

JESSICA WOOLNOUGH, Ph.D.

woolnoughjl@gmail.com | 321-266-0125 | Brookline, MA | linkedin.com/in/jessica-woolnough

SUMMARY

Computational and molecular biologist with a combined 7 years of hands-on experience in academia executing bioinformatic and experimental approaches in the fields of genetics and epigenetics.

- 7 years experience analyzing genomics data
- 3 years experience using R for genomics analysis, statistical analysis, and visualization
- In-depth knowledge of molecular biology, epigenetics, and genomics in the context of human disease

WORK EXPERIENCE

Postdoctoral Research Fellow (2016-present)

Mitzi Kuroda Lab | Harvard Medical School | Boston, MA

- Constructed a variant calling pipeline for Amplicon-seq data and executed Variant Allele Frequency (VAF) analysis critical for findings published in a recent manuscript from a collaborating lab. ¹
- Executed genome-wide profiling of key chromatin factors by ChIP-seq in human embryonic stem cells. ²
- Uncovered the existence of bivalent genes in a fly genetic model by developing and executing an innovative analytical approach centered on transcription start sites with the strongest Polycomb binding. This approach revealed previously undiscovered bivalent genes in the developing fly. ²
- Constructed bootstrapping analysis for statistical significance testing and used basic machine learning approaches (e.g. clustering) to dissect the defining genomic features of 'megadomains' that form in a subset of carcinomas.
- Constructed a Bash script, used widely in the lab, to collapse transcript annotations (based on a desired feature) to 'gene' annotations which contain a single line per unique transcription start site (e.g. collapse transcripts to gene outputting coordinates of the longest transcript).
- Integrated ChIP-seq and RNA-seq data from a collaborating lab to reveal functional consequences and targets of specific HDAC inhibitors in cancer.

Ph.D. student (2011-2016)

Keith Giles Lab | University of Alabama at Birmingham | Birmingham, AL

- Executed ChIP-seq, RNA-seq, statistical analysis of genomics data, and traditional molecular biology techniques that were critical for publication of four manuscripts. ^{3,4,6,8}
- Constructed Bash scripts to transform raw NGS data into metagene plots and binding profile heatmaps that were used in two published manuscripts. ^{6,8}
- Constructed Bash scripts for bootstrapping analysis of genomics data. ⁶
- Championed and introduced the use of R for statistical analysis and visualization in the lab.
- Authored and maintained user-friendly computational workflows for ChIP-seq and RNA-seq analysis used by numerous colleagues throughout the department.

SKILLS

Bioinformatics skills

- Extensive experience with design and execution of genomics experiments (e.g. ChIP-seq, RNA-seq)
- Extensive experience analyzing genomics data (e.g. quality control, sequence alignment, peak calling, variant calling, data manipulation, data format conversion)

- Extensive experience summarizing and visualizing genomics data (e.g. metagene profiles, heatmaps, volcano plots, box-and-whisker plots, correlation plots, VAF distributions, GO analysis)
- Extensive experience acquiring/analyzing publicly available data (e.g. GEO, UCSC, Roadmap, NCBI)
- Experience with statistical analysis of biological data (e.g. clustering, correlation, bootstrapping, regression, significance tests for parametric and non-parametric data)
- Experience with R/Bioconductor for a wide-range of genomics analyses, statistical analyses, and plotting
- Experience keeping notes using R Markdowns

Computational skills

- Experience in Linux/UNIX environment
- Experience with languages: R, Bash, AWK, sed
- Experience using high performance computing clusters (O2 at HMS, Cheaha at UAB)

Experimental skills

- Extensive experience with mammalian cell culture (including human embryonic stem cells)
- Extensive experience with NGS approaches and library preparation
- Extensive experience with basic molecular biology techniques (cloning, PCR, Western blotting, ChIP)

Soft skills

- Initiated and established collaborations with many researchers from diverse fields throughout career ^{1,8}
- Sought out by colleagues of all ranks for subject matter expertise and hands-on help with genomics
- Presented original research and was awarded “best presentation” at multiple meetings/conferences

EDUCATION

| | |
|--|-----------|
| Ph.D. in Biochemistry and Molecular Genetics University of Alabama at Birmingham (UAB), Birmingham, AL | 2011-2016 |
| Bachelor of Science in Biochemistry Auburn University, Auburn, AL | 2007-2011 |

PUBLICATIONS

Published under Makofske JL and Woolnough JL

1. Chu SH, Song EJ, Chabon JR, Minehart J, Matovina CN, **Makofske JL**, Frank ES, Ross K, Koche RP, Feng Z, Xu H, Krivtsov A, Nussenzweig A, Armstrong SA. (2018). Inhibition of MEK and ATR is effective in a B-cell Acute Lymphoblastic Leukemia model driven by MLL-Af4 and activated Ras. *Blood Adv.* 2018 Oct 9. PMID: 30266823
2. Kang H, Jung YL, McElroy KA, Zee BM, Wallace HA, **Woolnough JL**, Park PJ, Kuroda MI (2017). Bivalent complexes of PRC1 with orthologs of BRD4 and MOZ/MORF target developmental genes in Drosophila. *Genes & Dev.* 2017 Oct 1. PMCID: PMC5710143
3. **Woolnough JL**, Atwood BL, Liu Z, Zhao R, Giles KE (2016). The Regulation of rRNA Gene Transcription during Directed Differentiation of Human Embryonic Stem Cells. *PLoS One.* 2016 Jun 14. PMCID: PMC4907514
4. Atwood BL, **Woolnough JL**, Lefevre GM, Saint Just Ribeiro M, Felsenfeld G, Giles KE. (2016). Human Argonaute 2 is tethered to ribosomal RNA through microRNA interactions. *J Biol Chem.* 2016 Jun 10. PMCID: PMC5016180
5. Giles KE, **Woolnough JL**, Atwood BL (2015). Epigenetic Gene Regulation and Expression: ncRNA function in chromatin organization (Elsevier, San Diego, CA, 2015), Book chapter p. 117-142.
6. **Woolnough JL**, Atwood BL, Giles KE (2015). Argonaute 2 binds directly to tRNA genes and promotes gene repression in cis. *Mol Cell Biol.* Spotlight Article. 2015 Jul. PMCID: PMC4456445
7. Daniels JB, Scofield J, **Woolnough JL**, Silo-Suh L. (2014). Impact of glycerol-3-phosphate dehydrogenase on virulence factor production by *Pseudomonas aeruginosa*. *Can J Microbiol.* 2014 Dec. PMID: 25409940
8. Yang W, Lee YH, Jones AE, **Woolnough JL**, Zhou D, Dai Q, Wu Q, Giles KE, Townes TM, Wang H (2014). The histone H2A deubiquitinase USP16 regulates embryonic stem cell gene expression and differentiation. *Nat Commun.* 2014 May 2. PMCID: PMC4060806