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On the analysis of the SIR epidemic model for small networks: an application in hospital settings

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Biology and Medicine Through Mathematics Conference 2017

On the analysis of the SIR epidemic model for small networks: an application in hospital settings

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I will show in this talk how to analyse the SIR epidemic model in an exact way when the population under study is formed by a small highly heterogeneous group of N individuals, represented by means of a network. This approach, which amounts to the analysis of the exact 3^N -states continuous-time Markov chain (CTMC), makes special focus on algorithmic aspects, and requires a creative organization of the space of states $\mathcal{S} = \{S, I, R\}^N$ of the CTMC. The analysis of the epidemic dynamics is carried out in terms of a number of summary statistics for the disease: (i) the length and size of the outbreak; (ii) the maximum number of individuals simultaneously infected during the outbreak; (iii) the fate of a particular individual within the population; and (iv) the number of secondary cases caused by a certain individual until she/he recovers. I will illustrate this methodology by studying the spread of the nosocomial pathogen *Methicillin-resistant Staphylococcus Aureus* among the patients within an intensive care unit (ICU). The interest here is in analysing the effectiveness of different control strategies which intrinsically incorporate heterogeneities among the patients within the ICU. The talk is based on the following references

M. López-García (2016) *Stochastic descriptors in an SIR epidemic model for heterogeneous individuals in small networks*. *Mathematical Biosciences* **271**: 42-61.

A. Economou, A. Gómez-Corral, M. López-García (2015) *A stochastic SIS epidemic model with heterogeneous contacts*. *Physica A: Statistical Mechanics and its Applications* **421**: 78-97.