

# End-to-end Statistical Model Checking for ODEs

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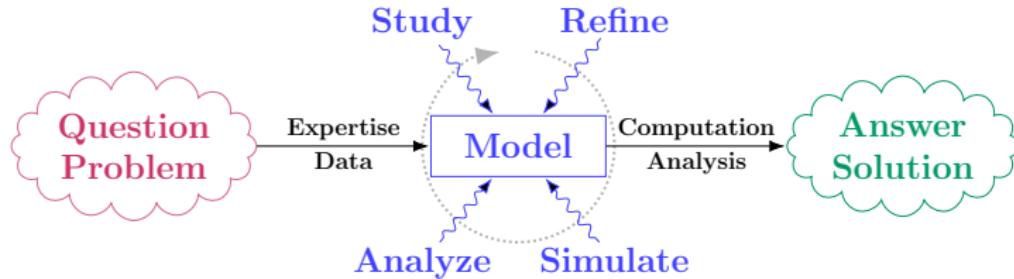
# Outline

- 1 Context
- 2 SMC for ODE models
- 3 Application to parameterization
- 4 Perspectives

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# Science of Models

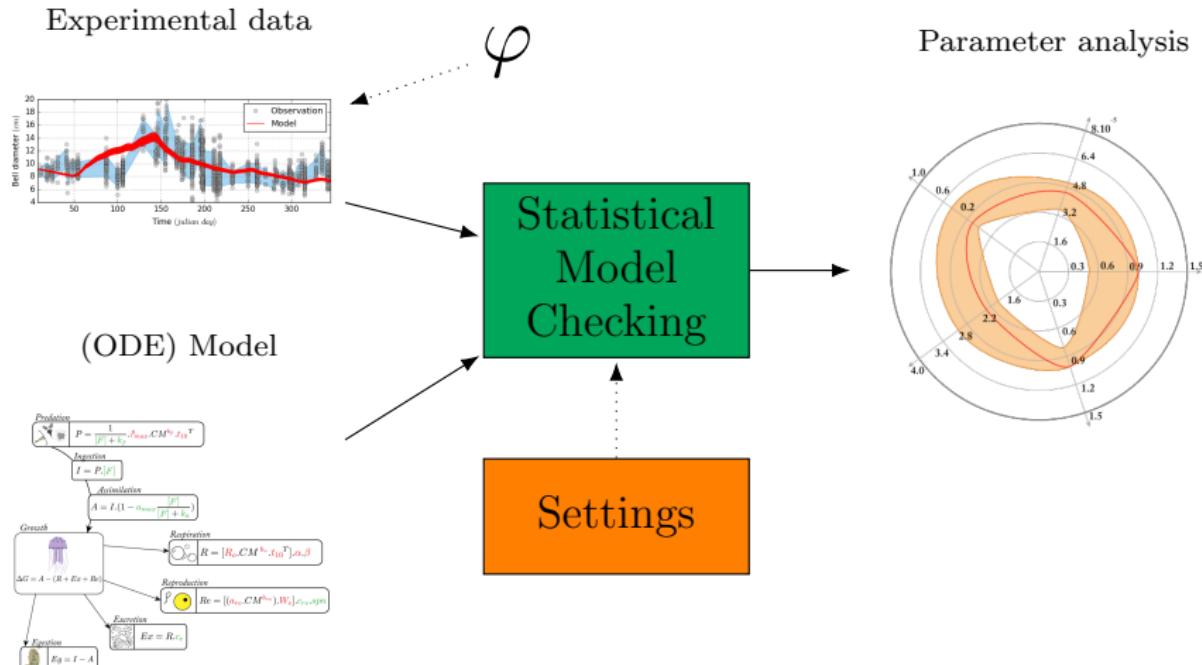


## Motivations

Provide mathematical **guarantees** and **tools** for building and analyzing models

- usable by any scientist;
- answering real-life questions.

