A patient centred disease comorbidity network

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Even if concomitant presence of two or more diseases represent a significant problem in preventive medicine the underlying molecular basis are poorly understood. Based on the analysis of patient specific expression signatures, we have developed a network based approach for the prediction of the risk of developing secondary diseases at the individual level (1).

In the first place, we build a network of patients based on the similarity of their expression profiles and estimate relative disease co-ocurrence risks. The network overlaps and complements the previously general trends detected in EHR by the Barabási and Brunak's groups. In a second step, we include in the network inverse relations between gene expression profiles that correspond to known inverse comorbidity relationships, such as the protection Alzheimer's disease provides to lung cancer patients. Inverse comorbidities add a new orthogonal dimension to the previous disease networks. Third, we deconstruct the network in patient subgroups. Subgroups reflect more accurately the inherent heterogeneity of human diseases and help to explain the differences in tendencies to acquire secondary diseases observed in real clinical cases. Finally, we associate drugs to the patient subgroup to dissect possible molecular causes of comorbidities and to explore possible drug repositioning options.

In the long run, our intention is to explore the use of the patient-to-patient disease networks to prevent the possible incidence of secondary diseases at the personal level in real clinical scenarios.

(1) Unveiling the molecular basis of disease co-occurrence towards personalized comorbidity profiles. by J Sánchez-Valle, H Tejero, JM Fernández, D Juan, S Capella-Gutiérrez, F AlShahrour, R Tabarés-Seisdedos, V Pancaldi and A. Valencia. submitted.