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Identifying driving gene clusters in complex diseases through critical transition theory NATHANIEL WOLANYK, The Department of Physics University of Alabama at Birmingham, XUJING WANG, NHLBI, NIH, MARTIN HESSNER, Medical College of Wisconsin, SHOUGUO GAO, YE CHEN, NHLBI, NIH, SHUANG JIA, Medical College of Wisconsin — A novel approach of looking at the human body using critical transition theory has yielded positive results: clusters of genes that act in tandem to drive complex disease progression. This cluster of genes can be thought of as the first part of a large genetic force that pushes the body from a curable, but sick, point to an incurable diseased point through a catastrophic bifurcation. The data analyzed is time course microarray blood assay data of 7 high risk individuals for Type 1 Diabetes who progressed into a clinical onset, with an additional larger study requested to be presented at the conference. The normalized data is 25,000 genes strong, which were narrowed down based on statistical metrics, and finally a machine learning algorithm using critical transition metrics found the driving network. This approach was created to be repeatable across multiple complex diseases with only progression time course data needed so that it would be applicable to identifying when an individual is at risk of developing a complex disease. Thusly, preventative measures can be enacted, and in the longer term, offers a possible solution to prevent all Type 1 Diabetes.

Nathaniel Wolanyk
University of Alabama at Birmingham

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