Biyo- kütüphaneleri

BIOJAVA

THE OPEN-SOURCE JAVA FRAMEWORK FOR BIOINFORMATICS

GET STARTED

LEARN MORE
↓

https://biojava.org/
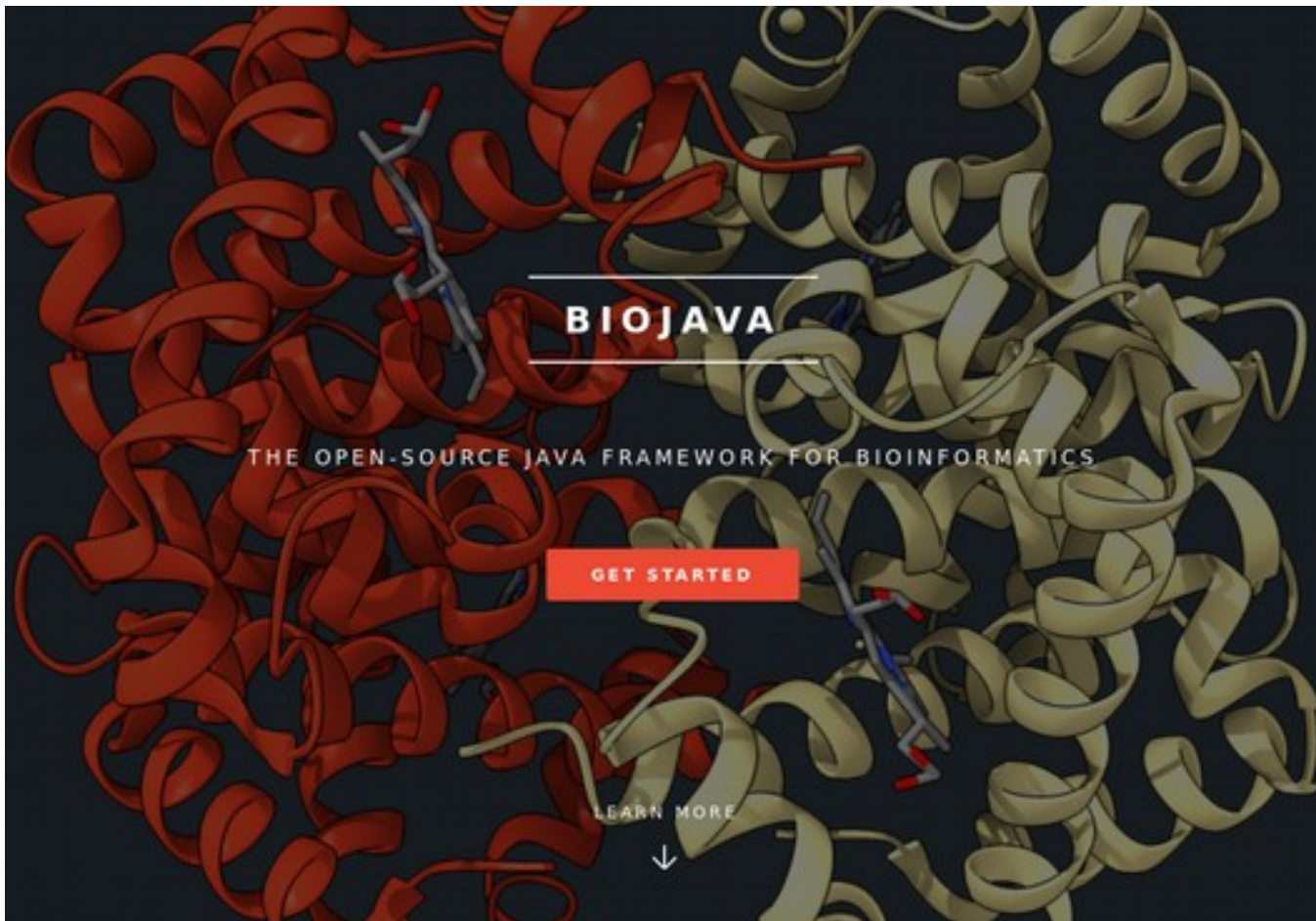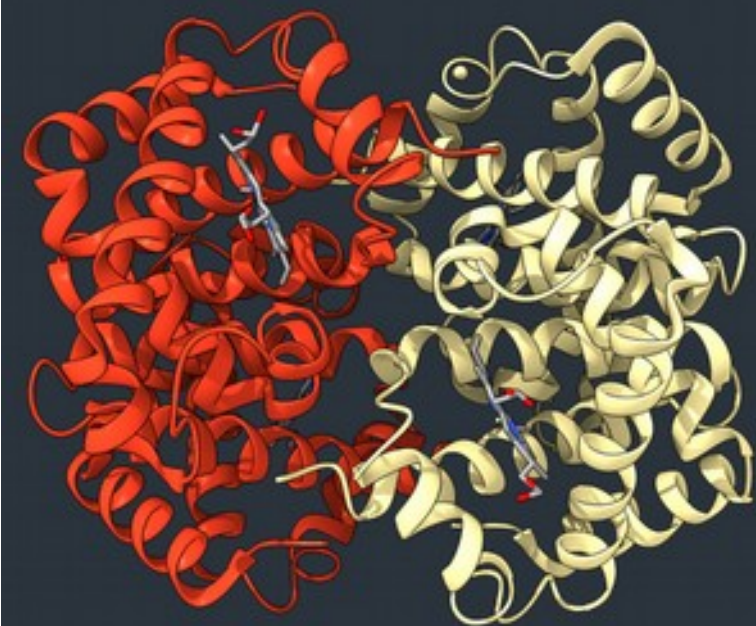
PROTEIN STRUCTURES

