Data Science/Bioinformatics Opportunity in Cancer Immunology

The laboratory of Dr. Pamela Ohashi at the Princess Margaret Cancer Centre (https://www.ohashilab.ca/) has an opening for a summer student. The scientific project is to decipher how immune cells interact with each other to shape the outcome of the immune response to cancer. You will work at the intersection of computer science, applied statistics and cancer immunology under the supervision of an experienced bioinformatician and a fellow immunologist. This a full-time paid position for 35 hour per week. The hourly pay will meet the minimum requirements of the department and is further negotiable. The applicant requires a Canadian SIN number and can work remotely within Canada.

What you'll be exposed to in this project:
- Analyzing lung cancer CyTOF data by applying and modifying established computational approaches
- Using data visualization, transformation and other exploratory techniques to explore data and inform further analysis
- Applying dimensionality reduction and clustering approaches to discover cell populations within and across samples
- Using regression-based approaches to find markers differentiating across populations and samples
- Examining published scientific literature on the performance of alternative CyTOF analysis approaches and using this information to inform analysis pipeline choices
- Implementing and sharing a reproducible data analysis pipeline using R and R markdown

This position is best suited to 3rd or 4th year students. The following areas of knowledge, and representative courses, are most helpful for this position:
- Statistics applied to data analysis (from STA247H1/STA255H1/STA257H1, STA302H1/STA303H1)
- Machine Learning (from courses CSC311H1, STA314H1, STA414H1)
- Bioinformatics (from courses BCH441H1, BCB410H1, BCB420H1)

You should have a level of comfort (ideally some experience) with the following:
- R programming and data handling
- Exploratory data visualization
- Basic statistical tests and Multiple Linear Regression
- Basic dimensionality reduction (e.g.: PCA)
- Basic clustering (e.g.: Hierarchical Clustering)
- Basic model evaluation (e.g.: Cross-Validation, train-test-validate split, False Positives/Negatives, Sensitivity/Specificity, ROC curves, Precision-Recall curves)

Get in touch with us and let's chat!
Who: Azin Sayad (asayad@gmail.com) and Maryam Ghaedi (maryam.ghaedi@uhnresearch.ca)
Email subject line: "Ohashi Lab CyTOF Bioinformatics Opening" (or comparable description)