sc-toolbox

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Installation New to *sc-toolbox*? Check out the installation guide.

API reference The API reference contains a detailed description of the sc-toolbox API.

Discussion Need help? Reach out on our forum to get your questions answered!

GitHub Find a bug? Interested in improving sc-toolbox? Checkout our GitHub for the latest developments.

CHAPTER

ONE

INSTALLATION

1.1 Stable release

To install sc-toolbox, run this command in your terminal:

```
$ pip install sc-toolbox
```

This is the preferred method to install sc-toolbox, as it will always install the most recent stable release.

If you don't have pip installed, this Python installation guide can guide you through the process.

1.2 From sources

The sources for sc-toolbox can be downloaded from the Github repo. Please note that you require poetry to be installed.

You can either clone the public repository:

```
$ git clone git://github.com/schillerlab/sc-toolbox
```

Or download the tarball:

```
$ curl -OJL https://github.com/schillerlab/sc-toolbox/tarball/master
```

Once you have a copy of the source, you can install it with:

```
$ make install
```

CHAPTER

TWO

USAGE

Import the sc-toolbox API as follows:

```
import sc_toolbox as sct
```

You can then access the respective modules like:

```
sct.pl.cool_fancy_plot()
```

2.1 Preprocessing

2.2 Tools

tools.generate_expression_table	Generates a table of cells by genes of expression values as a Pandas DataFrame.
tools.relative_frequencies	Calculates the relative frequencies of conditions grouped by an observation.
tools.relative_frequency_per_cluster	Calculates relative frequencies per cluster
tools.correlate_to_signature	Correlations Score (based on cell type signature (logFC)) - alternative to sc.tl.score
tools.remove_outliers	Remove outlying cells based on UMAP embeddings with DBScan (density based clustering).
tools.add_percentages	Add columns to existing diffxpy table specifying percentage of expressing cells.
tools.ranksums_between_groups	Perform Wilcoxon Rank-sum test between two groups.
tools.generate_count_object	@Meshal what is this really supposed to do?
tools.tidy_de_table	Sorts diffxpy de table and adds percentages of expression per group
tools.correlate_means_to_gene	Calculate gene to gene correlation based on a mean expression table
tools.extended_marker_table	Generates an extended marker table with cell types and percentages of expressed cell types per cluster.
tools.generate_pseudobulk	Generates a pseudobulk for a given key of groups in the AnnData object.
tools.automated_marker_annotation	Calculates a marker gene overlap based on pre-existing annotations.
tools.de_res_to_anndata	Add a tabular differential expression result to AnnData as if it was produced by scanpy.tl.rank_genes_groups.

2.2.1 sc_toolbox.tools.generate_expression_table

sc_toolbox.tools.**generate_expression_table**(*adata*, *cluster='all'*, *subset_by='cell_type'*, *xlabel=None*, *condition=None*, *use_raw=None*)

Generates a table of cells by genes of expression values as a Pandas DataFrame.

Parameters

- **adata** – Anndata object
- **cluster** (str) – Which label of the subsets to generate the table for. Use 'all' if for all subsets.
- **subset_by** (str) – Which label to subset the clusters by
- **xlabel** (Optional[str]) – Label that will be used for subsequent line plots as x-axis label. Typically a time series such as "days".
- **condition** (Optional[str]) – Column name of the condition to include.
- **use_raw** (Optional[bool]) – Whether to use adata.raw.X for the calculations

Returns

Gene expression table.

2.2.2 sc_toolbox.tools.relative_frequencies

sc_toolbox.tools.**relative_frequencies**(*adata*, *group_by='cell_type'*, *xlabel='days'*, *condition='batch'*)

Calculates the relative frequencies of conditions grouped by an observation.

Parameters

- **adata** – AnnData Objet containing the data
- **group_by** (str) – Column name to group by
- **xlabel** (str) – x-axis label
- **condition** (str) –

Returns

Relative frequencies in a Pandas DataFrame

2.2.3 sc_toolbox.tools.relative_frequency_per_cluster

sc_toolbox.tools.**relative_frequency_per_cluster**(*adata*, *group_by='cell_type'*, *xlabel='days'*, *condition=None*)

Calculates relative frequencies per cluster

Parameters

- **adata** – AnnData object containing the data
- **group_by** (str) – The label to group by for the clusters
- **xlabel** (str) – x-axis label
- **condition** – condition to combine by

Returns

Pandas DataFrame of relative frequencies

2.2.4 sc_toolbox.tools.correlate_to_signature

sc_toolbox.tools.**correlate_to_signature**(*adata*, *marker*, *log_fc_threshold=0.7*, *cell_type='AT2 cells'*, *cell_type_label='cell_type'*, *log_fc_label='logfoldchange'*, *gene_label='gene'*, *use_raw=True*)

Correlations Score (based on cell type signature (logFC)) - alternative to sc.tl.score

Parameters

- **adata** – AnnData object containing the data
- **marker** (DataFrame) – Pandas DataFrame containing marker genes
- **log_fc_threshold** (float) – Log fold change label
- **cell_type** (str) – Cell type to calculate the correlation for
- **cell_type_label** (str) – Label of all cell types in the AnnData object
- **log_fc_label** (str) – Label of fold change in the AnnData object
- **gene_label** (str) – Label of genes in the AnnData object
- **use_raw** (bool) – Whether to use adata.raw.X

Returns
List of correlations

2.2.5 sc_toolbox.tools.remove_outliers

sc_toolbox.tools.**remove_outliers**(*cords*, *eps=1*, *min_samples=2*)

Remove outlying cells based on UMAP embeddings with DBScan (density based clustering).

