

# VISUALIZING GENOMIC DATA WITH PYTHON.

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# What are genomic data?

Genomic data refers to the genome and DNA data of an organism. They are used in bioinformatics for collecting, storing and processing the genomes of living things.



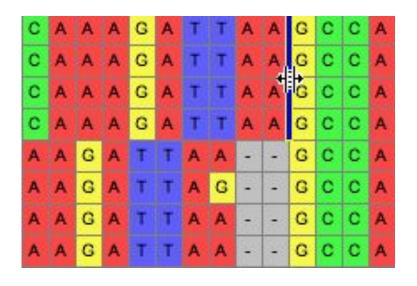


# **Challenges for visualization data**

- 1. What message should be conveyed by a particular plot?
- 2. Which methodologies should be used to represent the results in an easy, clear and accurate way to the users? I
- 3. Interpretation and visualization of genomic data, often consisting of thousands to billions of data points, and extracting biological meaning remains a serious challenge.



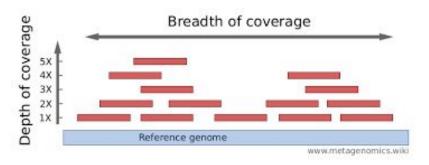
# **Alignment**

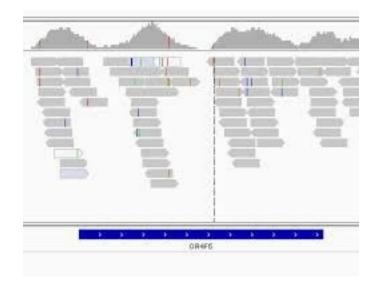




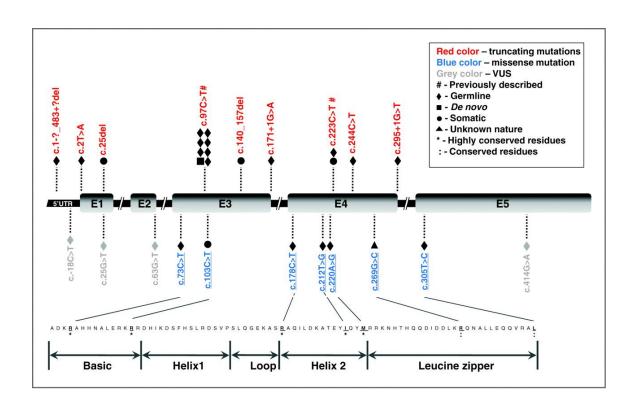


# **Coverage**



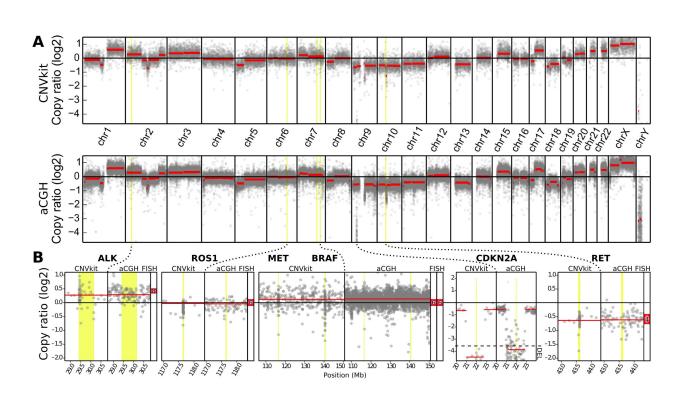


### **Variations**



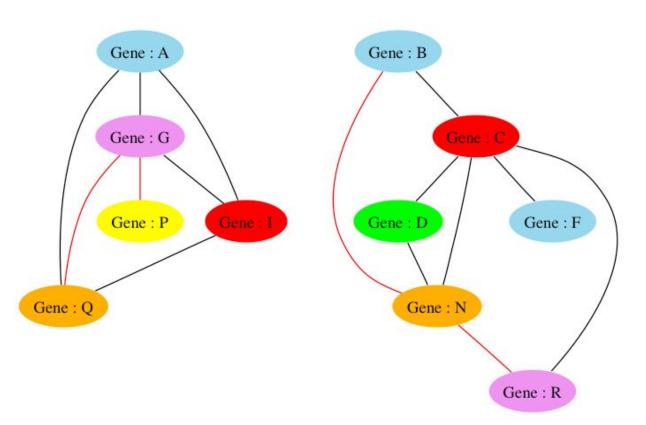


# **Copy Number Variation**



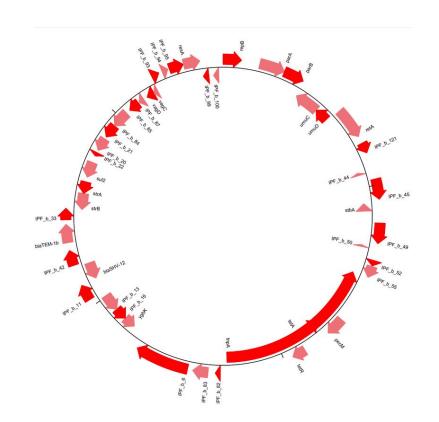


### **Gene network**





### Genome





### Visualization of genomic data

```
classmethod
def from_settings(
```

### DASH

Dash is a productive Python framework for building web applications.

Written on top of Flask, Plotly.js, and React.js, Dash is ideal for building data visualization apps with highly custom user interfaces in pure Python. It's particularly suited for anyone who works with data in Python.





# **DASH Component Libraries**

### Dash Core Components

The Dash Core Component library contains a set of higher-level components like sliders, graphs, dropdowns, tables, and more.

### Dash HTML Components

Dash provides all of the available HTML tags as user-friendly Python classes. This chapter explains how this works and the few important key differences between Dash HTML components and standard html.

### Dash DataTable

(New! Released Nov 2, 2018) The Dash DataTable is our latest and most advanced component. It is an interactive table that supports rich styling, conditional formatting, editing, sorting, filtering, and more.

