

Curriculum Vitae

Rajiv C. McCoy

November 16, 2022

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Professional experience

- 2018–Present Assistant Professor, Department of Biology
Johns Hopkins University, Baltimore, MD
- 2017–2018 Postdoctoral Research Associate, Department of Ecology and Evolutionary Biology
Princeton University, Princeton, NJ
- 2015–2017 Senior Fellow, Department of Genome Sciences
University of Washington, Seattle, WA

Education

- 2015 PhD in Biology
Stanford University, Stanford, CA
- 2010 BS in Biology; Ecosystem Science & Policy, *summa cum laude*
University of Miami, Coral Gables, FL

Fellowships, honors, & awards

- 2022 Johns Hopkins University Institutional Nominee, Moore Inventor Fellows Program
- 2022 Discovery Award, Johns Hopkins University
- 2021-2022 Technology Fellowship, Center for Educational Resources, Johns Hopkins University
- 2020 Johns Hopkins University Institutional Nominee, Pew Scholars Program
- 2020 Johns Hopkins University Institutional Nominee, Searle Scholars Program
- 2015–2017 Genome Training Grant (NIH/NHGRI T32), U. of Washington, Dept. of Genome Sciences
- 2015 Epstein Trainee Award for Excellence in Human Genetics Research – Finalist, ASHG
- 2014 Office of Graduate Education Travel Award, Stanford University
- 2013 & 2012 Excellence in Teaching Award, Stanford University, Department of Biology
- 2012 Rosemary Grant Award, Society for the Study of Evolution
- 2012 Arthropod Genomics Consortium i5K Workshop Fellowship Award
- 2010–2013 Stanford University Graduate Fellowship in Science & Engineering
- 2010 Phi Beta Kappa Society

Research support

ACTIVE

- 2022–2024 Discovery Award
 Johns Hopkins University
 Role: PI
 Co-PIs: Alexis Battle and Winston Timp
 Title: “A high-resolution view of human gene expression and splicing diversity with single-molecule long-read sequencing”
 Total Award: \$100,000
- 2019–2024 NIH/NIGMS R35GM133747
 Maximizing Investigators’ Research Award for Early Stage Investigators
 Role: PI
 Title: “Functional and fitness consequences of human genetic variation”
 Total Award: \$2,046,875

Publications & presentations

- * denotes co-first authors
- † denotes co-corresponding authors
- ‡ denotes presentations postponed or cancelled due to COVID-19
- § denotes lab members or rotation students

ARTICLES UNDER REVIEW

- *DeBoy, E. A., *§Tassia, M. G., Schratz, K. E., §Yan, S. M., Cosner, Z. L., McNally, E. J., Gable, D. L., Xiang, Z., Lombard, D. B., Antonarakis, E. S., Gocke, C. D., **McCoy, R. C.**, Armanios, M. A pronearoid long telomere syndrome predisposes to familial clonal hematopoiesis.
- Yang, X., Wang, X., Zou, Y., Zhang, S., Xia, M., Vollger, M. R., Chen, N., Taylor, D. J., Harvey, W. T., Logsdon, G. A., Meng, D., Shi, J., **McCoy, R. C.**, Schatz, M. C., Li, W., Eichler, E. E., Lu, Q., Mao, Y. Characterization of large-scale genomic differences in the first complete human genome.
- **McCoy, R. C.**, Summers, M. C., McCollin, A., Ottolini, C. S., Ahuja, K., Handyside, A. H. Meiotic and mitotic aneuploidies drive arrest of in vitro fertilized human preimplantation embryos. *bioRxiv*: 2022.07.03.498614. DOI: [10.1101/2022.07.03.498614](https://doi.org/10.1101/2022.07.03.498614)
- *§Carioscia, S. A., *§Weaver, K. J., §Bortvin, A. N., §Ariad, D., Bell, A. D., **McCoy, R. C.** Strict adherence to Mendel’s First Law across a large sample of human sperm genomes. *bioRxiv*: 2021.07.12.452063. DOI: [10.1101/2021.11.19.469261](https://doi.org/10.1101/2021.11.19.469261)
- Hadyniak, S. E., Eldred, K. C., Brenerman, B., Hussey, K. A., **McCoy, R. C.**, Sauria, M. E. G., Kuchenbeker, J. A., Neitz, M., Neitz, J., Taylor, J., Johnston, R. J. Temporal regulation of green and red cone specification in human retinas and retinal organoids. *bioRxiv*: 2021.03.30.437763. DOI: [10.1101/2021.03.30.437763](https://doi.org/10.1101/2021.03.30.437763)

RESEARCH ARTICLES (PEER REVIEWED)

