

Signal description is done quite differently in single genomes and in multiple genomes. In single genomes very complex models are often designed to describe the common features of a set of patterns, where these patterns are evolutionary unrelated and assumed to be independent instances from the same underlying distribution. Major classes of techniques are i. Position Weight Matrix (PWM), ii. Hidden Markov Models (HMMs), iii. Bayesian Networks (BNs), iv. Neural Networks (NNs) and v. Vector Support Machines (VSMs).

In multiple genomes comparative methods and evolutionary models are used, but the equilibrium of these models, what is what would be relevant in a single sequence, is typically much simpler than the non-evolutionary models will assume.