

Kelly Sovacool

Bioinformatician seeking to build open source software for reproducible data science

Skills

Languages & Tools	R, Python, C++, Bash, Snakemake, git, GitHub, R Markdown, Jupyter, Quarto, LaTeX, conda/mamba, Docker, Singularity, SLURM, UNIX CLI
Research	supervised machine learning pipelines, data visualization, reproducible reports & manuscripts
Software	package maintenance, test-driven development, continuous integration, documentation, collaboration & peer review, high performance computing

Education

2018-2023	PhD Bioinformatics , <i>University of Michigan</i> , Advisor: Patrick D. Schloss
2014-2018	BS Biology , <i>University of Kentucky</i> , Minor: Computer Science

Experience

2019-present	Graduate Student Researcher , Schloss Lab , University of Michigan <ul style="list-style-type: none">○ Develop, benchmark, and maintain bioinformatics workflows and software packages in R & Python.○ Build machine learning pipelines for human gut microbiome classification and prediction problems in colorectal cancer and <i>C. difficile</i> infection.○ Collaborate with other scientists on microbiome projects and mentor junior lab members.
Jan-Apr 2023	Graduate Student Instructor , <i>Dept. of Computational Medicine & Bioinformatics</i> , University of Michigan, BIOINF 576: Tool Development for Bioinformatics <p>Develop curriculum and teach students the principles of software development in R & Python. Topics: software design, implementation, testing, documentation, issue tracking, peer review, and release.</p>
2019-2022	Executive Committee Member: Open Source Technical Lead , Girls Who Code at U-M Dept. of Computational Medicine & Bioinformatics <p>Facilitated collaborative design, development, and maintenance of our curriculum on Python for data science to teach young women+ via Girls Who Code clubs.</p>
2015-2018	Undergraduate Lab Assistant , <i>Moseley Bioinformatics Lab</i> , University of Kentucky <p>Developed a Python package to identify homologous gene products for comparative genomics.</p>

Open Source Contributions

Maintainer	mikropml . User-Friendly R Package for Supervised Machine Learning Pipelines
Maintainer	mikropml snakemake workflow . Snakemake template for building reusable and scalable machine learning pipelines with mikropml (Python + R)
Maintainer	schtools . Schloss Lab tools for reproducible microbiome research (R package)
Contributor	mothur . Command-line tool for processing microbial amplicon sequence data (C++)
Co-author	mothur snakemake workflow . Template for microbial amplicon sequence analysis with mothur (Python + R)

Continuing Education

Jan 2020	Building Tidy Tools workshop at rstudio::conf . RStudio, PBC. San Francisco, CA
Dec 2019	Winter School in Research Software Engineering . URSSI. Seattle, WA
Jun 2019	Software Carpentry Instructor Training . The Carpentries. University of Michigan

Publications

 see list here: sovacool.dev/pubs