Evaluating targeted interventions via meta-population models with multi-level mixing

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A B S T R A C T

Among the several means by which heterogeneity can be modeled, Levins’ (1969) meta-population approach preserves the most analytical tractability, a virtue to the extent that generality is desirable. When model populations are stratified, contacts among their respective sub-populations must be described. Using a simple meta-population model, Feng et al. (2015) showed that mixing among sub-populations, as well as heterogeneity in characteristics affecting sub-population reproduction numbers, must be considered when evaluating public health interventions to prevent or control infectious disease outbreaks. They employed the convex combination of preferential within- and proportional among-group contacts first described by Nold (1980) and subsequently generalized by Jacquez et al. (1988). As the utility of meta-population modeling depends on more realistic mixing functions, the authors added preferential contacts between parents and children and among co-workers (Glasser et al., 2012). Here they further generalize this function by including preferential contacts between grandparents and grandchildren, but omit workplace contacts. They also describe a general multi-level mixing scheme, provide three two-level examples, and apply two of them. In their first application, the authors describe age- and gender-specific patterns in face-to-face conversations (Mossong et al., 2008), proxies for contacts by which respiratory pathogens might be transmitted, that are consistent with everyday experience. This suggests that meta-population models with inter-generational mixing could be employed to evaluate prolonged school-closures, a proposed pandemic mitigation measure that could expose grandparents, and other elderly surrogate caregivers for working parents, to infectious children. In their second application, the authors use a meta-population SEIR model stratified by 7 age groups and 50 states plus the District of Columbia, to compare actual with optimal vaccination during the 2009–2010 influenza pandemic in the United States. They also show that vaccination efforts could have been adjusted month-to-month during the fall of 2009 to ensure maximum impact. Such applications inspire confidence in the reliability of meta-population modeling in support of public health policymaking.

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1. Introduction

Agent-based, network and population models each have features that, for particular applications, make one the obvious choice. For others, identifying the best approach involves weighing their respective strengths and weaknesses. While each can incorporate structural heterogeneity, agent-based and meta-population modeling sacrifice and preserve, respectively, the most analytical tractability. As analyses invariably increase understanding, we seek to augment the usefulness of systems of weakly coupled large sub-populations, or meta-populations [11], in modeling the spread of pathogens, arguably the most important of several challenges that Ball et al. [1] describe.

In consolidating and extending earlier contributions to our understanding of the impact of heterogeneity (in characteristics affecting sub-population reproduction numbers) and non-random mixing, Feng et al. [5] used a convex combination of preferential within- and proportional among-group contacts [10]. In that mixing function, the fraction of within-group contacts and their complements correspond to Ball et al.’s [1] coupling strength, which determines location on a continuum whose limiting meta-populations behave as one or as multiple independent sub-populations. The simplicity of this function facilitates theoretical studies, but it is too simple for most applications.

Accordingly, we generalized the function of Jacquez et al. [10] by including preferential contacts between parents and

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