





Synthetic Biology and Biosystems Control Lab Valencia UPV



 $\stackrel{f}{=} K_{A}[Lu_{X}I]_{i} + d([AHL]_{i} - [AHL]_{e}) - \gamma_{A}[AHL]_{i}$

Modeling: ODEs and Hill Functions

Section 2: Derivation of the Hill Function

by Alejandro Vignoni (alvig2@upv.es)

An iGEM Measurement Committee Webinar Week 2, June 23rd, 2020

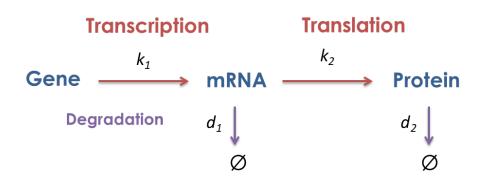


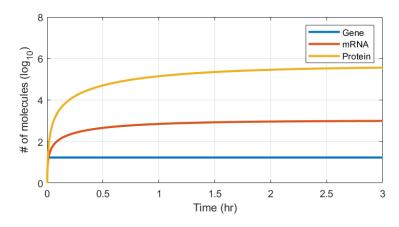
Today Webinar's Topics



- Section 1: ODEs, the law of mass action, and the central dogma (15 min)
- A Section 2: Derivation of a Hill function from the law of mass action (15 min)
- A Section 3: Hill function examples and intuitions: effects of parameters on activators, repressors, hybrid promoters, using a Matlab exploration package. (15min)
- △ Q&A (at the end of each 15 minutes block, total 15 min)

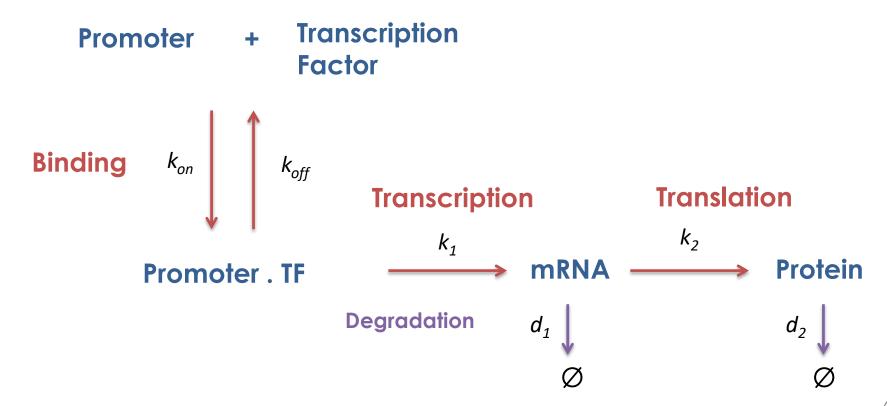
Remember: Constitutive gene expression

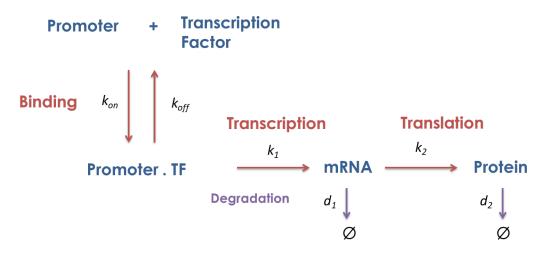




$$[mRNA] = k_1[Gene] - d_1[mRNA]$$

 $[Protein] = k_2[mRNA] - d_2[Protein]$





We will get: -5 Equations -with 7 parameters

Problems:

Danger Hazard area

Do not enter k_1 , k_2 , d_1 and d_2 become indistinguishable when we measure only the protein amount.

→ k_{on}, k_{off}, are very difficult to measure.

