Position: Temporal Measurement Interval Determines Computational and Model Complexity in Single-Cell Perturbation Analysis

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Github: https://github.com/alireza-jafari/SingleCellPerturbationPrediction-TrackabilityRegimes

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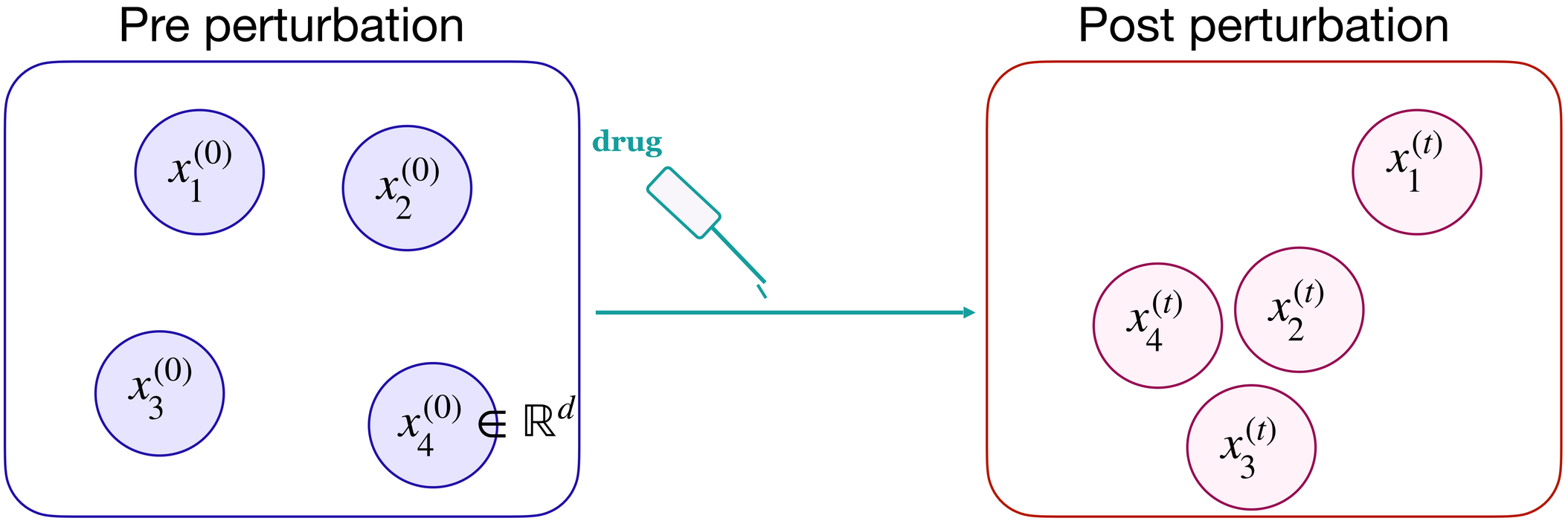
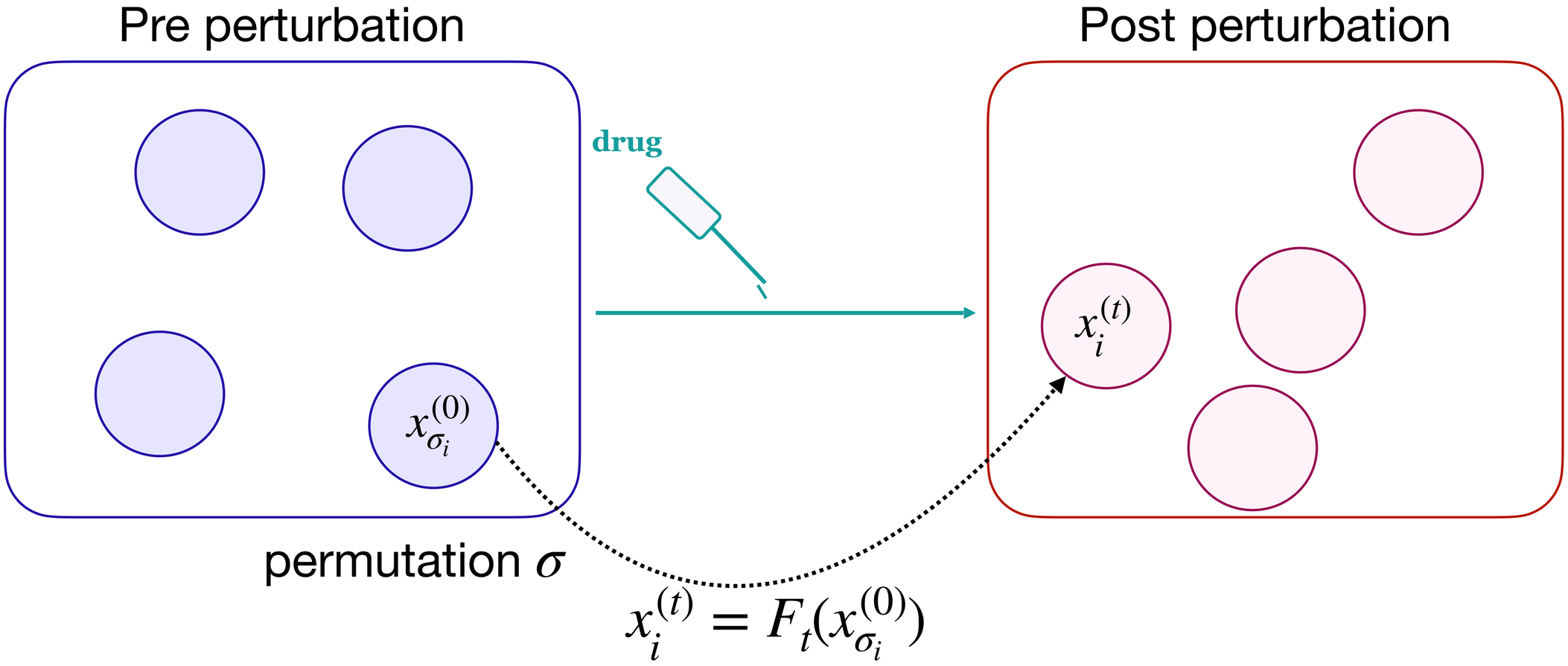
Problem Settings: Single cell perturbation



