

Fastcov

Fast Multiple Covariance Detector. <http://yanlilab.github.io/fastcov>
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Introduction

Single genetic mutations are always followed by a set of compensatory mutations. Thus, multiple changes commonly occur in biological sequences and play crucial roles in maintaining conformational and functional stability. Although many methods are available to detect single mutations or covariant pairs, detecting non-synchronous multiple changes at different sites in sequences remains challenging. Here, we develop a novel algorithm, named Fastcov, to identify multiple correlated changes in biological sequences using an independent pair model followed by a tandem model of site-residue elements based on inter-restriction thinking. Fastcov performed exceptionally well at harvesting co-pairs and detecting multiple covariant patterns. By 10-fold cross-validation using datasets of different scales, the characteristic patterns successfully classified the sequences into target groups with an accuracy of greater than 98%. Moreover, we demonstrated that the multiple covariant patterns represent co-evolutionary modes corresponding to the phylogenetic tree, and provide a new understanding of protein structural stability. In contrast to other methods, Fastcov provides not only a reliable and effective approach to identify covariant pairs but also more powerful functions, including multiple covariance detection and sequence classification, that are most useful for studying the point and compensatory mutations caused by natural selection, drug induction, environmental pressure, etc.

Install

Visit [download page \(http://yanlilab.github.io/fastcov/download/\)](http://yanlilab.github.io/fastcov/download/).

Usage

Read [manual \(http://yanlilab.github.io/fastcov/manual\)](http://yanlilab.github.io/fastcov/manual).

Please cite

Wei Shen, Yan Li*. A novel algorithm for detecting multiple covariance and clustering of biological sequences (submitted)

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