Resource Summary Report

Generated by NIF on May 5, 2025

Hybrid Pattern Library

RRID:SCR_008193
Type: Tool

Proper Citation

Hybrid Pattern Library (RRID:SCR_008193)

Resource Information

URL: http://bibiserv.techfak.uni-bielefeld.de/HyPa/

Proper Citation: Hybrid Pattern Library (RRID:SCR_008193)

Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented on July 15, 2013. It contains annotated structural elements characteristic for certain classes of structural and/or functional RNAs. These elements are described in a language specifically designed for this purpose. The language allows convenient specification of hybrid patterns, i.e. motifs consisting of sequence features and structural elements together with sequence similarity and thermodynamic constraints. A system that searches complex patterns (on nucleic-acid or protein level) in large biosequence-databases. As patterns, they allow hybrid patterns, which combine sequence similarity, structure similarity and arbitrary characteristics, like thermodynamic constraints. Applications are in the research of highly specific Protein/RNA-interactions or in the search of RNA-tertiary-structure-interactions. They developed a declarative pattern description language, which is implemented by known and new pattern-matching algorithms and an optimizing backtracking procedure. To achieve high efficiency when screening large data sets, the patterns are divided and queries are composed. The significance of patterns is estimated by a Monte-Carlo procedure. Complex results of queries are processed by a visualizing component. A library of biologically relevant patterns is developed and it is provided on the WWW together with the search-tool. The evaluation of the tool w.r.t. to the biosequence databases will in some cases mean to make laboratory-experiments, in order to check algorithmically developed functional hypothesis. Sponsors: This project is supported by a grant from the Deutsche Forschungsgemeinschaft. It is part of the special program on Computational Methods for the Analysis and Interpretation of large genomic data

Abbreviations: HyPaLib

Synonyms: Hybrid Pattern Library

Resource Type: data or information resource, database

Keywords: element, functional, biologically, biosequence, characteristic, class, constraint, hybrid, interaction, nucleic acid, pattern, protein, rna, screening, structural, tertiary, thermodynamic

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Hybrid Pattern Library

Resource ID: SCR_008193

Alternate IDs: nif-0000-21208

Record Creation Time: 20220129T080246+0000

Record Last Update: 20250505T053903+0000

Ratings and Alerts

No rating or validation information has been found for Hybrid Pattern Library.

No alerts have been found for Hybrid Pattern Library.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We have not found any literature mentions for this resource.