

NICOLE B. ROCKWEILER, PhD

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SUMMARY

Computational and systems biology scientist who is innovative, diligent, and passionate about genomics research and teaching.

EDUCATION

- | | |
|---|-----------|
| Washington University in St. Louis, St. Louis MO | 2013-2021 |
| Doctor of Philosophy | |
| Thesis: The Origins & Functional Effects of Postzygotic Mutations Throughout the Human Lifespan | |
| Computational and Systems Biology, Division of Biology and Biomedical Sciences | |
| GPA: 4.00 | |
| | |
| Washington University in St. Louis, St. Louis MO | 2006-2010 |
| Bachelor of Science, <i>summa cum laude</i> | |
| Double major in Biomedical Engineering (biomolecular track) and Mathematics (applied mathematics track) | |
| GPA: 3.93 | |

AWARDS AND HONORS

- **Washington University in St. Louis, Genome Analysis Training Program, *fellow*, 2016-2020**
- Leena Peltonen School of Human Genomics, *fellow*, 2019
- St. Jude Children's Research Hospital Future Fellow Research Conference, *fellow*, 2018
- Monsanto Graduate Fellowship in the Life Sciences, *finalist*, 2015
- National Science Foundation Graduate Research Fellowship, *honorable mention*, 2015
- Precision Medicine Special Emphasis Pathway Fellowship, 2014-2016
- Washington University merit-based Dean's Honorary Scholarship, 2006-2010
- Dean's List, all semesters, 2006-2010
- Sigma Xi Scientific Research Society
- Alpha Eta Mu Beta Biomedical Engineering Honor Society
- Tau Beta Pi Engineering Honor Society

RESEARCH EXPERIENCE

Postdoctoral Associate Fall 2021-present
Stanley Center for Psychiatric Research, Broad Institute of MIT and Harvard; and Dept. of Genetics, Harvard Medical School
Dr. Steven McCarroll

Graduate Research Assistant

Roy and Diana Vagelos Division of Biology and Biomedical Sciences, Washington University in St. Louis
Thesis lab, Dr. Don Conrad, Dept. of Genetics Fall 2016-Summer 2021

- Developed a variant calling algorithm to detect postzygotic mutations in bulk RNA-seq data
- Characterized landscape of postzygotic mutations in 17,000 normal adult human tissues
- Designed and implemented analysis pipelines for cloud computing

Previous thesis lab, Dr. Ting Wang, Dept. of Genetics

Fall 2014-Fall 2016

- Co-developed a cost-effective experimental and computational machine learning technology to predict DNA methylomes and hydroxymethylomes

Rotations

Fall 2013-Fall 2014

- *Dr. Max Artymov, Dept. of Pathology and Immunology; Dr. Chris Maher, Dept. of Medical Oncology; and Dr. Ting Wang, Dept. of Genetics*

Research Assistant at the Brent Lab

Spring 2013-Summer 2013

Dr. Michael Brent, Dept. of Computer Science, Washington University in St. Louis

- Defined a gene regulatory network for neural fate acquisition in mouse embryonic stem cells using RNA-seq and ChIP-chip data
- Investigated central carbon metabolism of *S. cerevisiae* in chemostat cultures

Bioinformatician at the Genome Technology Access Center

2010-2013

Dr. Robi Mitra and Dr. Paul Cliften, Dept. of Genetics, Washington University in St. Louis School of Medicine

- **Designed and optimized analysis pipelines for whole genome-seq, exome-seq, RNA-seq, and ChIP-seq in Perl and Python and analyzed over 8,000 next-generation sequencing (NGS) datasets**
- Designed and implemented NGS analysis pipelines in Perl, Python, R, and XML for Galaxy, a web-based bioinformatics platform
- Created automated NGS quality control reports in Perl, R, HTML, and CSS for internal and external use
- Developed algorithm to detect rare single nucleotide variants in pooled amplicon sequencing

Senior Design Project

Spring 2010

Dr. Dan Moran, Dept. of Biomedical Engineering, Washington University in St. Louis

- Developed an automated image processing algorithm in Matlab to determine a subject's line of vision in live video

Engineering Intern at Boston Scientific

Summer 2009

Dr. Scott Meyer, Research and Development, Boston Scientific, St. Paul, MN

- Created semi-automatic image processing and data analysis software in Matlab to determine efficacy of a cardioprotection therapy in porcine cardiac tissues
- Made protocol recommendations to senior management for future cardioprotection animal studies

Research Intern at the Center for Computational Biology

Summer 2008-Spring 2009

Dr. Garland Marshall, Dept. of Biochemistry and Molecular Biophysics, Washington University School of Medicine

- Performed preliminary stages of drug development using Sybyl, a computational informatics software, and validated computational models with various wet-lab assays
- Optimized algorithm parameters for Galahad and Unity programs in Sybyl

