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
2022 Nominated for Vice President of the AAAG
2023-2024 Faculty Writing Scholar (Georgia Tech)
2023-2025 Doc Blanchard Professorship (Georgia Tech)
2024 CIOS Honor Roll (Georgia Tech)

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 equilibrium and random mating. Invited book chapter for the *Encyclopedia of Evolutionary Biology,* edited by Kliman RM. Academic Press. Vol. 1, pp. 208-211.
[This publication is solely a product of the Lachance Lab at Georgia Tech]

* 2. **Hazra U**[G] and **Lachance J** (2024) Polygenic evolution of germline variants in cancer. Invited book chapter for *Cancer through Lens of Evolution and Ecology*, edited by Somarelli J and Johnson NA. pp 58-68.
[This publication is solely a product of the Lachance Lab at Georgia Tech]

* 3. **Janivara R**[G] and **Lachance J** (2024) The genetic hitchhiker's guide to tumor evolution. Invited book chapter for *Cancer through Lens of Evolution and Ecology*, edited by Somarelli J and Johnson NA. pp 26-41.
[This publication is solely a product of the Lachance Lab at Georgia Tech]

* 4. **Lauder IH**[G] and **Lachance J** (2026). Hardy-Weinberg equilibrium and randomly mating Invited book chapter for the *Encyclopedia of Evolutionary Biology,* edited by Wolf JB and Russo CAM. Academic Press. Vol. 2. pp. 177-182
[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, Fortier B, Hayward A, Lederman R, Petersen L, McBride J, Persersen D, Asjayi O, ... **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]

* 28. **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. *Human Genetics and Genomics Advances* 100083.
[This publication is solely a product of the Lachance Lab at Georgia Tech]

* 29. Darst BF, Hughley R, **Pfennig A**[G], **Hazra U**[G], ... **Lachance J**, Rebbeck TR, Conti DV, and Haiman CA (2021) A rare germline *HOXB13* variant contributes to risk of prostate cancer in men of African ancestry. *European Urology.* 81(5): 458-462.
[Lachance Lab contributions: supplied African genomic data and performed allele age analyses]

* 30. **Pfennig A**[G] and **Lachance J** (2022) Hybrid fitness effects modify fixation probabilities of introgressed alleles. *G3*: *Genes*|*Genomes*|*Genetics* 12(7), jkac113
[This publication is solely a product of the Lachance Lab at Georgia Tech]

* 31. Chen F, Darst BF, Madurri RK, ... **Lachance J**, ... Ambs S, Gaziano JM, Justice AC, Conti DV, and Haiman CA (2022) Validation of a multi-ancestry polygenic risk score and age-specific risks of prostate cancer: a meta-analysis within diverse populations. *eLife* 11:e78304

[Lachance Lab contributions: performed QC and supplied African genomic data]

* 32. **Kim MS**[G], Naidoo D, **Hazra U**[G], **Simonti CN**[PD], Chen WC, **Quiver MH**[G], Kachambwa P, **Harlemon M**[G], ... Rebbeck TR, and **Lachance J** (2022) Testing the generalizability of ancestry-specific polygenic risk scores to predict prostate cancer in sub-Saharan Africa. *Genome Biology* 12:194

* 33. Dyson CJ, **Pfennig A**[G], Ariano-Sanchéz D, **Lachance J**, Mendelson JR, and Goodisman MAD (2022) Draft genome of the highly endangered Guatemalan Beaded Lizard, *Heloderma charlesbogerti*, reveals evolutionary relationships of squamates and declines in effective population sizes. *G3*: *Genes*|*Genomes*|*Genetics* 12(12), jkac276

[Lachance Lab contributions: validated genomic data, performed PSMC analysis, and co-wrote the paper]

* 34. **Pfennig A**[G] and **Lachance J** (2023) Challenges of accurately estimating sex-biased admixture from X chromosomal and autosomal data. *American Journal of Human Genetics* 110:359-367.

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

* 35. Chen F, Madurri RK, Rodriguez AA, ... **Lachance J**, ... Blot WJ, Gaziano JM, Justice AC, Conti DV, and Haiman CA (2023) Evidence of novel susceptibility variants for prostate cancer and a multiancestry polygenic risk score associated with aggressive disease in men of African ancestry. *European Urology* 84(1):13-21.

[Lachance Lab contributions: performed QC and supplied African genomic data]

* 36. **Pfennig A**[G], Petersen L, Kachambwa P, and **Lachance J** (2023) Evolutionary genetics and admixture in African populations. *Genome Biology and Evolution* 15(4), evad054.

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

* 37. Wang A, Shen J, Rodriguez AA, Saunders EJ, Chen F, **Janivara R**[G]**,** ... **Lachance J**, ... Kote-Jarai Z, Madduri R, Conti DV, and Haiman CA (2023) Characterizing prostate cancer risk through multi-ancestry genome-wide discovery of 187 novel risk variants. *Nature Genetics* 55: 2065–2074.

[Lachance Lab contributions: performed polygenic risk score analyses and supplied African genomic data]

* 38. **Brown LM**[T], **Elbon M**[T], **Bharadwaj A**[G], **Damle G**[G], and **Lachance J** (2024) Does effective population size govern evolutionary differences in telomere length? *Genome Biology and Evolution* 16(5) evae111.

