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90% of cancer treatment failures are linked to drug resistance driven by tumor evolution (1). This evolutionary process can be modeled as interacting cell populations evolving under treatment pressure(2).

01. PROBLEM STATEMENT

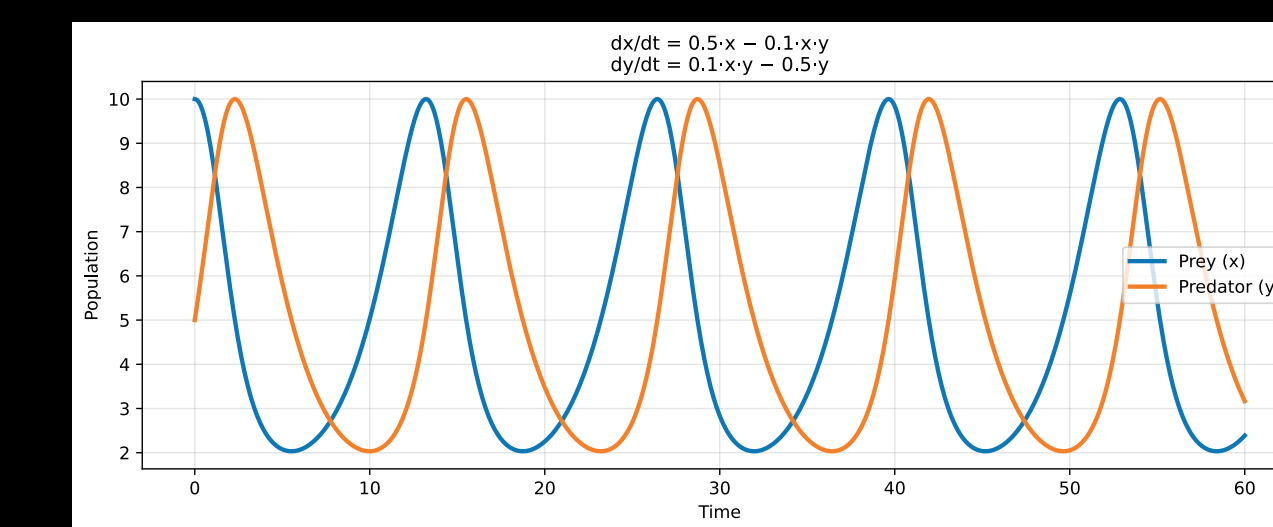
- We seek to extract maximum insight from time-series tumor dynamics.
- Traditional mechanistic models offer interpretability but rely on rigid assumptions.
- Machine-learning models capture complex behavior but often lack transparency.
- As a result, building trustworthy, biologically meaningful models remains challenging.

02. OBJECTIVES

- Discover interpretable equations directly from time-series tumor population data.
- Generate multiple candidate models to capture diverse plausible interaction dynamics.
- Filter and interpret equations using Evolutionary Game Theory to retain biologically plausible dynamics.

