduate author*
T *indicates Lachance Lab technician author*

A. Published Books, Book Chapters, and Edited Volumes

A1. Books

No data

A2. Refereed 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.
[This publication is solely a product of the Lachance Lab at Georgia Tech]

A3. Edited Volumes

No data

B. Refereed Publications and Submitted Articles

B1. Published and Accepted Journal Articles

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* 3:1143.
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 (2013) 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 (2013) 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.
[Lachance Lab contributions: supplied genomic data and assisted in writing the paper]

* 17. Hsieh PH, Veeramah KR, **Lachance J**, Tishkoff SA, Wall JD, Hammer MF, and 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.
[Lachance Lab contributions: supplied genomic data, interpreted demographic simulations, and assisted in writing the paper]

* 18. Hsieh PH, Woerner AE, Wall JD, **Lachance J**, Tishkoff SA, Gutenkunst RN, and Hammer MF (2016) Model-based analyses of whole genome data reveal a complex evolutionary history involving archaic introgression in Central African Pygmies. *Genome Research* 26:291-300.
[Lachance Lab contributions: supplied genomic data and helped supervise archaic introgression analyses]

* 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.
[Lachance Lab contributions: supplied genomic data and assisted in writing the paper]

* 20. **Berens AJ**[PD], **Cooper TL**[UG], and **Lachance J** (2017) The genomic health of ancient hominins. *Human Biology* 89:7-19.
[This publication is solely a product of the Lachance Lab at Georgia Tech]

* 21. **Lachance J**, **Berens AJ**[PD], Hansen MEB, **Teng AK**[G], Tishkoff SA, and Rebbeck TR (2018) Genetic hitchhiking and population bottlenecks contribute to prostate cancer disparities in men of African descent. *Cancer Research* 78(9):2432-2443.
[Lachance Lab contributions: conceived and supervised project, analyzed data, ran demographic simulations, and wrote the paper - collaborators supplied datasets]

* 22. Rishishwar L, Wang L, Wang J, Yi S, **Lachance J**, Jordan K (2018) Evidence for positive selection on recent human transposable element insertions. *Gene* 675:69-79.
[Lachance Lab contributions: supervised selection analyses, conceived and supervised demographic simulations, and assisted in writing and revising the paper]

* 23. Andrews C, ... **Lachance J** (author 31 of 79) ... Rebbeck TR, (2018) Development, evaluation, and implementation of a pan-African cancer research network: Men of African Descent and Carcinoma of the Prostate (MADCaP). *Journal of Global Oncology* Sept(4):1-14.

[Lachance Lab contributions: led array working group, supervised population genetics analyses, and assisted in the writing paper]

* 24. Hey J, Chung Y, Sethuraman A, **Lachance J** Tishkoff SA, Sousa VC, and Wang Y (2018) Phylogeny estimation by integration over isolation with migration models. *Molecular Biology and Evolution* 35(11):2805-2818.

[Lachance Lab contributions: supplied genomic data and assisted in writing the paper]

* 25. **Kim MS**[G], **Patel KP**[UG], **Teng AK**[G], **Berens AJ**[PD]**,** and **Lachance J** (2018) Genetic disease risks can be misestimated across global populations. *Genome Biology* 19:179.

[This publication is solely a product of the Lachance Lab at Georgia Tech]

* 26. Waldetoft KW, Gurney J, **Lachance J**, Hoskisson PA, and Brown S (2019) Evolving antibiotics against resistance: a potential platform for natural product development. *mBio* 10:e02946-19.

[Lachance Lab contributions: provided expert advice re: the genetics of adaptation and assisted in writing the paper]

* 27. **Harlemon M**[G], Ajayi O, Kachambwa P, **Kim MS**[G], **Simonti CN**[PD], **Quiver MH**[G]**,** Peterson D, Mittal A, ..., and **Lachance J**, (2020) A custom genotyping array reveals population-level heterogeneity for the genetic risks of prostate cancer and other cancers in Africa. *Cancer Research* 80:2959-2969.

[Lachance Lab contributions: conceived the study, designed the MADCaP genotyping array, conducted genetic analyses, and wrote the paper]

B2. Conference Presentations with Proceedings (Refereed)

* 1. **Lachance J** (2016) Ancient introgression in Africa and the evolutionary genetics of hybrid fitness effects. *American Journal of Physical Anthropology* 159:199.

[This publication is solely a product of the Lachance Lab at Georgia Tech]

* 2. **Lachance J**, **Berens AJ**[PD], Hansen MEB, **Teng AK**[G], Tishkoff SA, and Rebbeck TR (2017) Population and evolutionary genomics of prostate cancer-associated variants: implications for health disparities in men of African descent. *Cancer Research* 77 (22 Supplement):A33.

[Lachance Lab contributions: conceived and supervised project, analyzed data, ran demographic simulations, and wrote the paper - collaborators supplied datasets]

* 3. **Lachance J**, **Harlemon M**[G], Kachambwa P, Ajayi O, **Kim MS**[G], Adams M, Pugh E, Petersen, and Rebbeck TR (2019) Development of a custom genotyping platform and genetic prediction of prostate cancer risks in sub-Saharan Africa. *Cancer Research* 79 (13 Supplement):2410.

[Lachance Lab contributions: conceived the study, designed the MADCaP genotyping array, and performed tests of polygenic risk scores]

* 4. **Lachance J** (2020) Ancient DNA reveals that few disease-associated loci have been strongly selected during recent human history. *American Journal of Physical Anthropology* 171:153.

