

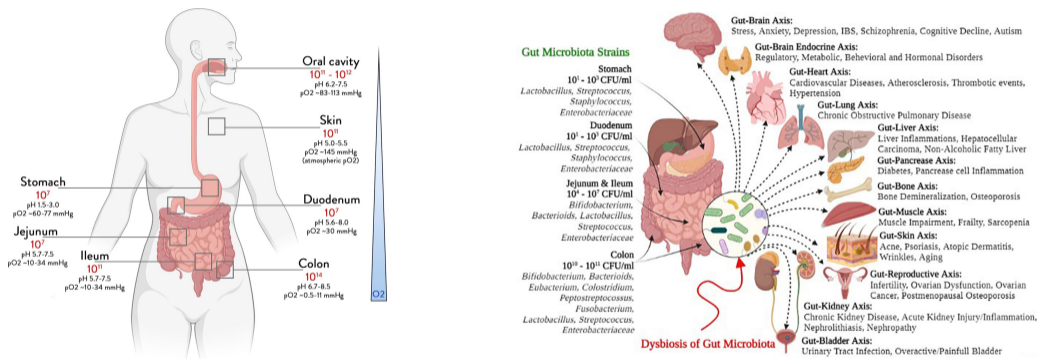
# Estimation of interactions in microbial communities via a neural network-based generalized smoothing algorithm

Nicolas Brunel, Paguiel Javan Hossie, Béatrice Laroche, Lucas Perrin,  
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Our body's equilibrium is partly ensured by billions of bacteria that form assemblages called microbiota in different sites.



**Figure 1:** Left, microbiota repartition in different sites; Right, gut microbial strains and negative health outcomes of gut microbial dysbiosis.

## Advances in gut microbiota analysis techniques:

- ▶ Targeted or respiratory faecal tests
- ▶ 16S RNA sequencing
- ▶ Shotgun metagenomics
  - ▶ Receipt of your stool sample,
  - ▶ DNA extraction,
  - ▶ Preparation of DNA libraries,
  - ▶ Sequencing of DNA fragments: identification of the nucleotides present on the DNA strands,
  - ▶ Interpretation and reception of results.

**Main objectives:** comprehend the interactions between these bacteria, their relationship with pathogens, and their functions within the ecosystem.

## CEMRACS Project

- ▶ Generalized Lotka–Volterra to model microbial interaction.
- ▶ From a data set obtained through experiments, we want to **estimate the parameters** involved in a model.
- ▶ In a previous work<sup>1</sup>, this was done using the **Generalized Smoothing Algorithm** with **splines** as data interpolation.

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**Disadvantage:** data interpolation with **splines** is the **costly** part of the estimation process.

- ▶ Main objective of the project: neural network to replace the spline smoothing.
- ▶ As this part tries to fit data points **and** a differential equation: investigate a **Physics-Informed Neural Network** approach.

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## Modeling biological data

- ▶ Models are not exact,
- ▶ Several experiments, different initial values, and conditions,
- ▶ Sparse and irregular sampling, depending on the experiment,
- ▶ Noise and missing data.

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### Notations:

- ▶  $N_s$ : number of species studied,
- ▶  $N_{\text{exp}}$ : number of experiments conducted,
- ▶  $N_{\text{obs}}^e$ : number of noisy observations of the bacterial population of species  $i$  at times  $t_k^{(e)}$ ,
- ▶  $U_{i,k}^{(e)}$  data measured for the experiment  $e$ , on species  $i$ , at time  $t_k^{(e)}$ .



## Generalized Lotka–Volterra Model<sup>2</sup> (GLV)

- ▶ For  $i \in \llbracket 1, N_s \rrbracket$ ,  $x_i(t)$  represent the quantity of bacteria of population  $i$ .
- ▶ This quantity follows the ODE:

$$\frac{\partial}{\partial t} x_i(t) = \mu_i x_i(t) + \sum_{j=1}^{N_s} a_{ij} x_i(t) x_j(t), \quad t \in [0, t_{\max}]$$

where:

- ▶  $\mu_i$  represents the **intrinsic growth** rate of the bacterial population in the absence of interaction with other bacterial populations,
- ▶  $a_{ij}$  describes the **interaction** coefficient representing the direct effect of species  $j$  on the species  $i$ .

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<sup>2</sup>V. Volterra and M. Brelot. *Leçons sur la théorie mathématique de la lutte pour la vie.* eng. Paris : Gauthier-Villars, 1931.

## Generalized Lotka–Volterra Model<sup>2</sup>

Setting  $\boldsymbol{\mu} = [\mu_1, \dots, \mu_{N_s}]^T$ ,  $\mathbf{A} = (a_{ij})_{1 \leq i, j \leq N_s}$  and  $u_i = \log(x_i)$ , the GLV model can be written under the matrix form:

$$\frac{\partial}{\partial t} \begin{bmatrix} u_1(t) \\ \vdots \\ u_{N_s}(t) \end{bmatrix} = \boldsymbol{\mu} + \mathbf{A} \cdot \exp \left( \begin{bmatrix} u_1(t) \\ \vdots \\ u_{N_s}(t) \end{bmatrix} \right) \quad (\text{GLV})$$

The elements of  $\boldsymbol{\mu}$  and  $\mathbf{A}$  are gathered in a matrix  $\boldsymbol{\theta}$  of size  $(N_s, N_s + 1)$ :

