



Genome Sciences Seminar

Monday, 4.23.18 | 3:30 | Foege Auditorium



Dr. John Marioni

University of Cambridge

<http://www.cruk.cam.ac.uk/research-groups/marioni-group>

“Using single cell genomics to understand cell fate decisions”

The Marioni laboratory

The human body is composed of billions of individual cells, which use different combinations of genes to fulfil their relevant functions. Unsurprisingly, cells that play very different roles (e.g., neurons and hepatocytes) use very different sets of genes as well as displaying clear morphological differences.

However, even within supposedly homogeneous populations of cells there exists tremendous heterogeneity, some of which can have important biological consequences. Studying this heterogeneity has been technically challenging due to the tiny amount of molecular material contained within a cell. However, these challenges have recently been overcome and we can now look at the sets of genes that are used in single cells.

Making sense of these, and other types of biological data, requires the development of appropriate computational tools and methods – this is commonly referred to as the “Big Data” challenge. My research team is motivated by developing computational tools to handle such big data and, importantly, to use them to answer key biological questions in collaboration with outstanding colleagues. We focus particularly on how cells decide what fate they are going to commit to, with a particular emphasis on early development. Moving forward, insights gleaned from these studies will provide us with important information about how cells within the human body acquire cancerous potential.

Refreshments served outside the Auditorium at 3:20pm

Questions? Contact Brian Giebel at bgiebel@uw.edu or visit the Seminar website at <http://www.gs.washington.edu/news/seminars.htm>

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