

Identification of cell signaling pathways based on biochemical reaction kinetics repositories

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Introduction

Cell Signaling

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Understanding the functioning of cell signaling is important in many biological areas.

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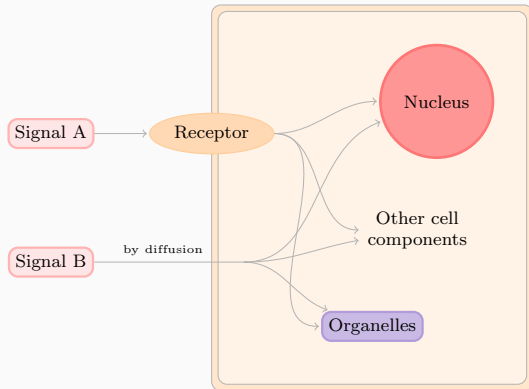


Figura 1: A general cell signaling mechanism.

Cell Signaling Pathways

A cell signaling network can be characterized by a sequence of chemical reactions that allows the presence of a signal to modify the state or behaviour of a cell.

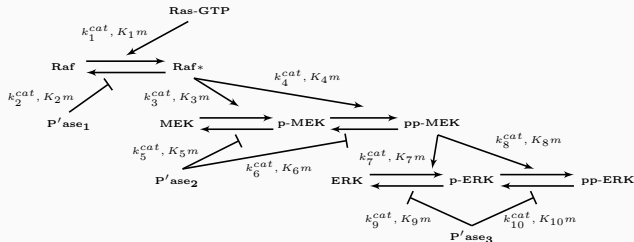


Figure 2: An example of a signaling pathway.

Mathematical Models of Signaling Networks

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Using biochemical and enzymatic kinetics, we can write equations that represent the rate of change of concentration for a chemical species.

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Repeating this procedure for all reactions of a pathway allows us to derive a system of ordinary differential equations that can model the signaling pathway.

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- a model composed by a set of chemical reactions that are relevant for the biological experiment;
- information about the reaction rate constants of the model.

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Hence, it is desirable to construct a method that can systematically modify these models and choose the one that better represents the experiment.

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On her work, the problem of identification of cell signaling pathways is treated as a feature selection problem.

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The feature selection problem is a combinatorial optimization problem:

Given a set of features S and a cost function c , find subset $X \in \mathcal{P}(S)$, with minimum cost $c(X)$.

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Feature Selection for Identification of Signaling Pathways

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The methodology proposed by Wu defines the set of features as a set of chemical reactions that can be added to a starting model. This set of chemical reactions is fetched from KEGG and stored in a database of interactions.

Wu's Search Algorithm for Feature Selection

The search algorithm used by Wu is the Sequential Forward Selection (SFS).

Wu's Cost Function for Feature Selection

Wu defines the cost function as the minimum distance between experimental and simulated data.

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- the database of interactions used could be more nearly complete;
- the search algorithm could also consider removing interactions;
- the cost function could implement a proper penalization of models;

What we Propose on this Project

We propose to create a methodology that uses a feature selection approach for identification of signaling pathways, tackling the difficulties encountered by Wu.

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To create new search algorithms, we intend to use more general algorithms that can also remove interactions.

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To define new cost functions, we intend to use Bayesian approaches of model selection that allow us to create estimates of probabilities such as $p(M|D)$ or $p(D|M)$.

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- Apply the methodology on a real case.

Fundamental Concepts

Kinetics Modeling of Chemical Reactions

Mathematical Modeling of Reactions

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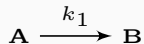
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- first order interaction kinetics;
- second order interaction kinetics;
- Michaelis-Menten enzymatic kinetics.

