

Inference and dynamical modeling of regulatory networks controlling hematopoiesis

Jose Teles

Computational Biology and Biological Physics – Lund University

Hematopoiesis is the differentiation process from which all mature blood cells are generated. During differentiation, hematopoietic cells can undergo different pathways leading to self-renewal, lineage commitment or apoptosis. Transcription factors are known to be regulators of these decisions, acting sequentially in combinatorial fashion and forming specific regulatory networks that drive the expression of specific genetic programs. To identify these regulators and understand the underlying networks is of great importance for clinical applications. This project follows a cross-disciplinary approach to identify novel regulators of hematopoietic stem cells and study the mechanism of action of known regulatory genes as well as their role on the complex molecular interplay that forms transcriptional networks driving hematopoiesis. An integrated computational approach, encompassing bioinformatics searches, network inference and dynamical modeling will be applied to extensive gene expression, proteomic and functional data hoping to provide a more complete view on the structural and functional principles of hematopoiesis.