[This publication is solely a product of the Lachance Lab at Georgia Tech]

B3. Other Refereed Material

* 1. **Lachance J** (2019) Book Review: Molecular Population Genetics by Hahn. *Evolution* 73:860-861.
[This publication is solely a product of the Lachance Lab at Georgia Tech]

* 2. **Lachance J**, **Simonti CN**[PD], and Weitz JS (2020) Large sample spaces do not imply biological systems are 'fine-tuned'. *Journal of Theoretical Biology.* 507:110457. doi: 10.1016/j.jtbi.2020.110457
[This letter was conceived and written by members of the Lachance Lab at Georgia Tech]

* 3. **Lachance J** (2020) Beyond stamp collecting: evolutionary and functional genomics advance our understanding of cancer biology. Cancer Research 81:1637-1638.
[This letter was conceived and written by members of the Lachance Lab at Georgia Tech]

B4. Submitted Journal Articles

* 1. **Simonti CN**[PD] and **Lachance J** (2021) Ancient DNA reveals that few GWAS loci have been strongly selected during recent human history.
[This publication is solely a product of the Lachance Lab at Georgia Tech]

* 2. **Elbon M**[T], **Bharadwaj A**[G], **Damle G**[G], **Brown L**[T], and **Lachance J** (2021) Does effective population size govern population and species-level differences in telomere length?
[This publication is solely a product of the Lachance Lab at Georgia Tech]

* 3. **Pfennig A**[G] and **Lachance J** (2021) Estimating sex-biased admixture when ancestry proportions don't add up.
[This publication is solely a product of the Lachance Lab at Georgia Tech]

* 4. **Kim MS**[G], Naidoo D, **Simonti CN**[PD], Chen WC, **Quiver MH**[G], Kachambwa P, **Harlemon M**[G], ... Rebbeck TR, and **Lachance J** (2021) Testing the generalizability of ancestry-specific polygenic risk scores to predict prostate cancer in sub-Saharan Africa
[Lachance Lab contributions: conceived the study, conducted genetic analyses, and wrote the paper]

* 5. **Quiver MH**[G] and **Lachance J** (2021) Adaptive eQTLs reveal the evolutionary impacts of pleiotropy and tissue-specificity, while contributing to health and disease in human populations. *bioRxiv preprint* doi:10.1101/444737
[This publication is solely a product of the Lachance Lab at Georgia Tech]

* 6. Darst BF, Hughley R, Pfennig A[G], Hazra UG, ... **Lachance J**, Rebbeck TR, Conti DV, and Haiman CA, (2021) Germline *HOXB13* variants contributes to risk of prostate cancer in men of African ancestry
[Lachance Lab contributions: supplied African genomic data and performed allele age analyses]

B5. Articles in Preparation

* 1. **Lachance J**, **Quiver MH**[G], Mullen K, Hansen MEB, **Berens AJ**[PD], Chen MA, Hsieh PH, Veeramah KR, and Tishkoff SA (2021) Genomic evidence of a male-biased migration out of Africa from X chromosome-autosome comparisons.
[Lachance Lab contributions: conceived and supervised project, analyzed data, developed mathematical models, and wrote the paper - collaborators supplied datasets

* 2. **Pfennig A**[G] and **Lachance J** (2021) Adaptive introgression and the evolutionary genetics of hybrid fitness effects.
[This publication is solely a product of the Lachance Lab at Georgia Tech]

* 3. **Janivara R**[G], **Harlemon M**[G], **Simonti CN**[PD], **Kim MS**[G], **…** Rebbeck TR, Adebiyi A, Agalliu I and **Lachance J** (2021) The genetic architecture of male pattern baldness differs between Europe and sub-Saharan Africa

[Lachance Lab contributions: conceived the study, applied polygenic risk scores, conducted a baldness GWAS, and wrote the paper]

* 4. **Simonti CN**[PD], Baños H, Silliman K, Heitsch C, **Lachance J,** and Paaby A (2021) Mutational load, compensatory evolution, and tRNA structure in *C. elegans*.

[Lachance Lab contributions: performed bioinformatics and evolutionary genomics analyses, as well as assisting in writing the paper]

* 5. Hansen MEB, **Kim MS**[G], Raj S, Fan S, Haut J, Ranciaro A, Mpoloka SW, Mokone GG, Nyambo T, Meskel DW, Bekay G, **Lachance J**, and Tishkoff SA (2021) Genomic analysis of complex traits in a continent-wide African cohort.

[Lachance Lab contributions: conceived the project, performed all analyses regarding replication of GWAS results across continents, and helped write the paper]

* 6. **Lachance J**, **Janivara RS**[G], **Hazra U**[G], **Kim MS**[G], Agalliu I, and Rebbeck TJ (2021) Challenges to generalizing genetic predictions of cancer risks to diverse populations.

[Lachance Lab contributions: conceived the study, conducted genetic analyses, and wrote the paper]

* 7. **Cruz G**[G], **Kim MS**[G], and **Lachance J** (2021) PRSproxy: a bioinformatics tool for selecting proxy SNPs for polygenic risk scores.

[This publication is solely a product of the Lachance Lab at Georgia Tech]

* 8. **Hazra U**[G] and **Lachance J** (2021) Polygenic adaptation is not a major driver of health disparities across global populations

[This publication is solely a product of the Lachance Lab at Georgia Tech]

* 10. **Kim MS**[G], **Simonti CN**[PD], and **Lachance J** (2021) Incorporating dominance and recessivity improves polygenic predictions of disease risk.

