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| **COLTON ROBBINS** | Snohomish, Wa 98296 | **Portfolio-CMR.github.io/Directory/** |
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| **OBJECTIVE**  Results-oriented data specialist with 6+ years’ experience in analytical research. Skilled at identifying trends, patterns, and opportunities for improvement. Seeking a challenging role where I can make a meaningful impact on business outcomes. | **TECHNICAL SKILLS**  **Programming -** SQL, Python, R, Git, Linux, AWS  **Data visualization –** Tableau, Looker, Plotly  **Statistics -** Linear regression, Principle component analysis, Hypothesis testing, Machine Learning |

**EXPERIENCE**

**FRED HUTCHINSON CANCER CENTER**, Seattle, WA

**Research Data Specialist**, March 2023 – January 2024

* Improved cell-type classification by 20% by implementing machine learning models on large-scale biological datasets (500+ million data points).
* Reduced processing time for gene expression data sets from 2 hours down to 5 minutes through automated data pipelines using Python and R.
* Visualized real-time complex experimental data using interactive dashboards fed from 3 disparate SQL database sources connected to Tableau.
* Automated large dataset processing with AWS cloud computing in conjunction with workflow management software to achieve efficient and scalable data analysis.
* Presented technical research findings in over 40 weekly meetings and led discussions in 3 departmental meetings.
* Successfully managed 5 concurrent projects within a 6-month period, achieving a 100% completion rate.

**NANOSTRING TECHNOLOGIES**, Seattle, WA

**Computational Biologist**, December 2021 – November 2022

* Reduced assay failure response time by 25% through the development and deployment of a cloud-based SQL database for real-time quality control monitoring and anomaly detection.
* Accelerated time-to-insight by 70% and reduced human error by 10% through the engineering of end-to-end automated data analysis pipelines.
* Increased sensitivity and specificity of spatial molecular assays by 20% through rigorous statistical analysis (ANOVA, t-tests, regression modeling).
* Successfully developed and validated a novel spatial biology prototype, exceeding target performance metrics by 12% and accelerating the product's path to commercialization.
* Translated complex biological questions into actionable data analysis plans through effective collaboration with a team of 15+ biologists, engineers, chemists, and software developers.
* Boosted molecular detection efficiency by 10% by analyzing 100+ terabytes of spatial microscopy images using an automated Fast-Fourier Transform algorithm.
* Communicated key experimental findings to diverse audiences through the creation of interactive Tableau and Looker Studio dashboards, presented at over 20 bi-weekly team meetings and 2 quarterly departmental reviews.

**WASHINGTON STATE UNIVERSITY**, Pullman, WA

**Molecular Biologist**, September 2018 – August 2021

* Developed a novel classification pipeline that improved cell population segmentation accuracy by 18%, enabling more precise identification of rare cell types in multi-species datasets.
* Analyzed large biological datasets (e.g., 700+ million data points) using NumPy and Pandas, uncovering statistically significant gene expression patterns.
* Integrated automated cell counting software into existing data collection protocols, reducing manual data entry errors by 30% and improving data accuracy by 10%.

**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