



BioJS²Galaxy

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seb@wilzba.ch



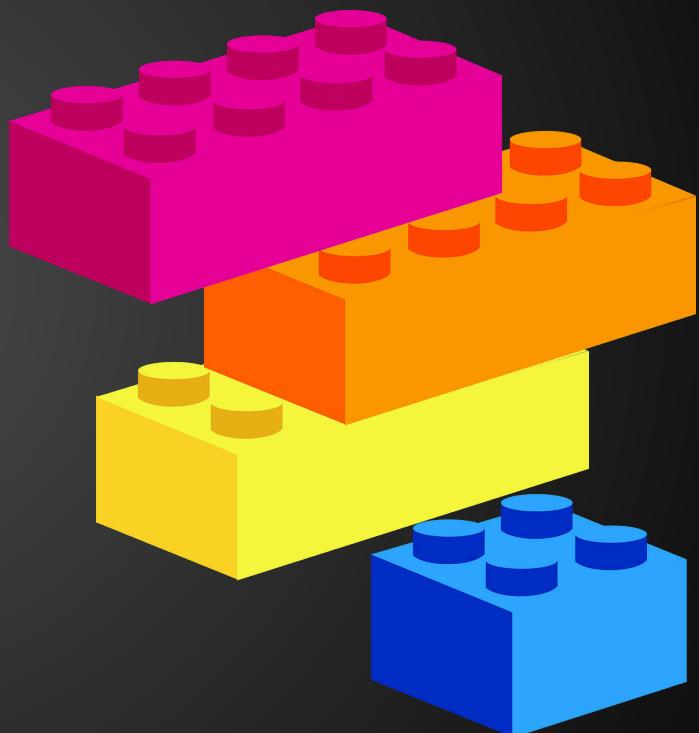
@MrGreenify



@greenify

What is BioJS?

- open source JavaScript library
- build & share biological visualizations
- stop to reinvent the wheel
- modularity



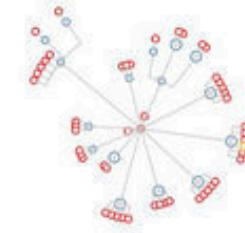
Building blocks



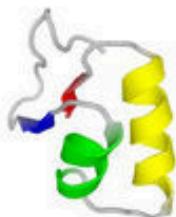
Tree Viewer

I	S	G	T	M	I	S	T	S	F	L	P	R	K	P	A	V	T	S	L	-	K	A	I
I	S	G	T	M	I	S	T	S	F	L	P	R	K	P	V	V	T	S	L	-	K	A	I
L	S	G	A	T	M	S	T	A	F	A	P	K	-	-	T	P	P	M	T	A	A	L	P
M	M	G	-	-	M	A	T	T	F	V	P	K	P	Q	A	P	P	M	M	A	A	L	P
L	S	S	A	I	V	G	T	S	F	I	R	R	S	P	A	P	I	S	L	R	S	L	P
L	S	S	A	I	V	S	T	S	F	L	R	R	Q	Q	T	P	I	S	L	R	S	L	P
L	Y	G	T	A	V	S	T	S	F	L	R	T	Q	P	M	P	M	S	V	-	T	T	T
L	Y	G	T	A	V	S	T	S	F	M	R	R	Q	P	V	P	M	S	V	-	A	T	T
A	P	A	F	F	S	S	S	S	L	R	A	A	P	A	T	V	-	-	A	L			

MSA viewer



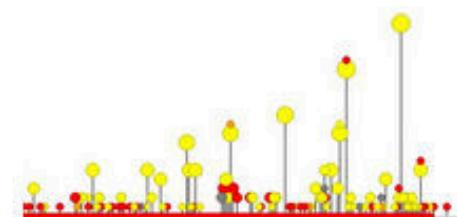
Proteome



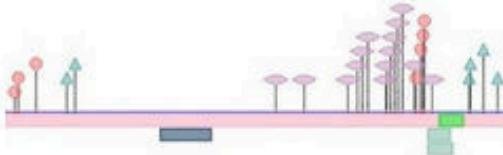
3D structures



Dot-bracket



Muts-needle plot



Protein Feature Viewer



Plasmids



Pathway visualization

BioJS.io - discover components



[Submit](#) [Wish a component](#) [Stats](#) [About us](#)

