Subject: Internship Opportunity at Genentech (ML or Mass-Spec Bioinformatics)

Target Start Date: May 2019
Length of Internship: 6 months
Work hours: 40 hours per week

In a collaboration between Genentech and Roche Diagnostics, we are interested in developing automated quality control and system suitability tools to enhance our mass spectrometry analytical pipeline capabilities. Current LC-MS systems are operated in semi-automatic modes, where an
operator manually reviews the results and visually inspects raw chromatograms to make decisions about data validity and system maintenance. The limitations of the manual review approach are: slow throughput due to the involvement of an operator; subjective assessment of the data; biased decisions; and sample loss due to QC failure that could have been prevented by early intervention. We are interested in taking advantage of machine learning and advanced analytics to automate LC-MS system monitoring through flagging individual measurements as valid or invalid, and identifying trends of degrading instrument performance for early intervention.

We are looking for an enthusiastic intern with experience in machine learning, or mass spectrometry bioinformatics to join our team and expand upon the work we have done. This is a great opportunity for you to:

- Develop a bioinformatics tool that can be integrated into commercial or open-source mass spectrometry analytics solutions. There is also opportunity for publication.
- Hone your programming and analytical skills.
- Gain further knowledge of mass spectrometry bioinformatics.
- Learn about drug, diagnostics and biomarker development.

Qualifications

- Candidates must be pursuing a MS or PhD (preferred) in biomedical engineering, bioinformatics, computational biology, computer science, physics or a related field or recent graduates of similar fields within the past two years.
- Understanding of statistics and machine learning concepts and algorithms and proven record of applying advanced analytical techniques to solve problems in biology, engineering, business or medicine.
- Time commitment of 6 months needed starting in Spring or Summer 2019 in South San Francisco, CA. Part-time and/or off-campus participation may be arranged for exceptional candidates.
- Excellent coding skills in at least one of the following programming languages: R (preferred), Python, Matlab
- Proven record of delivering results (e.g. publications or open-source tools)
- Familiarity with LC-MS data analysis is a plus.
- Experience in front-end programming and developing production-ready code is a plus.

About the team

We are the Technology group within the OMNI Biomarker Development function of Development Sciences at Genentech. Our group is responsible for design and implementation of mass spectrometry, flow cytometry and mass cytometry biomarker assays for programs in clinical development in diverse disease areas including Immunology, Inflammation and Autoimmune Diseases, Ophthalmology, Metabolism, Neuroscience and Oncology. We utilize and develop bioinformatics technologies and tools to improve and optimize our workflow for assay development, characterization and implementation as well as for exploratory analysis of high dimensional biomarker data.

At Roche Centralized and Point of Care Solutions we develop products to support health care professionals in clinical decision making in a wide field of indications including Cardiovascular,
Hematology, Infectious Diseases, Metabolism, Oncology and Women’s Health. It is important to us to ensure high quality of the acquired data. In the group of New Systems Statistics, we employ and develop state-of-the-art algorithms from the fields of data science, machine learning, bioinformatics and statistics to solve challenging problems to enable automated processing of mass spectrometry data.

If you are interested in this opportunity or have any questions, please contact:

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And

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