[This publication is solely a product of the Lachance Lab at Georgia Tech]

* 11. **Quiver MJ**[G], **Ma J**[G], and **Lachance J** (2021) Ancestral state reconstruction of primate genomes reveals tissue-specific evolutionary constraint acting on eQTLs

[This publication is solely a product of the Lachance Lab at Georgia Tech]

C. Other Publications and Creative Products

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, Ulijaszek, and Capelli. *Quarterly Review of Biology* 91:234-235.
11. * **Lachance J** (2018) Book Review: Crumbling Genome: The Impact of Deleterious Mutations on Humans by Kondrashov. *Quarterly Review of Biology* 93:274.
12. * **Kim MS**[G] and **Lachance J** (2018) Challenges to globalizing genetic predictions of health and disease. *On Biology* (invited guest blog).
13. * **Lachance J** (2020) Book Review: Cellular and Animal Models in Human Genomics Research by Walz and Young. *Quarterly Review of Biology* 95:269-270.
14. * **Lachance J** (2020) Book Review: The Genetics of African Populations in Health and Disease by Ibrahim and Rotimi. *Quarterly Review of Biology* 95:340-341.

D. PRESENTATIONS

D1. 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 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).
* 20. Evolutionary history and hereditary disease risks in ancient and modern humans. (Emory University - 2017).
* 21. Evolutionary history and hereditary disease risks in ancient and modern humans. (Pennsylvania State University - 2017).
* 22. Evolutionary history and hereditary disease risks in ancient and modern humans. (Auburn University - 2018).
* 23. Evolutionary history and hereditary disease risks in ancient and modern humans. *Gene Forum 2018* (Tartu, Estonia - 2018).
* 24. Evolutionary genetics of prostate cancer in men of African descent. *Prostate Cancer Seminar Series* (Winship Cancer Institute of Emory University - 2018).
* 25. Evolutionary history and hereditary disease risks in ancient and modern humans. *2018 International Symposium of Evolutionary Genomics and Bioinformatics* (National Taiwan University - 2018).
* 26. Evolutionary history and hereditary disease risks in ancient and modern humans. (National Central University, Taiwan - 2018).
* 27. Genetics of prostate cancer in men of African descent. *Grand Rounds* (Winship Cancer Institute of Emory University - 2018).
* 28. Development of the MADCaP array: a custom genotyping platform optimized for the detection of genetic associations with prostate cancer in men of African descent. *Prostate cancer in Africa: Connecting Clinical to Basic Science Research* (Abuja, Nigeria - 2019).
* 29. Population genomics of prostate cancer and the pitfalls of generalizing genetic predictions of cancer risk to African populations. *MADCaP Prostate Cancer Symposium* (Abuja, Nigeria - 2019).

* 30. Evolution and genetic prediction of prostate cancer risks in African men. *ICRC Cancer Symposium - Cancer from an Evolutionary Perspective* (Georgia Institute of Technology - 2019).

* 31. Evolution and genetic prediction of hereditary disease risks in ancient and modern humans. *Genetics Seminar Series* (University of Georgia - 2019).

* 32. Challenges to globalizing genetic predictions of cancer risks. *Indo-US Workshop on Human Diversity and Health Disparities* (CCMB in Hyderabad, India - 2020).

* 33. Evolution and genetic prediction of prostate cancer risks in African populations. *5th Annual Cancer Health Disparities Symposium* (SUNY Downstate Medical Center - 2020).

* 34. Challenges to globalizing genetic predictions of prostate cancer risks. *University of Southern California's Center for Genetic Epidemiology* (virtual seminar - 2020).

* 35. Evolution and prediction of genetic disease risks in ancient and modern humans. *School of Biological Sciences* (Georgia Institute of Technology - 2020).

* 36. Evolution and prediction of genetic disease risks in ancient and modern humans. *Department of Bioinformatics and Genomics Seminar Series* (UNC Charlotte - 2020). *[talk rescheduled due to coronavirus pandemic]*

* 37. Ancient DNA, Neanderthals, and the evolution of human health. *Department of Biology Seminar Series* (Williams College - 2021).

* 38. Ancestry-matched polygenic risk scores moderately improve predictions of prostate cancer in men of African descent. *Annual meeting of the International Society for Evolution, Medicine, and Public Health* (Virtual Meeting - 2021).

* 39. Genotyping technologies, ascertainment bias, and limitations of generalizing genetic predictions to Africa. *GTRI Friday Morning Seminar Series* (Georgia Institute of Technology - 2021).

* 40. Evolution and prediction of genetic disease risks in ancient and modern humans. *University Program in Genetics and Genomics Seminar Series* (Duke University 2021).

* 41. Challenges to globalizing genetic predictions of disease risks. *Department of Genetics Seminar Series* (Rutgers University - 2021).

D2. 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 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, UT - 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 in Black Men Conference* (Orlando, FL - 2016).

* 19. The genomic health of ancient hominins. *Annual Meeting of the Society for Molecular Evolution* (Austin, TX - 2017).

* 20. Ascertainment bias can create the illusion of genetic health disparities. *Annual Meeting of the Society for Molecular Biology and Evolution* (Austin, TX - 2017).
[presented by Lachance Lab Ph.D. student: ***Michelle Kim****]*

* 21. Adaptive eQTLs in human populations. *Annual Meeting of the American Society of Human Genetics* (Orlando, FL - 2017).
[lightning talk presented by Lachance Lab Ph.D. student: ***Melanie Quiver****]*

* 22. Ancient DNA reveals that few disease-associated loci have been strongly selected during recent human history. *Annual Meeting of the Society for the Study of Evolution* (Providence, RI - 2019).