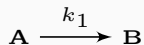
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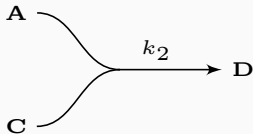


has rate of:

$$k_1[\mathbf{A}].$$

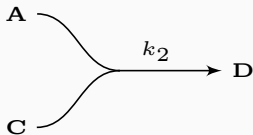
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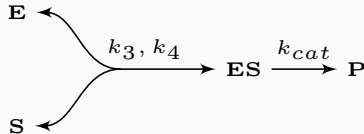


has rate of:

$$k_2[A][C].$$

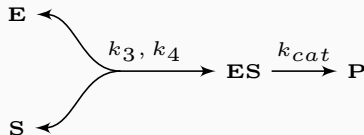
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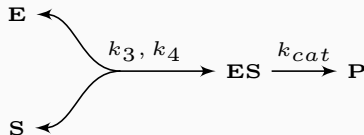
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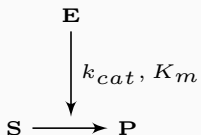
An enzymatic reaction:



Can be divided in two first order reactions plus a second order reaction. However, with the appropriate assumptions, it is possible to use a Michaelis-Menten simplification of this reaction.

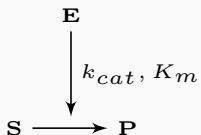
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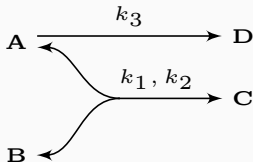


and it has rate of:

$$k_{cat} \frac{[\mathbf{E}][\mathbf{S}]}{K_M + [\mathbf{S}]}.$$

Kinetics of a System of Reactions

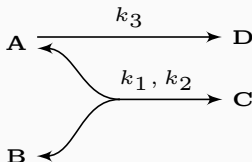
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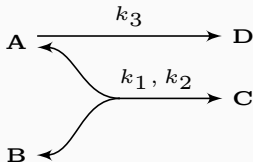


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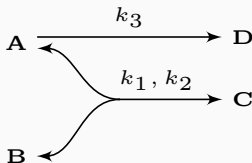


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- $A \longrightarrow D$, with rate $k_3[A]$.

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Then, the differential equation that models the concentration change of A is:

$$\frac{d[A]}{dt} = -k_1[A][B] + k_2[C] - k_3[A].$$

Bayesian Methods for Biochemical Model Selection

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State of the Art Methods for Model Selection

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For both methods, we resort to Metropolis-Hastings algorithm to generate samples of distributions.

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5. Increase t by one and repeat from Step 2 if not reached iteration limit.

Model Selection

Ranking with Marginal Likelihood Estimation

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If we consider that a model M with parameters θ correctly represent the signaling pathway and that there is a Gaussian observation error on D . Then, the likelihood of observing experimental data D is:

$$p(D|M, \theta) = p_{\mathcal{N}(\bar{0}, \Sigma)}(\phi(M, \theta) - D).$$

Where $\phi(M, \theta)$ is the simulated observation.

Marginal Likelihood of Data

We can marginalize the likelihood to obtain:

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Calculating this integral is hard, therefore we resort to estimating another integral.

Power-posterior distributions

We define a power-posterior distribution as:

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$$p_{\beta=1}(\theta) = \frac{p(D, \theta|M)}{\int_{\Theta} p(D, \theta|M) d\theta} = \frac{p(\theta|D, M)p(D|M)}{p(D|M)} = p(\theta|D, M).$$

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$$\ln p(D|M) = \int_0^1 \mathbb{E}_{p_\beta(\theta)} [\ln p(D|\theta, M)] d\beta.$$

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$$\sum_{t=0}^{T-1} (\beta_{t+1} - \beta_t) \frac{\mathbb{E}_{p_{\beta_{t+1}}(\theta)}[\log p(D|M, \theta)] + \mathbb{E}_{p_{\beta_t}(\theta)}[\log p(D|M, \theta)]}{2}$$

Estimating the Thermodynamic Integral

To produce the estimates of

$$\mathbb{E}_{p_{\beta_t}(\theta)}[\log p(D|M, \theta)] \text{ for } t \in \{0, \dots, T\}$$

we need to produce samples of the power-posteriors $p_{\beta_t}(\theta)$.

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On the second and third step, the covariance matrix of the jump distributed is estimated with the current sample of the posterior.

Sampling from the Power-posteriors

On the third step a Populational Monte Carlo Markov Chain is performed. This algorithm allows us to mix samples from different temperatures.