We want to approximate and simplify the problem and obtain a model easier to relate with experimental data:

We will

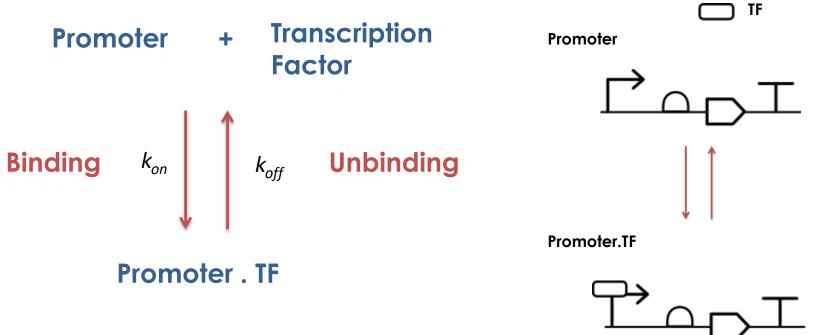
- 1. We will obtain all the equations.
- 2. Approximate and reduce them.

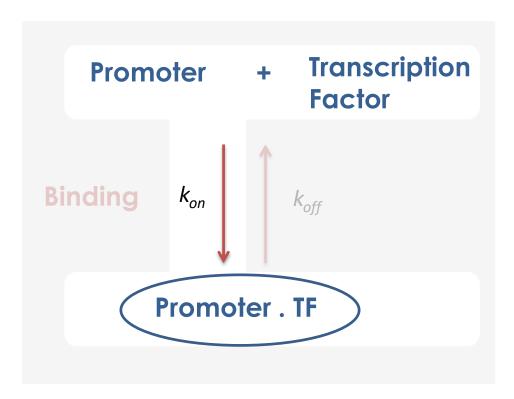
guishable ein



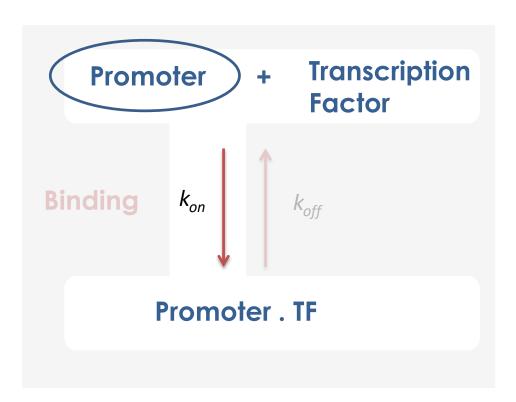
Problems: $\langle k_{on}, k_{off}, are very difficult to measure.$

