BioISI - Biosystems & Integrative Sciences Institute

A SYNTHETIC PORTUGAL TO MODEL COVID-19 SPREAD

Place of work: FCUL

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Abstract / MSc thesis project proposal

For the last twelve months, data on the pandemic have been all over the news, and the results of mathematical models became part of our everyday life. At the same time, much debate has been going on about the efficacy of containment measures, and the scientific literature devoted to their assessment exploded. We have developed the first study of this type devoted to Portugal. The study is still undergoing peer-review [1], but it already received much attention from the media [2].

The matrix that represents the frequency of personal contacts according to age class is a key ingredient of all mathematical models of COVID-19 spread. However, this matrix for Portugal available in the most recent literature [3] is outdated. The goal of this thesis is then to build a synthetic population for Portugal, including the features that are more relevant for COVID-19, and to assess the importance of introducing this level of detail in transmission models of COVID-19.

The student will learn how to model the viral spread in the population using differential equations and how to fit the model to various data sources using Hamiltonian Monte Carlo method [4]. We anticipate that this work will have a significant impact in our capacity to control the spread of COVID-19 in Portugal in the post-pandemic stage. This project will be developed in collaboration with Professor Manuel Gomes who is one of the key advisors on the COVID-19 pandemic for the Ministry of Health and with researchers from the Utrecht University, The Netherlands.

Bibliography:

[1] Viana J, van Dorp CH, Nunes A, et al. Controlling the pandemic during the SARS-CoV-2 vaccination rollout: a modeling study, 24 March 2021, PREPRINT (Version 1) available at Research Square [https://doi.org/10.21203/rs.3.rs-358417/v1]
[2] https://www.rtp.pt/noticias/pais/portugal-pode-enfrentar-quarta-vaga-de-covid-19-ja-no-proximo-mes_v1310404
[3] Mistry D, Litvinova M, Pastore y Piontti A, Chinazzi M, Fumanelli L, Gomes MFC, et al. Inferring high-resolution human mixing patterns for disease modeling. Nature Communications. 2021;12(1):323. doi:10.1038/s41467-020-20544-y.
[4] Rozhnova G, van Dorp CH, Bruijning-Verhagen P, Bootsma MCJ, van de Wijgert JHHM, Bonten MJM, et al. Model-based evaluation of school- and non-school-related measures to control the COVID-19 pandemic. Nature Communications. 2021;12(1):1614.