Research Intern at the Computational Electromagnetics Laboratory

Summer 2007

Dr. Susan Hagness, Dept. of Electrical and Computer Engineering, University of Wisconsin-Madison

- Discovered electric-field intensity thresholds for electroporation of cells exposed to pulsed electric fields
- Independently researched and designed protocol for the characterization of protein cytotoxicity

Summer Scholar in Biology and Biomedical Research

Summer 2006

Dr. Colin Nichols, Dept. of Cell Biology and Physiology, Washington University School of Medicine

- Investigated chronic effects of an anti-diabetic drug on insulin and glucose levels in mice
- Performed various hormone level assays, dissected mice, and isolated pancreatic cells

Research Intern at the Laboratory for Molecular Scale Engineering

Summer 2005

Dr. Robert Blick, Dept. of Electrical and Computer Engineering, University of Wisconsin-Madison

- Used electric fields to manipulate silicon nanotubes for potential use in drug delivery
- Designed, fabricated, and optimized circuit boards using AutoCAD

PUBLICATIONS

9. **Rockweiler, N. B.**, Ramu, A., Nagirnaja, L., Wong, W. H., Michiel, J., Drubin, C. W., Huang, N., Miller, B., Todres, E. Z., Vigh-Conrad, K. A., Zito, A., Small, K. S., Ardlie, K. G., Cohen, B. A., Conrad, D. F. (2023). The origins and functional effects of postzygotic mutations throughout the human lifespan. *Science*, 380. <https://doi.org/10.1126/science.abn7113> [preprint] [almetric]
8. Mahyari, E., Guo, J., Lima, A. C., Lewinsohn, D. P., Stendahl, A. M., Vigh-Conrad, K. A., Nie, X., Nagirnaja, L., **Rockweiler, N. B.**, Carrell, D. T., Hotaling, J. M., Aston, K. I., Conrad, D. F. (2021). Comparative single-cell analysis of biopsies clarifies pathogenic mechanisms in Klinefelter syndrome. *American Journal of Human Genetics*, 108, 1924–1945. <https://doi.org/10.1016/j.ajhg.2021.09.001>
7. Nagirnaja, L., Leon-Ricardo, B., **Rockweiler, N. B.**, Ramu, A., Noordam, M., Wong, W. S., Carrell, D., Aston, K. I., & Conrad, D.F. Detection and quantification of human germline mosaicism. *In preparation*.
6. Zhou, J., Sears, R. L., Xing, X., Zhang, B., Li, D., **Rockweiler, N. B.**, ..., Wang, T. (2017). Tissue-specific DNA methylation is conserved across human, mouse, and rat, and driven by primary sequence conservation. *BMC Genomics*, 18(1), 724. <https://doi.org/10.1186/s12864-017-4115-6>
5. Sankar, S., Yellajoshyula, D., Zhang, B., Teets, B., **Rockweiler, N. B.**, & Kroll, K. L. (2016). Gene regulatory networks in neural cell fate acquisition from genome-wide chromatin association of Geminin and Zic1. *Scientific Reports*, 6(November), 37412. <https://doi.org/10.1038/srep37412>
4. **Roadmap Epigenomics Consortium**, et al. (2015). Integrative analysis of 111 reference human epigenomes. *Nature*, 518, 317–330. <https://doi.org/10.1038/nature14248>
3. Zhou, X., Li, D., Zhang, B., Lowdon, R. F., **Rockweiler, N. B.**, Sears, R. L., ..., Wang, T. (2015). Epigenomic annotation of genetic variants using the Roadmap Epigenome Browser. *Nature Biotechnology*, 33(4), 345–346. <https://doi.org/10.1038/nbt.3158>
2. Taylor, C. M., **Rockweiler, N. B.**, Liu, C., Rikimaru, L., Tunemalm, A.-K., Kisselev, O. G., & Marshall, G. R. (2010). Using ligand-based virtual screening to allosterically stabilize the activated state of a GPCR. *Chemical Biology & Drug Design*, 75(3), 325–32. <https://doi.org/10.1111/j.1747-0285.2009.00944.x>
1. Kennedy, S. M., Ji, Z., **Rockweiler, N. B.**, Hahn, A. R., Booske, J. H., & Hagness, S. C. (2009). The Role of Plasmalemmal-Cortical Anchoring on the Stability of Transmembrane Electropores. *IEEE Transactions on Dielectrics and Electrical Insulation: A Publication of the IEEE Dielectrics and Electrical Insulation Society*, 16(5), 1251–1258. <https://doi.org/10.1109/TDEI.2009.5293935>

