

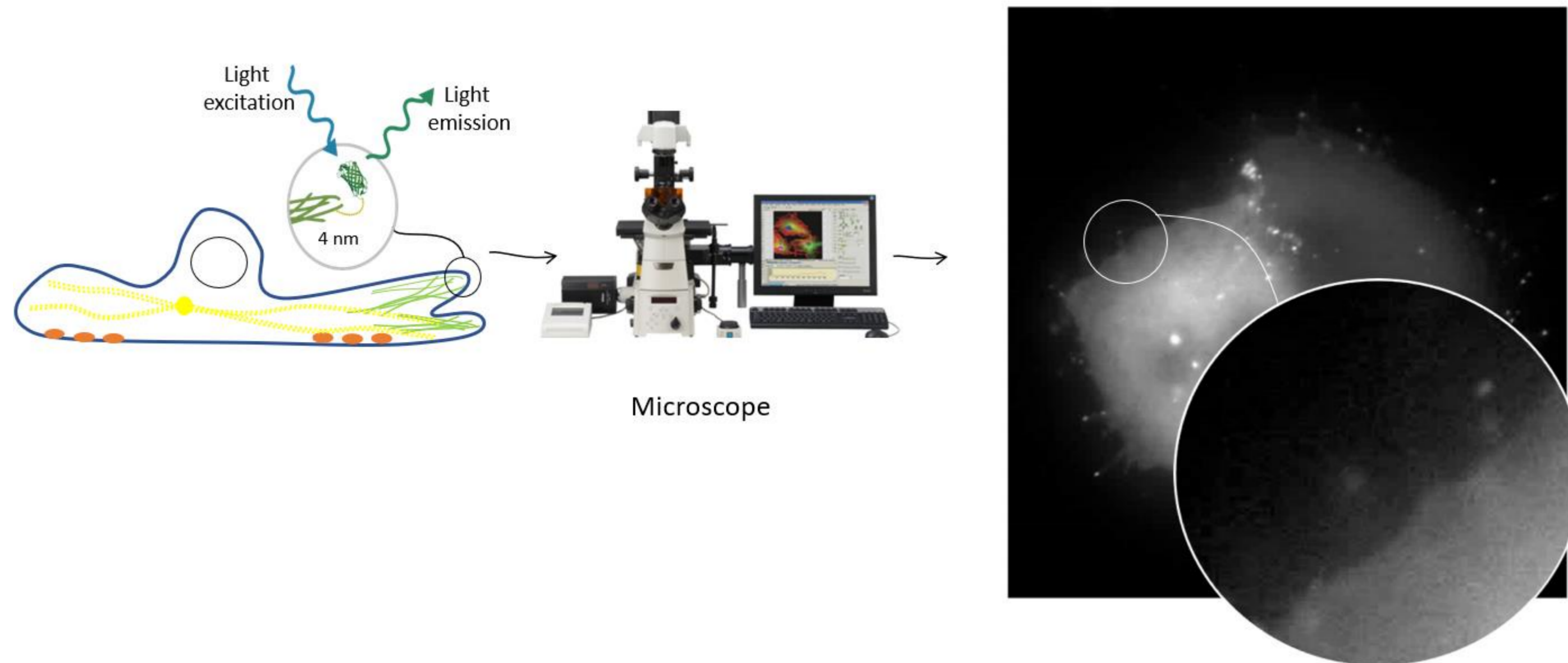
# Weakly-supervised inferences of molecular dynamics for fluorescence imaging in physiological environments

