Abstract: Mutational processes shape the genomes of cancer patients, leaving distinct mutational signatures, and their understanding has important applications in diagnosis and treatment. Current approaches for mutational signature discovery and analysis are based to a large extent on non-negative matrix factorization and make multiple assumptions about mutation category repertoire, data richness and independence of mutational processes. In this talk I will challenge each of these assumptions and present alternative probabilistic and algebraic models that can capture spatial dependencies among mutations, handle sparse data as typical in the clinic and derive informative mutation categories. The talk does not require previous biological background and will mainly emphasize the computational techniques involved.