

Report from project SAD2

1 Datasets and Ground Truth

Datasets (simulated trajectories) and their corresponding ground-truth Boolean networks are generated by sweeping the following parameter grid:

Parameter	Values
<i>Network parameters</i>	
<code>n_nodes</code>	{5, 8, 11, 16}
<code>network_seed</code>	{0, 1}
<i>Trajectory parameters</i>	
<code>n_trajectories</code>	{1, 5, 20}
<code>sync transition</code>	{True, False}
<code>trajectory_len</code>	{5, 20, 100}
<code>sampling_frequency</code>	{1, 3}

Table 1: Parameter grid used for generating datasets and ground-truth networks.

Larger networks (e.g., `n_nodes` > 12) significantly increased runtime for both dataset generation and BNFinder inference, so instead of exhaustively testing all sizes we used a representative set spanning the range [5, 16]. In total, the sweep contains $4 \times 2 \times 2 \times 3 \times 3 \times 2 = 288$ parameter combinations, which already requires substantial computational effort during evaluation. In addition, we tracked the `attractor_state_percentage`, which varies between 0 and 1 depending on the trajectory. Overall, the chosen grid allowed us to assess which conditions favor accurate graph-structure inference.

2 Evaluation

- **Reconstruction setup.** We used the simplest BNFinder invocation: `bnf -e input1.txt -n output1.sif -l 3`. The key adjustment was `-l 3`, which limits each Boolean function to at most three parents; this greatly reduces the search space and speeds up reconstruction.
- **Scoring functions.** We evaluated candidate network structures using two BNFinder-recommended scores: *Minimal Description Length (MDL)* and *BDe (Bayesian-Dirichlet equivalence)*.
- **Loss functions (accuracy metrics).** We measured structural prediction error using `edge jaccard distance` and `graph edit distance`: together they capture both *local edge overlap* (exact wiring agreement) and *global topological discrepancy* (how many edits are needed to transform one graph into the other). We chose these metrics because they are widely used in graph-structure evaluation and provide complementary views of reconstruction quality.

- Final conclusions** We ran a wide range of parameter configurations, and presenting all plots here would be unreadable - we chosen the most significant ones. The results varied substantially—from near-perfect reconstruction to almost no correct edges. Overall, the most influential factor was dataset size: more trajectories and longer trajectories consistently improved performance (Figure 3). This matches intuition, since larger datasets provide more information for inference. In contrast, we did not observe a clear difference between synchronous and asynchronous transitions, nor between the MDL and BDe scoring methods. Finally, we observed a slight negative (figure 4) correlation between network size and reconstruction accuracy, which is also intuitive: larger networks are generally harder to infer accurately.

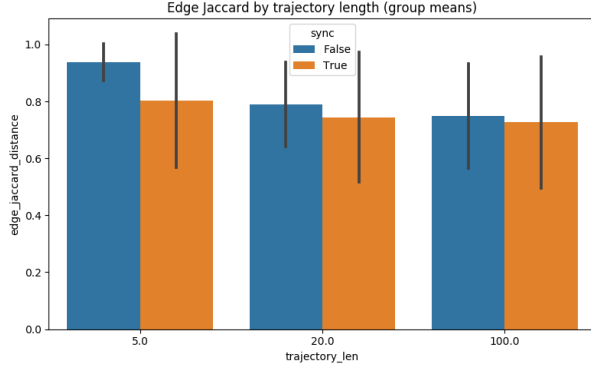


Figure 1: *

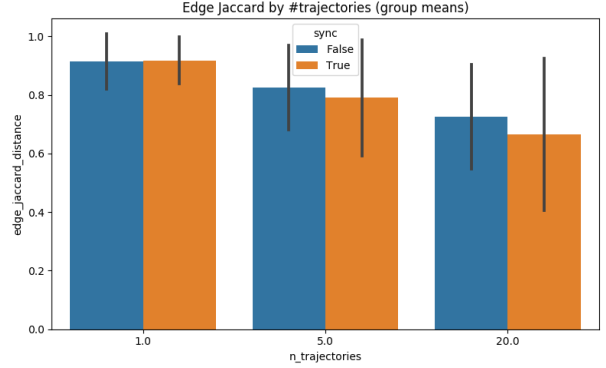


Figure 2: *

Jaccard vs. trajectory length (MDL)

Jaccard vs. number of trajectories (MDL)

Figure 3: Edge Jaccard distance under MDL for two dataset axes.

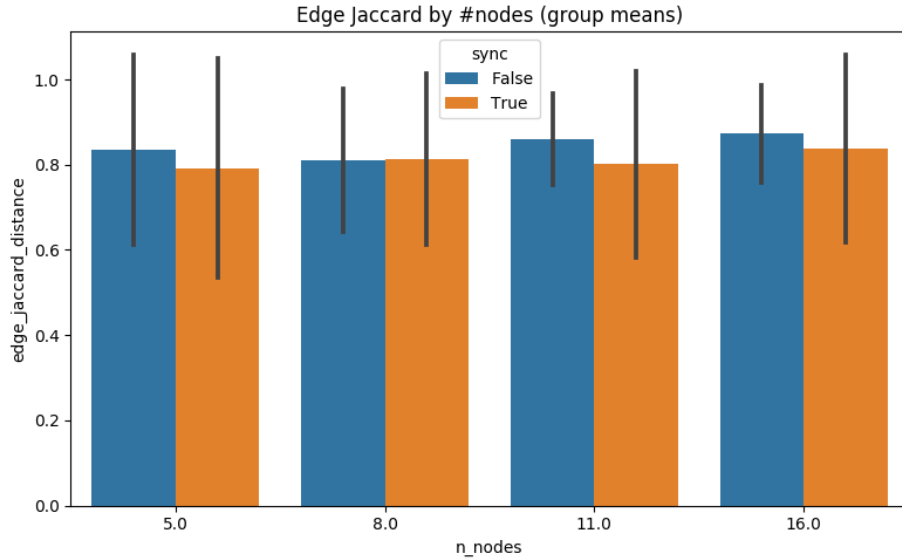


Figure 4: Edge Jaccard distance under MDL as a function of network size (n_nodes).

3 Challenges encountered

- **Legacy environment constraints.** One of the biggest challenges was setting up a fully compatible Python 2.7 environment (libraries, type checking, and tooling), since BNFinder does not support Python 3+. This turned out to be a valuable lesson in reproducibility: some of us managed the setup via `pyenv`, while others had to rely on Docker due to limited compatibility of their local machines with that early of a Python version.
- **Computational cost of the sweep.** To meaningfully assess how inference quality depends on key parameters (e.g., transition mode, network size etc.), we needed to run evaluations for a few hours, which limited how many additional combinations we could explore. To reduce runtime, we parallelized runs where possible and used BNFinder’s `-l` option to cap the maximum number of parents per node, substantially decreasing computational burden.