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APPLIED LIFE SCIENCES | MASTERSTUDIENGANG BIOINFORMATIK

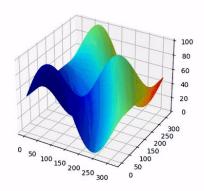


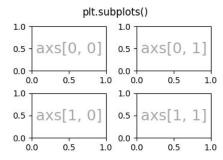


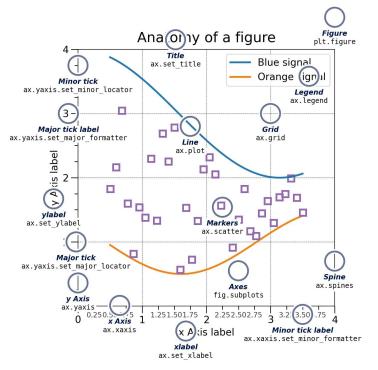
Motivation und Überblick

- Python-Library zur Erstellung statischer und interaktiver Datenvisualisierungen
- Sehr customizable
- Gut mit numpy integriert (und pandas)
 - Arbeiten mit Arrays
- Python-Alternative zu MatLab
- Animation von Daten möglich

import matplotlib.pyplot as plt
import numpy as np



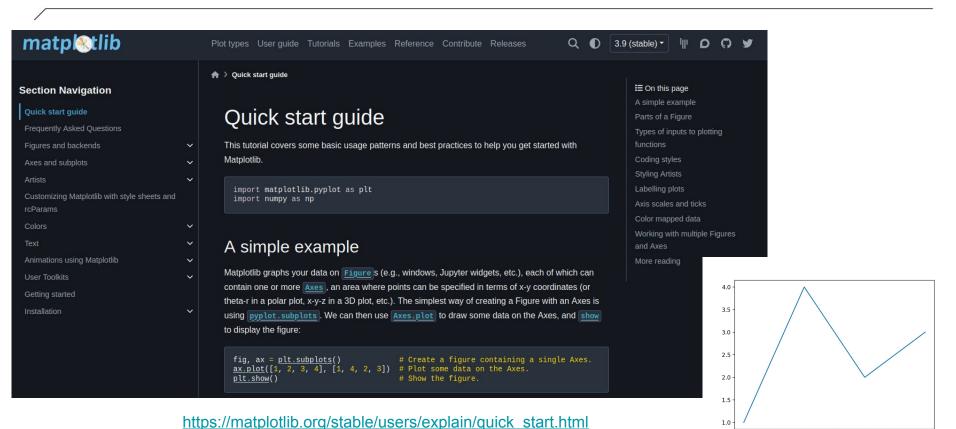




```
fig, ax = plt.subplots(figsize=(5, 2.7), layout='constrained')
categories = ['turnips', 'rutabaga', 'cucumber', 'pumpkins']
ax.bar(categories, np.random.rand(len(categories)))
```

```
fig, ax = plt.subplots()
ax.set_title("This is the title")
ax.set_xlabel("This is the x-Axis label")
ax.grid(True)
plt.show()
```





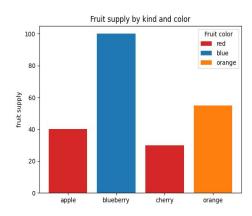
1.5

2.5

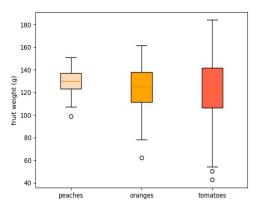
3.0



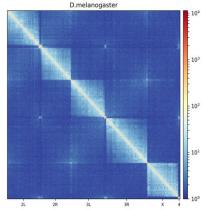
Diagramm- und Datentypen



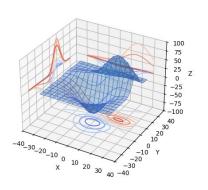
Pairwise data (x,y)



Statistical distributions



Gridded data
(arrays and images plotted on coordinate grids)



3D and volumetric data



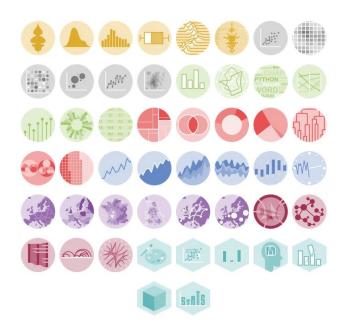
Diagramm- und Datentypen (2)

Python graph gallery

 Nützliche Ressource für mögliche Darstellungsarten

Matplotlib Cheat-Sheets

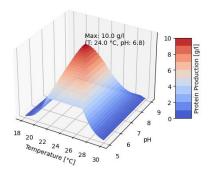
 Schnelle Hilfestellung zum Formatieren & Erstellen von Plots





Bioinformatische Anwendungen

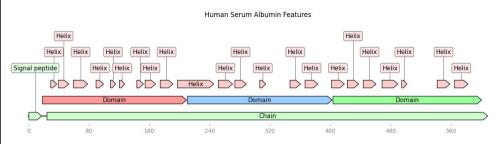
- Datenvisualisierung allgemein
- Verwendung in Kombination mit Biopython
- Phylogenetische Bäume
- Operative taxonomische Einheit (OTE) Visualisierung
- Genome/Sequenz Visualisierung (z.B. GC content, duplication rates)
- Genexpression Heatmaps
- Design of Experiment (DoE)
- Proteinstruktur
- ... und viel mehr





Beispiel: DNA Features Viewer Package

```
import matplotlib.pyplot as plt
from dna_features_viewer import GraphicFeature, GraphicRecord
def filter_short_features(features, min_length):
   return [feature for feature in features if feature.end - feature.start + 1 ≥ min_length]
def set_feature_color(feature_type, domain_index, domain_colors):
   if "domain" in feature_type.lower():
        color = domain_colors[domain_index % len(domain_colors)]
        domain_index += 1
   elif "helix" in feature_type.lower():
        color = "#ffcccc"
   elif "beta" in feature_type.lower():
       color = "#cceeff"
        color = "#ccffcc"
   return color, domain_index
record = GraphicRecord(sequence_length=sequence_length, features=features)
ax, _ = record.plot(figure_width=15, with_ruler=True)
plt.title("Human Serum Albumin Visualization (Capitalized Labels)")
plt.savefig("human_serum_albumin.png")
plt.show()
```





Beispiel: Quick Live Coding Session

Collab Link (download or view):

Copy of Input Matplotlib.ipynb