Fork me on GitHub

e.g. proteins

94 components found

Component

Stars

Downloads

Modified

Demos



msa 0.4.6

Sebastian Wilzbach

Display multiple sequences

bio galaxy-vis msa alignment sequence

24

2454

12 hours ago

9



biojs-vis-sequence 0.1.7

BioJS

Display sequence

sequence galaxy-vis

0

2597

12 hours ago

2



pileup 0.2.0

Dan Vanderkam

JavaScript track viewer

genome track bam gene bioinformatics genomics sequencing
reads interactive

24

822

5 days ago

2



bio-pv 1.7.0

Marco Biasini

WebGL protein viewer

protein 3d webgl

57

824

9 days ago

2

Preview the visualization

msa Display multiple sequences

Sebastian Wilzbach , Tatyana Goldberg , Guy Yachdav

bio galaxy-vis msa alignment sequence

[View Code](#) [Report/Flag](#)

`npm install msa`

[New window](#) [Edit \(JSBin\)](#) [Edit \(Codepen\)](#) [Edit \(Plunker\)](#) [All \(9\)](#)

[fer1](#) ▾ 9 examples available.

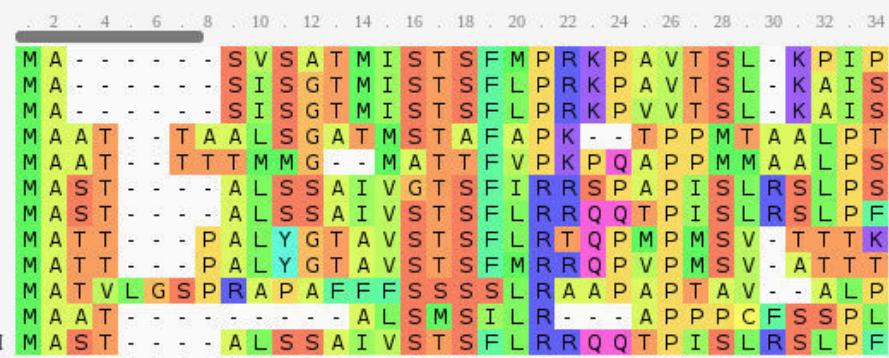
Import Ordering Filter Selection Vis.elements Color scheme Extras Export Help

ID	Label	Gaps	Ident	Links
1	FER_CAPAN	8%	0.75	
2	FER1_SOLLC	8%	0.81	
3	Q93XJ9_SOLTU	8%	0.80	
4	FER1_MESCR	6%	0.84	
5	FER1_SPIOL	6%	0.71	
6	FER1_ARATH	6%	0.83	
7	FER2_ARATH	6%	0.81	
8	FER1_PEA	5%	0.75	
9	Q7XA98_TRIPR	3%	0.78	
10	FER1_MAIZE	4%	0.70	
11	O80429_MAIZE	11%	0.68	
12	Q93Z60_ARATH	25%	0.83	
13	FER_CAPAA	38%	0.80	
14	FER3_RAPSA	39%	0.89	
15	FER_BRANA	39%	0.91	

Interactive workspace (JSBin)

Output

ID	Label
1	FER_CAPAN
2	FER1_SOLLC
3	Q93XJ9_SOLTU
4	FER1_MESCR
5	FER1_SPIOL
6	FER1_ARATH
7	FER2_ARATH
8	FER1_PEA
9	Q7XA98_TRIPR
10	FER1_MAIZE
11	O80429_MAIZE
12	Q93Z60_ARATH
13	FER_CAPAA
14	FER3_RAPSA
15	FER_BRANA



Super-powered by github

- no central, large repository
- own github repos

- pull requests



- issues

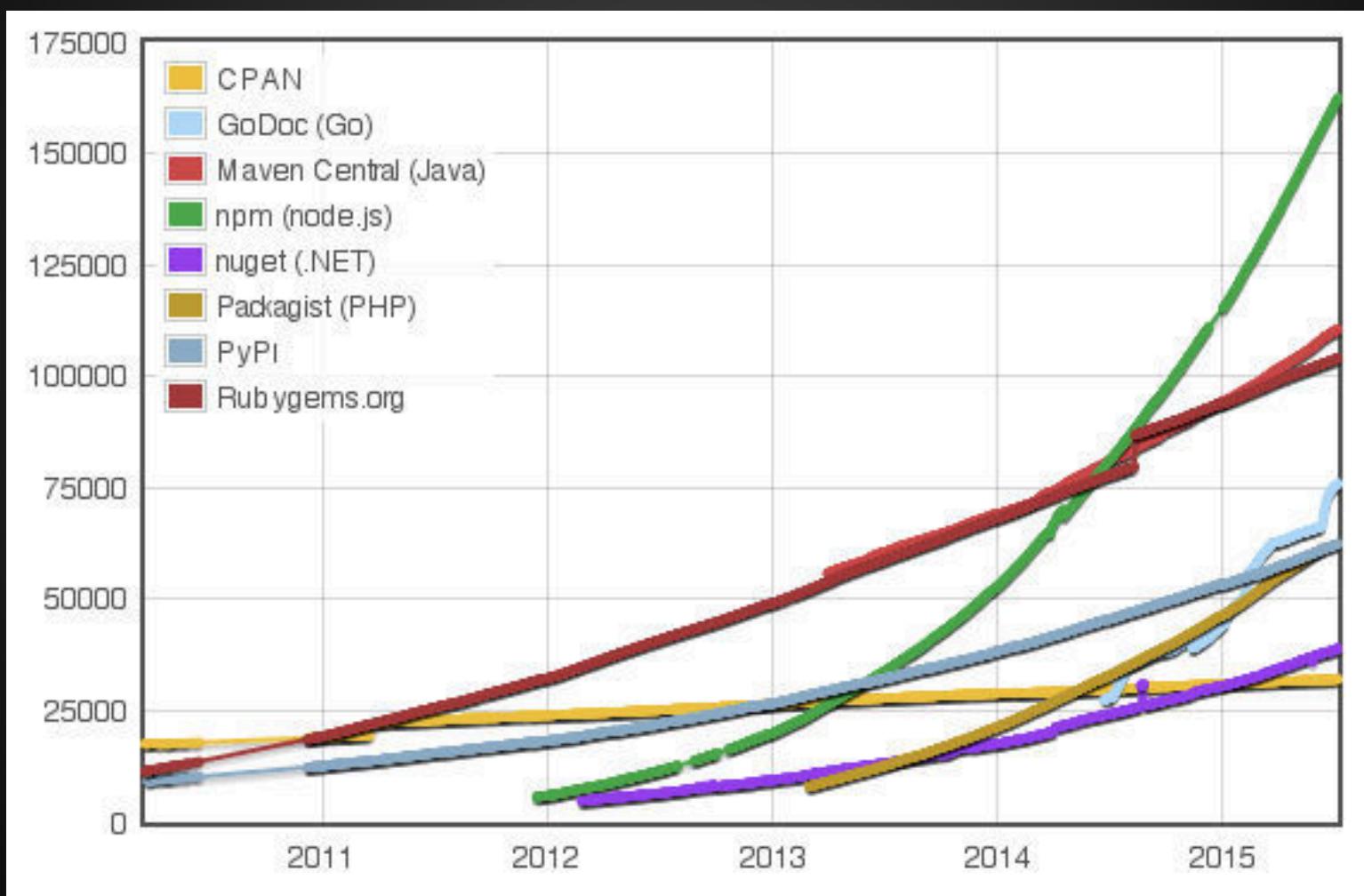


- forks



github
