

PyComplexHeatmap: A Python package to visualize multimodal genomics data

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<https://github.com/DingWB/PyComplexHeatmap>

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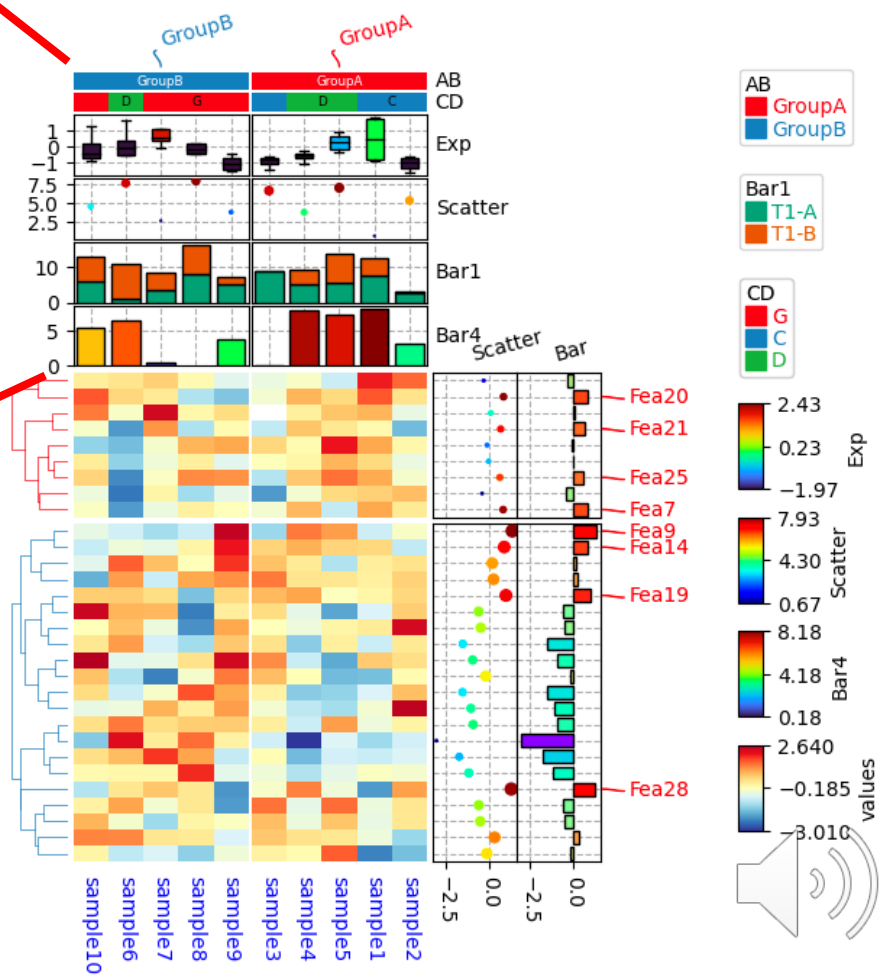
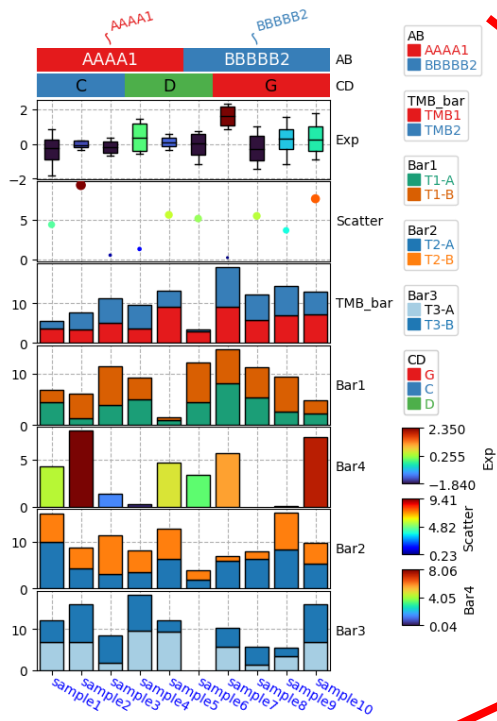
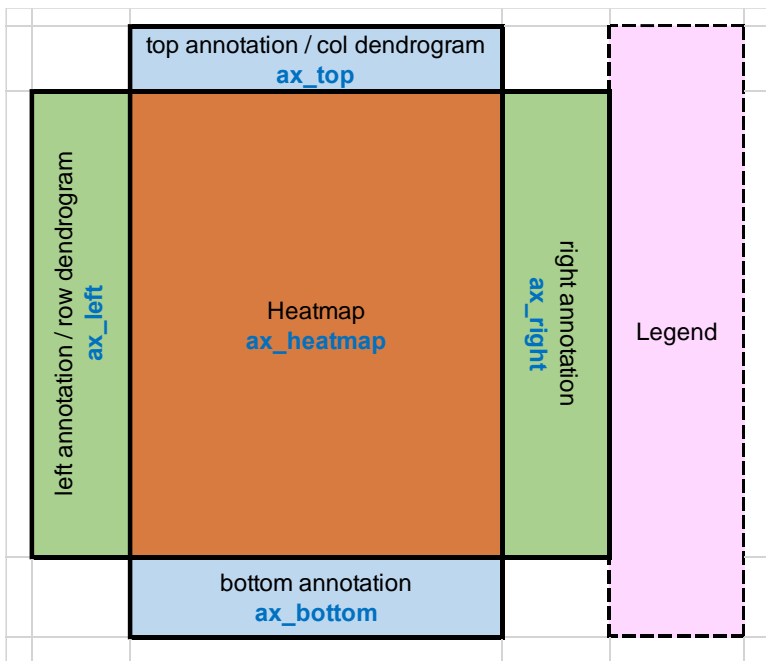