### Dash DAQ Components

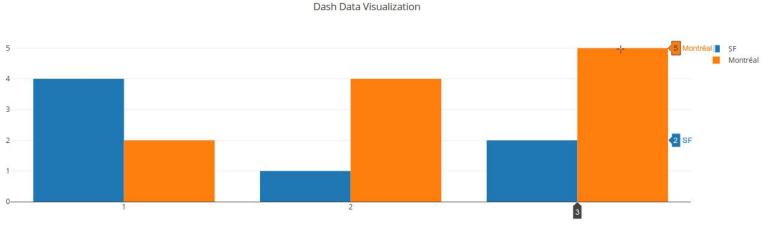
Beautifully styled technical components for data acquisition and engineering applications.

More info in https://dash.plot.ly/



### Hello Dash

Dash: A web application framework for Python.











# **DASH Component Libraries**

### Dash Canvas

(New! Released March 2019) Drawing and annotations for image processing.

### Dash Cytoscape

(New! Released Feb 5, 2019) Dash Cytoscape is our new network visualization component. It offers a declarative and pythonic interface to create beautiful, customizable, interactive and reactive graphs.

### Dash Bio Components

(New! Released April 2019) Components dedicated to visualizing bioinformatics data.

More info in https://dash.plot.ly/



### **DASH Bio**

pip install dash-bio==0.1.4

Dash is a web application framework that provides pure Python abstraction around HTML, CSS, and JavaScript.

Dash Bio is a suite of bioinformatics components that make it simpler to analyze and visualize bioinformatics data and interact with them in a Dash application.

The source can be found on GitHub at plotly/dash-bio.

These docs are using Dash Bio version 0.1.4.

```
>>> import dash_bio
>>> print(dash_bio.__version__)
0.1.4
```

More info in https://dash.plot.ly/



W-031011555.1	XM_USIBILESSS.I PREDUCTED: COFFICE GOFFICE GOFFICE GENERAL TESSOCIATED (EMENT), TRANSCRIPT VARIANT AF, RMWN
XM_031011554.1	>XM_031011554.1 PREDICTED: Gorilla gorilla BRCA1 DNA repair associated (BRCA1), transcript variant X3, mRNA

About

Explorer Controls

Enter a single GenBank accession ID or multiple ID's separated by commas and select the button to generate an alignment or the sequence of the dataset. Enter additional datasets to add these sequences to the alignment.

Example: Single Dataset - NR\_108049

Multiple Datasets - JF806202, HM161150, FJ356743, JF80620, JQ073190, GU457971, FJ356741, JF806

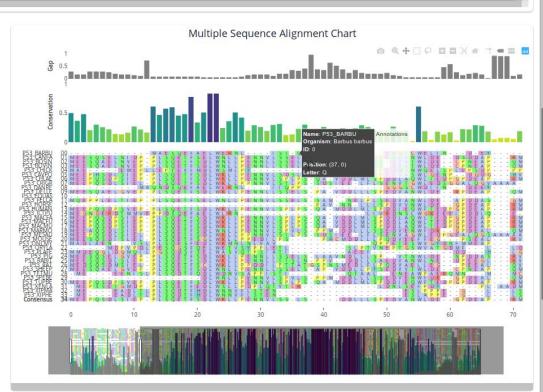
Enter an Accession ID...

