Multi-Tensor Decompositions for Personalized Cancer Diagnostics, Prognostics, and Therapeutics

I will describe the development of novel, multi-tensor generalizations of the singular value decomposition, and their use in the comparisons of, e.g., brain, lung, ovarian, and uterine cancer and normal genomes. They uncover patterns of DNA copy-number alterations that predict survival and response to treatment, statistically better than, and independent of, the best indicators in clinical use and existing laboratory tests. I will also describe a recent retrospective clinical trial that validates the brain cancer pattern. Recurring alterations have been recognized as a hallmark of cancer for over a century, and observed in these cancers’ genomes for decades; however, copy-number subtypes predictive of patients’ outcomes were not identified before. The data had been publicly available, but the patterns remained unknown until the data were modeled by using the multi-tensor decompositions. I will conclude that the decompositions underlie a mathematically universal description of the genotype-phenotype relationships in cancer that other machine learning methods miss.

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