**Github: a Powerful Resource for Scientific Communication**

Github is an online version control service built on top of the Git distributed version control software. Originally developed for software development teams, Github has evolved into a resource that has broad communication and resource sharing potential. Clearly hosting files with integrated support for version control is built in. Many users may not realize the ease of web hosting functionality Github provides via markdown, and its ability to run and display Jupyter notebooks.

Proteomics data analysis involves many steps that can be difficult to encapsulate and communicate in traditional forms of scientific communication. There is sample preparation, chromatography separations, instrument settings, and lengthy informatics pipelines. Quantitative experiments will also need additional statistical analyses. Increasingly, scientific projects involve more than just proteomics experiments. Methods sections of publications are getting harder to create and understand. Describing all of the pieces is daunting, let alone communicating how all of the pieces were used to address the scientific questions.

I will show how Github’s combination of features can present proteomics data analyses in effective and transparent ways. The <https://github.com/pwilmart/Sea_lion_urine_SpC> repository will be used as an example where publicly available data from PRIDE (PXD009019) for Seal lion urine samples was re-analyzed. The repository hosts results files, has experimental and analysis details fully described in the README.md file, and has Jupyter notebooks for quality control and statistical analyses with R. Notebooks offer unique ways to describe and share R scripting (or Python), rich data visualizations, and full analysis narratives.

A particularly useful part of this example will be how to find appropriate protein databases for non-model organisms, such as Sea lion, and how to make sense of the (un-annotated) identified proteins. I will discuss some ortholog mapping and annotation tools hosted at Github to facilitate data interpretation and follow up work.