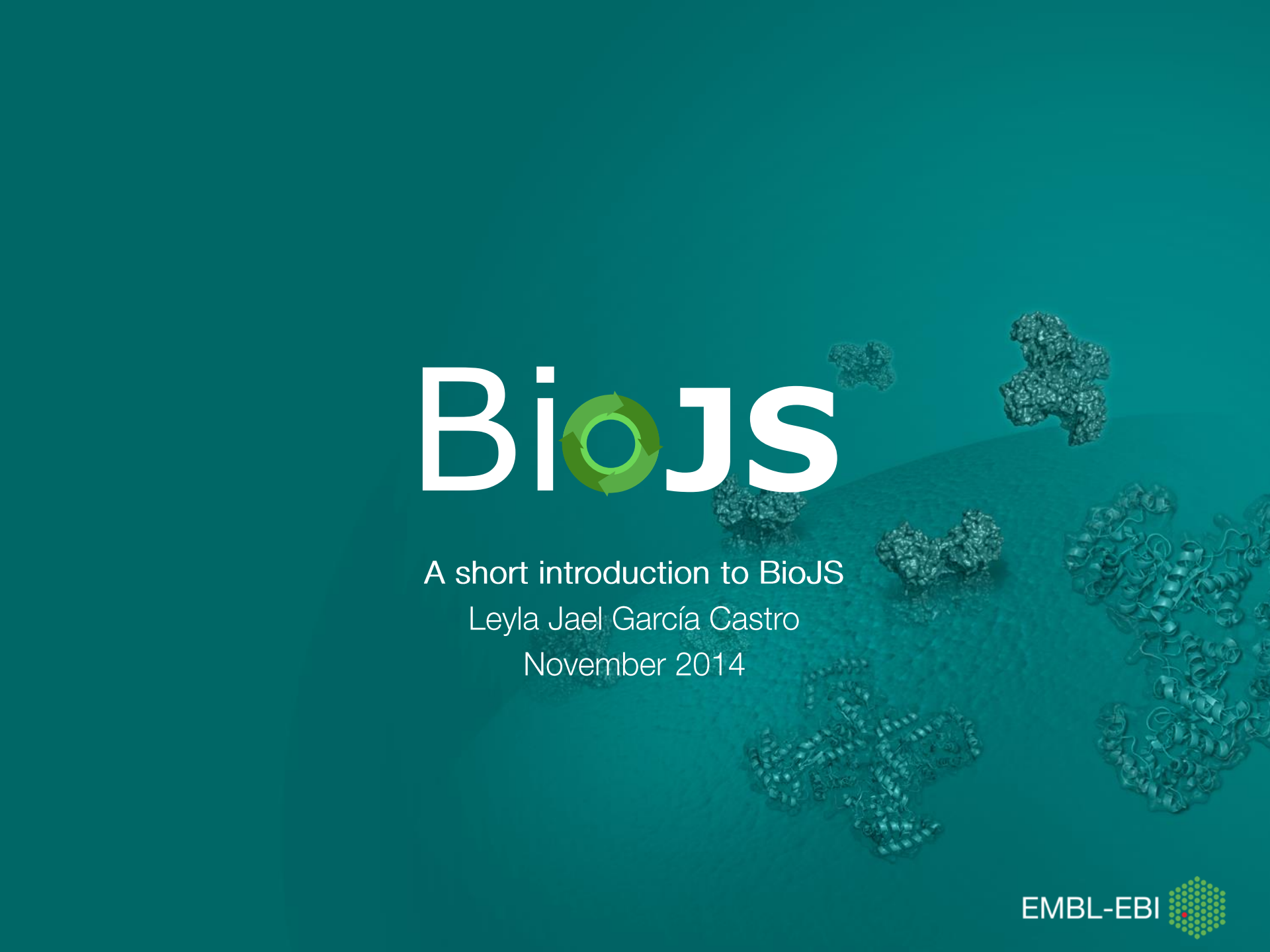


A short introduction to BioJS

Leyla Jael García Castro

November 2014

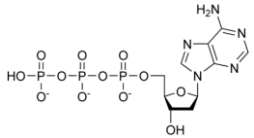
EMBL-EBI

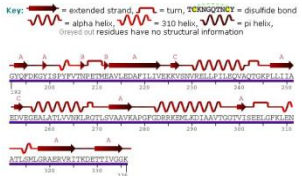
BioJS

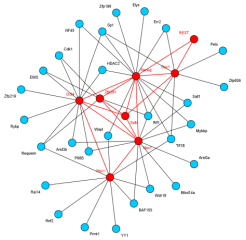
Motivation

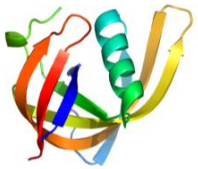
Discoverability, modularity and reuse
Unify efforts, avoid duplication