Introduction

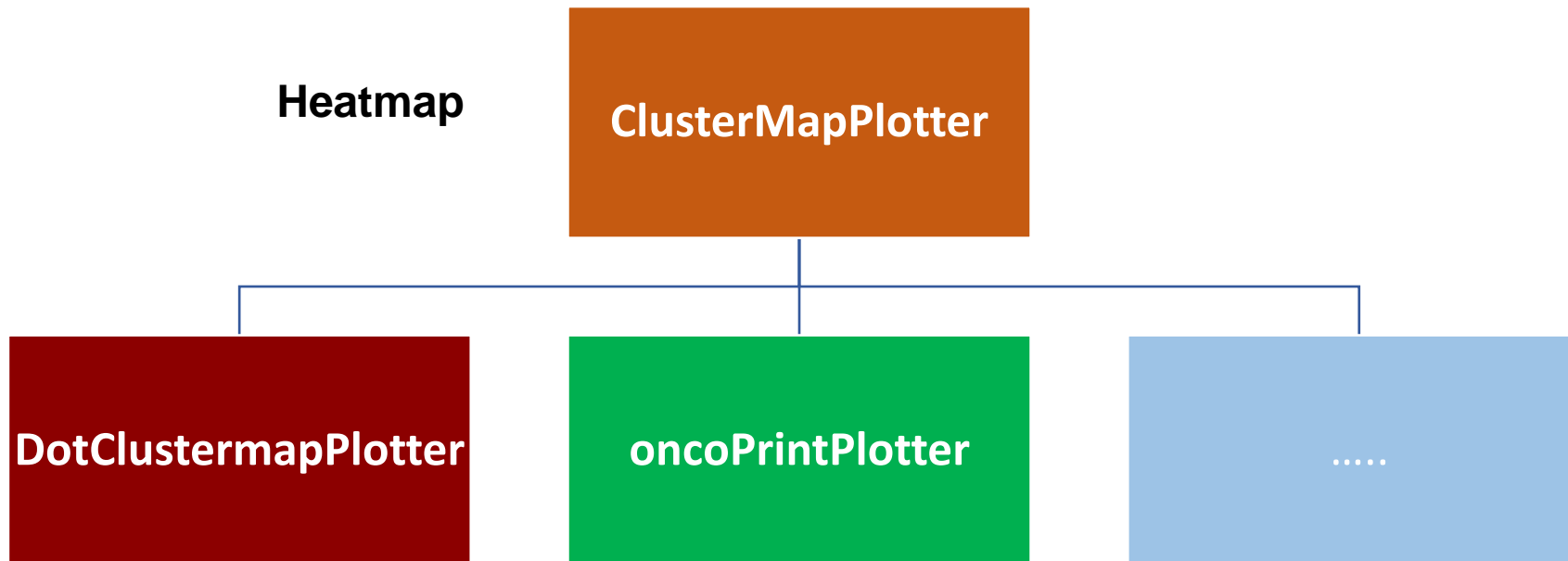
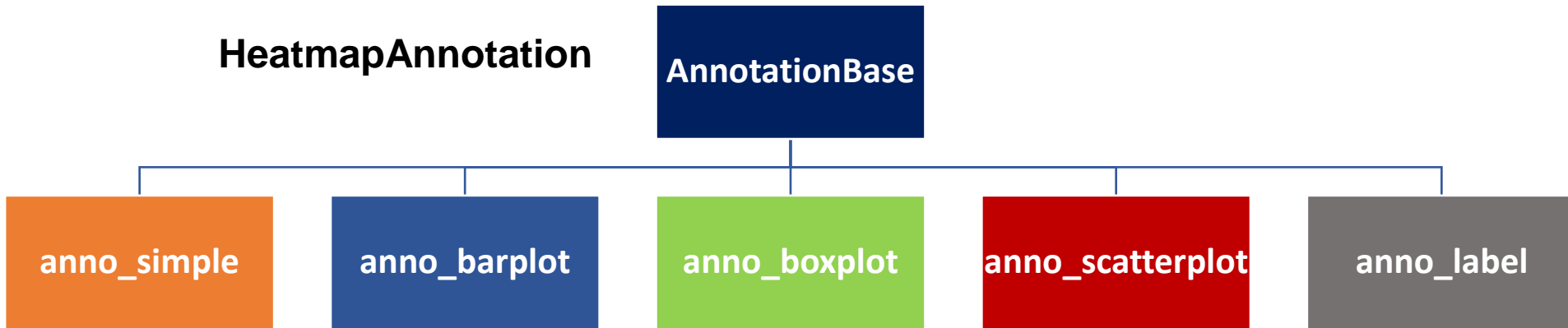
- The popularity of Python in bioinformatic single cell data analysis and **machine learning & deep learning** (SCANPY, EpiScanpy, scVelo, PyDESeq2, GSEAPy and so on).
- Compared with R, what hinders the application of python in single-cell data analysis is data visualization, especially for the complex heatmaps.
- To fill this gap in Python, we developed a Python package, PyComplexHeatmap, which allow Python user to visualize **multidimensional biological data** easily.