- 2022 Griffin, D. K., Brezina, P. R., Tobler, K., Silvestri, G., **McCoy, R. C.**, Anchan, R., Benner, A., Cutting, G. R., Kearns, W. G. (2022). The human embryonic genome is karyotypically complex, with chromosomally abnormal cells preferentially located away from the developing fetus. *Human Reproduction*, in press. DOI: [10.1093/humrep/deac238](https://doi.org/10.1093/humrep/deac238)
- 2022 *Aganezov, S., *[§]Yan, S. M., *Soto, D. C., *Kirsche, M., *Zarate, S., Avdeyev, P., [§]Taylor, D. J., Shafin, K., Shumate, A., Xiao, C., Wagner, J., McDaniel, J., Olson, N. D., Sauria, M. E. G., Vollger, M. R., Meredith, M., Martin, S., Koren, S., Rosenfeld, J. A., Paten, B., Layer, R., Chin, C., Sedlazeck, F. J., Hansen, N. F., Miller, D. E., Phillippy, A., Miga, K., †**McCoy, R. C.**, †Dennis, M. Y., †Zook, J. M., †Schatz, M. C. (2022). A complete reference genome improves analysis of human genetic variation. *Science*, 375: eabl3533. DOI: [10.1126/science.abl3533](https://doi.org/10.1126/science.abl3533)
- 2022 Nurk, S., Koren, S., Rhie, A., Rautiainen, M., Bzikadze, A. V., Mikheenko, A., Vollger, M. R., Altemose, N., Uralsky, L., Gershman, A., Aganezov, S., Hoyt, S. J., Diekhans, M., Logsdon, G. A., Alonge, M., Antonarakis, S. E., Borchers, M., Bouffard, G. G., Brooks, S. Y., ..., [§]Yan, S. M., ..., **McCoy, R. C.** (89/99), ..., Eichler, E. E., Miga, K. H., Phillippy, A. M. (2022). The complete sequence of a human genome. *Science*, 376: eabj6987. DOI: [10.1126/science.abl3533](https://doi.org/10.1126/science.abl3533)
- 2021 [§]Ariad, D., [§]Yan, S. M., Victor, A. R., Barnes, F. L., Zouves, C. G., Viotti, M., **McCoy, R. C.** (2021), Haplotype-aware inference of human chromosome abnormalities. *Proceedings of the National Academy of Sciences USA*, 118(46): e2109307118. DOI: [10.1073/pnas.2109307118](https://doi.org/10.1073/pnas.2109307118)
- 2021 [§]Yan, S. M., Sherman, R. M., [§]Taylor, D. J., [§]Nair, D. R., [§]Bortvin, A. N., Schatz, M. C., **McCoy, R. C.** (2021), Local adaptation and archaic introgression shape global diversity at human structural variant loci. *eLife*, 10, e67615. DOI: [10.7554/eLife.67615](https://doi.org/10.7554/eLife.67615)
- 2021 Ranallo-Benavidez, T. R., Lemmon, Z. H., Soyk, S., Aganezov, S., Salerno, W. J., **McCoy, R. C.**, Lippman, Z. B., Schatz, M. C., Sedlazeck, F. J. (2021), SVCcollector: Optimized sample selection for cost-efficient long-read population sequencing. *Genome Research*, 31: 910-918. DOI: [10.1101/gr.264879.120](https://doi.org/10.1101/gr.264879.120)
- 2020 [§]Starostik, M. R., Sosina, O. A., **McCoy, R. C.** (2020), Single-cell analysis of human embryos reveals diverse patterns of aneuploidy and mosaicism. *Genome Research*, 30: 814-825. DOI: [10.1101/2020.01.06.894287](https://doi.org/10.1101/2020.01.06.894287)
- 2020 Tyc, K. M., **McCoy, R. C.**, Schindler, K., Xing, J. (2020), Mathematical modeling of human oocyte aneuploidy. *Proceedings of the National Academy of Sciences USA*, 117(19): 10455-10464. DOI: [10.1073/pnas.1912853117](https://doi.org/10.1073/pnas.1912853117)
- 2020 Sharma, R., Singh, P., **McCoy, R. C.**, Lenz, S. M., Donovan, K., Ochoa, M. T., Estrada-Garcia, I., Silva-Miranda, M., Jurado-Santa Cruz, F., Balagon, M. F., Stryjewska, B., Scollard, D. M., Pena, M. T., Lahiri, R., Williams, D. L., Truman, R. W., Adams, L. B. (2020), Isolation of *Mycobacterium lepromatosis* and development of molecular diagnostic assays to distinguish *M. leprae* and *M. lepromatosis*. *Clinical Infectious Diseases*, 71(8): e262-e269. DOI: [10.1093/cid/ciz1121](https://doi.org/10.1093/cid/ciz1121)
- 2019 Gruhn, J. R., Zielinska, A., Shukla, V., ..., **McCoy, R. C.** (23/28), ..., Hoffmann, E. R. (2019), Chromosome errors in human eggs shape natural fertility over reproductive lifespan. *Science*, 365(6460): 1466-1469. DOI: [10.1126/science.aav7321](https://doi.org/10.1126/science.aav7321)
- 2019 Victor, A. R., Tyndall, J. C., Brake, A. J., Lepkowski, L. T., Murphy, A., Griffin, D. K., **McCoy, R. C.**, Barnes, F. L., Zouves, C. G., Viotti, M. (2019), One hundred mosaic embryos

