Disease Networks - Reconstruction, Topology, Dynamics. Towards an automated pipeline from static representations to executable disease models.

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Disease maps have been an emerging concept as a useful and intuitive way of describing disease mechanisms in a systematic fashion. Based on information mining, human curation and experts' advice, they summarize current biological pathway knowledge in a standard, comprehensive representation that is both human and machine readable. Disease maps can serve as templates for visualization and analysis of *omic* datasets, or they can be analyzed in terms of their underlying network structure. However, their static nature provides relatively limited understanding concerning the emerging behavior of the system under different conditions. Computational modelling can reveal dynamical properties of the network by *in silico* simulations and perturbations and can be further used for hypotheses testing and predictions. In order to address the lack of kinetic data and the large size of the biological pathways described in a Disease map, Boolean modelling can be employed to study the system's qualitative dynamic behavior. In this talk I will present our efforts to establish an automated pipeline starting from a fully detailed Disease map and its analysis as a complex network, all the way to the automated inference of a dynamical (Boolean) model, based on network topology and semantics, creating thus "executable" disease networks. I will use Rheumatoid Arthritis as case study.