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Fairlie Reese

Bioinformatics PhD Candidate

github.com/fairliereese
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Education

PhD, Developmental and Cell Biology, *University of California, Irvine*, GPA: 3.988 2018-Present
MS, Developmental and Cell Biology, *University of California, Irvine*, GPA: 3.983 2018-2021
BS, Bioengineering: Bioinformatics, *University of California, San Diego*, GPA: 3.724, Cum Laude 2013-2017

Research experience

Graduate student in Developmental and Cell Biology **January 2019 - Present**
Advisor: Ali Mortazavi *Irvine, CA*

- *Currently developing and applying novel bioinformatic tools and analyses to both bulk and single-cell long-read RNA-seq datasets in a variety of biological systems and contexts as a part of the ENCODE consortium's effort to profile full-length transcriptomes in human and mouse.*

Rotation student in Microbiology and Molecular Genetics **October 2018 - December 2018**
Advisor: Klemens Hertel *Irvine, CA*

- *Investigated the relationship between alternative splicing rates and exon sequence and length conservation scores.*

Research associate in Acoustic Ecology **June 2016 - August 2018**
Advisor: Simone Baumann-Pickering *La Jolla, CA*

- *Developed computational tools and pipelines to analyze acoustic data.*

Publications

* These authors contributed equally

Published

1. **F Reese***, E Rebboah*, K Williams, G Balderrama-Gutierrez, C McGill, D Trout, I Rodriguez, H Liang, BJ Wold, and Ali Mortazavi. Mapping and modeling the genomic basis of differential RNA isoform expression at single-cell resolution with LR-Split-seq. *Genome Biology.* (2021).

2. A Krumpel, A Rice, KE Frasier, **F Reese**, JS Trickey, AE Simonis, JP Ryan, SM Wiggins, A Denzinger, H Schnitzler, and S Baumann-Pickering. Long-Term Patterns of Noise From Underwater Explosions and Their Relation to Fisheries in Southern California. *Frontiers Marine Science.* (2021).

3. JE Moore, X Zhang, SI Elhajjajy, K Fan, HE Pratt, **F Reese**, A Mortazavi, and Z Weng. Integration of high-resolution promoter profiling assays reveals novel, cell type-specific transcription start sites across 115 human cell and tissue types. *Genome Research.* (2021).

4. **F Reese**, and A Mortazavi. Swan: a library for the analysis and visualization of long-read transcriptomes. *Bioinformatics.* (2020).

5. M Movassat, E Forouzmand, **F Reese**, KJ Hertel. Exon size and sequence conservation improves identification of splice-altering nucleotides. *RNA.* (2019).

In review / preparation

1. JE Childs, S Morabito, S Das, C Santelli, V Pham, K Kusche, V Alizo Vera, RR Campbell, DP Matheos, **F Reese**, A Mortazavi, V Swarup, and MA Wood. Medial Habenula *Nr4a2* is necessary for reinstatement of cocaine self-administration and related transcriptome changes identified using single nuclei RNA-seq. *Manuscript in preparation* (2022).

2. Z Liu, G Quinones-Valdez, T Fu, M Choudhury, **F Reese**, A Mortazavi, X Xiao. L-GIREMI uncovers RNA editing sites in long-read RNA-seq. *bioRχiv.* (2022).

3. **F Reese***, F Pardo-Palacios*, S Carbonell-Sala*, M Diekhans*, C Liang*, D Wang*, B Williams*, M Adams, A Behera, J Lagarde, H Li, A Prjibelski, G Balderrama-Gutierrez, MH Çelik, M De María, N Denslow, N Garcia-Reyero, S Goetz, M Hunter, J Loveland, C Menor, D Moraga, J Mudge, H Takahashi, A Tang, I Youngworth, P Carninci, R Guigó, H Tilgner, BJ Wold, C Vollmers, G Sheynkman, A Frankish, KF Au, A Conesa, A Mortazavi, and A Brooks. Systematic assessment of long-read RNA-seq methods for transcript identification and quantification. *Accepted registered report, Nature Methods.* (2021)

4. **F Reese***, D Wyman*, G Balderrama-Gutierrez*, S Jiang, S Rahmanian, S Forner, D Matheos, W Zeng, B Williams, D Trout, W England, S Chu, RC Spitale, AJ Tenner, BJ Wold, and A Mortazavi. A technology-agnostic long-read analysis pipeline for transcriptome discovery and quantification. *bioRχiv.* (2020).

