

Introduction to exploring morphological profile data with Morpheus

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Morpheus - <https://software.broadinstitute.org/morpheus/>



Open

All data is processed on your computer and never sent to any server.

My Computer

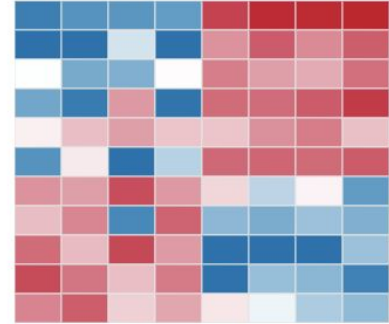
URL

Dropbox

Preloaded Datasets

Select File

or Copy and Paste Clipboard Data, Drag and Drop



MORPHEUS

Versatile matrix visualization and analysis software

View your dataset as a heat map, then explore the interactive tools in Morpheus. Cluster, create new annotations, search, filter, sort, display charts, and more.

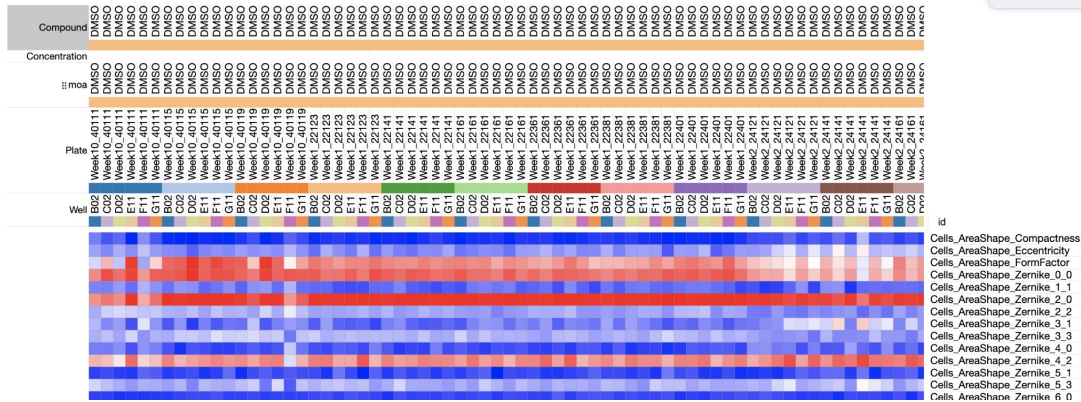
30,000+ users

100,000+ matrices analyzed.

If you use Morpheus for published work, please cite:
Morpheus, <https://software.broadinstitute.org/morpheus>