* 23. Ancient DNA reveals that few disease-associated loci have been strongly selected during recent human history. *Annual Meeting of the Society for Molecular Biology and Evolution* (Manchester, United Kingdom - 2019).
[presented by Lachance Lab postdoc: ***Corinne Simonti****]*

* 24. Evolution and genetic prediction of prostate cancer risks in African men. *Annual Meeting of the Society for Molecular Biology and Evolution* (Manchester, United Kingdom - 2019).

* 25. A custom genotyping array for detecting disease associations in men of African descent reveals population-level heterogeneity in the genetic risks of prostate and other cancers. *AORTIC's 12th Annual International Conference on Cancer in Africa* (Maputo, Mozambique - 2019).

* 26. Ancient DNA reveals that few disease-associated loci have been strongly selected during recent human history. *Annual Meeting of the American Association of Physical Anthropology* (Los Angeles, CA - 2020).
[meeting canceled due to coronavirus pandemic]

* 27. How accurate are genetic predictions of prostate cancer risk in Africa? *AORTIC Cancer Genomics Conference: African Genomic Diversity, a Roadmap to Global Equity in Cancer Control* (Virtual Meeting - 2021).

D3. 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 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****]*

* 17. Adaptive eQTLs in human populations. *Annual Meeting of the American Society of Human Genetics* (Orlando, FL - 2017). Received a Reviewer's Choice Award.
[presented by Lachance Lab Ph.D. student: ***Melanie Quiver****]*

* 18. The genomic health of ancient hominins. *Annual Meeting of the American Society of Human Genetics* (Orlando, OR - 2017).

* 19. Adaptive eQTLs in human populations. *SMBE Satellite Meeting on Modern Methods for the Study of Ancient DNA* (Providence, RI - 2018).
[presented by Lachance Lab Ph.D. student: ***Melanie Quiver****]*

* 20. Adaptive eQTLs in human populations reveal the evolutionary impacts of pleiotropy and tissue-specificity. *Annual Meeting of the Society for Molecular Biology and Evolution* (Yokohama, Japan - 2018).

* 21. How genetic disease risks can be misestimated. *Annual Meeting of the American Society of Human Genetics* (San Diego, CA - 2018).
[presented by Lachance Lab Ph.D. student: ***Michelle Kim****]*

* 22. Ancient DNA reveals signatures of selection on disease-associated loci from GWAS. *Annual Meeting of the American Society of Human Genetics* (San Diego, CA - 2018).
[presented by Lachance Lab postdoc: ***Corinne Simonti****]*

* 23. Investigating the contribution of runs of homozygosity and genetic ancestry to elevated risks of prostate cancer in men of African descent. *5th Biennial Science of Global Prostate Cancer Disparities in Black Men Conference* (Ilorin, Nigeria - 2018).
[presented by Lachance Lab Ph.D. student: ***Maxine Harlemon****]*

* 24. Development of a custom genotyping platform and genetic prediction of prostate cancer risks in sub-Saharan Africa. *Annual Meeting of the American Association for Cancer Research* (Atlanta, GA - 2019).

* 25. Scans of selection in urban African populations reveal recurrent targets of adaptation. *Annual Meeting of the American Society of Human Genetics* (Houston, TX - 2019).
[presented by Lachance Lab Ph.D. student: ***Melanie Quiver****]*

* 26. Polygenic risk scores generated from European populations poorly predict prostate cancer risks in African populations. *Annual Meeting of the American Society of Human Genetics* (Houston, TX - 2019).
*[presented by Lachance Lab Ph.D. student: **Michelle Kim**]*

* 27. A custom genotyping array for detecting disease associations in men of African descent reveals population-level heterogeneity in the genetic risks of prostate and other cancers. *Annual Meeting of the American Society of Human Genetics* (Houston, TX - 2019).
*[presented by Lachance Lab Ph.D. student: **Maxine Harlemon**]*

* 28. Limited transferability of polygenic trait scores and asymmetric replication of GWAS results between Europe and sub-Saharan Africa. *Annual Meeting of the Society for Molecular Biology and Evolution* (Quebec City, Canada - 2020).
*[meeting canceled due to coronavirus pandemic, poster by Ph.D. student: **Michelle Kim**]*

* 29. Scans of positive selection in African populations reveal a large X effect and a key role for blood-related traits. *Annual Meeting of the Society for Molecular Biology and Evolution* (Quebec City, Canada - 2020).
*[meeting canceled due to coronavirus pandemic, poster by Ph.D. student: **Melanie Quiver**]*

* 30. Limited transferability of polygenic trait scores and asymmetric replication of GWAS results between Europe and sub-Saharan Africa. *Annual Meeting of the American Society of Human Genetics* (Virtual Meeting - 2020).
*[presented by Lachance Lab Ph.D. student: **Michelle Kim**]*

* 31. Genetics of male-pattern baldness in sub-Saharan Africa. *Annual Meeting of the American Society of Human Genetics* (Virtual Meeting - 2021).

