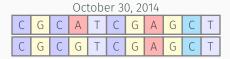
## **HUMAN GENETIC VARIATION VIEWER**

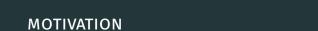
Saket Choudhary <sup>1</sup>, Leyla Garcia<sup>2</sup> and Andrew Nightingale<sup>2</sup>



<sup>&</sup>lt;sup>1</sup>University of Southern California and <sup>2</sup>EMBI-EBI

## **OUTLINE**

- Motivation
- · Solution
- · Demo and Use-Cases
- · Implementation
- · Future Work



## **VISUALIZATIONS ARE POWERFUL!**

The power of the unaided mind is highly overrated. The real powers come from devising external aids that enhance cognitive abilities. – Donald Norman

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- Exploratory visualization is the first step towards discovering patterns
- · Variation viewers are absent, if not, provide limited flexibility

# **SOLUTION**

· A graphical hub to present annotated variants from different sources

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- · Present information at different levels in a coherent manner

#### SOLUTION

- · A graphical hub to present annotated variants from different sources
- · Present information at different levels in a coherent manner
- · Scalable, and Interactive exploration on the browser

**DEMO** 

http://saketkc.github.io/biojs

# DETAILS

# **IMPLEMENTATION**

· Entirely written in javascript using the d3js library

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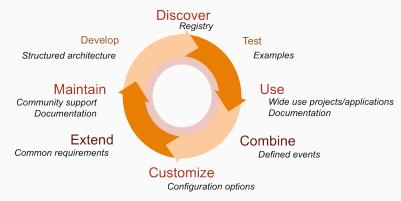
- · Entirely written in javascript using the d3js library
- · Deployed as a BioJS component
- · Events system that triggers events on user actions, allows cross-component communication

# WHY BIOJS

· BioJS is a javascript library for developing visualization of the biological data

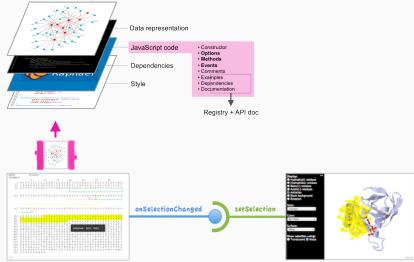
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# WHY BIOJS

# Reusable components that can talk to each other



```
"id":"P00533_variant226",
"sourceIds":["COSM1090877","COSM1090879"],
"position":541,
"wild type":"L",
"mutation":"I",
"frequency": 0.0,
"polyphenPrediction": "benign",
"polyphenScore":0.0,
"siftPrediction":"tolerated",
"siftScore":0.86,
"somaticStatus":1,
"consequenceTypes": "missense variant",
"cvtogeneticBand": "7p11.2",
"genomicLocation":"7:g.55229314C>A"
```

#### DATA INPUT

- · Pre-generated JSON files
- · Current version uses files generated by an unpublished webservice at EBI
- · Protein variants, though not specific to it

#### **FEATURES**

- · Supports JSON formatted files, alpha VCF support
- · User defined scoring criteria
- Different levels of information, tooltips
  - · Overview: Condensed information
  - · Zoomed View: All annotations
- · Loading proteins through URL parameters
- · SIFT, Polyphen, ....
- · Scalable, adaptable to new scores, mutation categories

# **USE CASES**

 $\cdot$  Identifying most or least mutated sites across proteins

## **USE CASES**

- · Identifying most or least mutated sites across proteins
- · Discover differences between different scoring criteria

#### **USE CASES**

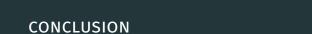
- · Identifying most or least mutated sites across proteins
- · Discover differences between different scoring criteria
- Benchmarking predictions

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- · Integration with Galaxy, web based bioinformatics workflows
- · Performance improvements
- · Interaction with 3D Protein viewer to highlight domains



#### **SUMMARY**

- · A tool for visualizing genetic variants
- · Supports visualization of different levels of information
- · Cross component talks
- · User defined and user controlled

## **ACKNOWLEDGEMENTS**

Google | Google Summer of Code 2014 BioJS Community USC MCB

