

The kinetics of Interferon- γ induced RNA flow

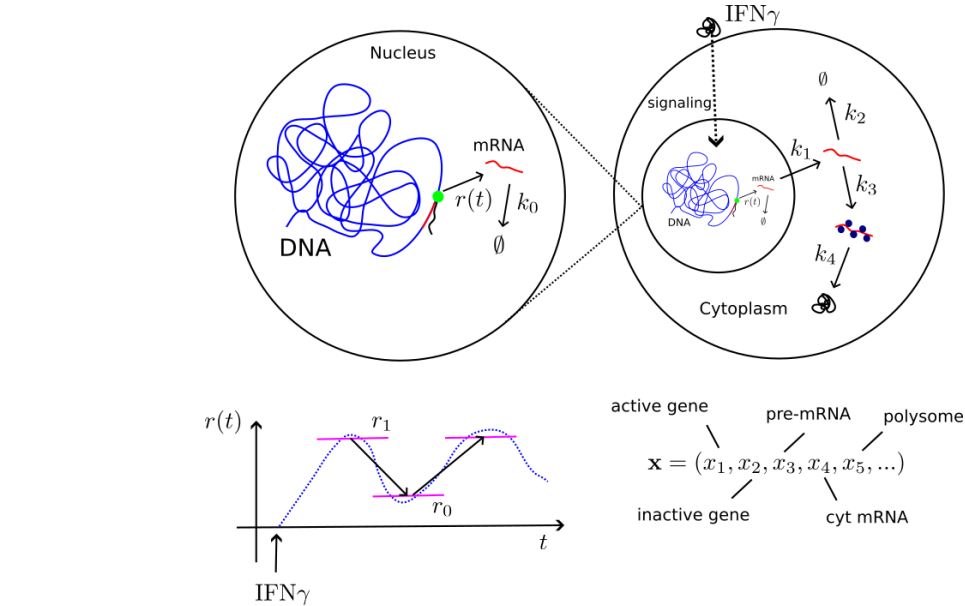
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Summary

- ▶ Recap of the compartment model for RNA flow
- ▶ Gene selection based on RNA flow
- ▶ Brief comments on probe design

A model for RNA Flow



Bayesian inference of RNA flow parameters

It is well-known that using just means and variances gives poor estimates of the model parameters (Munsky et al. PNAS 2018)

Let $\theta = (k_{on}, k_{off}, k_t, k_{exp}, \gamma)$. 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 $P(X|\theta)$ (the hard part) and specify a prior $P(\theta)$

Generally we have to resort to Monte Carlo methods to find $P(X|\theta)$

RNA Flow: parameter inference

Gene selection is based on hypothesized differences in rates k_i or the behavior of $r(t)$ in different experimental conditions

The selection method chosen where is based on expected differences in $r(t)$

The principle of Interferon- γ induced transcriptional memory

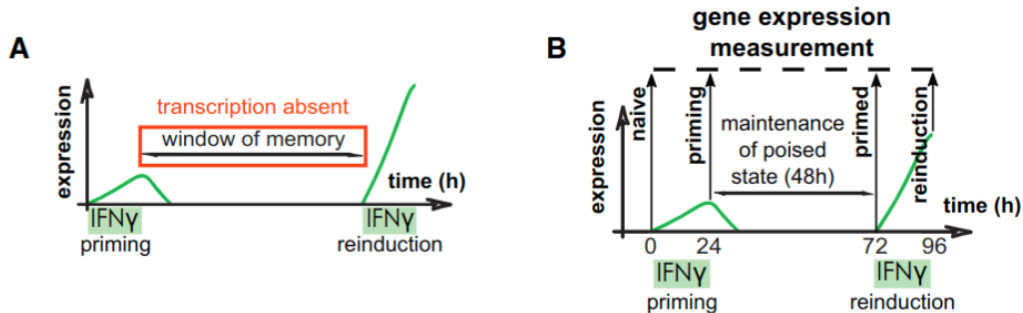
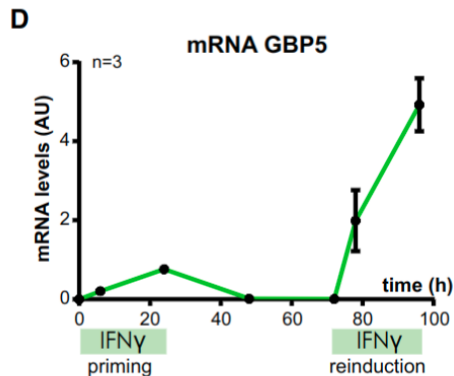
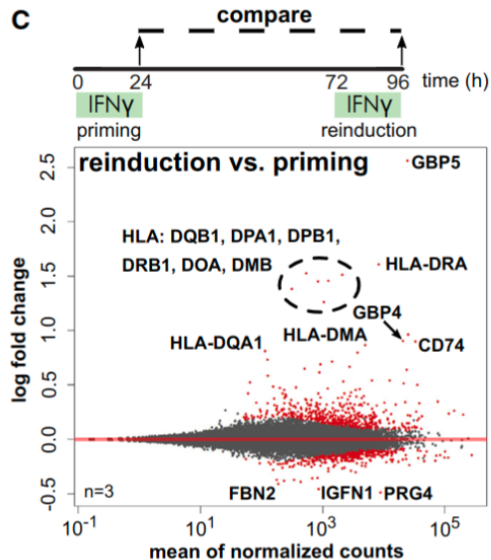


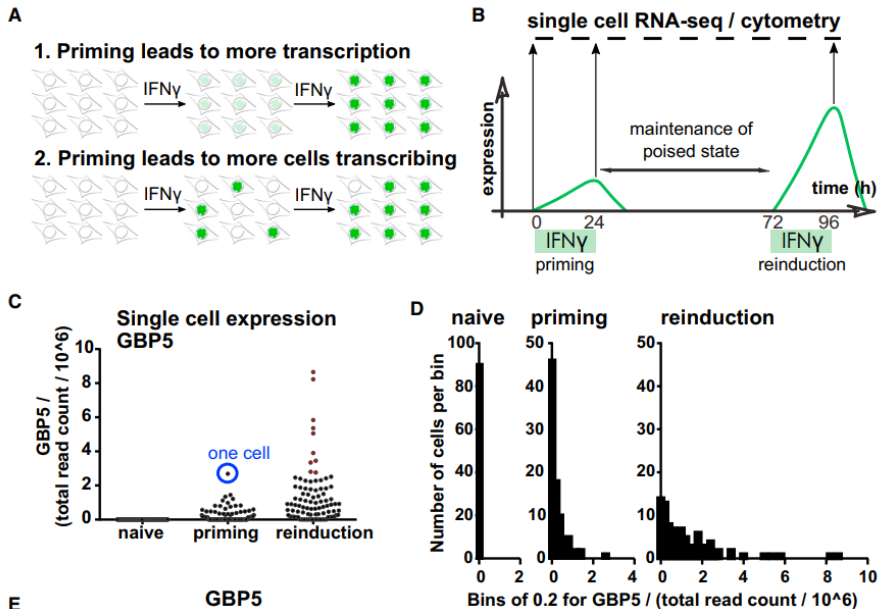
Figure 1

Siwek et al. *Activation of Clustered IFN γ Target Genes Drives Cohesin-Controlled Transcriptional Memory*. Molecular Cell 2020

Total RNA-seq identifies GBP5 as a memorized gene



Single-cell RNA-seq identifies GBP5 as a memorized gene



BLASTing probes for GPB5 and CD274