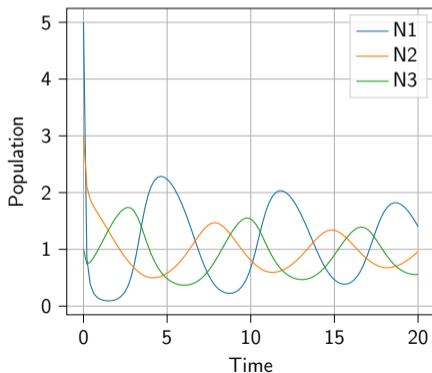
$$\boldsymbol{\theta} = \begin{bmatrix} \mu_1 & a_{11} & \dots & a_{1, N_s} \\ \vdots & \vdots & \ddots & \vdots \\ \mu_{N_s} & a_{N_s 1} & \dots & a_{N_s N_s} \end{bmatrix}$$

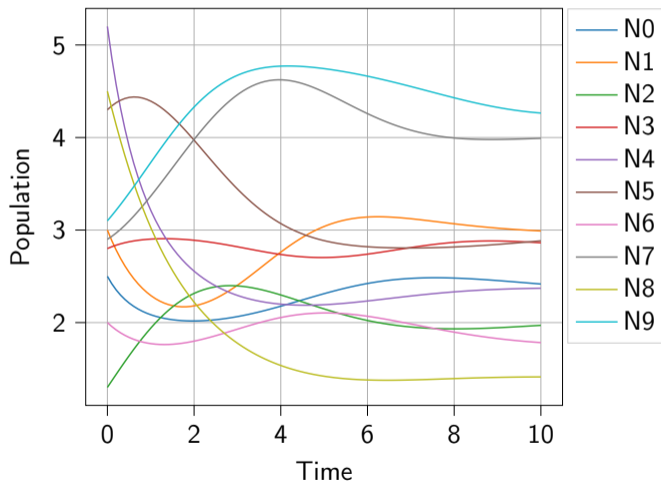
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## Example with $N_s = 3$

We set  $\mathbf{A} = \begin{bmatrix} -2 & -5 & -0.5 \\ -0.5 & -1 & -1.2 \\ -1 & -0.5 & -1 \end{bmatrix}$ , from an initial population of  $\mathbf{u}_0 = [5, 3, 1]^T$  and the intrinsic growth rate  $\boldsymbol{\mu} = [7.5, 2.6, 2.5]^T$



Example with  $N_s = 10$ 

## Framework of the study

**Main objective:** determine the optimal parameters  $a_{ij}$  and  $\mu_i$  of (GLV) from observed data throughout multiple experiments.

### Challenge:

- ▶ bacterial data has a significantly lower sample number than bacterial species
- ▶ Direct estimation of GLV model parameters, such as maximum likelihood estimation with smoothing of observation, Bayesian estimation with smoothing of observation, ....., even genetic algorithm is not easy (local minima, instability of the system in certain parameter regions).

*Here we present the Generalised Smoothing PINN algorithm: a mixture algorithm between PINN and Generalised Smoothing Algorithm.*

# Generalized Smoothing Algorithm

- ▶ Introduced by Ramsay and co-authors<sup>3</sup>
- ▶ Method to estimate parameters  $\theta$  in a nonlinear differential equation of the form

$$\partial_t \mathbf{u}(t) = \mathbf{f}(\mathbf{u}, t; \theta).$$

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- ▶ Previously used for the GLV model<sup>4</sup>

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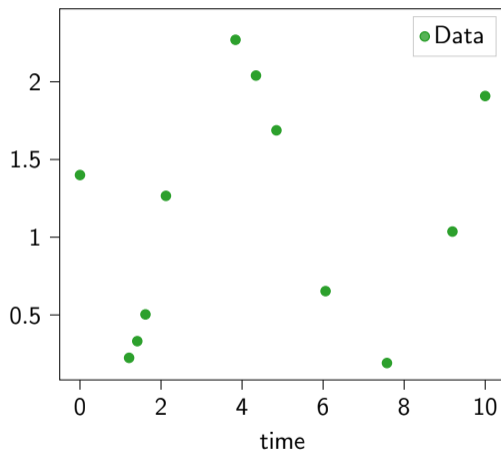
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## Generalized Smoothing Algorithm - Least Squares (GSA-LS)

- Step 0 Spline smoothing of the data.** The coefficients of the spline function fitting the data are stored in a matrix  $\mathbf{C}$ .
- Step 1** Estimate of  $\theta$  with the proximal gradient descent technique.
- Step 2** New coefficients of the spline  $\mathbf{C}$  basis are computed using a **least squares minimization approach**.

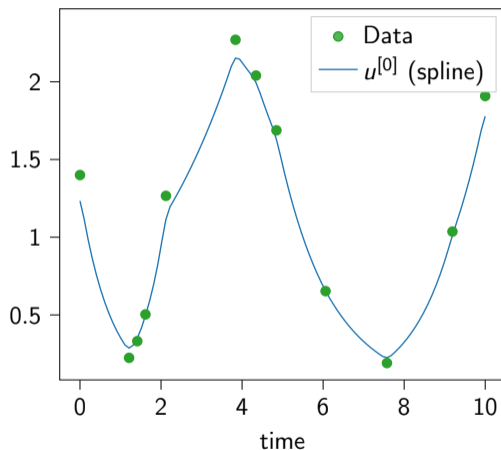


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Step 0: Spline smoothing

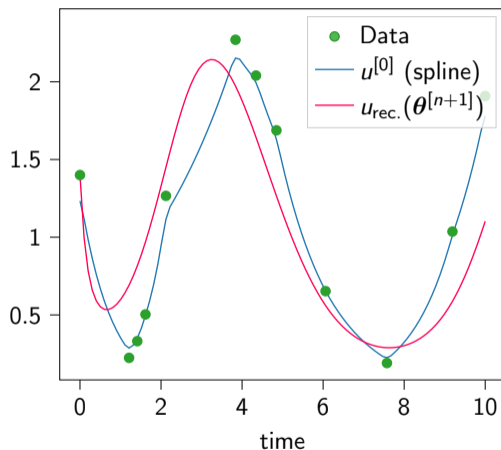


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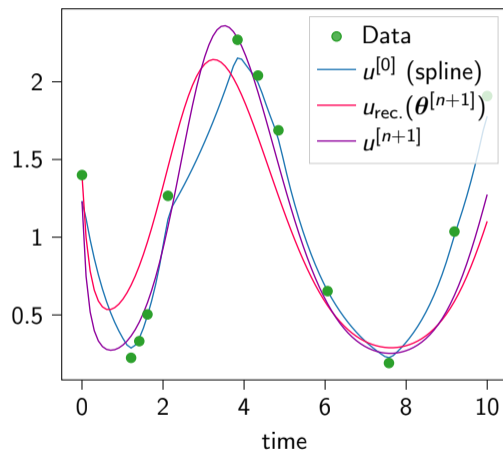
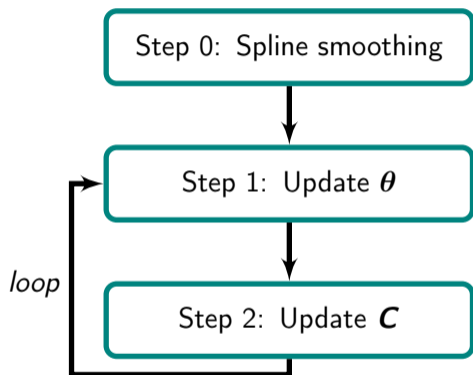
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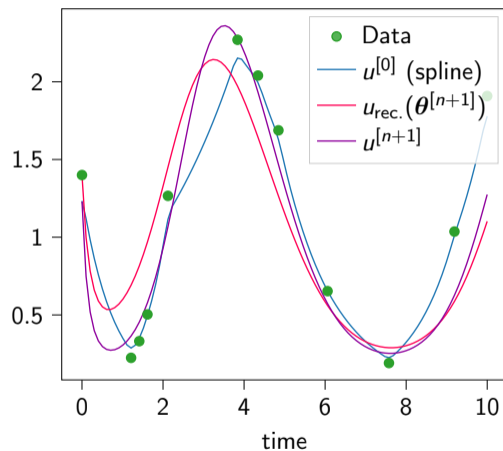
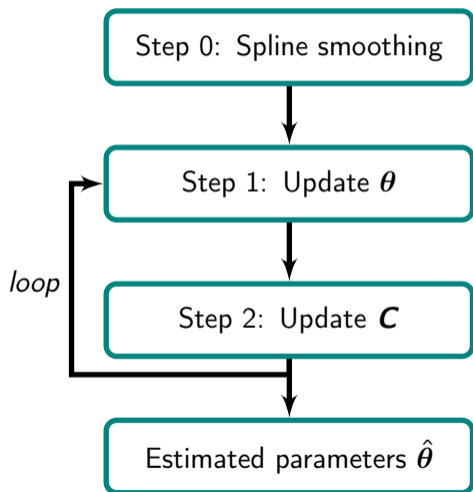
Step 1: Update  $\theta$



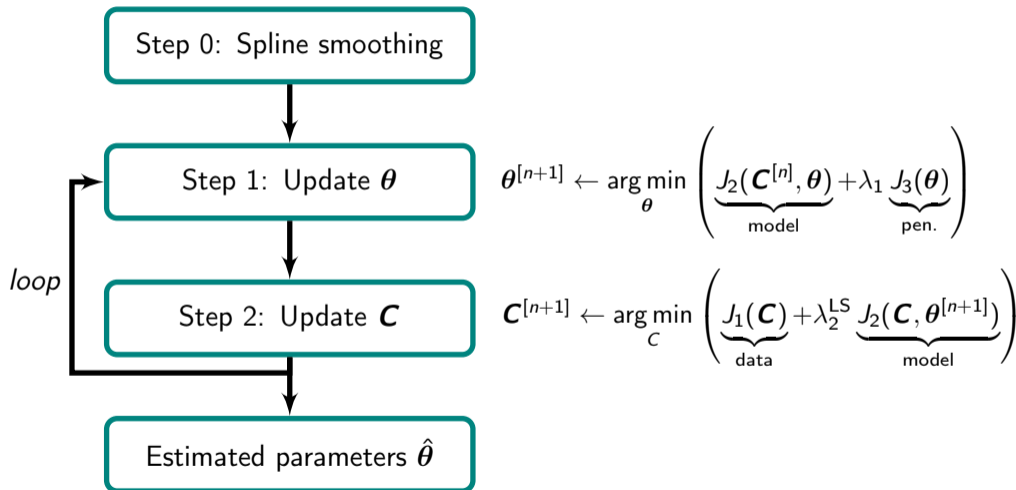
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- **Data:** we want to fit the data points

$$J_1(\mathbf{C}) = \sum_{e=1}^{N_{\text{exp}}} \sum_{k=1}^{N_{\text{obs}}^{(e)}} \sum_{i=1}^{N_s} \left| \hat{u}_i^{(e)}(t_k^{(e)}) - \mathbf{u}_{i,k}^{(e)} \right|^2$$

where  $\tilde{u}_i^{(e)}(t) = C^{(e)}\Phi(t)$  is the spline reconstructed solution for the species  $i$ , and the experiment  $e$ .

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- **Model:** we want to fit the dynamic

$$J_2(\mathbf{C}, \boldsymbol{\theta}) = \sum_{e=1}^{N_{\text{exp}}} \frac{1}{N_f} \sum_{j=1}^{N_f} \left\| \partial_t \hat{\mathbf{u}}^{(e)}(t_j) - \mathbf{f}(\hat{\mathbf{u}}^{(e)}(t_j), t_j, \boldsymbol{\theta}) \right\|_2^2$$

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- **Penalization on  $\boldsymbol{\theta}$ :** we want our parameters matrix to be sparse

$$J_3(\boldsymbol{\theta}) = \text{Pen}(\boldsymbol{\theta}) = \|\boldsymbol{\theta}\|_1$$

## Advantages of GSA

- ▶ **Flexibility:** can handle functional data with complex structures,
- ▶ **Nonparametric:** no assumptions about the underlying distribution,
- ▶ Effective for **denoising** and recovering underlying patterns in data,
- ▶ Provides **interpretable and smooth estimates**,
- ▶ **Widely applicable** in diverse fields for analyzing complex functional data.

## PINN to solve the GLV model for a given parameter and initial condition

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Let us consider a normalized version of (GLV) written as

$$\frac{\partial}{\partial t} \mathbf{u}(t) = t_{\max} (\boldsymbol{\mu} + \mathbf{A} \cdot \exp(\mathbf{u}(t))) \quad \text{for } t \in [0, 1]. \quad (\text{GLV-norm})$$

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**Objective:** construct a neural network approximation  $\hat{\mathbf{u}}(t)$  of the solution  $\mathbf{u}(t)$  of (GLV-norm) **given some parameters  $\boldsymbol{\mu}$  and  $\mathbf{A}$**  (and some data points).

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Let  $\mathcal{L}$  be the *residual* of the prediction  $\hat{\mathbf{u}}(t)$  defined as:

$$\mathcal{L}(t) := \partial_t \hat{\mathbf{u}}(t) - t_{\max}(\boldsymbol{\mu} + \mathbf{A} \exp(\hat{\mathbf{u}}(t))) \quad \forall t \in [0, 1].$$

## Loss function

We introduce 2 types of errors:

- ▶ The mean squared misfit by the data:

$$MSE_{\text{data}}\left(t^{(e)}\right) = \frac{1}{N_s N_{\text{obs}}^e} \sum_{i=1}^{N_s} \sum_{k=1}^{N_{\text{obs}}^e} \left\| \hat{\mathbf{u}}^i(t_k^{(e)}) - \mathbf{u}_{i,k}^{(e)} \right\|^2$$

- ▶ The mean squared residual, with collocation points  $t_r = \{t_j\}_{j=1}^{N_f} \subset [0, 1]$ :

$$MSE_{\mathcal{L}}(t_r) = \frac{1}{N_s N_f} \sum_{i=1}^{N_s} \sum_{j=1}^{N_f} \|\mathcal{L}_i(t_j)\|^2$$



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Target loss to be minimized, involving hyper-parameters  $\lambda_2^{\text{PINN}} > 0$ :

$$\text{Loss} = MSE_{\text{data}}(t^{(e)}) + \lambda_2^{\text{PINN}} MSE_{\mathcal{L}}(t_r)$$

# PINN prediction

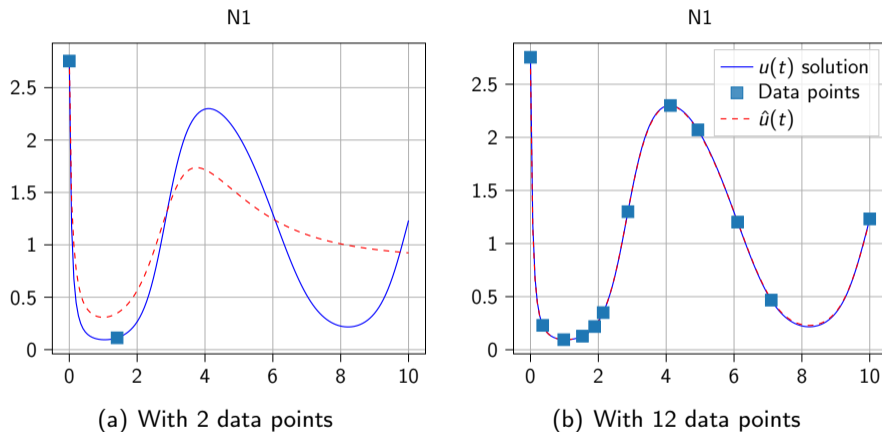


Figure 2: Prediction of the PINN with various numbers of points used for the training set

## Tuning the hyperparameters

### Hyperparameters of interest:

- ▶  $\lambda_2^{\text{PINN}}$
- ▶ architecture (number of layers, size of layers)

