Bayesian ranking of biochemical system models

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An error occurred in the text of the above article. Figure 1(a) and Figure 1(d) in the article and in the supplementary material must be depicted as in Figure 1 here.

The differential equation for $\dot{S}$ in Models 1 and 4 in the supplementary material should be $\dot{S} = -k_1 \cdot S - k_2 \cdot S \cdot R + k_3 \cdot RS$.

The SBML models supplied with the original article are correct and can be used without any changes.

These changes do not undermine the validity of the methods discussed in the article, nor do they change the justification of the approach used.

Fig. 1. Schematic diagrams of biochemical models used in this study

(a) Model 1: A model of a signal transduction cascade. Protein $S$ represents the input signal. $S$ can degrade to $dS$. At the same time $S$ activates protein $R$ from its inactive state, to an active state $Rpp$ by binding and activation. Protein Rpp can then be deactivated. This model was used to generate the experimental data.

(d) Model 4: A more complex version of Model 1. This model mechanistically describes how protein Rpp is deactivated by phosphatase PhA.