

Predictive models for gene regulation

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In the field of systems biology, "big data" refers to the massive amounts of information that can be collected, stored and analyzed computationally and which can reveal previously unseen patterns or associations important to understanding, treating or preventing disease.

Modern statistical tools, however, are not very accurate when it comes to predicting the discrete and non-symmetric behaviors of individual cells.

It's not [big data](#)'s fault, assert Gregor Neuert, PhD, and colleagues from Vanderbilt University and Colorado State University. The wrong tools are being used.

In a study of the stress response in yeast published last month in the *Proceedings of the National Academy of Sciences*, they show how single-molecule measurements and advanced computational analysis yield far more precise, reproducible and predictive models of the complex mechanisms that [control gene expression](#) profiles over time and space.

These approaches should aid efforts to predict how, for example, mutations and environmental perturbations affect cellular function and behavior, and how diseases respond to drug combinations.

More information: Brian Munsky et al. Distribution shapes govern the discovery of predictive models for gene regulation, *Proceedings of the National Academy of Sciences* (2018). [DOI: 10.1073/pnas.1804060115](https://doi.org/10.1073/pnas.1804060115)

Provided by Vanderbilt University

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