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SOFTWARE

Swan
Swan is a Python library designed to visualize and analyze transcriptome data. It can produce traditional genome browser-style and graph-based transcript visualizations, perform differential expression testing on the gene and transcript level, call isoform / transcription start site / transcription end site switching events, detect novel intron retention and exon skipping events, and generate gene-level reports that summarize the usage of each isoform across multiple datasets. Also compatible with single-cell RNA-seq data and short-read RNA-seq data quantified on the transcript level. Code, DOI

LR-splitpipe
LR-splitpipe is a tool designed to demultiplex and debarcode long-read single-cell RNA-seq data prepared with the Split-seq barcoding protocol. Code, DOI

TALON
TALON is used to identify and quantify known and novel isoforms from long-read RNA-seq data. It is currently implemented as the pipleline to process all long-read RNA-seq data for ENCODE. Also compatible with single-cell long-read RNA-seq data. Code, DOI

cerberus
cerberus aggregates transcriptome annotations from a variety of sources. Allows for representation of transcription start and end sites in the form of bed regions rather than single base pair coordinates, and iterative improvement upon existing cerberus annotations.

OUTREACH

UCI GenPALS Leadership **December 2020 - Present**
The UCI Genomics Practical Applications Learning Seminar (GenPALS) is a seminar series and community of genomics researchers at UCI. This group is for the technicians, graduate students, and post-docs that actually analyze genomics data to discuss new methods and share personal experiences with using genomics tools in their research, with an emphasis on code sharing and reproducibility. Currently, GenPALS hosts seminar speakers every other week to talk about genomics tools they've either developed or have used.

- *Co-founder of UCI GenPALS*
- *Responsible for helping recruit and schedule speakers each quarter*
- *Organized a well-attended workshop consisting of both presentations and hands-on data analysis sessions for analyzing single-cell genomics data in fall 2021*

CMB Peer Mentor **2020**

Speaker at local elementary school **2016-2017**
Gave talks about current research

WORKSHOPS AND TUTORIALS

UCI GenPALS scRNA-seq Workshop **2021, 2022**
Led an interactive workshop in 2021 and again in 2022 for the CaSB short course on dimensionality reduction and clustering in single-cell RNA-seq data using Scanpy with an emphasis on exploring what the effect of different parameters is. Code

UCI GenPALS scRNA-seq Workshop **2021, 2022**
Led an interactive workshop in 2021 and again in 2022 for the CaSB short course on how to map and quantify single-cell RNA-seq reads using Kallisto Bustools. Code

UC Davis IsoSeq Workshop **2021**
Led an interactive workshop on how to use TALON and Swan, two software libraries I have developed or contributed to to analyze long-read RNA-seq data. Code

UCI GenPALS Seminar **2021**
Gave a presentation with accompanying code on how to use TALON and Swan. Code

AWARDS

DCB Research Excellence Award	*UC Irvine*	2022
Cum laude	*UC San Diego*	2017
Provost Honors	*UC San Diego*	2014-2017

PRESENTATIONS

Invited short talk	*UCI CCBS Retreat*	2022
Invited speaker	*UCI CaSB Short Course*	2022
Seminar speaker	*UCI Developmental and Cell Biology RIP talk*	2022
Invited speaker	*ENCODE Consortium Meeting*	2022
Seminar speaker	*UCI GenPALS*	2022
Poster	*Society for Neuroscience*	2022
Invited speaker	*ENCODE Consortium Meeting*	2021
Seminar speaker	*UCI GenPALS scRNA-seq Workshop*	2021
Invited speaker	*UC Davis IsoSeq Workshop*	2021
Invited speaker	*PacBio IsoSeq Social Club*	2021
Invited speaker	*Genetics Virtual Week*	2021
Seminar speaker	*UCI GenPALS*	2021
Invited speaker	*ENCODE Consortium Meeting*	2021
Seminar speaker	*UCI Systems Biology RIP talk*	2020
Poster	*Genome Informatics*	2020
Accepted short talk	*Genome Informatics*	2020
Poster	*Intelligent Systems for Molecular Biology*	2020
Accepted speaker	*Intelligent Systems for Molecular Biology*	2020
Poster	*ENCODE Consortium Meeting*	2019
Poster	*Genome Informatics*	2019
Accepted short talk	*Genome Informatics*	2019
Invited speaker	*ENCODE Long-read RNA-seq Meeting*	2019

TEACHING

Teaching assistant	*COSMOS (Genes, Genomes, and Skeletal Muscle Dystrophies)*	SU 2021
Teaching assistant	*Intro to Precision Medicine (D132)*	FA 2020, 2021
Tutor	*UCI Systems Biology Short Course*	January 2020
Teaching assistant	*Metabolic Biochemistry (BIBC 102)*	SP 2017

(FA = fall, WI = winter, SP = spring, SU = summer)