Call as: sub.obs["d_cluster"] = remove_outliers(sub.obsm["X_umap"], min_samples = 10)

Parameters

- **cords** – adata UMAP coordinates, typically adata.obsm["X_umap"]
- **eps** (int) – Maximum distance between two clusters to still be considered neighbors
- **min_samples** (int) – Minimum samples of a cluster

Return type
Categorical

Returns
Pandas Categorical of clusters

2.2.6 sc_toolbox.tools.add_percentages

sc_toolbox.tools.**add_percentages**(*adata*, *table*, *ids*, *group_by*, *threshold=0*, *gene_label='gene'*)

Add columns to existing diffxpy table specifying percentage of expressing cells.

Parameters

- **adata** – AnnData object containing the data
- **table** – Table as generated by diffxpy
- **ids** – Identifiers to add percentages for.
- **group_by** (str) – Label to group by
- **threshold** (int) – Cell count threshold.
- **gene_label** (str) – Label of the genes

Returns
Table containing percentage of expressing cells

2.2.7 sc_toolbox.tools.ranksums_between_groups

sc_toolbox.tools.**ranksums_between_groups**(*table*, *id1='bystander'*, *id2='infected'*, *xlabel='condition'*, *cells=None*, *score='Axin2'*)

Perform Wilcoxon Rank-sum test between two groups.

Parameters

- **table** –
- **id1** (str) –
- **id2** (str) –

- **xlabel** (str) – x-axis label
- **cells** –
- **score** (str) –

Returns
Pandas DataFrame containing test statistic and p-value

2.2.8 sc_toolbox.tools.generate_count_object

sc_toolbox.tools.**generate_count_object**(*adata*, *hue='disease'*, *cell_type_label='cell_type'*, *cell_type=None*, *min_samples=2*, *min_cells=5*, *ref='healthy'*, *subset=None*, *layer='counts'*, *outliers_removal=False*)

@Meshal what is this really supposed to do?

Parameters

- **adata** – AnnData object
- **hue** (str) – Value to color by
- **cell_type_label** (str) – Label containing cell types
- **cell_type** (Optional[List[str]]) – Cells type to generate counts for
- **min_samples** (int) – Minimum samples for outlier removal with DBScan
- **min_cells** (int) – Minimal number of cells
- **ref** (str) –
- **subset** (Optional[List[str]]) –
- **layer** (str) –
- **outliers_removal** (bool) – Whether to remove outliers or not

Returns
AnnData object containing counts

Example Call: subset = [‘3d PI-KO’, ‘3d PI-WT’]

raw_counts = generate_count_object(adata,
condition = “grouping”, cell_type_label = “celltype_refined”, cell_type = [“AT2”], ref = “3d PI-WT”, subset = subset)

2.2.9 sc_toolbox.tools.tidy_de_table

sc_toolbox.tools.**tidy_de_table**(*de_test*, *adata*, *cells*, *ids=None*, *qval_thresh=0.9*, *group_by='treatment'*, *cols=None*)

Sorts diffxpy de table and adds percentages of expression per group

Parameters

- **de_test** – diffxpy de test
- **adata** – AnnData object
- **cells** –
- **ids** –

- **qval_thresh** (float) –
- **group_by** (str) –
- **cols** –

Returns
Pandas Dataframe of diffxpy table with percentages

2.2.10 sc_toolbox.tools.correlate_means_to_gene

sc_toolbox.tools.**correlate_means_to_gene**(*means*, *corr_gene='EOMES'*)

Calculate gene to gene correlation based on a mean expression table

Parameters

- **means** (DataFrame) –
- **corr_gene** (str) –

Returns
Pandas DataFrame of correlations

2.2.11 sc_toolbox.tools.extended_marker_table

sc_toolbox.tools.**extended_marker_table**(*adata*, *qval_thresh=0.05*, *cell_type_label='cell_type'*, *gene_ranks_key='rank_genes_groups'*)

Generates an extended marker table with cell types and percentages of expressed cell types per cluster.

Run scanpy.tl.rank_genes_groups before using this function.

Parameters

- **adata** (AnnData) – AnnData object containing ranked genes
- **qval_thresh** (float) – Threshold to filter the log fold change for
- **cell_type_label** (str) – Label containing all cell types
- **gene_ranks_key** (str) – Key for the ranked gene groups (generated by sc.tl.rank_genes_groups)

Returns
A Pandas DataFrame

2.2.12 sc_toolbox.tools.generate_pseudobulk

sc_toolbox.tools.**generate_pseudobulk**(*adata*, *group_key='identifier'*, *sep='\\t'*, *save=None*)

Generates a pseudobulk for a given key of groups in the AnnData object.

