

William J. Rowell

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<http://wirowell.info> • <http://github.com/williamrowell>

Skills and Qualifications

Computational: shell scripting, HPC clusters & version control • Python, Jupyter, NumPy, pandas & Matplotlib • reproducible analysis • next generation sequencing and third generation sequencing applications, including whole genome sequencing, targeted sequencing, RNASeq, and Iso-Seq • interpreting the quality of sequencing data • bioinformatic tools including BWA, Bowtie, STAR, GATK, minimap2, samtools, bedtools, bcftools, whatshap • designing and maintaining production grade bioinformatics analysis workflows • 20 years of experience administering home Linux servers and workstations

Molecular biology and genetics: quality control, critical interpretation & troubleshooting problems with NGS data • nucleic acid isolation, manipulation, cloning & analysis • RNA in situ hybridization & visualization • bacterial genetics, fruit fly husbandry & classical eukaryotic genetics

Technical: adapting techniques, off-the-shelf products & custom hardware and software • experimental design & protocol refinement • equipment testing, calibration & maintenance • logistics for high-throughput operation • wide field microscopy & confocal fluorescence microscopy • image acquisition & analysis

Professional: proven track record in collaborative science • determined problem solver & data-driven process improvement • training researchers in biological techniques & laboratory management skills • training researchers in introductory programming & best practices • liaising and translating between research staff & operations staff • consulting for sales, project managers & clients • presenting data in written & oral formats

Professional Experience

Sr Scientist, Bioinformatics [Pacific Biosciences of California](#) Feb 2017 — Present

Department: Bioinformatics Applications Team

Description: I work with customers and internal teams to develop new or improve existing applications and analysis workflows for single molecule, long-read sequencing. I help my associates in sales and marketing turn proof of principle or pilot experiments into equipment sales or marketing collateral.

Accomplishments: developed workflow for phasing of targeted capture long-read sequencing data • collaborated with wet lab scientists to improve targeted capture sequencing protocols • provided data analysis solutions and expertise for multiple targeted sequencing collaborations

Scientific Programmer [Q² Solutions | EA Genomics](#) Sep 2015 – Feb 2017

Department: Lab Operations - Bioinformatics Data Services

Description: I delivered high-quality next-generation sequencing data to our clients in a timely manner.

Accomplishments: guided the development of delivery and analysis pipeline enhancements • developed tools for tracking tasks and errors • data-driven process improvement • provided exceptional customer service

Consulting Research Specialist [Howard Hughes Medical Institute, Janelia Research Campus](#) Sep 2015 – Feb 2017

Research Specialist I (2013 – 2015) • **Research Technician III** (2011 – 2013) • **Research Technician II** (2010 – 2011)

Department: [Project Technical Resources](#) (2012 – 2015)

Description: I supported the research of the project teams and labs at Janelia by providing consultation, conducting experiments, analyzing data, and writing software.

Accomplishments: acted as liaison and translator between different disciplines • screened over 200 *Drosophila melanogaster* lines through high-throughput locomotor/optomotor/phototaxis assay • screened over 300 *D. melanogaster* lines through high-throughput olfactory assay • curated and analyzed data and metadata • aided in design of novel behavioral assays, including instrument design and testing, protocol refinement, and data analysis tools • wrote suite of tools for analysis of *D. melanogaster* activity/sleep data • wrote and maintained automated pipeline for fluorescence imagery analysis

Department: [Fly Olympiad Team Project](#) (2010 – 2012)

Description: I investigated the role of individual neurons or groups of neurons in altering behavior by screening *Drosophila melanogaster* lines through high-throughput behavioral assays.

Accomplishments: acted as liaison and translator between different disciplines in large-scale scientific collaboration • screened over 2000 *D. melanogaster* lines through high-throughput locomotor/optomotor/phototaxis assay • aided in establishing guidelines for storing data and metadata • curated and analyzed data and metadata • aided in establishing a more flexible scheme for describing line nomenclature and relationships

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Education

MA Molecular and Cell Biology	University of California, Berkeley	May 2012
BS Biology with minor in Chemistry	University of North Carolina, Chapel Hill	May 2002

Related Experience

Contributor	Genome in a Bottle Consortium	2018 – Present
Contribute data and analysis to develop reference materials and methods for human genome sequence analysis.		
Volunteer Instructor	Software Carpentry	2013 – Present
George Washington University	Ashburn, VA	April 2014
Howard Hughes Medical Institute	Ashburn, VA	July 2014
Conduct on-site workshops to train researchers in core software skills to improve their efficacy, such as use of the Unix shell and Python for data analysis.		
Instructor	Introduction to Python Programming	March 2015, July 2015
Howard Hughes Medical Institute	Ashburn, VA	
Organized, planned curriculum, wrote lessons, and led instruction for class tailored to the needs of JRC researchers.		