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

* 39. **Janivara R**[G], Chen WC**, Hazra U**[G], Baichoo S, Agalliu I, S, Kchambwa P, **Simonti CN**[PD], **Tambe SN**[G], **Brown LM**[T], **Kim MS**[G], **Harlemon M**[G], … ,Petersen L, **Lachance J**, and Rebbeck TR (2024) Heterogeneous genetic architectures of prostate cancer susceptibility in sub-Saharan Africa. *Nature Genetics* 56(10):2093-2103.

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

* 40. Hoffman TJ, Graff RE, Madduri RK, Rodriguez A, … , **Lachance J**, Andrews CA, Adebiyi A, Aisuodionoe-Shadrach O, Pedro Fernandez P, Jalloh M, **Janivara R**[G], … , Justice AC, Kachuri L, and Witte JS (2025) Genome-wide association study of prostate-specific antigen levels in 392,522 men identifies new loci and improves cross-ancestry prediction. *Nature genetics* 57:334-344.

[Lachance Lab contributions: supplied African genomic data]

* 41. **Janivara R**[G], **Hazra U**[G], **Pfennig A**[G], **Harlemon M**[G], **Kim MS**[G], **Muthukrishnan E**[PD], **…**, Adebiyi AO, Agalliu I and **Lachance J** (2025) Uncovering the genetic architecture and evolutionary roots of androgenetic alopecia in African men. *Human Genetics and Genomics Advances* 100428.

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

* 42. Chen F, Sheng X, Wang A, Xu Y, … **Lachance J**, Multigner L, Darst BF, Rebbeck TR, Brureau L, Watya S, Conti D, and Haiman C (2025) Integrating pathogenic variants, polygenic risk score, and family history for prostate cancer risk estimation in men of African ancestry. *European Urology* (accepted).

[Lachance Lab contributions: supplied African genomic data]

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 L, 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]

* 5. Chen F, Darst BF, Sheng X, Wang A, … **Lachance J**, … Chanock SJ, Conti DV, and Haiman CA (2023) Association of prostate cancer candidate genes with overall and aggressive prostate cacer in men of African ancestry. *Cancer Research* 84 (7 Supplement):1182.

[Lachance Lab contributions: supplied African genomic data]

* 6. Wang A, Xu Y, Sheng X, Hughley R, … **Lachance J**, … Darst BF Conti DV, and Haiman CA 2023) Association between clonal hematopoiesis and risk of prostate cancer in a large cohort of African ancestry men. *Cancer Research* 84 (7 Supplement):3508.

[Lachance Lab contributions: supplied African genomic data]

* 7. Rebbeck TR, **Janivara R**[G], Chen WC**, Hazra U**[G], MADCaP Network, and **Lachance J** (2024) Genetic architecture, evolutionary genomics, and genomic risk of prostate cancer in Sub-Saharan Africa. *Cancer Research* 84 (6 Supplement):774.
[Lachance Lab contributions: conceived the study, conducted genetic analyses, and wrote the paper]

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** (2021) 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. **Hazra U**[G] and **Lachance J** (2025) The evolutionary genetics of polygenic diseases with the largest global burden in mortality rates
[This publication is solely a product of the Lachance Lab at Georgia Tech]

* 2. **Carvalho N**[UG], **Lauder IH**[G], **Harris A**[G], and **Lachance J** (2025) The different genetic architecture of complex traits and their relevance to polygenic score performance in diverse populations.
[This publication is solely a product of the Lachance Lab at Georgia Tech]

* 3. **Pfennig A**[G] and **Lachance J** (2025) The evolutionary fate of Neanderthal alleles in recently admixed African American genomes.
[This publication is solely a product of the Lachance Lab at Georgia Tech]

* 4. Odole I, Andrews C, Agalliu I, Rohan T, …, **Janivara R**[G], **Lachance J**, … and Rebbeck TR (2025) Association of family history and polygenic risk scores with prostate cancer in Africa. *Submitted to JCO Global Oncology*
[Lachance Lab contributions: supplied genomic data and generated polygenic risk scores]

* 5. Cho E, Agalliu I, Rohan T, Neugut AI, Baichoo S, **Lauder IH**[G], **Rajesh A**[G], ... **Lachance J**, and Rebbeck TR (2025) Polygenic and epidemiological determinants of PSA levels in Africans. *Submitted to BMC Cancer*
[Lachance Lab contributions: supplied genomic data and generated polygenic risk scores]

* 6. Hansen MEB, **Hazra U**[G], **Kim MS**[G], Raj S, Fan S, Beggs, W, Mpoloka SW, Mokone GG, Nyambo T, Ibrahim ME, Meskel DW, Belay G, Hirbo J, Ranciaro A, **Lachance J**, and Tishkoff SA (2025) Anthropometric and cardio-metabolic trait variation and genetic associations in sub-Saharan Africa. Submitted to *American Journal of Human Genetics*.
[Lachance Lab contributions: conceived the project, performed all analyses regarding replication of GWAS results across continents, and helped write the paper]

* 7. Bell AD, **Simonti CN**[PD], Baños H, Silliman K, Heitsch C, **Lachance J,** and Paaby A (2025) 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]

B5. ARTICLES IN PREPARATION

* 1. **Hazra U**[G], **Choi J**[G], and **Lachance J** (2025) Machine learning reveals functional and evolutionary genetic features of GWAS hits that replicate well across ancestries.
[This publication is solely a product of the Lachance Lab at Georgia Tech]

