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Aqib Hasnain* (aqib@ucsb.edu) and **Enoch Yeung** (eyeung@ucsb.edu). *Structured dynamic mode decomposition to quantify the impact of a genetic circuit on its host.*

Biophysical systems often exhibit emergent behavior when new elements are incorporated. Biophysical models typically fail to reconcile these emergent dynamics when confronted with data. Existing biophysical models do not account for the added interactions, arguably the leading obstacle in building robust synthetic genetic circuits. Often these models are created independent of data to describe only genetic circuit components; they lack a mechanism for incorporating whole cell data. We improve on these models through a learning process which takes advantage of the experimental process involved in collecting sequencing data. The learning process approximates the Koopman operator, K , an infinite-dimensional operator that acts on observables to produce linear dynamics. Sequencing measurements are not handled well by the state-of-the-art Dynamic Mode Decomposition (DMD) algorithms to approximate K . The data are high-dimensional, noisy, and typically contain a low number of timepoints. To overcome these difficulties, we develop structured DMD and integrate it with the learning algorithm for sparse DMD, which is a regularized DMD that can handle sparse time-series data. We demonstrate our method on a real dataset collected from a NAND gate built in *Escherichia coli*. (Received March 03, 2020)