

1. Introduction

Aim: Discover non-linear epidemic dynamics directly from data.

Method: Use a modified Monte Carlo Graph Search (MCGS) for Dynamical Symbolic Regression (DSR).

Motivation (1): Epidemic model discovery

ODE system: $\frac{d\mathbf{x}_t}{dt} = \dot{\mathbf{x}}_t = f(\mathbf{x}_t, \theta)$.

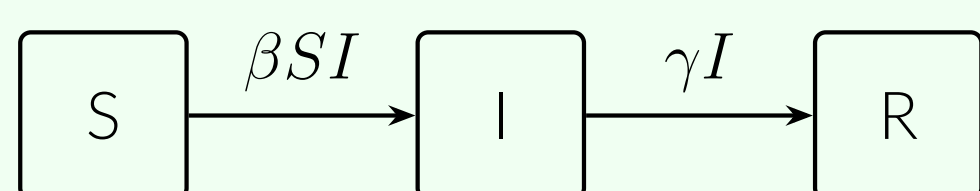
We simultaneously learn the **functional form** of the ODEs, $f(\mathbf{x}_t, \theta)$, and estimate its **parameters**, θ . This avoids **restrictive assumptions** of traditional models.

Motivation (2): Interpretability

DSR outputs **explicit, parsimonious mathematical expressions** for ODEs. Interpretability is key for policymakers who require more than ‘black-box’ reasoning to justify public health decisions.

2. SIR Dynamics

Figure 1. Dynamics of the Susceptible-Infectious-Recovered (SIR) model.



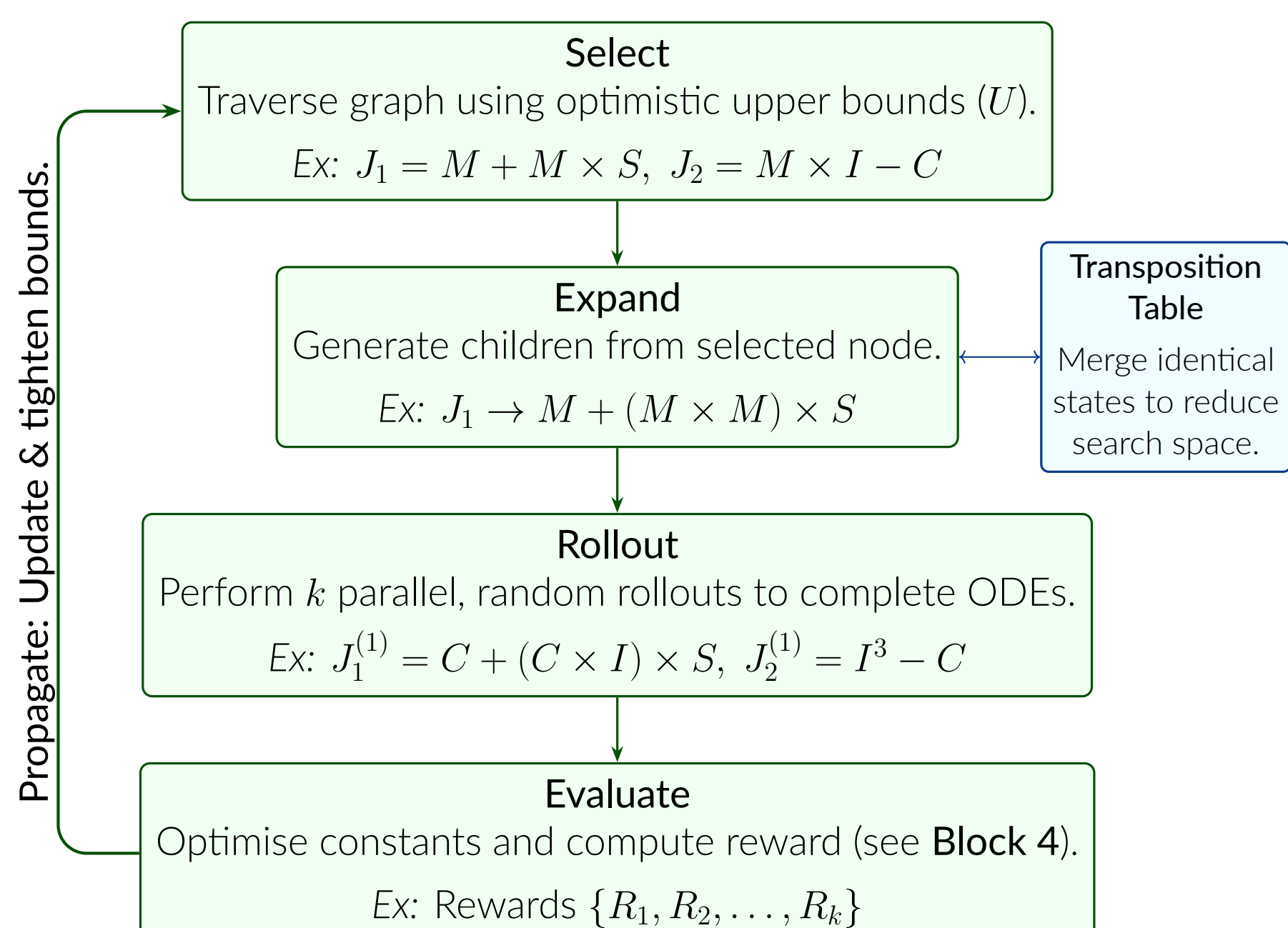
We leverage system stoichiometry to perform flux discovery as opposed to full model discovery:

$$\begin{bmatrix} \dot{S} \\ \dot{I} \\ \dot{R} \end{bmatrix} = \underbrace{\begin{bmatrix} -1 & 0 \\ +1 & -1 \\ 0 & +1 \end{bmatrix}}_{\text{stoichiometry}} \times \underbrace{\begin{bmatrix} J_1 \\ J_2 \end{bmatrix}}_{\text{fluxes}} = \underbrace{\begin{bmatrix} -J_1 \\ J_1 - J_2 \\ J_2 \end{bmatrix}}_{\text{coupled ODEs}}$$

- Infection flux, J_1 , should learn βSI .
- Recovery flux, J_2 , should learn γI .
- Fluxes $[J_1, J_2]$ are learnt simultaneously.

3. Method

- **Grammar:** Context-free grammar describing valid actions.
- **Symbolic graph:** Nodes represent partial/complete generated ODEs; edges represent grammar rules.
- **Transposition table:** Track existing states to allow merging of identical states reached via different paths.
- **Bounds:** Optimistic upper bound U and guaranteed lower bound L .



4. Reward Function

- Generated ODEs undergo **constant optimisation** to minimise trajectory MSE.
- Estimated trajectories are computed by applying **Euler's integration method** to generated ODEs.
- Reward function evaluates ODEs, balancing **parsimony** and **fit**:

$$R = \frac{\eta^c}{1 + \text{MSE}} \in (0, \eta)$$

where:

- η is a hyperparameter controlling equation parsimony ($\eta < 1$).
- c measures equation complexity of the fluxes.
- MSE represents the mean-squared error between true and estimated trajectories.
- Rewards are also used to update the **guaranteed lower bounds** (L) of nodes.

5. Results

The method successfully reconstructs trajectories given multiple realisations, even in noisy data settings.

