Epidemic Processes on Networks, Viral Marketing and Optimal Vaccination

Alberto Guggiola
a.guggiola@gmail.com

École Normale Supérieure de Paris

NETADIS Scientific Kick-off Meeting
Torino (Italy), February 5th, 2013

Outline

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Who I Am

- Bachelor Degree in *Physics* at the University of Torino
- Master Degree in *Physics of Complex Systems* at the University of Torino

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- Now PhD student at the École Normale Supérieure de Paris

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1. Presentation
2. Previous Research Projects
3. The NETADIS Project
4. Possible Secondments

Previous Research Projects

Bachelor Thesis

Spreading of Information on Dynamical Contact Networks

With **Ciro Cattuto**, ISI Foundation, Torino

Master Thesis

Statistical Sequence Analysis of Protein Families

With **Andrea Pagnani**, HuGeF Foundation, Torino

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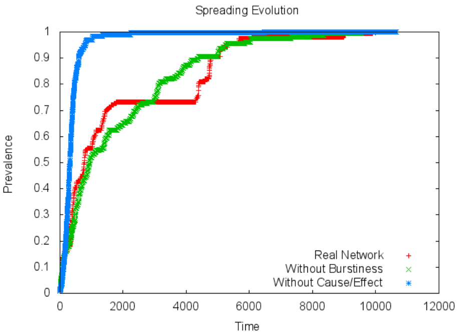
Spreading of Information on Dynamical Contact Networks

- Real World networks:
  - Small world effect
  - Slow propagation of information

    M. Karsai et al., 2011: *Small But Slow World: How Network Topology and Burstiness Slow Down Spreading*, arXiv:1006.2125

- Which topological characteristics slow down the spreading?



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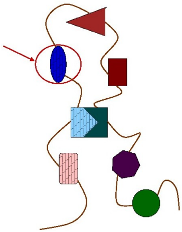
Statistical Sequence Analysis of PF

Objective

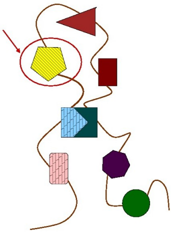
Inference of protein structures using statistics of the sequences

F. Morcos, A. Pagnani et al. Direct-coupling analysis of residue coevolution captures native contacts across many protein families, PNAS 2011

- Contact points are more correlated than generic ones



Original Sequence



Independent Modifications

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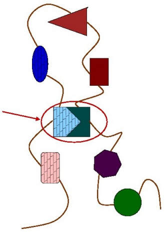

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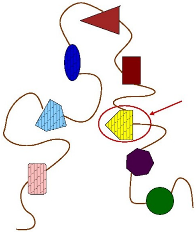

One-site Modified Sequence

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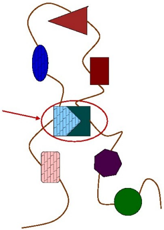

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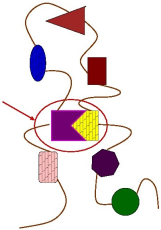

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Statistical Sequence Analysis of PF

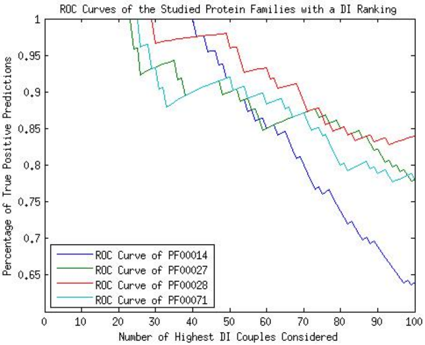
- *Direct Information* ranking of the couples of sites

Result

Percentage of TP among the x top ranked couples

Possible Improvement

Generate modified datasets, then rank according to mean DI



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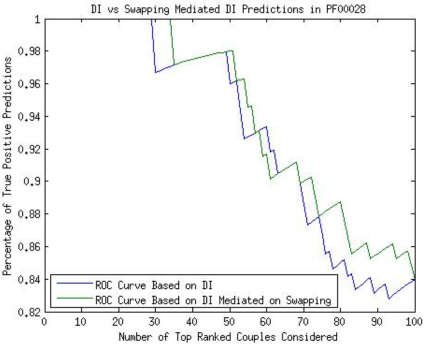

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The NETADIS Project

Project 1 ⇝ Socio-economical sciences

With **Guilhem Semerjian**:

Epidemic processes on networks, viral marketing and optimal vaccination

Which initial conditions lead a system to a certain final state within a given dynamical process?

Project 2 ⇝ Biology

With **Rémi Monasson**:

Statistical mechanical study of the dynamics of interacting genomical sequences

PDZ proteic domains and their ligands are highly specific.
How is such an **optimal** result obtained through the two independent, local evolutions of the sequences?