- How to predict response of (the same or different) cell type to the same drug?

Citations: Schiebinger, G., Shu, J., et al. Cell 2019; Lotfollahi, M., Wolf, F. A., and Theis, F. Nature Methods 2019, Bunne, Stark, et al. Nature Methods 2023

Problem Settings: Single cell perturbation

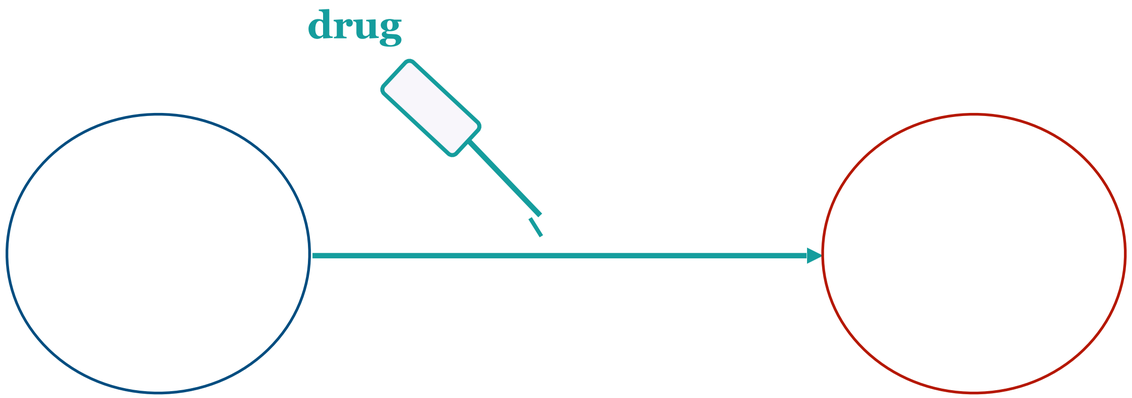


- **Problem:** Finding F_t and permutation σ

Current Approach: Post Experiment Model Selection

- As in many biological applications, model selection is after data collection.