Layout



Implementation

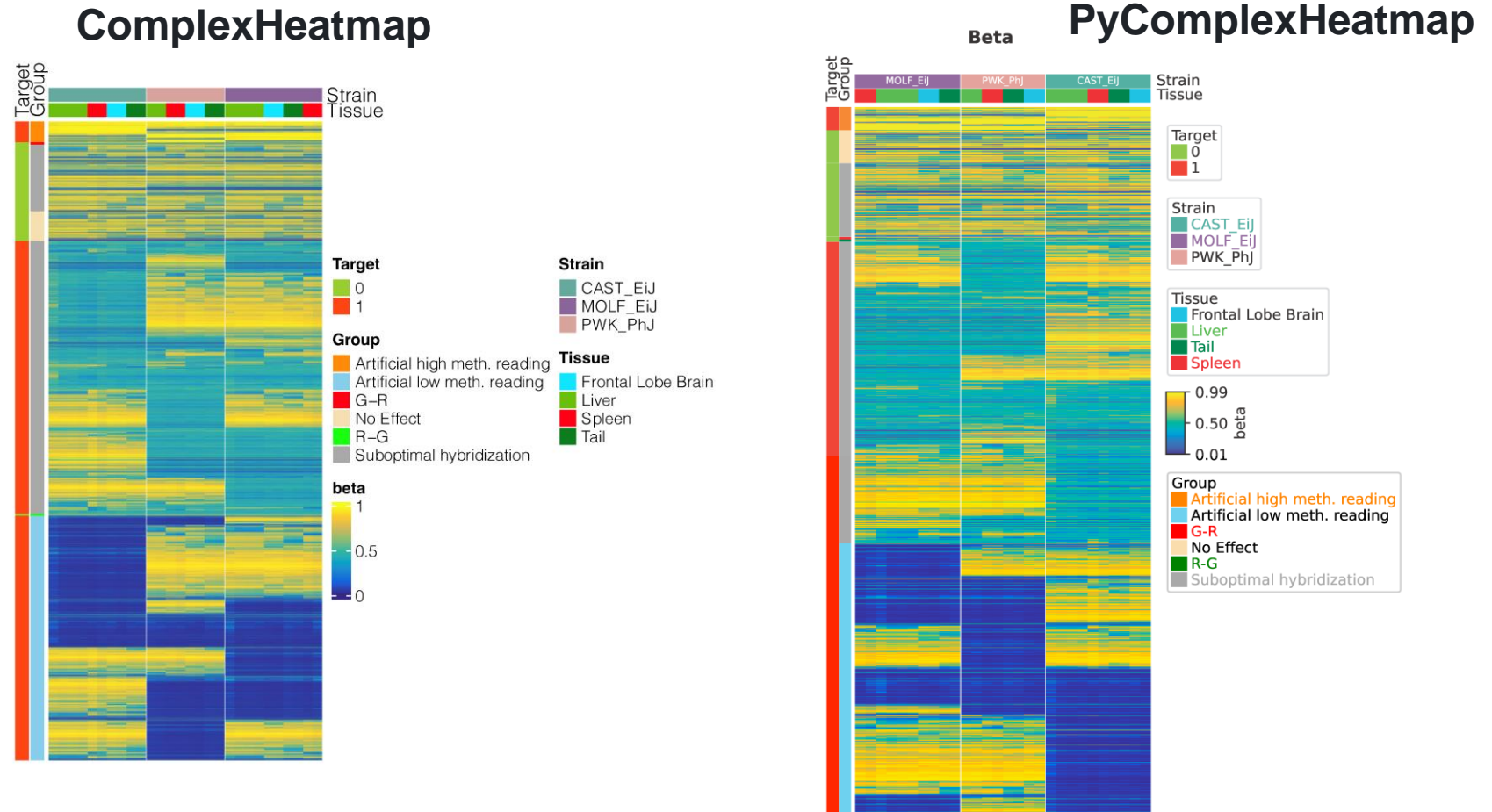


Compared with other Python packages

	PyComplexHeatmap	matplotlib	seaborn	ComplexHeatmap	Description
Version	1.3.8	3.7.1	0.12	2.13.1	Test version
URL	https://github.com/DingWB/PyComplexHeatmap	https://github.com/matplotlib/matplotlib	https://github.com/mwaskom/seaborn	https://github.com/ioker/goo/ComplexHeatmap	Github link
Language	Python	Python	Python	R	Programming Language
Row / Columns scale	✓	×	✓	×	Scale rows or columns using standard scale or z score
Clustering	✓	×	✓	✓	Clustering rows and columns using different clustering methods and metrics
Heatmap Split	✓	×	×	✓	Split rows or columns using int number or given annotations
Support Missing Values	✓	×	×	✓	Whether support matrix containing NaN (missing values)
Heatmap Annotations	✓	×	custom function	✓	Add different kinds of annotations, including simple annotation, barplot, boxplot and scatterplot annotations
Text Annotations	Automatically	×	×	anno_block	Add text on the top of simple annotations
Float Annotated Heatmaps	✓	custom function	✓	custom function	Add float values on the top of heatmap cells
Heatmap Splicing	✓	×	×	✓	Combine multiple heatmap vertically or horizontal to generate a joint figure
Support Dot Heatmap	✓	×	✓	custom function	Plot dot heatmap using different size, colormap and marker for different categories
Dot Heatmap Annotations	✓	×	custom function	✓	Add rows/cols annotations to scatterplot heatmap
Plot Legends Separately	✓	×	×	packLegend	Plot the figure legends together or separately in another figure
Plot Annotations Separately	✓	×	×	✓	Plot the heatmap annotations together or separately in another figure
OncoPrint	✓	×	×	✓	Support oncoPrint
Label Annotations	Automatically Distributed	×	×	Manually Distributed	Add labels annotations to show the interested rows or columns and merge the labels of the rows/cols belonging to the same group and distribute them evenly throughout the axis without overlapping



