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On the reproduction number of enteropathogenic bacteria

The linear model reflecting the dynamics of a population at low densities is the main mathematical tool the (deterministic) modeler has at hand in order to answer if the population tends to grow or, alternatively, becomes extinct. This question can be addressed by computing the population ratio between successive generations, so that values above one imply proliferation whereas values below one imply regression. Classically, two successive generations have been characterized as one would expect: the individuals in the later generation are the offspring of the former one. When this definition is taken into account the ratios between successive generations converge to the famous basic reproduction number, roughly defined as the mean number of offspring produced by each member of the population. However different interpretations of what a birth event is give rise to different generational schemes, and hence alternative reproduction numbers can be obtained. In this talk we illustrate, by means of an example, why some of such alternative reproduction numbers are easier to compute empirically than others.

Joint work with Angel Calsina and Jordi Ripoll.