


Bayesian inference of transcription dynamics from population snapshots of single-molecule RNA FISH in single cells

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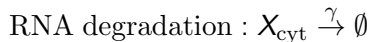
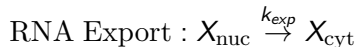
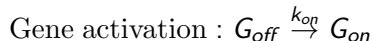


BayFish: Bayesian inference of transcription dynamics from population snapshots of single-molecule RNA FISH in single cells

Mariana Gómez-Schiavon^{1,2}, Liang-Fu Chen³, Anne E. West^{3*} and Nicolas E. Buchler^{4,5,6*} 

A spatial model for induced gene expression

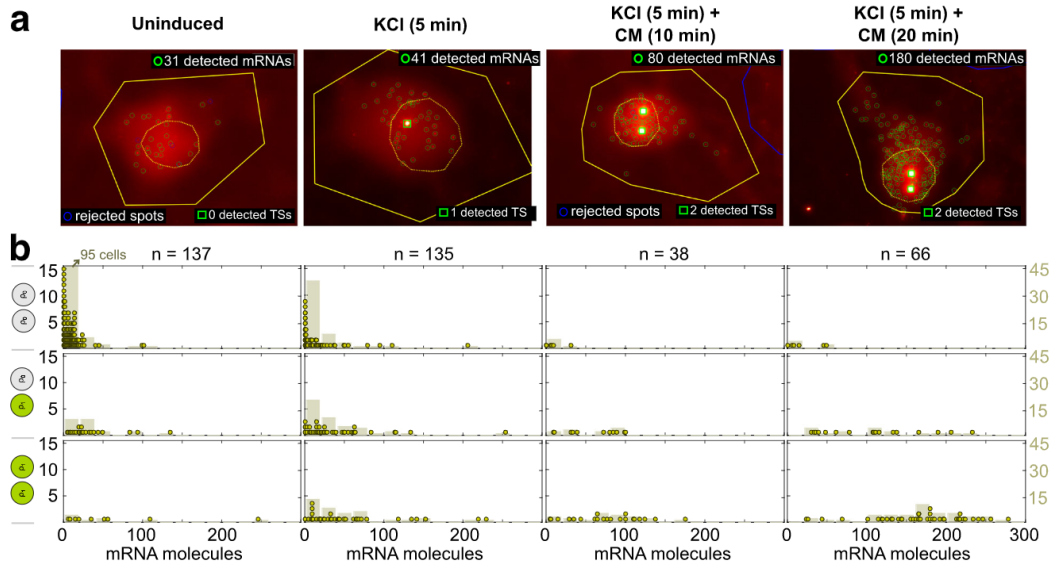
Let X represent an arbitrary RNA transcript of an induced gene G . Assume two promoter states (on and off)



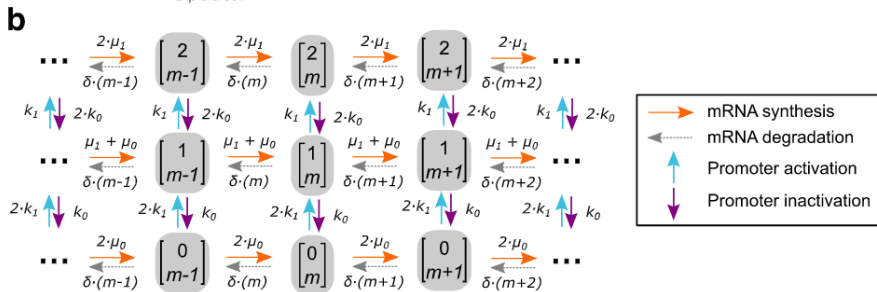
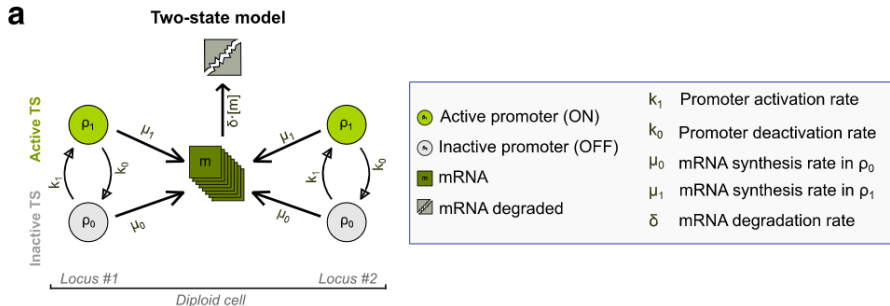
Raw data collected post induction can be used to infer parameters

$$\theta = (k_{\text{on}}, k_{\text{off}}, k_t, k_{\text{exp}}, \gamma)$$

smFISH data of Npas4 mRNA in primary neurons after membrane depol.



