

# Utilizing non-negative least squares for data-driven discovery of dynamics

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Biological networks are complex and discovering dynamics for these large systems can prove difficult, especially in a low-data, high noise environment. Our approach utilizes the Non-negative Least Squares (NNLS) algorithm to infer the dynamics of a (biological) network from data. We will discuss how this approach can be used to identify dynamics for both mass-action systems as well as those akin to Michaelis–Menten kinetics. Both NNLS and similar methods will be tested on low-data, high-noise systems to compare how accurately they infer dynamics.