About

Relate Tools

HMMer

HMMER is used for searching sequence databases for sequence homologs, and for making sequence alignments. It implements methods using probabilistic models called profile hidden Markov models (profile HMMs).

HMMER is often used together with a profile database, such as Pfam or many of the databases that participate in Interpro. But **HMMER** can also work with query sequences, not just profiles, just like BLAST. For example, you can search a protein query sequence against a database with phmmer, or do an iterative search with jackhmmer.

HMMER is designed to detect remote homologs as sensitively as possible, relying on the strength of its underlying probability models. In the past, this strength came at significant computational expense, but as of the new HMMER3 project, **HMMER** is now essentially as fast as BLAST.

HMMER can be downloaded and installed as a command line tool on your own hardware, and now it is also more widely accessible to the scientific community via new search servers at the European Bioinformatics Institute.

Antismash

The **antiSMASH** framework allows the detection of clusters of co-occurring biosynthesis genes in genomes, called Biosynthetic Gene Clusters (BGCs). BGCs often contain all the genes required for the biosynthesis of one or more Natural Products (NPs), also known as specialized or secondary metabolites. NPs show interesting biological activities and many of them have been developed into essential medicines, including antibiotics (penicillin, streptomycin), anti-cancer drugs (bleomycin, doxorubicin), or cholesterol-lowering agents (lovastatin). This makes NPs and their encoding BGCs highly relevant from both a commercial and scientific perspective.

BLAST+

The NCBI provides a suite of command-line tools to run BLAST called **BLAST+** . This allows users to perform BLAST searches on their own server without size, volume and database restrictions. BLAST+ can be used with a command line so it can be integrated directly into your workflow.

The Basic Local Alignment Search Tool (BLAST) finds regions of local similarity between sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance of matches. BLAST can be used to infer functional and evolutionary relationships between sequences as well as help identify members of gene families.