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$$E_{\text{PINN}} = \frac{1}{N_s} \sum_{j=1}^{N_s} \frac{\|\hat{\mathbf{u}}^j - \mathbf{u}_{\text{truth}}^j\|_{L^2([0, t_{\max}])}^2}{\|\mathbf{u}_{\text{truth}}^j\|_{L^2([0, t_{\max}])}^2}$$

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- ▶  $\lambda_2^{\text{PINN}} = 10^{-3}$
- ▶ best architecture is  $[1, N_s, 7 \cdot N_s, 7 \cdot N_s, N_s]$

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Regarding the architecture:

- ▶ compromise between speed of training and precision
- ▶ wanted an increasing size of layers (N. Brunel)

## GSA with a PINN

**Step 0:**  $\mathbf{u}^{[0]}$  ← spline smoothing of data  
+ « loop 0 »: First training of the PINN

## GSA with a PINN

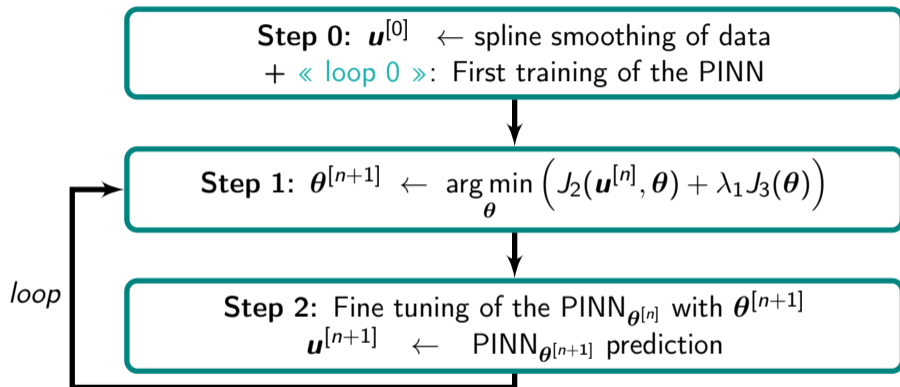
**Step 0:**  $\mathbf{u}^{[0]} \leftarrow$  spline smoothing of data  
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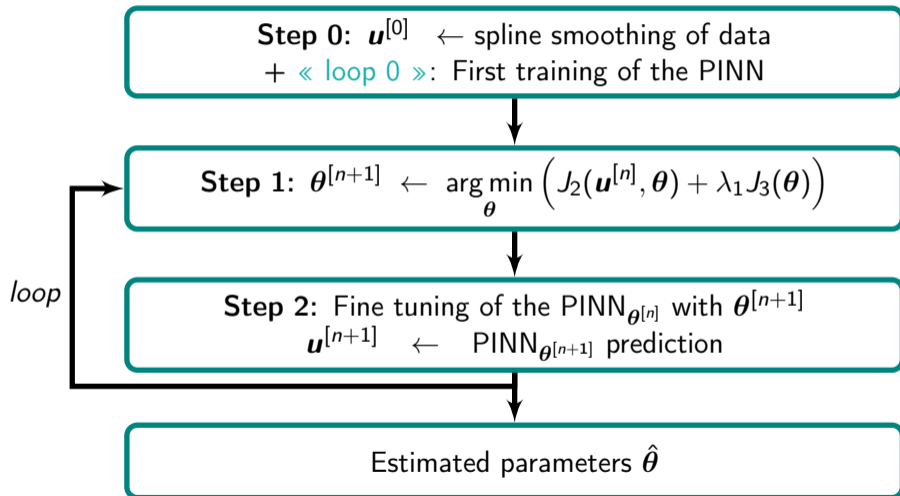
**Step 1:**  $\theta^{[n+1]} \leftarrow \arg \min_{\theta} \left( J_2(\mathbf{u}^{[n]}, \theta) + \lambda_1 J_3(\theta) \right)$



## GSA with a PINN



## GSA with a PINN



## Epoch management

### How many epochs should we do for the PINN ?

We have to do a trade-off between precision and computation time.

Hyperparameters tuning methods no so helpful as they appeared to be very problem dependent.

Chose an **adaptative method**: do fewer epochs if there is a smaller change in the estimated parameters.

- ▶ do  $k$  epochs, with  $k = \min \left\{ 1 + \left\lfloor 10^3 \cdot \frac{\|\boldsymbol{\theta}^{[n]} - \boldsymbol{\theta}^{[n+1]}\|_F}{\|\boldsymbol{\theta}^{[n]}\|_F} \right\rfloor, 200 \right\}$
- ▶ stop if  $\text{Loss} \leq 10^{-3}$

## Stop criterion

- ▶ We use a relative error between two consecutive iterations to stop the algorithm:

$$err^{[n]} = \frac{\|\mathbf{u}^{[n]} - \mathbf{u}^{[n+1]}\|_{L^2[0, t_{\max}]}}{\|\mathbf{u}^{[n]}\|_{L^2[0, t_{\max}]}} + \frac{\|\boldsymbol{\theta}^{[n]} - \boldsymbol{\theta}^{[n+1]}\|_{\text{F}}}{\|\boldsymbol{\theta}^{[n]}\|_{\text{F}}}$$

- ▶ We stop when  $err^{[n]}$  reaches a given tolerance `errMax`,
- ▶ We also stop if the number of iterations reaches a maximal number of iterations `maxIter`.

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- ▶ We stop when  $err^{[n]}$  reaches a given tolerance `errMax`,
- ▶ We also stop if the number of iterations reaches a maximal number of iterations `maxIter`.
- ▶ But  $err^{[n]}$  decreasing really slowly,
- ▶ Adaptive stop criterion: every 30 steps, if we have not improved the minimal error, we multiply the tolerance by 10.