Publications

Wenger AM, Peluso P, **Rowell WJ**, Chang P-C, Hall RJ, Concepcion GT, Ebler J, Fungtammasan A, Kolesnikov A, Olson ND, Töpfer A, Along M, Mahmoud M, Qian Y, Chin C-S, Phillippy AM, Schatz MC, Myers G, DePristo MA, Ruan J, Marschall T, Sedlazeck FJ, Zook JM, Li H, Koren S, Carroll A, Rank DR, Hunkapiller MW. 2019. Accurate circular consensus long-read sequencing improves variant detection and assembly of a human genome. *Nat. Biotechnol.* 74:1-13. [doi:10.1038/s41587-019-0217-9](https://doi.org/10.1038/s41587-019-0217-9)

Tseng E, **Rowell WJ**, Glenn O-C, Hon T, Barrera J, Kujawa S, and Chiba-Falek O. 2019. The Landscape of *SNCA* Transcripts Across Synucleinopathies: New Insights From Long Reads Sequencing Analysis. *Front. Genet.* 10:354-359. [doi:10.3389/fgene.2019.00584](https://doi.org/10.3389/fgene.2019.00584)

Aso Y, Sitaraman D, Ichinose T, Kaun K, Vogt K, Belliard-Guérin G, Plaçais P, Robie A, Yamagata N, Schnaitmann C, **Rowell WJ**, Johnston RM, Ngo TT, Chen N, Korff W, Nitabach MN, Heberlein U, Preat T, Branson K, Tanimoto H, Rubin GM. 2014. Mushroom body output neurons encode valence and guide memory-based action selection in *Drosophila*. *eLife* 3:e04580. [doi:10.7554/eLife.04580](https://doi.org/10.7554/eLife.04580)

Senger K, Armstrong GW, **Rowell WJ**, Kwan JM, Markstein M, Levine M. 2004. Immunity regulatory DNAs share common organizational features in *Drosophila*. *Mol. Cell* 13:19–32. [doi:10.1016/S1097-2765\(03\)00500-8](https://doi.org/10.1016/S1097-2765(03)00500-8)

Selected Talks and Posters

Rowell WJ, Wenger AM, Kolesnikov A, Chang P-C, Carroll A, Hall RJ, Peluso P. (Poster 16.85A) Comprehensive variant detection in a human genome with highly accurate long reads. European Human Genetics Conference. Gothenburg, Sweden. June 15-18, 2019.

Rowell WJ. (Talk) Advantages of HiFi reads for variant discovery and genome assembly. SMRTLeiden SMRT Scientific Symposium. Leiden Netherlands. May 8, 2019.

Fijneman RJA, Mekkes N, van den Broek E, Stringer B, Glas RA, Komor MA, Rausch C, van Lieshout S, Cuppen E, Smith ML, Sebra RP, **Rowell WJ**, Ashby M, Carvalho B, Heringa J, Meijer GA, Abeln S. (Poster 1738) Characterization of structural variants within MACROD2 in the pathogenesis of colorectal cancer. American Society for Cancer Research Annual Meeting. Atlanta, GA, United States. Mar 29-Apr 3, 2019.

Rowell WJ, Peluso P, Harting J, Qian Y, Wenger AM, Hall RJ, Rank DR. (Poster) Comprehensive Variant Detection in a Human Genome with PacBio High-Fidelity Reads. CSH Biological Data Science Meeting. Cold Spring Harbor, NY, United States. Nov 7-9, 2018.

Professional Enrichment

- Lean Six Sigma Yellow Belt training (2016), Q2 Solutions.
- High Functioning Leadership Program (2012), Janelia Research Campus.