networks theoretically have $R_0 = \infty$ because there will be some individuals with arbitrarily large numbers of contacts (Albert et al. 2000; May and Lloyd 2001). However, in any practical scenario, the maximum number of contacts is always limited and the success of the epidemic depends on encountering these core individuals early.

In contrast, the lattice and two-dimensional small-world networks show much slower epidemic growth rates. In fact, as predicted in Section 7.3, the lattice network leads to an expanding wave of infection and hence an (almost) linear initial increase in the number of cases. As long-range contacts are added to this basic lattice, forming a Small-World network (Watts and Strogatz 1998), the infection is able to spread to new susceptible areas of the network and therefore the infection grows more rapidly.

In general, networks display slower epidemic dynamics compared to randomly mixed models. As a consequence, networks that are most like the random-mixing models— with short-average path length (Small-World, Random, and Scale-free) and little clustering (Random, and Scale-Free)—show the fastest epidemic growth rates for a given average number of contacts per individual.

7.7. WHICH MODEL TO USE?

With such a vast array of possible spatial models, it may be daunting to try to choose between them. As with all model choices, the type of model required will reflect the problem being addressed, the availability of data, and the form of results required. At some fundamental level, *all* spatial models can ultimately be expressed as both metapopulation models or individual-based models with carefully constructed interaction terms. However, the following guide may help discriminate between the model classes:

- *All individuals interact at random.* A spatial model is not required.
- *The population is naturally separable into groups, with strong (random) interaction within each group.* This is the classical metapopulation ideal, and is frequently the preferred model for human disease dynamics at a national scale where the population can be generally grouped by town or city.
- *The population is densely distributed across the entire space.* Here we may safely treat the population as continuous and deterministic; therefore, either PDE or integro-differential models can be appropriate.
- *The environment and distribution of hosts is approximately uniform and a qualitative understanding of spatial effects is required.* In such situations, the approximate lattice-based models may be suitable. It should be noted, however, that such models are unlikely to provide an accurate prediction of the quantitative behavior of any real problem.
- *Hosts have a low density or patchy distribution and stochasticity effects are important.* Here we must resort to individual-based modeling; this has the extra advantage that greater behavioral complexity can be easily included. Note that parameters are generally defined at the individual level, such that aggregate population-level data is difficult to use.
- *Hosts have few contacts to whom they can pass infection.* In such cases, networks are the preferred modeling tool. Again, this is an individual-based approach, such that individual-level data is required for parameterization.