## Stop criterion

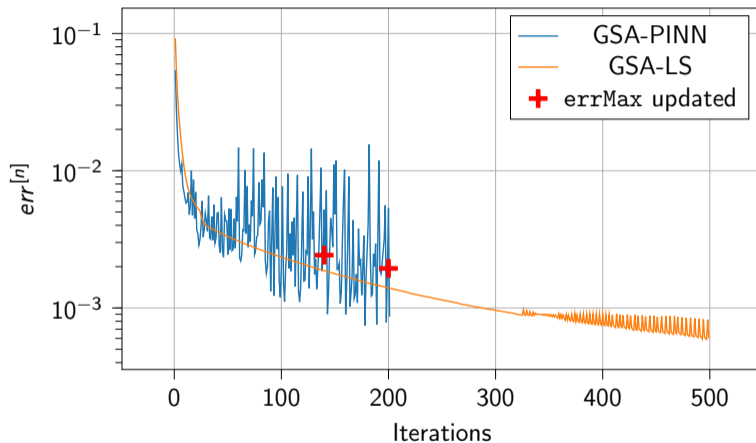
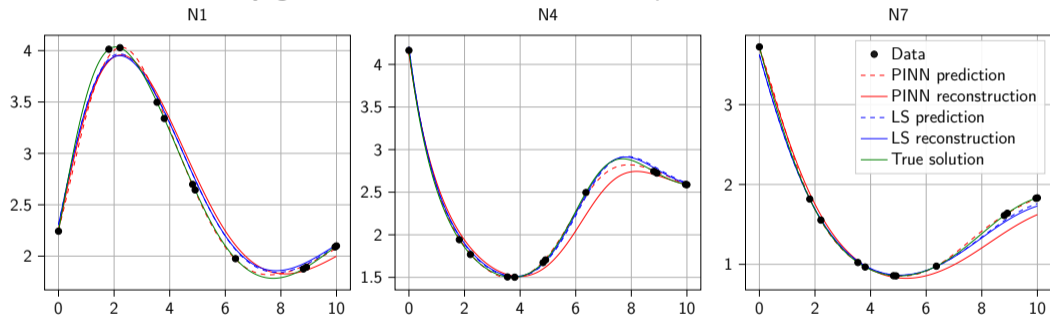


Figure 3: Evolution of the error in the GSA-PINN algorithm, test case with 3 populations

## First comparison: 10 experiments for 10 species are performed

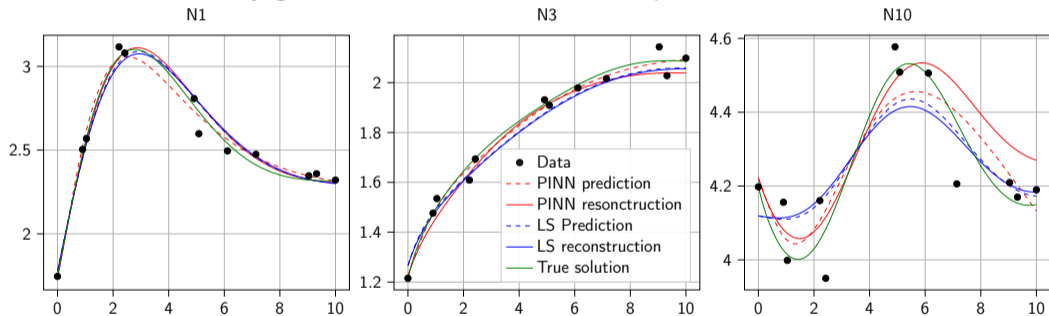
We use data manually generated from a known set of parameters.



(a) Data without noise

## First comparison: 10 experiments for 10 species are performed

We use data manually generated from a known set of parameters.



(b) Noisy data



## First comparison: comparison between the two algorithms

- ▶  $Err_{\theta,1} := \frac{\|\hat{\theta} - \theta_{\text{truth}}\|_F}{\|\theta_{\text{truth}}\|_F}$ ,
- ▶  $Err_{\theta,2}$  defined as the number of coefficients where  $\hat{\theta}$  and  $\theta_{\text{truth}}$  have the same sign, divided by the number of coefficients of the matrices.

$$\text{▶ } Err_{\mathbf{u},1} := \frac{1}{N_s N_{\text{exp}}} \sum_{i=1}^{N_s} \sum_{e=1}^{N_{\text{exp}}} \frac{\|\hat{\mathbf{u}}_j^{(e)} - \mathbf{u}_j^{(e)}(\theta_{\text{truth}})\|_2^2}{\|\mathbf{u}_j^{(e)}(\theta_{\text{truth}})\|_2^2},$$

$$\text{▶ } Err_{\mathbf{u},2} := \frac{1}{N_s N_{\text{exp}}} \sum_{i=1}^{N_s} \sum_{e=1}^{N_{\text{exp}}} \frac{\|\mathbf{u}_j^{(e)}(\hat{\theta}) - \mathbf{u}_j^{(e)}(\theta_{\text{truth}})\|_2^2}{\|\mathbf{u}_j^{(e)}(\theta_{\text{truth}})\|_2^2},$$

## Comparison between Matlab original code and our Python code

Uniformly distributed data (non-random), 10 data, 10 species, 1 experiment, no noise

