

Visualizing ensemble time-evolving probability landscapes of stochastic networks

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Introduction

The computational study of dynamic and stochastic gene regulatory networks is a challenging topic in systems biology. Such studies result in large numbers of stochastic simulations, which feature many states across many timesteps. Visualizing and comparing the resulting time-evolving probability landscapes can help the biologists understand the phenotypic behavior associated with specific genes. However, visualizing this highly-dimensional, spatiotemporal information is difficult. Figure 1 shows an example of probability landscapes, with only two proteins, from N simulations and T timesteps.

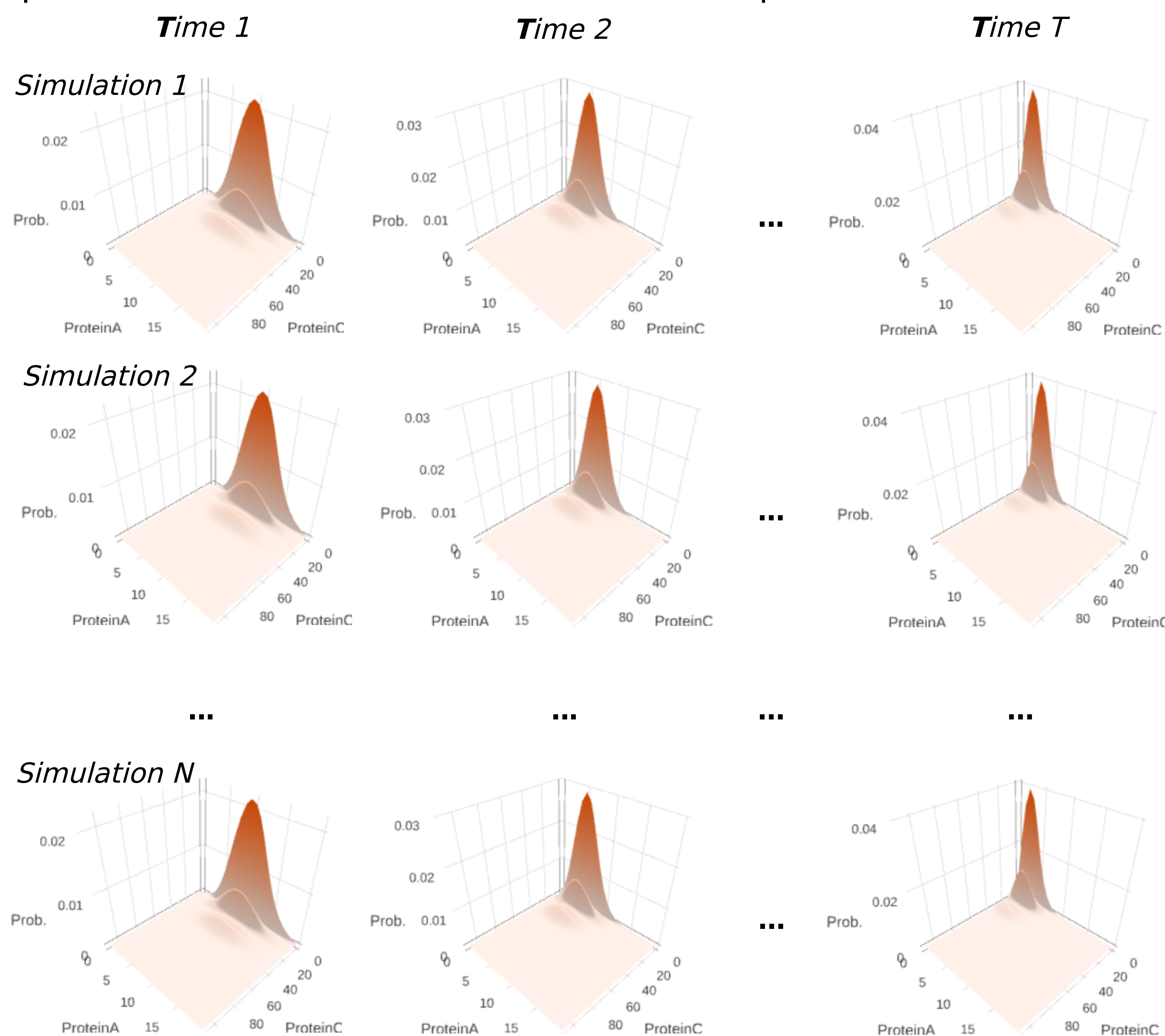


Figure 1. An example of probability landscapes over T time steps from N simulations.

Approach

To address the challenges related to the comparison of peak spatiotemporal distributions among multiple simulations, we propose a web-based visual analysis tool that combines multiple linked views to capture ensemble time-evolving probability landscapes.

