Towards network level modeling of tumor heterogeneity

Uncovering and interpreting genotype/phenotype relationships are among the most challenging open questions in disease studies. In cancer, uncovering of this relationship is complicated further by the heterogeneous nature of the disease. We have recently developed two complementary approaches to address this challenge. First, called module cover [1], captures differences between patients by identifying differences in dys-regulated modules. The second approach is based on a probabilistic mixture modeling [2]. Based on phenotypic similarity between the patients and a spectrum of possible disease causes/explanation such as mutations, copy number variation, microRNA levels, etc. the method identifies disease subtypes together with their causes and models the disease of each patient as a mixture of the subtypes. I will demonstrate the applicability of these approaches to GMB and preliminary results on applications to Pancancer data. Taken together, these approaches help to fill a significant gap between the general current understanding of cancer and existing approaches to model cancer diversity.

References

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