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General Framework

Microscopically Irreversible Process

- **Binary variables** $x_i^t \in \{0, 1\}$ $i \in \{1, ..., N\}$ and $t \in \{0, ..., \infty\}$
- **State of the system at time t**: $\vec{x}^t = \{x_1^t, x_2^t, ..., x_N^t\}$
- **Only flips $0 \rightarrow 1$ allowed**: $x_i^t = 1 \rightarrow x_i^{t'} = 1 \quad \forall t' \geq t, \forall i$

Dynamics: Bootstrap Percolation

$$x_i^{t+1} = \begin{cases} 1 \text{ if } x_i^t = 1 \text{ or } \sum_{j \in \partial_i} x_j^t \geq \theta \\ 0 \text{ otherwise} \end{cases}$$

Applications

Financial contagion, failures in power grids, viral marketing ...

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The Spread Optimization Problem

Statement

Given a graph $\mathcal{G} = \mathcal{G}(\mathcal{V}, \mathcal{E})$, find the minimal set of seeds such that, at a certain time T, all the nodes of the network become active

F. Altarelli, A. Braunstein, L. Dall'Asta, R. Zecchina, The Spread Optimization Problem, arXiv:1203.1426

Energy function

$$\varepsilon(\vec{t}) = \sum_{i=1}^{N} \varepsilon_i = \sum_{i=1}^{N} \left(\mu \mathbb{I}[t_i = 0] + \varepsilon \mathbb{I}[t_i = \infty] \right)$$

where t_i is the **activation time** of the i^{th} node s.t. $x_i^{t_i - 1} = 0$ and $x_i^{t_i} = 1$

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The seeds are **not** randomly chosen $\rightsquigarrow$ Extremal properties of the process under exam

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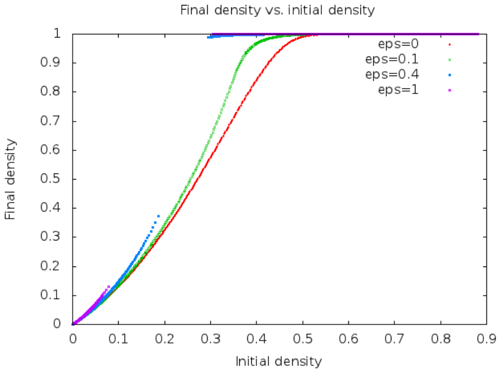
Optimization vs. Random Choice of the Seeds

- If $\varepsilon > 0$, the fraction of seeds needed to activate all the network is smaller with respect to the case where no optimization is imposed (i.e. $\varepsilon = 0$)

Random Regular Graph, K=3, $\Theta = 2$, $T = 20$



Phase Transitions in rCSP

Constraint Satisfaction Problems

A CSP consists in a set of constraints to be simultaneously satisfied by a set of variables.

- As $\alpha = \frac{\#constraints}{\#variables}$ changes $\Rightarrow$ **Phase transitions**

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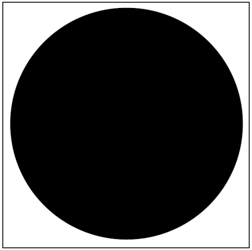

$\alpha = \alpha_S \Rightarrow$

SAT-UNSAT TRANSI-TION

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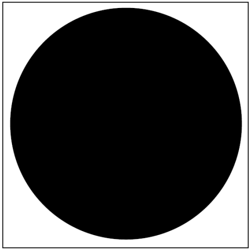
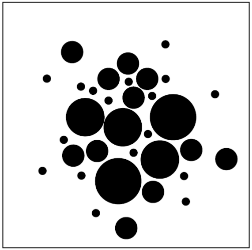


$\alpha = \alpha_C < \alpha_S \Rightarrow$ **CLUSTERING TRANSITION**



Beyond the RS Phase in the Spreading Problem

- For certain values of the parameters μ and ϵ the BP equations do not converge any more
- The hypothesis on which they hold are then no more fulfilled because of the **replica symmetry breaking**: the space of the solutions splits into separate pure states
- The problem should then be approached in a more general framework (i.e. **1 RSB**), so to study the statistics of sets of solutions instead of trying to find a unique one

$$\eta_{ij}(t_i, t_j) \quad \rightsquigarrow \quad P[\eta_{ij}(t_i, t_j)]$$

First Results and Perspectives

First Result

In the region where BP equations do not converge, the **complexity** (i.e. the logarithm of the number of pure states) has been seen to be strictly positive: **the 1 RSB approach seems then to be justified**

BUT a deeper analysis is needed in order to extract useful information about the spreading process

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Possible Intersections with Other Projects

KCL1: Sub-network analysis using projection methods

What can be said about extreme trajectories in networks if the structure is partially unknown?

KCL2: Contagion dynamics across credit networks
ICTP: Inference in finance and socio-economic networks

Applications of the theory of spreading events developed to socio-economic data (epidemics, financial contagion...)

Thank you for your attention!!

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