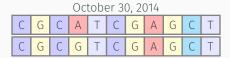
HUMAN GENETIC VARIATION VIEWER

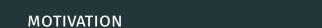
Saket Choudhary ¹, Leyla Garcia² and Andrew Nightingale²



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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, comparing consensus, aggregating predictions
- · Variation viewers are practically *absent*, those present provide limited flexibility

SOLUTION

· A graphical hub to present annotated variants from different sources

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- · Incremental levels of abstractions
- · Scalable and Interactive exploration on the web browser

OVERVIEW



Figure: Overview

ZOOMED VIEW

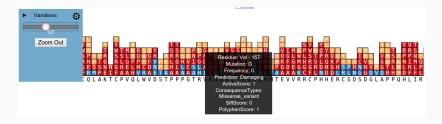


Figure: Zoomed View

DEMO

http://saketkc.github.io/biojs

DETAILS

IMPLEMENTATION

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- · Deployed as a BioJS component

IMPLEMENTATION

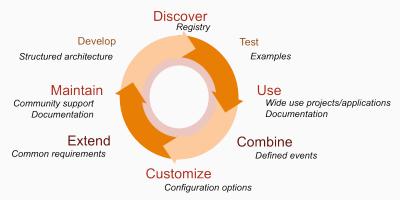
- · Written in javascript using the d3js library
- · Deployed as a BioJS component
- · Flexible system with ability to capture and react to user-actions

WHY BIOJS

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

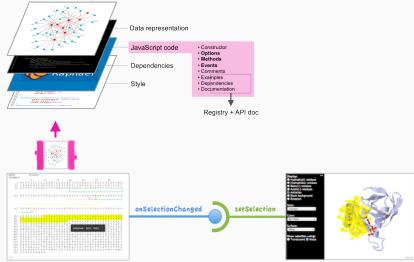
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WHY BIOJS

Reusable components that can talk to each other



DATA INPUT

- · Pre-generated JSON files
- · Current version uses files generated by an unpublished webservice at EBI
- · Protein variants only

```
"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",
"cytogeneticBand": "7p11.2",
"genomicLocation":"7:g.55229314C>A"
```

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- · Different levels of abstractions, tooltips

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 - · Zoomed View: All annotations
- · SIFT, Polyphen,
- · Scalable, adaptable to new scores, mutation categories

USE CASES

 \cdot Identifying most or least mutated sites on a protein

USE CASES

- · Identifying most or least mutated sites on a protein
- · Discover differences between different scoring criteria

USE CASES

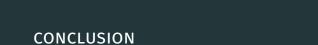
- · Identifying most or least mutated sites on a protein
- · Discover differences between different scoring criteria
- Benchmarking predictions

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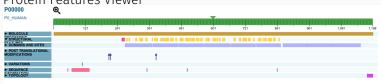
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- · Integration with Galaxy, web based bioinformatics workflows
- · Performance improvements
- · Interaction with 3D Protein viewer to highlight domains



SUMMARY

- · A tool for visualizing genetic variants
- · Limited applications as a standalone tool, more usable with Protein Features Viewer



- · Supports visualization of different levels of information
- · Cross component talks
- · User defined and user controlled
- Open Sourced(MIT License): https://github.com/saketkc/ biojs-genetic-variation-viewer

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