

Fastcov

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

Single genetic mutation always brings along with a set of compensatory mutations, therefore multiple changes commonly occur in the biological sequences, which play crucial roles to maintain the conformational and functional stability. Although there are a lot of methods to detect single mutation or covariant pairs, it is still a great challenge to explore the non-synchronous multiple changes at different sites in the sequences.

Here we developed a novel algorithm, named Fastcov, to identify multiple correlated changes of biological sequences, by using an independent pair model followed by a tandem model of site-residue elements, based on an inter-restriction thinking. The results showed that Fastcov has excellent performances on harvesting co-pairs and detecting multiple covariant patterns. By 10-fold cross-validation in different scales of datasets, the characteristic patterns successfully classified the sequences into their target groups with an accuracy of 98% above. Moreover, it demonstrated the multiple covariant patterns represented co-evolutionary modes, corresponding to the phylogeny tree, and it provided new understanding of the structural stability of protein during the evolution. In contrast to other methods, Fastcov, as an original algorithm, provides not only a reliable and effective approach to harvest covariant pairs of site-residues, but also more powerful functions including multiple covariance detection and sequence classification.

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

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