

William Raymond

Bioengineering PhD

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https://will-raymond.github.io/will_raymond_cv

Education

Colorado State University

Doctorate of Philosophy - Bioengineering

Fort Collins, CO

Fall 2018 - Spr 2024

- Dissertation title: Stochastic modeling to explore the Central Dogma of molecular biology and to design more informative single-molecule live-cell fluorescence microscopy experiments.
- Focused on mechanistic modeling, machine learning, and statistical techniques on biological data types such as live-cell fluorescence microscopy, smFISH, and transcriptomics for studying gene expression.
- Gained a life-long love for the intricacies of RNA biology.

Colorado State University

Bachelor of Science - Chemical and Biological

Bachelor of Science - Biomedical Engineering

Fort Collins, CO

Fall 2012 - Spr 2017

Research Experience

Postdoctoral Research Assistant - Colorado State University

May 2024 - Present

- Continued software development on the Munsky lab's open source Python packages: rSNAPsim and rSNAPed.

Graduate Research Assistant - Colorado State University

Sept 2017 - May 2024

- As a PhD student, completed tasks for academic publications for multiple lab projects.
- Developed open source Python packages aimed at providing our lab's research to the public and allow fellow scientists to quickly build mRNA translation models.
- Built an ML based experimental design pipeline for Nascent Chain Tracking experiments, allowing more sophisticated experiments to be performed.
- Performed statistical model fitting for mechanistic models of gene expression in-house and collaborators experimental data leading to novel insights on transcriptional regulation.
- Provided mentorship to junior lab members with a focus on fostering computational skills and coding capabilities.

Undergraduate Research Assistant - Colorado State University

Fall 2016 - Summer 2017

- Completed an honors thesis focusing on a Python GUI for solving bursting gene models
- Provided support to a research laboratory with implementing models in Python.

Peer-Reviewed Publications

Aguilera LU, Weber L, Ron E, King CR, Kaan O, Poppinga A, Cook J, May MP, **Raymond WS**, 2025
Fox ZR, Forero-Quintero LS, Forman J, David A, and Munsky B. Methods in Quantitative Biology –
from Analysis of Single-Cell Microscopy Images to Inference of Predictive Models for Stochastic Gene
Expression. UNDER REVIEW. **Contributions:** Course material generation, writing.

Raymond WS, DeRoo J, and Munsky B. Identification of potential riboswitch elements in *Homo Sapiens* 2025
mRNA 5'UTR sequences using Positive-Unlabeled machine learning. *PLOS One*. 20(4), 2025.
doi: 10.1371/journal.pone.0320282 **Contributions:** Conceptualization, design, data curation, ML implementation,
computation analyses, writing, editing. As the primary corresponding author, conceptualized this project, selected and
curated the data-sets and performed the machine learning, and analyzed the results to produce a ranked list of human 5'UTRs
most likely to harbor a riboswitch RNA structure.

Raymond WS, Ghaffari S, Aguilera LU, Ron E, Morisaki T, Fox ZR, May MP, Stasevich TJ, and 2023
Munsky B. Using mechanistic models and machine learning to design single-color multiplexed nascent chain
tracking experiments. *Frontiers in Cell and Developmental Biology*. 11, 2023. doi: 10.3389/fcell.2023.1151318
Contributions: Conceptualization, design, ML implementation, computation analyses, writing, editing. Implemented
the computational pipeline and analyses using our custom mechanistic modeling software to generate machine learning guided
design for fluorescent microscopy experiments.

Forero-Quintero LS, **Raymond WS**, Munsky B, and Stasevich TJ. Visualization, quantification and 2022
Modeling of Endogenous RNA Polymerase II Phosphorylation at a Single-copy Gene in Living Cells.
Bio-protocol. 12(14) 2022. doi: 10.21769/BioProtoc.4482.
Contributions: Computation, writing, editing. As first computational author, wrote the code that recreates the entire
computational protocol for publishing.

Forero-Quintero LS, **Raymond WS**, Handa T, Saxton MN, Morisaki T, Kimura H, Bertrand E, Munsky B, 2021
and Stasevich TJ. Live-cell imaging reveals the spatiotemporal organization of endogenous RNA polymerase II

phosphorylation at a single gene. *Nature Communications*. 12(1):3158 2021. doi: 10.1038/s41467-021-23417-0.