E. GRANTS AND CONTRACTS

[$3.0M since arriving at Georgia Tech, including $2.8M as a PI]

E1. AS PRINCIPAL INVESTIGATOR

2019-2024 Evolution of Genetic Disease Risks Over Time and Space
NIH R35GM133727
Role: PI
Direct funding: $1,882,000 total to Georgia Tech
Period of contract: 9/5/2019 – 7/31/2024
Candidate's share: 100%

2021-2024 Georgia Tech GAANN Graduate Fellowships in Biology
Dept. of Education: DSP200A210046
Role: PI
Direct and indirect funding: $1,241,000 total ($913,000 to Georgia Tech)
Period of contract: 10/1/2021 – 9/31/2024
Candidate's share: 100%

Previously Funded

2007 King-Miller Travel Award (Stony Brook University)
Funding: $500 total
Candidate's share: 100%

2008 Research Access Project Travel Grant (Stony Brook University)
Funding: $500 total
Candidate's share: 100%

2009 Summer Institute in Statistical Genetics Fellowship (University of Washington)
Funding: $2000 total
Candidate's share: 100%

2011-2014 Population Genomics of Geographically and Ethnically Diverse Africans
NIH F32HG006648
Role: PI
Direct and indirect funding: $154,000 total
Period of contract: 12/15/2011 – 12/14/2014
Candidate's share: 100%

2019 Globalizing Genetic Predictions of Prostate Cancer
Integrated Cancer Research Center Seed Grant (Georgia Tech)
Role: PI
Direct funding: $30,000 total
Period of contract: 1/1/2019 – 6/30/2019
Candidate's share: 100%

2015-2020 Genetic Epidemiology of Prostate Cancer in Africa
NIH U01CA184374
Role: Subcontractor
Collaborator: Timothy Rebbeck (PI)
Direct and indirect funding: $8,890,000 total ($184,000 to Georgia Tech)
Period of contract: 9/1/2015 – 8/31/2020
Candidate's share: 2%

E2. AS CO-PRINCIPAL INVESTIGATOR

No data

E3. AS SENIOR PERSONNEL OR CONTRIBUTOR

No data

E4. PENDING PROPOSALS

2021-2026 Genomic Diversity of Prostate Cancer Across the African Diaspora
NIH R01 CA259100-01A1
Role: Subcontractor
Collaborator: Timothy Rebbeck (PI)
Direct and indirect funding: $7,750,000 total ($465,000 to Georgia Tech)
Period of contract: 8/1/2021 – 7/31/2026
Candidate's share: 6%

E5. PROPOSALS SUBMITTED BUT NOT FUNDED (LAST TWO YEARS)

NIH NHGRI R01
Evolutionary trajectories of cryptic genomic structural variants in primates

International Centre for Genetic Engineering and Biotechnology (Short Course Award)
Topic: Foundations in Genomics

Accurate Genetic Prediction of Cancer Risks in Diverse Human Populations

Mark Foundation for Cancer Research: Emerging Leader Award

F. Other Scholarly and Creative Accomplishments

No data

G. Societal and Policy Impacts

Media coverage of African hunter-gatherer genomes and ancient introgression: *New York Times (front page), Washington Post (front page), Philadelphia Inquirer, Veja, Medium, Science, Nature, Nature Genetics, Scientific American, Chronicle of Higher Education, ScienceNews, io9, GenomeWeb, PBS,* and the cover of *Cell*

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, LiveScience, NPR, Pacific Standard, Phys.Org, Science Daily*, *Slate, The Conversation, The Hindu,* and the *Washington Post*

Media coverage of how evolution has shaped the genomes of African Pygmies: *New York Times, Smithsonian Magazine, Science* News, and *Nature*

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

Media coverage of the migration out-of-Africa and ancient introgression: *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, and the cover of Nature*

Media coverage of the genomic health of ancient hominins: *American Association of Anthropological Genetics, American Society of Human Genetics, Front Line Genomics*, *Men's Health UK*, *National Geographic Explorer, phys.org, PLoS Blogs, Research Horizons*, *Science Daily, Technique,* and the cover of *Human Biology*

Media coverage of the genetic risks of prostate cancer in Africans: *Gene Expression*

Media coverage of the challenges to globalizing genetic prediction of disease risks: *BMC Blog Network*, *GenomeWeb, Genome Medicine*

Media coverage of a custom genotyping array that is optimized for detecting associations with prostate cancer in African populations: *ThermoFisher's Life in the Lab*, selected as one of the NCI's Epidemiology and Genomics Research Program highlights of 2020

Interviewed for a news feature in the journal *Science* about the evolution of polygenic risk scores for immune responses to pathogens.

H. Other Professional Activities

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.

Led discussions and interviewed director Christian Frei at a screening of "Genesis 2.0" at the Jimmy Carter Presidential Library and Museum. This documentary film follows the lives of tusk hunters in Siberia, as well as geneticists attempted to clone woolly mammoths. This event was hosted by the Swiss Consulate of Atlanta and was part of the Atlanta Science Tavern series.

Two student groups from my BIOL 3600 class had films that were finalists in the Evolution-

Themed Film Festival held at the SSE's 2019 conference. Only 15 films were selected as finalists in this international contest.

Led discussions of the film "Human Nature" at the Jimmy Carter Presidential Library and Museum. This documentary film examines the implications of CRISPR technology. This event was part of the Atlanta Science Tavern series.

Gave a public talk entitled "Ancient DNA, Neanderthals, and the evolution of human health" as part of the Atlanta Science Tavern series.

Teamed up with an artist (Birney Robert) as part of the Science.Art.Wonder program. This collaboration resulted in artwork that conveyed the concept of gene flow between divergent populations, entitled: *Gene Flow: A Constellation of Vital Phenomena*.

