

Jenny Leopoldina Smith, MSc

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Bioinformatician and R programmer applying methods in data science to biomedical research questions with expertise in next generation sequencing (NGS) data.

Research and Work Experience

Bioinformatician, Fred Hutchinson Cancer Research Center, *Seattle, WA*

January 2017 - Current

- Principal Investigator: Dr. Soheil Meshinchi
- Transcriptional profiling of pediatric acute myeloid leukemia using RNA-sequencing with supervised and unsupervised clustering ML algorithms, as well as statistical regression and classification, in a multidisciplinary and collaborative environment with molecular biologists, bioinformaticians, and lead investigators.
- Production of complex visualizations of sequencing and mutation data including heatmaps, circos plots, oncoprints, 3D scatter plots, genomic tracks, network graphs, and volcano plots, among others to identify actionable biological insights and gene targets from multivariate biological datasets derived from NGS and public databases such as NCBI and Ensembl using R and Rmarkdown.
- Development of genomics workflows for cloud computing on AWS using Nextflow for processing raw RNA-seq data for gene expression quantification and fusion detection.

Postbaccalaureate Fellow, National Institutes of Health, *Bethesda, MD*

June 2014 - July 2016

- Principal Investigator: Dr. Maria Morasso
- Conducted biomedical research on the function of homeodomain protein DLX3 at NIAMS. Bioinformatics analysis of ATAC-seq and ChIP-seq from murine mouse models using command line tools for genomic alignment, MACS peak calling, motif analysis, NGS.plot, and Deeptools.

Science Teacher, Agua Fria High School, *Avondale, AZ*

June 2012 - May 2014

- Teach For America Phoenix corps member; certified for secondary biology and chemistry education. Courses taught: general biology, AP biology, general chemistry and integrated science.

Research Assistant, University of San Diego, *San Diego, CA*

August 2009 - May 2012

- Principal Investigator: Dr. Terry Bird
- Investigated the role of CHPT in the cellular differentiation of the bacterium *Rhodospirillum centenum* by utilizing site-directed mutagenesis.

Education

Applied Bioinformatics and Genomics, M.Sc. June 2016 – September 2017
University of Oregon, *Eugene, OR*

Secondary Education in Science, M.Ed. August 2012 – May 2014
Arizona State University, *Phoenix, AZ*

Biology, B.A., magna cum laude August 2008 – May 2012
University of San Diego, *San Diego, CA*

Experience with NGS Data

- RNA-sequencing – Illumina
- RNA-sequencing – PacBio
- miRNA-seq
- ChIP-seq
- ATAC-seq

Bioinformatics and Statistics

- Unsupervised clustering with dendrograms, PCA, NMDS, and UMAP
- Statistical regression, classification, regularization
- Differential gene expression with Limma and EdgeR
- Survival and time-to-event analysis
- Data visualization with ggplot2, ComplexHeatmap, plotly R, and Gviz

Experience with Software

- Github Version Control
- R programming: base R and Tidyverse
- R package development
- Bash shell scripting
- SLURM on-prem HPC job scheduler
- Amazon Web Services: AWS S3 and Batch
- Nextflow Bioinformatics workflows on AWS
- Python programming
- MultiQC and FastQC for NGS quality control
- Genomic alignments: STAR-aligner and Bowtie
- Fusion detection algorithms for RNA-seq: STAR-Fusion
- Long-read RNA-seq (PacBio) transcriptional profiling with Isoseq3 pipeline

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Publications

- Huang, B., **Smith, J. L.**, Wang, J., Taghizadeh, K., ... Meshinchi, S. *CBFB-MYH11* Fusion Transcripts Distinguish Acute Myeloid Leukemias with Distinct Molecular Landscapes and Outcomes. *Blood Advances* **2021**. DOI: 10.1182/bloodadvances.2021004965
- Chisholm, K., Heerema-McKenney, A., Choi, J., **Smith, J.L.** ... Kahwash, B. Acute erythroid leukemia is enriched in NUP98 fusions: a report from the Children's Oncology Group. *Blood Advances* **2020**. DOI: 10.1182/bloodadvances.2020002712
- Noort, S., Wander, P., Alonzo, T. A., **Smith, J.L.**, ... Meshinchi, S. The clinical and biological characteristics of NUP98-KDM5A in pediatric acute myeloid leukemia. *Haematologica* **2020**. DOI: 10.3324/haematol.2019.236745
- **Smith, J. L.**, Ries, R. E., Hylkema, T., Alonzo, T. A., ... Meshinchi, S. Comprehensive Transcriptome Profiling of Cryptic CBFA2T3-GLIS2 Fusion-positive AML Defines Novel Therapeutic Options – A COG and TARGET Pediatric AML Study. *Clinical Cancer Research* **2019**. DOI: 10.1158/1078-0432.CCR-19-1800
- **Smith, J.L.**, Maden S. K., Lee, D., Buie, R., ... Busby, B. Consensus Machine Learning for Gene Target Selection in Pediatric AML Risk. *bioRxiv* **2019**. DOI: 10.1101/632166
- Noort, S., Zimmermann, M., Reinhardt, D., Cuccuini, W., Pigazzi, M., **Smith, J.**, ... Zwaan, C. M. Prognostic impact of t(16;21)(p11;q22) and t(16;21)(q24;q22) in pediatric AML: a retrospective study by the I-BFM Study Group. *Blood* **2018**. DOI: 10.1182/blood-2018-05-849059

Additional Publications: <https://orcid.org/0000-0003-0402-2779>

Presentations

- **American Society for Hematology**, poster on ETS Family Transcription Factor Fusions in Childhood AML: Distinct Expression Networks and Clinical Implications (Virtual, 2021).
- **American Society for Hematology**, poster on The Transcriptomic Landscape of NUP98-Rearranged Pediatric Acute Myeloid Leukemia (Virtual, 2020).
- **Molecular Medicine Tri-conference**, panelist on AI in Genomics and Precision Medicine (San Francisco, CA, 2020).
- **American Society for Hematology**, poster on Long Non-Coding RNAs (lncRNAs) Are Highly Associated with Disease Characteristics and Outcome in Pediatric Acute Myeloid Leukemia - a COG and Tpm1 Study (Orlando, FL, 2019).
- **Brotman Baty Pediatric Sequencing Symposium**, oral presentation on Long Non-coding RNAs Associate with Outcome in Pediatric Acute Myeloid Leukemia (Seattle, WA, 2019).
- **American Society for Hematology**, oral presentation on Comprehensive Transcriptome Profiling of Cryptic *CBFA2T3-GLIS2* Fusion-Positive AML Defines Novel Therapeutic Options — a COG and Target Pediatric AML Study (San Diego, CA, 2018).
- **American Society for Hematology**, oral presentation on The LSC17 Leukemic Stem Cell Signature Predicts Outcome in Pediatric Acute Myeloid Leukemia. Abstract Achievement Award Recipient (Atlanta, GA, 2017).

- HOMER motif analysis for ChIP-seq
- Differential peak binding identification for ChIP-seq: DiffBind R

Continuing Education and Volunteering

- SnpReportR package, Carnegie Mellon and DNAnexus Hackathon, January 2021
- RLadies, Seattle, WA 2018-2021
- Pacific Biosciences Isoseq Transcriptome Analysis Training, July 2020
- Nextflow workflow development training, May 2020
- Women In Biology, MAPS Mentorship Group, 2017-2019
- ConsensusML, Machine learning classification in AML, NCBI Hackathon February 2018
- Fred Hutch Summer High School Internship Mentor, June-August 2018
- Summer Institute in Statistics for Big Data (SISBID), University of Washington, June 2017