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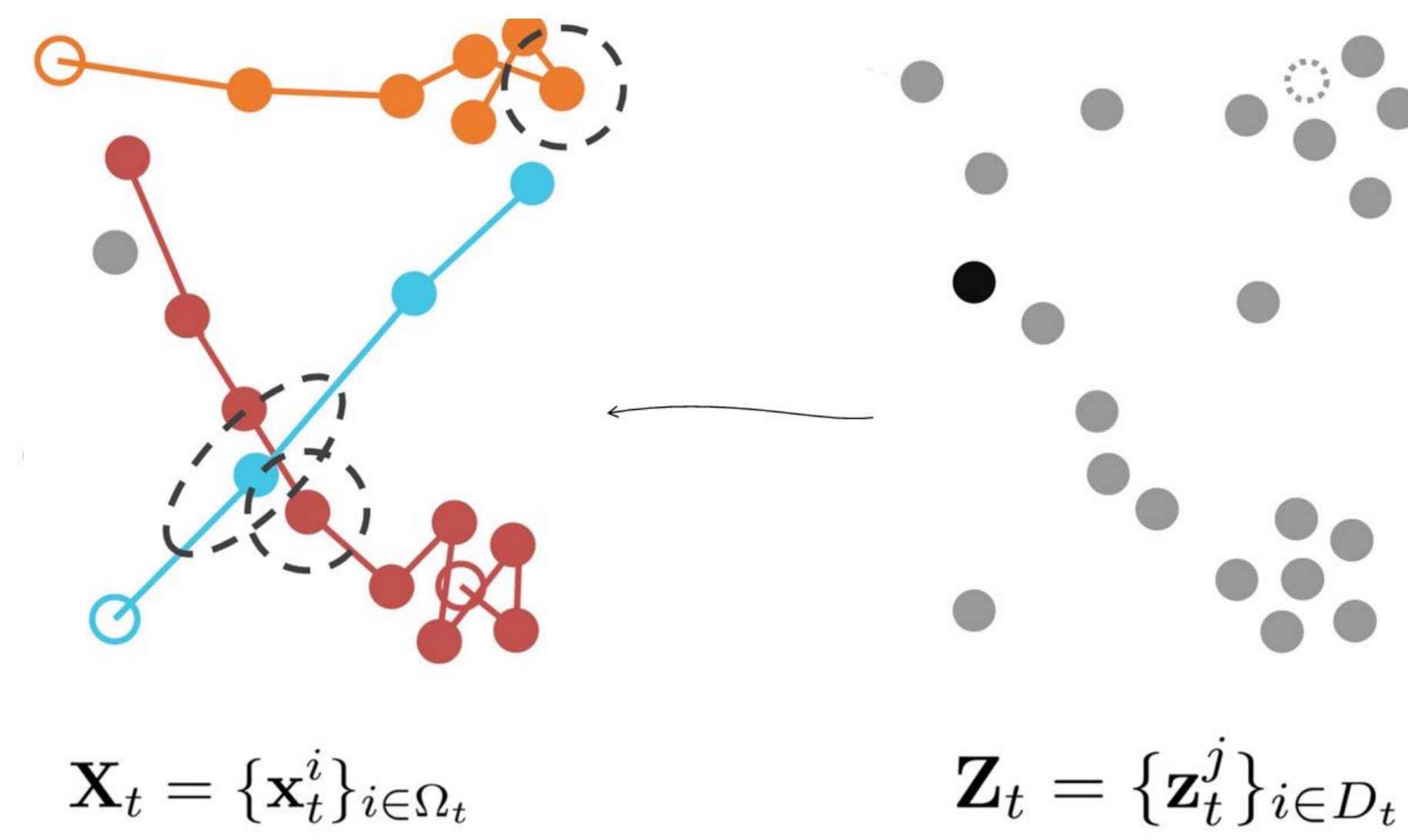
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## A. Context

