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Subject

Investigation of RNA metabolism using pulseR

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Abstract

Motivation: Results: Availability: Contact: alexey.mipt@gmail.com **Supplementary information:** Supplementary data are available at *Bioinformatics* online.

1 Introduction

2 Methods

First-order reaction kinetics is one of simplified models, which can help to describe RNA dynamics *in vivo*[**?**]. Given

- constant synthesis rate s and
- degradation rate d,

RNA concentration r follows the ordinary differential equation

$$\dot{r} = s - dr, \tag{1}$$

where $\dot{r}$ stands for the time derivative of the r[**?**].

During synthesis, a new RNA molecule incorporates labelled uridine bases[**?**]. For zero initial condition $r_L(0) = 0$, the solution is

$$r_{\mathrm{L}}(t) = \frac{s}{d}\left(1 - e^{-dt}\right). \tag{2}$$

With time, the labelled fraction tends to the steady state level of concentration μ, $\lim_{t\to\infty} r_{\mathrm{L}}(t) = \frac{s}{d} = \mu$. In contrast, the unlabelled molecules are only being degraded during the *pulse*-experiment. Hence, assuming initial level of unlabelled RNA to be the steady-state one, $r_U = \mu$, the the amount of unlabelled fraction at a time t is

$$r_{\mathrm{U}}(t) = \mu e^{-dt}. \tag{3}$$

The example model includes only two parameters and does not consider RNA maturation and existence of several isoforms. For more complex approaches we refer to [**?**].

For completeness we provide the formulas, which describe expression levels for *chase*-experiments. In this case, we assume that no synthesis of labelled RNA occurs after labelling period t_L:

$$r_{\mathrm{T}} = \mu \tag{4}$$

$$r_{\mathrm{L}} = \mu\left(1 - e^{-dt_{\mathrm{L}}}\right)e^{-dt_{\mathrm{C}}} \tag{5}$$

$$r_{\mathrm{L}} = \mu\left(1 - \left(1 - e^{-dt_{\mathrm{L}}}\right)e^{-dt_{\mathrm{C}}}\right), \tag{6}$$

where t_{C} stands for the longitude of the chase period.

3 Results

4 Discussion

5 Conclusion

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References