# Example: Parameterization of a jellyfish model <sup>1</sup>



<sup>1</sup> [Ramondec et al. 2020] Probabilistic modeling to estimate jellyfish ecophysiological properties and size distribution. *Scientific Reports*

# Formal verification of ODE models

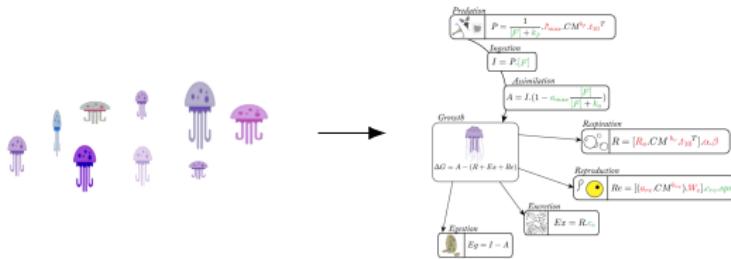
System



# Formal verification of ODE models

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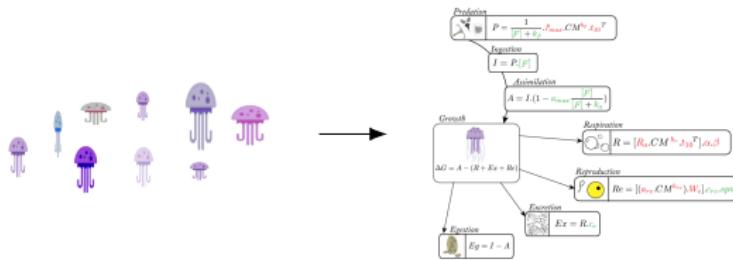
(ODE) Model



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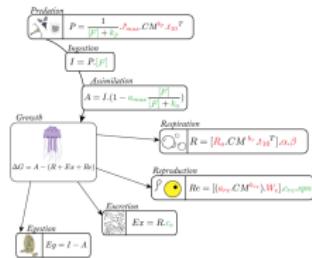


$\varphi$

# Formal verification of ODE models

System

(ODE) Model



Some models may be verified directly (automata, graphs...).

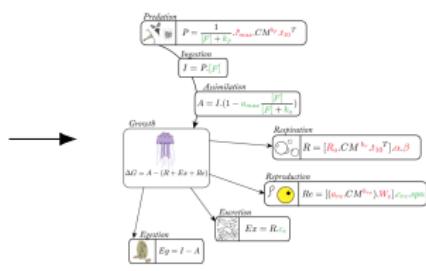
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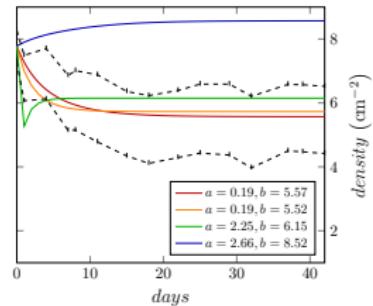
System



