a- plotly | Graphing Libraries (https://plotly.com/)(/graphing-libraries/)



Python (/python) > (/python/) > Alignment Chart

cutm_campaign=studio_cloud_launch&utm_content=sidebar)

• Suggest an edit to this page(https://github.com/plotly/plotly.py/edit/doc-prod/doc/python/bio-alignment-chart.md)

Alignment Chart in Python

tion

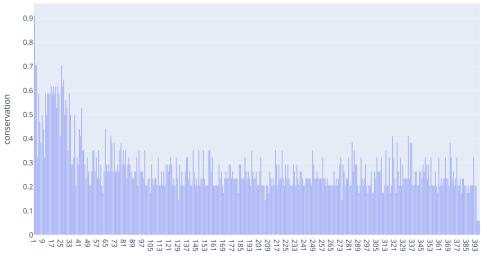
Plotly Studio: Transform any dataset into an interactive data application in minutes with Al. Sign up for early access now. (https://plotly.com/studio/?utm_medium=graphing_libraries&utm_campaign=studio_early_access&utm_content=sidebar)

Alignment Viewer

The Alignment Viewer (MSA) component is used to align multiple genomic or proteomic sequences from a FASTA or Clustal file. Among its extensive set of features, the multiple sequence alignment viewer can display multiple subplots showing gap and conservation info, alongside industry standard colorscale support and consensus sequence. No matter what size your alignment is, Alignment Viewer is able to display your genes or proteins snappily thanks to the underlying WebGL architecture powering the component. You can quickly scroll through your long sequence with a slider or a heatmap overview.

Note that the AlignmentChart only returns a chart of the sequence, while AlignmentViewer has integrated controls for colorscale, heatmaps, and subplots allowing you to interactively control your sequences.

Bar Chart for conservation visualization





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tion

Alignment Chart in dash_bio

```
import urllib.request as urlreq
from dash import Dash, html
                                                                                                                                                                                                                                          DOWNLOAD
import dash_bio as dashbio
app = Dash(__name__)
data = urlreq.urlopen('https://git.io/alignment_viewer_p53.fasta').read().decode('utf-8')
app.layout = html.Div([
       dashbio.AlignmentChart(
              id='alignment-viewer',
              data=data
])
if __name__ == '__main__':
      app.run(debug=True)
                       0.8
                      0.6
                       0.2
    P53_BARBU
  P53_BARBU
P53_CANFA
P53_BOSIN
P53_CHICK
P53_CHICK
P53_CHLAE
P53_CRIGR
P53_DANRE
P53_DAURE
P53_EQUAS
P53_FELCA
P53_FELCA
P53_HUMAN
P53_ICTPU
P53_MACFA
P53_MACFA
P53_MACFA
  P53_MACFU
P53_MACMU
P53_MASMO
P53_MESAU
P53_MOUSE
P53_ONCMY
P53_ORYLA
P53_PLAFE
P53_PLAFE
    P53_RABIT
P53_RAT
P53_SHEEP
   P53_SEEP
P53_TETMU
P53_SPEBE
P53_TUPBE
P53_XENLA
P53_XIPMA
```



What About Dash?

<u>Dash (https://dash.plot.ly/)</u> is an open-source framework for building analytical applications, with no Javascript required, and it is tightly integrated with the Plotly graphing library.

Learn about how to install Dash at https://dash.plot.ly/installation (https://dash.plot.ly/installation).

Everywhere in this page that you see fig.show(), you can display the same figure in a Dash application by passing it to the figure argument of the <u>Graph component</u> (https://dash.plot.ly/dash-core-components/graph) from the built-in dash_core_components package like this:

tion

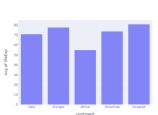
```
import plotly.graph_objects as go # or plotly.express as px
fig = go.Figure() # or any Plotly Express function e.g. px.bar(...)
# fig.add_trace( ... )
# fig.update_layout( ... )

from dash import Dash, dcc, html

app = Dash()
app.layout = html.Div([
    dcc.Graph(figure=fig)
])

app.run(debug=True, use_reloader=False) # Turn off reloader if inside Jupyter
```





(https://dash.plotly.com/tutorial?utm_medium=graphing_libraries&utm_content=python_footer)

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