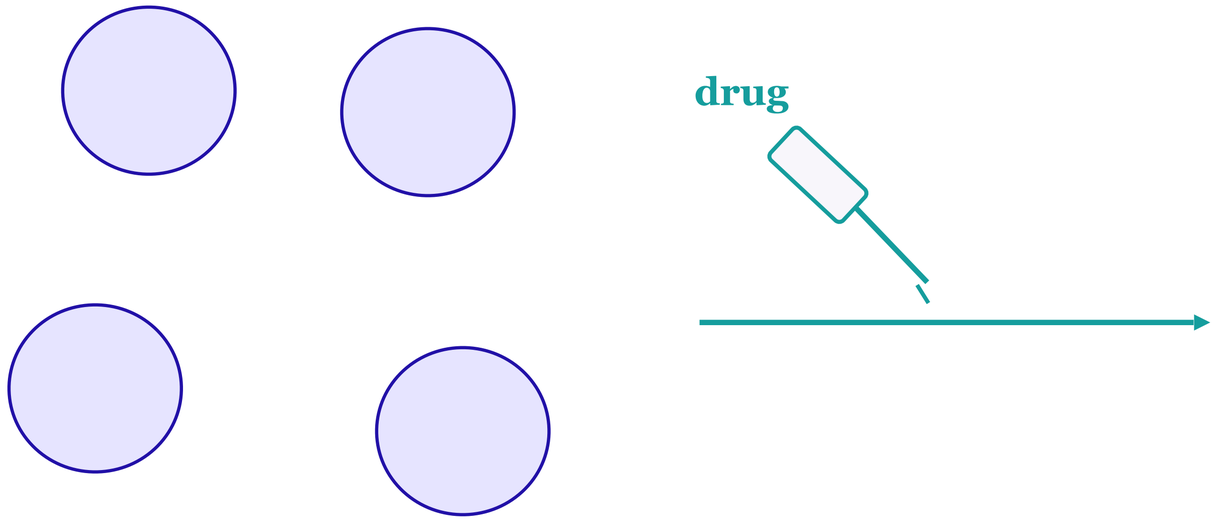
experimental measurements



model selection

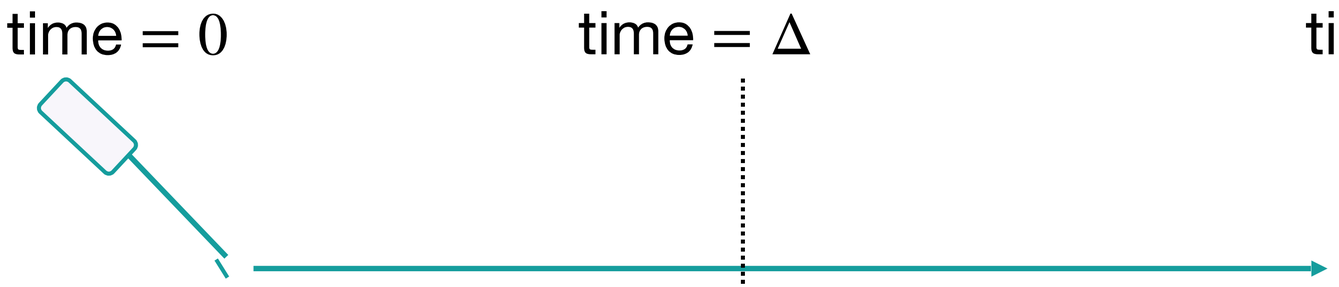
- VAEs [Lotfollahi et al. 2019]
- Convex Neural Nets [Bunne, Stark, et al. 2023]
- Transformers [Adduri, Gautam, et al. 2025]

The Challenge of Computational Complexity



- Even for linear perturbation, the problem is NP-hard
- Based on casting to unlabeled regression problem [Pananjady, Wainwright, and Courtade 2016]

Main Result: Time Determines Complexity



- **Theorem:** there is a Δ such that recovery of perturbation map and permutation

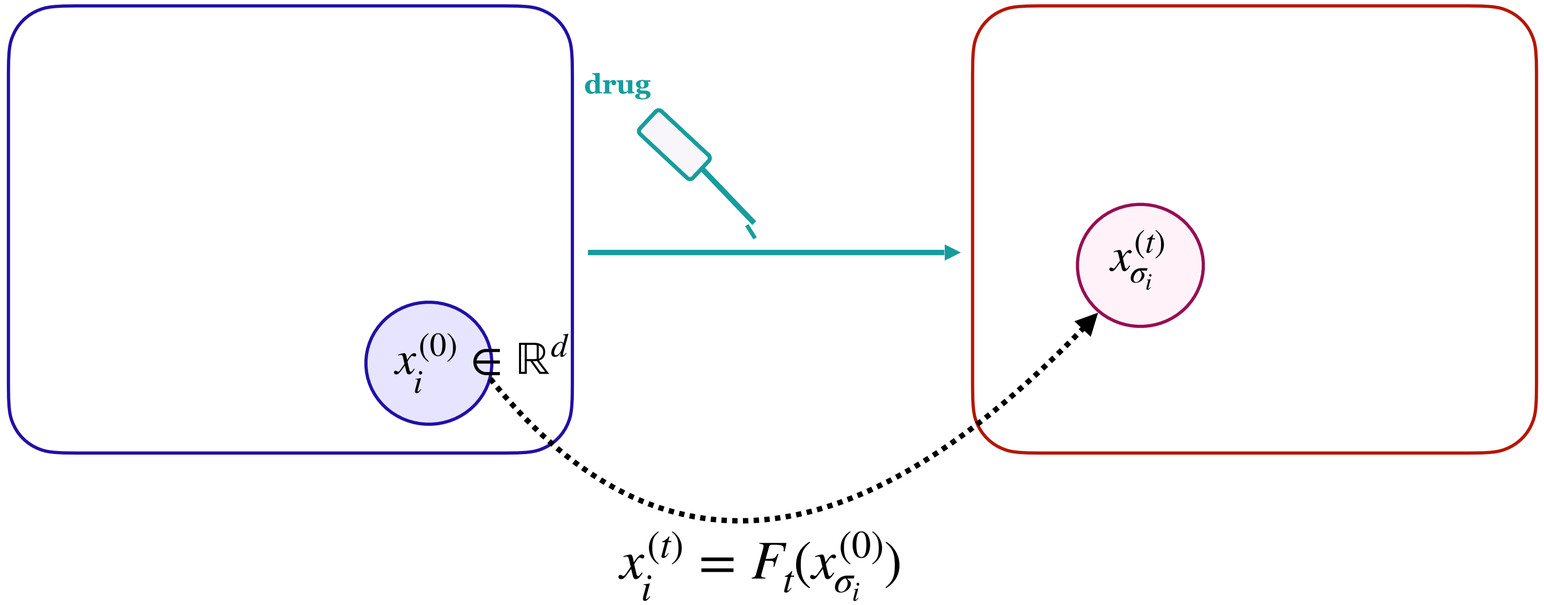
$t \leq \Delta$ Casts to supervised learning