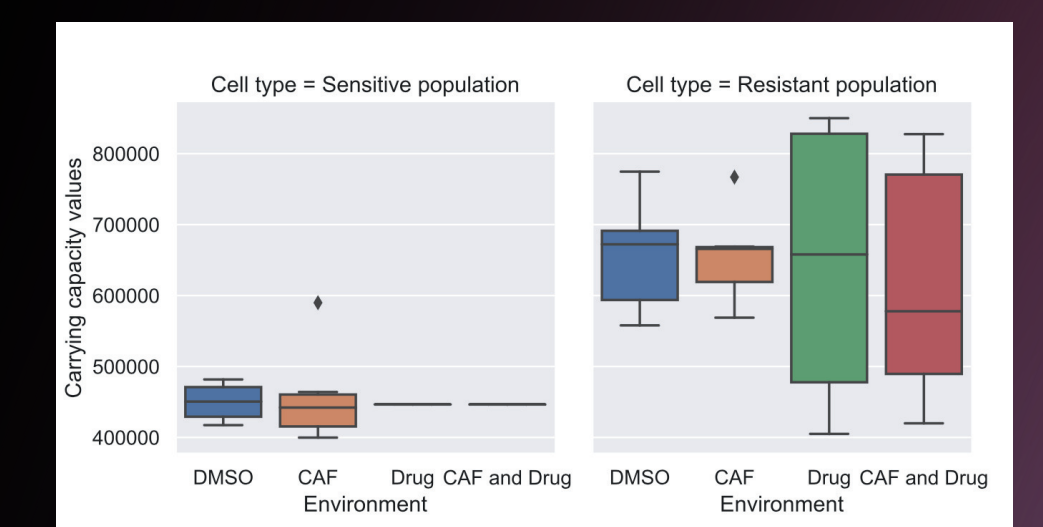
03. DATASET

Simulated dynamics



Used to validate equation discovery and filtering under known dynamics

Real experimental data

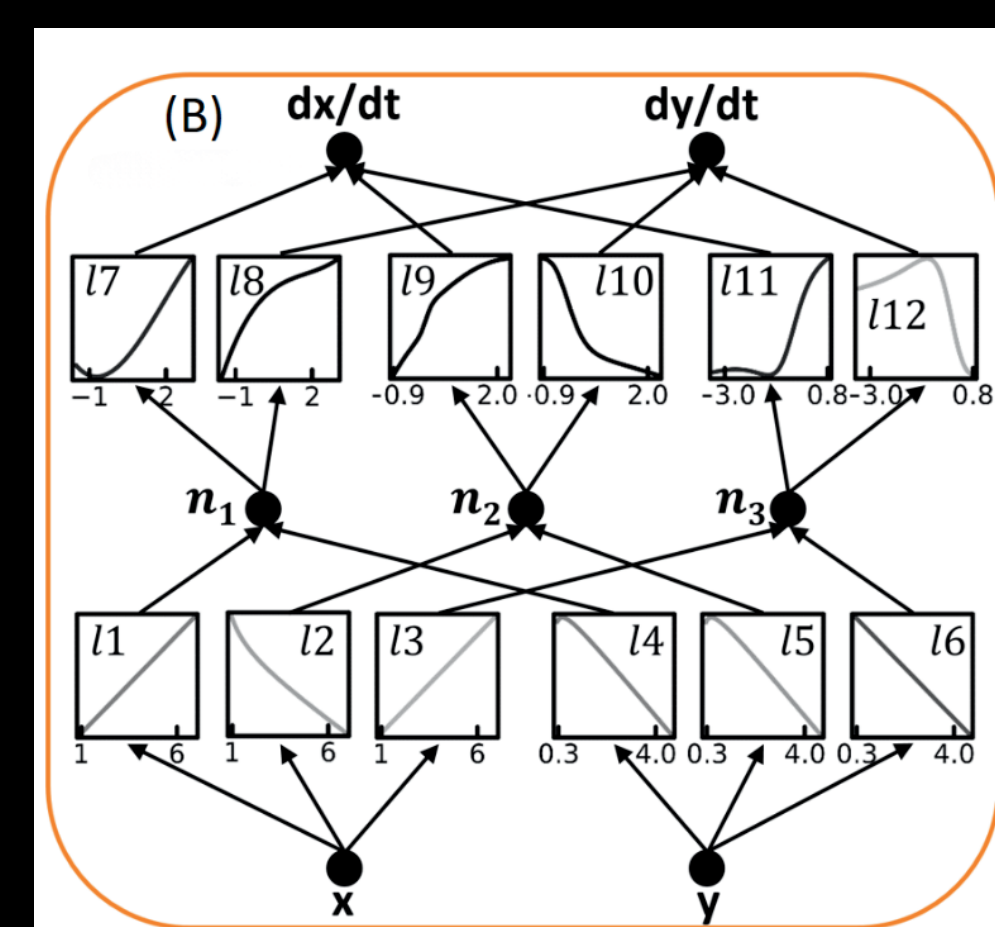


In vitro NSCLC time-series under multiple experimental conditions (3)

