Resource Summary Report

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HMM-TM

RRID:SCR_006186
Type: Tool

Proper Citation

HMM-TM (RRID:SCR_006186)

Resource Information

URL: http://bioinformatics.biol.uoa.gr/HMM-TM/

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Description: A web tool using the Hidden Markov Model method for the topology prediction of alpha-helical membrane proteins that incorporates experimentally derived topological information. Hidden Markov Models (HMMs) have been extensively used in computational molecular biology, for modelling protein and nucleic acid sequences. In many applications, such as transmembrane protein topology prediction, the incorporation of limited amount of information regarding the topology, arising from biochemical experiments, has been proved a very useful strategy that increased remarkably the performance of even the top-scoring methods. However, no clear and formal explanation of the algorithms that retains the probabilistic interpretation of the models has been presented so far in the literature. We present here, a simple method that allows incorporation of prior topological information concerning the sequences at hand, while at the same time the HMMs retain their full probabilistic interpretation in terms of conditional probabilities. We present modifications to the standard Forward and Backward algorithms of HMMs and we also show explicitly, how reliable predictions may arise by these modifications, using all the algorithms currently available for decoding HMMs. A similar procedure may be used in the training procedure, aiming at optimizing the labels of the HMM''s classes, especially in cases such as transmembrane proteins where the labels of the membrane-spanning segments are inherently misplaced. We present an application of this approach developing a method to predict the transmembrane regions of alpha-helical membrane proteins, trained on crystallographically solved data. We show that this method compares well against already established algorithms presented in the literature, and it is extremely useful in practical applications.

Abbreviations: HMM-TM

Synonyms: HMM-TM: Prediction of Transmembrane Alpha-Helical Proteins

Resource Type: data analysis service, production service resource, analysis service resource, service resource

Defining Citation: PMID:16597327

Keywords: hidden markov model, topology, prediction, alpha-helical membrane protein, protein, transmembrane, transmembrane alpha-helical protein, bio.tools

Funding:

Availability: Free for academic use

Resource Name: HMM-TM

Resource ID: SCR_006186

Alternate IDs: nlx_151731, biotools:hmm-tm

Alternate URLs: https://bio.tools/hmm-tm

Record Creation Time: 20220129T080234+0000

Record Last Update: 20250410T065425+0000

Ratings and Alerts

No rating or validation information has been found for HMM-TM.

No alerts have been found for HMM-TM.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 5 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Tamposis IA, et al. (2021) Hidden neural networks for transmembrane protein topology prediction. Computational and structural biotechnology journal, 19, 6090.

Abdollahi S, et al. (2021) Physicochemical and structural characterization, epitope mapping and vaccine potential investigation of a new protein containing Tetratrico Peptide Repeats of

Acinetobacter baumannii: An in-silico and in-vivo approach. Molecular immunology, 140, 22.

Paes JA, et al. (2018) Comparative proteomics of two Mycoplasma hyopneumoniae strains and Mycoplasma flocculare identified potential porcine enzootic pneumonia determinants. Virulence, 9(1), 1230.

Jamet A, et al. (2015) A new family of secreted toxins in pathogenic Neisseria species. PLoS pathogens, 11(1), e1004592.

Bagos PG, et al. (2006) Algorithms for incorporating prior topological information in HMMs: application to transmembrane proteins. BMC bioinformatics, 7, 189.