Looks like:

Genes	Group Member 1	Group Member 2
Gene 1	Value 1	Value 2
Gene 2	Value 2	Value 3

Parameters

- **adata** (AnnData) – AnnData object
- **group_key** (str) – The key to group by. E.g. by mice, by condition, … (default: 'identifier')
- **sep** – Separator to use when saving the pseudobulk table (default: ' ')
- **save** (Optional[str]) – Path to save the pseudobulk table to (default: None)

Return type
DataFrame

Returns
A Pandas DataFrame containing the pseudobulk table

2.2.13 sc_toolbox.tools.automated_marker_annotation

sc_toolbox.tools.**automated_marker_annotation**(*adata*, *organism*, *tissue*, *marker_file*, *key='rank_genes_groups'*, *normalize='reference'*, *p_value=0.05*, *log_fold_change=2*)

Calculates a marker gene overlap based on pre-existing annotations.

Currently supported marker files:

Organism	Tissue	Marker File
Mouse	Lung	lung_particle_markers.txt
Human	NA	

Parameters

- **adata** (AnnData) – AnnData object containing ranked genes
- **organism** (str) – Currently supported: 'mouse'
- **tissue** (str) – Currently supported: 'lung'
- **marker_file** (str) – Name of the marker file to be used - refer to table
- **key** (str) – Key of ranked genes in adata (default: 'rank_genes_groups')
- **normalize** (Optional[Literal['reference', 'data']]) – Normalization option for the marker gene overlap output (default: 'reference')
- **p_value** (float) – p-value threshold for existing marker genes (default: 0.05)
- **log_fold_change** (float) – log fold change threshold for existing marker genes (default: 2)

Returns
Pandas DataFrame of overlapping genes. Visualize with a Seaborn Heatmap

2.2.14 sc_toolbox.tools.de_res_to_anndata

sc_toolbox.tools.**de_res_to_anndata**(*adata*, *de_res*, ***, *groupby*, *gene_id_col='gene_symbol'*, *score_col='score'*, *pval_col='pvalue'*, *pval_adj_col=None*, *lfc_col='lfc'*, *key_added='rank_genes_groups'*)

Add a tabular differential expression result to AnnData as if it was produced by scanpy.tl.rank_genes_groups.

Parameters

- **adata** (AnnData) – Annotated data matrix
- **de_res** (DataFrame) – Tablular DE result as Pandas DataFrame
- **groupby** (str) – Column in *de_res* that indicates the group. This column must also exist in *adata.obs*.
- **gene_id_col** (str) – Column in *de_res* that holds the gene identifiers
- **score_col** (str) – Column in *de_res* that holds the score (results will be ordered by score).
- **pval_col** (str) – Column in *de_res* that holds the unadjusted pvalue
- **pval_adj_col** (Optional[str]) – Column in *de_res* that holds the adjusted pvalue. If not specified, the unadjusted p values will be FDR-adjusted.
- **lfc_col** (str) – Column in *de_res* that holds the log fold change
- **key_added** (str) – Key under which the results will be stored in adata.uns

Return type
None

2.3 Plots

plot.Colormaps(value)	Useful Colormaps for e.g.
plot.custom_plot_size(width, height, dpi)	Create a custom axis object of desired sizes.
plot.standard_lineplot(data, order, xlabel, ...)	Draws a standard line plot based on Seaborn's lmplot.
plot.average_expression(gene_expression, ...)	Draw a line plot showing the gene expression over time.
plot.average_expression_per_cluster(...[, ...])	Plots gene expression over time split by cluster identity.
plot.average_expression_split_cluster(...[, ...])	Plot average gene expression as line plots for multiple clusters at once.
plot.average_expression_per_cell(...[, ...])	Plots the average gene expression as a line plot per cell.
plot.gene_expression_dpt_ordered(data, ...)	Plot smoothed expression of all cells ordered by pseudo time.
plot.relative_frequencies_boxplots(...[, ...])	Plots the relative frequencies as split boxplots.
plot.split_boxplot(table, order, xlabel, ylabel)	Draws a boxsplit split by hue.
plot.marker_dendrogram(marker_table[, ...])	Plots a dendogram of used marker genes.
plot.volcano_plot(table[, fdr_thresh, ...])	Scatter plot of differential gene expression results generated by diffxpy
plot.cluster_composition_stacked_barplot(...)	Plot relative frequencies as a stacked barplot.
plot.gene_boxplot(table, palette[, xlabel, ...])	Plot gene values as split boxplots.
plot.colors_overview(colors[, ncols, ...])	Draw an overview plot of all used colors.
plot.relative_frequencies_lineplot(...[, ...])	Plot relative frequencies as a line plot.
plot.annotated_cell_type_umap(adata, ...[, ...])	Plots a UMAP which is colored by the primary_color, but also draws all labels on top of all clusters.
plot.genotype_vs_genotype_umaps(adata, ...)	Plots a two UMAPs of genotypes next to each other displaying only the colors of the second UMAP.

2.3.1 sc_toolbox.plot.Colormaps

class sc_toolbox.plot.**Colormaps**(*value*)

Useful Colormaps for e.g. UMAPs.

