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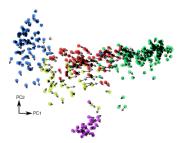
Some mathematical aspects of RNA velocity

Loïc DEMEULENAERE

Université de Liège - GIGA-Genomics

Liège, January 9, 2019

Purpose: summary of the mathematical aspects of the paper "*RNA velocity of single cells*" ([1])



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A mathematical model

RNA velocity

Estimation of parameters and prediction

Appendix

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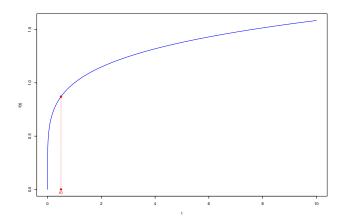
The notion of derivatives

Let f be a function and t_0 a point of its domain.

Appendix

The notion of derivatives

Let f be a function and t_0 a point of its domain.

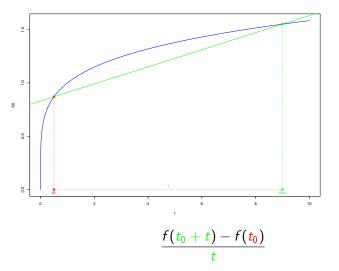


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App en dix

The notion of derivatives

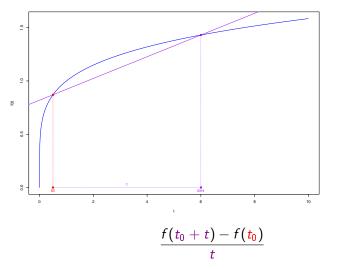
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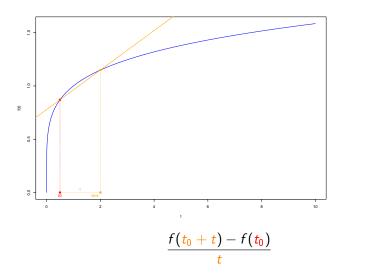
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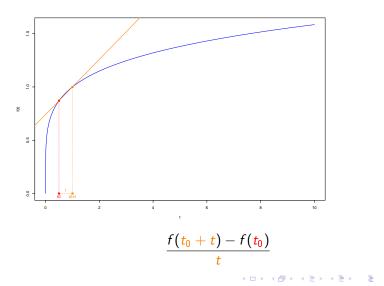
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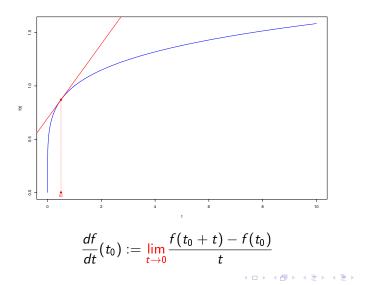
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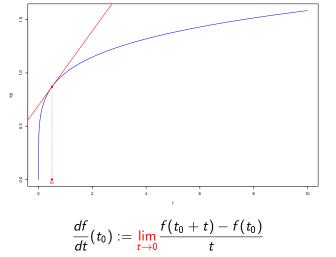


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The notion of derivatives

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(if this limit exists and is finite).

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Variations with respect to time

$$\frac{df}{dt}(t_0) := \underbrace{\lim_{t \to 0} \quad \underbrace{f(t_0 + t) - f(t_0)}_{t}}_{t}$$



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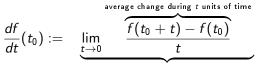
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Variations with respect to time



Instantaneous rate of varation with respect to time

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Examples (Physics)

• f(t) = x(t): motion (1D) of a particle;