* 2. **Janivara R**[G], Cheng S, **Lauder IH**[G], **Rajesh A**[G], Agasaro O, Goss L, … , Haiman CA, Rebbeck TR, Darst B and **Lachance J** (2026) Population genetic analysis of rare coding variants at *HOXB13* and prostate cancer susceptibility in Sub-Saharan Africa. *To be submitted to BMC Cancer*
[Lachance Lab contributions: designed the study, performed bioinformatics and evolutionary genomics analyses, and wrote the paper]

* 3. **Quiver MH**[G], **Mack D**[UG], and **Lachance J** (2026) Testing whether human accelerated regions are enriched for signals of recent positive selection and functional genomic impacts.
[This publication is solely a product of the Lachance Lab at Georgia Tech]

* 4. Narh CT, Jalloh M, **Lauder IH**[G], ... and **Lachance J,** and Rebbeck TR (2025) Does benign prostate hyperplasia play a role in prostate cancer clinical presentation and genetics in Africa?
[Lachance Lab contributions: performed the genome-wide association study, ran genetic architecture analyses, and assisted in the writing of the paper]

* 5. Maley CC, Lawson-Michod K, Carter H, Curtis K, Houlahan, Fisk N, Liu L, **Lachance J**, DeGregori J, Swanton C, Compton ZT, Aktipis A, Hiatt, and Navarro A (2025) Evolutionary cancer epidemiology. *To be submitted to Cancer, Epidemiology, Biomarkers, and Prevention.*
[Lachance Lab contributions: wrote the "genetic legacies of human demography" section]

* 6. Chen WC, **Lauder IH**[G], **Janivara R**[G], Baichoo S, ... **Arthur AV**[U], ... Haiman CA, **Lachance J**, and Rebbeck TR (2026) Comparative analysis of germline genetic variation in cancer, diabetes, obesity and lipid-associated gene panels among men from four African countries.
[Lachance Lab contributions: designed the study, performed tests of genetic load, performed evolutionary genetic analyses, and wrote the paper]

* 7. **Chen JL**[G], **Janivara R**[G], Chen CW, ... , Rebbeck TR, and **Lachance J** (2026) Gene burden tests of rare alleles and prostate cancer risk in Senegal, Ghana, Nigeria, and South Africa. *To be submitted to BMC Cancer*
[Lachance Lab contributions: designed the study, performed gene burden tests, performed population genetic analyses, and wrote the paper]

* 8. **Chen JL**[G], ... Rebbeck TR, and **Lachance J** (2026) Tests of positive selection in urban African populations from Senegal, Ghana, Nigeria, and South Africa.
[Lachance Lab contributions: designed the study, performed evolutionary genomics analyses, and wrote the paper]

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.

* 15. **Simonti CN**[PD] and **Lachance J** (2021) Ancient DNA reveals that few GWAS loci have been strongly selected during recent human history*. bioRxiv.* DOI:10.1101/2021.04.13.439742.

* 16. **Lachance J** (2022) Book Review: Human Population Genomics: Introduction to Essential Concepts and Applications by Lohmueller and Nielsen. *Quarterly Review of Biology* 97:229.

* 17. **Lachance J** (2023) Book Review: Combining human genetics and causal inference to understand human disease and development by Davey Smith, Richmond, and Pingault. *Quarterly Review of Biology* 98:104-105.

* 18. Rebbeck TR and **Lachance J** (2024) Pan-African analysis identifies genetic differences in prostate cancer risk (Research Briefing). *Nature Genetics* 56: 2006-2007.

* 19. **Lachance J** (2025) Book Review: Genetic reconstruction of the past by Erlich. *Quarterly Review of Biology* 100:42-43.

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 Humans 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. Evolutionary genetics and challenges to generalizing predictions of disease risks across populations. *Department of Genetics Seminar Series* (Rutgers University - 2021).

* 42. Ascertainment bias, evolutionary history, and challenges facing the generalization of genetic findings across ancestries. *Division of Genome Sciences Seminar Series* (University of Washington - 2022).

* 43. How ascertainment bias and differences in genetic architecture impair the generalizability of polygenic risk scores for prostate cancer. *Departmental seminar* (CIC bioGUNE - 2023).

* 44. Evolution of hereditary disease risks and the portability of genetic predictions to African populations. *Health Systems: The Next Generation* (Georgia Institute of Technology - 2023).

* 45. Evolution of hereditary disease risks and the portability of genetic predictions to African populations. *UGA's Global Health Seminar Series* (University of Georgia - 2024).

* 46. Heterogeneous genetic architectures and the portability of polygenic predictions to Africa. *Center for Global Genomics and Health Equity seminar* (University of Pennsylvania - 2024).

* 47. African population genetics and the portability of polygenetic predictions. *University of North Texas Health Science Center seminar* (Fort Worth, TX - 2025).

* 48. Population genetics and heterogeneous genetic architectures of prostate cancer in Africa. *Prostate Cancer Foundation: Population Sciences Working Group* (virtual seminar - 2025). *[presented by Lachance Lab Ph.D. student:* ***Rohini Janivara****]*

* 49. Heterogeneous genetic architectures of prostate cancer susceptibility in sub-Saharan Africa. *Center for Cancer Research and Therapeutic Development - 14th National Symposium on Prostate Cancer* (Clark Atlanta University - 2025).

* 50. Heterogeneous genetic architectures and the portability of polygenic predictions to Africa. *Institute for Genomics and Evolutionary Medicine seminar* (Temple University - 2025).

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).

