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# On the reproduction number in different infectious diseases models

The classical Kermack-McKendrick homogeneous SIR (susceptible, infected and removed) model is well known. Its general solution is a function of the unique parameter (the reproduction number) that is equal to a mean number of secondary cases produced by a typical infected individual in a completely susceptible population. If the reproduction number is more than one (the threshold value) its value describes an epidemic level larger values correspond to stronger epidemics. This model bases on two assumptions 1) all members of the population have the equal probability to get infected and 2) mixing in the population is uniform. It is clear that both of these assumptions are nonrealistic for any large human population. In the more complex compartment SIR models the population is divided into several non-overlapping groups. It allows us to partly remove assumptions of the classical model. Twenty years ago Diekmann et al 1 showed that for this kind of models, just as for the classical model there is the threshold parameter R0. Usually it is called by the same name the reproduction number though the physical meaning of this parameter has changed. However, this new parameter is a not unique measure of an epidemic severity (it will be proven during my talk). In particular it means that for such models comparison of the severity of two epidemics by simple comparing values of their reproduction numbers is incorrect. Since the more realistic model has to contain much more parameters for more detailed descriptions of the population and epidemic itself, we can be sure that the last conclusion is valid for the real epidemics too. Individual-based models (IBMs) are more complex in comparison with the compartment ones since they use overlapping groups (school children are members of a family also, for example). This peculiarity of IBMs makes Diekmanns calculation method of the reproduction number inapplicable. Moreover there is no usual mathematical formulation for the IBMs (by differential equations, for example). It means that we may not use analytic methods of research and therefore, an existence of any similarity parameter in the solution (for example, a threshold condition or some analog of the reproduction number) has to be proved numerically. Unfortunately, papers with misunderstandings of the IBMs peculiarities continue to appear.

## References

[1] Diekmann, O., J. A. P. Heesterbeek, J. A. J. Metz, 1990. On the definition and computation of the basic reproduction ratio R0 in models for infectious diseases in heterogeneous populations. J. Math. Biol., 28, pp.365-382.