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In 3D: likewise! If x(t) := (x(t), y(t), z(t)) is the position of a particle in the space, then its velocity is

$$ec v(t) := rac{dec x}{dt}(t) := \left(rac{dx}{dt}(t), rac{dy}{dt}(t), rac{dz}{dt}(t)
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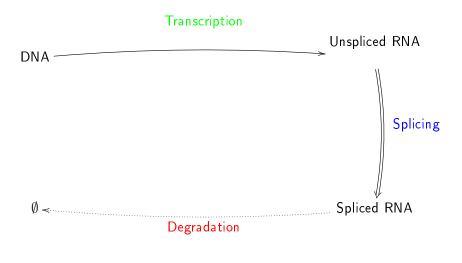
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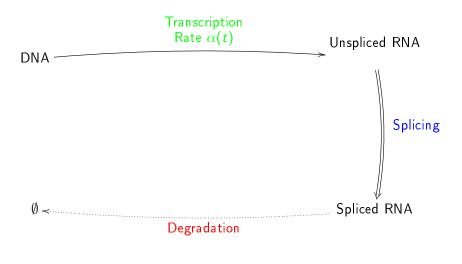
RNA dynamics: the idea



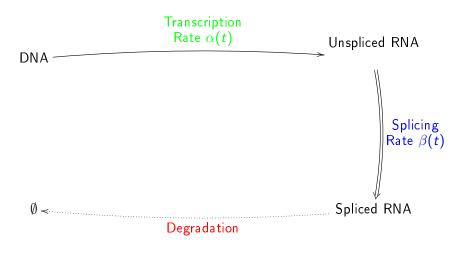


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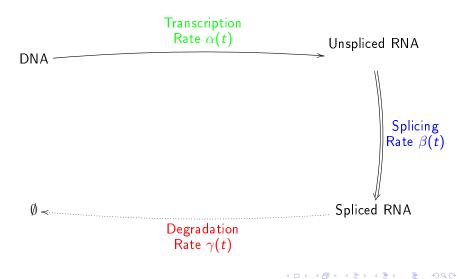
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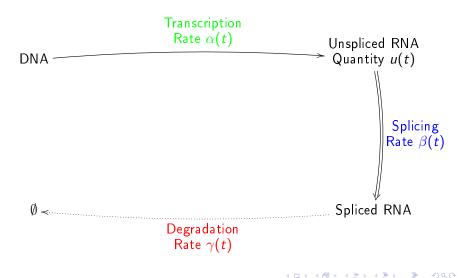


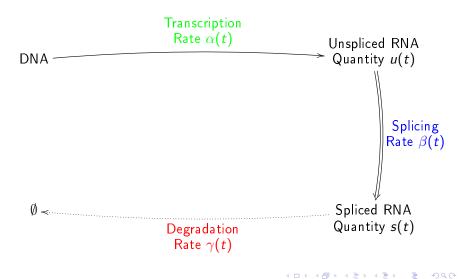
In one cell, for one gene ...

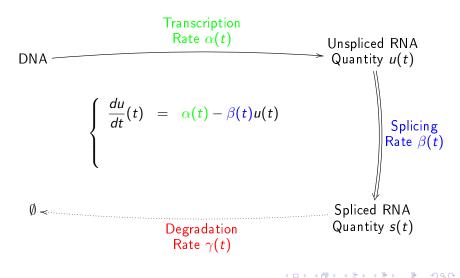


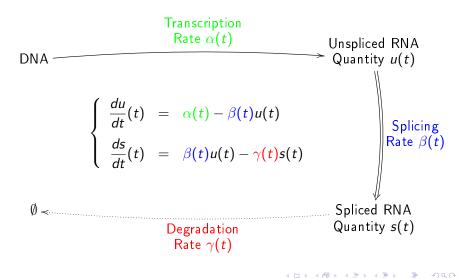
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In this context

 u(t) and s(t) are the expected values of the numbers of molecules of unspliced and spliced RNA (at time t)

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App en dix

In this context

- u(t) and s(t) are the expected values of the numbers of molecules of unspliced and spliced RNA (at time t)
- <u>Real</u> numbers of molecules (at time t) have a bivariate Poisson distribution with parameters (expected values) u(t) and s(t).

RNA dynamics

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- <u>Real</u> numbers of molecules (at time t) have a bivariate Poisson distribution with parameters (expected values) u(t) and s(t).