Ranking with Approximate Bayesian Computation

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4. Repeat until some iteration limit.

The result of the algorithm is a sample of the distribution

$$p(\theta, M | d(\phi(M, \theta), D) < \epsilon).$$

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We can use the accepted parameters of tolerance ϵ and model M to estimate

$$p(M|d(\phi(M, \theta)) < \epsilon).$$

Experiments on Model Selection

Software used for Model Ranking Experiments

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- **SigNetMS**: an implementation of the Marginal Likelihood method created in this project.
- **ABC-SysBio**: an implementation of ABC-SMC.

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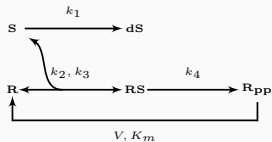
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- Rank the four models.

Experiment #1

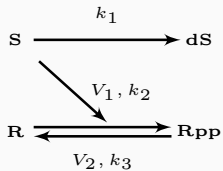
Experiment #1

This experiment is originally from Vyshemirsky and Girolami (2007), in which they present results of Annealing Melting Integration.

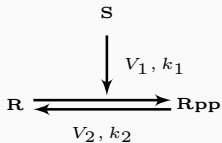
Experiment #1



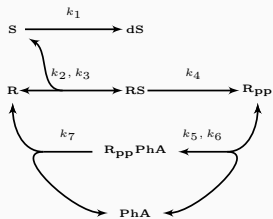
Model 1



Model 2



Model 3



Model 4

Experiment #1

The model used to create the observations was Model 1.

Experiment #1

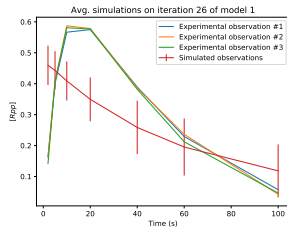
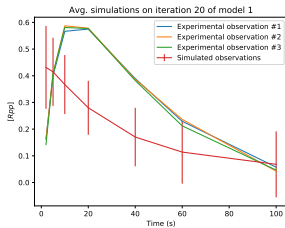
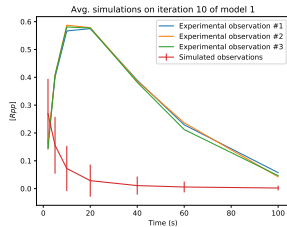
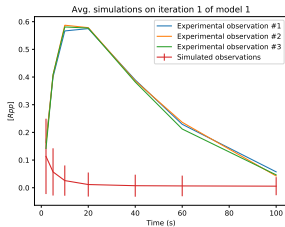
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The priors distribution used for all parameters is $\text{Gamma}(1, 3)$.

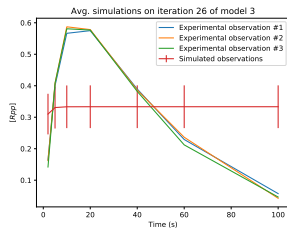
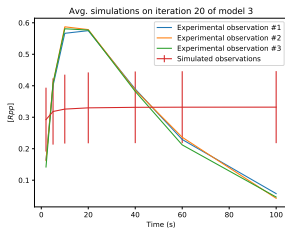
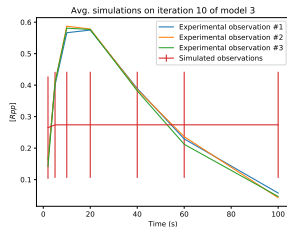
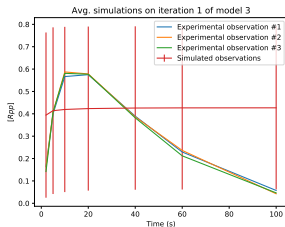
The ABC-SysBio software returned the following ranking of models:

$$3 > 2 > 4 > 1$$

Results on ABC-SysBio



Results on ABC-SysBio



The ranking returned by SigNetMS on the first experiment is:

$$1 > 2 > 4 > 3;$$

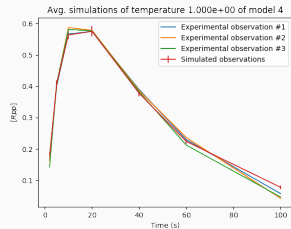
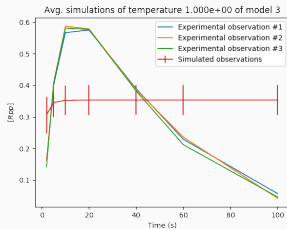
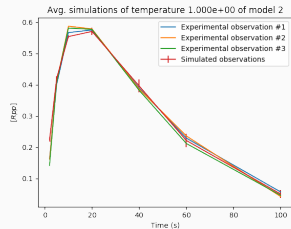
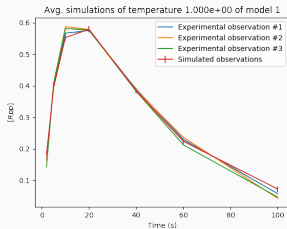
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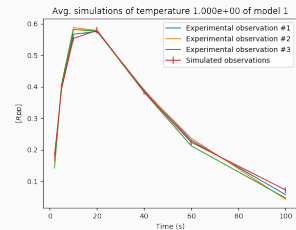
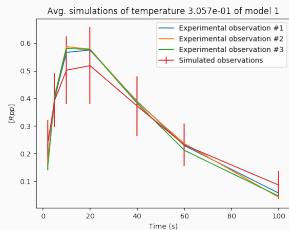
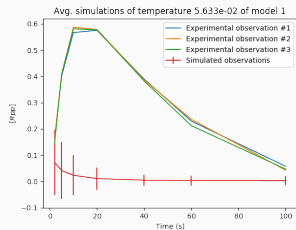
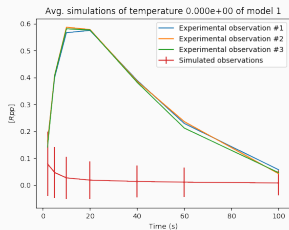
which is very similar to the ranking presented originally by Vyshemirsky and Girolami (2007):

$$1 > 4 > 2 > 3.$$

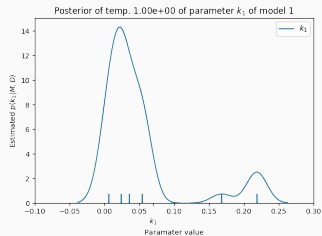
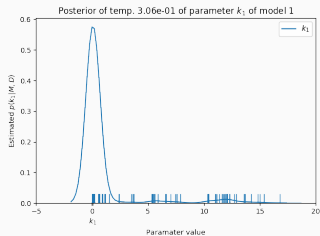
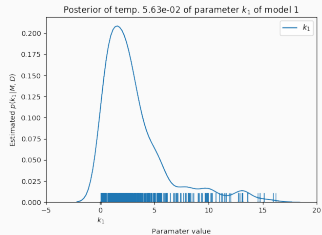
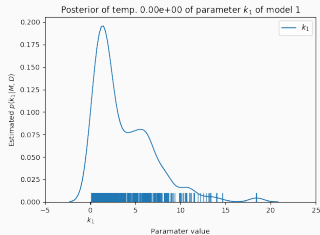
Results on SigNetMS



Results on SigNetMS



Results on SigNetMS

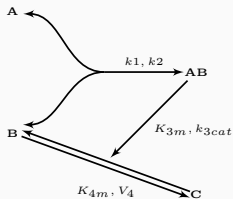


Experiment #2

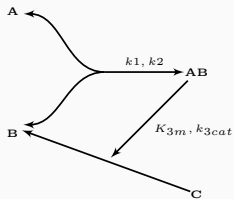
Experiment #2

This experiment is very similar to the later and it was designed by us.