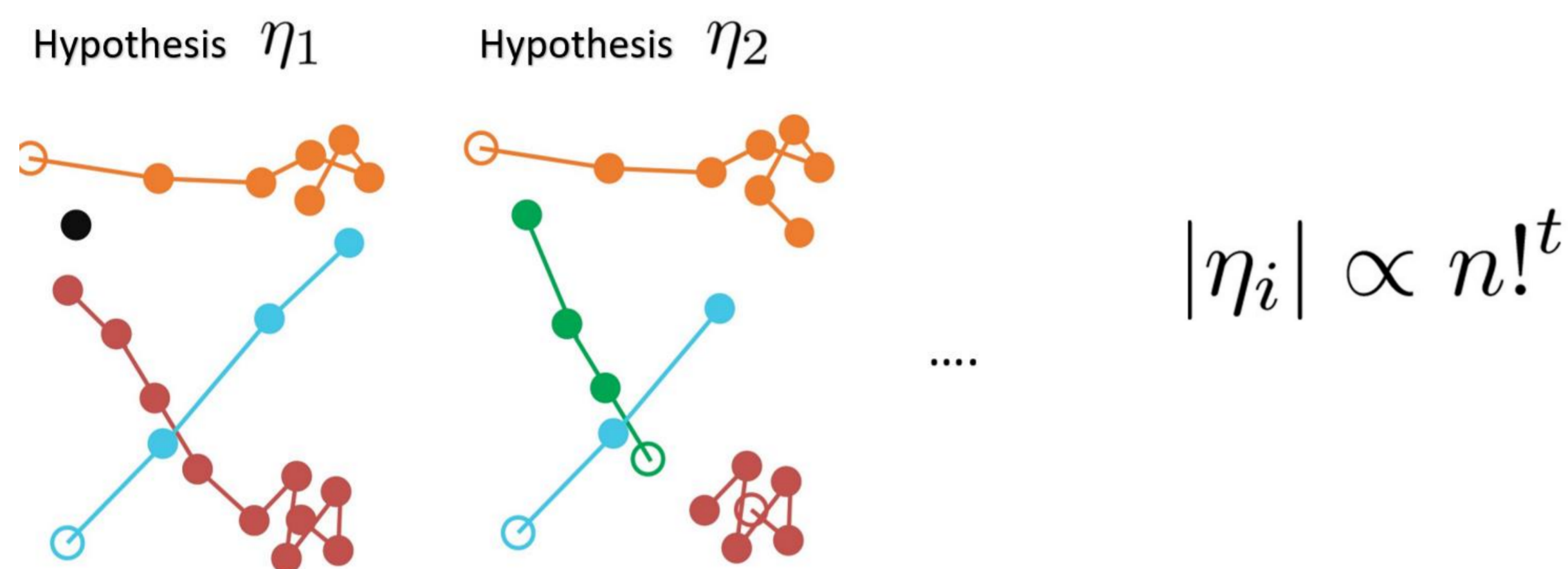
Measurements from fluorescence microscopy are noisy & cluttered [1]



Mapping measurements to trajectories is an inverse data association problem [2]



Data association is a combinatorially hard problem [3]



Conventional methods (like MHT) are untractable

$$p(X_t|Z_{1:t}) = p(Z_t|X_t) \int p(X_t|X_{t-1})p(X_{t-1}|Z_{1:t-1})dX$$

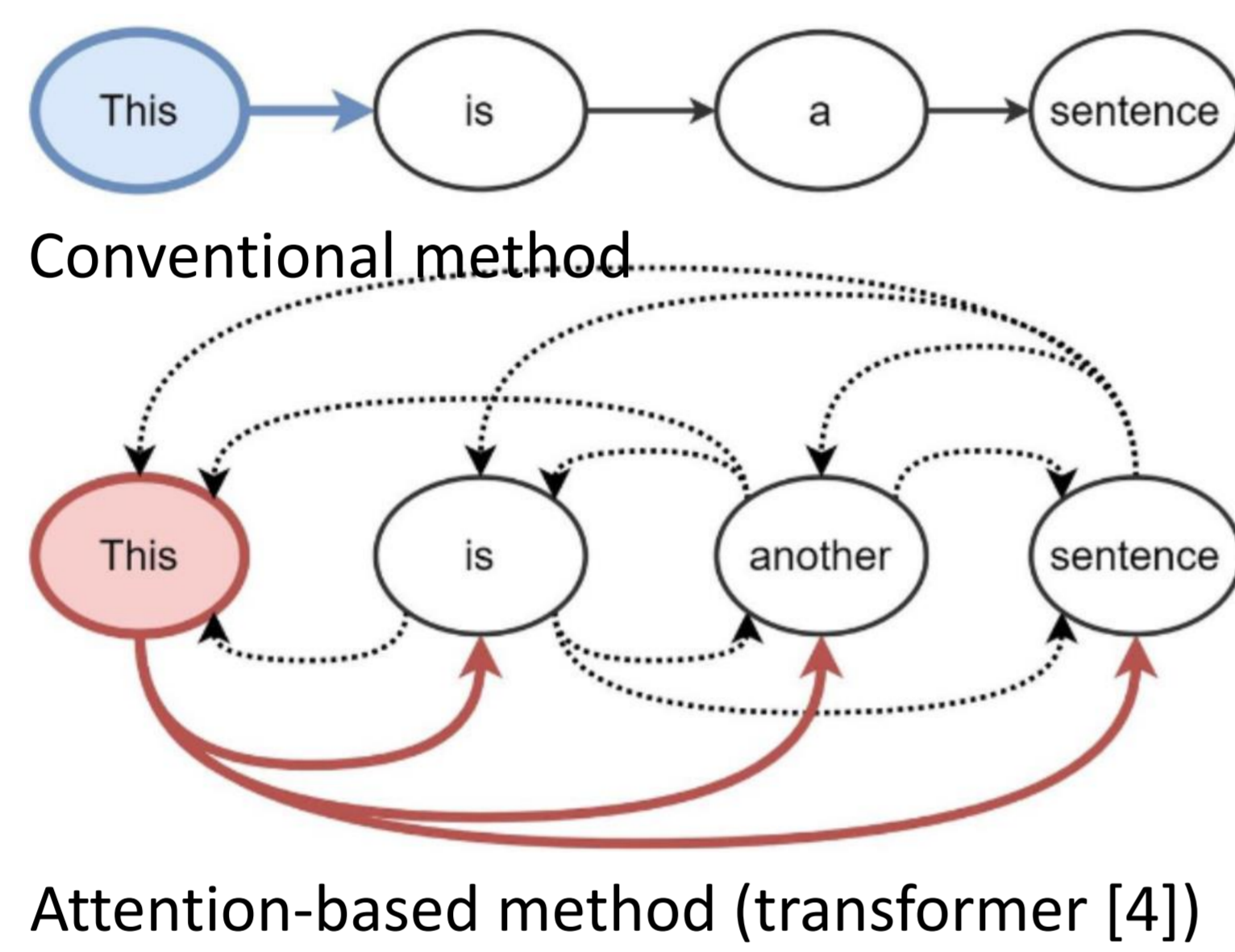
$$\sum_{\eta_i \in H_t} p(Z_t|X_t, \eta_i^t) p(\eta_i^t|X_t) \int p(X_t|X_{t-1})p(X_{t-1}|Z_{1:t-1})dX$$