Our equations

$$\begin{cases} \frac{du}{dt}(t) = \alpha(t) - \beta(t)u(t) \\ \frac{ds}{dt}(t) = \beta(t)u(t) - \gamma(t)s(t) \end{cases}$$

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RNA dynamics

Assumptions

• The rates α , β , γ are constant: $\alpha \geq 0$, $\beta > 0$, $\gamma > 0$.

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RNA dynamics

Assumptions

- The rates α , β , γ are constant: $\alpha \geq$ 0, $\beta >$ 0, $\gamma >$ 0.
- $\beta = 1$ (all units expressed in terms of β , i.e. everything divided by β).

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Final equations

$$\begin{cases} \frac{du}{dt}(t) = \alpha - u(t) \\ \frac{ds}{dt}(t) = u(t) - \gamma s(t) \end{cases}$$

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"(Linear) differential equations"

Solution of the first equation

$$\frac{du}{dt}(t) = \alpha - u(t)$$

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Solution of the first equation

$$\frac{du}{dt}(t) = \alpha - u(t)$$

Solution If $u_0 := u(0)$,

$$u(t) = \alpha + (u_0 - \alpha)e^{-t}.$$

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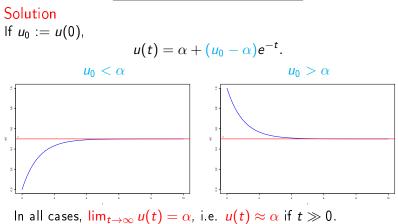
$$\frac{du}{dt}(t) = \alpha - u(t)$$

Solution If $u_0 := u(0)$, $u(t) = \alpha + (u_0 - \alpha)e^{-t}.$ $u_0 < \alpha$ $u_0 > \alpha$ 5 ę

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Solution of the first equation

$$\frac{du}{dt}(t) = \alpha - u(t)$$



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Solution of the second equation

$$rac{ds}{dt}(t) = u(t) - \gamma s(t)$$

Solution

$$s(t) = \frac{\alpha}{\gamma} + \frac{u_0 - \alpha}{\gamma - 1} e^{-t} + \left(s_0 + \frac{\alpha - u_0}{\gamma - 1} - \frac{\alpha}{\gamma}\right) e^{-\gamma t}.$$

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Many graphical possibilities...

Solution of the second equation

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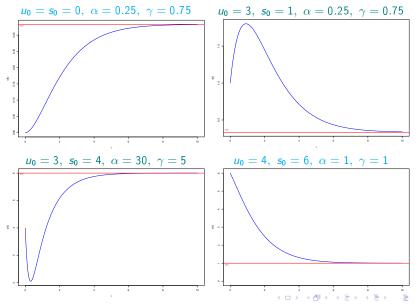
Many graphical possibilities... But we always have

$$\lim_{t\to\infty} s(t) = \frac{\alpha}{\gamma},$$

i.e. $s(t) \approx \frac{\alpha}{\gamma}$ if $t \gg 0$.

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Solution of the second equation: graphical examples



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RNA dynamics: summary

There exist solutions u, s, depending on u_0 , s_0 (initial conditions) and on α , γ (parameters), with

$$\lim_{t\to\infty} u(t) = \alpha \quad \text{and} \quad \lim_{t\to\infty} s(t) = \frac{\alpha}{\gamma}.$$

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In particular,

$$\lim_{t\to\infty}\frac{u(t)}{s(t)}=\gamma.$$

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Steady state

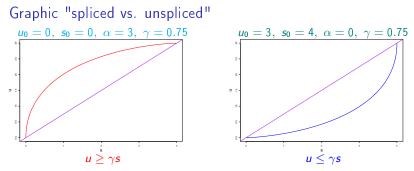
When $t \gg 0$, the system reaches a steady state, with

$$u(t) pprox lpha, \quad s(t) pprox rac{lpha}{\gamma}, \quad ext{and} \quad u(t) pprox \gamma s(t).$$

Some recalls

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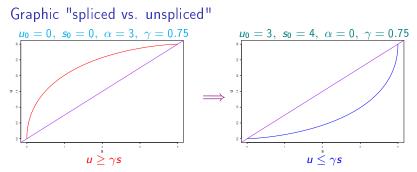
Phase portrait



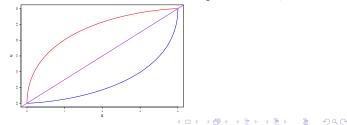
The system reaches the steady state, i.e. the straight line $u = \gamma s$.