- transferred prospectively in a single clinic: exploring when and why they result in normal pregnancies. *Fertility & Sterility*, 111(2): 280–293. DOI: [10.1016/j.fertnstert.2018.10.019](https://doi.org/10.1016/j.fertnstert.2018.10.019)
- 2019 Victor, A. R., Griffin, D. K., Brake, A. J., Tyndall, J. C., Murphy, A., Lepkowsky, L. T., Lal, A., Zouves, C. G., Barnes, F. L., **McCoy, R. C.**, Viotti, M. (2019), Assessment of aneuploidy concordance between clinical trophectoderm biopsy and blastocyst. *Human Reproduction*, 34(1): 181–192. DOI: [10.1093/humrep/dey327](https://doi.org/10.1093/humrep/dey327)
- 2018 Tucci, S., Vohr, S. H., **McCoy, R. C.**, Vernot, B., Robinson, M., Barbieri, C., Fu, W., Purnomo, G. A., Sudoyo, H., Barbujani, G., Visscher, P. M., Akey, J. M., Green, R. E. (2018), Evolutionary history and adaptation of a human pygmy population of Flores Island, Indonesia. *Science*, 361(6401): 511–516. DOI: [10.1126/science.aar8486](https://doi.org/10.1126/science.aar8486)
- 2018 Press, M. O., **McCoy, R. C.**, Hall, A. N., Akey, J. M., Queitsch, C. (2018), Short tandem repeats with massive variation and functional consequences across strains of *Arabidopsis thaliana*. *Genome Research*, 28: 1169–1178. DOI: [10.1101/gr.231753.117](https://doi.org/10.1101/gr.231753.117)
- 2018 ***McCoy, R. C.**, *Newnham, L. J., Ottolini, C. S., Hoffmann, E. R., Chatzimeletiou, K., Cornejo, O. E., Zhan, Q., Zaninovic, N., Rosenwaks, Z., Petrov, D. A., Demko, Z. P., Sigurjonsson, S., Handyside, A. H. (2018), Tripolar chromosome segregation drives the association between maternal genotype at variants spanning *PLK4* and aneuploidy in human preimplantation embryos. *Human Molecular Genetics*, 27(14): 2573–2585. DOI: [10.1093/hmg/ddy147](https://doi.org/10.1093/hmg/ddy147)
- 2018 Kort, J. D., **McCoy, R. C.**, Demko, Z. P., Lathi, R. B. (2018), Are blastocyst aneuploidy rates different between fertile and infertile populations? *Journal of Assisted Reproduction and Genetics*, 35(3): 403–408. DOI: [10.1007/s10815-017-1060-x](https://doi.org/10.1007/s10815-017-1060-x)
- 2017 **McCoy, R. C.**, Wakefield, J., Akey, J. M. (2017), Impacts of Neanderthal-Introgressed Sequences on the Landscape of Human Gene Expression. *Cell*, 168(5): 916–927.e12. DOI: [10.1016/j.cell.2017.01.038](https://doi.org/10.1016/j.cell.2017.01.038)
- 2016 Vernot, B., Tucci, S., Kelso, J., Schraiber, J. G., Wolf, A. B., Gittelman, R. M., Dannemann, M., Grote, S., **McCoy, R. C.**, Norton, H., Scheinfeldt, L. B., Merriwether, D. A., Koki, G., Friedlaender, J. S., Wakefield, J., Pääbo, S., Akey, J. M. (2016), Excavating Neandertal and Denisovan DNA from the genomes of Melanesian individuals. *Science*, 352(6282): 235–239. DOI: [10.1126/science.aad9416](https://doi.org/10.1126/science.aad9416)
- 2016 Demko, Z. P., Simon, A. L., **McCoy, R. C.**, Petrov, D. A., Rabinowitz, M. (2016), Effects of maternal age on euploidy in a large cohort of embryos analyzed with 24 chromosome single nucleotide polymorphism-based preimplantation genetic screening. *Fertility & Sterility*, 105(5): 1307–1313. DOI: [10.1016/j.fertnstert.2016.01.025](https://doi.org/10.1016/j.fertnstert.2016.01.025)
- 2015 **McCoy, R. C.**, Demko, Z., Ryan, A., Banjevic, M., Hill, M., Sigurjonsson, S., Rabinowitz, M., Petrov, D. A. (2015), Evidence of selection against complex mitotic-origin aneuploidy during preimplantation development. *PLoS Genetics*, 11(10): e1005601. DOI: [10.1371/journal.pgen.1005601](https://doi.org/10.1371/journal.pgen.1005601)
- 2015 **McCoy, R. C.**, Demko, Z., Ryan, A., Banjevic, M., Hill, M., Sigurjonsson, S., Rabinowitz, M., Fraser, H. B., Petrov, D. A. (2015), Common variants spanning *PLK4* are associated with mitotic-origin aneuploidy in human embryos. *Science*, 348(6231): 235–238. DOI: [10.1126/science.aaa3337](https://doi.org/10.1126/science.aaa3337)
- 2014 Ahola, V., Lehtonen, R., Somervou, P., ..., **McCoy, R. C.** (18/45) , ..., Hanski, I. (2014), The Glanville fritillary genome retains an ancient karyotype and reveals selective chromosomal fusions in Lepidoptera. *Nature Communications*, 5. DOI: [10.1038/ncomms5737](https://doi.org/10.1038/ncomms5737)
- 2014 **McCoy, R. C.**, Taylor, R., Blauwkamp, T. A., Kelley, J. L., Kertesz, M., Pushkarev, D., Petrov, D. A., Fiston-Lavier, A. S. (2014), Illumina TruSeq synthetic long reads empower *de novo* assembly and resolve complex, highly repetitive transposable elements. *PLoS*

ONE, 9(9): e106689. DOI: [10.1371/journal.pone.0106689](https://doi.org/10.1371/journal.pone.0106689)