(ODE) Model



Set of traces

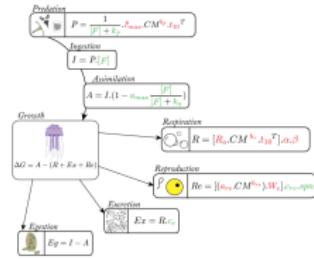
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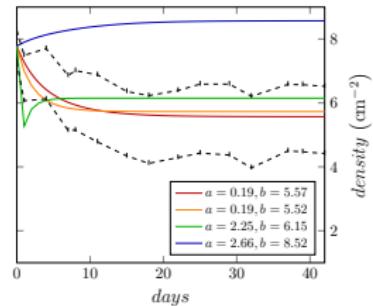
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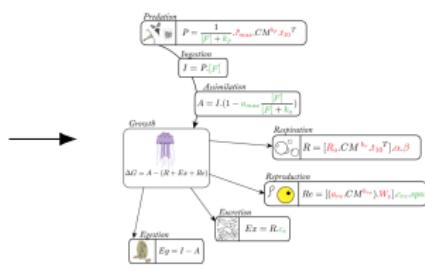
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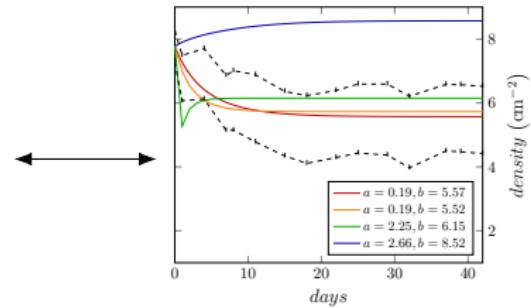
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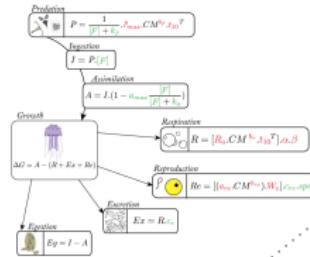
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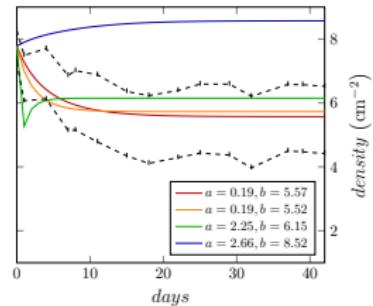
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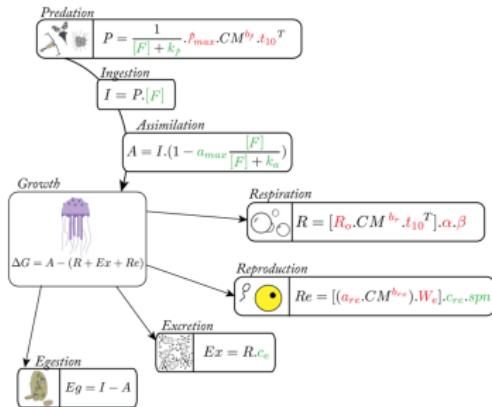


If Model  $\sim$  Traces

$\Rightarrow$  Checking  $\varphi$  on the traces is equivalent to checking it on the model.

$\varphi$

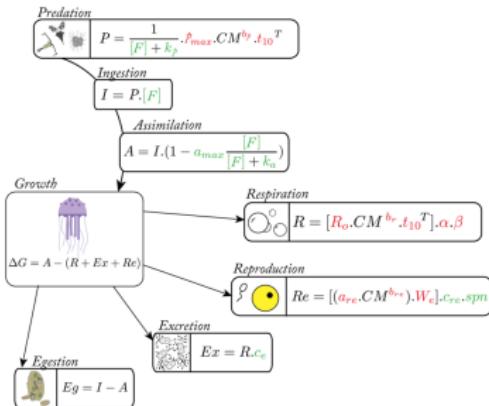
# Probabilistic models



## Uncertainty and variability

- Several experiments  
⇒ data uncertainty.
- Family of systems  
⇒ parameters variability.

# Probabilistic models



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- Several experiments  
⇒ data uncertainty.
- Family of systems  
⇒ parameters variability.

⇒ Parametric model with probabilistic parameter values.

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# SMC: answering “how good is a model?”

The Monte-Carlo procedure:

1. Randomly generate  $N$  samples  $(\sigma_1, \dots, \sigma_N)$  from the model.
2. Check whether the sample  $i$  satisfies the property  $\varphi$ .

$$X_i = 1 \Leftrightarrow \sigma_i \models \varphi$$

3. Compute the estimator  $\hat{p} = \frac{\sum X_i}{N}$ .  
 $\Rightarrow \mathbb{P}(p \in [\hat{p} - \alpha, \hat{p} + \alpha]) \geq 1 - \theta$

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## Central Limit Theorem

- $\hat{p} \sim \mathbb{E}(X)$   
 $\Rightarrow \hat{p}$  is a good estimation of  $\mathbb{P}(M \models \varphi)$ .
- **precision, error.**

## Application to ODE models

[Liu et al. 2019] Statistical Model Checking-Based Analysis of Biological Networks.