Some recalls

Phase portrait



The system reaches the steady state, i.e. the straight line $u = \gamma s$.



Some recalls

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RNA velocity

Context

• Here, we consider <u>one</u> cell, with *p* genes.



RNA velocity

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- Let $s_j(t)$ be the (expected value of the) quantity of spliced RNA associated to the j^{th} gene (at time t).

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- Let $s_j(t)$ be the (expected value of the) quantity of spliced RNA associated to the j^{th} gene (at time t).
- Each $s_j(t)$ verifies the previous equations, with its own parameters $\alpha_j \ge 0$, $\beta_j = 1$, and $\gamma_j > 0$.

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- Each s_j(t) verifies the previous equations, with its own parameters α_j ≥ 0, β_j = 1, and γ_j > 0.

Warning! Implicit assumption!

 $\beta_j = 1$ for all j: the rates of splicing are equal for all genes!

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Definition

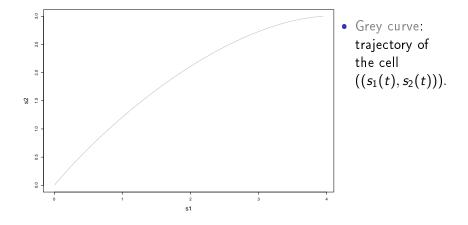
The RNA velocity of the cell (at time t) is

$$\frac{d\vec{s}}{dt}(t) := \left(\frac{ds_1}{dt}(t), ..., \frac{ds_p}{dt}(t)\right).$$

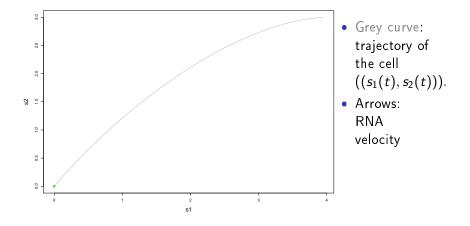
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- A cell with 2 genes...
- $\alpha_1 = 2$, $\gamma_1 = 0.5$; $\alpha_2 = 3$, $\gamma_2 = 1$

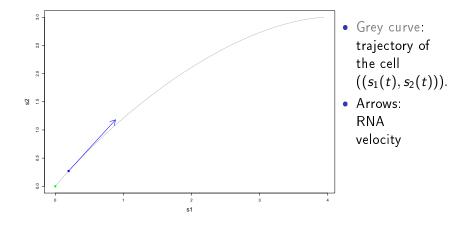
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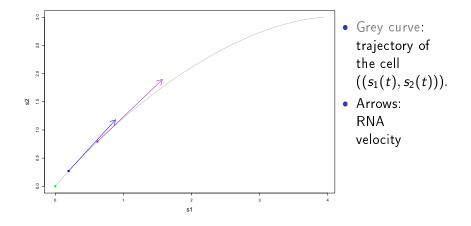
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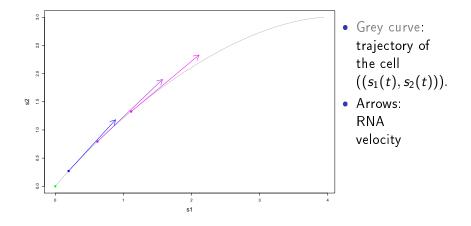
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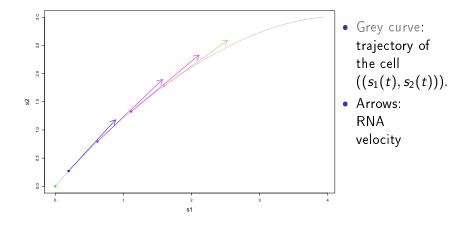