V. EDUCATION

A. COURSES TAUGHT

Spring, 2015	BIOL 2400	Mathematical Models in Biology CIOS overall effectiveness: 4.6/5	24 students
Spring, 2016	BIOL 4803/8803	Human Evolutionary Genomics CIOS overall effectiveness: 4.9/5	16 students
Fall, 2016	BIOL 8803	Frontiers in Molecular Cell Biology CIOS overall effectiveness: 4.9/5	9 students
Spring, 2017	BIOL 2400	Mathematical Models in Biology CIOS overall effectiveness: 4.9/5	21 students
Fall, 2017	BIOL 4803/8803	Human Evolutionary Genomics CIOS overall effectiveness: 5/5	26 students
Spring, 2018	BIOL 3600	Introduction to Evolutionary Biology CIOS overall effectiveness: 4.7/5	49 students
Fall, 2018	BIOL 8803	Frontiers in Molecular Cell Biology CIOS overall effectiveness: 4.9/5	6 students
Spring, 2019	BIOL 4803/8803	Human Evolutionary Genomics CIOS overall effectiveness: 5.0/5	17 students
Spring, 2019	BIOL 2344	Genetics CIOS overall effectiveness: 4.8/5	57 students
Spring, 2020	BIOS 3600/6600	Introduction to Evolutionary Biology *No CIOS scores due to coronavirus pandemic*	75 students
Fall, 2020	BIOS 4530/8530	Human Evolutionary Genomics CIOS overall effectiveness: 5/5	17 students
Spring, 2021	BIOS 3600/6600	Introduction to Evolutionary Biology CIOS overall effectiveness: 4.7/5	93 students
Fall, 2021	BIOS 3600/6600	Introduction to Evolutionary Biology	75 students

B. Individual Student Guidance

B1. Ph.D. Students

2015- Melanie Quiver (biology)
- Joined Lachance Lab in January 2015
- NIH T32 training grant fellowship
- 2nd place poster award at the 2015 AISES Conference in Phoenix, AZ
- Jackson Lab short course on the genetics of addiction - travel award
- Summer internship for indigenous peoples in genomics fellowship
- American Indian Education Fund fellowship
- Poster award at the 2017 ASHG meeting in Orlando, FL
- Dissertation title: *Local adaptation of regulatory DNA and disease-associated loci in diverse human populations*

2015-2020 Maxine Harlemon (biology, affiliation: Clark Atlanta University)
- Joined Lachance Lab in January 2015
- Co-advisor: Nathan Bowen
- Travel award to attend the 2018 CAPTC Conference in Ilorin, Nigeria
- Session chair at the 2019 AC3 conference in Kingston, Jamaica
- Dissertation title: *Prostate cancer and genetics in men of African descent*
- PhD successfully defended May 2020

2016-2020 Michelle Kim (bioinformatics)
- Session chair at the 2019 ASHG conference in San Diego, CA
- Joined Lachance Lab in August 2016
- Advanced to candidacy March 2019
- Dissertation title: *Prediction of disease risks across multiple populations using evolutionary genetics*
- PhD successfully defended October 2020
- Placed into a postdoc job at the Fred Hutchinson Cancer Center

2021- Rohini Janivara. (bioinformatics)
- Joined Lachance Lab in January 2021
- Summer Institute in Statistical Genetics 2021 scholarship recipient

2021- Uzani Hazra (bioinformatics)
- Joined Lachance Lab in January 2021
- Summer Institute in Statistical Genetics 2021 scholarship recipient

2021- Aaron Pfennig (QBioS)
- Joined Lachance Lab in January 2021
- Summer Institute in Statistical Genetics 2021 scholarship recipient
- Sam Nunn Security Program Fellow

B2. M.S. Students

2015-2016 Binbin Huang (bioinformatics)
- Joined Lachance Lab in January 2015, graduated May 2016
- Research focus: comparing different whole genome sequencing technologies
- Placed into a Ph.D. program at Michigan State University

2015-2016 Andrew Teng (bioinformatics)
- Joined Lachance Lab in August 2015, graduated December 2016
- NIH/NCI summer internship
- Research focus: polygenic risk scores for breast and prostate cancer
- Placed into a Ph.D. program at the University of Washington

2016-2017 Venna Wang (bioinformatics)
Joined Lachance Lab in August 2016, graduated December 2017
Research focus: branch-specific rates of adaptive evolution
Placed into a developer/data scientist job at Kx Systems/First Derivatives

2017-2018 Mohit Thakur (bioinformatics)
Joined Lachance Lab in August 2017, graduated December 2018
Research focus: genetic ancestry painting (comparisons between methods)
Placed into a metagenomics fellow position at the CDC

2018-2019 Nishant Gerald (bioinformatics)
Joined Lachance Lab in August 2018, graduated December 2019
Genomics data scientist intern at AncestryDNA
Research focus: genetic ancestry and prostate cancer risk in African men
Placed into a bioinformatics engineer position at General Dynamics

2018-2019 Preethi Gowrishankar (bioinformatics)
Joined Lachance Lab in August 2018, graduated December 2019
Research focus: generalizing polygenic risk scores
Placed into a data analyst job at Slalom Consulting

2018-2019 Jialin Ma (bioinformatics)
Joined Lachance Lab in August 2018, graduated December 2019
John Chambers Statistical Software Award runner-up
Research focus: ancestral state reconstruction
Placed into an associate software engineer position at the Broad Institute

2018-2020 Siddhartha Sharma (bioinformatics)
Joined Lachance Lab in August 2018, graduated May 2020
Intern at the Jackson Laboratory for Genomic Medicine
Research focus: genetic ancestry painting (STRUCTUREpainter)

2019 Will Hutwagner (bioinformatics)
Joined Lachance Lab in June 2019, graduated August 2019
Research focus: phylogenetic analysis of different dog breeds
Placed into an EMT job