2014 **McCoy, R. C.**, Garud, N. R., Kelley, J. L., Boggs, C. L., Petrov, D. A. (2014), Genomic inference accurately predicts the timing and severity of a recent bottleneck in a non-model insect population. *Molecular Ecology*, 23(1): 136–150. DOI: [10.1111/mec.12591](https://doi.org/10.1111/mec.12591)

REVIEW ARTICLES (PEER REVIEWED)

2022 Brosens, J. J., Bennett, P. R., Abrahams, V., Ramhorst, R., Coomarasamy, A., Quenby, S., Lucas, E. S., **McCoy, R. C.** (2022), Maternal selection of human embryos in early gestation: insights from recurrent miscarriage. *Seminars in Cell and Developmental Biology*: in press. DOI: [10.1016/j.semcdb.2022.01.007](https://doi.org/10.1016/j.semcdb.2022.01.007)

2021 Quenby, S., Gallos, I. D., Dhillon-Smith, R. K., Podesek, M., Stephenson, M. D., Fisher, J., Brosens, J., Brewin, J., Ramhorst, R., Lucas, E. S., **McCoy, R. C.**, Anderson, R., Daher, S., Regan, L., Al-Memar, M., Bourne, T., MacIntyre, D. A., Rai, R., Christiansen, O. B., Sugiura-Ogasawara, M., Odendaal, J., Devall, A. J., Bennett, P. R., Petrou, S., Coomarasamy, A. (2021), Miscarriage matters: the epidemiological, physical, psychological, and economic costs of early pregnancy loss. *The Lancet*, 397: 1658-1667. DOI: [10.1016/S0140-6736\(21\)00682-6](https://doi.org/10.1016/S0140-6736(21)00682-6)

2021 Levy, B., Hoffmann, E. R., **McCoy, R. C.**, Grati, F. R. (2021), Chromosomal mosaicism: origins and clinical implications in preimplantation and prenatal diagnosis. *Prenatal Diagnosis*, 41: 631-641. DOI: [10.1002/pd.5931](https://doi.org/10.1002/pd.5931)

2021 Wartosch, L., Schindler, K., Schuh, M., Gruhn, J. R., Hoffmann, E. R., **McCoy, R. C.**, Xing, J. (2021), Origins and mechanisms leading to aneuploidy in human eggs. *Prenatal Diagnosis*, 41, 620-630. DOI: [10.1002/pd.5927](https://doi.org/10.1002/pd.5927)

2020 [§]Yan, S. M., **McCoy, R. C.** (2020), Archaic hominin genomics provides a window into gene expression evolution. *Current Opinion in Genetics & Development*, 62: 44–49. DOI: [10.1016/j.gde.2020.05.014](https://doi.org/10.1016/j.gde.2020.05.014)

2017 **McCoy, R. C.** (2017), Mosaicism in preimplantation human embryos: when chromosomal abnormalities are the norm. *Trends in Genetics*, 33(7): 448–463. DOI: [10.1016/j.tig.2017.04.001](https://doi.org/10.1016/j.tig.2017.04.001)

EDITORIALS AND COMMENTARIES

2021 Viotti, M., **McCoy, R. C.**, Griffin, D. K., Spinella, F., Greco, E., Madjunkov, M., Madjunkova, S., Librach, C. L., Victor, A. R., Barnes, F. L., Zouves, C. G. Let the data do the talking: The Need To Consider Mosaicism During Embryo Selection. *Fertility & Sterility*: in press.

2019 [§]Yan, S. M., **McCoy, R. C.** (2019), Functional divergence among hominins. *Nature Ecology & Evolution*, 3: 1507–1508. DOI: [10.1038/s41559-019-0995-y](https://doi.org/10.1038/s41559-019-0995-y)

2019 **McCoy, R. C.**, Kort, J. D. (2019), Quantifying the transcriptional impacts of aneuploidy in human blastocysts. *Fertility & Sterility*, 111(5): 888–889. DOI: [10.1016/j.fertnstert.2019.02.126](https://doi.org/10.1016/j.fertnstert.2019.02.126)

2017 **McCoy, R. C.**, Akey, J. M. (2017), Selection plays the hand it was dealt: evidence that human adaptation commonly targets standing genetic variation. *Genome Biology*, 18: 139. DOI: [10.1186/s13059-017-1280-5](https://doi.org/10.1186/s13059-017-1280-5)

2017 Adashi, E. Y., **McCoy, R. C.** (2017), Technology versus biology: the limits of pre-implantation genetic screening. *EMBO Reports*: e201743941. DOI: [10.1038/embo.2017.43941](https://doi.org/10.1038/embo.2017.43941)

[10.15252/embr.201743941](https://doi.org/10.15252/embr.201743941)

2016 **McCoy, R. C., Akey, J. M.** (2016), Patterns of deleterious variation between human populations reveal an unbalanced load. *Proceedings of the National Academy of Sciences USA*, 113(4): 809–811. DOI: [10.1073/pnas.1524016113](https://doi.org/10.1073/pnas.1524016113)