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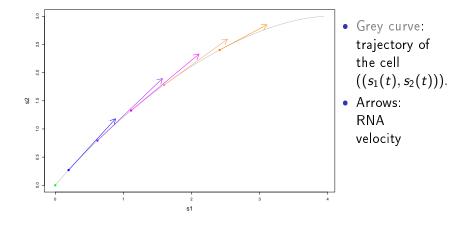


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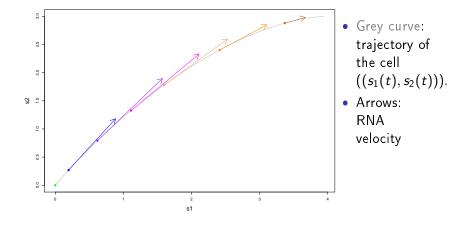
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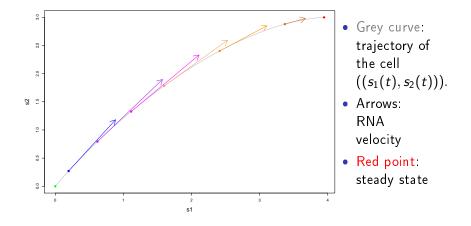
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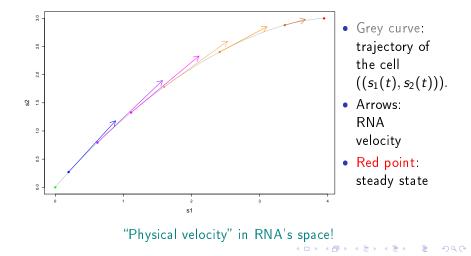
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Representation: an unreal world...

• A cell with 2 genes...

•
$$\alpha_1 = 2$$
, $\gamma_1 = 0.5$; $\alpha_2 = 3$, $\gamma_2 = 1$



Representation of RNA velocity

And if p > 3?

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Representation of RNA velocity

And if p > 3?

• Principle component analysis: quite natural, projection on P.C.;

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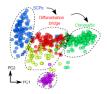
Representation of RNA velocity

And if p > 3?

- Principle component analysis: quite natural, projection on P.C.;
- t-SNE? Possible, but more tricky...

Representation of RNA velocity

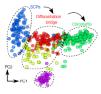
Example: Schwann cell precursors (coming from [1])

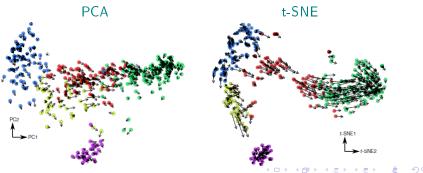




Representation of RNA velocity

Example: Schwann cell precursors (coming from [1])





Some recalls

A mathematical model

RNA velocity

Estimation of parameters and prediction

Appendix

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Estimation of γ

We study <u>one</u> gene (i.e. its parameters) through a sample of **several** cells.

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Estimation of γ

We study <u>one</u> gene (i.e. its parameters) through a sample of **several** cells.

Assumptions

- The sample of cells is sufficiently large to cover all the "RNA cycle" (from beginning of production to steady state).
- The rate of degradation γ of the gene is the same in all cells.

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Estimation of γ

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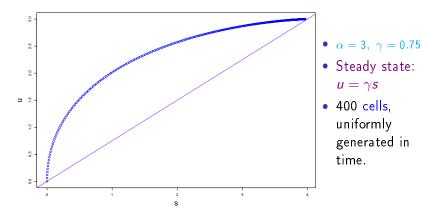
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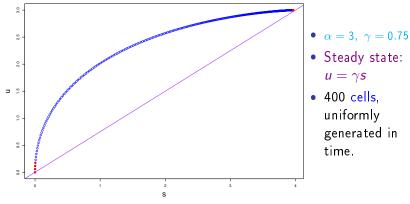
 \rightsquigarrow Estimation of γ with phase portraits...