* 28. Adaptive introgression and the evolutionary genetics of hybrid fitness effects. *Population, Evolutionary, and Quantitative Genetics Conference of the Genetics Society of America* (Pacific Grove, CA - 2022).
[presented by Lachance Lab Ph.D. student: ***Aaron Pfennig****]*

* 29. Generalizing genetic predictions of prostate cancer risk to sub-Saharan Africa / Scans of selection in African populations. *MADCaP Investigator's Meeting* (Somone, Senegal - 2022).
[presented by Lachance Lab Ph.D. student: ***Ujani Hazra****]*

* 30. Heterogeneous genetic architectures of prostate cancer in African populations / Genetic predictions of baldness generalize poorly to Africa. *MADCaP Investigator's Meeting* (Somone, Senegal - 2022).
[presented by Lachance Lab Ph.D. student: ***Rohini Janivara****]*

* 31. Genetic demography of MADCaP populations / Genomic imputation of African data. *MADCaP Investigator's Meeting* (Somone, Senegal Africa - 2022).

* 32. A multi-population African GWAS for prostate cancer reveals novel disease associations and within-continent heterogeneity of cancer risk. *Annual Meeting of the American Society of Human Genetics* (Los Angeles, CA - 2022)
[presented by Lachance Lab Ph.D. student: ***Rohini Janivara****]*

* 33. The genetic architecture of complex traits and its relevance to polygenic score performance. *Annual Meeting of the American Society of Human Genetics* (Los Angeles, CA - 2022)

* 34. Hybrid fitness effects modify fixation probabilities of introgressed alleles. *PopGroup 56 Conference* (London, UK - 2023)
[presented by Lachance Lab Ph.D. student: ***Aaron Pfennig****]*

* 35. Heterogeneous genetic architectures of prostate cancer in African populations. *14th International Congress of Human Genetics* (Cape Town, South Africa - 2023).

* 36. Differences in disease burdens across human populations are driven more by neutral evolution than by recent polygenic selection. *Annual Meeting of the Society for Molecular Biology and Evolution* (Ferrara, Italy - 2023).
[presented by Lachance Lab Ph.D. student: ***Ujani Hazra****]*

* 37. Heterogeneous genetic architectures and evolutionary genomics of prostate cancer in sub-Saharan Africa. *Annual Meeting of the Society for Molecular Biology and Evolution* (Puerto Vallarta, Mexico - 2024).
[presented by Lachance Lab Ph.D. student: ***Rohini Janivara****]*

* 38. Complex neutral processes drive the evolutionary fate of Neanderthal alleles in 30,780 admixed genomes with African-like and European-like ancestry. *Annual Meeting of the Society for Molecular Biology and Evolution* (Puerto Vallarta, Mexico - 2024).
[presented by Lachance Lab Ph.D. student: ***Aaron Pfennig****]*

* 39. Does effective population size govern evolutionary differences in telomere length? *3rd Joint Congress on Evolutionary Biology* (Montreal, Canada - 2024).

* 40. Does effective population size govern evolutionary differences in telomere length? *School of Biological Sciences retreat* (Georgia Institute of Technology - 2024).

* 41. Clonal interference in forward-time simulations of tumor evolution. *Annual Meeting of the Society for the Study of Evolution* (Athens, GA - 2025).
[presented by Lachance Lab Ph.D. student: ***Rohini Janivara****]*

* 42. Uncovering the genetic architecture and evolutionary roots of androgenetic alopecia in African men. *Annual Meeting of the Society for the Study of Evolution* (Athens, GA - 2025).

* 43. Machine learning identifies the genomic and statistical features that predict cross-population replication of GWAS signals. *Annual Meeting of the American Society of Human Genetics* (Boston, MA - 2025).

* 44. Genomic analyses of MADCaP Network datasets: scans of positive selection, gene burden tests, and population genetics of pathogenic variants in HOXB13. *MADCaP Network Investigator's Meeting* (Hammamet, Tunisia - 2025).

* 45. Pan-African GWAS reveals heterogeneous genetic architectures of prostate cancer across Africa. *AORTIC's 15th Annual International Conference on Cancer in Africa* (Hammamet, Tunisia - 2025).

* 46. Tracing founder *HOXB13* variants in African populations: insights into prostate cancer susceptibility. *AORTIC's 15th Annual International Conference on Cancer in Africa* (Hammamet, Tunisia - 2025).

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).

* 32. Polygenic adaptation is not a major driver of health disparities across global populations. *Population, Evolutionary, and Quantitative Genetics Conference of the Genetics Society of America* (Pacific Grove, CA - 2022).
[presented by Lachance Lab Ph.D. student: ***Ujani Hazra****]*

* 33. Challenges of accurately estimating sex-biased admixture from X chromosomal and autosomal data. *Annual Meeting of the Society for Molecular Biology and Evolution* (Ferrara, Italy - 2023).
[presented by Lachance Lab Ph.D. student: ***Aaron Pfennig****]*

* 34. Modeling clonal interference and context dependency of mutations that affect different hallmarks of cancer. *Biology of Cancer: Microenvironment & Metastasis conference at CSHL* (Cold Spring Harbor, NY - 2023).
[presented by Lachance Lab Ph.D. student: ***Rohini Janivara****]*

* 35. Different genetic architectures of complex traits and their relevance to polygenic score performance in diverse populations. *Harvard T.H Chan School of Public Health 17th Annual Program in Quantitative Genomics Conference: Diversity in Genetics and Genomics* (Boston, MA - 2023).
*[presented by Lachance Lab undergraduate student: **Nuno Carvalho**]*