SOCIAL CODING

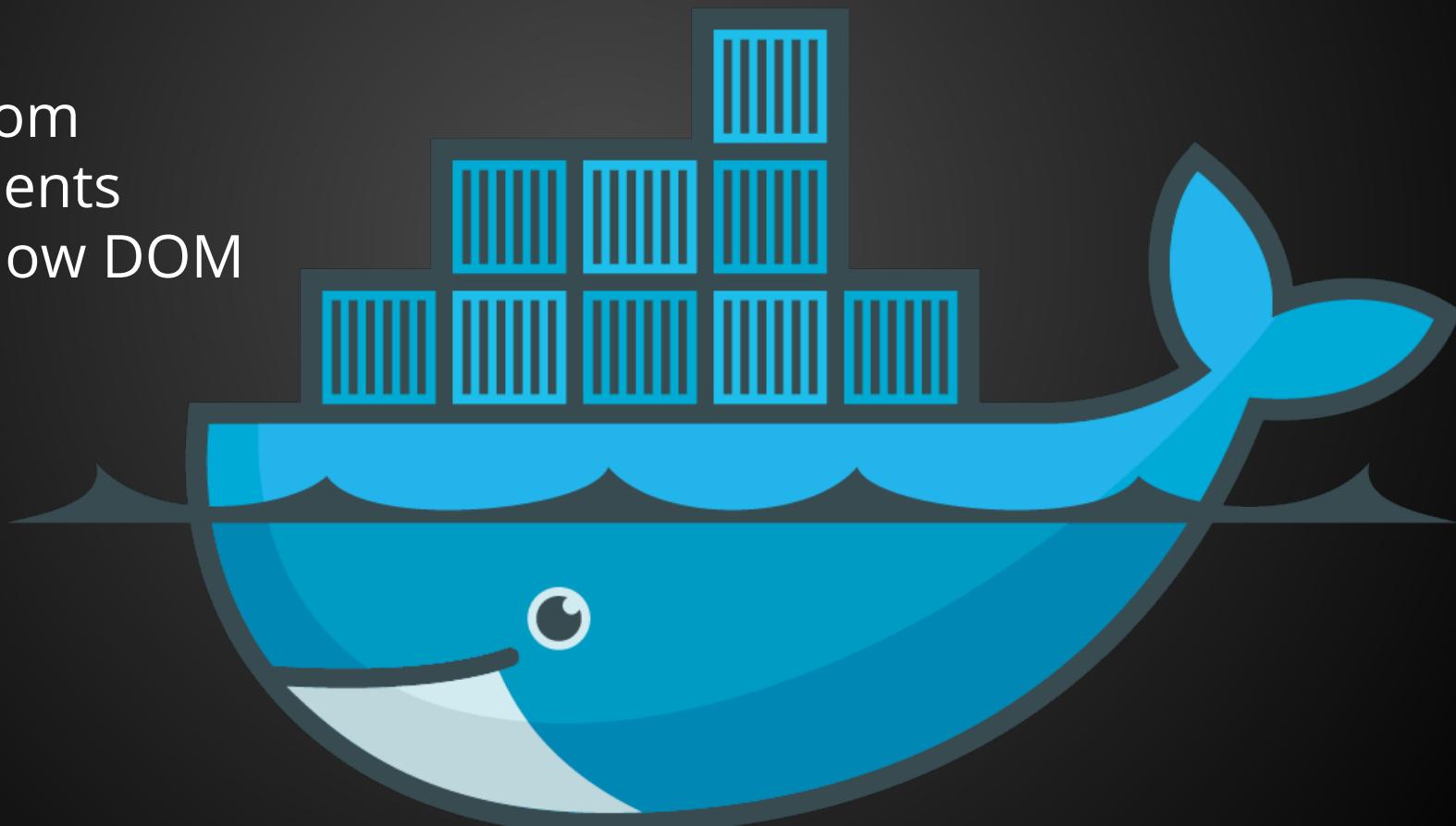
NPM (Node packaged modules)



Web Components

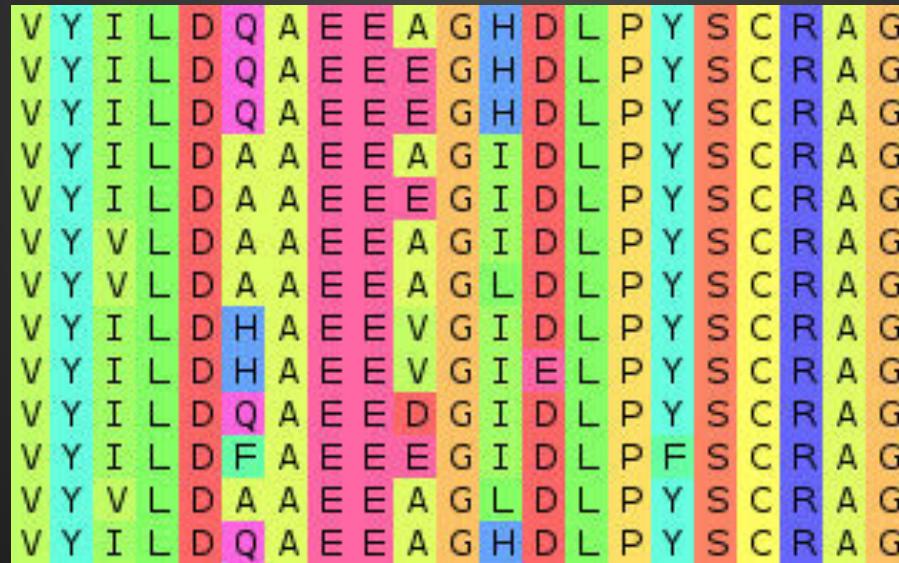
“Docker of the Web”