2019 Winnie Zheng (bioinformatics)
Research focus: bioinformatics of ancient genomes
Joined Lachance Lab in August 2019, left lab in December 2020

2019- Gabriel Cruz (bioinformatics)
Research focus: proxy markers for polygenic risk scores
Joined Lachance Lab in October 2019

2020- Gargi Damle (bioinformatics)
Research focus: uncertainty in polygenic risk scores
NIH Graduate Data Science Summer Program intern
Joined Lachance Lab in August 2020

2020- Ajay Bharadwaj (bioinformatics)
Research focus: evolution of polygenic risk scores
Joined Lachance Lab in August 2020
Received J. Leland Jackson Award (top MS student)

2020- Adrian Harris (bioinformatics)
Research focus: SQL database of ancient DNA
Joined Lachance Lab in August 2021

2020- Ashika Ramesh (bioinformatics)
Research focus: ascertainment bias
Joined Lachance Lab in August 2021

B3. UNDERGRADUATE STUDENTS

2015	Anna Paulino (biochemistry)
2015	Imon Ghosh (biochemistry)
2015	Claire Hanson (biology) Obtained PURA salary award
2015-2016	Kane Patel (biology) Obtained PURA travel award Georgia Tech research symposium: 2nd place poster award Placed into an epidemiologist job at the CDC
2015-2017	Taylor Cooper (biology) School of Biological Sciences Fast-Track to Research Scholar SSE/BEACON Undergraduate Diversity in Evolution travel award Cherry L. Emerson Research Award Placed into a lab manager job at Zoo Atlanta
2016-2017	Collin Spencer (biology) School of Biological Sciences Fast-Track to Research Scholar
2017-2018	Greg Johnston (computer science) Obtained PURA salary award Placed into a Silicon Valley cloud computing start-up job
2017	Nigel Blackwood (computational biology, affiliation: University of Pennsylvania)
2017	Courtney Wong (biomedical engineering)
2017-2018	Keerthi Ramachandran (biology) School of Biological Sciences Fast-Track to Research Scholar
2018	Ashley Salen (biology) College of Sciences Dean's Intern
2019-2020	Subbarao Garlapati (mathematics) Obtained PURA salary award
2019	Ryan Sequeira (biology) Stamp's Presidential Scholar
2020-	Chenming Fan (computer science)
2020-	Michelle Seeler (biology) ECSEL scholar
2021	Hanna Dancy (biochemistry)
2021	Kia Safai (computer science)
2021	Zharia Redhead (business)
2021	Dhairya Patel (biology)

B4. SERVICE ON THESIS OR DISSERTATION COMMITTEES

2015	Jing Zhao (biology)
2015-2018	Diana Williams (biology)
2015-2018	Biao Zeng (bioinformatics)
2015-2019	Dan Sun (biology
2016-2019	Yuehui Zhao (biology)
2016-2019	Emily Norris (bioinformatics)
2018-2020	Aroon Chande (bioinformatics)
2019-2021	Angela Mo (bioinformatics)
2019-	Sashwat Nagar (bioinformatics)

2019- Ross Lindsey (biology)
2020- Sini Nagpal (biology)
2020- Devika Singh (bioinformatics)
2021- Ling Wang (biology)
2021- George Gruenhagen (bioinformatics)
2021- Sydney Popsuj (biology)
2021- Vahab Rajaei (biochemistry)

B5. Mentorship of Postdoctoral Fellows or Visiting Scholars

2016 Annachiara Korchmaros (bioinformatics M.S. rotation student)
Research focus: using genetic ancestry proportions to predict complex traits

2015-2017 Ali Berens (postdoctoral researcher)
Joined Lachance Lab in August 2015, obtained industry position in April 2017
Research focus: ancient genomic health
Placed into a private-sector data scientist job at Monsanto

2017- Corinne Simonti (postdoctoral researcher)
Research focus: population genetics and the evolution of disease risks
Joined Lachance Lab in December 2017

2020-2021 Mia Elbon Pfennig (research technician)
Placed into Georgia Tech's MS in public policy program

2021 Ujani Hazra Pfennig (research technician)

2021 Nyssa Morgan (biology Ph.D. rotation student)

C. Educational innovations and Other Contributions

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 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
Topic: Molecular diversity (undergraduate level - BIO 367)

2011 Guest instructor: Perelman School of Medicine
Topic: Population genetics (M.D. level - Core Principles Module 1)

2012 Guest instructor: University of Pennsylvania
Topic: 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
Topic: Human evolutionary genetics (undergraduate level - BIOL 3600)

2015	Guest instructor: Georgia Institute of Technology Topic: Human evolutionary genetics (undergraduate level - BIOL 3600)
2015	Guest instructor: Georgia Institute of Technology Topic: African genetic variation (undergraduate level - BIOL 4545)
2016-2019	Developed a new course at Georgia Tech Course name: Human Evolutionary Genomics Course number: BIOS 4530/BIOL 8530
2016	Instructor: Summer Institute in Statistical Genetics Introduction to genetics and genomics (Ph.D. level - Module 2) Teaching ratings: 4.53/5
2017	Instructor: Summer Institute in Statistical Genetics Introduction to genetics and genomics (Ph.D. level - Module 2) Teaching effectiveness: 4.71/5
2019	Instructor: MADCaP Investigator's Meeting in Maputo, Mozambique Working with genetic data from the MADCaP Array (training workshop)
2020	Instructor: Summer Institute in Statistical Genetics Introduction to genetics and genomics (Ph.D. level - Module 2) Teaching effectiveness: 4.81/5
2020	Guest instructor: Georgia Institute of Technology Topic: Genetics and adaptive introgression (Ph.D. level - BIOL 8801)
2021	Instructor: Summer Institute in Statistical Genetics Introduction to genetics and genomics (Ph.D. level - Module 2) Teaching effectiveness 4.68/5

