

fastcov

Fast Covariant Mutation Detector. <http://yanlilab.github.io/fastcov>

Introduction

Covariant mutations are very important to maintain the structural characteristics and consequently to maintain the protein conformational and functional stability. In this study, we developed a novel algorithm to identify correlated changes by using an independent pair model followed by a correlated tandem model.

Fastcov is based on a correlation idea of interaction restriction among site-residue elements, which is very suitable for natural co-variances analysis. In contrast to other complex methods, the lightweight and fast Fastcov algorithm significantly improves the processing efficiency.

By tests on the genotyping, phylogeny and divergence analysis, the results demonstrated that this approach has an excellent performance on detecting covariant residue patterns. Based on the covariant pattern clustering, the genotyping performance reached a sensitivity of 99.42%, a specificity of 99.94% and an accuracy of 99.77%; The covariant patterns displayed co-evolutionary modes corresponding to the phylogeny tree; Moreover, it found an important evidence involving in the structural stability of protein during the evolution. As an original algorithm, Fastcov provides not only a fast and reliable approach to achieve the data analysis, but also much more powerful functions including multiple variance detection and evolutionary classification.

Install

Fastcov is very easy to install, no dependencies are needed. It is implemented in [Golang](#) programming language.

Just download the single binary executable file of your platform in [release](#) page and run it in command-line interface.

Usage

See [MANUAL](#)

Please cite

Wei Shen, Yan Li*. A novel algorithm for covariant analysis and clustering of biological sequences (submitted)

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