ORAL PRESENTATIONS

Summer 2023 ReproUnion, Sweden and Denmark
Summer 2023 Globe Institute, University of Copenhagen, Denmark
Summer 2023 Department of Molecular and Cellular Medicine, University of Copenhagen, Denmark
2022 Origins of Human Aneuploidy Meeting, Paris, France
2022 Annual Meeting of the American Society of Human Genetics, Los Angeles, CA
2022 Annual Meeting of the American Society for Reproductive Medicine, Anaheim, CA (presented by co-author, Michael Summers, due to scheduling conflict with ASHG)
2022 Department of Genetic Medicine, Johns Hopkins School of Medicine, Baltimore, MD
2022 Joint Didactic Session, Reproductive Endocrinology & Infertility / Medical Genetics Fellowship Program, Johns Hopkins School of Medicine, Baltimore, MD
2022 Maimon M. Cohen Genetics Colloquium, Greater Baltimore Medical Center (Online), Towson, MD
2021 Chromatin, Chromosomes, and Epigenomes Workshop, Johns Hopkins University (Online), Baltimore, MD
2021 Cell Bio Virtual, American Society of Cell Biology / European Molecular Biology Organization, Online
2021 Howard and Georgeanna Jones Endowed Symposium on Assisted Reproductive Technology, Annual Meeting of the American Society for Reproductive Medicine, Baltimore, MD
2021 Origins of Human Aneuploidy Meeting, Online
2021 Division of Biomedical Sciences, Warwick Medical School (Online), Coventry, United Kingdom
2021 Center for Reproductive Medicine, Weill Medical College of Cornell University (Online), New York, NY
2020 Zouves Foundation for Reproductive Medicine (Online), Foster City, CA
2020 World Congress on Controversies in Obstetrics, Gynecology and Infertility, Online
2020 ‡Department of Molecular and Cellular Biology, Harvard University, Cambridge, MA
2020 Origins of Human Aneuploidy Meeting, Online
2020 Department of Embryology, Carnegie Institution, Baltimore, MD
2020 Computational Biology Department, Carnegie Mellon University, Pittsburgh, PA
2020 CReATe Fertility Centre, Toronto, Canada
2019 Annual Conference of the Foundation for Reproductive Medicine, New York, NY
2019 Origins of Human Aneuploidy Meeting, Paris, France
2019 Annual Meeting of the American Society of Human Genetics, Houston, TX
2019 Department of Genetics, Rutgers University, Piscataway, NJ
2019 Department of Biology, Catholic University, Washington, DC
2018 Annual Conference of the Foundation for Reproductive Medicine, New York, NY

2018 Genomics & Bioinformatics Symposium, Johns Hopkins University, Baltimore, MD
 2018 Johns Hopkins University Graduate Program in Cell, Molecular, Developmental Biology, and Biophysics Retreat, Rocky Gap State Park, MD
 2018 Origins of Human Aneuploidy Meeting, Toronto, Canada
 2017 Marabou Symposium on Nutrition and Human Development, Stockholm, Sweden
 2017 1st Origins of Human Aneuploidy Meeting, Barcelona, Spain
 2017 Department of Genomes Sciences / Computational Molecular Biology Program Combi Seminar, University of Washington, Seattle, WA
 2017 Annual International Conference on Preimplantation Genetics, Valencia, Spain
 2016 Genotype-Tissue Expression (GTEx) Project Community Meeting, Stanford, CA
 2015 Annual Meeting of the American Society of Human Genetics, Baltimore, MD
 2014 Bay Area Population Genomics Meeting, University of California, Davis, CA
 2014 Illumina Long-Reads Applications Symposium, University of California, Davis, CA
 2014 Presentation to Management Team at Natera, Inc., San Carlos, CA

SENIOR AUTHORSHIP OF TRAINEE ORAL PRESENTATIONS

2022 Yan, S. M., Telomere-to-Telomere Face-to-Face, Santa Cruz, CA
 2022 Taylor, D. J., Telomere-to-Telomere Face-to-Face, Santa Cruz, CA
 2022 Yan, S. M., Advances in Genome Biology and Technology (AGBT), Orlando, FL
 2022 Ariad, D., The Biology of Genomes, Cold Spring Harbor Laboratory, NY
 2021 Yan, S. M., *eLife* Virtual Symposium on Evolutionary Medicine (Online)
 2021 Zarate, S., Annual Meeting of the American Society of Human Genetics (Online)
 2021 Ariad, D., Genomics & Bioinformatics Symposium, Johns Hopkins University (Online)
 2021 Ariad, D., RECOMB-Genetics Satellite Meeting (Online)
 2021 Yan, S. M., The Biology of Genomes, Cold Spring Harbor Laboratory (Online)
 2020 Yan, S. M., Annual Meeting of the American Society of Human Genetics (Online)
 2020 ‡Yan, S. M., Society for Molecular Biology & Evolution, Québec City, Canada
 2019 Seyedian, A., RECOMB-Genetics Satellite Meeting, George Washington University, Washington, DC

POSTER PRESENTATIONS

2020 ‡Society for Molecular Biology & Evolution, Québec City, Canada
 2020 ‡The Allied Genetics Conference, Genetics Society of America
 2019 Society for Molecular Biology & Evolution, Manchester, England
 2017 67th Annual Meeting of the American Society of Human Genetics, Orlando, FL
 2017 NHGRI Annual Training and Career Development Meeting, St. Louis, MO
 2016 66th Annual Meeting of the American Society of Human Genetics, Vancouver, Canada
 2016 NHGRI Annual Training and Career Development Meeting, Bethesda, MD
 2014 Bay Area Population Genomics Meeting, University of California, Davis, CA
 2014 Stanford Biosciences Student Association Poster Session, Stanford, CA