VI. Service

A. Professional Contributions

A1. Reviewed Publications

American Journal of Physical Anthropology, BMC Genomics, *Cancer* Research, EBioMedicine, eLife, *Evolution*, *Evolutionary Applications, G3*: *Genes*|*Genomes*|*Genetics, Genes and Genetic Systems*, *Genetica*, *Genetics*, *Genome Biology*, *Genome Biology and Evolution*, *Genome Research, Heredity*, *Human Biology*, *Human Genetics*, *Journal of Theoretical Biology*, *Molecular Biology and Evolution*, *Molecular Ecology*, *Nature Reviews Genetics, Oxford University Press*, *Philosophical Transactions of the Royal Society B, Physical Biology*, *PLoS Genetics*, *PLoS One*, *Proceedings of the National Academy of Sciences*, *Quarterly Review of Biology*, *Science Advances, Sinauer Associates*, *Theoretical Population Biology, Trends in Genetics, and the Yearbook of Physical Anthropology*

A2. Guest Editor

2015	PLoS Genetics (one manuscript)
2020	PLoS Genetics (one manuscript)

A3. Grant Reviewing

2008	King Miller Fellowship
2015	Leakey Foundation
2017-2019	National Science Foundation (Biological Anthropology)
2019	Swiss National Science Foundation

2020 Center for Transplantation and Immune-mediated Disorders at Emory University
2021 Wellcome Trust
2021 NIH study section (KNOD – Kidney, Nutrition, Obesity & Diabetes)
2021 National Science Foundation (Division of Environmental Biology)

A4. 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 seven meetings)
2010- American Society of Human Genetics
(attended seven meetings)
2015- American Association of Anthropological Genetics
(attended three meetings)
2016- International Society for Evolution, Medicine, and Public Health
(attended two meetings)
2016- American Association for Cancer Research
(attended three meetings)
2021- African Organization for Research and Training in Cancer
(attended three meetings)

B. Public and Community Service

2015 Science Olympiad judge (CEISMC)
2020 Assisted a high school teacher (Chris Sikich) in developing an active learning activity that focused on genetic signatures of natural selection

C. Institute Contributions

2015 Evolution@Tech seminar series organizer
2015-2019 Active participant in the College of Sciences New Faculty Mentoring Workshop
2015 Commencement alignment volunteer
2015 Organized the School of Biology holiday party
2015- Member of the Petit Institute for Bioengineering and Bioscience
2015- Member of the Integrated Cancer Research Center
2015- Member of the Center for Integrated Genomics
2015-2017 Member of the Integrative BioSystems Institute
2016- Organized Darwin Day events and an evolution-themed film festival
2016 Participated in the Best Practices Forum on Mentoring
2016 Assisted in the Research Bound in STEM workshop
2016 Faculty-staff advisory committee for EBB
2016-2017 School of Biological Sciences graduate committee
2016 Petit Scholars review committee
2017 Reviewed student applications for bioinformatics T32 training grant
2017-2018 Reviewed student applications for the Leland Jackson award
2017- Member of the Institute for Data Engineering and Science
2020- School of Biological Sciences ECSEL committee
2020- Reviewed student applications for McCallum Scholar awards
2020 Reviewed applications for Suddath student awards
2020- School of Biological Sciences research faculty promotion committee
2020 Helped increased diversity at Georgia Tech as part of the FOCUS program
2021 Reviewed applications for CTL teaching awards

2021 Reviewed applications for the Borodovsky Prize

D. 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 Teaching assistant workshop panelist (Stony Brook University)
2009-2010 Student representative on the executive committee of the Graduate Program in Genetics (Stony Brook University)
2009-2015 Associate member of the Faculty of 1000 (Development & Evolution) Seven recommendations to Faculty Opinions as an associate member
2012-2014 Organized Department of Genetics journal club (University of Pennsylvania)
2015 Represented Georgia Tech at the National Science South Big Data Hub and Spokes meeting (Atlanta, GA)
2016 Represented Georgia Tech at the Atlanta area Quantitative Biology Workshop (Spelman College)
2016- Full member of the Faculty of 1000 (Evolutionary & Comparative Genetics) Thirteen recommendations to Faculty Opinions as a full member
2016 Organized a networking event for members of Georgia Tech's School of Biology and global experts in Neanderthal and Denisovan genomics
2016-2018 Men of African Descent and Carcinoma of the Prostate (MADCaP) network: co-chair of the array working group
2017- Presented Lachance Lab research to Georgia Tech's chapter of TriBeta (biology undergraduate honors society) – three presentations in total
2019 Hamilton Award judge at Evolution 2019 (Society for the Study of Evolution)
2019 Faculty diversity mentor at Evolution 2019 (Society for the Study of Evolution)
2019 Evaluated a candidate for Research Professor of Evolutionary Genomics at the Institute of Genomics (University of Tartu)
2019- Men of African Descent and Carcinoma of the Prostate (MADCaP) network: co-chair of the genomics working group
2019- Member of the Winship Cancer Institute of Emory University
2019- Executive committee of the American Association of Anthropological Genetics
2020 ERC^2 faculty mentor (Society for the Study of Evolution)
2021 Outstanding Trainee Presentation in Anthropological Genetics judge (American Association for Anthropological Genetics)
2021 CIMER mentoring training (University of Wisconsin – Madison)