Two-state model of gene expression



Bayesian inference of model parameters

Transcription is stochastic so we observe samples $X \sim P(X|\theta)$

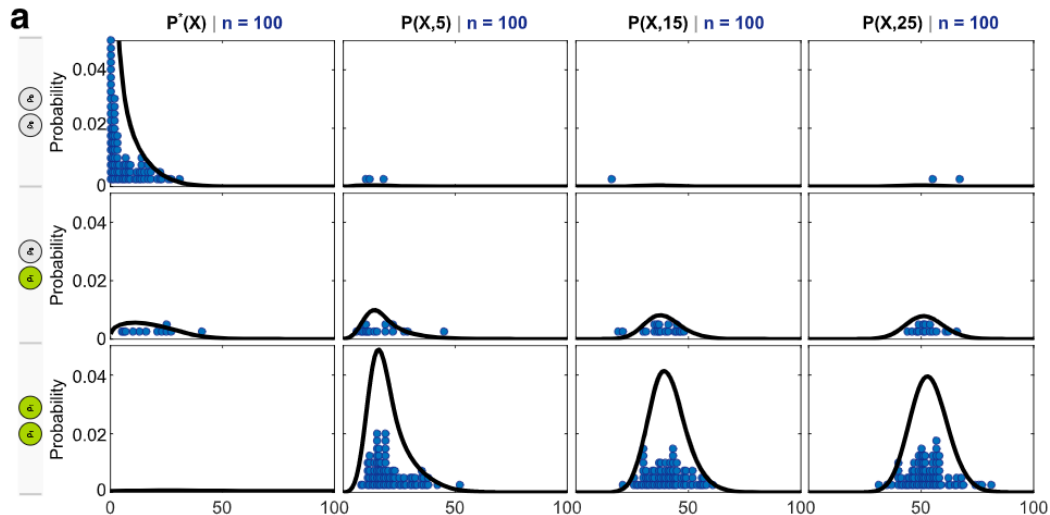
Let $\theta = (k_0, k_1, \mu_0, \mu_1, \delta)$. Using Bayes Rule:

$$P(\theta|X) = \frac{P(X|\theta)P(\theta)}{\int P(X|\theta)P(\theta)} \propto P(X|\theta)P(\theta)$$

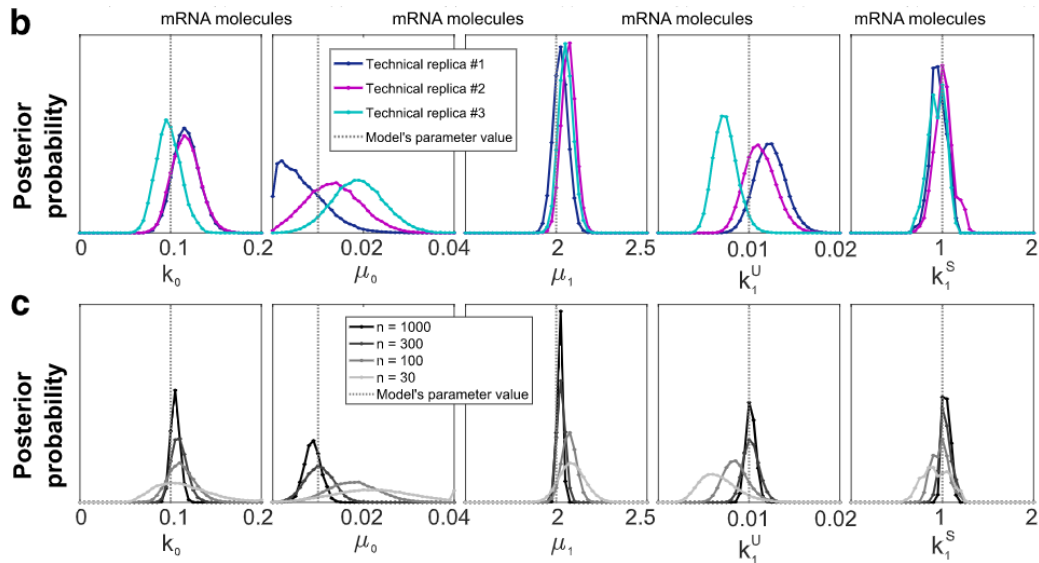
Can infer θ if we know the likelihood $P(X|\theta)$ and specify a prior $P(\theta)$

Generally we have to resort to Monte Carlo methods to find $P(X|\theta)$ (Gillespie algorithm). BayFISH evaluates $P(X|\theta)$ directly

Validating BayFish on synthetic smFISH data



Validating BayFish on synthetic smFISH data



Posterior distribution for (k1,k0)-stimulus model run on Npas4 data

