MetaCast: A package for broadCASTing epidemiological and ecological models over META-populations.

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Summary

`MetaCast` is a Python package for broadcasting epidemiological and ecological Ordinary Differential Equation (ODE) based models over metapopulations (structured populations). Users define a function describing the subpopulation model. `MetaCast`'s `MetaCaster` then broadcasts the subpopulation model function over dimensions of metapopulations. These dimensions can be defined and redefined flexibly, allowing for comparisons of multidimensional metapopulation models that can have migration (flows) of populations between subpopulations. In addition to the metapopulation suite, `MetaCast` has several features. A multinomial seeder allows users to randomly select infected stages to place an infected population in, based on the occupancy time of infected states. `MetaCast`'s event queue suite can handle discrete events within simulations, such as movement of populations between compartments and changes in parameter values. Sensitivity analysis can be done in `MetaCast` using parallelisable Latin Hypercube Sampling and Partial Rank Correlation Coefficient functions. All of this makes `MetaCast` an ideal package not only for modelling metapopulations but for wider scenario analysis.

Statement of Need

`MetaCast` was developed from the code base used in a project modelling the spread of COVID-19 at Mass Gathering Events (MGEs), such as the FIFA 2022 World Cup (Grunnill et al., 2024). During this project there were a number of MGEs that we considered as potential case studies before settling on the FIFA 2022 World Cup. As such, even though our epidemiological model was remaining much the same, the resulting change in metapopulation structure between potential case study models meant we had to extensively recode the model. In order to expedite this recoding due to changes in metapopulation structure, we developed the code in Grunnill et al. (2024). This code allowed us to broadcast our COVID-19 subpopulation model over different two-dimensional metapopulations (based on clusters of people and their vaccination status, Grunnill et al., 2024), whilst calculating the force of infections for all subpopulations (Keeling & Rohani, 2008). `MetaCast` builds upon and improves the code used in Grunnill et al. (2024). These improvements mean that metapopulations are no longer limited to two dimensions. Furthermore, metapopulation dimensions do not have to be based on clusters of

people and their vaccination status. MetaCast also includes more user-friendly versions of the discrete event, sensitivity analyses and infectious population seeding features from Grunnill et al. (2024). These features make MetaCast an ideal package for scenario analyses based around metapopulation models within epidemiology or ecology.

State of Field

There are a number of packages that can be used for epidemiological or ecological modelling accross a number of platforms including Python. However, to our knowledge, none bring together all the features for scenario analyses based around ODE metapopulation models as described above.

Ordinary Differential Equation (ODE) Modelling Packages for Epidemiology and Ecology

R's EpiMode (Jenness et al., 2018) has some pre-coded epidemiological ODE models (such as SIR and SIS), as does the Python package Eir (Jacob, 2021). EpiMode (Jenness et al., 2018) can also perform sensitivity analyses on these pre-coded models. PyGOM (Tye et al., 2018) and Epipack (Maier, 2021) are Python packages that can produce ODE models from a list of transitions defining the flow between epidemiological compartments. Both PyGOM (Tye et al., 2018) and Epipack (Maier, 2021) can then simulate the ODE models deterministically or stochastically, with PyGOM having some extra stochastic methods. PyGOM (Tye et al., 2018) also has a suite of maximum likelihood based and Approximate Bayesian Computation fitting procedures.

Individual Based Modelling (IBM) Packages for Epidemiology and Ecology

Python's Epipack (Maier, 2021) has modules for defining transitions between states for nodes in network modelling. The Python open-source package Covasim (COVID-19 Agent-based Simulator, Kerr et al., 2021) provides detailed demographic data tailored to specific countries, encompassing age distributions and population sizes, offering sophisticated transmission networks for various social settings (households, schools, workplaces, long-term care facilities, etc). It also incorporates age-specific disease outcomes, viral load dynamics, and a wide array of intervention strategies. R's EpiMode (Jenness et al., 2018) implements agent-based modelling based around contacts as discrete events or as a static network model. There are a number of other R epidemiological IBM packages that take spatial or network contact based approaches: individual (Charles & Wu, 2021), hybridModels (Marques et al., 2020) and EpiILMCT (Al-mutiry et al., 2021). The Python package Eir (Jacob, 2021) provides epidemiological models that incorporate the movements of people. Pathogen.jl (Angevaare et al., 2022) is a Julia package for continuous time simulation and inference of transmission network individual level models (TN-ILMs).

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