Precision medicine and personalized networks

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The paradigm in cancer treatment has shifted from the traditional "one-size-fits-all" approach towards developing personalized treatments that account for individual variability in genes and in clinical and environmental characteristics for each person. The development and progression of cancer is driven by sub-networks within the functional regulatory networks of genes and their products, which undergo changes in response to different patient-specific characteristics. To this end, recovering both population-level and subject-level gene regulatory networks and monitoring the changes in gene regulatory relationships as a function of a given patient's clinical characteristics may assist in developing personalized treatment regimes that target specific pathway disruptions. We consider the problem of modeling conditional independence structures in heterogeneous data in the presence of additional subject-level covariates, and propose a novel specification of a conditional (in)dependence function of covariates - which allows the structure of a directed graph to vary flexibly with the covariates. This approach produces both subject-specific and predictive graphs, and is computationally tractable. We illustrate our approach in a cancer genomics-based precision medicine paradigm, where-in we explore gene regulatory networks in multiple myeloma taking prognostic clinical factors into account to obtain both population-level and subject-level gene regulatory networks.