Drag and drop CSVs, GCTs, or Morpheus- created JSON files

1 - Change column annotations to something useful



Options

Annotations

Color Scheme

Display

Row annotations

id

All | None

Column annotations

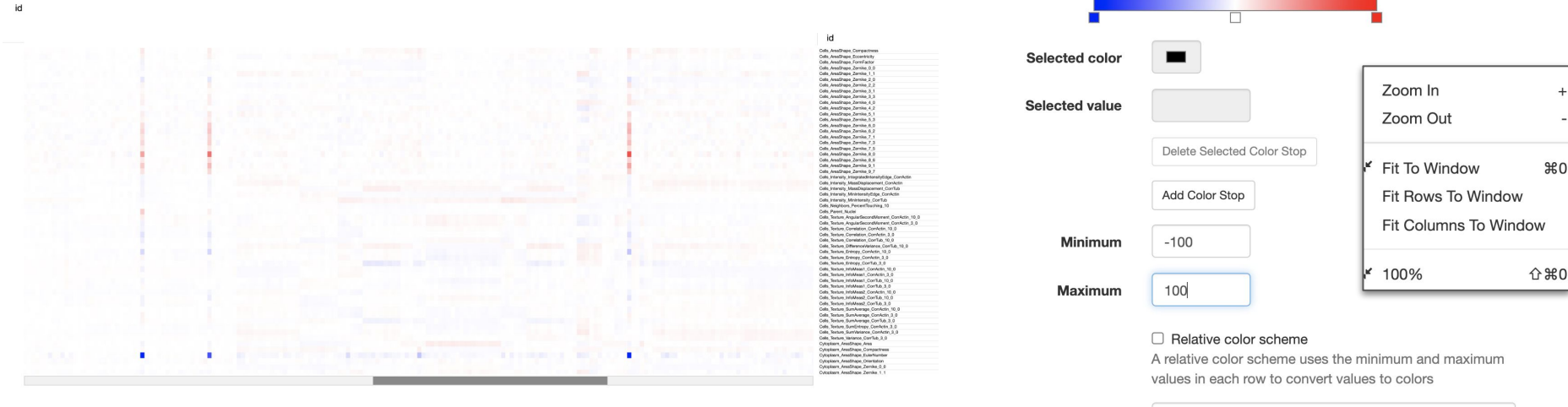
5 items selected


Compound
Concentration
id
moa
Plate
Well

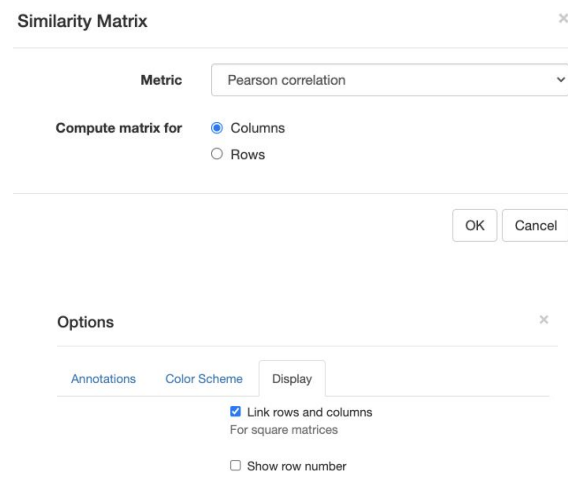




Options -> Annotation, optionally then right click each annotation to add color

2 - Change color displays to make it easier to look for aberrant rows/columns

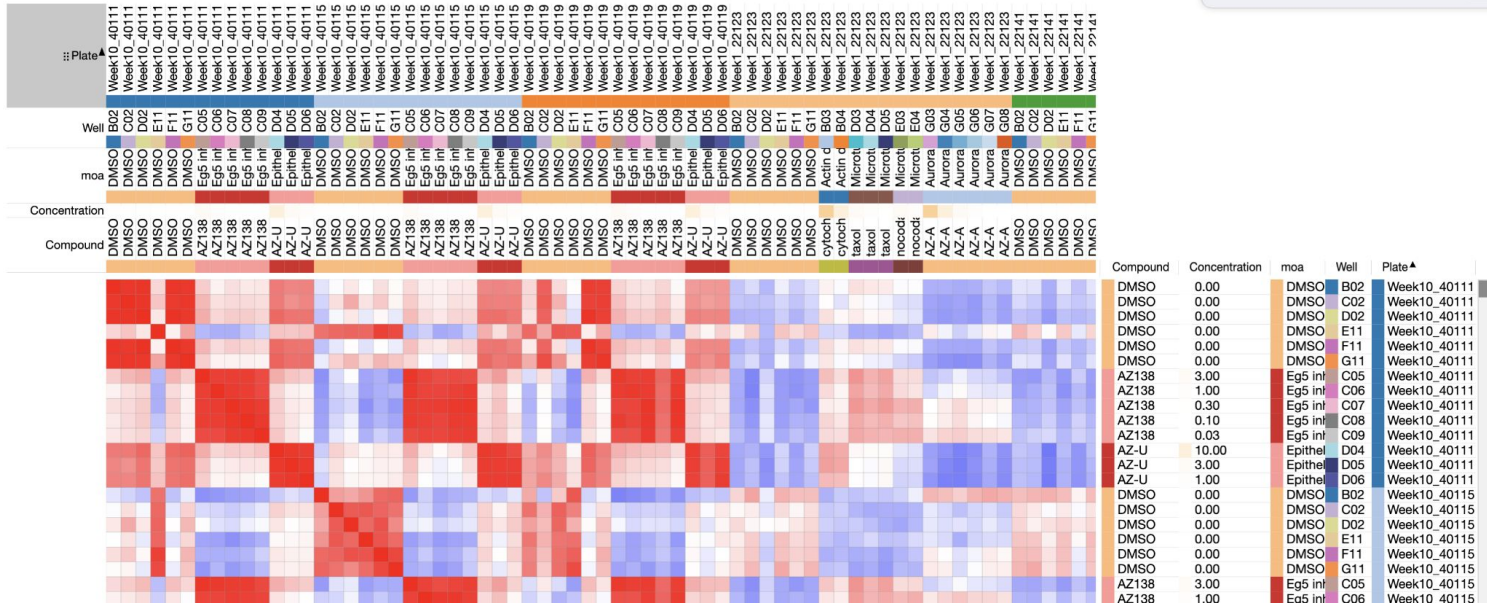


Options -> Color Scheme, then uncheck “Relative color scheme” and set minimum and maximum to -100 and 100. Close, and then  zoom to “fit to window”. Be sure to return display to “Relative color scheme” before continuing.