Attributes table

grey_red
grey_green
grey_yellow
grey_violet
grey_blue

Attributes

grey_red

Colormaps.**grey_red** = <matplotlib.colors.LinearSegmentedColormap object>

grey_green

Colormaps.**grey_green** = <matplotlib.colors.LinearSegmentedColormap object>

grey_yellow

Colormaps.**grey_yellow** = <matplotlib.colors.LinearSegmentedColormap object>

grey_violet

Colormaps.**grey_violet** = <matplotlib.colors.LinearSegmentedColormap object>

grey_blue

Colormaps.**grey_blue** = <matplotlib.colors.LinearSegmentedColormap object>

2.3.2 sc_toolbox.plot.custom_plot_size

sc_toolbox.plot.**custom_plot_size**(*width*, *height*, *dpi*)

Create a custom axis object of desired sizes.

Parameters

- **width** (int) – Desired plot width
- **height** (int) – Desired plot height
- **dpi** (int) – Desired plot DPI.

Returns: Axis of desired sizes

2.3.3 sc_toolbox.plot.standard_lineplot

sc_toolbox.plot.**standard_lineplot**(*data*, *order*, *xlabel*, *ylabel*, *hue=None*, *gene=None*, *smooth=None*, *palette=None*, *title=None*, *rotation=None*, *figsize=(15, 5)*, *tick_size=None*, *label_size=None*, *order_smooth=3*, *confidence_interval=None*, *scatter=None*, *save=None*)

Draws a standard line plot based on Seaborn's lmplot.

Parameters

- **data** – Data frame containing averaged expression values
- **order** (List) – Order of x-axis labels from left to right

- **xlabel** (str) – x-axis label
- **ylabel** (str) – y-axis label
- **hue** – Subsets of the data which will be drawn on separate facets in the grid. Example: "condition"
- **gene** – Gene of interest
- **smooth** (Optional[bool]) – Whether to smoothen (interpolate) the curve
- **palette** – Color palette. For example a list of colors.
- **title** – Title of the plot
- **rotation** (Optional[int]) – Rotation of the x-axis labels
- **figsize** (Tuple[int, int]) – Size of the figure as specified in matplotlib
- **tick_size** – Size of the ticks as specified in matplotlib
- **label_size** – Size of the labels as specified in matplotlib
- **order_smooth** (int) – If greater than 1, numpy.polyfit is used to estimate a polynomial regression
- **confidence_interval** – Confidence interval
- **scatter** – Set to true in order to add mean expression per sample in form of scatter point
- **save** (Optional[str]) – Path to save the plot to

2.3.4 sc_toolbox.plot.average_expression

sc_toolbox.plot.**average_expression**(*gene_expression*, *genes*, *order*, *id_label='identifier'*, *xlabel='days'*, *cluster='all'*, *hue=None*, *palette='tab:blue'*, *figsize=(15, 6)*, *smooth=None*, *rotation=None*, *order_smooth=None*, *conf_int=None*, *scatter=None*, *save=None*)

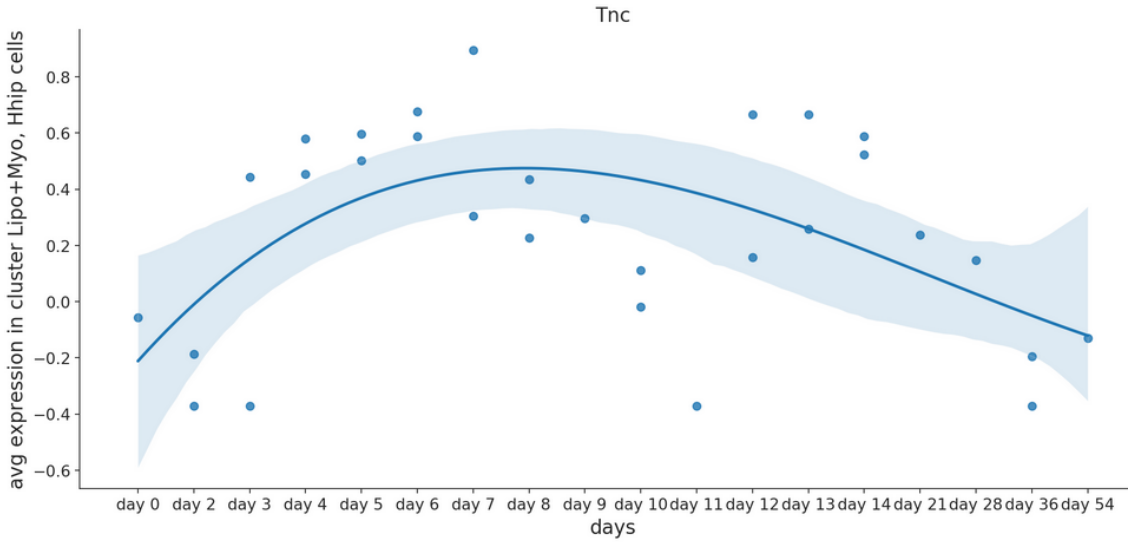
Draw a line plot showing the gene expression over time. Expression values are averaged by individual sample.