Algo.	Mean $Err_{\theta,1}$	Mean $Err_{\theta,2}$	Mean $Err_{\mathbf{u},1}$	Mean $Err_{\mathbf{u},2}$	Elapsed time
GSA-LS	1.02	0.69	$4.73 \cdot 10^{-2}$	$4.94 \cdot 10^{-2}$	5.54 sec
GSA-PINN	1.06	0.6	$1.62 \cdot 10^{-2}$	$2.2 \cdot 10^{-2}$	4.46 sec

## Comparison between Matlab original code and our Python code

Uniformly distributed data (non-random), 10 data, 20 species, 1 experiment, no noise

Algo.	Mean $Err_{\theta,1}$	Mean $Err_{\theta,2}$	Mean $Err_{\mathbf{u},1}$	Mean $Err_{\mathbf{u},2}$	Elapsed time
GSA-LS	1.09	0.8	$3.4 \cdot 10^{-2}$	$3.53 \cdot 10^{-2}$	8.75 sec
GSA-PINN	0.98	0.74	$1.35 \cdot 10^{-2}$	$1.92 \cdot 10^{-2}$	10.48 sec

## Comparison between Matlab original code and our Python code

Uniformly distributed data (non-random), 10 data, 10 species, 10 experiments, no noise

Algo.	Mean $Err_{\theta,1}$	Mean $Err_{\theta,2}$	Mean $Err_{\mathbf{u},1}$	Mean $Err_{\mathbf{u},2}$	Elapsed time
GSA-LS	0.19	0.21	0.32	0.26	16.81 sec
GSA-PINN	0.22	0.18	$1.5 \cdot 10^{-2}$	$2.18 \cdot 10^{-2}$	35.53 sec

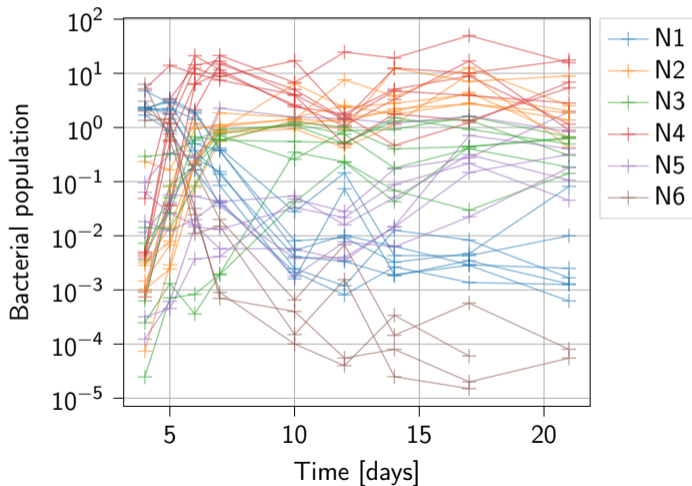
## Comparison between Matlab original code and our Python code

Uniformly distributed data (non-random), 10 data, 10 species, 20 experiments, with some noise

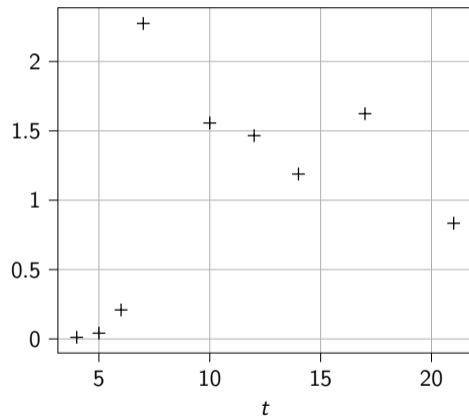
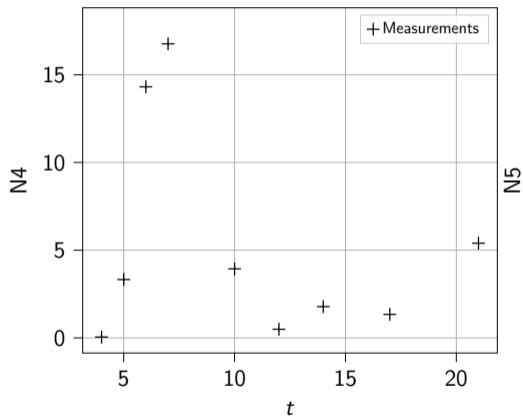
Algo.	Mean $Err_{\theta,1}$	Mean $Err_{\theta,2}$	Mean $Err_{\mathbf{u},1}$	Mean $Err_{\mathbf{u},2}$	Elapsed time
GSA-LS	0.16	0.13	0.44	0.28	98.65 sec
GSA-PINN	0.18	0.15	$1.49 \cdot 10^{-2}$	$2.08 \cdot 10^{-2}$	70 sec