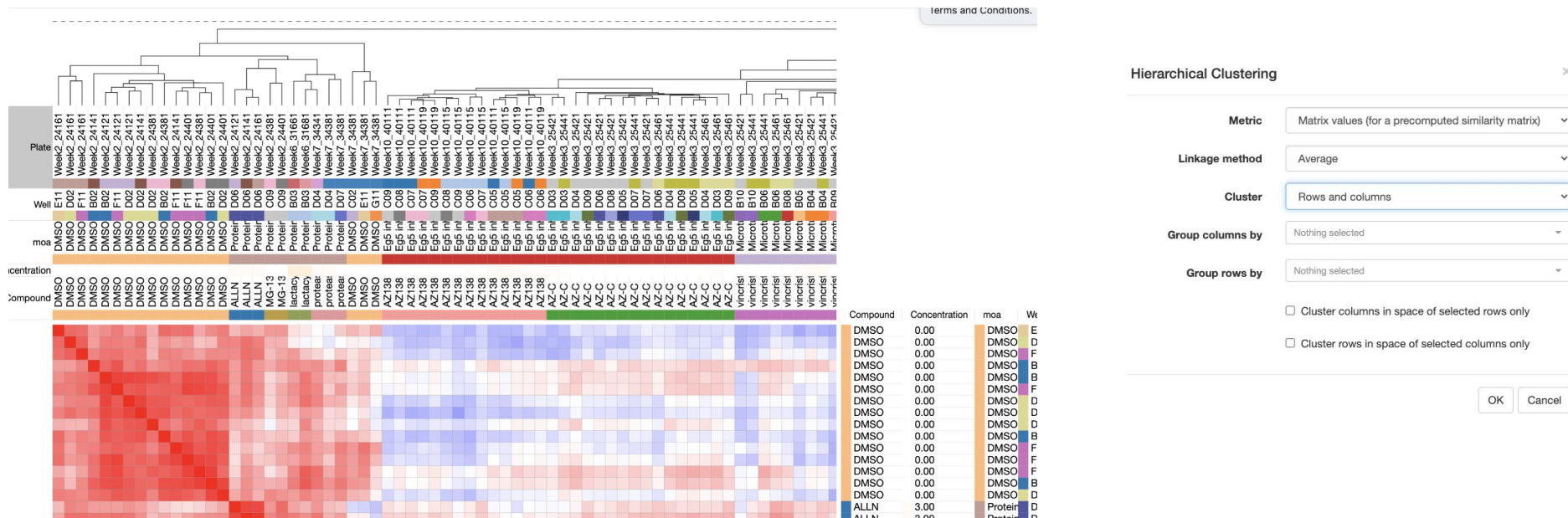
Tools -> Similarity Matrix -> Pearson/Columns then  Options -> Display -> Link rows and columns.  Zoom in and out as needed.

4 - Create a similarity matrix, look clustering by plate



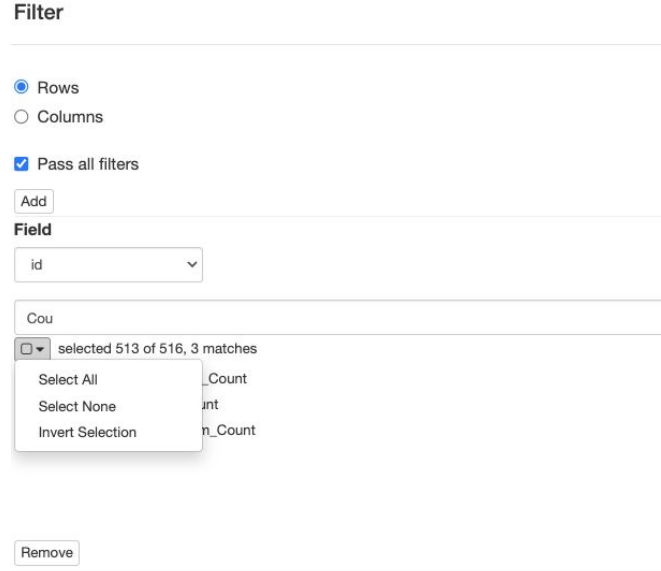
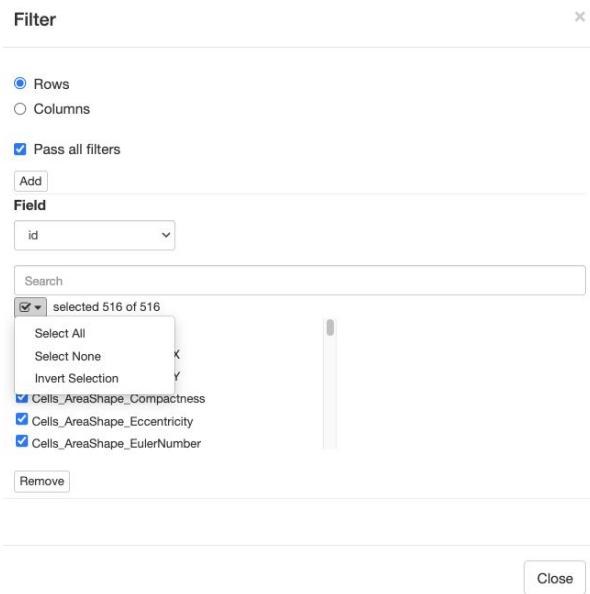
Change sorting by clicking the variable you want to sort by. Holding shift before clicking an additional variable (or variables) will allow you to sort by multiple variables, with the sorting tier indicated by a number next to the arrow.