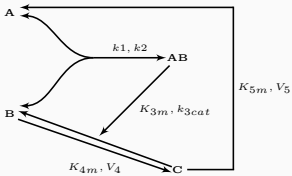
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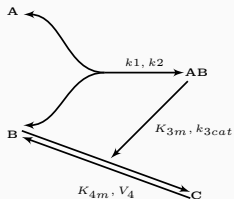
Model 1



Model 2



Model 3



Model 4

Experiment #2

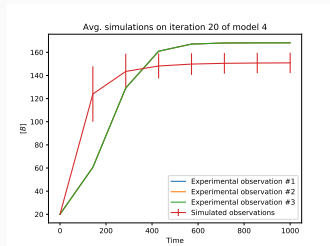
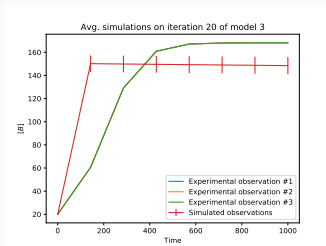
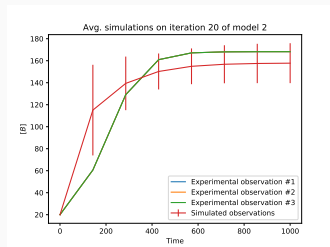
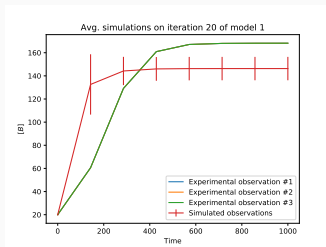
We used the following prior distributions for model parameters:

Parameter	Models	Prior
k_1	1, 2, 3, 4	$\text{Gamma}(1, 0.01)$
k_2	1, 2, 3, 4	$\text{Gamma}(2, 0.5)$
k_{3cat}	1, 2, 3, 4	$\text{Gamma}(4, 1)$
K_{3m}	1, 2, 3, 4	$\text{Gamma}(2, 1500)$
V_4	1, 3, 4	$\text{Gamma}(2, 1)$
K_{4m}	1, 3, 4	$\text{Gamma}(2, 100)$
V_5	3	$\text{Gamma}(2, 0.4)$
K_{5m}	3	$\text{Gamma}(2, 100)$

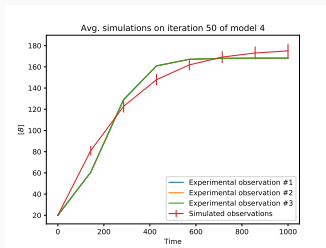
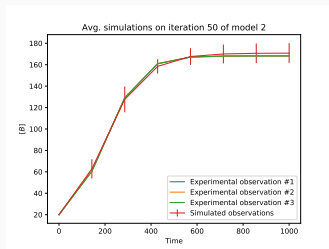
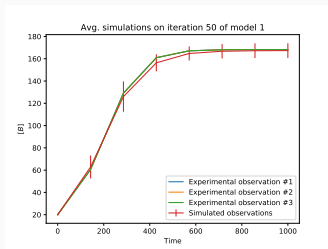
The ABC-SysBio software returned the following ranking of models:

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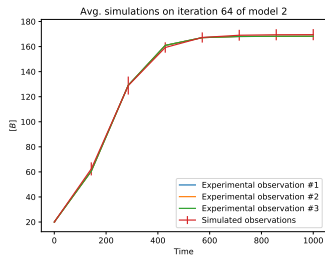
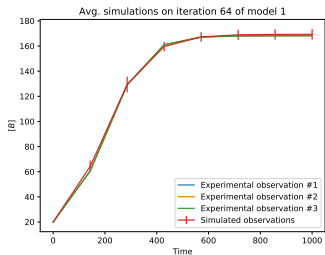
Results on ABC-SysBio



