



Thursday, 16th June, 9.30am, Online Host: Prof. Aitziber L. Cortajarena

Genealomics, single cell lineage tracing of blood cell production through next generation sequencing

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How heterogeneous systems of cells constituting multicellular organisms establish, organize and achieve coordination persists as a central question in natural sciences. Whereas stochastic gene or protein expressions have clearly demonstrated their role in cellular heterogeneity and are widely studied, the role of cell heterogeneity in the organization of multicellular organisms has been less interrogated. Addressing this question requires adequate tools that quantitatively study ensembles of cells individually rather than group of cells.

My research aims at addressing cell heterogeneity in dynamical and complex systems of cells using the hematopoietic system as a model of study. Strikingly hematopoietic cells (immune cells, platelets and red blood cells) compose over 90% of total human cells and correspond to approximately ten trillions of cells. More importantly they all originate from the same cells, the hematopoietic stem cells (HSC), through a process called hematopoiesis. In addition, as immune and blood cells have a short life span (from hours to months) and can response to perturbations like infections, this process is highly dynamical. It is therefore an interesting and challenging model to study differentiation in a complex system at the single cell level.

Genealomics, which use high throughput sequencing methods to track the descendant of individual cells, is a powerful tool to study differentiation at the single cell level. In my research, we take advantage of genealomics methods to study the hematopoietic differentiation pathway both in mice and human. I will present some recent results using genealomics to study blood cell production.