Genomics

Distance Scan

A tool for finding pairs of transcription factor binding sites.
Further information: www.omnifung.hki-jena.de/omnifung/Rpad/Distance_Scan/index.htm

SiTaR

The method is based on the idea that we can calculate the number of motifs with given nucleotide content and given number of mismatches in a random sequence. These predicted numbers can then be compared with the real occurrences of motifs in a query sequence.
Further information: sbi.hki-jena.de/sitar

Reference:

cDAIoptimizer

A tool for characterization of the gene expression and translation efficiency of gene sequences based on CAI (Codon Adaptation Index) and dCAI (Dicodon Adaptation Index).
Further information: www.omnifung.hki-jena.de/Rpad/dCAIoptimizer.Rpad

Orthology R package

This R package enables the assignment of orthologous genes by utilization of multiple databases

FungiFun2

FungiFun is a user-friendly Web tool for functional enrichment analysis of fungal genes and proteins. The
novel tool FungiFun2 uses a completely revised data management system and thus allows enrichment analysis for 298 currently available fungal strains published in standard databases.

https://elbe.hki-jena.de/fungifun/fungifun.php

References:
