**This file contains information about the different configurations that can be adjusted while running the ‘mofa\_workflow’ pipeline.**

[mandatory parameters that need to be set by the user and are not filled in as default parameters are highlighted in ‘orange’ ; for other parameters default values will be added during the execution but modifications might still be necessary]

**Global\_Configs**

* *‘data\_path’:*

*‘Value*’: text

*‘Description’:* add path to folder where all input files are stored; in case the path is wrongly specified the data cannot be read in during the execution and execution will fail

* *‘result\_path’:*

*‘Value’*: text

*‘Description’*: add path to folder where all result data will be stored; in case the path is wrongly specified the data cannot be read in during the execution and execution will fail

* *‘configuration\_name’:*

*‘Value*: any text

*‘Description’*: add a name that should be added as file extension to all the files that will be generated during the workflow execution

**01\_Pre\_Processing\_SC\_Data**

Only needs to be specified/ adjusted if sc data will be used. By default the names of all datasets in the specified folder for the input data will be added. If this is correct no modifications are necessary.

* ‘configuration\_name’:

*‘Value*: any text

*‘Description’*: add a name that should be added as file extension to all the files that will be generated during the workflow execution

(by default the value of ‘Global\_Configs.csv’ is added but another extension can be chosen here)

* *'data\_name':*

‘Value’: text

*‘Description’*: enter name of the sc datasets that are included in the folder specified in ‘data\_path’ in the previous file and should be used in the analysis; the dataset needs to be of format '.h5ad' and contain two meta-data columns in the cell annotations:

* + 'cluster\_id' [specifies the cell-type, cluster for aggregation to pseudobulk];
  + 'sample\_id' [sample identifier; needs to be the same across all integrated datasets]

**02\_Pre\_Processing\_Configs\_SC**

Only needs to be specified/ adjusted if sc data will be used. Default values for all ‘.h5ad’ files in the specified input data folder are added when executing the ‘00\_Configuration\_Update.ipynb’ script of the pipeline.

* *'configuration\_name'* :

*‘Values*: any text

*‘Description’*: : add a name that should be added as file extension to all the files that will be generated during the workflow execution

(by default the value of ‘Global\_Configs.csv’ is added but another extension can be chosen here)

* *'data\_name':*

*‘Values’: text*

*‘Description’*: enter name of the sc datasets that are included in the folder specified in ‘data\_path’ in the previous file and should be used in the analysis (one row per dataset) ; the dataset needs to be of format '.h5ad' and contain two meta-data columns in the cell annotations:

* + 'cluster\_id' [specifies the cell-type, cluster for aggregation to pseudobulk];
  + 'sample\_id' [sample identifier; needs to be the same across all integrated datasets]

*‘Misspecification’:* in case names of datasets are added here that are not within the input\_dataset folder the execution of the scripts will fail

* *'data\_type':* 'h5ad'
* *'cell\_expr\_thres1':*

‘Values’: two numbers separated by ‘;’ (‘x;y’ - Default: ’50;10’)

‘Description’: defines threshold for filtering of genes

* first number: percentage value (x%) - gene needs to be expressed in at least x% of cells to be used as input,
* second number: average minimum amount of cells per sample - gene needs to be expressed in at least y \* number of samples cells

Both thresholds need to apply

*‘Relevance of specification’:* with this parameter genes should be filtered out that are not expressed in a high amount of cells. It might be set to 0 but this would mean that all genes will be included in the analysis, even genes that have low quality due to being measured only on a couple of cells, this might influence the results of the analysis. If the threshold is set to high and all genes are filtered out this might lead to no single-cell data being used in the MOFA analysis of the script execution to fail.

* *'cell\_expr\_thres2'*: same as cell\_expr\_thres1; different numbers may be entered; gene will be used in analysis if either thres1 **or** thres2 applies (Default: ’40;20’)
* *'cell\_type\_exclusion'*:

*‘Values*’: enter names from the ‘cluster\_id’ column of the sc-data file separated by ‘,’

*‘Description’:*

* + specify cell-types that should be excluded from further analysis (e.g. because of low amount of cells)
  + names need to match exactly to values in 'cluster\_id' information
  + values need to be entered comma seperated without space in between
  + Default: by default all cell-types cluster\_id’s are added to the file which have less than 50 cells

**02\_Pre\_Processing\_Configs**

Specify one row for each dataset that should be included

* ‘configuration\_name’:

*‘Value*: any text

*‘Description’*: add a name that should be added as file extension to all the files that will be generated during the workflow execution