PRESENTATIONS*Invited presentations*

- **Rockweiler, N. B.**, Sears, R. L., Meuleman, W., & Wang, T. “Epigenomics 2016 Workshop.” *Epigenomics 2016*, Rio Grande, PR, Feb 2016.
Workshop materials: <http://epigenomegateway.wustl.edu/support/workshop2016Epigenomics.html>
- **Rockweiler, N. B.**, Sears, R. L., & Wang, T. “Roadmap Epigenomics Workshop.” *The 1st International Epigenomics Conference*, Shanghai, China, Oct 2015.
Workshop materials: <http://epigenomegateway.wustl.edu/support/workshop2015IEC.html>
- **Rockweiler, N. B.**, Wang, T. “Expanding the DNA alphabet: computational integration of DNA methylation and hydroxymethylation.” Department of Genetics seminar, Washington University School of Medicine, St. Louis, MO, Oct 2016.

Selected by PhD program directors to give seminar for PhD recruits for 2 years*Selected presentations*

- **Rockweiler, N. B.**, Ramu, A., Gelfand, E., Drubin, C., Ardlie K., Huang, N., Kunisaki, J., Griffith, M., The GTEx Consortium, & Conrad, D. F. Whole-body maps of postzygotic mutations in 964 normal individuals. *The 12th Leena Peltonen School of Human Genomics*, Les Diablerets, Switzerland, August 2019.

- **Rockweiler, N. B.**, Ramu, A., Gelfand, E., Drubin, C., Ardlie K., The GTEx Consortium, & Conrad, D. F. "Whole-body Maps of Postzygotic Mutations in Humans." *The 2019 Biology of Genomes Annual Meeting*, Cold Spring Harbor, NY, May 2019.
Tweets: <https://tinyurl.com/bog19-rockweiler>
- **Rockweiler, N. B.**, Ramu, A., Gelfand, E., Drubin, C., Ardlie K., The GTEx Consortium, & Conrad, D. F. "Whole-body Maps of Somatic Mutations." *Molecular Genetics and Genomics, Computational and Systems Biology, and Human Statistical Genetics Annual Retreat*, Potosi, MO, Sept 2017.
Awarded best graduate student talk
- **Rockweiler, N. B.**, Ramu, A., Gelfand, E., Drubin, C., Ardlie K., The GTEx Consortium, & Conrad, D. F. "Whole-body Maps of Somatic Point Mutations in 550 Healthy Individuals." *The 2017 NHGRI Research Training and Career Development Annual Meeting*, St. Louis, MO, April 2017.

POSTERS

- **Rockweiler, N. B.**, Ramu, A., Gelfand, E., Drubin, C., Ardlie K., Huang, N., Kunisaki, J., Griffith, M., The GTEx Consortium, & Conrad, D. F. "Whole-body maps of postzygotic mutations in normal humans." *The 2019 NHGRI Research Training and Career Development Annual Meeting*, St. Louis, MO, April 2019.
- **Rockweiler, N. B.**, Ramu, A., Gelfand, E., Drubin, C., Huang, N., Kunisaki, J., Griffith, M., Ardlie K., The GTEx Consortium, & Conrad, D. F. "Whole-body Maps of Somatic Mutations in Humans." *The 2018 NHGRI Research Training and Career Development Annual Meeting*, Los Angeles, CA, March 2018.
- **Rockweiler, N. B.**, Ramu, A., Gelfand, E., Drubin, C., Ardlie K., The GTEx Consortium, & Conrad, D. F. "Whole-body Maps of Somatic Mutations in 550 Healthy Individuals." *The 2017 Washington University Graduate Research Symposium*, St. Louis, MO, Feb 2017.
- **Rockweiler, N. B.**, Zhou, X., Li D., Zhang, B., Lowdon, R. F., Zhang, B., Lowdon, R. F., & Wang, T. "Epigenomic annotation of genetic variants using the Roadmap EpiGenome Browser." *The 2015 Cold Spring Harbor Laboratory Biology of Genomes*, Cold Spring Harbor Laboratory, NY, May 2015 and *The American Society for Biochemistry and Molecular Biology Evolution and Core Processes in Gene Regulation*, St. Louis, MO, June 2015.
- **Rockweiler, N. B.**, Taylor, C. M., Liu, C., Kisselev, O. G., & Marshall, G. R. "Using ligand-based virtual screening to modulate rhodopsin-transducin interaction." *The 38th Great Lakes Regional Meeting of the American Chemical Society*, Chicago, IL, May 2009 and *Washington University Undergraduate Research Symposium*, St. Louis, MO, Oct 2009.
- Kennedy, S. M., Ji, Z., **Rockweiler, N. B.**, Hahn, A. R., Booske, J. H., & Hagness, S. C. "A locally constrained surface tension model based on cortical anchoring predicts stable electropore development." *The 31st Annual Bioelectromagnetics Society Meeting*, Davos, Switzerland, June 2009.