2014 Society for Molecular Biology & Evolution, San Juan, Puerto Rico [1/2]
 2014 Society for Molecular Biology & Evolution, San Juan, Puerto Rico [2/2]
 2014 Ctr. for Computational, Evolutionary, and Human Genomics Symposium, Palo Alto, CA
 2013 Bay Area Population Genomics Meeting, Stanford, CA
 2013 Annual Meeting of the Society for Integrative & Comparative Biology, San Francisco, CA
 2012 Arthropod Genomics Symposium, Kansas City, MO
 2012 1st Joint Congress on Evolutionary Biology, Ottawa, Canada

SENIOR AUTHORSHIP OF TRAINEE POSTER PRESENTATIONS

2022 Ariad, D., RECOMB, La Jolla, CA
 2022 Taylor, D. J., The Biology of Genomes, Cold Spring Harbor Laboratory, NY
 2021 Weaver, K. J., RegSys COSI, International Society for Computational Biology / European Conference on Computational Biology (Online)
 2021 Ariad, D., RECOMB (Online)
 2021 Ariad, D., Annual Meeting of the American Society of Human Genetics (Online)
 2021 Carioscia, S. A., Genomics & Bioinformatics Symposium, Johns Hopkins University (Online)
 2021 *Weaver, K. J., *Bortvin, A. N., Genomics & Bioinformatics Symposium, Johns Hopkins University (Online)
 2021 *Carioscia, S. A., *Weaver, K. J., The Biology of Genomes, Cold Spring Harbor Laboratory (Online)
 2021 Ariad, D., The Biology of Genomes, Cold Spring Harbor Laboratory (Online)
 2020 Ariad, D., Annual Meeting of the American Society of Human Genetics (Online)
 2020 Taylor, D. J., Annual Meeting of the American Society of Human Genetics (Online)
 2020 Yan, S. M., The Allied Genetics Conference, Genetics Society of America (Online)
 2020 Carioscia, S. A., The Allied Genetics Conference, Genetics Society of America (Online)
 2019 Yan, S. M., Genomics & Bioinformatics Symposium, Johns Hopkins University, Baltimore, MD
 2019 Carioscia, S. A., Genomics & Bioinformatics Symposium, Johns Hopkins University, Baltimore, MD
 2019 Yan, S. M., Society for Molecular Biology & Evolution, Manchester, England
 2018 Farney, S., Genomics & Bioinformatics Symposium, Johns Hopkins University, Baltimore, MD

Teaching

2022 Guest Lecturer, Human Genome Variation (020.319, Spring; 3 hours), Johns Hopkins University
 2022 Guest Lecturer, Genetics (020.303, Spring; 1 hour), Johns Hopkins University
 2021 Guest Lecturer, Biology of Disease (020.314, Fall; 2.5 hours), Johns Hopkins University

- 2021 Co-Instructor, Quantitative Biology Lab (020.617, Fall; 14 hours), Johns Hopkins University
- 2021 Co-Instructor, Quantitative Biology Bootcamp (020.607, Fall; 13 hours), Johns Hopkins University
- 2021 Guest Lecturer, Genetics (020.303, Spring; 1 hour), Johns Hopkins University
- 2021 Instructor, Computation Lab: Human Genome Variation (020.321 / 020.323, Spring; 13 hours), Johns Hopkins University
- 2021 Co-Instructor, Human Genome Variation (020.319 / 020.321, Spring; 4 hours), Johns Hopkins University
- 2020 Co-Instructor, Human Genome Variation (020.319, Fall; 4 hours), Johns Hopkins University
- 2020 Co-Instructor, Quantitative Biology Lab (020.617, Fall; 14 hours), Johns Hopkins University
- 2020 Co-Instructor, Quantitative Biology Bootcamp (020.607, Fall; 13 hours), Johns Hopkins University
- 2020 Instructor, Human Genome Variation Module: Analysis of Genomic Data (020.321, Spring; 13 hours), Johns Hopkins University
- 2020 Guest Lecturer, Human Genome Variation (020.319, Spring; 3 hours), Johns Hopkins University
- 2019 Guest Instructor, Quantitative Biology Bootcamp (020.607, Fall; 3 hours), Johns Hopkins University
- 2019 Guest Lecturer, Human Genome Variation (020.319, Spring; 3 hours), Johns Hopkins University
- 2019 Participant, Best Practices in University Teaching Workshop, Johns Hopkins University
- 2018 Guest Lecturer, Quantitative Biology Bootcamp (020.607, Fall; 1 hour), Johns Hopkins University
- 2017–2018 Science Teaching Experience for Postdocs (STEP) Program, University of Washington
- 2017 Participant, Undergraduate Faculty Genetics Education Workshop, American Society of Human Genetics
- 2014 Teaching Assistant Mentor, Department of Biology, Stanford University
- 2013 & 2011 Teaching Assistant: Ecology, Evolution, and Plant Biology, Stanford University
- 2013 & 2012 Biocore Explorations Course Instructor, Department of Biology, Stanford University
- 2012 Teaching Assistant: Conservation Biology, Stanford University
- 2010 Undergraduate Workshop Leader: Evolution and Biodiversity, University of Miami
- 2009–2010 Peer Tutor, Camner Academic Resource Center, University of Miami

Research mentoring

GRADUATE PROGRAMS

- 2022–Present Faculty Preceptor, Predoctoral Training Program in Human Genetics, Johns Hopkins School of Medicine
- 2018–Present Training Faculty, Predoctoral Training Program in Cell, Molecular, Developmental Biology and Biophysics (CMDDB), Johns Hopkins University

