Numerical computation of the basic reproduction number

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The twentieth century has witnessed the emergence of the basic reproduction number as a key player in assessing the growth of a population or the spread of a disease. Only in the nineties this quantity has been rigorously characterized as the spectral radius of a positive linear operator, promoting since then the use of increasingly realistic, yet more complicated, models. In this talk we would like to present some recent developments [1, 2, 3] in the numerical approximation of this number, first illustrating a spectrally accurate discretization framework and then discussing its convergence. As an application we consider models of epidemics structured by individual traits as, e.g., age or immunity.

References

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