* 36. The evolutionary fate of introgressed Neanderthal alleles in recently admixed African American individuals. *Annual Meeting of the American Society of Human Genetics* (Washington, DC - 2023).
*[presented by Lachance Lab Ph.D. student: **Aaron Pfennig**]*

* 37. Leveraging site frequency spectra to infer clonal interference and identify cryptic driver mutations. *International Society for Evolution, Ecology and Cancer: Leveraging Evolutionary Theory to Understand and Treat Cancer* (Hinxton, UK - 2023).
*[presented by Lachance Lab Ph.D. student: **Rohini Janivara**]*

* 38. Uncovering the genetic architecture and evolutionary roots of androgenetic alopecia in African men. *Annual Meeting of the Society for Molecular Biology and Evolution* (Puerto Vallarta, Mexico - 2024).
*[presented by Lachance Lab Ph.D. student: **Ujani Hazra**]*

* 39. Evaluating functional and evolutionary genomic predictors of polygenic score portability using machine learning and explainable AI. *Annual Meeting of the American Society of Human Genetics* (Denver, CO - 2024).
*[presented by Lachance Lab Ph.D. student: **Ujani Hazra**]*

* 40. Evaluating genetic architectures of complex traits with simulated GWAS data. *Annual Meeting of the American Society of Human Genetics* (Boston, MA - 2025).
*[presented by Lachance Lab Ph.D. student: **Ianne Lauder**]*

E. GRANTS AND CONTRACTS

[$3.33M since arriving at Georgia Tech, including $3.15M as a PI]

E1. AS PRINCIPAL INVESTIGATOR

2019-2025 Evolution of Genetic Disease Risks Over Time and Space
NIH R35GM133727
Role: PI
Funding: $1,882,000 total to Georgia Tech
Period of contract: 9/5/2019 – 7/31/2025 (including no cost extension)
Candidate's share: 100%

2021-2025 Georgia Tech GAANN Graduate Fellowships in Biology
Dept. of Education: P200A210046
Role: PI
Funding: $913,000 to Georgia Tech + $326,000 matching funds
Period of contract: 10/1/2021 – 9/30/2025 (including no cost extension)
Candidate's share: 100%

2023-2025 Doc Blanchard Professorship
Role: PI
Total funding: $60,000
Period of contract: 7/1/2023 – 6/30/2025
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%

2021-2022 Computational Biomedical Genomics
Georgia Tech IDEaS Cloud Computing Credit Award
Role: Co-PI
Collaborator: Gregory Gibson (PI)
Funding credits: $25,000
Period of contract: 10/1/2021 – 6/31/2022

2023-2024 Google Cloud Research Credits
Role: PI
Direct and indirect funding: $5,000
Period of contract: 8/31/2023 – 8/30/2024
Candidate's share: 100%

E2. As Co-Principal Investigator

2023 Integrative Genomics for Health Equity
Georgia Tech IDEaS Workshop
Role: Co-PI
Collaborator: Gregory Gibson (PI)
Funding credits: $8,000
Period of contract: 1/1/2023 – 12/31/2023

E3. As Senior Personnel or Contributor

2021-2026 Genomic Diversity of Prostate Cancer Across the African Diaspora
NIH R01CA259200
Role: Subcontractor
Collaborator: Timothy Rebbeck (PI)
Direct and indirect funding: $6,434,000 total ($386,000 to Georgia Tech)
Period of contract: 1/1/2022 – 12/31/2026
Candidate's share: 6%

E4. Pending proposals

2026-2031 Human Evolutionary History and the Portability of Polygenic Predictions of Disease Risk
NIH R35GM163947
Role: PI
Funding: $1,850,765 total to Georgia Tech
Period of contract: 4/16/2026 – 4/14/2031
Candidate's share: 100%

E5. Proposals Submitted But Not Funded (Last Two Years)

2025-2029 Evolution of Genetic Disease Risks Over Time and Space
NIH R35GM133727 (renewal)
Role: PI
Funding: $2,247,000 total to Georgia Tech
Period of contract: 8/1/2025 –11/30/2029

2026-2031 Evolution's Mechanism of Cancer Avoidance: Learning from Nature's Billion-Year Experiment
Cancer Grand Challenges (Cancer Research UK & National Cancer Institute)
Role: Subcontractor
Funding: $25,000,000 total ($1,960,765 to Georgia Tech)
Period of contract: 3/1/2026 – 3/1/2031
Candidate's share: 2%

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 rain forest hunter-gatherers: *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 evolutionary genetics of prostate cancer risk 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

The benefits of ancestry-matched polygenic risk scores for prostate cancer were featured the yearly highlights of the NCI's Epidemiology and Genetics Research Program

My lab's review paper on African admixture was featured as a highlight in *Genome Biology and Evolution*

Media coverage of the first pan-African GWAS of prostate cancer: ASCO Post, JUTA Medical Brief, Medical Xpress, Nature Africa, and News-Medical

Interviewed by the Atlanta Journal Constitution about the impact of cuts to science funding at the Atlanta Stand up for Science rally

Featured in a College of Sciences faculty profile

H. Other Professional Activities

Guest interview 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*.

Guest interview for "The Mark Arum Show" on WSB 95.5. This interview focused ancient DNA and de-extinction, including the so-called dire wolves that were engineered by \Colossal Biosciences.