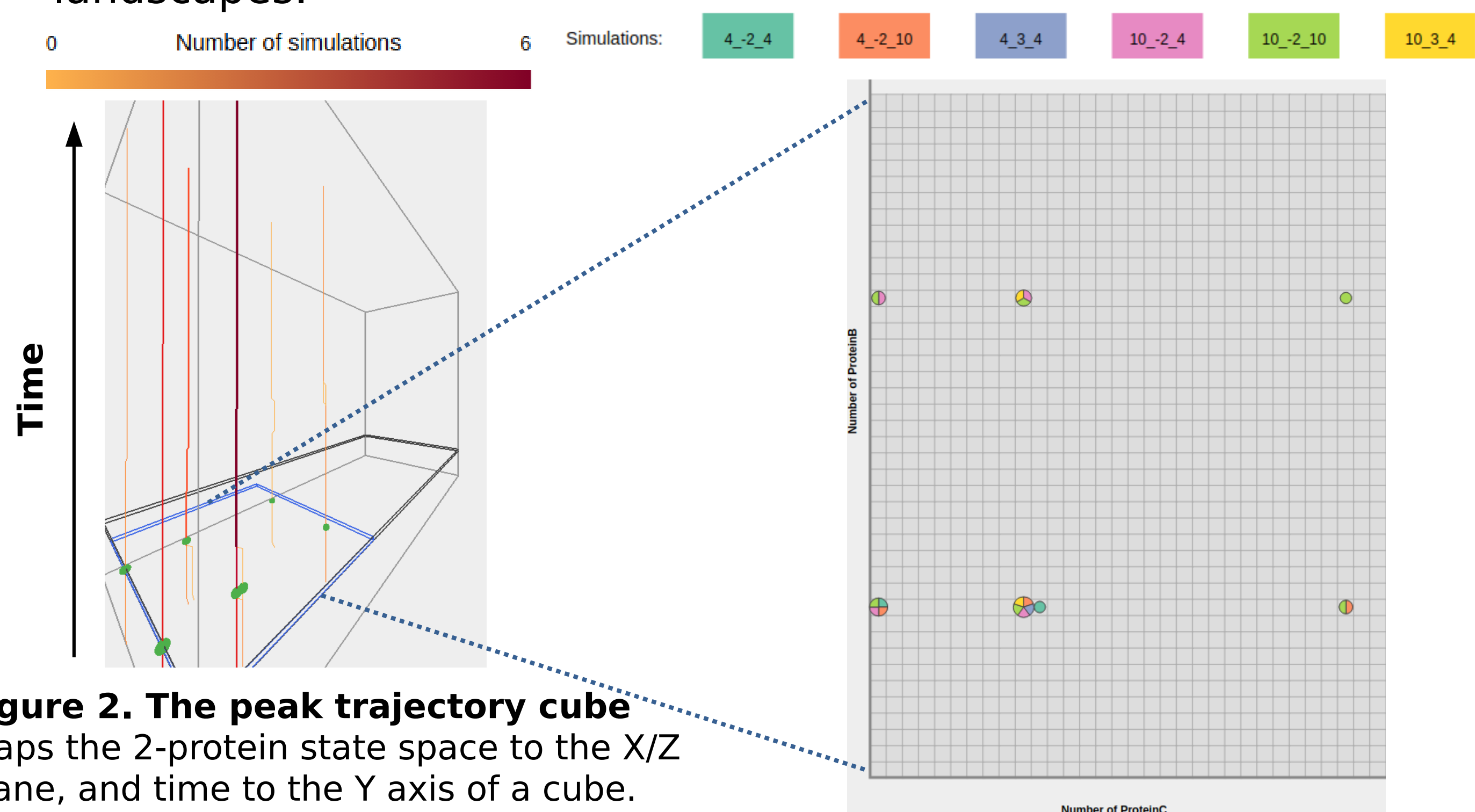


Figure 2. The peak trajectory cube maps the 2-protein state space to the X/Z plane, and time to the Y axis of a cube. Yellow-red polylines map the peaks' (highest probability points) location in this spatiotemporal space, across 6 simulations. The redder the polyline, the more peaks are sharing that trajectory across the simulations. For the selected time (dark gray horizontal rectangle), green dots mark peak locations. Peak locations converge over time. The blue state subarea is mapped to Fig. 3.

Figure 3. The x/y plane of the peak trajectory view is a detailed view of the blue subarea in Fig 2. A glyph encodes with color which simulation runs contain a peak at that glyph location; colors are mapped to simulations. The green simulation has the most peaks among all six simulations.

Overview:

- A peak trajectory cube (Fig. 2) provides an overview of peak distributions in state space and time space across multiple simulations.

For each user selected timestep:

- A peak projection map (Fig. 3) shows the exact peak locations of multiple simulations.