Compared with R ComplexHeatmap



Package Name	Processing Time (s)	Memory (kb)
ComplexHeatmap	40.21	3,366,768
PyComplexHeatmap	22.57	1,037,944



Applications

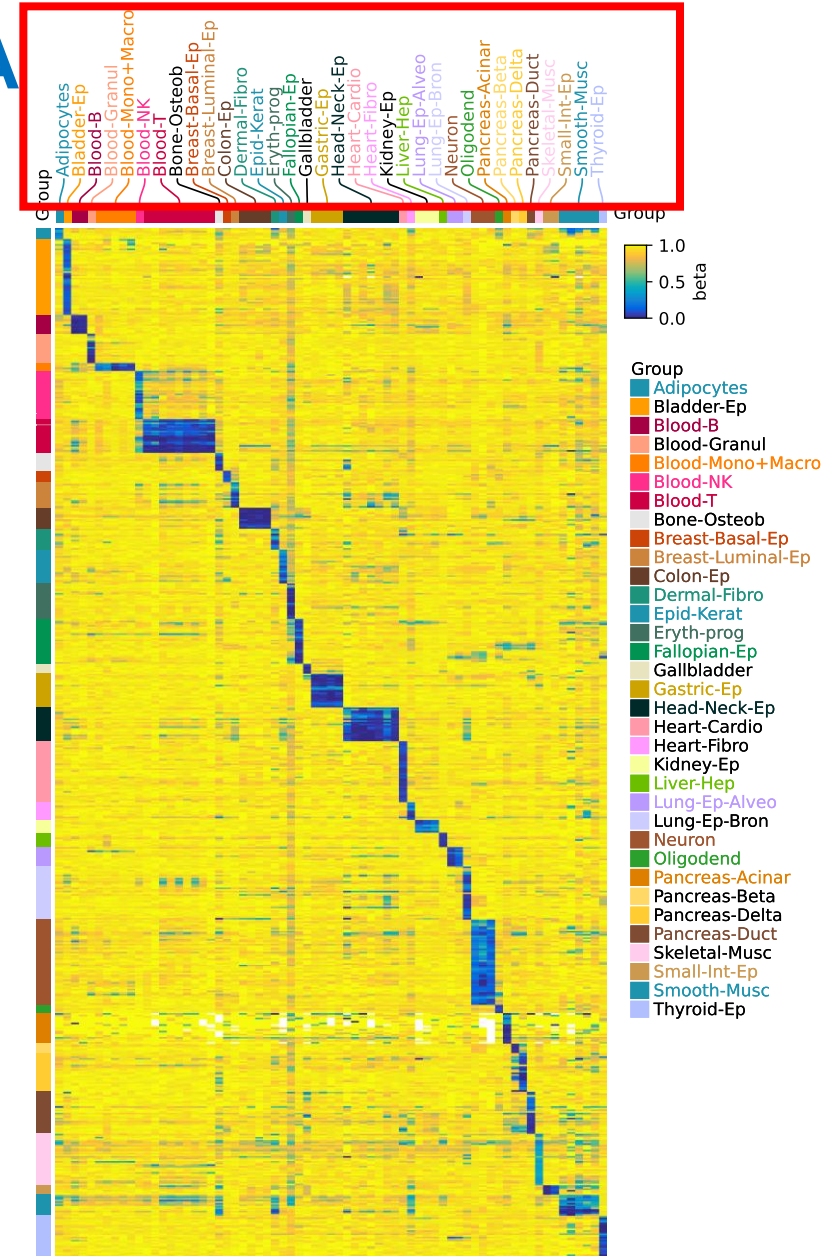
Visualization of cell type specific DNA methylation markers

```
col_colors_dict={
    'Adipocytes': '#1E93AE', 'Bladder-Ep': '#FF9C00', 'Blood-B': '#A40043', 'Blood-Granul': '#FF9F
    'Blood-Mono+Macro': '#FF7F00', 'Blood-NK': '#FF2E8D', 'Blood-T': '#CC0043', 'Bone-Osteob': '#E
    'Breast-Basal-Ep': '#CC4407', 'Breast-Luminal-Ep': '#CC843D', 'Colon-Ep': '#663D28', 'Dermal-
    'Epid-Kerat': '#1E93AE', 'Eryth-prog': '#40705F', 'Fallopian-Ep': '#009351', 'Gallbladder': '#
    'Gastric-Ep': '#CCA300', 'Head-Neck-Ep': '#002929', 'Heart-Cardio': '#FF99AA', 'Heart-Fibro':
    'Kidney-Ep': '#F6FF99', 'Liver-Hep': '#6CBF00', 'Lung-Ep-Alveo': '#BA99FF', 'Lung-Ep-Bron': '#
    'Neuron': '#9e542e', 'Oligodend': '#2ca02c', 'Pancreas-Acinar': '#DF7F00', 'Pancreas-Beta': '#
