COLTON ROBBINS

Data Analyst (5+ years)

+1 206-552-4365 www.linkedin.com/in/colton-robbins73

Coltonrobbins73@gmail.com

Seattle, WA

WORK EXPERIENCE

Data Analyst - Fred Hutch Cancer Research, Seattle, WA

Mar 2023 – Jan 2024

Skills: SQL, Python, PostgreSQL, Machine Learning, Multiple Linear Regression, Decision Trees, Cloud Computing

- Attained a 20% improvement in cell-type classification by implementing deep language models (scBERT transformer) on large-scale biological datasets (500+ million data points).
- Reduced processing time by 95% for RNA expression analysis through Python automation scripts, Slurm job scheduler, and workflow management software on high-performance computing clusters.
- Led 30 weekly meetings and 3 departmental meetings to discuss technical research findings and future directions using Tableau, Looker, and plotly visualizations.
- Saved \$80k annually by automating end-to-end single-cell analysis pipeline using the severse annual at toolkit executed on a 600GB memory high-performance computing cluster.
- Achieved 100% completion rate for 5 concurrent projects within a 6-month period.

Research Data Specialist - Nanostring Technologies, Seattle WA

Dec 2021 - Nov 2022

Skills: SQL, Python (Pandas, Scikit-learn, Plotly, OpenCV), MySQL, Tableau, ANOVA, Regression, Causal Inference

- Achieved 25% reduction in assay failure response time 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% through the development of Python-based automated data analysis pipelines leveraging pandas, scikit-learn, and Tableau visualization.
- Realized a 20% increase in sensitivity and specificity for spatial molecular assays through rigorous statistical analysis (ANOVA, t-tests, regression modeling) of spatial biology performance metrics.
- Automated analysis of 100+ terabytes of spatial microscopy images to directly quantify improvements to key protocol changes reducing product iteration intervals by 1-week on average; an estimated savings of 100k per year.
- Effectively translated \$500k budget for spatial biology prototype to first phase product delivery 6-weeks ahead of schedule while surpassing molecular detection efficiency requirements of 80%.

Computational Biologist – Washington State University, Pullman WA

Sep 2018 – Aug 2021

Skills: Python (Pandas, Scikit-learn, Matplotlib), R (Bioconducter, Ggplot2, Tidyverse), Regression, Hypothesis Testing

- Achieved a 20% improvement in cell-type classification on large multi-species multi-temporal single-cell data sets (e.g., 700+ million data points across 3 species across 15 time points).
- Reduced processing time by 40% for immunofluorescent cell counting by authoring automated image analysis software using ImageJ macros, R scripting, and Bioconducter packages.
- Saved ~\$2000 quarterly on lab reagents by integrating an online ordering database with direct vendor purchasing.
- Automated analysis on 200 core computing cluster to quickly align genomic sequencing fragments (300 GB memory).
- Trained and mentored 7 lab technicians in advanced laboratory protocols and computational methods.

EDUCATION

M.S in Molecular Biology – Washington State University, Pullman WA – Honors Distinction – GPA 3.96 / 4.00

Thesis Research Paper: Multi-Species and Multi-Dimensional Comparison of the Developmental Porcine Testis

Relevant coursework: Bioinformatics (Python, R. Unix), Advanced Genetics (Python, SOL, Unix)

B.S. in Biochemistry – Washington State University, Pullman WA – Magna Cum Laude – GPA 3.87 / 4.00 Relevant coursework: Statistics (Regression), Calculus, Introduction to Bioinformatics (Python, Perl)

CERTIFICATIONS

AWS cloud practitioner - 2024

PUBLICATIONS

<u>Donor-derived spermatogenesis following stem cell transplantation in sterile NANOS2 knockout males.</u> (2020) Proceedings of the National Academy of Sciences, 117(39), 24195-24204

<u>Proper timing of a quiescence period in precursor Prospermatogonia is required for stem cell pool establishment in the male germline.</u> (2021) Development, 148(9)