V. EDUCATION

A. COURSES TAUGHT

Spring, 2015	BIOL 2400	Mathematical Models in Biology	24 students
	CIOS overall effectiveness: 4.64/5		
Spring, 2016	BIOL 4803/8803	Human Evolutionary Genomics	16 students
	CIOS overall effectiveness: 4.85/5		
Fall, 2016	BIOL 8803	Frontiers in Molecular Cell Biology	9 students
	CIOS overall effectiveness: 5.00/5		
Spring, 2017	BIOL 2400	Mathematical Models in Biology	21 students
	CIOS overall effectiveness: 4.91/5		
Fall, 2017	BIOL 4803/8803	Human Evolutionary Genomics	26 students
	CIOS overall effectiveness: 4.97/5		
Spring, 2018	BIOL 3600	Evolutionary Biology	49 students
	CIOS overall effectiveness: 4.70/5		
Fall, 2018	BIOL 8803	Frontiers in Molecular Cell Biology	6 students
	CIOS overall effectiveness: 4.90/5		
Spring, 2019	BIOL 4803/8803	Human Evolutionary Genomics	17 students
	CIOS overall effectiveness: 5.00/5		
Spring, 2019	BIOL 2344	Genetics	57 students
	CIOS overall effectiveness: 4.79/5		
Spring, 2020	BIOS 3600/6600	Evolutionary Biology	75 students
	No CIOS scores due to coronavirus pandemic		
Fall, 2020	BIOS 4530/8530	Human Evolutionary Genomics	17 students
	CIOS overall effectiveness: 4.92/5		
Spring, 2021	BIOS 3600/6600	Evolutionary Biology	93 students
	CIOS overall effectiveness: 4.67/5		
Fall, 2021	BIOS 3600/6600	Evolutionary Biology	75 students
	CIOS overall effectiveness: 4.84/5		

Spring, 2022	BIOS 3600/6600	Evolutionary Biology	89 students
	CIOS overall effectiveness: 4.27/5		
Fall, 2022	BIOS 4530/8530	Human Evolutionary Genomics	30 students
	CIOS overall effectiveness: 4.95/5		
Spring, 2023	BIOS 4530/8530	Evolutionary Biology	98 students
	CIOS overall effectiveness: 4.52/5		
Fall, 2023	BIOS 3600/6600	Evolutionary Biology	77 students
	CIOS overall effectiveness: 4.82/5		
Spring, 2024	BIOS 4530/8530	Human Evolutionary Genomics	36 students
	CIOS overall effectiveness: 4.92/5		
Fall, 2024	BIOL 8050	Professional Development in QBioS	16 students
	CIOS overall effectiveness: 4.50/5		
Fall, 2024	BIOS 3600/6600	Evolutionary Biology	94 students
	CIOS overall effectiveness: 4.83/5		
Spring, 2025	BIOS 3600/6600	Evolutionary Biology	87 students
	CIOS overall effectiveness: 4.39/5		
Fall, 2025	BIOS 3600/6600	Evolutionary Biology	94 students
	CIOS overall effectiveness: tbd		

B. Individual Student Guidance

B1. Ph.D. Students (8 in total)

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

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

2021-2024 Aaron Pfennig (QBioS)
Joined Lachance Lab in March 2021
Summer Institute in Statistical Genetics 2021 scholarship recipient
Sam Nunn Security Program Fellow
IHE-LeaD Fellow
Travel award to attend PopGroup56 in London, England
QBioS Best Paper in Ecology, Evolution, and Population Biology (2022)
QBioS Service Award (2022)
O'Hara Graduate Scholarship recipient
Travel award to attend PopGroup57 in St. Andrews, Scotland
Dissertation title: *Theoretical and empirical population genetics of admixture and archaic introgression*
PhD successfully defended June 2024
Placed into a postdoc position in Josh Akey's lab at Princeton University

2021- Rohini Janivara. (bioinformatics)
Joined Lachance Lab in January 2021
Advanced to candidacy July 2024
Summer Institute in Statistical Genetics 2021 scholarship recipient
J. Leland Jackson Award for best bioinformatics paper
Presidential Membership Award (Genetics Society of America)
Georgia Tech College of Sciences Career Connect Travel Award

2021- 2025 Ujani Hazra (bioinformatics)
Joined Lachance Lab in January 2021
Advanced to candidacy February 2024
Summer Institute in Statistical Genetics 2021 scholarship recipient
Presidential Membership Award (Genetics Society of America)
SMBE Graduate Student Excellence Award
Peer Review Training Program (Genetics Society of America)
PhD successfully defended April 2025
Placed into a Senior Data Scientist/Statistical Genetics job at Valo Health
Dissertation title: *Studying polygenic traits across populations: evolutionary insights and predictive models of replication*

2024- Ianne Lauder (bioinformatics)
Joined Lachance Lab in August 2024
Selected to be an International Teaching Assistant Liason

2025- Jing-Lian Chen (bioinformatics)
Joined Lachance Lab in August 2025

B2. M.S. STUDENTS (21 in total)

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 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 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

2018-2020 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)

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

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

2019-2021 Gabriel Cruz (bioinformatics)
Research focus: proxy markers for polygenic risk scores
Joined Lachance Lab in October 2019
Placed into bioinformatics contractor at the CDC (via Weems Design Studio)

2020-2021 Gargi Damle (bioinformatics)
Research focus: uncertainty in polygenic risk scores
NIH Graduate Data Science Summer Program intern
Joined Lachance Lab in August 2020, graduated December 2021
Placed into a bioinformatics position at Mount-Sinai Health System

