Publicacions més rellevants de la línia de recerca:

Xarxes complexes i dinàmica de poblacions

Referència: Garcia-Domingo, J.L., Juher, D., Saldaña, J. Degree correlations in growing networks with deletion of nodes. *Physica D*, **237** (2008), pp. 640-651.

Abstract:

In this paper we study the degree distribution and the two-node degree correlations in growing networks generated via a general linear preferential attachment of new nodes together with a uniformly random deletion of nodes. By using a continuum approach we show that, under some suitable combinations of parameters (deletion rate and node attractiveness), the degree distribution not only loses its scale-free character but can even be supported on a small range of degrees. Moreover, we obtain new results on two-vertex degree correlations showing that, for degree distributions with finite variance, such correlations can change under a nonselective removal of nodes.

Referència: Saldaña, J. Continuous-time formulation of reaction-diffusion processes on heterogeneous metapopulations. *Physical Review E*, **78** (2008), 012902.

Abstract:

We present the derivation of the continuous-time equations governing the limit dynamics of discrete-time reaction-diffusion processes defined on heterogeneous metapopulations. We show that, when a rigorous time limit is performed, the lack of an epidemic threshold in the spread of infections is not limited to metapopulations with a scale-free architecture, as it has been predicted from dynamical equations in which reaction and diffusion occur sequentially in time.

Referència: Juher, D., Ripoll, J., Saldaña, J. Analysis and Monte Carlo simulations of a model for the spread of infectious diseases in heterogeneous metapopulations. *Physical Review E*, **80** (2009), 041920.

Abstract:

We present a study of the continuous-time equations governing the dynamics of a susceptible-infectedsusceptible model on heterogeneous metapopulations. These equations have been recently proposed as an alternative formulation for the spread of infectious diseases in metapopulations in a continuous-time framework. Individual-based Monte Carlo simulations of epidemic spread in uncorrelated networks are also performed revealing a good agreement with analytical predictions under the assumption of simultaneous transmission or recovery and migration processes.