Master thesis proposal:

Simulation of a proteomics mass spectrometry experiment

In developing computational tools for proteomics mass spectrometry, one recurring problem is the acquisition of suitable test data, were the sample composition is completely known. This thesis will attempt to tackle this problem through construction of a deep computational model of a modern mass spectrometer (the Thermo Q-Exactive). Such a model could allow improved benchmarking of analysis algorithms and deepen understanding of instrument operation, ultimately enabling increased analytical power in clinical and biological applications.

Why would you want to do this?
Apart for general master thesis experience of communication a complex topic over various written and spoken channels, this thesis will give the student
- Deep knowledge of high-tech instrument worth several million
- Experience in a modern programming language
- A chance expand the frontiers of science
- A nice time in a multidisciplinary research group

The task
Depending on progress, the thesis will consist of
- Acquiring an understanding of the target mass spectrometer
- Developing a suitable model representing the mass spectrometer, that mimics instrument population wide behavior
- Benchmarking the model against experimental data

The programming will preferably be carried out in scala, a modern and extremely concise language that will make you not want to use Java/C++ ever again.

The candidate
This thesis will suit a student with a passion for software development and general interest in statistical modeling. Previous expertise in chemistry is not required.

Don't wait, please send a mail to johan.teleman@immun.lth.se with your CV and some examples of courses or free time programming projects that you think makes you suitable for this thesis project.