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Theoritical estimation of γ



Theoritical estimation of γ

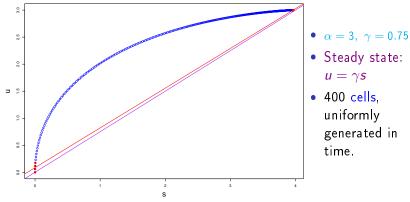


Process

1. Selection of the extreme cells (here smallest and greatest 1%'s)

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Theoritical estimation of γ



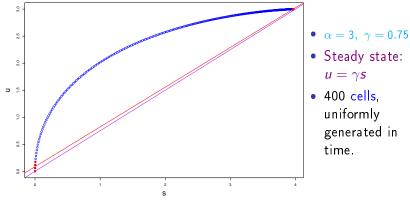
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- 1. Selection of the extreme cells (here smallest and greatest 1%'s)
- 2. Linear regression on the extreme cells

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Theoritical estimation of γ



Process

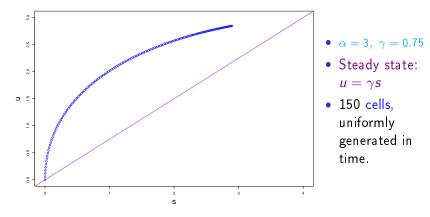
- 1. Selection of the extreme cells (here smallest and greatest 1%'s)
- 2. Linear regression on the extreme cells

Here, estimation of γ (slope): 0.73493

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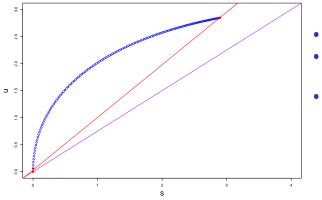
Difficulties of estimation for γ ...

Assumption 1 not respected...



Difficulties of estimation for γ ...

Assumption 1 not respected...



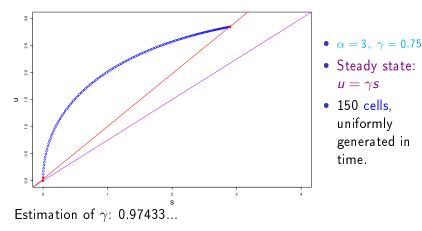
- $\alpha = 3, \ \gamma = 0.75$
- Steady state: $u = \gamma s$
 - 150 cells, uniformly generated in time.

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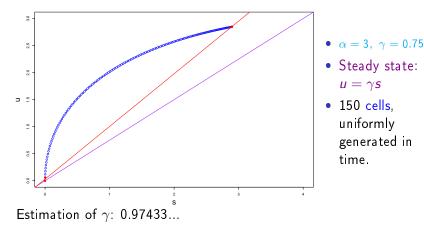
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Difficulties of estimation for γ ...

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Corrections?

Estimation on very correlated genes, filtering some cells...

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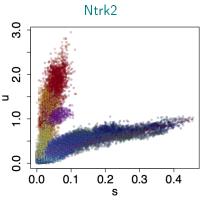
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Multiple splicing

- In [1], \pm 89 % of studied genes showed a unique degradation rate $\gamma...$

Multiple splicing

- In [1], \pm 89 % of studied genes showed a unique degradation rate $\gamma...$ but 11 % showed several degradation rates!
- Example from [1]:



• Then the model fails...

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Estimation of α

According to [1], it is very difficult to estimate α ... Two approximations are considered:

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Estimation of α

According to [1], it is very difficult to estimate α ... Two approximations are considered:

• Model I:
$$v := rac{ds}{dt}$$
 is assumed to be constant; then, $s(t) = vt + s_0,$

with $v := u_0 - \gamma s_0$.