*Automated Reasoning for Systems Biology and Medicine*

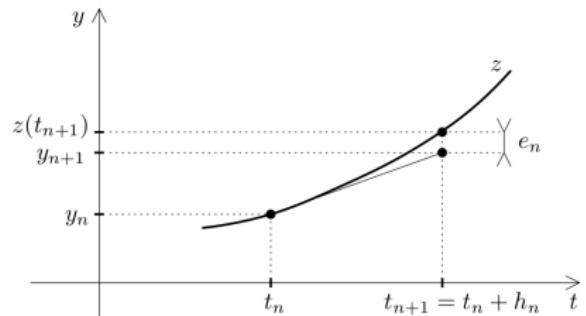
Parameter analysis of ODE models with variability.

# Problem: Approximations

Model  $\approx$  Traces

Approximation error stacks up at each step:  $\varepsilon = \max_n e_n$

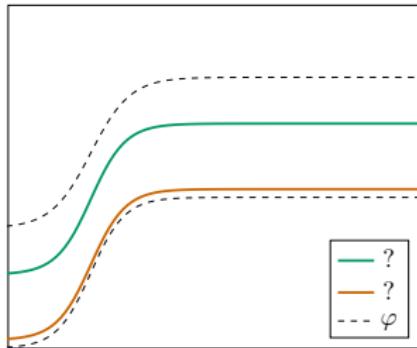
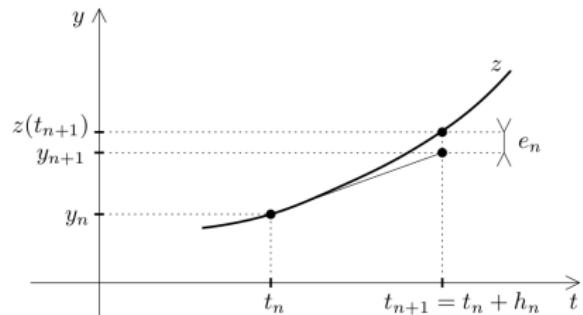
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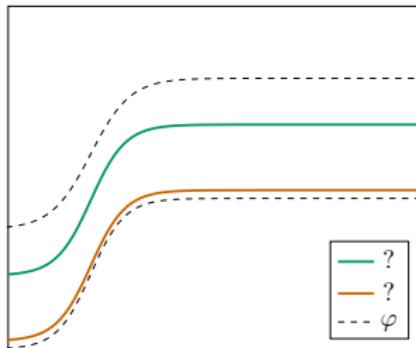
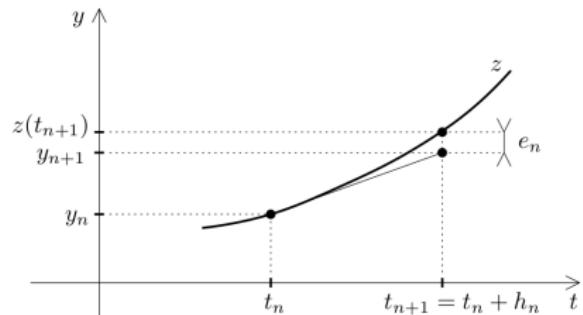
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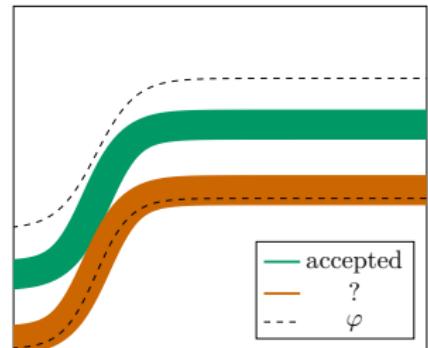
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Approximations



## Solution: Safety margins

- Bound approximation error  $\varepsilon$  on the parameter space.
- Define new properties  $\varphi_1$  and  $\varphi_2$ .