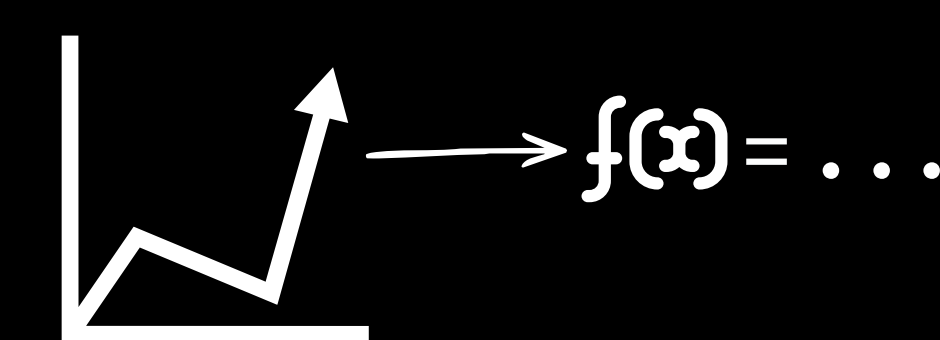
04. PIPELINE



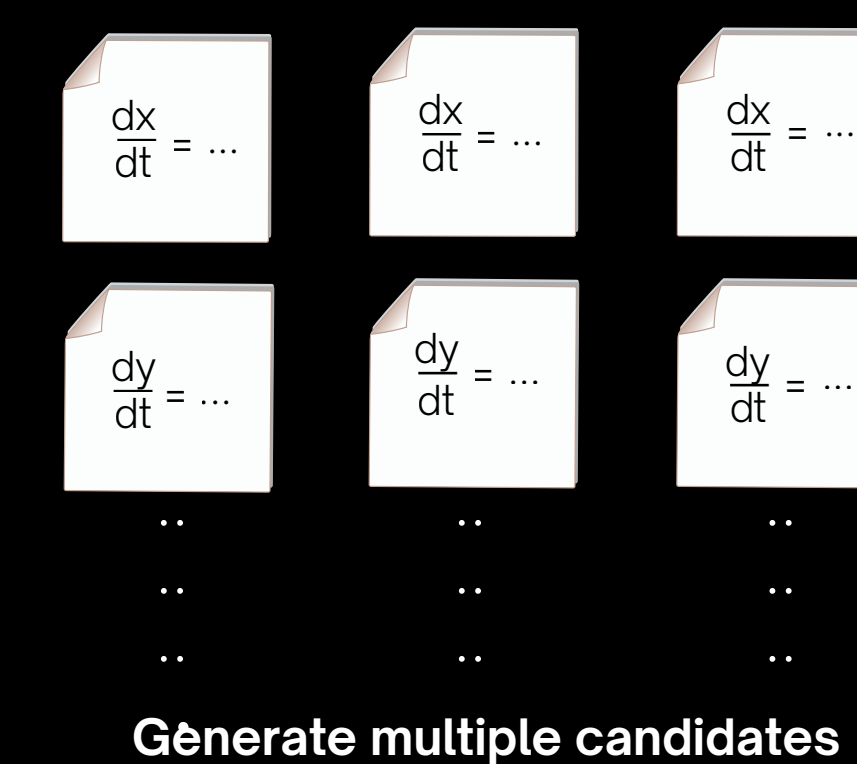
Learn dynamics via KAN-ODE (4)



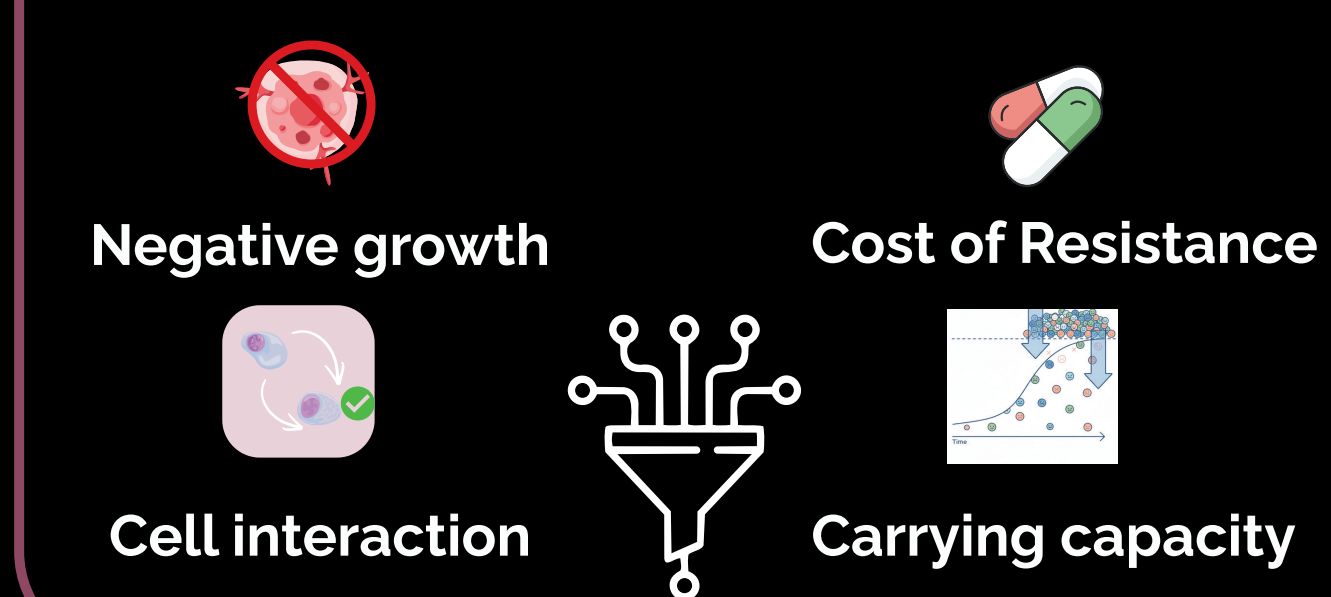
Symbolic Equation Extraction (4)