Part I: Getting the model



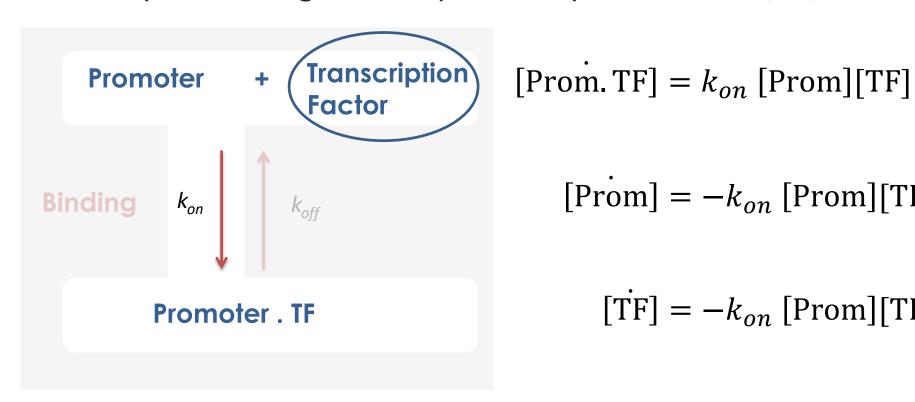


 $[Prom.TF] = k_{on} [Prom][TF]$



$$[Prom. TF] = k_{on} [Prom][TF]$$

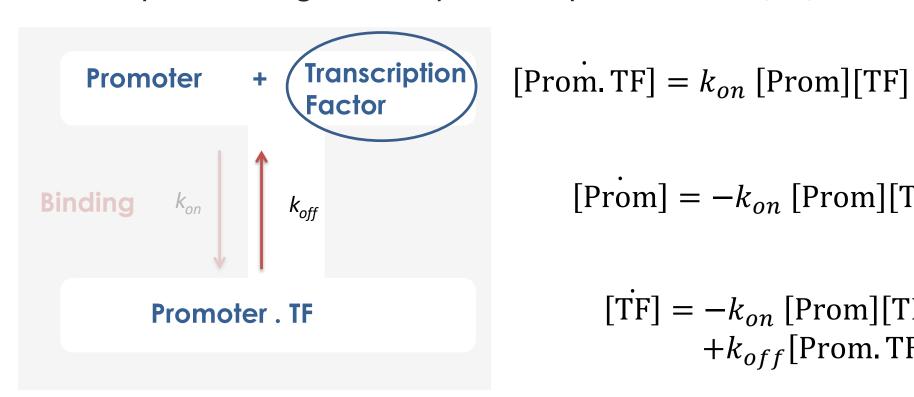
$$[Prom] = -k_{on} [Prom][TF]$$



$$[Prom. TF] = k_{on} [Prom][TF]$$

$$[Prom] = -k_{on} [Prom][TF]$$

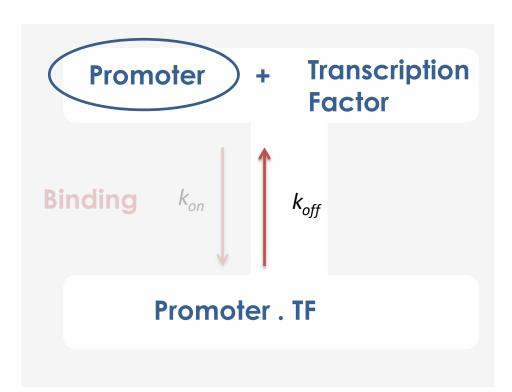
$$[TF] = -k_{on} [Prom][TF]$$



$$[Prom.TF] = k_{on} [Prom][TF]$$

$$[Prom] = -k_{on} [Prom][TF]$$

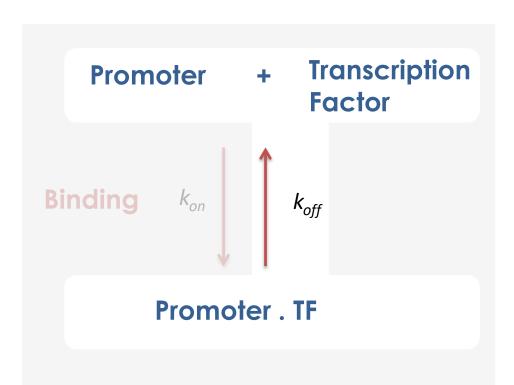
$$\begin{split} [\ddot{\text{TF}}] &= -k_{on} \, [\text{Prom}] [\text{TF}] \\ &+ k_{off} [\text{Prom.TF}] \end{split}$$



$$[Prom. TF] = k_{on} [Prom][TF]$$

$$[Prom] = -k_{on} [Prom][TF] + k_{off} [Prom. TF]$$

$$\begin{split} [\ddot{\text{TF}}] &= -k_{on} \, [\text{Prom}] [\text{TF}] \\ &+ k_{off} [\text{Prom.TF}] \end{split}$$



$$[Prom.TF] = k_{on} [Prom][TF]$$

$$-k_{off} [Prom.TF]$$

$$[Prom] = -k_{on} [Prom][TF]$$

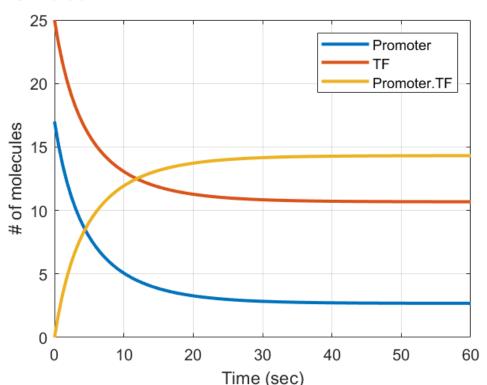
$$+k_{off} [Prom.TF]$$

$$[TF] = -k_{on} [Prom][TF]$$

$$+k_{off} [Prom.TF]$$



Simulation



$$[Prom.TF] = k_{on} [Prom][TF]$$

$$-k_{off} [Prom.TF]$$

$$[Prom] = -k_{on} [Prom][TF]$$

$$+k_{off} [Prom.TF]$$

$$[TF] = -k_{on} [Prom][TF]$$

 $+k_{off}[Prom.TF]$

Starting with:

