

Overview

MolDViewer is a multiplatform web based open-source software for interactive visualization of the kinetics of macromolecule processes. The MolDViewer enables the fast-graphical comparison between measured kinetics of hundreds of macromolecule interactions. In addition, it makes possible the side-by-side representation of the kinetic data and the mathematical models that describe the macromolecules` dynamics.

Features

MolDViewer provides a complete set of features required for deeper analysis and a convenient way to share and compare results.

Part of the features are listed below.

- Comparison between measured kinetic data and mathematical models;
- Comparison between proteins with high and low intensity macromolecule behavior;
- Comparison between proteins with rapid and slow recruitment speed;
- Several ways to animate the recruitment and removal processes;
- A set of features that provide a convenient work environment for handling hundreds of graphics plotted at a time;
- Friendly user interface to upload prepared files with mathematical models, measure kinetic data and animation parameters;
- Full capabilities to interactively modify and explore the mathematical models;
- Paper styling capabilities;
- Easy way to share and compare results.

Demo

Demo videos could be found on the following URL:

<https://github.com/yordanbabukov/MolDViewer/tree/master/Demo>

Training

Training material could be found here:

<https://github.com/yordanbabukov/MolDViewer/tree/master/Training/MolDViewer>