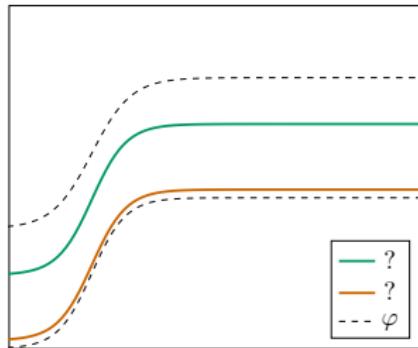
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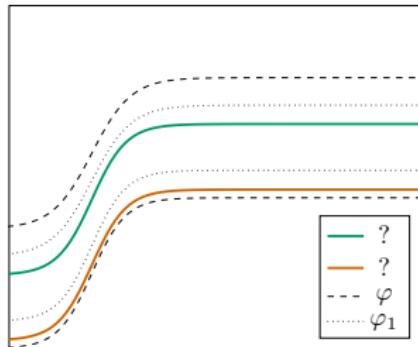


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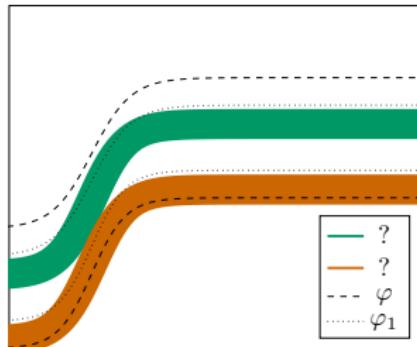


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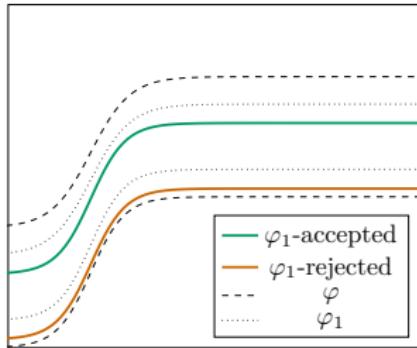


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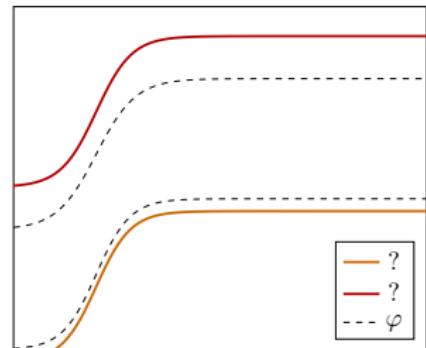
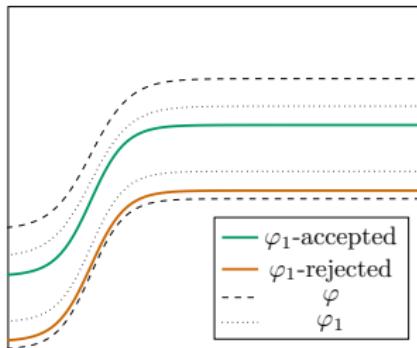


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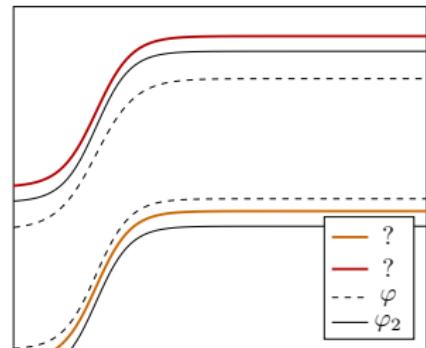
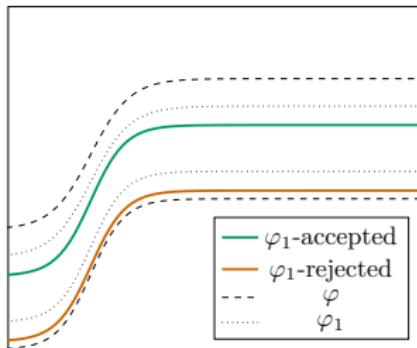