At each user selected state:

- Time-curves (Fig. 4) display the probability values over time.
- A profile-glyph view (Fig. 5) and a arrow glyphs view (Fig. 6) both show the local probability landscape shapes.

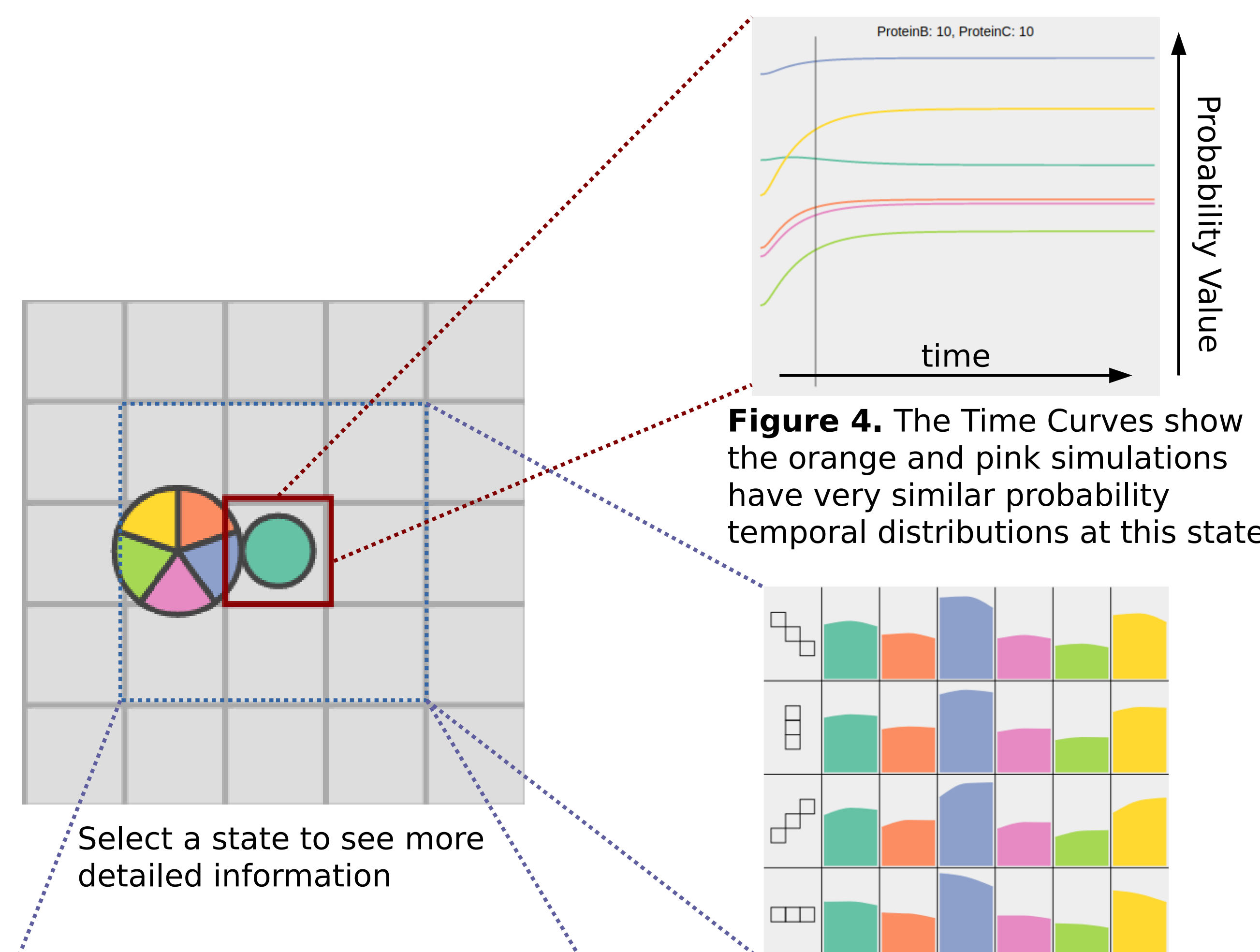


Figure 4. The Time Curves show the orange and pink simulations have very similar probability temporal distributions at this state.

Figure 5. Profile Glyphs show that the peaks in the blue and yellow simulations are steeper than the other four.

