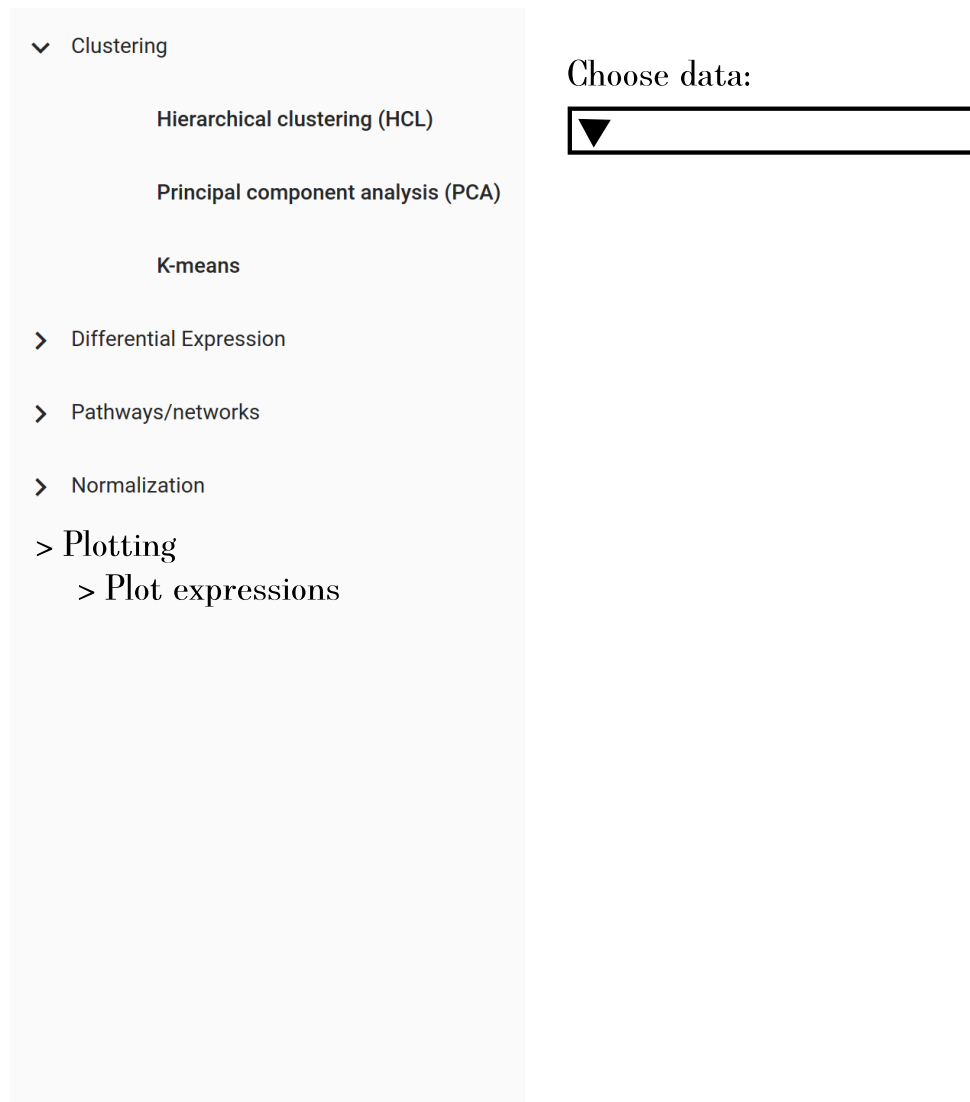


Some ideas for an additional frontend-only plotting module

I could see this being the output view for the normalization methods, but maybe it's better to make this as an additional "analysis" like the others? e.g. adding to the left-side menu

Here, the dropdown would give a list of options for files of type MTX, I_MTX, EXP_MTX, etc. (any numerical matrix)



After choosing the matrix, I suppose we could do two things:

- Make a request to `api/resources/<uuid>/contents/?page=1` to get the initial boxplot of expressions for "random" genes.
- *Do not* show the initial boxplot, but instead ask them to filter the table *or* select a `FeatureSet` from a dropdown. Additionally, could ask them to choose `ObservationSets`. When they are done with their choices, click "plot"

The second option probably makes the most sense (instead of wasting time plotting random data).

One consideration in terms of performance-- does it make more sense to get *everything* and then cache it front-end (the old MEV seems to do that)? Alternatively, I could look into caching mechanisms on the backend...loading the file from disk each time a request is made could be slow.

Anyway, if the user does not select any `ObservationSet`s, then we create a boxplot showing the distribution of expressions across all samples (for the selected genes).

▼ Clustering

Hierarchical clustering (HCL)

Principal component analysis (PCA)

K-means

> Differential Expression

> Pathways/networks

> Normalization

> Plotting

> Plot expressions

Plot genes by:
Feature set:

▼

or by filtering the table:

Gene	S1	S2	...	Sn
g1				
g2				
...				
gp				

Group observations by:

☐ Cntrl

☐ Exp

☐ groupA

☐ groupB

If the user selected more than one `ObservationSet`, then create a boxplot like we currently do for the differential expression analyses. Ideally, we could have any number of `ObservationSet`s shown in the plot.

▼ Clustering

Hierarchical clustering (HCL)

Principal component analysis (PCA)

K-means

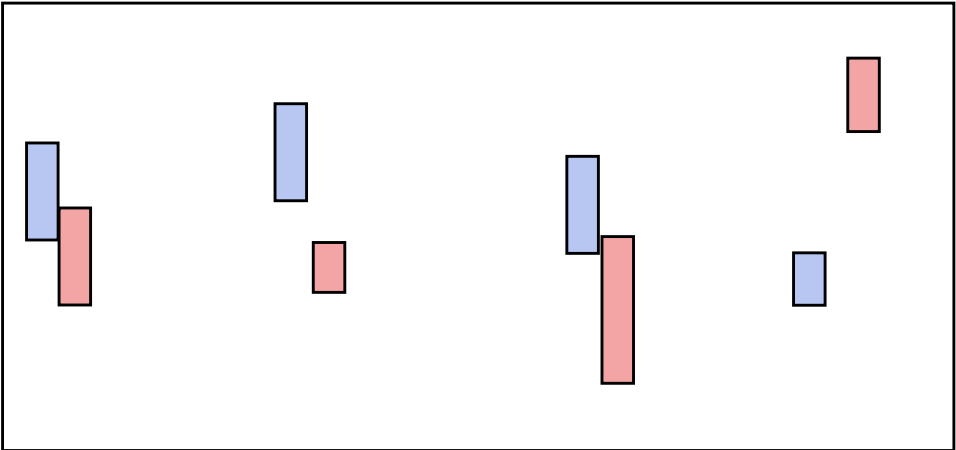
> Differential Expression

> Pathways/networks

> Normalization

> Plotting

>> Plot expressions



Plot genes by:
Feature set:

▼

or by filtering the table:

Gene	S1	S2	...	Sn
g1				
g2				
...				
gp				

Group observations by:

- ☒ Cntrl
- ☒ Exp
- ☐ groupA
- ☐ groupB

