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## Machine learning and complex networks for precision and systems biomedicine

*Tuesday, 4 July 2017 11:00 (30 minutes)*

### Abstract

The talk will present our research at the Biomedical Cybernetics Group that I established about three years ago in Dresden. We adopt a transdisciplinary approach integrating information theory, machine learning and network science to investigate the physics of adaptive processes that characterize complex interacting systems at different scales, from molecules to ecosystems, with a particular attention to biology and medicine. Our theoretical effort is to translate advanced mathematical paradigms typically adopted in theoretical physics (such as topology, network and manifold theory) to characterize many-body interactions in complex systems and quantitative biomedicine. We apply the theoretical frameworks we invent in the mission to develop computational tools for systems and network analysis. In particular, in biomedicine we deal with: prediction of wiring in biological networks, combinatorial and multiscale biomarkers design, precision biomedicine, drug repositioning and combinatorial drug therapy. In general, we devise theoretical models of structural organization in complex networks and we leverage this knowledge to create novel and more efficient algorithms and to perform advanced analyses and predictions of patterns in complex systems. This talk will focus on two main theories. Firstly, Minimum Curvilinearity, which is a theory for topological estimation of nonlinear relations in high-dimensional data<sup>1</sup> (or in complex networks<sup>2</sup>) and its relevance for machine learning applications in biomedicine. The new topic on the impact of Minimum Curvilinearity for network embedding in the hyperbolic space will be also treated<sup>3</sup>. Secondly, we will discuss the Local Community Paradigm (LCP)<sup>4,5</sup>, which is a theory proposed to model local-topology-dependent link-growth in complex networks and therefore it is useful to devise topological methods for link prediction in monopartite and bipartite<sup>5</sup> networks. In particular, we will discuss the impact of this new method for pioneering topological methods for network-based drug-target interaction prediction and repositioning<sup>6</sup>.

### References (\* indicates first co-authorship)

1. Cannistraci, C. V., Ravasi, T., Montecchi, F. M., Ideker, T. & Alessio, M. Nonlinear dimension reduction and clustering by minimum curvilinearity unfold neuropathic pain and tissue embryological classes. *Bioinformatics* 26, i531–i539 (2010).
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3. Thomas, J. M., Muscoloni, A., ..., & Cannistraci, C. V. Machine learning meets network science: dimensionality reduction for fast and efficient embedding of networks in the hyperbolic space. (2016). at <http://arxiv.org/abs/1602.06522>
4. Cannistraci, C. V., Alanis-Lobato, G. & Ravasi, T. From link-prediction in brain connectomes and protein interactomes to the local-community-paradigm in complex networks. *Sci. Rep.* 3, 1–13 (2013).
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### Short biography note

#### Biography

Carlo Vittorio Cannistraci is a theoretical engineer with a background in biomedical cybernetics. He is cur-

rently head of the Biomedical Cybernetics Group at the Centre for Molecular and Cellular Bioengineering (CMCB) and faculty member of the Department of Physics in the Technical University Dresden. His area of research embraces information theory, machine learning and complex network theory including also applications in computational network and systems biomedicine. Nature Biotechnology selected Carlo's article (Cell 2010)<sup>7</sup> on machine learning in developmental biology to be nominated in the list of 2010 notable breakthroughs in computational biology. Circulation Research featured Carlo's work (Circulation Research 2012)<sup>8</sup> on leveraging a cardiovascular systems biology strategy to predict future outcomes in heart attacks, commenting: "a space-aged evaluation using computational biology". The Technical University Dresden honoured Carlo of the Young Investigator Award 2016 in Physics for his recent work on the local-community-paradigm theory and link prediction in bipartite networks<sup>5</sup>.

References (\* indicates first co-authorship)

1. Ravasi, T., *Cannistraci C.V.*, et al. An atlas of combinatorial transcriptional regulation in mouse and man. *Cell* 140, (2010).
2. Ammirati, E., *Cannistraci, C.V.*, et al. Identification and predictive value of interleukin-6+ interleukin-10+ and interleukin-6-interleukin-10+ cytokine patterns in st-elevation acute myocardial infarction. *Circ. Res.* 111, 1336–1348 (2012).

**Primary author:** Dr CANNISTRACI, Carlo (Technische Universität Dresden)

**Presenter:** Dr CANNISTRACI, Carlo (Technische Universität Dresden)

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