

Automated, predictive, and interpretable inference of phenomenological models of biological dynamics

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The cost of an empirical bit in biophysics has fallen dramatically, and high-precision data are now abundant. However, biological systems are notoriously complex, multiscale, and inhomogeneous, so that we often lack intuition for transforming such measurements into theoretical frameworks. Modern machine learning can be used as an aid. I will discuss our Sir Isaac platform for automatic inference of phenomenological models of complex dynamics from noisy time series, even if the dynamics are nonlinear, and only a few of the relevant variables are measured. I will illustrate the method on applications to toy problems, including inferring the iconic Newton's law of universal gravitation, as well as a few synthetic biochemical reaction networks. Finally I will illustrate how the approach has been used for automatic construction of a model of *C. elegans* escape dynamics, which is more accurate than that curated manually, is biophysically interpretable, and makes nontrivial predictions about the system.

REFERENCES

- [1] Daniels BC et al. (2019) Automated, predictive, and interpretable inference of *Caenorhabditis elegans* escape dynamics. *PNAS* 116, 7226-7231.

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