POSTDOCTORATE

- 2022–Present Michael Tassia, Postdoctoral Fellow, Johns Hopkins University
2020–2022 Daniel Ariad, Postdoctoral Fellow, Johns Hopkins University

GRADUATE

- 2021–Present Andrew Bortvin, PhD Candidate in CMDB, Johns Hopkins University
2020–Present Kathryn Weaver, PhD Candidate in CMDB, Dean’s Teaching Fellow, Johns Hopkins University
2020–Present Dylan Taylor, PhD Candidate in CMDB, Johns Hopkins University
2020–Present Sara Carioscia, PhD Candidate in CMDB, NSF Graduate Research Fellow, Johns Hopkins University
2019–Present Stephanie Yan, PhD Candidate in CMDB, NIH/NHGRI NRSA Predoctoral Fellow (F31), Johns Hopkins University
2021 Taher Mun, PhD Candidate in Computer Science (Qualifying Project), Johns Hopkins University
2018–2020 Arta Seyedian, Masters of Science Student in Bioinformatics, Johns Hopkins University

GRADUATE ROTATION

- 2022 J. Noah Workman, PhD Rotation Student in Human Genetics, Johns Hopkins University
2022 Jack Dorman, PhD Rotation Student in CMDB, NIH Graduate Partnership Program
2022 Calvin Runnels, PhD Rotation Student in CMDB, Johns Hopkins University
2022 Matthew Isada, PhD Rotation Student in CMDB, Johns Hopkins University
2022 Joshua Schultz, PhD Rotation Student in CMDB, Johns Hopkins University
2022 Bradley Olinger, PhD Rotation Student in CMDB, NIH Graduate Partnership Program
2021 Rylee Genner, PhD Rotation Student in CMDB, NIH Graduate Partnership Program
2021 Sadhana Chidambaran, PhD Rotation Student in CMDB, Johns Hopkins University
2021 Catherine Henderson, PhD Rotation Student in CMDB, Johns Hopkins University
2021 Robyn Stix, PhD Rotation Student in CMDB, NIH Graduate Partnership Program
2021 Radhika Jangi, PhD Rotation Student in CMDB, Johns Hopkins University
2020 Simon Zhang, PhD Rotation Student in CMDB, Johns Hopkins University
2019–2020 Sara Debic, PhD Rotation Student in CMDB, Johns Hopkins University
2019 Natalie Murphy, PhD Rotation Student in CMDB, Johns Hopkins University
2018–2019 Margaret Starostik, PhD Rotation Student in CMDB, Johns Hopkins University
2018 Katie Farney, PhD Rotation Student in CMDB, NIH Graduate Partnership Program

UNDERGRADUATE

- 2022–Present Anika Misra, Bachelor of Science Student in Biology and Computer Science, Johns Hopkins University
2022–Present Hao Pan, Bachelor of Science Student in Biology and Applied Mathematics, Johns Hopkins University

Hopkins University

- 2020–Present Divya Nair, Bachelor of Science Student in Biology, Johns Hopkins University
- 2022 Katherine Gilbert, Research Experience for Undergraduates (REU) Student from Wesleyan University, Johns Hopkins University
- 2018–2020 Joel Espinoza, Bachelor of Science Student in Biology, Johns Hopkins University
- 2019–2020 Peter Huang, Bachelor of Science Student in Biology, Johns Hopkins University
- 2019–2020 Nicholas Parente, Bachelor of Science Student in Applied Mathematics & Statistics and Computer Science, Johns Hopkins University
- 2018 Vincent Huang, Bachelor of Science Student in Biology, Johns Hopkins University
- 2014–2015 Jack McGregor, Senior Honors Thesis (Co-Advised), Stanford University

HIGH SCHOOL

- 2022–Present Cosima Billotte Bermudez, Ingenuity Project, Baltimore Polytechnic Institute, Baltimore, MD
- 2020–2021 Miles Fancher, Ingenuity Project, Baltimore Polytechnic Institute, Baltimore, MD
- 2020–2021 Aram Zaprosyan, Ingenuity Project, Baltimore Polytechnic Institute, Baltimore, MD

Academic, community, & university service

DOCTORAL THESIS COMMITTEES

- 2022–Present Radhika Jangi, CMDB, Johns Hopkins University
- 2021–Present Danielle Nicklas, Pathobiology, Johns Hopkins University
- 2021–Present Dylan Sucich, CMDB, NIH Graduate Partnership Program, Johns Hopkins University
- 2020–Present Margaret Starostik, CMDB, Johns Hopkins University
- 2020–Present Jeremiah Miller, CMDB, Johns Hopkins University
- 2020–2021 T. Rhyker Ranallo-Benavidez, Biomedical Engineering, Johns Hopkins University

GRADUATE BOARD ORAL EXAMINATION COMMITTEES

- Oct. 2022 Jimmy Gonzalez Nunez, Physics and Astronomy, Johns Hopkins University
- Oct. 2022 Rylee Genner, CMDB, NIH Graduate Partnership Program, Johns Hopkins University
- 2022 Matthew Isada, CMDB, Johns Hopkins University
- 2022 Arun Das, Computer Science, Johns Hopkins University
- 2022 Christian Wesselborg, CMDB, Johns Hopkins University
- 2022 Samantha Zarate, Computer Science, Johns Hopkins University
- 2021 Radhika Jangi, CMDB, Johns Hopkins University
- 2021 Sadhana Chidambaran, CMDB, Johns Hopkins University
- 2021 Xiangning Chen, CMDB, Johns Hopkins University
- 2021 Katie Farney, CMDB, NIH Graduate Partnership Program, Johns Hopkins University
- 2021 Catherine Henderson, CMDB, Johns Hopkins University