Parameters

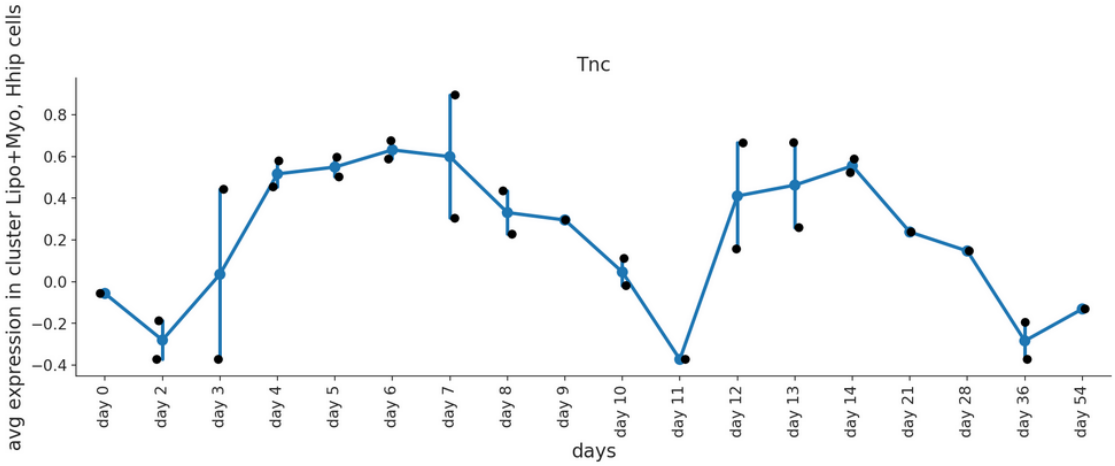
- **gene_expression** – Data frame containing gene expression values
- **genes** – List of genes for which individual line plots will be generated
- **order** (List[str]) – Order of x-axis labels from left to right
- **id_label** (str) – Adata column in which sample id information is stored
- **xlabel** (str) – x-axis label
- **cluster** (str) – Which clusters to plot. Select 'all" if all clusters should be drawn.
- **hue** – Which value to color by
- **figsize** (Tuple[int, int]) – Size of the figure as specified in matplotlib
- **smooth** – Set to true for smoothened line plot using polynomial regression
- **rotation** (Optional[int]) – set to True to rotate x-axis labels 90 degrees
- **order_smooth** – If greater than 1, use numpy.polyfit to estimate a polynomial regression
- **conf_int** – Size of the confidence interval for the regression estimate
- **scatter** – Set to True to add average expression values per sample ID as dots

- **save** (Optional[str]) – Path to save the plot to

Example smooth:



Example raw:



2.3.5 sc_toolbox.plot.average_expression_per_cluster

sc_toolbox.plot.**average_expression_per_cluster**(*gene_expression*, *genes*, *order*, *obs=None*, *id_label='identifier'*, *xlabel='days'*, *cluster='all'*, *hue=None*, *figsize=(15, 6)*, *smooth=None*, *rotation=None*, *tick_size=12*, *label_size=15*, *order_smooth=None*, *conf_int=None*, *palette=None*, *scatter=None*, *save=None*)

Plots gene expression over time split by cluster identity.

One line per cluster.

Parameters

- **gene_expression** – Data frame containing gene expression values

- **genes** – List of genes for which individual line plots will be generated
- **order** – Order of x-axis labels from left to right
- **obs** – Data frame containing meta data information
- **xlabel** (str) – x-axis label
- **cluster** (str) – Which clusters to plot. Select 'all" if all clusters should be drawn.
- **id_label** (str) – Meta data column in which sample id information is stored
- **hue** – Split expression values by this grouping, one line per category will be drawn
- **figsize** (Tuple[int, int]) – Size of the figure as specified in matplotlib
- **smooth** – Set to True for smoothened line plot using polynomial regression
- **rotation** – Set to True to rotate x-axis labels 90 degrees
- **tick_size** (int) – Size of the ticks as specified in matplotlib
- **label_size** (int) – Size of the labels as specified in matplotlib
- **order_smooth** – If greater than 1, use numpy.polyfit to estimate a polynomial regression
- **conf_int** – Size of the confidence interval for the regression estimate
- **palette** – Color palette that gets passed to Seaborn's lineplot. For example a list of colors.
- **scatter** – Set to True to add average expression values per sample ID as dots
- **save** (Optional[str]) – Path to save the plot to

2.3.6 sc_toolbox.plot.average_expression_split_cluster

sc_toolbox.plot.**average_expression_split_cluster**(*gene_expression*, *genes*, *order*, *id_label='identifier'*, *xlabel='days'*, *hue='genotype'*, *cluster=None*, *figsize=(15, 6)*, *smooth=None*, *rotation=None*, *cols=None*, *tick_size=12*, *label_size=15*, *order_smooth=None*, *conf_int=None*, *scatter=None*, *save=None*)

