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### **Automated adaptive inference of phenomenological dynamical models**

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Understanding the dynamics of biochemical systems can seem impossibly complicated at the microscopic level: detailed properties of every molecular species, including those that have not yet been discovered, could be important for producing macroscopic behavior. The profusion of data in this area has raised the hope that microscopic dynamics might be recovered in an automated search over possible models, yet the combinatorial growth of this space has limited these techniques to systems that contain only a few interacting species. We take a different approach inspired by coarse-grained, phenomenological models in physics. Akin to a Taylor series producing Hooke's Law, forgoing microscopic accuracy allows us to constrain the search over dynamical models to a single dimension. This makes it feasible to infer dynamics with very limited data, including cases in which important dynamical variables are unobserved. We name our method *Sir Isaac* after its ability to infer the dynamical structure of the law of gravitation given simulated planetary motion data. Applying the method to output from a microscopically complicated but macroscopically simple biological signaling model, it is able to adapt the level of detail to the amount of available data. Finally, using nematode behavioral time series data, the method discovers an effective switch between behavioral attractors after the application of a painful stimulus.