- Custom Elements
- Shadow DOM



BioJS & Web Components

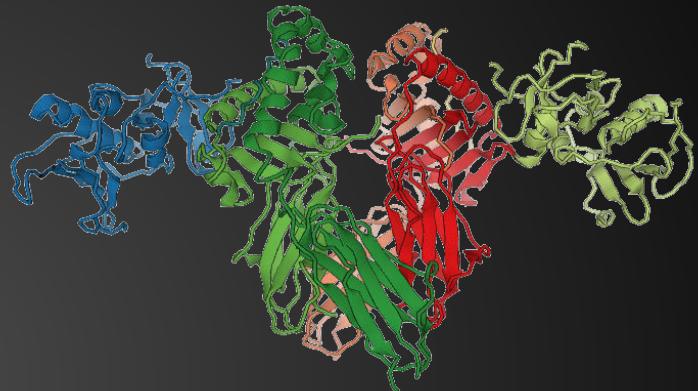
```
<bio-msa colorscheme="Taylor">
  <bio-io-clustal url="<path>/Q7T2N8.clustal" />
</bio-msa>
```



under development - see: github.com/biojs/biojs3

BioJS & Web Components

```
<bio-pv url="1SEB.pdb" />
```



```
<bio-tree>
```

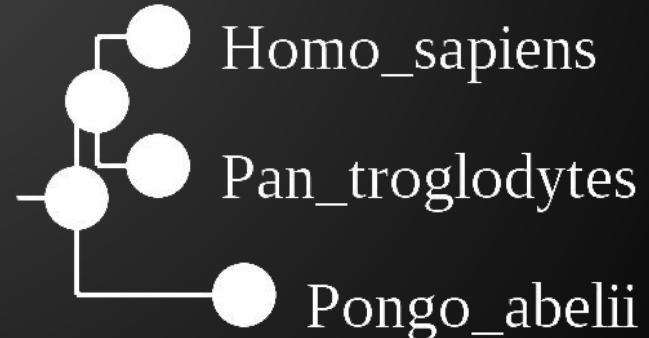
```
  <bio-io-newick>
```

```
    (pongo_abelii:3, (Pan_troglodytes:3,
```

```
      Homo_sapiens:5):3);
```

```
  </bio-io-newick>
```

```
</bio-tree>
```