## Bacterial population in mice guts

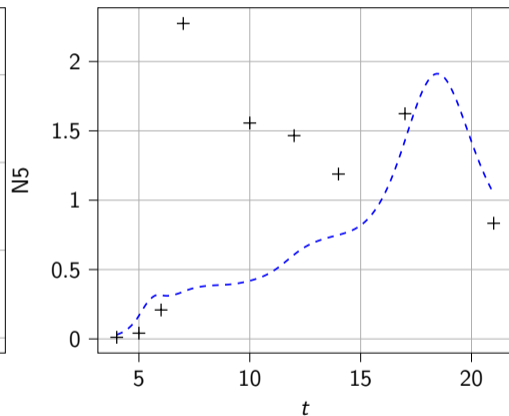
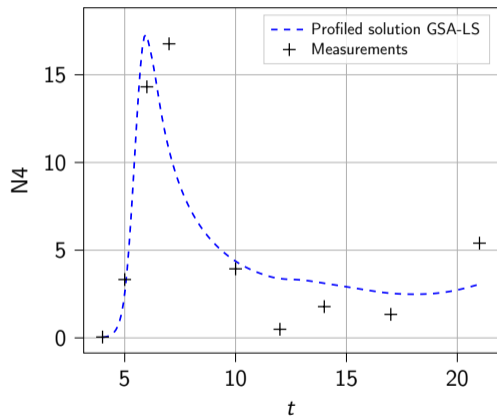
7 experiments were performed, to measure 6 various species



## Results of the GSA algorithms

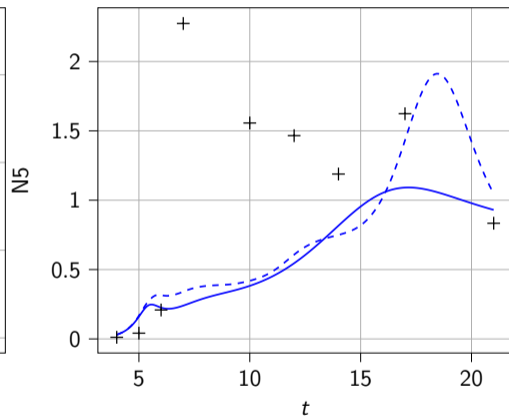
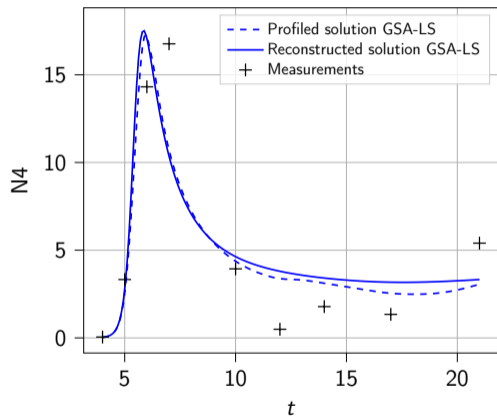


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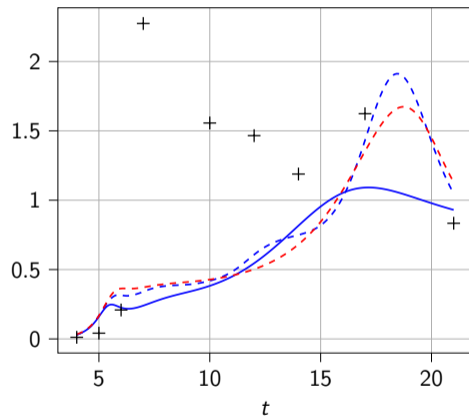
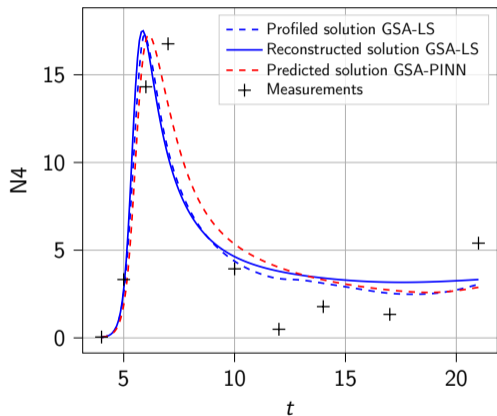




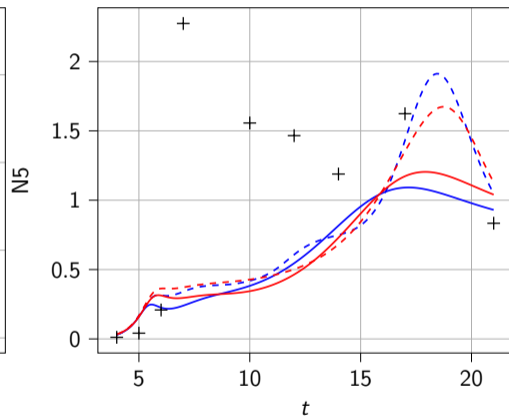
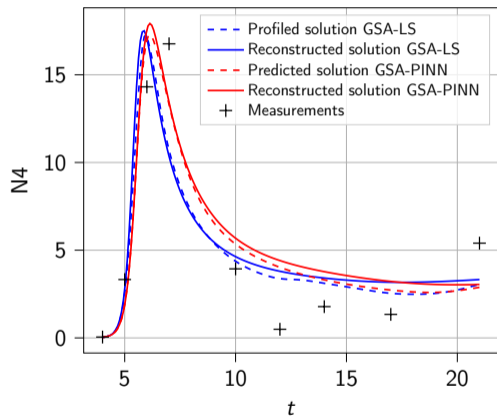
## Results of the GSA algorithms



## Results of the GSA algorithms



## Results of the GSA algorithms



## Conclusion and outlooks

- ▶ Inferring interaction coefficients from noisy data for the GLV model is a difficult question.
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  - ▶ Have a unique PINN for all experiments (★)
  - ▶ (★) + trained offline so it only has to predict during the alternate minimization
  - ▶ Study a PINN for the first step or « Last-step PINN »
- ▶ Tests on « almost real » simulated data

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Thanks for your attention !

## References

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