BioJava provides an API to maintain local installations of the PDB, load and manipulate structures, perform standard analysis such as sequence and structure alignments and visualize them in 3D.

BIOLOGICAL SEQUENCES

BioJava supports reading and writing popular sequence file formats, translating DNA sequences into proteins and other common bioinformatics routines.
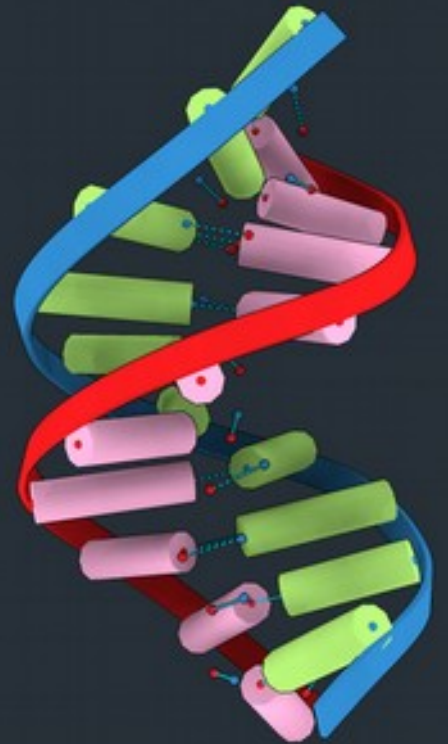
BioPerl

The Bioperl Project is an international association of users & developers of open source Perl tools for bioinformatics, genomics and life science

Installation
Installing the current version

Documentation
HOWTOs and Scrapbook code

Support
BioPerl Mailing Lists

Issues
Submit bugs or enhancement requests to GitHub

Code
BioPerl Packages at GitHub

OBF
The Open Bioinformatics Foundation

https://bioperl.org/#

Practical descriptions of BioPerl modules with a focus on common tasks.