17 Promoters (Plasmid copy number)
25 molecules of Transcription Factor (TF) $k_{on} = 0.5 \text{ molecules}^{-1} \text{ min}^{-1}$

$$k_{off} = 1 \text{ min}^{-1}$$

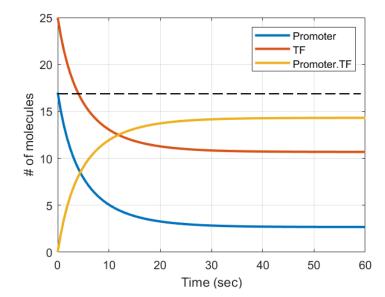


Part II: Model Reduction

$$[\overrightarrow{Prom}] = -k_{on} [\overrightarrow{Prom}][\overrightarrow{TF}] + k_{off} [\overrightarrow{Prom}.\overrightarrow{TF}]$$

$$[\overrightarrow{TF}] = -k_{on} [\overrightarrow{Prom}][\overrightarrow{TF}] + k_{off} [\overrightarrow{Prom}.\overrightarrow{TF}]$$

$$[Prom. TF] = k_{on} [Prom][TF] - k_{off}[Prom. TF]$$



Remarks

- A First two equations are equal (Blue and red)!
- A The sum of the first one and the third one is identically zero (Blue and yellow)!
- A We can use this fact (promoter invariance) to simplify the equations and reduce the model.

Promoter invariance (constant Plasmid Copy Number)

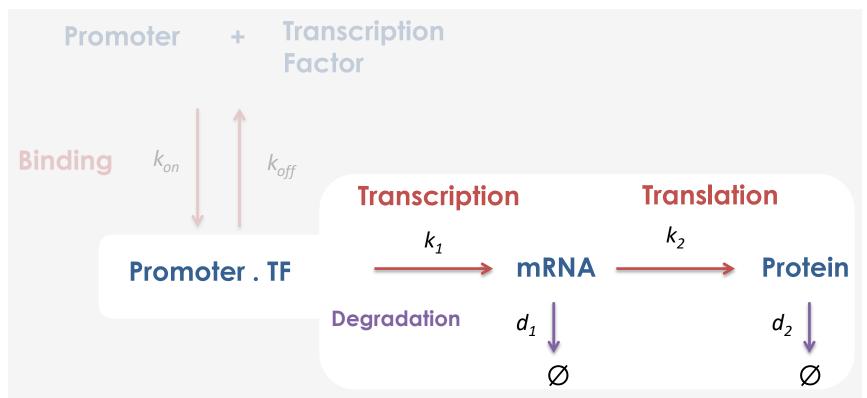
$$[Prom] = -k_{on} [Prom][TF] + k_{off} [Prom.TF]$$
+
$$[Prom.TF] = k_{on} [Prom][TF] - k_{off} [Prom.TF]$$