Estimation of α

According to [1], it is very difficult to estimate α ... Two approximations are considered:

• <u>Model I</u>: $v := \frac{ds}{dt}$ is assumed to be constant; then,

$$s(t)=vt+s_0,$$

with $v := u_0 - \gamma s_0$.

• Model II: *u* is assumed to be constant; then,

$$s(t) = rac{u_0}{\gamma} + \left(s_0 - rac{u_0}{\gamma}\right)e^{-\gamma t}$$

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Estimation of α

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• Model II: *u* is assumed to be constant; then,

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ight)e^{-\gamma t}.$$

These two models are correct in the short term; they have to be used "step by step" to predict the future (Markov process).

A mathematical model

RNA velocity Estimation of parameters and prediction

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Thank you for your attention!

Some recalls

A mathematical model

RNA velocity

Estimation of parameters and prediction

Appendix

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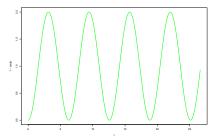
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And if the parameters are non-constant?

Much more complex...

Example

Assume that $\alpha(t) = 1 - \cos(t)$, $\beta = 1$, and $\gamma > 0$ is constant.

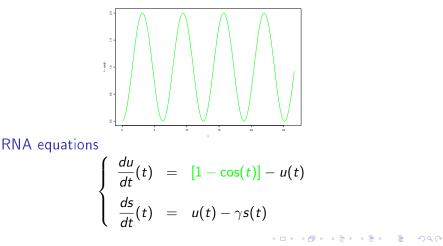


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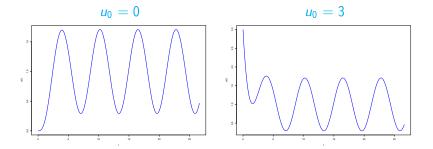


Appendix

Solutions

Unspliced RNA

$$u(t) = 1 - \frac{1}{2} \left(\cos(t) + \sin(t) \right) + \left(u_0 - \frac{1}{2} \right) e^{-t}.$$



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Solutions

Spliced RNA

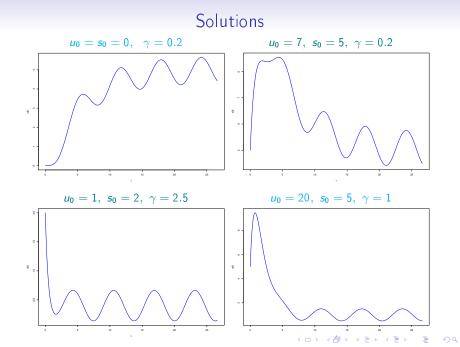
If $\gamma
eq 1$,

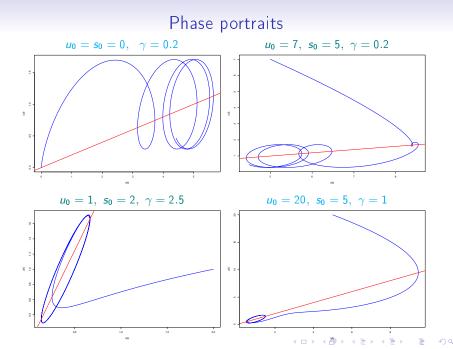
$$s(t) = \frac{1}{\gamma} - \frac{1}{2(1+\gamma^2)} \left((\gamma - 1) \cos(t) + (\gamma + 1) \sin(t) \right) \\ + \frac{u_0 - 1/2}{\gamma - 1} e^{-t} + \left(s_0 - \frac{1}{\gamma} + \frac{1/2 - u_0}{\gamma - 1} + \frac{\gamma - 1}{2(1+\gamma^2)} \right) e^{-\gamma t}$$

and, if $\gamma=$ 1,

$$s(t) = 1 - \frac{1}{2}\sin(t) + \left(\left(u_0 - \frac{1}{2}\right)t + s0 - 1\right)e^{-t}.$$

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References |

G. La Manno et al. RNA velocity of single cells. *Nature*, 560:494–516, 2018.