

Subject

Investigation of RNA metabolism using pulseR

Uvarovskii Aleksei^{1,2*}, Christoph Dieterich^{1,2}

¹ Section of Bioinformatics and Systems Cardiology Klaus Tschira Institute for Integrative Computational Cardiology Department of Internal Medicine III University Hospital Heidelberg, Im Neuenheimer Feld 669 69120 Heidelberg, and ² German Center for Cardiovascular Research (DZHK), Im Neuenheimer Feld 669 69120 Heidelberg

*To whom correspondence should be addressed.

Associate Editor: XXXXXXXX

Received on XXXXX; revised on XXXXX; accepted on XXXXX

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

$$\dot{r} = s - dr, \quad (1)$$

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

$$r_L(t) = \frac{s}{d} \left(1 - e^{-dt} \right). \quad (2)$$

With time, the labelled fraction tends to the steady state level of concentration μ , $\lim_{t \rightarrow \infty} r_L(t) = \frac{s}{d} = \mu$. 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

$$r_U(t) = \mu e^{-dt}. \quad (3)$$

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

where t_C stands for the longitude of the chase period.

© The Author 2015. Published by Oxford University Press. All rights reserved. For permissions, please e-mail: journals.permissions@oup.com

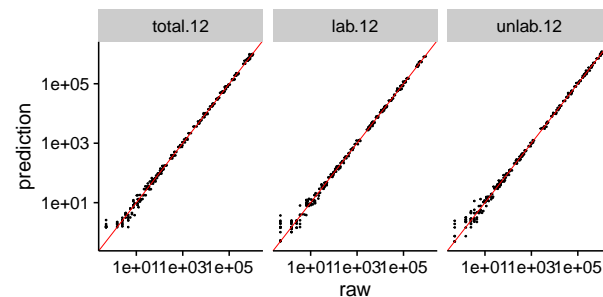


Fig. 1. Model predictions.

labelled RNA occurs after labelling period t_L :

$$r_T = \mu \quad (4)$$

$$r_L = \mu \left(1 - e^{-dt_L} \right) e^{-dt_C} \quad (5)$$

$$r_U = \mu \left(1 - \left(1 - e^{-dt_L} \right) e^{-dt_C} \right), \quad (6)$$

3 Results

4 Discussion

5 Conclusion

Acknowledgements

Funding

References

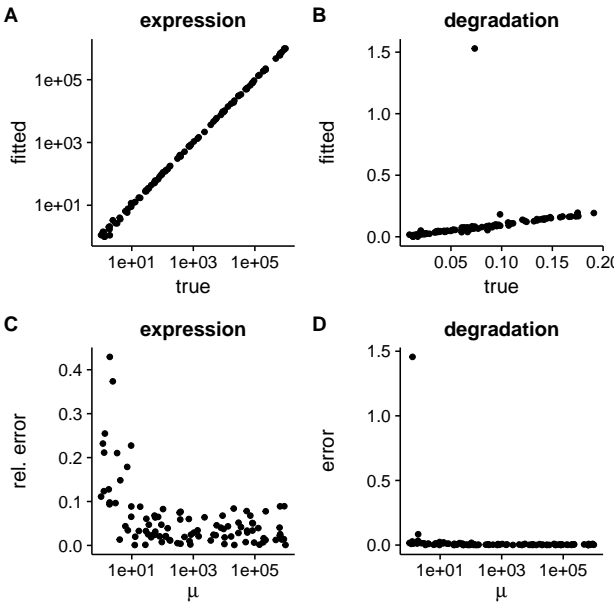


Fig. 2. Parameter misprediction.