2021 Nae-Chyun Chen, Computer Science, Johns Hopkins University

UNIVERSITY AND DEPARTMENTAL COMMITTEES

2022–Present CMDB Admissions Committee, Johns Hopkins University
2021–Present Diversity Advocate and Member, Search Committee for Computational Genomics, Department of Biology, Johns Hopkins University
2021–Present Biology Futures Committee, Department of Biology, Johns Hopkins University
2022–Present Graduate Curriculum Committee, Department of Biology, Johns Hopkins University
2020–Present Undergraduate Curriculum Committee, Department of Biology, Johns Hopkins University
2022 Faculty Focus Group Panelist, External Review of Research Compliance Program, Johns Hopkins University
2019 CMDB Thesis Award Committee, Department of Biology, Johns Hopkins University
2012 PhD Interview Visit Committee, Department of Biology, Stanford University
2011 New PhD Student Orientation Committee, Department of Biology, Stanford University

ACADEMIC AND PROFESSIONAL ORGANIZATIONS

2021–Present Co-Chair, Origins of Human Aneuploidy Research Consortium

CONFERENCES

2021–Present Organizing Committee, Origins of Human Aneuploidy Meeting, Online
2019 Pre-Conference Workshop Chair, Annual Conference of the Foundation for Reproductive Medicine, New York, NY
2019 Session Moderator, Reproductive Fitness - The Genetics of Infertility, 69th Annual Meeting of the American Society of Human Genetics, Houston, TX
2017 Session Moderator, Detection and Interpretation of Structural Variation, 67th Annual Meeting of the American Society of Human Genetics, Orlando, FL

PEER REVIEW

2013–Present Ad Hoc Reviewer, *American Journal of Human Genetics*, *American Journal of Obstetrics & Gynecology*, *BioData Mining*, *Bioinformatics*, *Cell Proliferation*, *Current Urology*, *Development*, *eLife*, *G3*, *Genes*, *Genetics*, *Genome Biology*, *Genome Biology and Evolution*, *Genome Research*, *Journal of Assisted Reproduction & Genetics*, *Journal of Biogeography*, *Journal of Heredity*, *Journal of Ovarian Research*, *Molecular Ecology*, *Nature*, *Nature Communications*, *Nature Ecology & Evolution*, *PLoS Biology*, *PLoS Genetics*, *PLoS One*, *Prenatal Diagnosis*, *Proceedings of the National Academy of Sciences U.S.A.*, *Proceedings of the Royal Society B*, *Reproduction*, *Science*, *Science Advances*

GRANT REVIEW

2022–Present College of Expert Reviewers, European Science Foundation

2022 Ad Hoc Reviewer, Kleberg Foundation Scholars Program Internal Competition, Office of Foundation Relations, Johns Hopkins University

2022 Outside Reviewer, Medical Research Council, United Kingdom Research and Innovation

2022 Outside Reviewer, Israel Science Foundation

2022 Ad Hoc Reviewer, NHGRI Genomic Data Science Analysis, Visualization, and Informatics Lab-space (AnVIL) Cloud Credits Continued Program (AC3)

2021 Outside Reviewer, Independent Research Fund Denmark, Danish Agency for Higher Education and Science

2021 Outside Reviewer, Biological Anthropology Program, National Science Foundation

2018–2019 Outside Reviewer, Biological Anthropology Program, National Science Foundation

EDUCATION, VOLUNTEERING, & OUTREACH

2022 Virtual Training Program Mentor, Society for Molecular Biology and Evolution

2022 Mock F31 Review Panelist, Communicating Science (020.619, Spring), Johns Hopkins University

2021 Mock F31 Review Panelist, Communicating Science (020.619, Spring), Johns Hopkins University

2020 Representative of JHU CMDB, NIH Virtual Graduate & Professional School Fair

2020 Visiting Fellow in Biology Assessment, AP Higher Education, The College Board

2019 Undergraduate Mentor, Society for Molecular Biology & Evolution, Manchester, England

2018–2019 Senior Project Mentor, School Without Walls, Washington, DC

2018 Mock F31 Review Panelist, Communicating Science (020.619, Spring), Johns Hopkins University

2018 Bioethics Panelist, Biology Club, Univ. of Maryland, Baltimore County, Catonsville, MD

2018 & 2017 Education Outreach Volunteer, University Prep Middle School, Seattle, WA

2018 Judge, NWABR Middle School Essay Contest, Seattle, WA

2017 Invited Speaker, Emerald City Rotary, Seattle, WA

2016 Volunteer, University of Washington Paws-On Science, Pacific Science Center, Seattle, WA

2016 Invited Speaker, Open Mic Science, Treehouse Cafe, Bainbridge Island, WA

2014 AP Biology E-mentor, Arroyo High School, San Lorenzo, CA

2012–2013 Copy Editor, *Six Degrees: The Stanford Journal of Human Rights*

2012 Judge, Synopsys Silicon Valley Science and Technology Championship, San Jose, CA