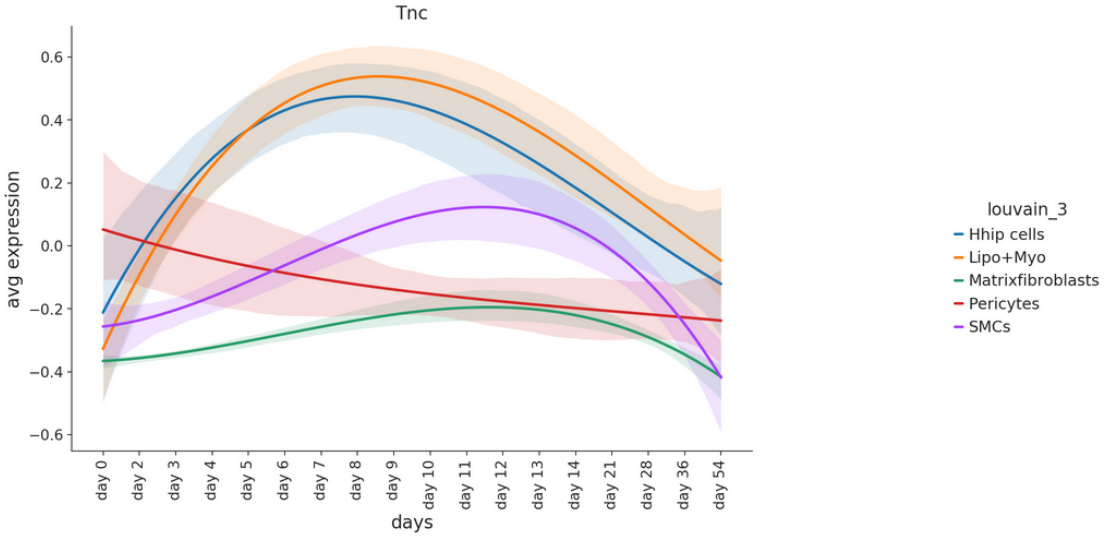
Plot average gene expression as line plots for multiple clusters at once.

Parameters

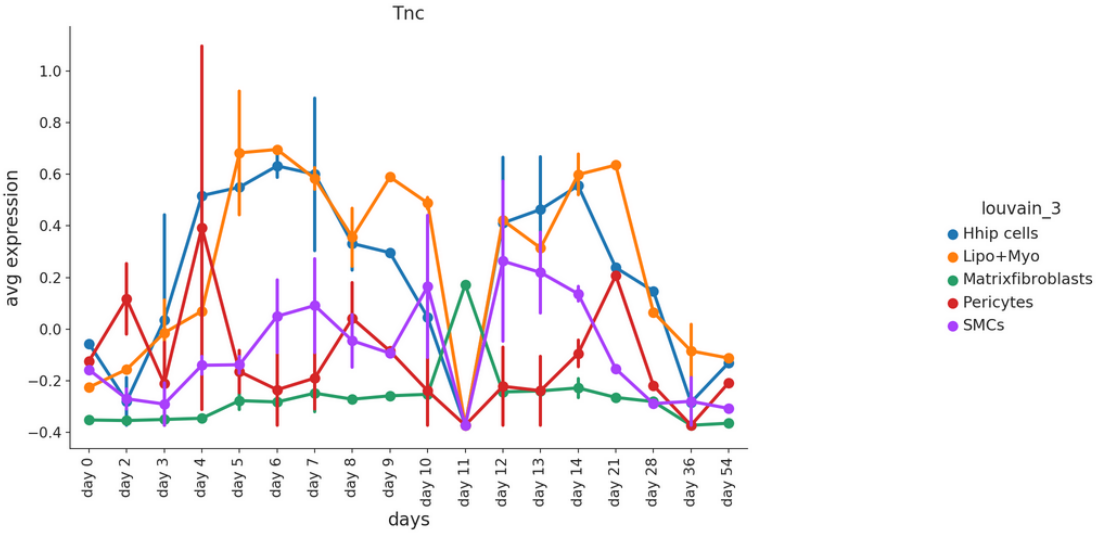
- **gene_expression** – Data frame containing gene expression values
- **genes** – List of genes for which individual line plots will be generated
- **order** – Order of x-axis labels from left to right
- **id_label** – Meta data column in which sample id information is stored
- **xlabel** – x-axis label
- **hue** – Split expression values by this grouping, one line per category, will be drawn
- **cluster** – Which clusters to plot. Select 'all" if all clusters should be drawn.
- **figsize** – Size of the figure as specified in matplotlib
- **smooth** – Set to True for smoothened line plot using polynomial regression
- **rotation** – x-axis label rotation
- **cols** – List of colors to use for line plot

- **tick_size** – Size of the ticks as specified in matplotlib
- **label_size** – Size of the labels as specified in matplotlib
- **order_smooth** – If greater than 1, numpy.polyfit is used to estimate a polynomial regression
- **conf_int** – Size of the confidence interval for the regression estimate
- **scatter** – Set to True to add average expression values per sample ID as dots
- **save** – Path to save the plot to

Example smooth:



Example raw:



2.3.7 sc_toolbox.plot.average_expression_per_cell

sc_toolbox.plot.**average_expression_per_cell**(*gene_expression*, *genes*, *order*, *xlabel='days'*, *cluster='all'*, *hue=None*, *figsize=(15, 6)*, *smooth=None*, *rotation=None*, *tick_size=12*, *label_size=15*, *order_smooth=None*, *conf_int=None*, *scatter=None*, *cols=None*, *save=None*)