difficult to account for the super-exponential increase in hypotheses

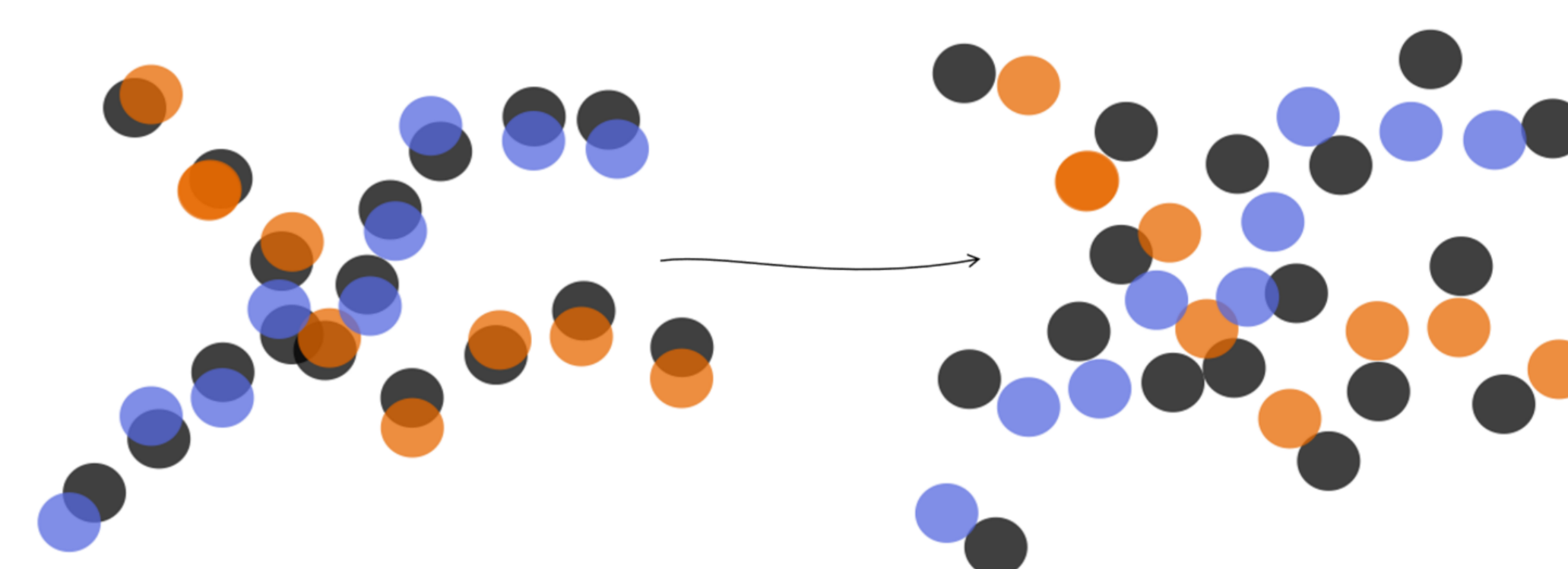
often, we don't have a priori information

Can LLMs be used for long-range sequence-dependencies & combinatorial complexity?