5 - Look at the clustering of the similarity matrix



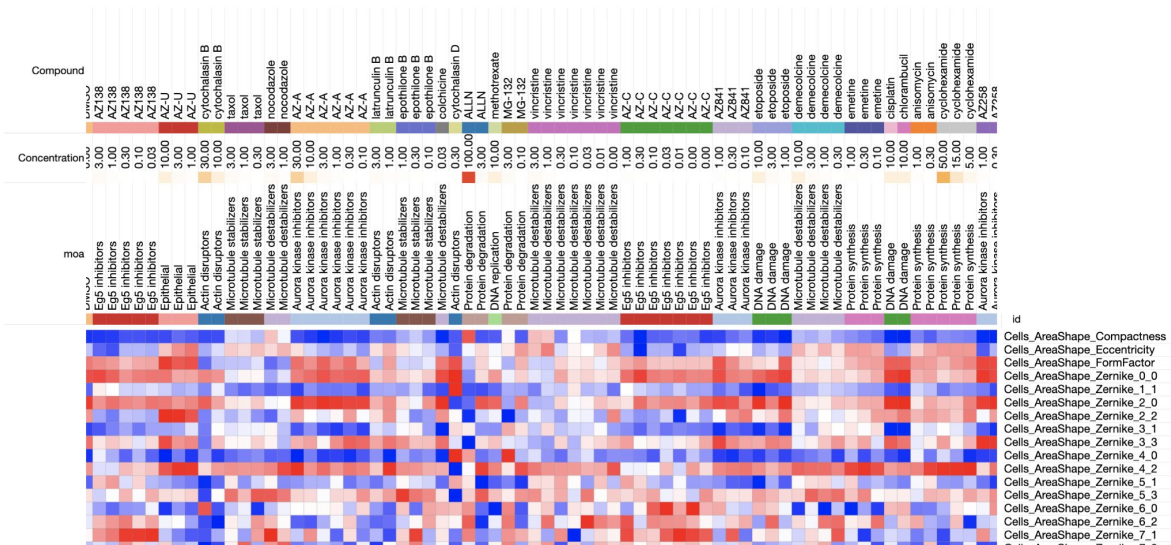
Tools -> Hierarchical Clustering -> Precomputed similarity matrix/ Rows and columns

6 - Filter out troubling features



Tools -> Filter -> Rows -> Add -> Select all, then type enough of the feature name you want to remove and uncheck it or hit “Select None”. Hit close when done.

7 - Collapse all replicates to make it easier to look at MOA associations



Collapse

Collapse method

Median

Collapse

☒ Columns

☐ Rows

Collapse to fields

Compound

Concentration

id

moa

...