(by default the value of ‘Global\_Configs.csv’ is added but another extension can be chosen here but it should be the same as in the previous file)

* *'data\_name':*

*Values:* enter names of the datasets which should be used in the MOFA analysis; all datasets listed here will be integrated (if single-cell data is used also set up the previous configuration file: ‘02\_Pre\_Processing\_Configs\_SC’)

* *'data\_type':*

*Values:*  'h5ad' or ‘csv’

* *‘remove\_sample\_ids’:*

*Values: ‘*sample\_id’ s separated by ‘,’ or empty

*Description:* specify in case samples should be removed from the analysis

* *‘sample\_filtering\_thres’*

*Values:* number between 0 and 1 (x)

*Description:* filters out samples for which across all features (e.g. genes) more than x% of the values are zero *(Usage filter out low quality samples)*

* *‘feature\_filtering\_thres’:*

*Values:* number between 0 and 1 (x)

*Description:* specifies whether features should be filtered out that are not expressed in a x% of samples [0: no features will be filtered; 1: all features will be filtered 🡪 error ; default: 0.2]

* *‘library\_adjustment’:*

*Values:* either ‘TRUE’ or ‘FALSE’

*Description:* specifies whether library size adjustment will be applied to data, meaning that all samples will have the same amount of counts across all features after the transformation [usually applied to single-cell and bulk RNA-seq data]

* *‘log\_transformation’:*

*Values:* either ‘TRUE’ or ‘FALSE’

*Description:* specify whether values should be log-transformed

* *‘variable\_gene\_filtering’:*

*Values:* between 0 and 1 (x)

*Description:* only the x% of the most variable genes (based on their variance across samples) will be kept

* *‘quantile\_normalization\_samples’:*

*Values:* either ‘TRUE’ or ‘FALSE’

*Description:* specify whether quantile normalization across samples should be applied [in our data applied to single-cell and bulk RNA-seq data]

* *‘ribosomal\_mitochondrial\_gene\_filtering’:*

*‘Values’:* either ‚TRUE‘ or ‘FALSE’

*Description:* specify whether ribosomal and mitochondrial genes should be excluded from analysis [note: this only works when gene names are given by their ‘SYMBOL’ annotation]

* *‘feature\_wise\_quantile\_normalization’:*

*Values:* either ‚TRUE‘ or ‘FALSE’ (needs to be the same for all entries)

*Description:* specifies whether feature-wise quantile normalization should be applied to all features or not

**03\_MOFA\_Configs:**

Specify one row for each different mofa configuration that should be run

* *'configuration\_name'*:

*Values:* any text

*Description:* enter the name of the configuration by which data in previous steps has been generated (‘02\_Preprocessing\_Configs.csv’)

* *‘mofa\_result\_name’:*

*Values:* any text

*Description:* enter a name that will be added to all resulting tables and figures that are generated as result of the MOFA model

* *‘amount\_of\_factors’*

*Values: numeric value* (max: amount of features -1; min: 1; default: 20)

*Description:* amount of latent factors that should be estimated by the MOFA model

* *‘weighting\_of\_views’*

*Values: ‘TRUE’ , ‘FALSE’*

*Description:* defines whether the views should be weighted based on the amount of features (if ‘TRUE’, views with a lower amount of features will receive a higher weight)

* *‘scale\_views’*

*Values: ‘TRUE’ , ‘FALSE’*

*Description:* defines whether the features should be scaled based on the corresponding MOFA functionality

**04\_Factor\_Analysis\_Configs:**

* *'configuration\_name'*:

*Values:* any text

*Description:* enter the name of the configuration by which data in previous steps has been generated and was used as input for the MOFA model (‘02\_Preprocessing\_Configs.csv’)

* *‘mofa\_result\_name’:*

*Values:* any text

*Description:* enter the name of the MOFA results output for which the analysis should be done (name used in: ‘03\_MOFA\_Configs.csv’)

* *‘relevant\_factors’:*

*Values*: text, factor names that should be plotted comma separated (e.g.: Factor1,Factor2,Factor3)

*Description:* subselection of the factors of the MOFA model that will be plotted (Default: ‘Factor1,Factor2,Factor3,Factor4,Factor5’)

* *‘numeric covariates’:*

*Values:* text, name of the numeric covariates that should be analyzed comma separated (e.g. Age,Weight); needs to correspond to columns in Sample\_Meta\_Data.csv)

*Description:* used to generate correlation plots between the specified covariates + factors

