

Jeremy Welsh

Email : jeremy@micromelody.net

Mobile : +1 (503) 890-1543

Linkedin: www.linkedin.com/in/jeremy-welsh

Github: github.com/jeremyiwk

EDUCATION

- **University of Oregon** Eugene, OR
Master of Science, Physics, GPA: 3.92 Sep 2020 - Jun 2022
- **University of Oregon** Eugene, OR
Bachelor of Science, Mathematics and Physics, GPA: 3.83 Sep 2016 - June 2020

WORK EXPERIENCE

- **Senior Intern** Jun 2022 – Present
Thermo Fisher Scientific Hillsboro, OR
 - ◊ Wrote Python scripts to automate milling and imaging procedures on dual-beam scanning electron microscope systems.
 - ◊ Performed image registration on ion beam images using cross-correlation and a TensorFlow convolutional neural network to detect ~100nm machining tolerances in ion column components.
 - ◊ Developed Python code to measure optical aberrations in ion beam images using computer vision tools from OpenCV and Skimage.
 - ◊ Wrote custom ion column elements in C for ion column simulations using GPT simulation software.
 - ◊ Performed and analyzed ~1TB of GPT simulation data using Python and shell scripts in a Linux HPC environment for the optimization of novel column designs.
 - ◊ Developed algorithms for regression of sparse simulation data to optimize ion column lenses.
 - ◊ Used Python libraries such as NumPy, SciPy, Pandas, Matplotlib, and Seaborn for data analysis, visualization, and presentation to a team of scientists in order to direct critical decisions about experimental design.
- **Graduate Research Assistant** Sep 2020 – Jun 2022
University of Oregon Eugene, OR
 - ◊ Developed theoretical models for organic macromolecules at multiple resolutions using mathematical tools from non-equilibrium statistical mechanics.
 - ◊ Validated theoretical models against experimental data using molecular dynamics and Monte Carlo simulation data.
 - ◊ Mentored undergraduate and graduate research assistants on projects related to molecular coarse-graining schemes and simulation data analysis
 - ◊ Performed and analyzed molecular dynamics simulations using GROMACS and LAMMPS molecular dynamics software on HPC clusters at San Diego Supercomputer Center.
 - ◊ Characterized performance and the degree of parallelism of molecular dynamics simulations to determine computational resources requirement on 128 Core/node HPC system.
 - ◊ Developed programs in Python and Fortran for data analysis of ~10TB of molecular dynamics simulation data.
 - ◊ Developed Fortran code to create input data for polymers of arbitrary length for MCCCSTowhee Monte Carlo molecular simulation software
 - ◊ Developed novel coarse-grained models of DNA and validated models using custom Python and Fortran code, leading to improved agreement between predicted and simulated correlation statistics over prior models.
 - ◊ Performed DBSCAN clustering on molecular dynamics simulation data to define regions for Markov Chain Monte Carlo simulation.
 - ◊ Validated coarse-grained molecular models against predictions of statistical models such as principal component analysis (PCA) and time-lagged independent component analysis (t-ICA).
 - ◊ Developed coarse-grained molecular model using PCA and an Autoencoder neural network to perform non-linear dimensionality reduction on the model parameter space.

TECHNICAL SKILLS

- **Programming Languages:** Python, Fortran, C++, C, R, MATLAB, Julia, Shell scripting (Unix/macOS), Mathematica, SQL
- **Frameworks:** NumPy, Pandas, SciPy, Scikit-Learn, TensorFlow, OpenCV, PyMC, Matplotlib, Numba, ggplot2
- **Software & Tools:** Git, Docker, AWS, General Particle Tracer (GPT), GROMACS, LAMMPS