PhD Position
Parametrization of Reaction Networks

Topic profile

theory/math

coding

wet-lab

Tags

#AI

#deep learning

#digital twins

#bioengineering

Supervision

Benedikt Bollig

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Matthias Függer

CNRS Researcher at ENS Paris-Saclay

Thomas Nowak

Professor at ENS Paris-Saclay

We are looking for

Prerequisites are a Master degree in a relevant subject (e.g., mathematics, computer science, or bioengineering), coding experience (in Python) and basic experience in AI (e.g., basic concepts and coding in pytorch). We expect a curious, driven attitude and interest to work both on the theory, coding, and experimental setup in the wet-lab.

The team

You will be part of an interdisciplinary research team at Laboratoire Méthodes Formelles in the ENS Paris-Saclay, near Paris, working at the interface between AI and bioengineering.

Research

Many products of industrial or biomedical relevance, such as pharmaceuticals, biofuels, vaccines, etc., are manufactured by cultivating cells in a bioreactor. Understanding the biological processes, and tracking it in real-time is central when optimizing this process for cost and yield.
In this research program, we are looking for ways to automate the discovery of bioproduction processes from experimental data. Focus of the PhD will be (i) assessing and improving existing approaches of parameter estimation as they are currently used for microbial growth processes, (ii) parameter estimation of processes for which the biochemical reactions are known but their reaction rates are unknown, and (iii) parameter estimation for highly stochastic processes.

You are interested or would like to join us?

Please mail your questions or, in case you would like to apply, a short statement of interest and a CV to Benedikt Bollig (bollig@lmf.cnrs.fr), Matthias Függer (mfuegger@lmf.cnrs.fr), and Thomas Nowak (thomas@thomas-nowak.net). Applications until the end of April 2024 will receive full consideration.

Literature

[1] Fabian Fröhlich, Barbara Kaltenbacher, Fabian J Theis, and Jan Hasenauer. Scalable parameter estimation for genome-scale biochemical reaction networks. *PLoS computational biology*, 13(1):e1005331, 2017.

[2] Ankit Gupta and Mustafa Khammash. Unbiased estimation of parameter sensitivities for stochastic chemical reaction networks. *SIAM Journal on Scientific Computing*, 35(6):A2598–A2620, 2013.

[3] Max Mowbray, Thomas Savage, Chufan Wu, Ziqi Song, Bovinille Anye Cho, Ehecatl A Del Rio-Chanona, and Dongda Zhang. Machine learning for biochemical engineering: A review. *Biochemical Engineering Journal*, 172:108054, 2021.