Plots the average gene expression as a line plot per cell. Ideally used when the scatter point should not be sample wise, but cell wise. :type gene_expression: :param gene_expression: Data frame containing gene expression values :type genes: :param genes: List of genes for which individual line plots will be generated :type order: :param order: Order of x-axis labels from left to right :type xlabel: `str` :param xlabel: x-axis label :type cluster: `str` :param cluster: Which clusters to plot. Select 'all" if all clusters should be drawn. :type hue: :param hue: Split expression values by this grouping, one line per category, will be drawn :type figsize: `Tuple`[`int`, `int`] :param figsize: Size of the figure as specified in matplotlib :type smooth: :param smooth: Set to true for smoothened line plot using polynomial regression :type rotation: :param rotation: Set to True to rotate x-axis labels 90 degrees :type tick_size: :param tick_size: Size of the ticks as specified in matplotlib :type label_size: :param label_size: Size of the labels as specified in matplotlib :type order_smooth: :param order_smooth: If greater than 1, use numpy.polyfit to estimate a polynomial regression :type conf_int: :param conf_int: Size of the confidence interval for the regression estimate :type scatter: :param scatter: Set to True to add average expression values per sample ID as dots :type cols: :param cols: List of colors to use for line plot :type save: `Optional`[`str`] :param save: Path to save the plot to

2.3.8 sc_toolbox.plot.gene_expression_dpt_ordered

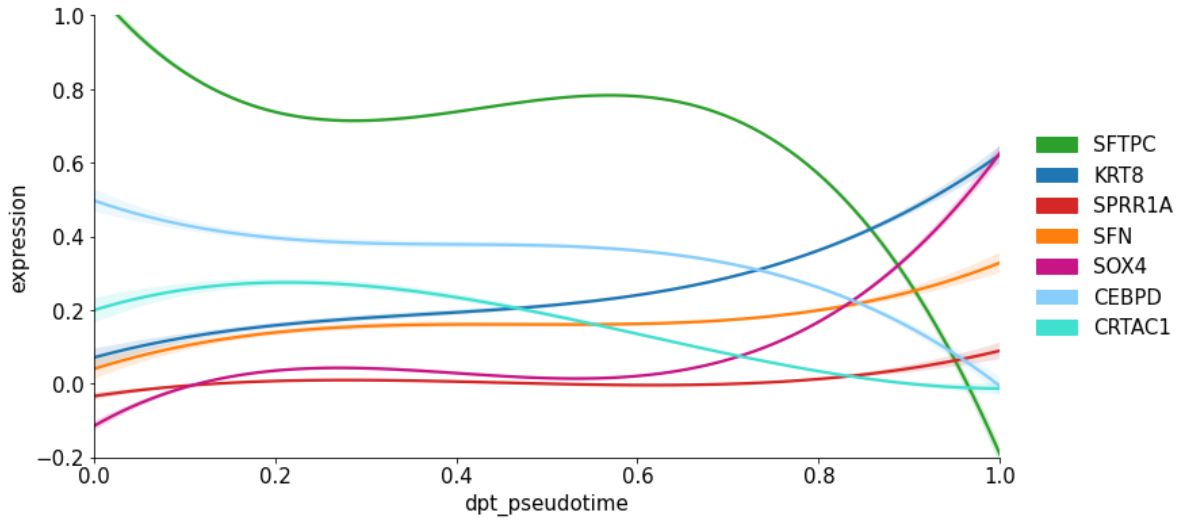
sc_toolbox.plot.**gene_expression_dpt_ordered**(*data*, *genes*, *xlabel*, *order=3*, *conf_int=95*, *figsize=(12, 6)*, *condition=None*, *label_size=15*, *cols=None*, *scale=None*, *ylim=None*, *save=None*)

Plot smoothed expression of all cells ordered by pseudo time.

