

Abstract Submitted
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Comparing large-scale computational approaches to epidemic modeling: agent based versus structured metapopulation models BRUNO GONÇALVES, Indiana University, Bloomington, IN, MARCO AJELLI, Bruno Kessler Foundation, Trento, Italy, DUYGU BALCAN, Indiana University, Bloomington, IN, VITTORIA COLIZZA, Institute for Scientific Interchange Foundation, Turin, Italy, HAO HU, Indiana University, Bloomington, IN, JOSÉ RAMASCO, Institute for Scientific Interchange Foundation, Turin, Italy, STEFANO MERLER, Bruno Kessler Foundation, Trento, Italy, ALESSANDRO VESPIGNANI, Indiana University, Bloomington, IN — We provide for the first time a side by side comparison of the results obtained with a stochastic agent based model and a structured metapopulation stochastic model for the evolution of a baseline pandemic event in Italy. The Agent Based model is based on the explicit representation of the Italian population through highly detailed data on the socio-demographic structure. The metapopulation simulations use the GLObal Epidemic and Mobility (GLEaM) model, based on high resolution census data worldwide, and integrating airline travel flow data with short range human mobility patterns at the global scale. Both models provide epidemic patterns that are in very good agreement at the granularity levels accessible by both approaches, with differences in peak timing of the order of few days. The age breakdown analysis shows that similar attack rates are obtained for the younger age classes.

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