under development - see github.com/biojs/biojs3

Integration with Galaxy

github.com/biojs/biojs2galaxy



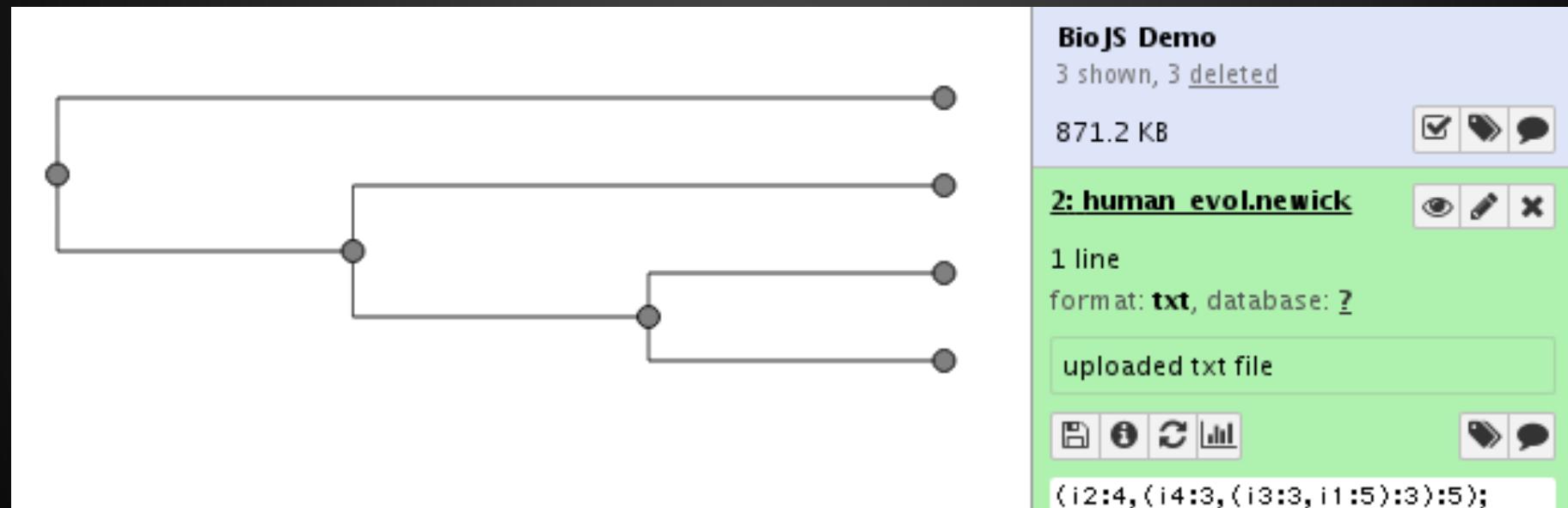
Multiple sequence alignments

Import Ordering Filter Selection Vis.elements Color scheme Extras Export Help Debug

