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2017 WORKSHOP SERIES

DECODING CELL IDENTITY FROM MODELS OF TRANSCRIPTION FACTOR NETWORKS

Presented by:

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The definition of epigenetic mechanisms that maintain the differentiated state of a cell has become a critical problem in this post-genomic era. Starting from bioinformatics analyses of large gene expression datasets, we specify the biochemical identity of a cell as a set of co-expressed gene modules. From these modules, we derive the corresponding network of transcription factors (TFs) that ultimately specify cell identity. The topology of TF networks is derived from prior knowledge and its dynamics simulated using logic-based mathematical modeling. Predicted network attractors represent differentiation states supported by a TF network, which can then be validated experimentally. We propose that with this workflow it is possible to predict single-cell state transitions in a cell population subjected to perturbations. We show examples of the usefulness of this approach in identifying cancer cell drug-sensitive or –resistant states.

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