Master's Thesis Proposal[1]

General Information

Title:	Dynamic correlations of epidemic spreading in complex networks
Expiry Date:	2012
Modality:	☐ technological project
	☒ research work
Advisor/s:	Sergio Gómez
Advisor's Dept. & Univ.:	DEIM, URV
Advisor/s e-mail:	sergio.gomez@urv.cat
Observations:	
Student's Name:	Javier Berlinches
(if already known)	

M.Sc. Thesis Description

Main issues / Brief Description [Mandatory]:

Study of the dynamic correlations found in epidemic processes in complex networks, which make Monte Carlo simulations deviate from the expected outputs from our Microscopic Markov-Chain Approach.

---

[1] **Each M.Sc. Th. Proposal should be in a separate file, named as follows: "MSc-Th-Proposal-2-or-3-title-first-words-Advisor/s-AcademicYear.pdf".**
   For Example: "MSc-Th-Proposal-Syntactic-and-Semantic-LluisMarquez&JesusGimenez-1011.pdf"
 The proposal could be elaborated with any text processor (Word, Openoffice, etc.), but **the file electronically delivered** to LSI Dept. Secretary (merce@lsi.upc.edu) **MUST BE a single PDF file**

Detailed Description including a task planning [Mandatory]:

Complex weblike structures describe a wide variety of systems of high technological and intellectual importance [1,2]. For example, the cell is best described as a complex network of chemicals connected by chemical reactions; the Internet is a complex network of routers and computers linked by various physical or wireless links; fads and ideas spread on the social network, whose nodes are human beings and whose edges represent various social relationships; the World Wide Web is an enormous virtual network of Web pages connected by hyperlinks. These systems represent just a few of the many examples that have recently prompted the scientific community to investigate the relationship between the topology of complex networks and the dynamics that take place on them.

A complex network is just a graph with several non-trivial topological properties, not present in simple models of networks. Some of them are: scale-free degree distributions, high clustering coefficients (i.e. more triangles than expected in a random network), assortativity (correlations between connected nodes' degrees), and community structure. On the contrary, simple graphs such as random networks or grids show a homogeneous structure in which all nodes are almost indistinguishable, unlike what is observed in real networks.

Our research group has been studying complex networks for a long time, and one of the topics we are more interested now is in the spreading of epidemics in complex networks. For example, taking the standard epidemiological susceptible-infected-susceptible (SIS) model [3], and running it in complex networks, it is possible to show, from theory and from Monte Carlo (MC) simulations, the existence of an epidemic threshold [4,5], i.e. a value of the infection rate above which the disease becomes pandemic.

In [6,7] we introduce a new mathematical framework, the Microscopic Markov-Chain Approach (MMCA), which is able to predict with high accuracy the total SIS epidemic spreading in a complex network, and even the probabilities of being infected of all the individual nodes, in almost perfect agreement with the corresponding MC simulations.

However, there are cases in which MMCA and MC show a non-negligible deviation, which need to be studied. The objective of this project is the study of the dynamic correlations between infected nodes in epidemic spreading processes, in order to extend the MMCA equations and to obtain more accurate predictions.

The working plan is the following:
1. Introduction to the problem: study of the basic bibliography on complex networks, structural parameters, and epidemic spreading dynamics.
2. Study of our implementations of MC and MMCA.
3. Analysis of the dynamic correlations in MC simulations of SIS epidemic spreading in different complex network structures, and near the epidemic threshold.
4. Extension of MMCA equations to take into account these dynamic correlations.
5. Numeric solution of the extended MMCA equations, and comparison with MC.

References [Mandatory]:

[1] M. E. J. Newman, The structure and function of complex networks, *SIAM Review* **45** (2003) 167-256

[2] S. Boccaletti, V. Latora, Y. Moreno, M. Chavez, D.-U. Hwang, Complex networks: Structure and dynamics, *Physics Reports* **424** (2006) 175-308

[3] L. J. S. Allen, Some Discrete-Time SI, SIR, and SIS Epidemic Models, *Math. Biosci.* **124** (1994) 83-105

[4] R. Pastor-Satorras, A. Vespignani, Epidemic dynamics in finite size scale-free networks, *Phys. Rev. E* **65** (2002) 035108(R)

[5] M. Boguñá, R. Pastor-Satorras, Epidemic spreading in correlated complex networks, *Phys. Rev. E* **66** (2002) 047104

[6] S. Gómez, A. Arenas, J. Borge-Holthoefer, S. Meloni, Y. Moreno, Discrete-time Markov chain approach to contact-based disease spreading in complex networks, *Europhysics Letters* **89** (2010) 38009

[7] S. Gómez, A. Arenas, J. Borge-Holthoefer, S. Meloni, Y. Moreno, Discrete-time Markov chain approach to contact-based disease spreading in complex networks, *International Journal of Complex Systems in Science* **1** (2011) 47-54

Minimal Requirements & Previous Knowledge [Optional]:

Other comments [Optional]:

Location and Date: Tarragona, 08-Mar-2011

To the Academic Commission of the Master in Artificial Intelligence (CAIMIA)