## B. Method



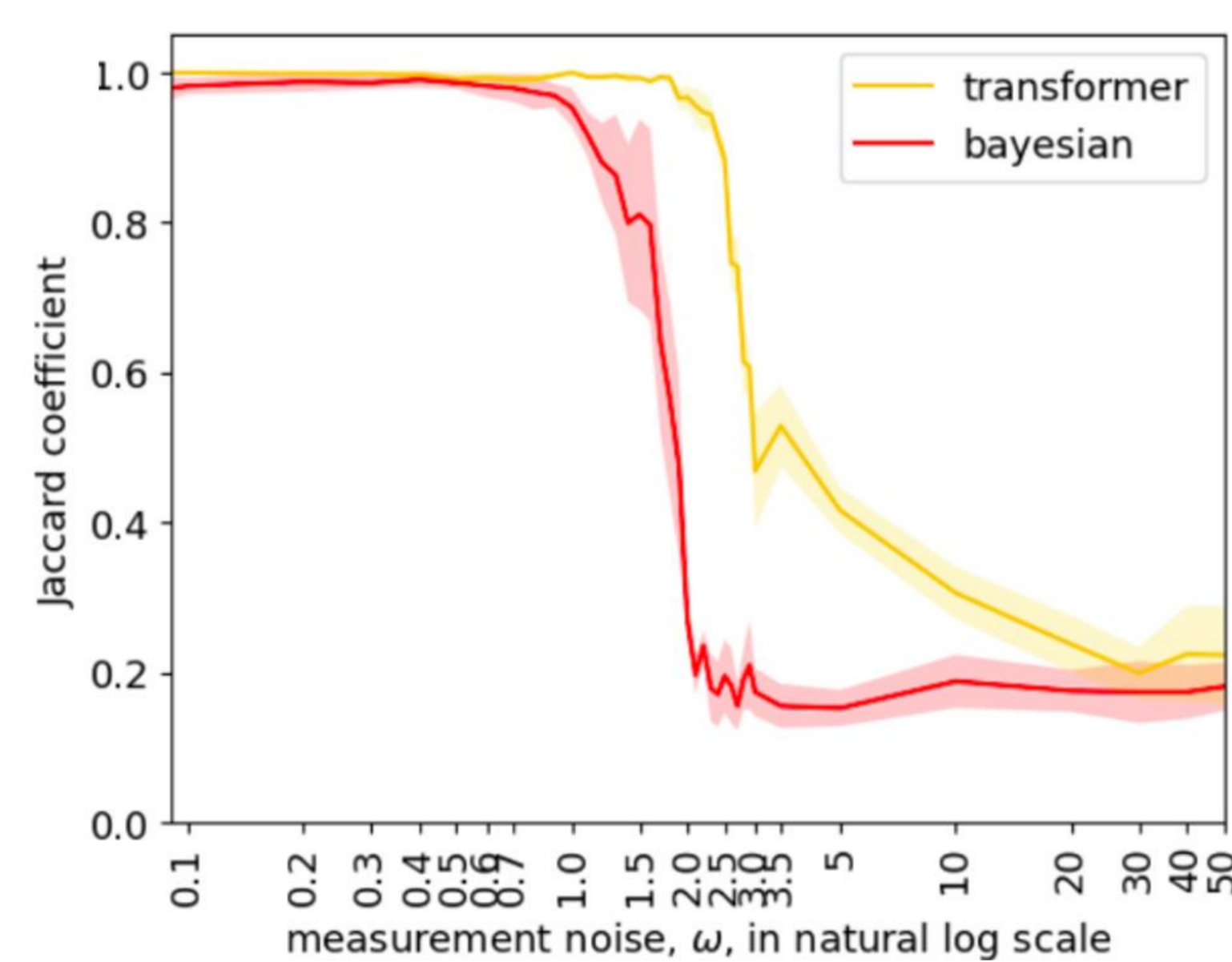
### Experimental setup



Simulation of a simple system of 2 particles in 2 dimensions without any false positives & increasing measurement noise following standard Brownian motion