TEACHING EXPERIENCE

- **Scientific communication & graduate school preparation course, designed and taught a summer course for underrepresented minorities through the Opportunities in Genomics Research program at the McDonnell Genome Institute** 2019
- The Teaching Citation Program at Washington University in St. Louis, *participant* 2013-2021
- Washington University in St. Louis graduate coursework and Becker Library workshops on scientific computing, *consultant* 2015-2021
- Washington University in St. Louis, Bio4933: Molecular Biology on the Cutting Edge, *guest lecturer* 2016-2018
- WU Center for the Integration of Research, Teaching, and Learning, *associate* 2017-2018
- The WU Teaching Center Course Design Institute, *participant* 2018
- **Bioinformatics Workshop, developed and taught a three-day bioinformatics workshop for scientists at Washington University in St. Louis** 2015
 - Course website: http://nrockweiler.github.io/bioinformatics_wkshp_washu/index.html
- Initiative for Maximizing Student Development, *programming and bioinformatics tutor* 2015-2016
- Washington University in St. Louis, *teaching assistant*

- Bio5488: Genomics (head teaching assistant) 2015-2016
- Bio5075: Fundamentals of Biostatistics for Graduate Students 2016
- Bio5495: Algorithms for Computational Biology 2013
- ESE330: Electromagnetic Principles 2009
- Bio2970: Principles of Biology II 2008
- Washington University in St. Louis School of Engineering and Applied Science tutoring program, *tutor for undergraduate STEM courses and Calculus Help Room* 2007-2011

MENTORING EXPERIENCE

- Washington University in St. Louis, undergraduate: *Algorithms for imputing methylation levels in transposable elements using bisulfite sequencing data* 2015
- University of Missouri-St. Louis' Students and Teachers as Research Scientists, high school student: *Ligand-based virtual screening of the rhodopsin-transducin interaction* 2008

SERVICE AND LEADERSHIP EXPERIENCE

Academic

- Annual Broad Institute Retreat, *organizer* 2023-present
- Medical and Population Genetics Scientific Retreat at the Broad Institute, *organizer* 2023
- Symposium for the Opportunities in Genomics Research program at the McDonnell Genome Institute, *judge* 2019
- The Teaching Center Graduate Student Advisory Group, *member* 2017-2019
- WUSTL Future Educators, *executive board member* 2016-2017
- Department of Genetics faculty search committee, *graduate student ambassador* 2016-2021
- **Young Scientists Program, Co-Director of IT and founder of the Robotics Teaching Team** 2013-2016
- Computational and Systems Biology Student Run Seminar, *organizer* 2014-2015
- Regional Business Council Mentor Network, *mentored by Colonel Lawrence Riddles* 2009-2010
- Tau Beta Pi Engineering Honor Society, *secretary* 2008-2010

Community

- Washington University in St. Louis LEAD Initiative, a network of emerging alumni leaders, *invited panelist and member* 2019-present
- Girls on the Run, *assistant coach* 2015-2017
- American Eskimo Rescue of St. Louis, *volunteer* 2014-2021
- Dent County Animal Welfare Society, *volunteer* 2010-2021
- Washington University in St. Louis Symphony and Chamber Orchestras and chamber music ensembles, *first violinist* 2007-2009

ADVANCED COURSEWORK

Graduate school

Machine Learning; Algorithms for Computational Biology; Genomics; Genetics and Genomics of Disease; Statistical Computation

Undergraduate

Biomedical Engineering Design; Engineering Math; Kinetics of Receptor-Mediated Processes; Numerical Applied Mathematics; Principles of Protein Structure; Protein Function and Interactions; Quantitative Physiology; Statistical Thermodynamics and Kinetics; Web Development

COMPUTER SKILLS

Programming

Python; R; Perl; C; Bash; SAS; Matlab; Java; Mathematica; VBA; WDL

Bioinformatics

Google Cloud Platform; Docker; Bowtie; Novoalign; BLAST; ClustalW2; Tophat; Cufflinks; EdgeR; MACS; Samtools; Bedtools; VCFtools; Picard; GATK; MySQL; BioPerl; Bioconductor; MEME suite; UCSC Genome Browser; WashU Epigenome Browser; Galaxy (system administrator & end-user); Annovar; SeattleSeq; Sybyl; Partek; Maestro; VMD; Chimera; ImageJ; Autodoc

Web

Django; Jekyll; HTML; CSS; Javascript

Version control

Git; SVN; Github; Bitbucket

Office

Microsoft Works; OpenOffice; Google Docs; LaTeX; Vim

Systems

Linux; Windows; Mac OS

REFERENCES

Don F. Conrad, Ph.D.

Associate Professor and Chief

Division of Genetics

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Department of Molecular & Medical Genetics

Oregon Health & Science University

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