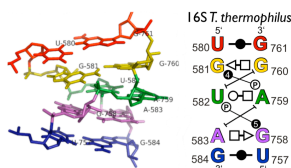# BGSU RNA Structural Bioinformatics

rna.bgsu.edu

Databases for RNA 3D motifs, non-redundant lists of RNA 3D structures, structural annotations

Web servers for searching, superimposing and predicting RNA 3D structures and RNA 3D motifs

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RNA 3D Motif Atlas

RNA 3D Motif Atlas is a representative collection of RNA 3D motifs. It is built upon a new automated RNA 3D motif clustering approach, which is based on exhaustive all-against-all geometric comparisons with the FR3D program. The Motif Atlas contains all hairpin and internal loop RNA 3D motifs including well-known motifs such as sarcin-ricin, C-, and kink-turn internal loops and T-, UNCG and GNRA hairpin loops, as well as many new motifs. The Motif Atlas is regularly updated. It also has a versioning system and a user friendly interface.

rna.bgsu.edu/motifs

Non-redundant Lists
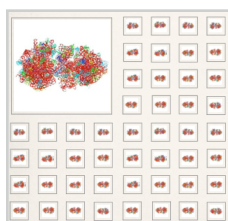
Many RNA 3D structures deposited at Protein Data Bank represent the same RNA molecule with small variations. We use sequence similarity, structure superposition and structure quality considerations to group similar files and select the best representative. Each release is archived and all releases can be compared. Users can get non-redundant lists at different resolution cutoffs.

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JAR3D
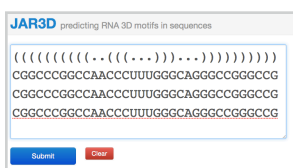
JAR3D is a web application for predicting RNA 3D motifs starting from sequence. It uses the RNA 3D Motif Atlas to build stochastic context free grammars for known motif instances, and it relies on the RNA base pair isostericity and the knowledge of RNA base stacking and base phosphate interactions to infer RNA 3D motifs even with previously unobserved sequences. JAR3D recognizes multiple types of input. The output shows the top scoring motifs from the RNA 3D Motif Atlas. Take a look at JAR3D tutorial online.

**rna.bgsu.edu/jar3d**

WebFR3D and WebR3DAlign
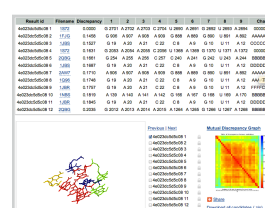
WebFR3D is the online version of FR3D, a suite of Matlab programs designed to search RNA 3D structures for user specified queries. New RNA structures can be searched by WebFR3D as they are made available at PDB. Take a look at WebFR3D tutorial online.

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WebR3DAlign is the online version of R3DAlign, a new algorithm to align large homologous RNA structures nucleotide by nucleotide using local superpositions that accommodate the flexibility of RNA molecules.

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RNA Base Triple Database
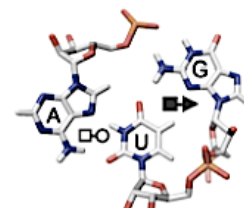
Base triples are recurrent clusters of three RNA nucleobases interacting edge-to-edge by hydrogen bonding. **RNA Base Triple Database** provides exemplars of all base triples observed in the structure database and models for unobserved, predicted triples, grouped by triple family, as well as by three-base combination. The classification helps to identify recurrent triple motifs that can substitute for each other while conserving RNA 3D structure.
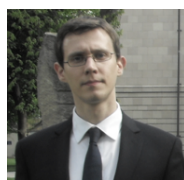
rna.bgsu.edu/triples

About Us

Professor Neocles Leontis
Professor of Chemistry, Bowling Green State University and program officer National Science Foundation BIO/MCB

Professor Craig Zirbel
Department of Mathematics and Statistics, Bowling Green State University

Anton Petrov, PhD
is developing RNA 3D Motif Atlas, WebFR3D, and is working on RNA 3D Hub, a new resource for RNA bioinformatics

James Roll
is working on JAR3D and stochastic context free grammars (SCFGs) to predict RNA 3D motifs from sequence

Blake Sweeney
is working on integrating RNA 3D structural data with RNA sequence alignments and building the next version of FR3D

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