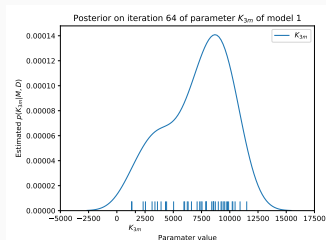
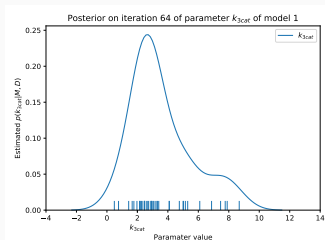
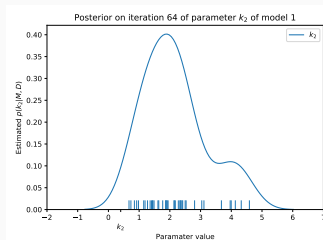
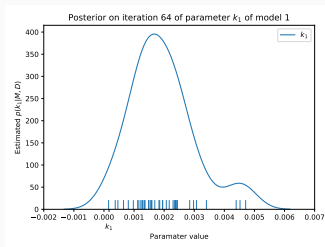
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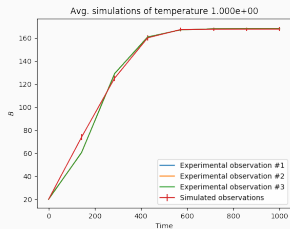
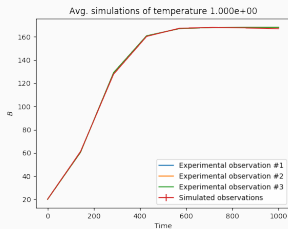
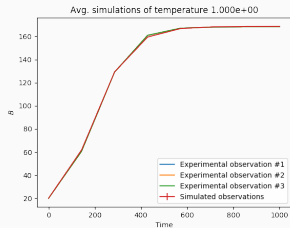
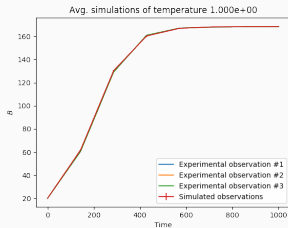
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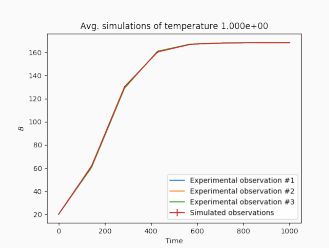
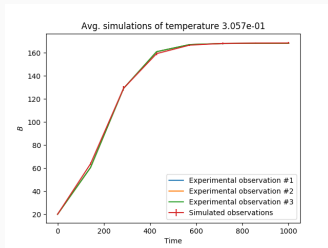
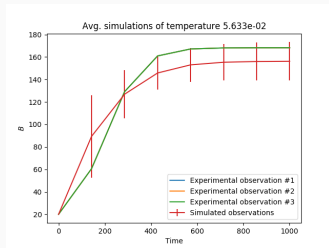
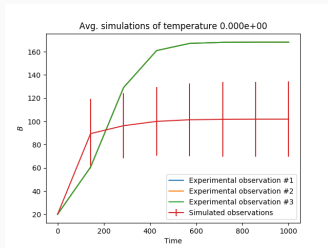
SigNetMS returned the following ranking of models:

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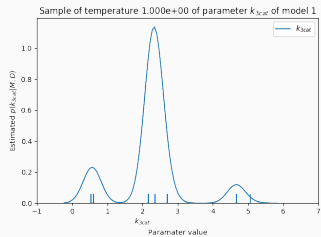
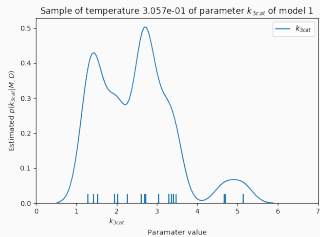
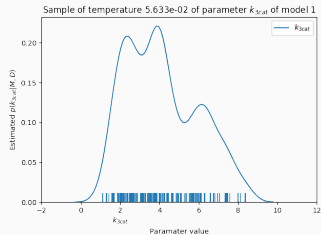
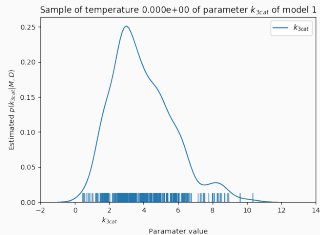
Results on SigNetMS



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Future Work

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- Studies of databases of chemical kinetics such as SABIO-RK and BRENDA.
- Creation of a relational database of chemical interactions that is able to store the topology and rate constants of reactions gathered from chemical kinetics databases.

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- Testing of the methodology developed on known pathways.
- Application of the method in ERK signaling pathways of tumor cell lines Y1 and HEK293.