Ensemble of Equations



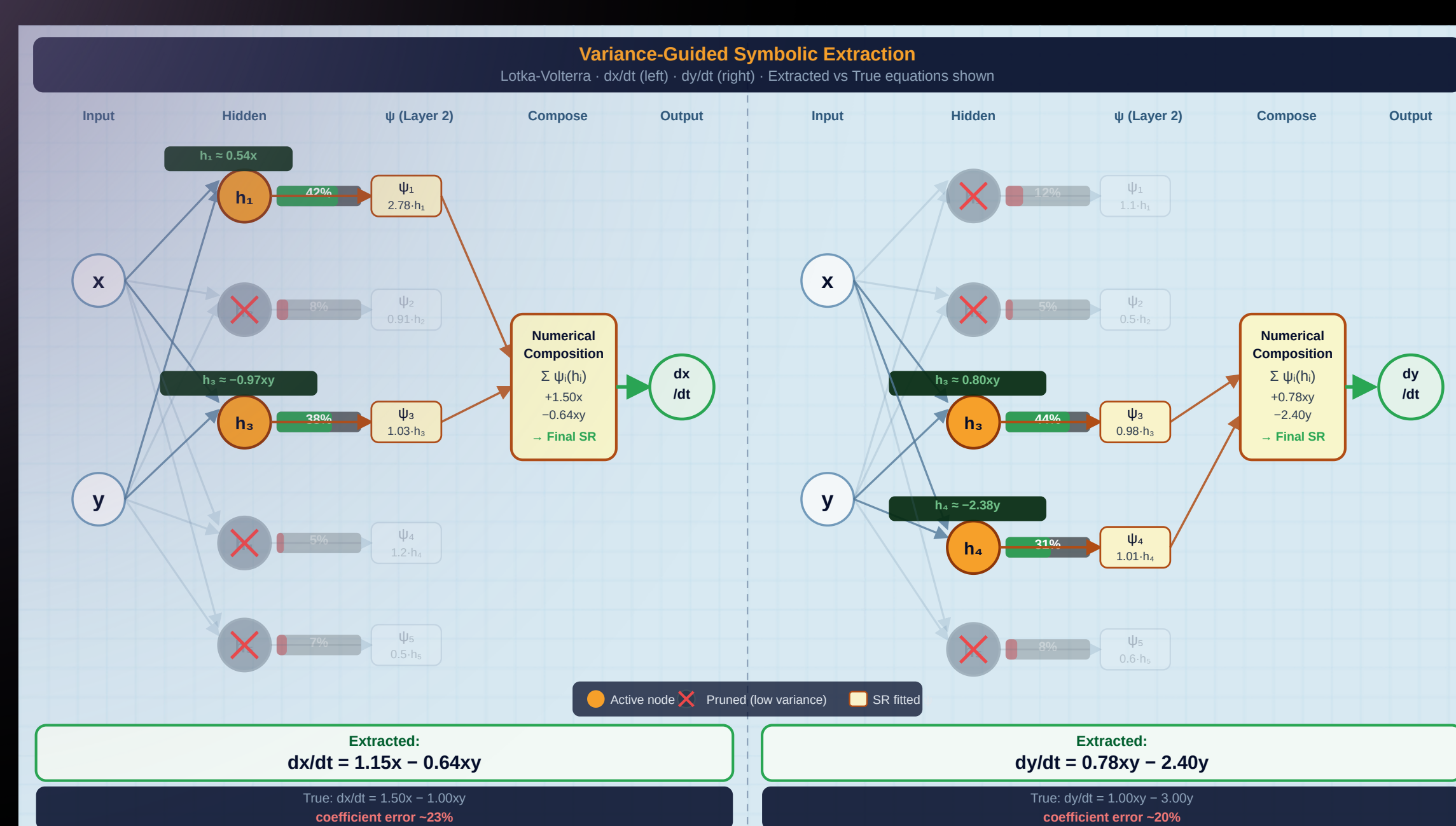
Biological and game theoretic filter



Final Valid Equation(s)