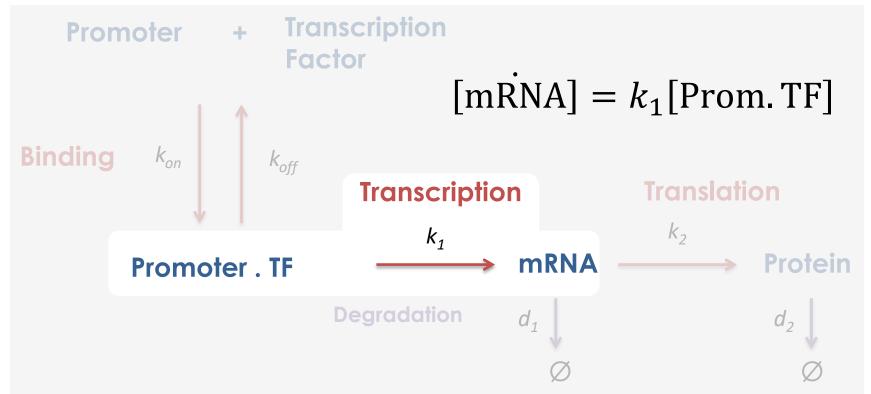
$$[Prom. TF] + [Prom] = 0$$

$$[Prom. TF] + [Prom] = C_N$$
 Plasmid Copy Number

$$[Prom] = C_N - [Prom. TF]$$

Part I: Getting the model





Fast Transcription Factor – Promoter binding

$$[Prom.TF] \approx 0$$

Because of the difference in time scales: Binding in the seconds, transcription/translation from minutes to hours; we can say that TF rapidly binds to the promoter and this reaction reaches equilibrium very fast.

This is called Quasy Steady State Approximation (QSSA).

$$[Prom.TF] = k_{on} [Prom][TF] - k_{off}[Prom.TF]$$

$$0 = k_{on} [Prom][TF] - k_{off}[Prom.TF]$$

From invariance (previous slide)

$$[Prom] = C_N - [Prom. TF]$$

Fast Transcription Factor – Promoter binding

$$[Prom.TF] \approx 0$$

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This is called Quasy Steady State Approximation (QSSA).

$$[Prom.TF] = k_{on} [Prom][TF] - k_{off}[Prom.TF]$$

$$0 = k_{on} [Prom][TF] - k_{off}[Prom.TF]$$

From invariance (previous slide)

$$[Prom] = C_N - [Prom. TF]$$

Using these two, we will derive the Hill function

Replacing the free promoter equation into the TF bound Promoter one:

[Prom] =
$$C_N$$
 – [Prom. TF]

$$0 = k_{on} \text{ [Prom][TF]} - k_{off} \text{[Prom. TF]}$$

$$0 = k_{on} (C_N - [Prom.TF])[TF] - k_{off}[Prom.TF]$$

Solving for the TF bound Promoter:

$$k_{on} (C_N - [Prom. TF])[TF] = k_{off}[Prom. TF]$$

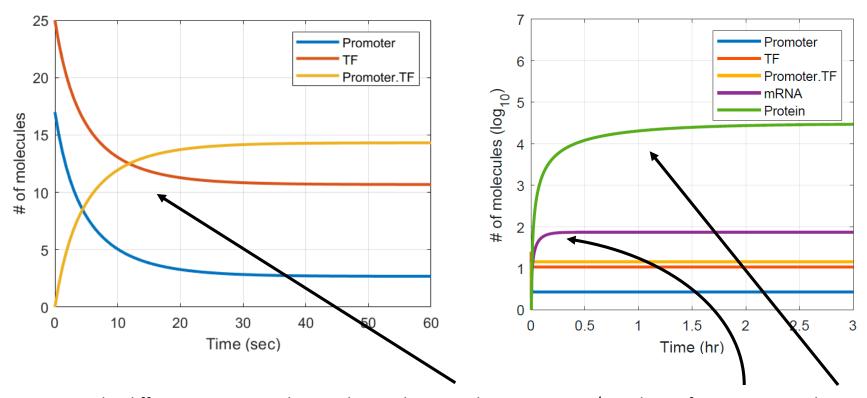
$$k_{on}$$
 [TF] $C_N - k_{on}$ [TF][Prom. TF] = k_{off} [Prom. TF]

$$k_{on}$$
 [TF] $C_N = k_{on}$ [TF][Prom. TF] + k_{off} [Prom. TF] A bit of algebra...