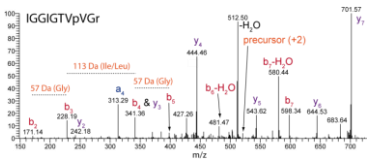
Components

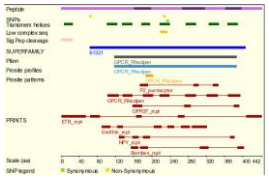




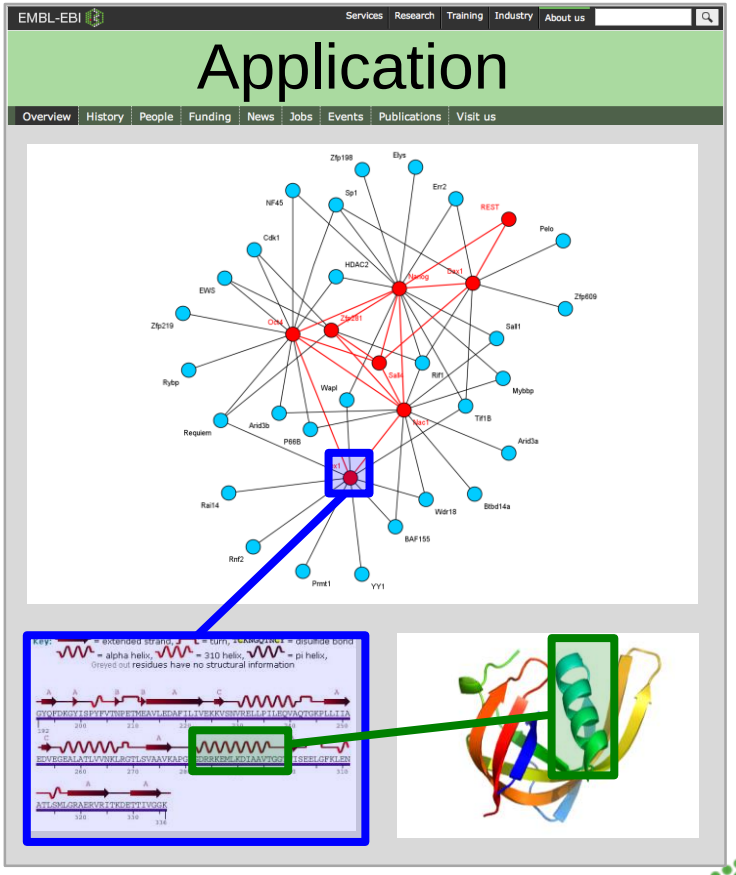








Application



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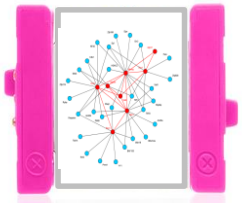
BioJS at a glance

What

A collection of **JavaScript** components following a **common guideline** to **visually** present **biological**



When

- Aug 2011 – Student project
- Dec 2012 – BioJS 1.0 at EBI
- Feb 2013 – AppNote in Bioinformatics
- Jan 2014 – F1000 collection
- May/Aug 2014 – Google Summer of Code
- July 2014 – BioJS 2.0 release

Who

Community of developers and collaborators

Where

Development: https://github.com/biojs/biojs

Learning: http://edu.biojs.net/

General information: http://biojs.net/

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From BioJS 1.0 to 2.0

- BioJS 1.0
  - Fixed core → Inheritance and event model
  - Built process with jsdoc + maven → not working for everybody
  - Not compatible with modern module and dependency management tools

- BioJS 2.0
  - No core but guidelines + event module
  - Better support for module and dependency management
  - Developers are free to use their preferred technologies

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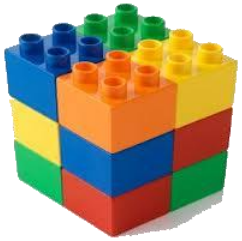
BioJS

Development

Guidelines

- Make it simple → one thing at a time
- Use modules → separate retrieval, process, visualization



- Make it open → GitHub
- Document → code and examples
- Share → publish your modules as a Node Packaged Module

npm

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BioJS

Development

Technology

- Highly recommended
  - Module management
  - Module dependency

- Either JavaScript or transpilers
- Dependency management → commonJS, require

- Test suits → choose your preferred and use it!

BioJS

Development

Community

- Participate → biojs google groups
- Share → submit your modules to BioJS registry

Name	Summary	Version	Avatar	Stars	Downloads	Modified	Demos	Build	Tests	
openphacts-vis-compoundinfo	Displays the information available in the Open PHA...	0.0.1		0	0	16 hours ago	X	X	X	openphacts compound
biojs-vis-inchlib	Interactive Cluster Heatmap library	1.1.2		0	236	a day ago	# 2	X	X	cluster heatmap clustering hierarchical clustering heatmap dendrogram
biojs-vis-circularnet	A circular network component	0.0.6		0	156	a day ago	# 2	X	X	vis network
biojs-vis-feature	A Feature viewer	0.0.5		0	156	a day ago	# 1	X	X	visualization features
biojs-io-graduates	Graduate parser for BioJS	0.0.7		0	325	2 days ago	X	build passing	X	tutorial
slush-biojs	A slush generator for BioJS modules	0.2.5		0	787	2 days ago	X	X	X	slushgenerator node npm module
biojs-util-colorschemes	Color schemes for residues	1.0.2		0	38	5 days ago	X	X	X	color schemes
biojs-vis-hpafeature	Component to represent one summary feature. Origin...	0.0.6		0	162	5 days ago	# 1	build passing	code climate 2.8	vis network
biojs-io-fasta	Parses FASTA files	0.0.11		0	1150	12 days ago	X	build passing	X	fasta sequence
biojs-io-snipspector	A simple snippet parser	0.0.7		0	371	13 days ago	X	build passing	X	snippets

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BioJS

- GSoC is a program designed to
  - Encourage students participation in open source software development.
  - Inspire young developers to begin participating in open source development
  - Get more open source code created and released for the benefit of all
- Participating Projects
  - Databases
  - Biology, Analytical Sciences, Health Care
- What does it mean for BioJS?
  - Ideal way to explore potential new ideas or bring ideas into production
  - Getting more people involved
  - First participation 2014
    - 5 successful projects → Genetic variations, proteome taxonomy, BAM file, MSA, phylogenetic tree
    - BioJS 2.0 initiative

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Thanks to:

The BioJS project members and collaborators

https://github.com/biojs/biojs

http://edu.biojs.net

http://biojs.net/

biojs@googlegroups.com

Main contributors

- UniProt
- EBI web development team
- The Proteomics Services Team
- GSoC: RostLab

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