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EQUATION AND DYNAMICS OF STATE TRANSITION FROM HEALTH TO LEUKEMIA

Russell C. Rockne[1]*, Sergio Branciamore[2], Jing Qi[3], Guerry J. Cook[3], Wei-Kai Hua[3], Emily Carnahan[3], Ayelet Marom[3], Herman Wu[3], Davide Maestrini[1], Xiwei Wu[4], Yate-Ching Yuan[5], Zheng Liu[5], Nadia Carlesso[3], Stephen J. Forman[3], Leo D. Wang[6,7] Ya-Huei Kuo[3] and Guido Marcucci[3]

[1]Department of Information Sciences, Division of Mathematical Oncology, City of Hope, National Medical Center, USA

[2]Department of Diabetes Complications & Metabolism, City of Hope Medical Center, USA

[3]Department of Hematology & Hematopoietic Cell Transplantation, Division of Hematopoietic Stem Cell and Leukemia Research, Gehr Family Center for Leukemia Research, City of Hope Medical Center, USA

[4]Department of Molecular and Cellular Biology; Integrative Genomics Core, City of Hope Medical Center, USA

[5]Department of Molecular Medicine; Bioinformatics Core, City of Hope Medical Center, USA

[6]Department of Immuno-Oncology, City of Hope Medical Center, USA

[7]Department of Pediatrics Beckman Research Institute, City of Hope Medical Center, USA

rrockne@coh.org (*corresponding author)

Leukemia evolves as a complex, dynamic system of multi-dimensional generic, epigenetic and micro-environmental alterations. System biology approaches to integrate a myriad of “omics” data over the course of disease progression offer promising opportunities of tracking disease evolution and predicting trajectory. However, satisfying methods and theories to model the dynamics and interpret these time series “omics” data are still lacking.

Here we present a mathematical model to describe the development and progression of leukemia in a two dimensional state-space constructed with time series genome-wide gene expression data obtained from blood cells of a mouse model of acute myeloid leukemia. The blood cell transcriptome is then represented by a particle moving in this space and its dynamics is determined

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by Langevin equation. We show that the transition of the transcriptome from a health state to a leukemia state can be understood in terms of mathematically-derived inflection points and energy states which characterize the dynamic probability of leukemia development. Our approach provides a framework that may be generalized to model dynamic state-transitions for other types of cancer.

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