



MARIE SKŁODOWSKA-CURIE POSTDOCTORAL FELLOWSHIPS 2024

EXPRESSION OF INTEREST FOR HOSTING MARIE CURIE FELLOWS

HOST INSTITUTION

Faculdade de Ciências e Tecnologias, Universidade Nova de Lisboa

RESEARCH GROUP AND URL

Center for Mathematics and Application (NOVA Math); <https://novamath.fct.unl.pt/>

SUPERVISOR (NAME AND E-MAIL)

Marta B. Lopes, marta.lopes@fct.unl.pt

SHORT CV OF THE SUPERVISOR

Marta Lopes is a Researcher at the Center for Mathematics and Applications (NOVA Math), NOVA School of Science and Technology, Universidade NOVA de Lisboa. Marta holds a PhD in Biotechnology, a Master's degree in Applied Mathematics and a 5-year degree in Biology. She specializes in developing advanced mathematical and computational tools to extract valuable insights from high-dimensional biological data, supporting informed decision-making.

5 SELECTED PUBLICATIONS

- Martins S, Coletti R, Lopes MB (2023). Disclosing transcriptomics network-based signatures of glioma heterogeneity using sparse methods. *BioData Mining* 2023;16(1):26, doi:10.1186/s13040-023-00341-1
- Peixoto C, Lopes MB, Martins M, Casimiro S, Sobral D et al. (2023). Identification of biomarkers predictive of metastasis development in early-stage colorectal cancer using network-based regularization. *BMC Bioinformatics*, 24(1):17, doi:10.1186/s12859-022-05104-z
- Cruz RC, Costa PR, Krippahl L, Lopes MB (2022). Forecasting biotoxin contamination in mussels across production areas of the Portuguese coast with Artificial Neural Networks 257(5):109895. *Knowledge-Based Systems* doi:10.1016/j.knosys.2022.109895
- Lopes MB, Vinga S (2020). Tracking intratumoral heterogeneity in glioblastoma via regularized classification of single-cell RNA-Seq data. *BMC Bioinformatics*, 21:50, doi:10.1186/s12859-020-3390-4
- Lopes MB, Casimiro S, Vinga S (2019). Twiner: correlation-based regularization for identifying common cancer gene signatures. *BMC Bioinformatics*, 20:356, doi:10.1186/s12859-019-2937-8

PROJECT TITLE AND SHORT DESCRIPTION

Integration of statistical learning and dynamic modeling for assisting clinical decision

This project aims to integrate statistical and machine learning methods with dynamic systems modeling for clinical applications. The abundance of large-scale biological data offers valuable insights into the mechanisms behind pathological conditions. Statistical and machine learning techniques can handle vast datasets, identifying significant variables and correlations, despite their limitations on the interpretability of the underlying processes. In contrast, dynamic systems modeling provides detailed predictive models of system evolution but requires knowledge of



underlying kinetics. By combining these approaches, the project aims to elucidate complex biological processes, through the analysis of time-series data.

SCIENTIFIC AREA WHERE THE PROJECT FITS BEST*

Mathematics (MAT)

***Scientific Area where the project fits best** – Please select/indicate the scientific area according to the panel evaluation areas: Chemistry (CHE) • Social Sciences and Humanities (SOC) • Economic Sciences (ECO) • Information Science and Engineering (ENG) • Environment and Geosciences (ENV) • Life Sciences (LIF) • Mathematics (MAT) • Physics (PHY)