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181 Longwood Avenue
Boston, Massachusetts 02115-5804

Department of Medicine
Channing Division of Network Medicine

Channing Network Science Seminar
May 15, 2015, 11am @ 5th floor conference room

Assieh Saadatpour, Ph.D
Postdoctoral Research Fellow
Dana-Farber Cancer Institute
Harvard T.H. Chan School of Public Health

Characterizing heterogeneity in leukemic cells using single-cell gene expression analysis

Abstract: A fundamental challenge in cancer therapy is that each tumor contains a highly heterogeneous cell population whose structure and mechanistic underpinnings remain incompletely understood. Recent advances in single-cell gene expression profiling have created new possibilities to characterize this heterogeneity and to dissect the potential intra-cancer cellular hierarchy. In this talk, I will present our recent work on using single-cell gene expression analysis to systematically characterize the heterogeneity within a leukemic cell population. First, we used a multiplexed quantitative PCR approach to assay the transcriptional profile of 175 carefully selected genes in the MLL-AF9 driven mouse model of acute myeloid leukemia (AML). Next, we employed a set of computational tools to map the cellular hierarchy and to elucidate the underlying transcriptional networks. In particular, by mapping to the normal hematopoietic cellular hierarchy, we identified two distinct subpopulations of leukemic cells: one similar to the granulocyte/monocyte progenitor (GMP) phenotype and the other to macrophage and dendritic cells. Further functional experiments suggested that these subpopulations differ in proliferation rates and clonal phenotypes. Finally, co-expression network analysis revealed similarities as well as organizational differences between leukemia and normal GMPs. Taken together, this study enabled pinpointing previously uncharacterized heterogeneity within leukemic cells, thereby providing insights into the molecular signatures of AML.

Reference: http://genomebiology.com/2014/15/12/525

Bio: Assieh Saadatpour received her Ph.D. in Mathematics with a Ph.D. minor in Computational Science from the Pennsylvania State University – University Park under the joint supervision of Profs. Reka Albert (Physics and Biology) and Mark Levi (Mathematics). After a one-year postdoc at Albert's lab, she joined the research group of Prof. Guo-Cheng Yuan as a Postdoctoral Research Fellow in Dana-Farber Cancer Institute and Harvard T.H. Chan School of Public Health. Her research interests include dynamic network modeling of biological systems, especially those related to disease, as well as developing computational methods for analyzing single-cell data.

hosted by Yang-Yu Liu

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