Cologne Evolution Colloquium
Joint Seminar with
Theory Colloquium

CRC 1310   Predictability in Evolution

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Can we precisely forecast the turning point and end of an epidemic by fitting past data?

No, we can't. The time at which the growth in the number of infected individuals halts and starts decreasing cannot be calculated with certainty before the turning point is actually attained. This assertion is illustrated by adding to a standard SIR model a new class for confined individuals. A Bayesian fit to the on-going COVID-19 pandemic in Spain shows that a slow-down in the number of newly infected individuals during the expansion phase allows to infer neither the precise position of the maximum nor whether the measures taken will bring the propagation to the inhibition regime. Our study warns against precise forecasts of the evolution of epidemics based on mean-field, effective models, and supports that only probabilities of different outcomes can be confidently given.

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