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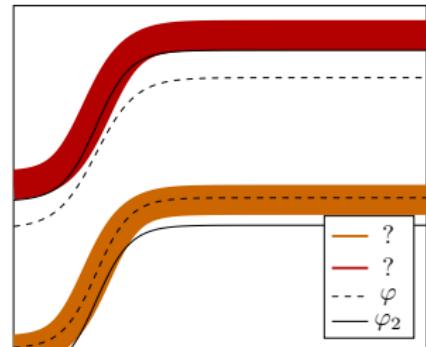
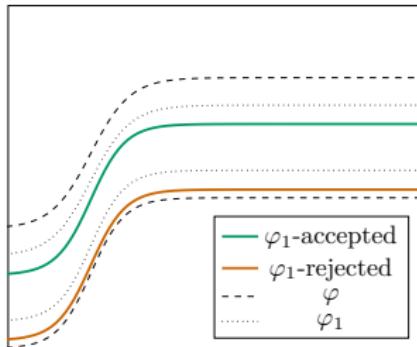


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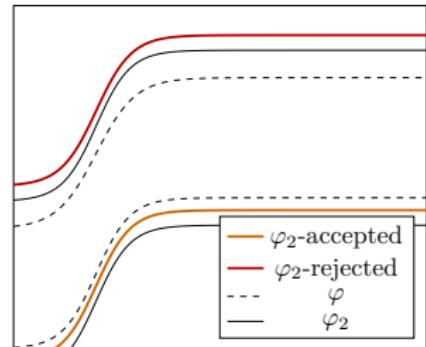
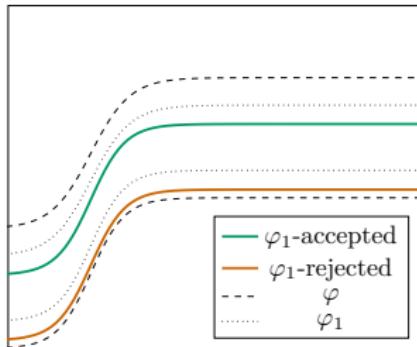


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$$\sigma \models \varphi_1 \Rightarrow M \models \varphi \Rightarrow \sigma \models \varphi_2 \quad \Rightarrow \quad p_1 \leq p \leq p_2$$



# Guarantees: global risk $\xi$ and precision $\alpha$

## Usual SMC

- $n = \frac{\log(2/\xi)}{2\alpha^2}$  simulations.

$$\Rightarrow \mathbb{P}(p \in [\hat{p} - \alpha, \hat{p} + \alpha]) \geq 1 - \xi$$

In our case (for each property)

- SMC risk  $\theta = 1 - \sqrt{1 - \xi} < \xi$
- $n' = \frac{\log(2/\theta)}{2\alpha^2} > n$  simulations

$$\Rightarrow \mathbb{P}(p_1 \in [\hat{p}_1 - \alpha, \hat{p}_1 + \alpha]) \geq 1 - \theta, \quad \mathbb{P}(p_2 \in [\hat{p}_2 - \alpha, \hat{p}_2 + \alpha]) \geq 1 - \theta$$

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Theorem 2 (Main theorem).

After performing  $N = 2 \times n'$  simulations, the following statements hold:

- $\mathbb{P}(p \in [\hat{p}_1 - \alpha, \hat{p}_2 + \alpha]) \geq 1 - \xi$ ;
- $\mathbb{P}(|\hat{p}_1 - \hat{p}_2| \leq 3\alpha) \geq 1 - \xi$ .

Bonus: extension to reward functions.

