

Stochastic model for gene expression in prokaryotes

Queueing theory meets protein production

Emanuele LEONCINI

INRIA Rocquencourt - INRA Jouy-en-Josas

March 22nd 2012



Biological context

- Proteins are the fundamental components of cells
- Most of the information contained in DNA concerns the production of proteins
- More than 85% of the resources of a *prokaryote* cell (organism without nucleus) are devoted to protein production
- In a *prokaryote* cell there are $\sim 3.5 \times 10^6$ proteins of ~ 2000 different types
- Protein production has been proved experimentally to be inherently stochastic

The bacterium dilemma

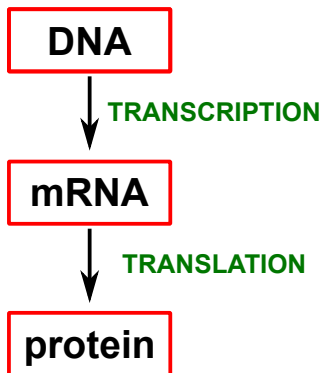
- Each cell needs a minimum amount of each type of protein in order to develop normally
- The cells also seeks to minimize the amount of excess proteins in order to save energy and resources

The bacterium dilemma

- Each cell needs a minimum amount of each type of protein in order to develop normally
- The cells also seeks to minimize the amount of excess proteins in order to save energy and resources

Q: what are the fundamental parameters ?

Central Dogma of molecular biology



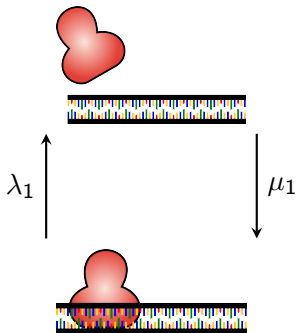
Gene Expression

mechanism by which a *gene* produces a protein through a series of complex steps.

Three Stage Model

Activation

$$N_1(t) \in \{0, 1\}$$

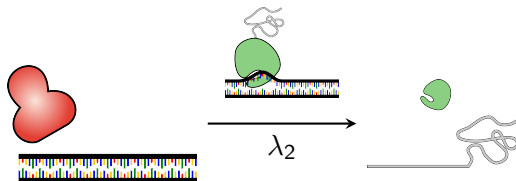


Three Stage Model

Transcription

$$N_1(t) \in \{0, 1\}$$

$$N_2(t) \in \mathbb{N}$$



Three Stage Model

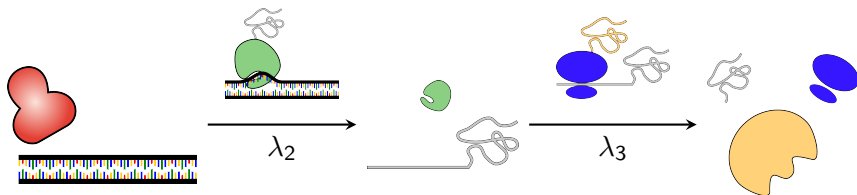
Transcription

Translation

$$N_1(t) \in \{0, 1\}$$

$$N_2(t) \in \mathbb{N}$$

$$N_3(t) \in \mathbb{N}$$



Three Stage Model

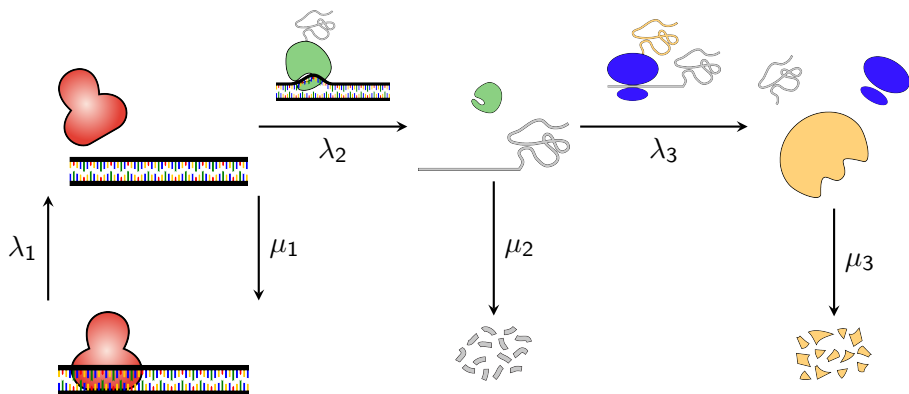
Transcription

Translation

$$N_1(t) \in \{0, 1\}$$

$$N_2(t) \in \mathbb{N}$$

$$N_3(t) \in \mathbb{N}$$



Three Stage Model

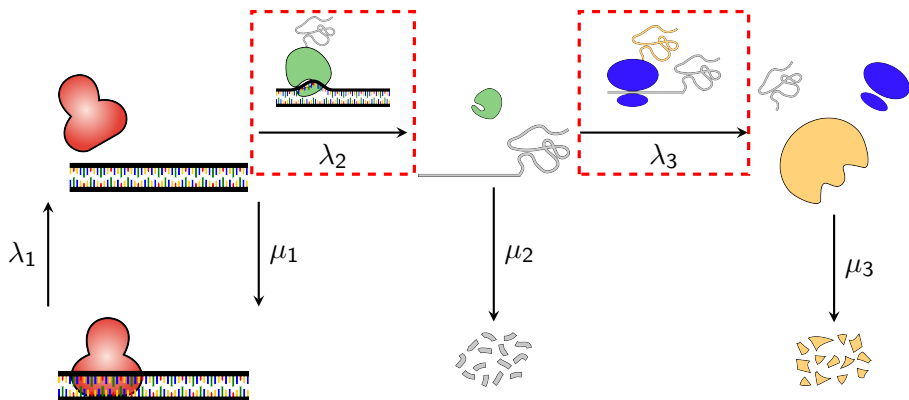
Transcription

Translation

$$N_1(t) \in \{0, 1\}$$

$$N_2(t) \in \mathbb{N}$$

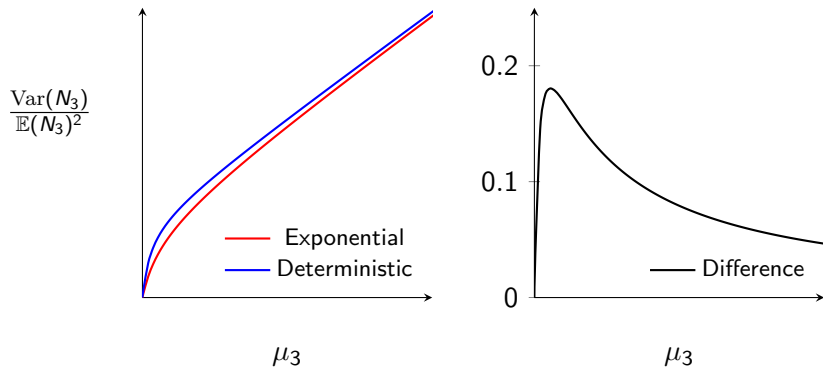
$$N_3(t) \in \mathbb{N}$$



Some results

- Probabilistic techniques similar to those used for *loss networks* (successive functional transformations of Poisson processes)
- Generalisation of the existing models to include more realistic assumptions: study of the impact of the probability distributions on variance of protein number

Protein degradation: deterministic vs. exponential



μ_3 : protein degradation rate.

Future work

- study a model of two interacting proteins;
- production of many interacting proteins: **mean field approximation**;
- biological experiments.