

BioJS 2.0: an open source standard for biological visualization

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Project Website: <http://biojs.net/>

Source Code: <https://github.com/biojs/biojs>

License: Apache license V 2.0

BioJS 2.0 is an open-source, JavaScript-based biological data visualization framework. The development of BioJS has been prompted by the growing need for bioinformatics visualization tools to be easily shared, reused and discovered. BioJS 2.0 features an open, inclusive framework for integration of visualization code (called components) that can be combined to create rich and interactive applications. Components can be quickly discovered on the BioJS 2.0 registry (<http://biojs.io>), a searchable and highly descriptive repository that highlights a component's usefulness by using a star rating system and a download counter. Applying modern best practices, BioJS 2.0 makes it easy for the end users to release and deploy new components. This in turn allows users with no or little technical skills to be able to test and reuse. Among the 90 currently published (and ready to be used) components, the BioJS 2.0 library already incorporates a set of commonly used components such as a Cytoscape network viewer, a 3D molecule viewer, a multiple sequence alignment viewer, a heat map viewer, a phylogenetic tree viewer and a BAM file viewer, applicable to a range of data visualization needs in the -omics fields. Some notable bioinformatics resources that have already integrated BioJS components include UniProt, ENSEMBL, PredictProtein, ApiNATOMY and the Galaxy project. The BioJS community of open source developers is heavily engaged in the organization of workshops, tutorials, hackathons and participates as a mentoring organization in the Google Summer of Code program. The BioJS registry, source code repository, extensive tutorials and documentation can be accessed through <http://biojs.net/>.