# Outline

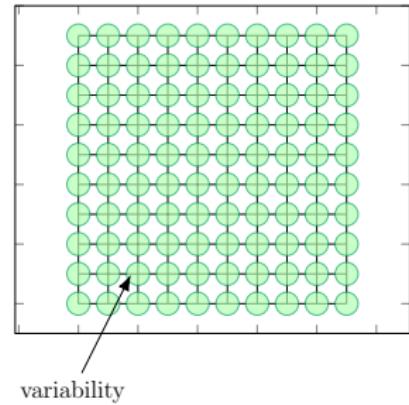
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# Generalities

- Parameterization: Find parameter values  $\lambda$  for a generic model.
- Goal: Find good values for  $\lambda$  w.r.t. score ( $\mathbb{E}(r)$ ) of  $\varphi$ -satisfaction.
- Any algorithm:
  - Local search: low execution time / superficial search;
  - **Global** search: more informative / higher execution time;
  - ...

# What we do

1. Compute the grid of parameters.
2. Compute the score of each value.
3. Select the best value.

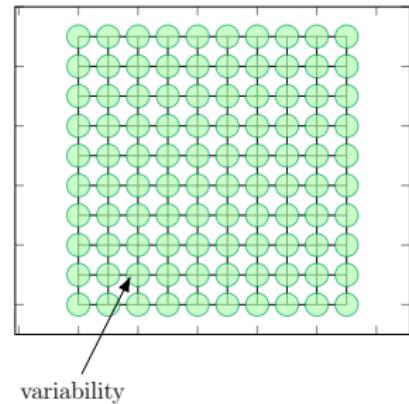


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It only works if we can bound the error  $\varepsilon$ !

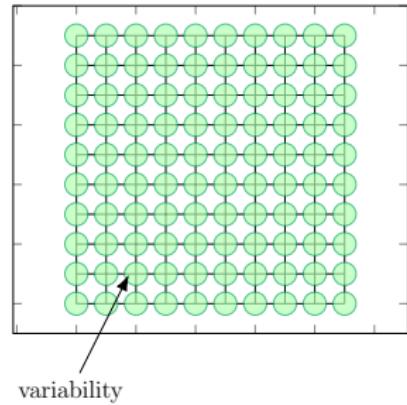


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Proposition

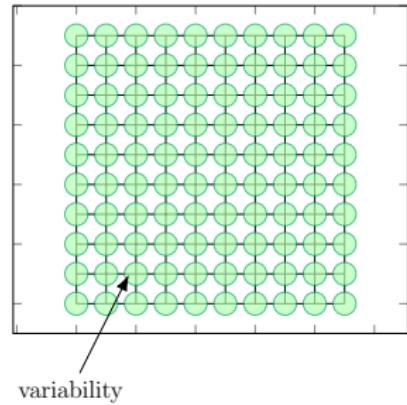
When solving an ODE, the error  $\varepsilon$  is bounded by a function of the integration step  $h$ .

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Lemma 1.

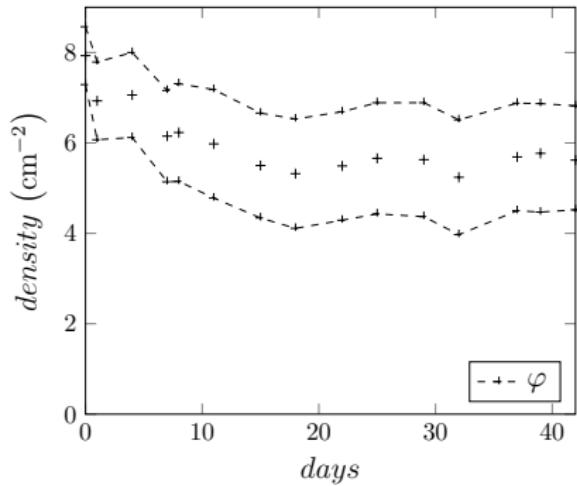
For any arbitrary  $\varepsilon > 0$ , there exists an integration step  $h$  such that

$$0 < \varepsilon_h < \varepsilon, \quad \forall \lambda.$$

# Aurelia Aurita<sup>2</sup>

Jellyfish species from the Adriatic Sea.

