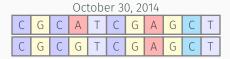
HUMAN GENETIC VARIATION VIEWER

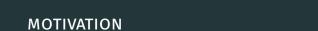
Saket Choudhary ¹, Leyla Garcia² and Andrew Nightingale²



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OUTLINE

- Motivation
- · Solution
- · Demo and Use-Cases
- · Implementation
- · Improvements



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
- · Scalable, and Interactive exploration on the browser



DETAILS

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IMPLEMENTATION

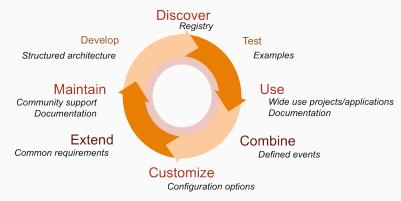
- · Entirely written in javascript using the d3js library
- · Deployed as a BioJS component
- · Events system that triggers events on user actions, allows cross-component communication

WHY BIOJS

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

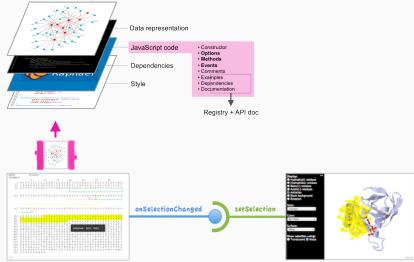
WHY BIOJS

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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

.

FEATURES

- · Supports JSON formatted files, alpha VCF support
- · User defined scoring criteria
- · Different levels of information
 - · Overview: Condensed information
 - · Zoomed View: All annotations
- · Loading proteins through URL parameters
- · SIFT, Polyphen,

USE CASES

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

IMPROVEMENTS

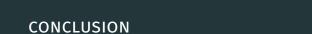
 \cdot VCF support, almost there

IMPROVEMENTS

- · VCF support, almost there
- · Integration with Galaxy, web based bioinformatics workflows

IMPROVEMENTS

- · VCF support, almost there
- · Integration with Galaxy, web based bioinformatics workflows
- · Performance improvements



SUMMARY

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

ACKNOWLEDGEMENTS

Google, for running the Google Summer of Code 2014.