☐ Compute percent

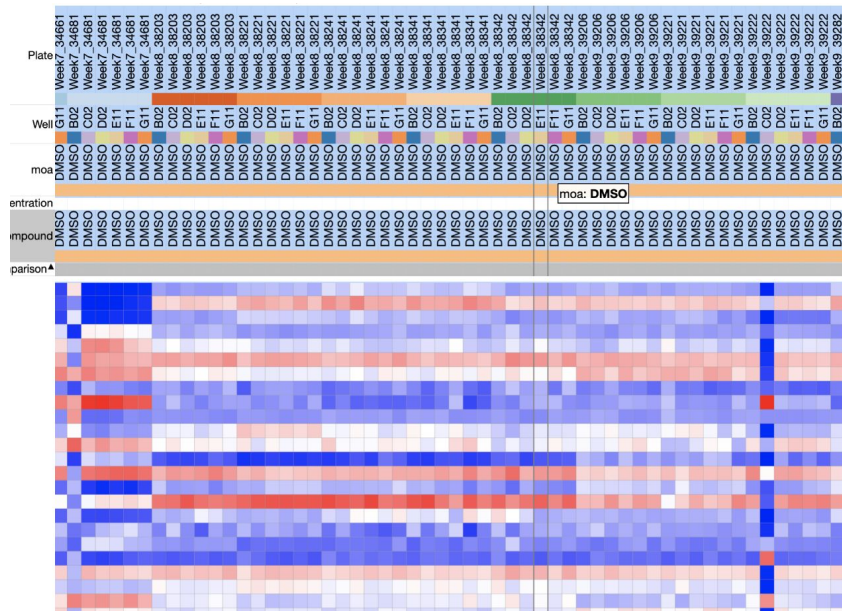
Whether to calculate the percentage of items in a collapsed group that passed an expression

OK

Cancel

From feature data -> Tools -> Collapse -> Median/Columns/Compound, Concentration, and moa (hold shift to select multiple options), then follow previous instructions to create a similarity matrix on the collapsed data

8 - See which features drive particular strong phenotypes



id	T-Test	p_value	FDR(BH) ▲
Cytoplasm_AreaShape_Area	-15.45	0.00	0.00
Cytoplasm_AreaShape_Zernike_2_0	-10.67	0.00	0.00
Cytoplasm_Intensity_IntegratedIntensity_CorrActin	-13.12	0.00	0.00
Cytoplasm_Texture_DifferenceVariance_CorrActin_10_0	10.90	0.00	0.00
Nuclei_Texture_Contrast_CorrActin_10_0	11.83	0.00	0.00
Nuclei_Texture_DifferenceVariance_CorrDAPI_10_0	12.00	0.00	0.00
Nuclei_Texture_InfoMeas2_CorrTub_10_0	12.21	0.00	0.00
Nuclei_Texture_Variance_CorrDAPI_3_0	10.51	0.00	0.00
Nuclei_Neighbors_PercentTouching_20	10.65	0.00	0.00
Nuclei_Texture_Correlation_CorrDAPI_10_0	-11.11	0.00	0.00
Cells_Intensity_IntegratedIntensityEdge_CorrActin	-9.95	0.00	0.00
Nuclei_Texture_Entropy_CorrActin_3_0	9.98	0.00	0.00
Nuclei_Texture_SumVariance_CorrTub_3_0	9.20	0.00	0.00
Cytoplasm_Texture_Entropy_CorrActin_3_0	9.58	0.00	0.00
Cytoplasm_Texture_AngularSecondMoment_CorrActin_3_0	-9.11	0.00	0.00
Nuclei_Texture_InfoMeas1_CorrTub_10_0	-8.45	0.00	0.00
Nuclei_Neighbors_SecondClosestDistance_20	-8.63	0.00	0.00
Cytoplasm_AreaShape_Zernike_3_1	8.21	0.00	0.00
Cytoplasm_Texture_Contrast_CorrTub_10_0	8.00	0.00	0.00
Nuclei_Texture_AngularSecondMoment_CorrDAPI_3_0	-8.35	0.00	0.00
Nuclei_Texture_Variance_CorrDAPI_10_0	8.02	0.00	0.00
Cells_Intensity_MassDisplacement_CorrActin	-8.31	0.00	0.00
Cells_Texture_Entropy_CorrActin_3_0	7.77	0.00	0.00

Marker Selection

Metric

T-Test

Field

moa

Class A

DMSO

Class B

2 items selected

Number of markers

Select All

Deselect All

Permutations

Actin disruptors

Aurora kinase inhibitors

Cholesterol-lowering

DMSO

DNA damage

DNA replication

Back to feature data -> Tools -> Marker Selection -> T-Test, Field is moa, Class A is DMSO, Class B are DNA damage and DNA replication, then sort by FDR

9 - Optionally save out your data

Save Image

File name

Format

☐ PDF

☒ PNG

☐ SVG

OK

Cancel

Save Dataset

File name

GCT 1.3 or GCT 1.2 file name

File format

☐ GCT version 1.2

☒ GCT version 1.3

☐ Save selection only

OK

Cancel

Save Session

File name

OK

Cancel

File -> Save Image allows you to save an image of the current tab in the format of your choice. File -> Save Dataset saves a GCT file of the DATA of your current tab. File -> Save Session saves the data AND settings (annotations, sortings, etc) of your current tab in a JSON file.