$$\frac{dx}{dt} = 1.5x - 1.0xy, \quad \frac{dy}{dt} = 1.0xy - 3.0y$$

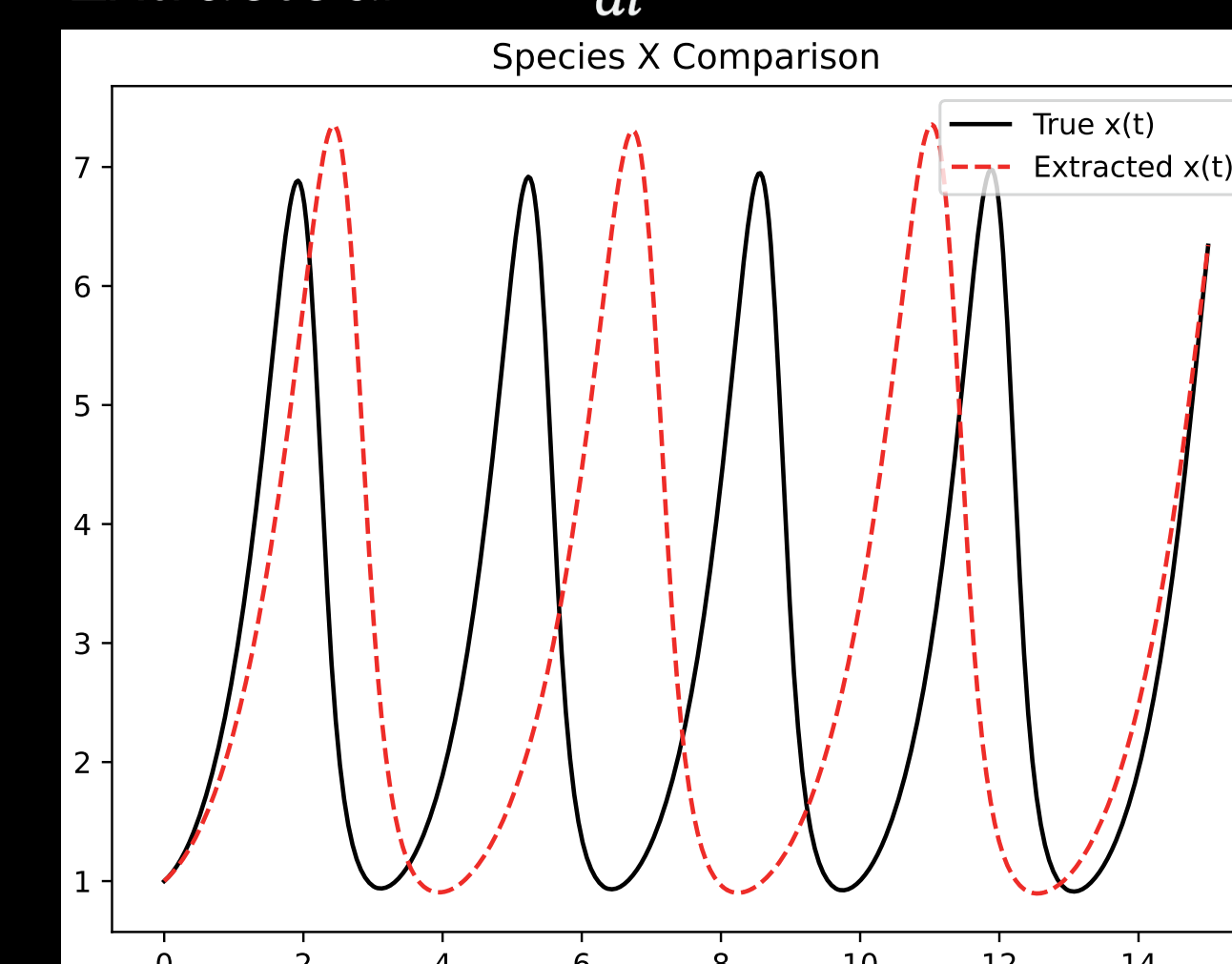
05. EQUATION EXTRACTION



06. RESULTS

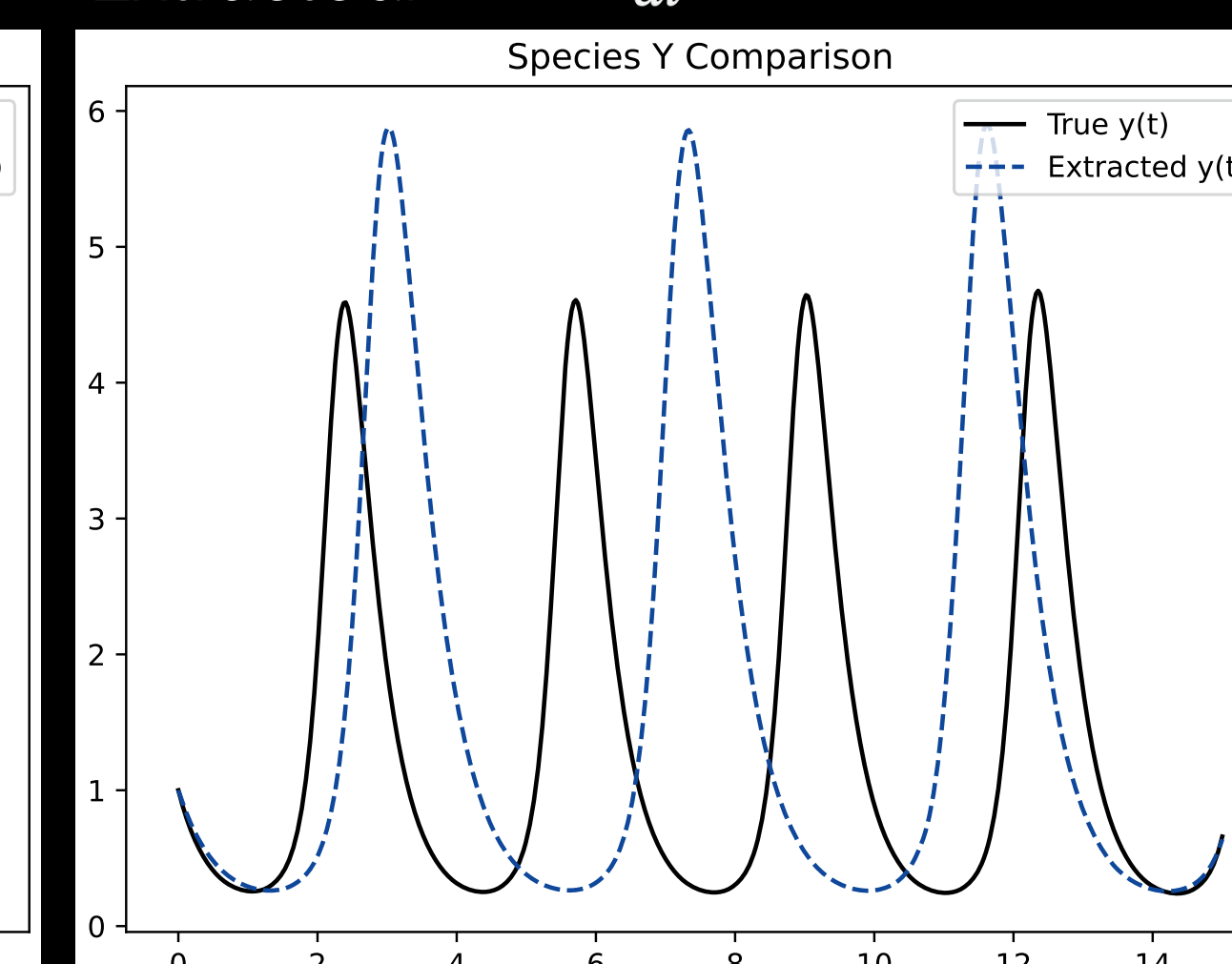
Ground Truth: $\frac{dx}{dt} = 1.5x - 1.0xy$

Extracted: $\frac{dx}{dt} = 1.15x - 0.64xy$



Ground Truth: $\frac{dy}{dt} = 1.0xy - 3.0y$

Extracted: $\frac{dy}{dt} = 0.78xy - 2.40y$



07. CHALLENGES

Multiple equations may fit the same trajectories

Filtering may remove valid but unconventional dynamics

Sensitivity to noise can affect extracted equations

Reliable parameter estimation is required for therapy simulation