

# 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, *summa cum laude*  
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., Yellajoshiyula, 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 1<sup>st</sup> 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 12<sup>th</sup> 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 38<sup>th</sup> 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 31<sup>st</sup> Annual Bioelectromagnetics Society Meeting*, Davos, Switzerland, June 2009.

## TEACHING EXPERIENCE

- Research Mentoring Training program through the [Center for the Improvement of Mentored Experiences in Research \(CIMER\)](#), *participant* 2023
- **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](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

Oregon National Primate Research Center

Department of Molecular & Medical Genetics

Oregon Health & Science University

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Email: [conradon@ohsu.edu](mailto:conradon@ohsu.edu)

Barak A. Cohen, Ph.D.

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Washington University School of Medicine

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Paul Cliften, Ph.D.

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