- $x'(t) = \textcolor{red}{a} \cdot x(t) \cdot \left(1 - \frac{x(t)}{\textcolor{red}{b}}\right)$
- $\varphi = \text{data} \pm \text{standard error}$

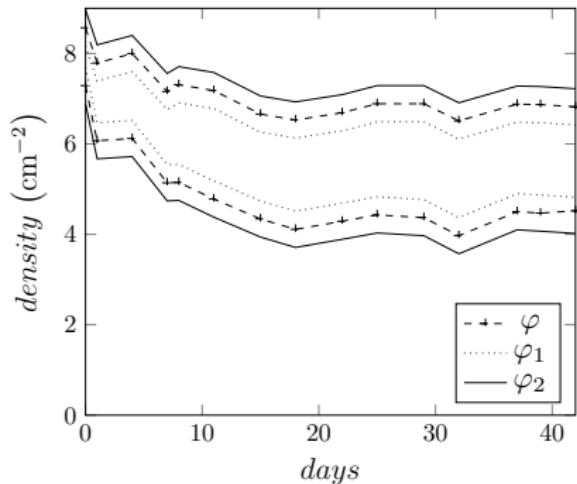


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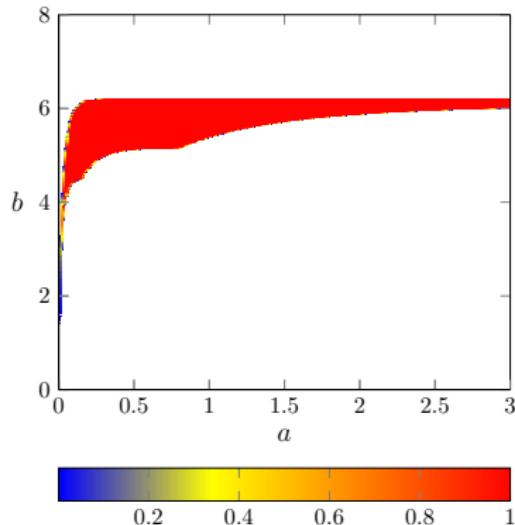
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- $\varphi_1 = \text{"}\varphi - \varepsilon\text{"}$
- $\varphi_2 = \text{"}\varphi + \varepsilon\text{"}$

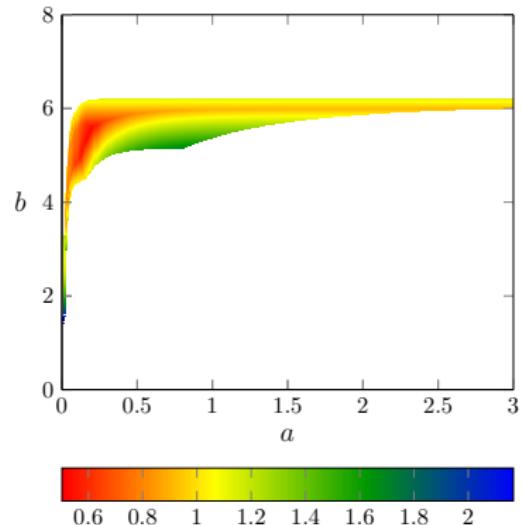


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# Parameter analysis



Probability of staying in the tunnel.



Expected distance to data.

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# Perspectives

## Mathematics

- Convergence speed of  $\hat{p}_1 - \hat{p}_2$ .
- Suitable values for  $\varepsilon$  and  $h$  in the general case.

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- Tool.
- Larger case studies.  
→ mixing models (humans/forest, epidemiology, ...)

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## Modeling

- **Structural properties** of ODE models.  
→ stability, attraction, cycles ...
- **Dynamic** discretization of the parameter grid.  
→ variance, score

# Thank you for your attention !