## C. Main Results: Transformers are robust for long sequences but MHT remains optimal for short sequences

### Robust to increasing noise

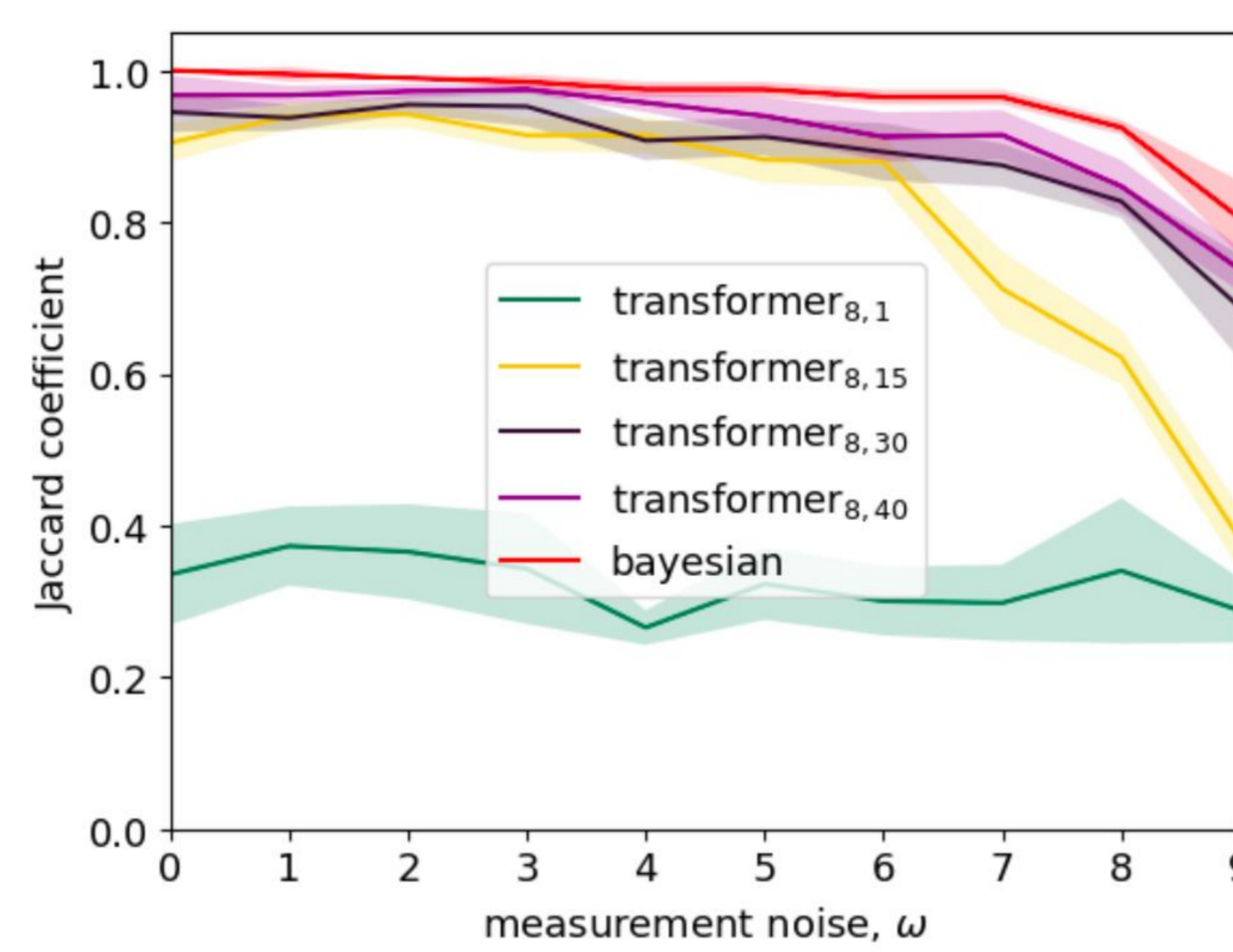


While attention prolongs the noise-cliff, it breaks the same way as MHT does

**Hypothesis: MHT would be optimal (and hence, perform best) if it could easily access the entire lookback window.**

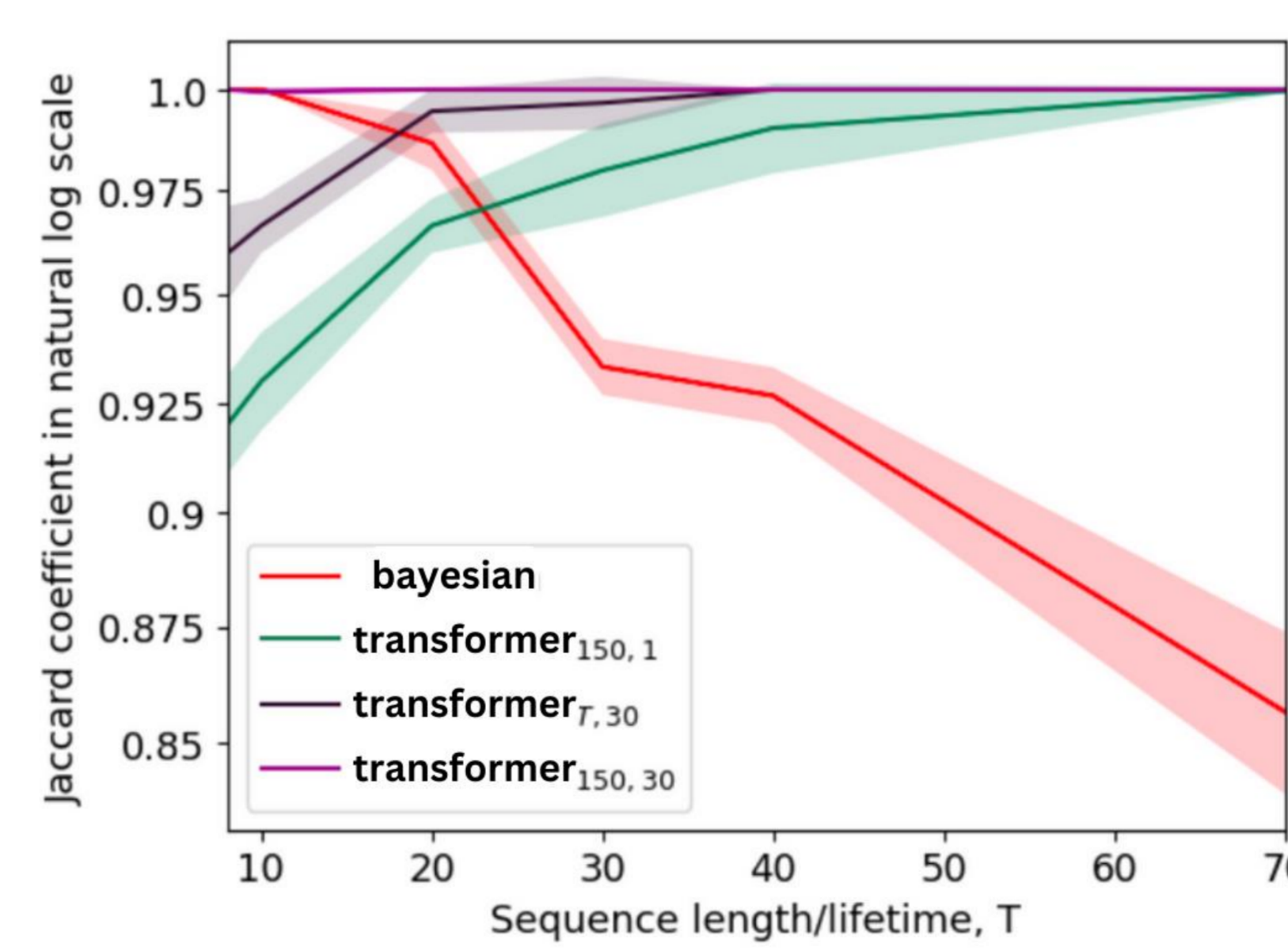
For small sequences, this is still feasible. What happens then?

### When MHT is optimal



When MHT is indeed optimal, i.e., for small sequences, attention is unable to match its accuracy

### Hint to hybridise?



Emergence of 2 regimes: small sequences where MHT performs better and big sequences where attention performs better

**If trained enough times, attention performs better in both regimes!**

### References:

- [1] Vonesch et al, 2006
- [2] P. Emami, P. M. Pardalos, 2020
- [3] Reid, 1979
- [4] Vaswani et al, 2017

### Acknowledgements:

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