 $k_{on} [TF]C_N = (k_{on} [TF] + k_{off}) [Prom. TF]$

[Prom. TF] =
$$C_N \frac{k_{on}[TF]}{k_{on}[TF]+k_{off}} = C_N \frac{[TF]}{\frac{k_{off}}{k_{on}}+[TF]} = C_N \frac{[TF]}{K_d+[TF]}$$





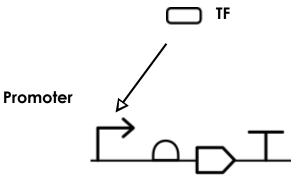
Note the difference in time scales: Binding in the seconds, transcription/translation from minutes to hours. $_{23}$

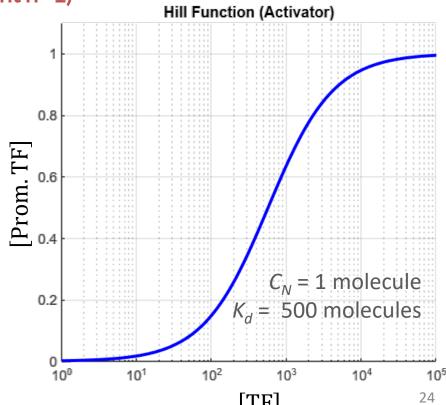


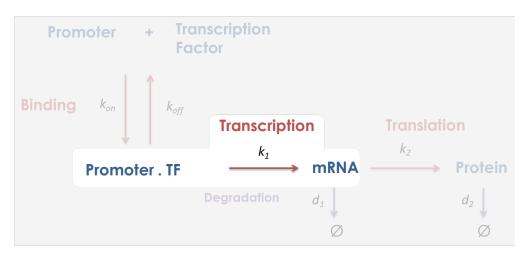
We get the Hill function (with Hill coefficient n=1)

[Prom. TF] =
$$C_N \frac{[TF]}{K_d + [TF]}$$

Activator







[Prom. TF] =
$$C_N \frac{[TF]}{K_d + [TF]}$$

$$[mRNA] = k_1[Prom.TF]$$

The complete equation for the mRNA

$$[m\dot{R}NA] = k_1 C_N \frac{[TF]}{K_d + [TF]} - d_1[mRNA]$$

Promoter + Transcription Factor

Binding
$$k_{on} \downarrow \uparrow k_{off}$$

Promoter . TF

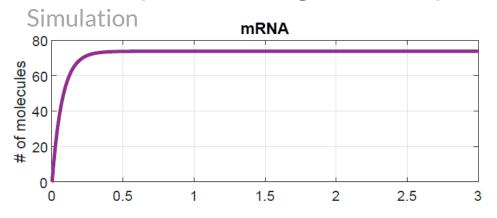
$$k_1 \atop \longrightarrow mRNA \longrightarrow Protein$$

Degradation $d_1 \downarrow d_2 \downarrow \emptyset$

$$\frac{d[\text{mRNA}]}{dt} = [\text{mRNA}] = k_1 C_N \frac{[\text{TF}]}{K_d + [\text{TF}]} - d_1[\text{mRNA}]$$

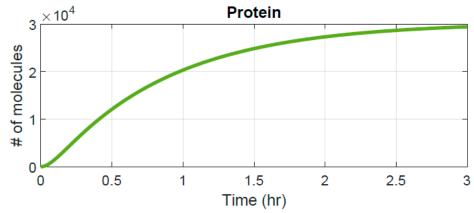
$$\frac{d[\text{Protein}]}{dt} = [\text{Protein}] = k_2[\text{mRNA}] - d_2[\text{Protein}]$$





$$[\overrightarrow{mRNA}] = k_1 C_N \frac{[TF]}{K_d + [TF]} - d_1[mRNA]$$

$$[Protein] = k_2[mRNA] - d_2[Protein]$$



Parameters:

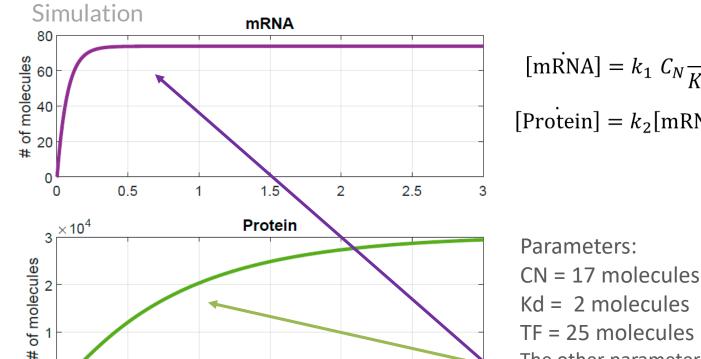
CN = 17 molecules (Plasmid copy number)

Kd = 2 molecules

TF = 25 molecules (Transcription Factor)

The other parameters same than constitutive





2

1.5 Time (hr)

0.5

$$[\overrightarrow{mRNA}] = k_1 C_N \frac{[TF]}{K_d + [TF]} - d_1[mRNA]$$

 $[Protein] = k_2[mRNA] - d_2[Protein]$

CN = 17 molecules (Plasmid copy number)

Kd = 2 molecules

TF = 25 molecules (Transcription Factor)

The other parameters same than constitutive

2.5

Now, as mRNA is much faster than Protein production... we use the same trick than before (QSSA):

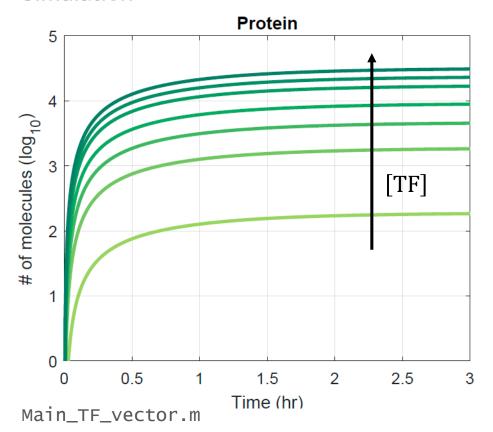
$$\begin{bmatrix} [mRNA] \approx 0 \\ 0 = k_1 C_N \frac{[TF]}{K_d + [TF]} - d_1[mRNA] \Longrightarrow [mRNA] = \frac{k_1}{d_1} C_N \frac{[TF]}{K_d + [TF]}$$

$$\frac{d[\text{Protein}]}{dt} = [\text{Protein}] = \alpha \frac{[\text{TF}]}{K_d + [\text{TF}]} - d_2[\text{Protein}]$$

$$\alpha = k_2 \frac{k_1}{d_1} C_N$$



Simulation



$$[\overrightarrow{\text{Protein}}] = \alpha \; \frac{[\text{TF}]}{K_d + [\text{TF}]} - d_2[\text{Protein}]$$

With:

 $\alpha = 720 \text{ molecules min}^{-1}$

 $K_d = 2$ molecules

 $d_2 = 0.02 \text{ min}^{-1}$

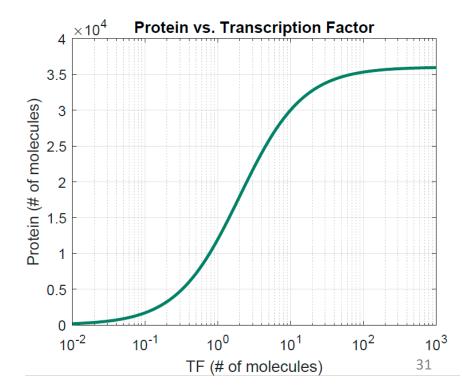
(this means 34 min of doubling time)

[TF]: from 0.1 molecule to 25 molecules of Transcription Factor

Now, if we want the steady state we can use the same trick (QSSA) that we used before (equilibrium expression of protein, data at the end of the experiment)

[Protein]
$$\approx 0$$

[Protein] =
$$\frac{\alpha}{d_2} \frac{[TF]}{K_d + [TF]}$$



protein_vs_TF.m

Questions? Ask writing in the chat or contact me by email (alvig2 [at] upv [dot] es)

Stay tuned, next Section 3:

Hill function examples and intuitions: effects of parameters on activators, repressors, hybrid promoters, using a Matlab exploration package.