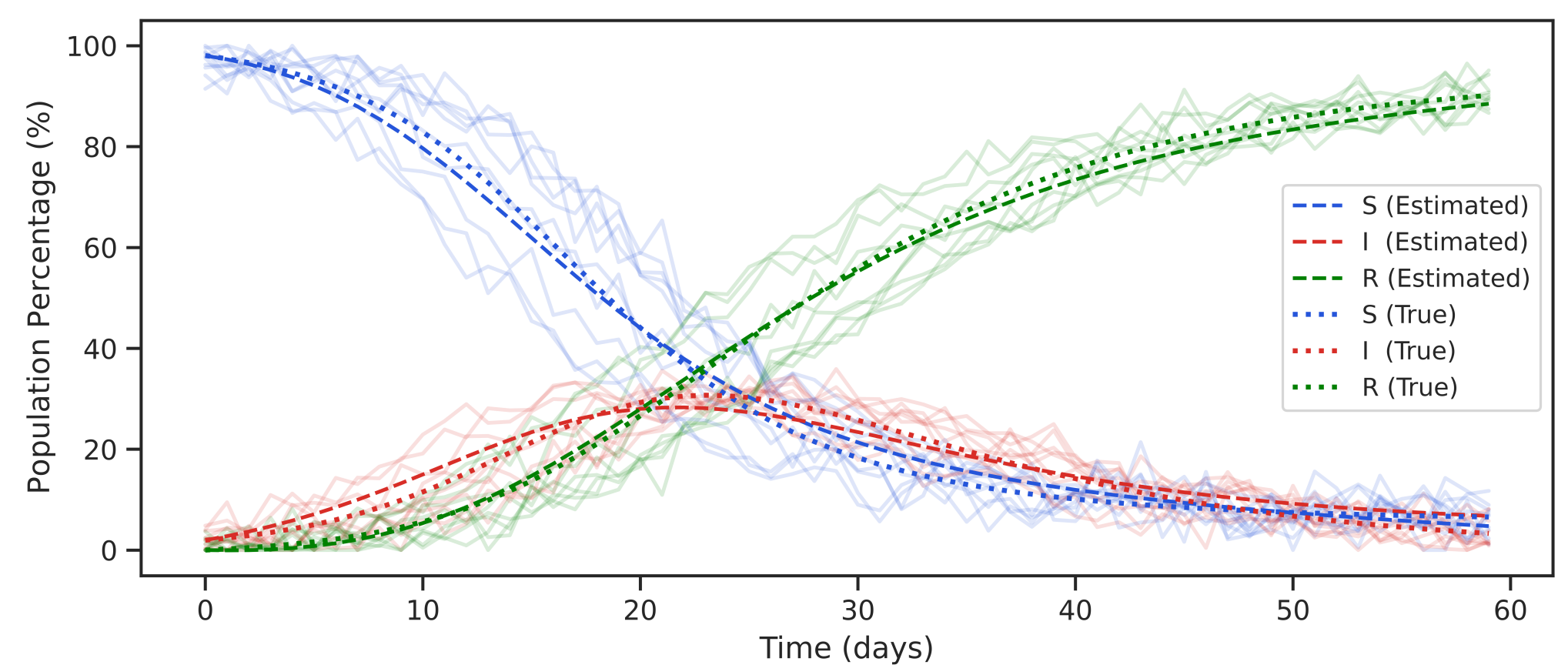


Figure 2. **Trajectory reconstruction:** Comparison of true vs. estimated SIR states. Light lines show the 10 noisy, independently simulated training trajectories, representing different regions.

The correct terms are largely identified in the top-scoring inferred equations.

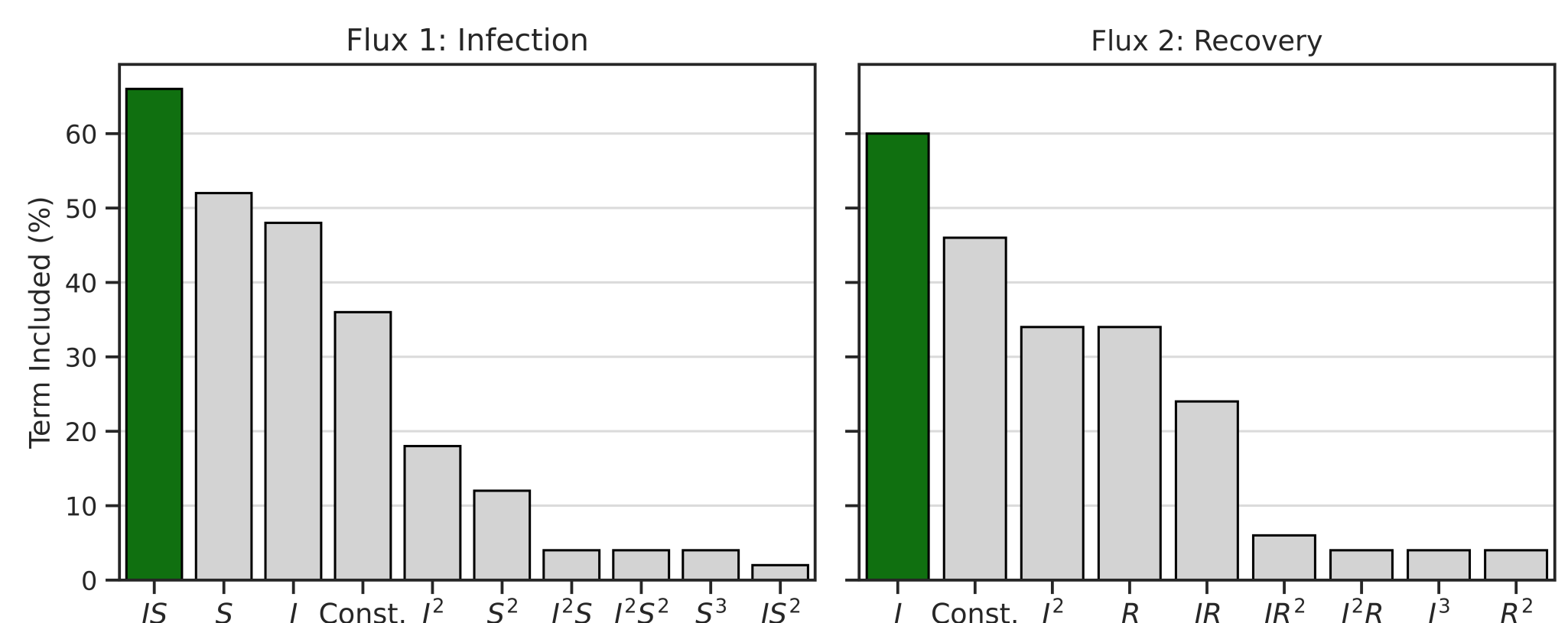


Figure 3. **Equation discovery frequency:** The proportion of times different terms appear in the top 50 equation sets. Green bars indicate the correct ground truth terms for the infection and recovery flux.

References

- [1] Edouard Leurent and Odalric-Ambrym Maillard. Monte-Carlo Graph Search: the Value of Merging Similar States. In *Asian Conference on Machine Learning*, pages 577–592. PMLR, 2020.
- [2] Fangzheng Sun, Yang Liu, Jian-Xun Wang, and Hao Sun. Symbolic Physics Learner: Discovering governing equations via Monte Carlo tree search. *arXiv preprint arXiv:2205.13134*, 2022.