$\Delta \leq t$ is NP-hard regime

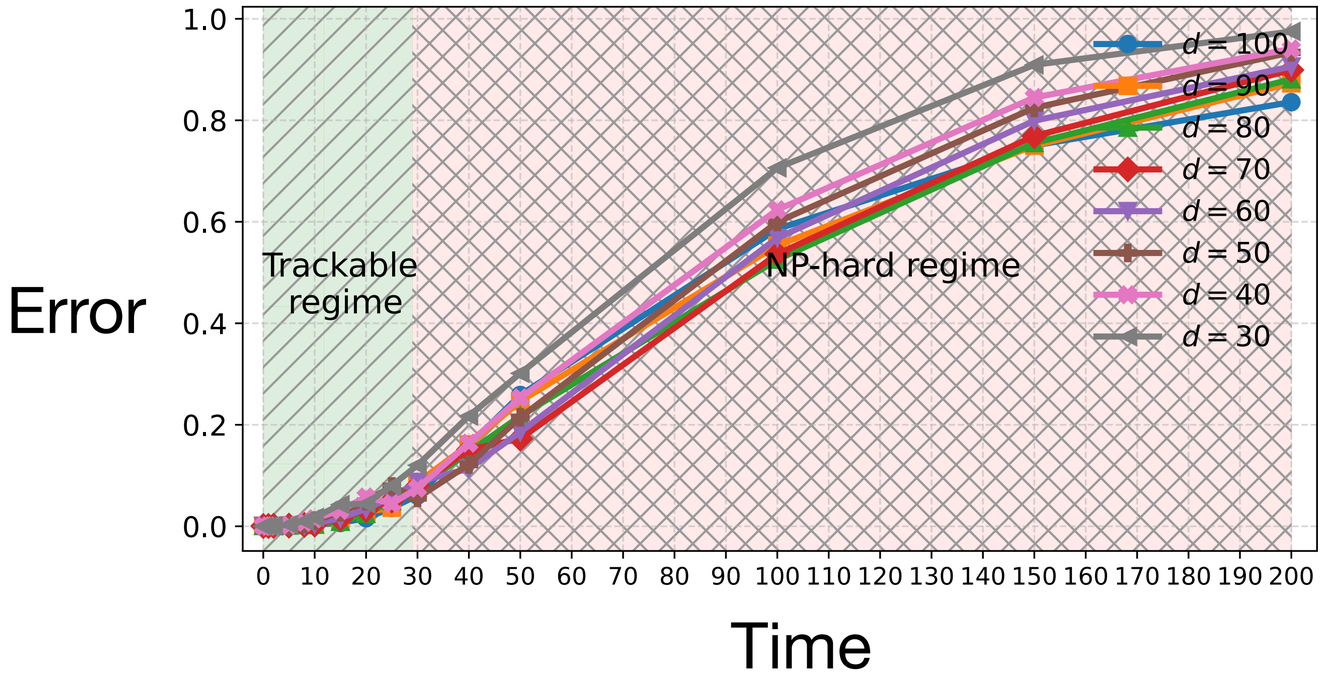
- under **two assumptions**

Assumptions

- The medicine takes time to take effect. Lipschitzness: $\|F_{t'}(x) - F_t(x)\| \leq L\,|t - t'|$
- Restricted Isometry Property (RIP) (Candes & Tao, 2005)



Experimental results



- Observation: Across several benchmarks in the trackable regime, **a linear model** achieves performance comparable to state-of-the-art **nonlinear models.**

Thank you very much for your attention

Poster Time and Location: Wed, Jul 8, 2026 • 10:30 AM – 12:15 PM KST @Coex: HALL A

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