2020-2021 Ajay Bharadwaj (bioinformatics)
Research focus: evolution of polygenic risk scores
Joined Lachance Lab in August 2020, graduated December 2021
Received J. Leland Jackson Award (top MS student)
Placed into a bioinformatics position at Cedar-Sinai Medical Center

2021-2022 Adrian Harris (bioinformatics)
Research focus: genetic architecture of complex traits
Joined Lachance Lab in August 2021
Placed into a bioinformatics job at the CDC

2021-2022 Ashika Ramesh (bioinformatics)
Research focus: genomic imputation and scans of selection
Joined Lachance Lab in August 2021
Placed into a bioinformatics position at Cedar-Sinai Medical Center

2022-2023 Joel Vaz (bioinformatics)
Research focus: GWAS and polygenic risk scores
Joined Lachance Lab in August 2022
Placed into a bioinformatics position at the Fred Hutchinson Cancer Center

2022-2023 Saanika Tambe (bioinformatics)
Research focus: allele ages and population genetics
Joined Lachance Lab in August 2022
Placed into a bioinformatics position at UVA Health

2022-2023 Jiyeong Choi (bioinformatics)
Research focus: replication of GWAS results across ancestries
Joined Lachance Lab in August 2022

2023-2024 Tarek Hachad (bioinformatics)
Research focus: local ancestry inference
Joined Lachance Lab in August 2023

2023-2024 Nia Meadows (bioinformatics)
Research focus: ancestry-specific shifts in polygenic scores
Joined Lachance Lab in August 2023

2024- Akkshaya Rajesh (bioinformatics)
Research focus: genomic impact
Joined Lachance Lab in August 2024

B3. UNDERGRADUATE STUDENTS (30 in total)

2015 Anna Paulino (biochemistry)

2015 Imon Ghosh (biochemistry)

2015 Claire Hanson (biology)
Obtained PURA salary award

2015-2017 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) Stamps Presidential Scholar
2020-2021	Chenming Fan (computer science)
2020-2021	Michelle Seeler (biology) Stamps Presidential Scholar
2021	Hanna Dancy (biochemistry)
2021	Kia Safai (computer science)
2021-2022	Zharia Redhead (business)
2021-2022	Dhairya Patel (biology) McCallum Fellow
2021-2024	Nuno Carvalho (biomedical engineering) GT ESTEEMED fellow Summer Institute in Biomedical Informatics at Harvard Medical School PURA travel award 2022 PURA salary award 2023 PURA travel award 2023
2022	Elliot Januzelli (biology) ECSEL scholar
2022-2023	Freddie Wright (biology)
2023-2024	Joey Haskell (computer science)
2023	Medina McCowin (biology) ECSEL scholar Obtained a Petit Undergraduate Research Scholar award
2023-2024	Dhruuv Devani (computer science)
2024-2025	Toby Cisco (biology)
2024-2025	Donovan Mack (biology)
2025	Anh Nguyen (biology)
2025-	Rebecca Anderson (biology)
2025-	Ananda Arthur (biology) Fast Track Scholarship

B4. SERVICE ON THESIS OR DISSERTATION COMMITTEES (31 in total)

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)

2019-2021 Shashwat Nagar (bioinformatics)
2019- Ross Lindsey (biology)
2020-2022 Sini Nagpal (bioinformatics)
2020-2021 Devika Singh (bioinformatics)
2021-2024 Ling Wang (biology)
2021-2023 George Gruenhagen (bioinformatics)
2021-2025 Sydney Popsuj (biology)
2021- Vahab Rajaei (biochemistry)
2021 Khalid Alhumimidi (bioinformatics)
2022- Nikesh Kumar (bioinformatics)
2022-2025 Emily Greenwood (bioinformatics)
2022-2023 Courtney Astore (bioinformatics)
2022- Shivam Sharma (bioinformatics)
2023 Dayna Smith (Stellenbosch University)
2023 Jared Collins (bioinformatics)
2023-2024 Ben Metcalf (bioinformatics)
2023- Mo Sun (bioinformatics)
2023- Lindsey Tucker (bioinformatics)
2024- Varsha Bhat (bioinformatics)
2024 Samishksa Kaul (biology)
2024- Colin Naughton (bioinformatics)
2025 Sophia Xu (biology)
2025- Paulius Kristupas (biology)
2025- Samantha Boudeau (Temple University)
2025- Parisa Pourroostaei Ardakani (chemistry)
2025- Ankit Raj (QBioS)

B5. MENTORSHIP OF POSTDOCTORAL FELLOWS OR VISITING SCHOLARS (11 in total)

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

2017-2022 Corinne Simonti (postdoctoral researcher)
Research focus: population genetics and the evolution of disease risks
Joined Lachance Lab in December 2017
Placed into an associate editor position at the journal *Science*

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

2021 Ujani Hazra (research technician)

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

2022 Prada House (Morehouse School of Medicine MS student)

2023 Akash Arani (QBioS Ph.D. rotation student)

2023-2024 Muthukrishnan Eaaswarkhanth (research scientist II)
Placed into a computational biologist position at Galatea Bio

2025 Sharon Kartika (QBioS Ph.D. rotation student)

2025- Marjorie Ntiwaa Quarchie (University of Ghana – African Cancer STARS fellow)