Contributions: First computational author, computation, writing, editing. Performed the mechanistic model fitting to live-cell fluorescent microscopy data to provide insights about transcriptional mechanisms at a single gene.

Aguilera LU, **Raymond WS**, Fox ZR, May MP, Djokic E, Morisaki T, Stasevich TJ, and Munsky B.

2019

Computational design and interpretation of single-RNA translation experiments. *PLOS Computational Biology*. 15(10) 2019. doi: 10.1371/journal.pcbi.1007425.

Contributions: Computation, writing, editing. Wrote the Python implementation of the model software, rSNAPsim.

Weber L, **Raymond WS**, and Munsky B. Identification of gene regulation models from single-cell data.

2018

Physical Biology. 15(5) 2018. doi: 10.1088/1478-3975/aabc31. *Modified from Chapter 30 of the textbook *Quantitative Biology: Theory, Computational Methods, and Models (2018)*

Contributions: Created a Python GUI to run the examples in the paper and textbook chapter.

Teaching and Mentoring Experience

Course Instructor - Colorado State University

Jan 2023 - May 2023

BIOM 421 - Transport Phenomena

- As a primary instructor of this upper division class, instructed senior undergraduate engineering students principles in transport phenomena including topics such as pharmacokinetics, fluid dynamics, mass transport, and FEM / FVM analyses.
- Created an engaging and vibrant learning environment and lecture materials with a focus on applicable real world examples.

Learning Assistant, Invited Lecturer, Course Designer - UQ-Bio summer school

Summer 2021, 2022, 2023 & 2024

- Taught various levels of student from undergraduate to senior PhD students at the Undergraduate Quantitative Biology Summer School (UQ-Bio) across many topics: ODE modeling, machine learning, Python coding, MCMC, stochastic simulation, image processing, and finite state projection.
- Generated lecture materials used for teaching students on topics for learning Python, mechanistic modeling, and machine learning. Provided these materials as open source Colab notebooks. These were used as the basis for a full lecture course at CSU.
- Fostered a welcoming and collaborative project-focused environment via mentoring small student teams.

Graduate Teaching Assistant - Colorado State University

Fall 2020, Fall 2021

BIOM 421 - Transport Phenomena

- Assisted undergraduate students during one-on-one sessions and office hours.

Presentations

Graduate Engineering and Research (GEARS) 2024 - Fort Collins, Colorado

Feb 2024

- Presented a poster on my publication “Identification of Potential Riboswitch Elements in Homo Sapiens 5’UTR Sequences using Positive-Unlabeled Machine Learning.”

qCMB Symposium - Fort Collins, Colorado

June 2024

- Presented a poster on my publication “Identification of Potential Riboswitch Elements in Homo Sapiens 5’UTR Sequences using Positive-Unlabeled Machine Learning.”

Rocky Mountain RNA Symposium - Aurora, Colorado

April 2024

- Presented a poster on my publication “Identification of Potential Riboswitch Elements in Homo Sapiens 5’UTR Sequences using Positive-Unlabeled Machine Learning.”

UQ-Bio 2023 Guest Lecturer - Fort Collins, Colorado

June 2023

- Gave a 15 minute talk on my dissertation project combining mechanistic mRNA models to extend the color palette of NCT experiments.
- Presented a poster on my publication “Using mechanistic models and machine learning to design single-color multiplexed nascent chain tracking experiments”

qCMB Symposium - Fort Collins, Colorado

June 2023

- Gave a 2.5 minute lightning talk advertising my poster.
- Presented a poster on my publication “Using mechanistic models and machine learning to design single-color multiplexed nascent chain tracking experiments”

APS March Meeting - Las Vegas, Nevada

March 2023

- Talk title: “Combining mechanistic and statistical models to enable Nascent Chain Tracking for multiple mRNAs using a single color” *accepted talk

SBME Seminar - Fort Collins, CO

March 2019

- Talk title: “Simulating mRNA Translation Dynamics under tRNA Depletion Conditions”

Skills

Expert:

Mechanistic modeling, machine learning, Python, RNA biology, MATLAB, stochastic simulation, bioinformatics

Intermediate:

Protein biology, graphic design, MCMC, image processing, big data

Beginner:

C++, R