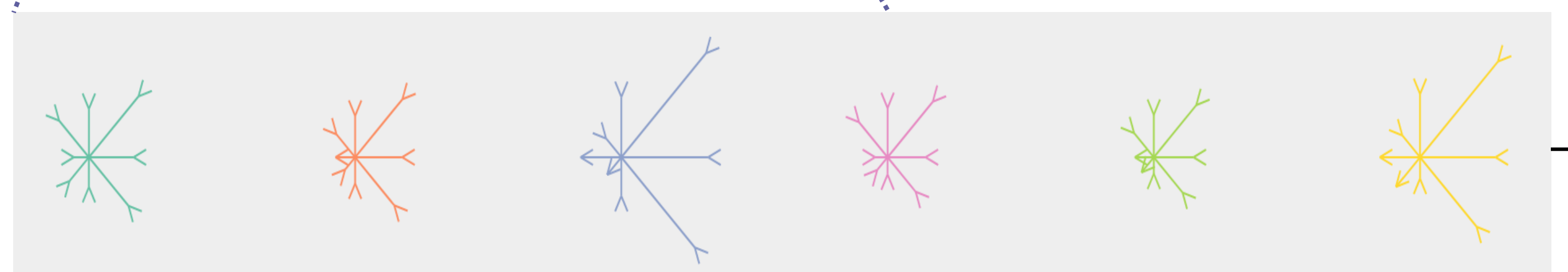


Figure 6. The arrow-glyph indicates that a state is a peak state when all the eight arrows in the glyph point towards the glyph center. The states shown in darker green and pink are peak states. However, the other four states shown are very near a peak state, but are not peaks themselves.

Results

In the figures above, we notice a disagreement between the arrow glyphs and the peak projection map.

This mismatch demonstrates that probability distributions over the genes in this system are not independent of each other.

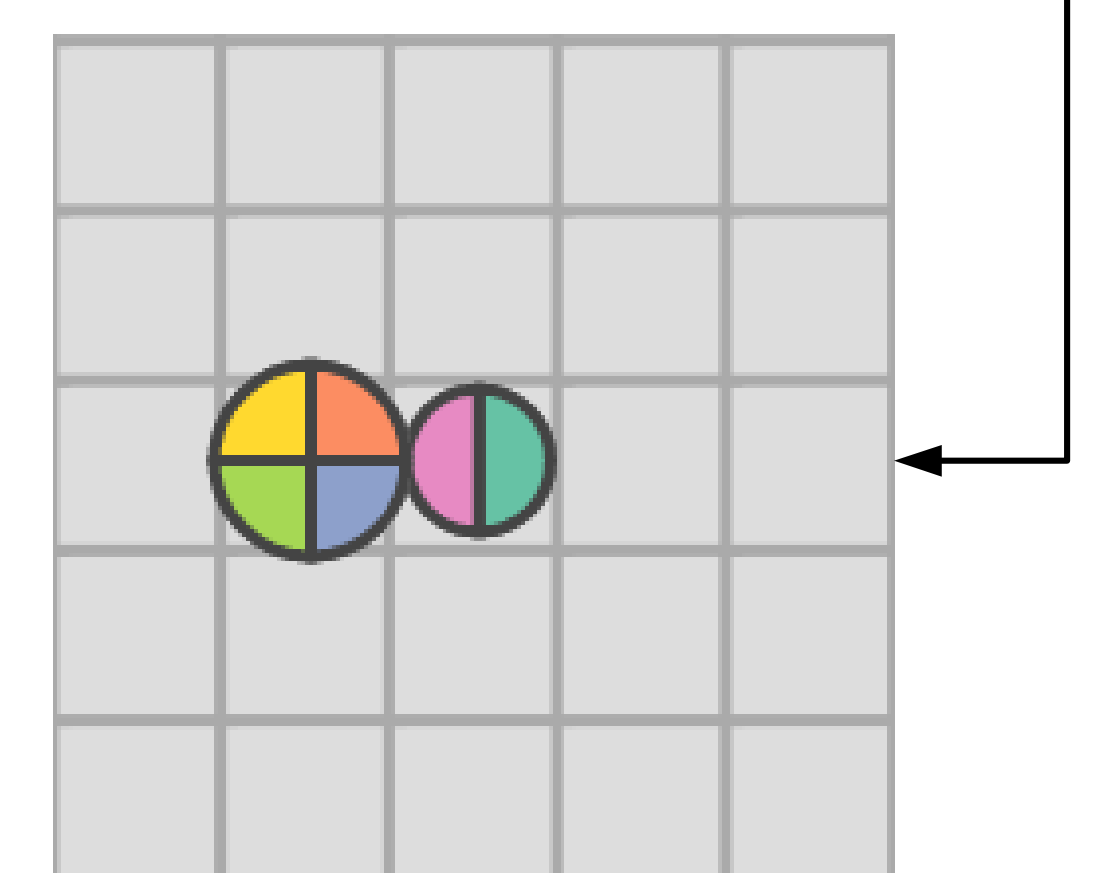


Figure 7. Detail of the state space shown in Fig. 3, with peak distributions derived from arrow glyphs in Fig. 6.

Conclusions

Our visual analysis tool allows bioinformatics researchers to explore and compare the time evolving characteristics of probability landscapes from multiple simulations efficiently, without running many small scripts and computing each characteristic separately.

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References

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