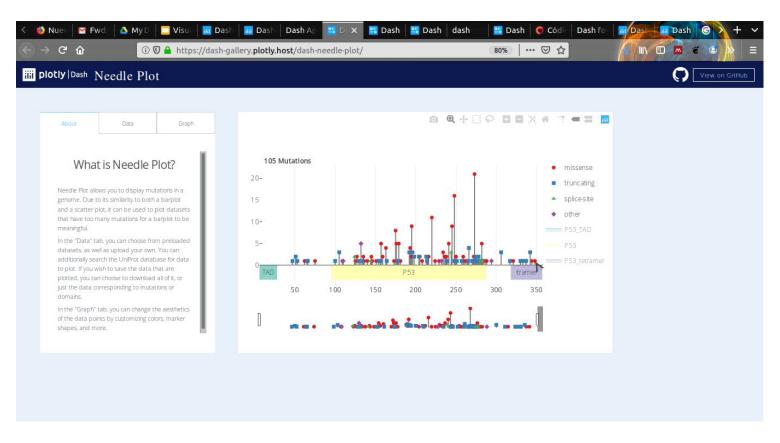
GENERATE SEQUENCE

GENERATE ALIGNMENT

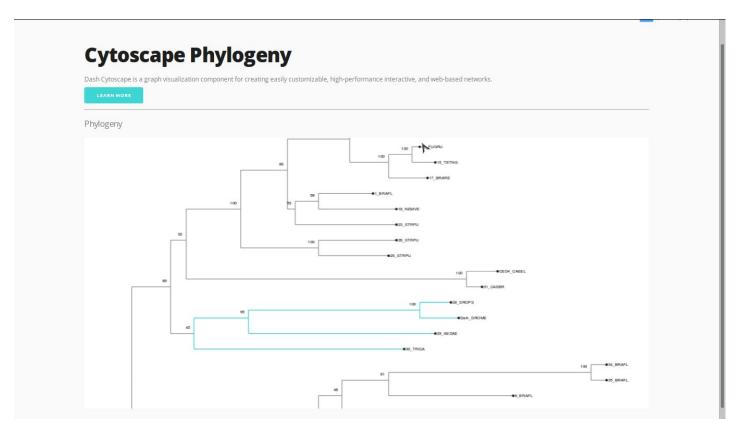
DOWNLOAD FASTA DATA

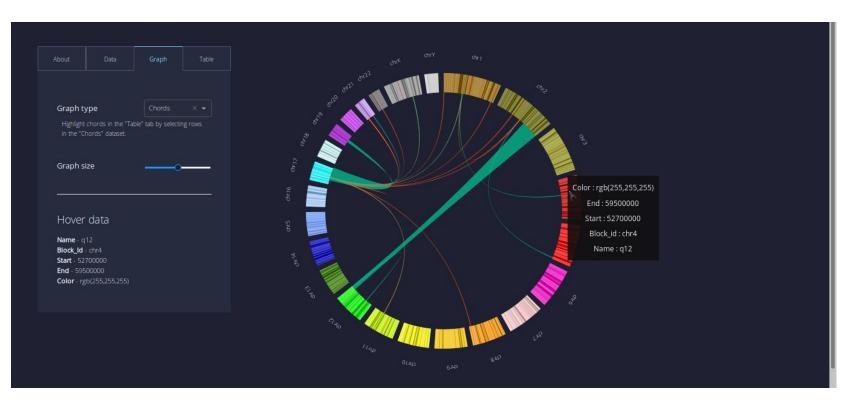
Drag and drop FASTA files or select files.













### Code

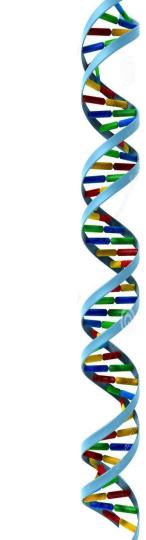
```
33
     @app.callback(
62
         dash.dependencies.Output('my-dashbio-manhattanplot', 'figure'),
         [dash.dependencies.Input('manhattanplot-input', 'value')]
64
     def update manhattanplot(threshold):
67
         return dashbio.ManhattanPlot(
             dataframe=df,
             genomewideline_value=threshold,
             suggestiveline_color='#AA00AA',
71
             genomewideline_color='#AA5500',
72
74
     if __name__ == '__main__':
         app.run_server(debug=True)
```



### **Video**

https://youtu.be/joVWIrmkEs4





Gracias ¿Preguntas?