

# Jeremy Welsh

Email : [jeremy@micromelody.net](mailto:jeremy@micromelody.net)

Mobile : +1 (503) 890-1543

Linkedin: [www.linkedin.com/in/jeremy-welsh](https://www.linkedin.com/in/jeremy-welsh)

Github: [github.com/jeremyiwk](https://github.com/jeremyiwk)

## TECHNICAL SKILLS

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

## WORK EXPERIENCE

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- **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.
  - ◇ Contributed to scientific software (Python) for parallelizing GPT simulations and processing data in a Linux HPC environment.
  - ◇ Developed algorithms for regression of sparse simulation data to optimize novel ion column designs, resulting in up to 300% improvement in ion beam performance.
  - ◇ 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.

## EDUCATION

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- **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