

LARGE SCALE EPIDEMIC SPREAD ON HIGH RESOLUTION MAPS: SIMULATING COMPLEX INDIVIDUAL BASED EPIDEMIC MODELS

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I will present a computational tool that permits to simulate the spread of infectious diseases on high resolution maps. The tool presents significant differences with existing computational tools: (1) it uses an individual based description with Gillespie dynamics; (2) it uses high resolution maps for the description of the human geographical distribution, in theory permitting to simulate the whole world with a resolution of 1 km; (3) it implements commuting of individuals: individual move to a preferred location and move back home; (4) it uses a code generator with a compact syntax for extremely fast implementation of any compartmental model; (5) it provides full control of the spatio-temporal dependence of any parameter as well as control of the outcome of any transition event and the simulation cycle via user defined C++ functions; (6) it provides a rich API for querying the simulation status as well as altering the simulation behaviour during the dynamics; (7) it permits to assign specific information to each individual, thus allowing heterogeneous populations; (8) it is fully parallelized, and thus provides virtually unlimited complexity, being limited only by computational resources.

The tool takes an input file specifying all the details of the simulations and produce an executable that can be submitted to a computer cluster for parallel execution. The executable is tailored to the specific needs of the simulations and thus uses optimizations dependent on the simulation requirements, aiming for minimal memory requirement and fast execution.

The tool is the result of several years of research driven development. I will show some examples of its use and illustrate its capabilities as well as discussing future extensions.