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	Pedagogical training via the University of Pennsylvania's College and University Teaching Seminar for PENNPort postdocs
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 Genetics and genomics (Ph.D. level - Module 2) Teaching ratings: 4.5/5
2017	Instructor: Summer Institute in Statistical Genetics Genetics and genomics (Ph.D. level - Module 2) Teaching effectiveness: 4.7/5
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 Genetics and genomics (Ph.D. level - Module 2) Teaching effectiveness: 4.8/5
2020	Guest instructor: Georgia Institute of Technology Topic: Genetics and adaptive introgression (Ph.D. level - BIOL 8801)
2021	Instructor: Summer Institute in Statistical Genetics Genetics and genomics (Ph.D. level - Module 2) Teaching effectiveness 4./5

2022 Instructor: Summer Institute in Statistical Genetics
Genetics and genomics (Ph.D. level - Module 2)
Teaching effectiveness 4.8/5

2022 Instructor: African Cancer STARS (D43)
Data visualization and interpretation

2022 Guest instructor: Georgia Institute of Technology
Topic: Human evolutionary genetics (undergraduate level - BIOL 3600)

2023 Guest instructor: Harvard Medical School Genetics Training Program
Topic: Anthropological genetics

2023 Instructor: Summer Institute in Statistical Genetics
Genetics and genomics (Ph.D. level - Module 2)
Teaching effectiveness 4.8/5

2023 Guest instructor: Washington University School of Medicine
Keystone Integrated Science Course on Precision Medicine
Topic: Population genetics

2024 Instructor: Summer Institute in Statistical Genetics
Genetics and genomics (Ph.D. level - Module 2)
Teaching effectiveness 97/100

2024 Developed a new module for the Summer Institute in Statistical Genetics
(Molecular Evolution)

2024 Instructor: Summer Institute in Statistical Genetics
Molecular evolution (Ph.D. level - Module 20)
Teaching effectiveness 96/100

2025 Guest instructor: Emory University
Topic: Human Population Genetics (undergraduate level - BIOL 385)

2025 Instructor: African Cancer STARS (D43)
Interpreting data and results

VI. Service

A. Professional Contributions

A1. Reviewed Publications

American Journal of Human Genetics, *American Journal of Physical Anthropology, BMC Genomics*, *Cancer Research*, *Cell*, *Communications Biology*, *Current Biology, EBioMedicine*, *eLife*, *Evolution*, *Evolution Medicine and Public Health, Evolutionary Applications, Fibonacci Quarterly, G3*: *Genes|Genomes|Genetics, Genes and Genetic Systems*, *Genetica*, *Genetics*, *Genetics in Medicine*, *Genome Biology*, *Genome Biology and Evolution*, *Genome Medicine, Genome Research, Heredity*, *Human Biology*, *Human Genetics*, *Human Genetics and Genomics Advances, Human Population Genetics and Genomics*, *iScience*, *Journal of Infectious Diseases*, *Journal of Theoretical Biology*, *Molecular Biology and Evolution*, *Molecular Ecology*, *Nature*, *Nature Communications, Nature Genetics, Nature Reviews Genetics, Oxford University Press*, *PCI Math & Comp Biol, 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, Science Advances, Scientific Reports, Sinauer Associates*, *Theoretical Population Biology, Trends in Genetics,* and the *Yearbook of Physical Anthropology* (51 different publications in total)

A2. Editorial Boards

2015 PLoS Genetics guest editor (one manuscript)
2020 PLoS Genetics guest editor (one manuscript)
2024- Human Population Genetics and Genomics - member of the editorial board

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)
2022 NIH study section (KNOD – Kidney, Nutrition, Obesity & Diabetes)
2023 NIH study section x2 (F08 – Fellowships: Genes, Genomes, and Genetics)
2024 National Science Foundation (Biological Anthropology)
2025 NIH study section (F08 – Fellowships: Genes, Genomes, and Genetics)
2025 Leakey Foundation

A4. Society Memberships

2002- Society for the Study of Evolution
(attended fifteen meetings)
2006- Genetics Society of America
(attended one meeting)

2009- Society for Molecular Biology and Evolution
(attended nine meetings)
2010- American Society of Human Genetics
(attended eleven meetings)
2015- American Association of Anthropological Genetics
(attended three meetings)
2016- International Society for Evolution, Medicine, and Public Health
(attended one meeting)
2016- American Association for Cancer Research
(attended three meetings)
2021- African Organization for Research and Training in Cancer
(attended five 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
2020-2022 School of Biological Sciences ECSEL committee
2020-2022 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
2021-2022 School of Biological Sciences search committee (quantitative genomics and neuroscience)
2022 CETL microteaching facilitator
2022- Bioinformatics graduate committee
2022-2023 Presented my lab's work to newly admitted undergrads as part of the College of Science's EXPLORE program: "Evolutionary genomics and human health"
2022-2023 SoBS search committee (computational genomics)
2023 Led round table discussion at the IDEaS workshop on Integrative Genomics for Health Equity
2023 Reviewed applications for the Leland Jackson Award
2024 Mentoring panel for new faculty (College of Sciences)
2024 School of Biological Sciences retreat committee
2025 Reviewed applications for the Leland Jackson Award

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-	Served as the external assessor for faculty seeking promotion – total number of candidates evaluated: three
2019-	Men of African Descent and Carcinoma of the Prostate (MADCaP) network: chair of the genomics working group
2019-	Member of the Winship Cancer Institute of Emory University
2019-2023	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)
2022-2023	AAAG Education Committee