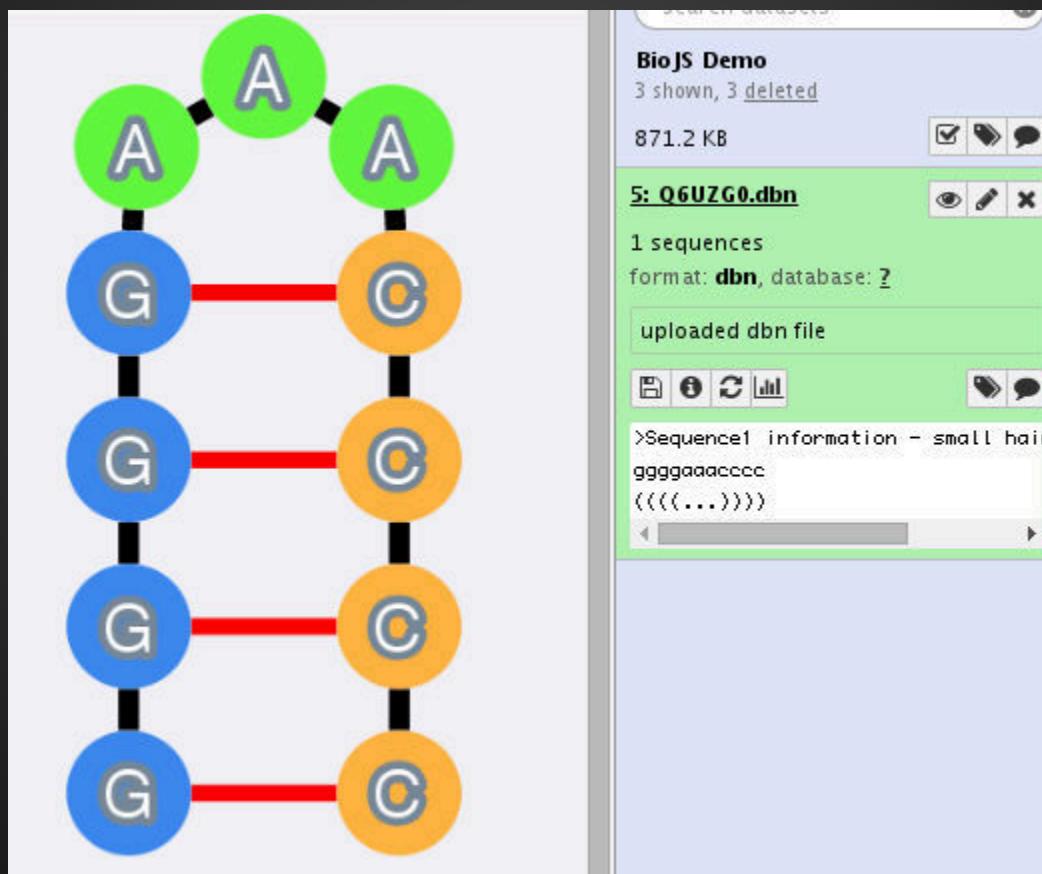
ID	Label	2	4	6	8	10	12	14	16	18	20	22	24	26	28	30	32	34	36																			
Q9W678	Cellular tumor an	M	A	E	S	Q	E	F	A	E	L	W	E	R	N	L	I	S	T	Q	E	A	G	T	C	W	E	L	I	N	D	E	Y	L	P	S	F	
Q29537	Cellular tumor an	M	E	E	S	Q	S	E	L	N	I	D	P	P	L	S	Q	E	T	F	S	E	L	W	N	L	L	P	E	N	N	V	L	S	S	E	L	C
P67938	Cellular tumor an	M	E	E	S	Q	A	E	L	N	V	E	P	P	L	S	Q	E	T	F	S	D	L	W	N	L	L	P	E	N	N	L	L	S	S	E	L	S
P67939	Cellular tumor an	M	E	E	S	Q	A	E	L	N	V	E	P	P	L	S	Q	E	T	F	S	D	L	W	N	L	L	P	E	N	N	L	L	S	S	E	L	S
P10360	Cellular tumor an	M	A	E	E	M	E	P	L	L	E	P	T	E	V	F	M	D	L	W	S	M	L	P	Y	S	M	Q	Q	L	P	L	P	E	D	H	S	N
Q9UR6	Cellular tumor an	M	E	E	P	H	S	D	L	S	I	E	P	P	L	S	Q	E	T	F	S	D	L	W	K	L	L	P	E	N	N	V	L	S	D	S	L	S
P13481	Cellular tumor an	M	E	E	P	Q	S	D	P	S	I	E	P	P	L	S	Q	E	T	F	S	D	L	W	K	L	L	P	E	N	N	V	L	S	P	L	P	S
O09185	Cellular tumor an	M	E	E	P	Q	S	D	L	S	I	E	L	P	L	S	Q	E	T	F	S	D	L	W	K	L	L	P	P	N	N	V	L	S	T	L	P	S
P79734	Cellular tumor an	M	A	Q	N	D	S	Q	E	F	A	E	L	W	E	K	N	L	I	I	Q	P	P	G	G	G	S	C	W	D	I	I	N	D	E	E	Y	L
Q8SPZ3	Cellular tumor an	M	E	E	S	Q	A	E	L	G	V	E	P	P	L	S	Q	E	T	F	S	D	L	W	K	L	L	P	E	N	N	L	L	S	S	E	L	S
Q29480	Cellular tumor an	Y	S	P	A	L	N	K	M	F	C	Q	L	A	K	T	C	P	V	Y	L	R	I	S	S	P	P	P	G	T	R	V	R	A	M	A	I	
P41685	Cellular tumor an	M	Q	E	P	P	L	E	L	T	I	E	P	P	L	S	Q	E	T	F	S	E	L	W	N	L	L	P	E	N	N	V	L	S	S	E	L	S
P79892	Cellular tumor an	P	A	V	N	N	L	L	S	P	D	V	V	N	W	L	D	E	G	P	D	E	A	P	R	M	P	A	A	P	L	A	P	A				
P04637	Cellular tumor an	M	E	E	P	Q	S	D	P	S	V	E	P	P	L	S	Q	E	T	F	S	D	L	W	K	L	L	P	E	N	N	V	L	S	P	L	P	S
O93379	Cellular tumor an	M	E	G	N	G	E	R	D	T	M	M	V	E	P	P	D	S	Q	E	F	A	E	L	W	L	R	N	L	I	V	R	D	N	S	L	W	G

BioJS Demo
1 shown, 5 deleted
871.2 KB
1: p53.fasta
34 sequences
format: fasta, database: ?
uploaded fasta file
uploaded sequence file
>sp|Q9W678 biojs-vis-sequence
MAESQEFAEL
VPVATDYPGE msa
IRATAIVKKSEHVAEVVRRCPHHERTPDGGLAPF
VVVPYEVPLQLGSEFTTVLYNFMCNSSCMGGMNRRP
CPCGRDRKTEESNFRKDQETKTLDKIPSANKRSLTH

Phylogenetic trees



RNA



What is a Galaxy vis plugin?