* *‘categorical\_covariates’:*

*Values:* text, name of the categorical covariates that should be analyzed comma separated (e.g. Gender,Disease); needs to correspond to columns in Sample\_Meta\_Data.csv)

*Description:* used to generate boxplots to analyze differences in factor values

* *‘top\_variable\_thres’:*

*Value:* numeric value between 0 and 1 (Default: 0.005)

*Description:* defines the selection of top features per factor that should be analyzed

**05\_Feature\_Analysis\_Configs:**

* *'configuration\_name'*:

*Values:* any text

*Description:* enter the name of the configuration by which data in previous steps has been generated and was used as input for the MOFA model that should be analyzed (‘02\_Preprocessing\_Configs.csv’)

* *‘mofa\_result\_name’:*

*Values:* any text

*Description:* enter the name of the MOFA results output for which the analysis should be done (name used in: ‘03\_MOFA\_Configs.csv’)

* *‘factor’:*

*Values:* factor name (e.g. Factor1, Factor2; Default: ‘Factor2’)

*Description:* select the MOFA Factor for which top features should be plotted in the heatmap

* *‘top\_variable\_thres’:*

*Values:* numeric value between 0 and 1 (x) (Default: 0.005)

*Description:* select the x% of top features (meaning having the highest weights) that should be displayed in heatmap (! if value is to large heatmap might include to many features and not be readable anymore)

* *‘faceting\_variable’:*

*Values:* name of a column in the ‘sample\_meta\_data.csv’ (needs to be a categorical column)

*Description:* faceting/ grouping of samples in the heatmap is done based on this parameter

* *‘type’:*

*Values:* name of a type/view for which features should be selected; if empty all views with top features will be displayed

*Description:* defines of which view features will be displayed in the heatmap

**06\_Pathway\_Configs:**

* *‘mofa\_result\_name’:*

*Values:* any text

*Description:* enter the name of the MOFA results output for which the analysis should be done (name used in: ‘03\_MOFA\_Configs.csv’)

* *‘factor\_set’:*

*Values:* numbers comma separated (e.g: ‘1,2,3’)

*Description:* defines the factors for which the enrichment analysis should be conducted by default for factors 1-5 (‘1,2,3,4,5’)

* *‘coverage\_par’:*

*Values:* numeric between 0 and 1 (x)

*Description:* within the MOFA feature set at least x% of the genes of the pathway need to be included in order to test the pathway for enrichment, i.e. pathways with a lot of genes that are not in the feature set will not be tested

* *‘types’:*

*Values:* name of a type/view for which the enrichment analysis should be executed

*Description:* for all names entered here a view-specific enrichment analysis will be executed

* *‘coverage\_plot’:*

*Values: :* numeric between 0 and 1 (x)

*Description:* after the execution of the pathway enrichment analysis a plot will be generated showing selected enriched pathways and the corresponding genes; this paremeter is used to filter the pathways shown in the plot and indicates to show only pathways for which x% of genes have been included in the MOFA feature set

* *‘p\_value\_plot’:*

*Values:* numeric between 0 and 1 (x)

*Description:* after the execution of the pathway enrichment analysis a plot will be generated showing selected enriched pathways and the corresponding genes; this paremeter is used to filter the pathways shown in the plot and indicates to show only pathways for which the p-value of the enrichment is smaller than x

* *‘enrichment\_plot:*

*Values:* either ‘positive’, ‘negative’ , ‘complete’

*Description:* pathway enrichment is executed in three directions: analyzing only features with positive weights, only negative weights and absolute values (‘complete’); this parameter is used to filter the pathways shown in the plot and indicates to show only pathways of a certain type of enrichment (‘positive’, ‘negative’ , ‘complete’)

* *‘top\_features\_plot’:*

*Values:* numeric between 0 and 1 (x)

*Description:* this parameter is used to filter the genes shown in the plot after the pathway enrichment analysis, so only features among the top x% of features will be shown in the plot

**07\_Comparison\_Configs:**

* *‘mofa\_result\_name’:*

*Values:* any text

*Description:* enter the name of the MOFA results output for which the comparisons should be done (name used in: ‘03\_MOFA\_Configs.csv’); add a new entry for each mofa result that should be compared

* *‘compare\_factors’:*

*Values:* factor names separated by ‘,’ (e.g. ‘Factor1,Factor2,Factor3’)

*Description:* the different MOFA models will be compared for the factors specified here (Default: ‘Factor1,Factor2,Factor3,Factor4,Factor5)