- Beginners HOWTO - Introduction to BioPerl for biologists.
- Features and Annotations HOWTO - Reading and writing detailed data associated with sequences.
- BlastPlus HOWTO - Create, manage, and query BLAST databases with NCBI blast+.
- EUtilities Cookbook HOWTO - Simple script examples using Bio::DB::EUtilities.
- SearchIO HOWTO - Parsing reports from sequence comparison programs like BLAST.
- SeqIO HOWTO - Sequence file input and output, with script examples.
- Getting Genomic Sequences HOWTO - Some examples of how to retrieve genomic sequences.
- AlignIO and SimpleAlign HOWTO - Create and analyze alignments using BioPerl.
- Writing BioPerl Tests HOWTO - A general guide on how to write BioPerl tests using Test::More.
- OBDA Flat Databases HOWTO - Indexing local sequence files for fast retrieval using OBDA.
- Tiling HOWTO - Use SearchIO to create robust alignments.
- Local Databases - Indexing local sequence files for fast retrieval.
- OBDA HOWTO - Using OBDA, a universal and customizable sequence retrieval system.
- Restriction Enzyme Analysis HOWTO - *in silico* restriction enzyme analysis.
- Short-read assemblies with BWA HOWTO - Using the *bwa* assembler in BioPerl.
- Short-read assemblies with maq HOWTO - Using the *maq* assembler in BioPerl.
- Trees HOWTO - Using BioPerl to analyze phylogenetic trees.
- EUtilities Web Service HOWTO - Query NCBI Entrez via the EUtilities.
- PAML HOWTO - Using the PAML package using BioPerl.
- PhyloXML HOWTO - Read and write phyloXML documents using BioPerl.
- Bioperl Objects HOWTO - The common and uncommon objects that represent sequence.
- Simple Web Analysis HOWTO - Submitting sequence data to Web forms and retrieving results.
- Best Practices HOWTO - The conventions to use when writing BioPerl code.
- Advanced BioPerl HOWTO - Notes on developing BioPerl code.
- PopGen HOWTO - Population genetics, molecular evolution, and BioPerl.
- SubmitPatch HOWTO - The steps needed to get your modification to BioPerl into the code base.
- Nexml HOWTO - A guide on how to read and write Nexml documents using BioPerl.
- Glyphs HOWTO - Extend Bio::Graphics using custom glyphs.
- BioGraphics HOWTO - Creating beautiful graphics for sequence display and annotation.
- Using Git HOWTO - Using Git with BioPerl.
- Submitting Issues HOWTO - How we suggest submission of bugs and feature requests.
- Scrapbook HOWTO - Donated scraps of BioPerl code for you to reuse.

Referans Biyo- kütüphanesi!!!

BioRuby

Open source bioinformatics library for Ruby

Announcements

- BioRuby 1.5.2 is released on September 20, 2018. (Download) (Release Notes) (ChangeLog)
- At the 16th Annual Bioinformatics Open Source Conference (BOSC 2015) held in Dublin on July 10-11, George Githinji and Pjotr Prins will be presenting a talk entitled "The biogems community: Challenges in distributed software development in bioinformatics" (Abstract).
- Biogem is community developed plugins for the BioRuby. See the complete list, generic information, README, HOWTO and Tutorial.

http://bioruby.org/

- Plotting ABI traces
- Represent an alignment from contig archived in ACE files.
- Retrieve and annotate Entrez Gene IDS with the Entrez module.
- Concatenating multiple alignments NEXUS files with the Bio.Nexus module.
- Converting sequence files with the Bio.SeqIO module.
- Mapping genetic coordinates with the Bio.SeqUtils.Mapper module.
- Methods for Degenerated Codons
- From gene sequence to predicted protein with the GFF module.
- Workflow to extract intergenic regions from a sequence.
- Bio.Phylo Cookbook.
- Reading data from UNIX pipes.
- Reading large PDB files with Biopython.
- Remove PDB disordered atoms with the Bio.PDB module.
- Retrieve nonmatching blast queries
- Sequence Cleaner
- Split large file

… ve daha bir çooooooook fonksiyon :)