- config (xml)
- templates (mako)
- static files (js, css)

config (xml)

1) Config

templates (mako)

static files (js, css)

> package.json

```
"galaxy": {  
    "datatypes": ["sequence.Fasta"]  
}
```

config (xml)

2) Hello world “vis”

templates (mako)

static files (js, css)

> helloworld.mako

```
galaxy.getData(function(data){  
    galaxy.el.textContent = data;  
});
```

config (xml)

templates (mako)

static files (js, css)

2) msa.mako

```
var msa = require("msa");
var fasta = require("biojs-io-fasta");
```

```
galaxy.getData(function(data){
    var seqs = fasta.parse(data);
    var m = new msa({
        el: galaxy.el,
        seqs: seqs,
    });
    m.render();
})
```

* slightly simplified version

2) Create template

config (xml)
templates (mako)
static files (js, css)

predefined `galaxy` (mini JS client)

- el
- dataType
- getData(cb)
- meta
- config
- ...

Where is step 3?

msa.min.js

msa.min.css

config (xml)

templates (mako)

static files (js, css)



How to run?

```
npm install --global biojs2galaxy
```

```
biojs2galaxy msa,biojs-vis-sequence --output  
<path/to/galaxy>/config/plugins/visualizations/
```

Enable visualization in Galaxy

```
> config/galaxy.ini
```

```
[...]
```

```
visualization_plugins_directory =config/plugins/visualizations
```

```
[...]
```

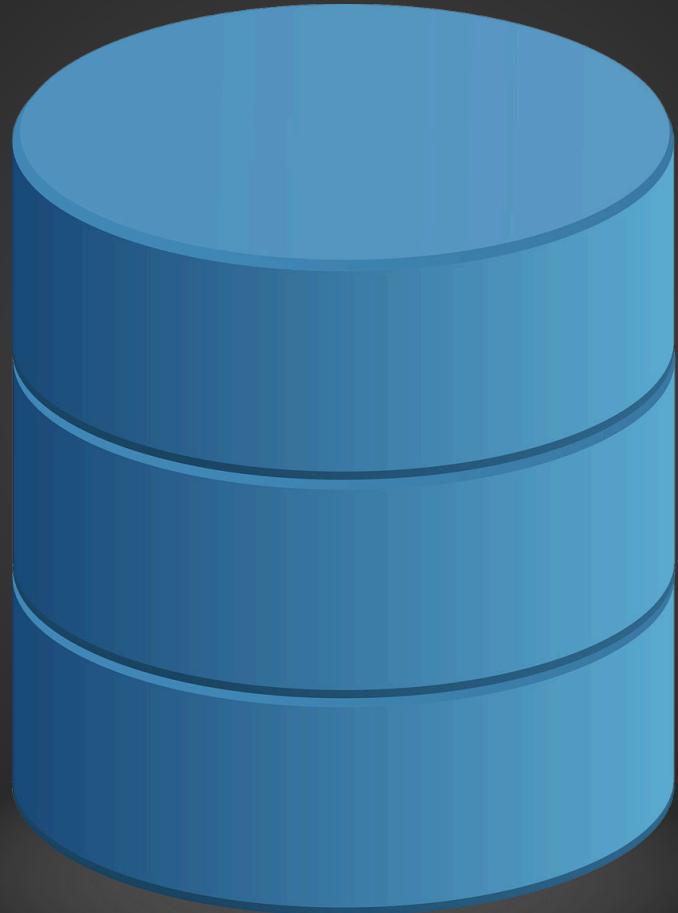
3) Downloading all

biojs2galaxy --all

> package.json

keywords: [. . . , "galaxy-vis" , ...]

biojs2galaxy ➔ galaxy vis toolshed?



To come: not only Galaxy



Shiny

IP[y]:



Project Chi

It's your turn!



Importer:
github.com/biojs/biojs2galaxy

Discover components:
biojs.io

Socialize @ github
github.com/biojs/biojs

BioJS & We Components:
github.com/biojs/biojs3



@BioJSLibrary



@biojs