COLTON ROBBINS

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BIOINFORMATICS SCIENTIST

Dedicated and detail-oriented biological scientist with over 7 years of experience in molecular biology and genetic research, seeking to leverage extensive background in data analysis and biological systems into a challenging bioinformatics role. Proficient in handling large transcriptomic datasets using cluster computing and statistical software. Eager to apply a robust foundation in computational biology and a proven track record of research publication and product development to drive innovation and discovery in a dynamic bioinformatics environment.

TECHNICAL SKILLS

Spatial Transcriptomics | Single-Cell RNA-seq | Bulk RNA-seq Image Processing | Python | SQL | R | Cloud Computing | Git | Workflow management | Linux shell scripting | Next-Generation Sequencing | Data Visualization | Statistical Analysis

EXPERIENCE

FRED HUTCHINSON CANCER CENTER, Seattle, WA
Lab Technician II, March 2023 – January 2024
- Led experimental design and data analysis for several *in vivo* and *in vitro* based research projects.
- Full-length smart-seq2 isoform analysis of *in vitro* cancer lines exposed to chemotherapeutics.
- Created a multi-species tissue atlas from previous single-cell RNA-seq data to characterize Double Homeobox (Dux) expression profile in putative tissues.
- Utilized Slurm Linux cluster manager to align and process large transcriptomic datasets.
- Mammalian cell culture operations including transgenic line generation, knockdown assays, immunocytochemistry, and RT-qPCR.

NANOSTRING TECHNOLOGIES, Seattle, WA
Research Associate III, December 2021 – November 2022
- Product design and development of spatial biology technologies.
- Conducted and analyzed biweekly CosMx spatial biology experiments in mouse, human, healthy, and cancerous tissues.
- Wrote and maintained statistical analysis software to evaluate CosMx experimental performance.
- Authored several computer vision programs to batch process thousands of spatial biology images.
- Designed a department-wide fully automated SQL database capable of tracking and comparing several thousand historical experiments.
- Developed and tested novel molecular constructs that improved signal to noise detection rate of transcripts by 20%.
- Worked closely with a team of 4 biological scientists to help develop tissue-cleared gel expansion 3D spatial imaging technology.

WASHINGTON STATE UNIVERSITY, Pullman, WA
Graduate Student, September 2019 – August 2021
- Spearheaded the world's first developmental pig testis cell atlas with multi-species integration encompassing human and mouse data across 12 studies and ~50 single-cell RNA-seq libraries.
- Trained 6 graduate/undergraduate students on single-cell/bulk RNA-seq analysis.
- Utilized Kamiak Linux cluster manager to align and process large transcriptomic data sets.
- Conducted immunofluorescent labeling and RT-qPCR to corroborate large data findings.
- Conveyed scientific discoveries at team meetings, conferences, and seminars.

Lab Manager, June 2018 – September 2019

- Coordinated day-to-day operations to support short-term and long-term laboratory goals.
- Managed mouse colony of 300+ animals consisting of about 12 unique mutation strains.
- Supervised onboarding, training, and management of 4 lab technicians and graduate students.
- Organized and implemented an online lab inventory and ordering database.

Lab Technician, September 2016 – May 2018
- Provided experimental support for team members and maintained laboratory spaces
- Wrote automated cell finding R script for batch processing multi-channel microscopy images.
- Performed various biomolecular assays such as genotyping PCR, RNA isolation, RT-qPCR, and tissue dissection

EDUCATION

Master of Science (M.S) Molecular Biology
Washington State University, Pullman, WA

Bachelor of Science (B.S) in Biochemistry - magna cum laude
Washington State University, Pullman, WA

PUBLICATIONS

Ciccarelli, M., Giassetti, M. I., Miao, D., Oatley, M. J., **Robbins, C.**, Lopez-Biladeau, B   Oatley, J. M. (2020). **Donor-derived spermatogenesis following stem cell transplantation in sterile NANOS2 knockout males**. Proceedings of the National Academy of Sciences, 117(39), 24195-24204

Du, G., Oatley, M. J., Law, N. C., **Robbins, C.**, Wu, X., & Oatley, J. M. (2021). **Proper timing of a quiescence period in precursor Prospermatogonia is required for stem cell pool establishment in the male germline.** Development, 148(9)

PRESENTATIONS

Washington State University Center for Reproductive Biology Retreat
September 2019, Leavenworth, WA
Developmental origins of spermatogonial stem cells

Gordon Conference on Germinal Stem Cell Biology
May 2019, Sha Tin, Hong Kong
Relationship between Dppa5a expression and spermatogonial stem cell fate determination in fetal prospermatogonia