    'Pancreas-Delta': '#FFCC32', 'Pancreas-Duct': '#7F4C33', 'Skeletal-Musc': '#FFCCEE', 'Small-I
    'Smooth-Musc': '#1E93AE', 'Thyroid-Ep': '#B2BFFF'}

col_ha = HeatmapAnnotation(label=anno_label(df_col['Group'],merge=True,rotation=90,extend=True,
    colors=col_colors_dict,adjust_color=True,luminance=0.75,
    relpos=(0.5,0)), #fontsize=10
    Group=anno_simple(df_col['Group'],colors=col_colors_dict), #legend_kws={'fon
    verbose=0,axis=1)

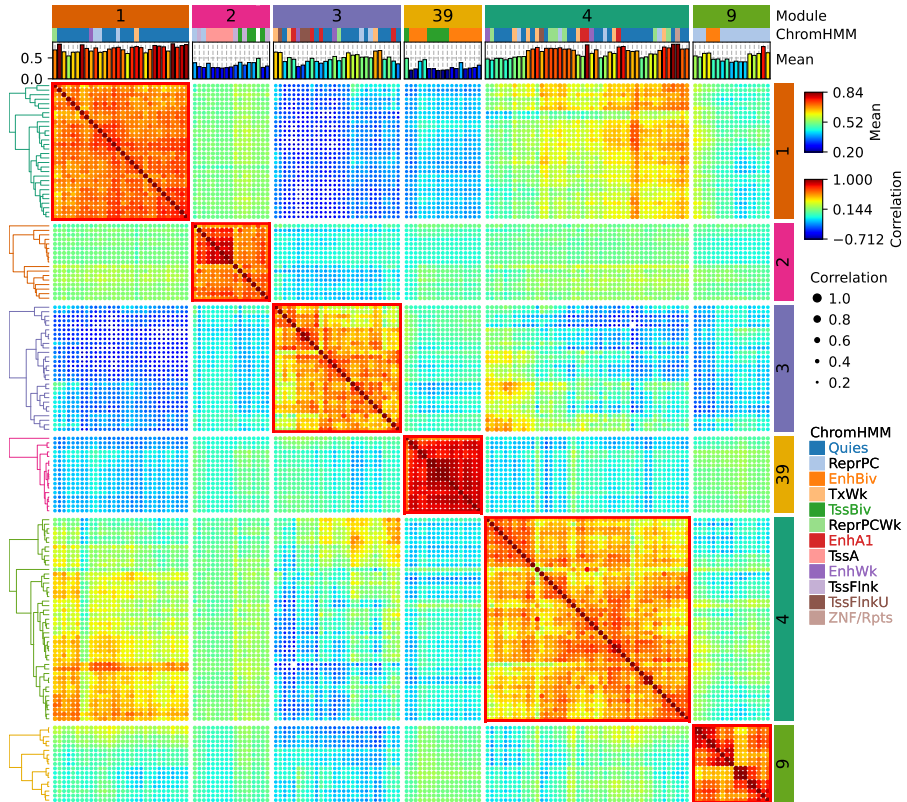
row_ha = HeatmapAnnotation(
    Group=anno_simple(df_row['Group'],legend=True,
    colors=col_ha.annotations[1].color_dict),
    verbose=0,axis=0,plot_legend=False) #label_kws={'rotation':90,'rotation_mode

plt.figure(figsize=(6, 10))
cm = ClusterMapPlotter(data=data.loc[df_row.index.tolist(),df_col.index.tolist()],
    top_annotation=col_ha, left_annotation=row_ha,
    row_cluster=False,col_cluster=False,
    label='beta', row_dendrogram=False,legend_gap=7,
    cmap='parula',rasterized=True)
plt.savefig("Loyfer2023_heatmap.pdf",bbox_inches='tight')
plt.show()
```

