Abstract

This paper mainly analyzes the applications of the Generator matrices in a Continuous Time Markov Chain (CTMC). Hidden Markov models [HMMs] together with related probabilistic
models such as Stochastic Context-Free Grammars [SCFGs] are the basis of many algorithms for the analysis of biological sequences. Combined with the continuous-time Markov chain theory of likelihood based phylogeny, stochastic grammar approaches are finding broad application in comparative sequence analysis, in particular the annotation of multiple alignments, simultaneous alignment. It was originally used to annotate individual sequences, then in later stages stochastic grammars were soon also combined with phylogenetic models to annotate the alignments. Thus, trees have been combined with HMMs to predict genes and conserved regions in DNA sequences, secondary structures and transmembrane topologies in protein sequences and base pairing structures in RNA sequences. The importance of Generator matrix is analyzed in deriving the various properties of continuous time Markov chains with examples from the phylogenetic tree.

References

An Analysis of Continuous Time Markov Chains using Generator Matrices


Index Terms

- Computer Science
- Applied Mathematics

Keywords

- Generator matrix
- Continuous Time Markov Chains
- Embedded
- Markov Chain (EMC)
- Transition probability matrix
- Stationary probabilities
- Ergodicity
- Jump process