

Gertz J, Siggia ED, Cohen BA, nature, vol 457, 8 january 2009

ANALYSIS OF COMBINATORIAL CIS-REGULATION IN SYNTHETIC AND GENOMIC PROMOTRES

Summary

• Model

thermodynamical model based on Shea & Ackers

- Organism
 - S. cerevisiae
- Assumptions
 - Gene regulation is completely controlled by DNAprotein/prot-prot binding
 - RNAP binding us directly proportional to fluorescence intensity

Parameters

- Model see Shea & Ackers
- Promoters:
 - 7 libraries à 80-600
 promoters, ∑ = 2807.
 - 18 building blocks
 - weak, strong, spacer
 - cooperativity
- Gene expression (FACS)
 - 25000 individual cells per promoter
 - Average FL : cell volume ratio

FACS: why volume against FL intensity?



Gertz J and Cohen BA, Mol Sys Biol, 2009

ENVIRONMENT-SPECIFIC COMBINATORIAL CIS-REGULATION IN SYNTHETIC PROMOTERS

Summary

- Basics: see Gertz et al. 2009
- Assumptions
 - Gene regulation is completely controlled by DNAprotein/prot-prot binding
 - RNAP binding us directly proportional to fluorescence intensity
- 4 Environments
 - + Glucose
 - + glycerol
 - amino acid
 - + diamide

Parameters

- Model see Shea & Ackers
- Expression measurement: FACS
 - Mean fluorescence divided by electronic volume (25000 events)
 - Include plate effect
- TD model: explanation of expression variation
 - $R^2 \approx 0.4$ with c(TF) = const.
 - $R^2 \approx 0.6$ with differential TF concentration
 - Cross validation

Cross-validation?

Pathways





$TNF\alpha$ -pathway – simplify?



Modeling edges



$HIF1\alpha$ -Pathway