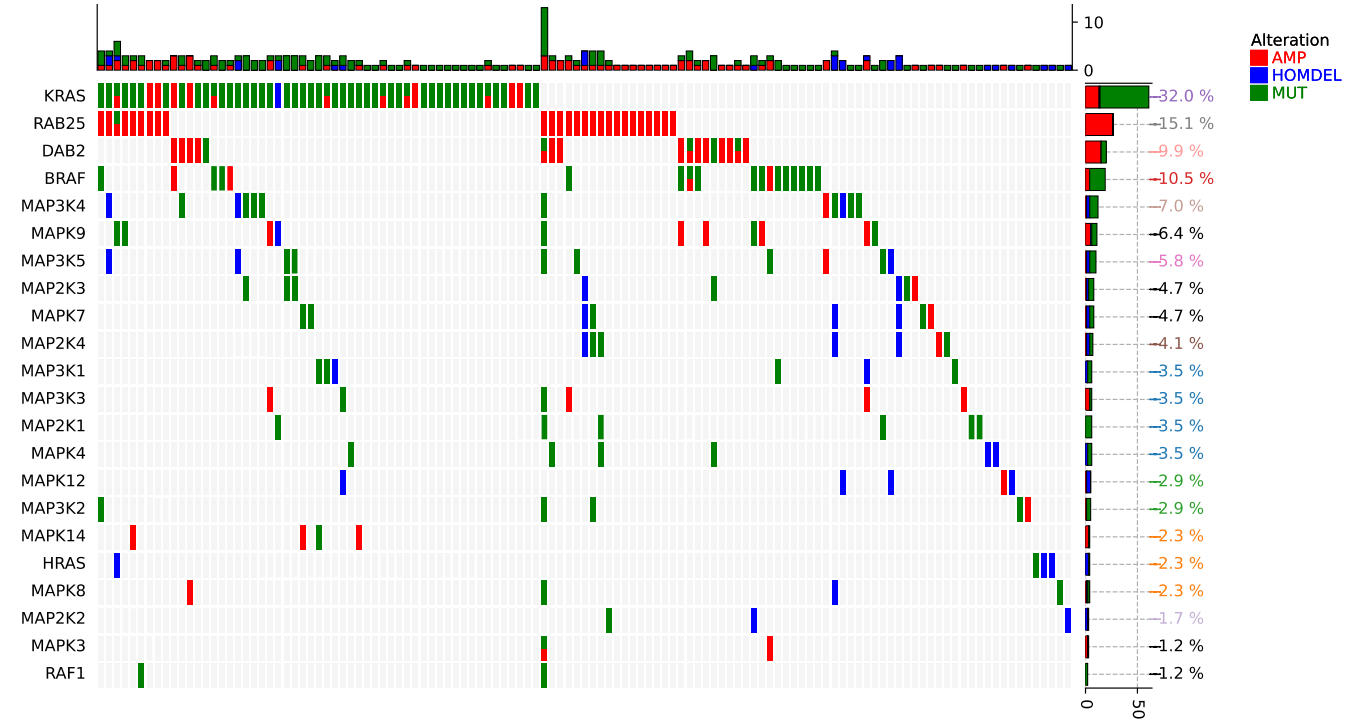


Applications

■ Dot heatmap



■ OncoPrint



Applications

- Combine two heatmaps horizontally



Conclusions

- We introduced PyComplexHeatmap, a versatile and user-friendly Python package, to fill the multidimensional data visualization gap in the Python-based data science ecosystem.
- We showcased the main features of PyComplexHeatmap in rendering complex biological datasets with rich annotations. Our benchmark indicated improved computational efficiency over the R implementation.
- We demonstrated its power in advanced genomics data analysis, including rendering the OncoPrint and dot heatmap.





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