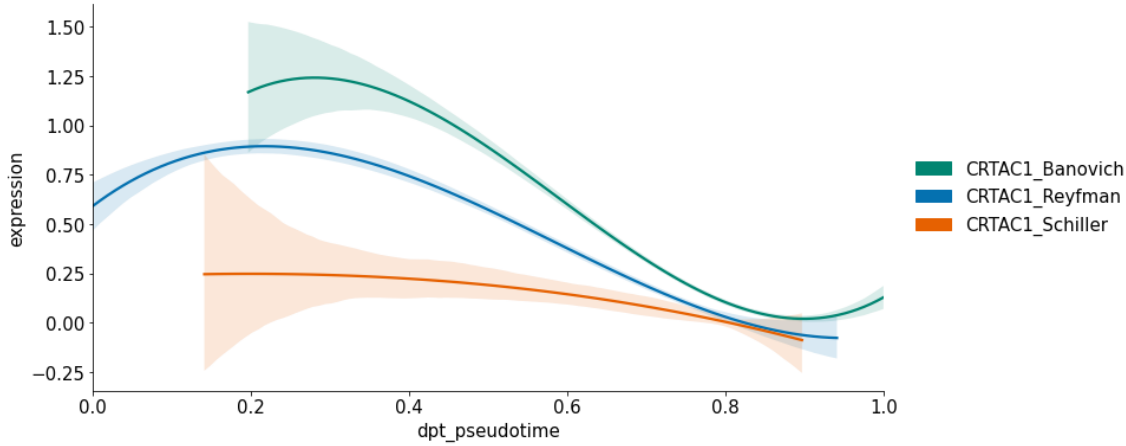
Parameters

- **data** – AnnData object
- **genes** – List of genes for which individual line plots will be generated
- **xlabel** – x-axis label
- **order** – Order of x-axis labels from left to right
- **conf_int** – Size of the confidence interval for the regression estimate
- **figsize** (`Tuple`[`int`, `int`]) – Size of the figure as specified in matplotlib
- **condition** – Split expression values by this grouping, one line per category will be drawn
- **label_size** (`int`) – Size of the labels as specified in matplotlib
- **cols** – List of colors to use for line plot
- **scale** – Set to True to scale expression value to a range between 0 and 1
- **ylim** – Upper limit on the y-axis if desired
- **save** (`Optional`[`str`]) – Path to save the plot to

Example



Example with columns:



2.3.9 sc_toolbox.plot.relative_frequencies_boxplots

sc_toolbox.plot.**relative_frequencies_boxplots**(*relative_frequencies*, *cluster*, *cols*, *order*, *xlabel='days'*, *hue='batch'*, *figsize=(15, 6)*, *width=0.5*, *jitter=None*, *save=None*)

Plots the relative frequencies as split boxplots.

Use calc_relative_frequencies to get the required input format.

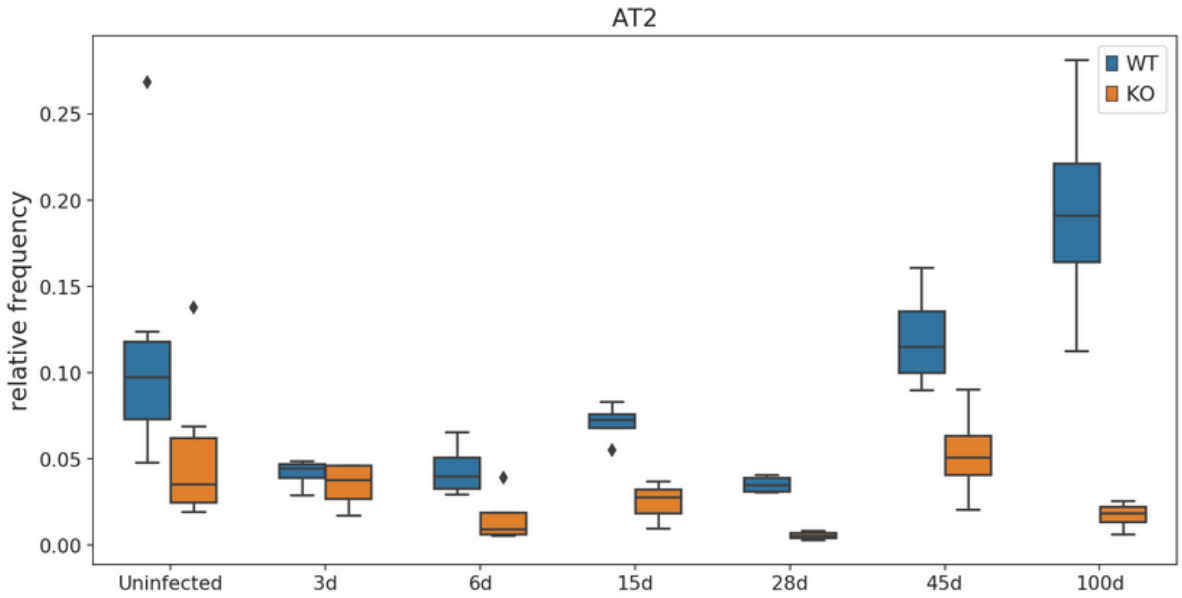
Parameters

- **relative_frequencies** (DataFrame) – Calculated by calc_relative_frequencies as Pandas DataFrame
- **cluster** – Cluster to be plotted
- **cols** – List of colors to use for boxes
- **order** – Order of x-axis labels from left to right
- **xlabel** (str) – x-axis label

- **hue** (str) – Value to color by
- **figsize** (Tuple[int, int]) – Size of the figure as specified in matplotlib
- **width** (float) – Width of the plot as specified in matplotlib
- **jitter** – Set to True for individual dots per sample
- **save** – Path to save the plot to

Return type
None

Example



2.3.10 sc_toolbox.plot.split_boxplot

sc_toolbox.plot.**split_boxplot**(*table*, *order*, *xlabel*, *ylabel*, *column=None*, *hue=None*, *cols=None*, *width=1*, *title=None*, *figsize=(15, 6)*, *jitter=None*, *save=None*)

Draws a boxsplit split by hue.

Parameters

- **table** – Table containing the data to draw the boxplots for
- **order** – Order of the boxplot labels
- **xlabel** (str) – x-axis label
- **ylabel** (str) – y-axis label
- **column** –
- **hue** – Value to split relative frequencies by
- **cols** – List of colors to use for boxes
- **width** (float) – Width of the desired plot

- **title** – Title of the plot
- **figsize** (Tuple[int, int]) – Size of the figure as specified in matplotlib
- **jitter** – Set to True for individual dots per sample
- **save** (Optional[str]) – Path to save the plot to

Return type
None

2.3.11 sc_toolbox.plot.marker_dendrogram

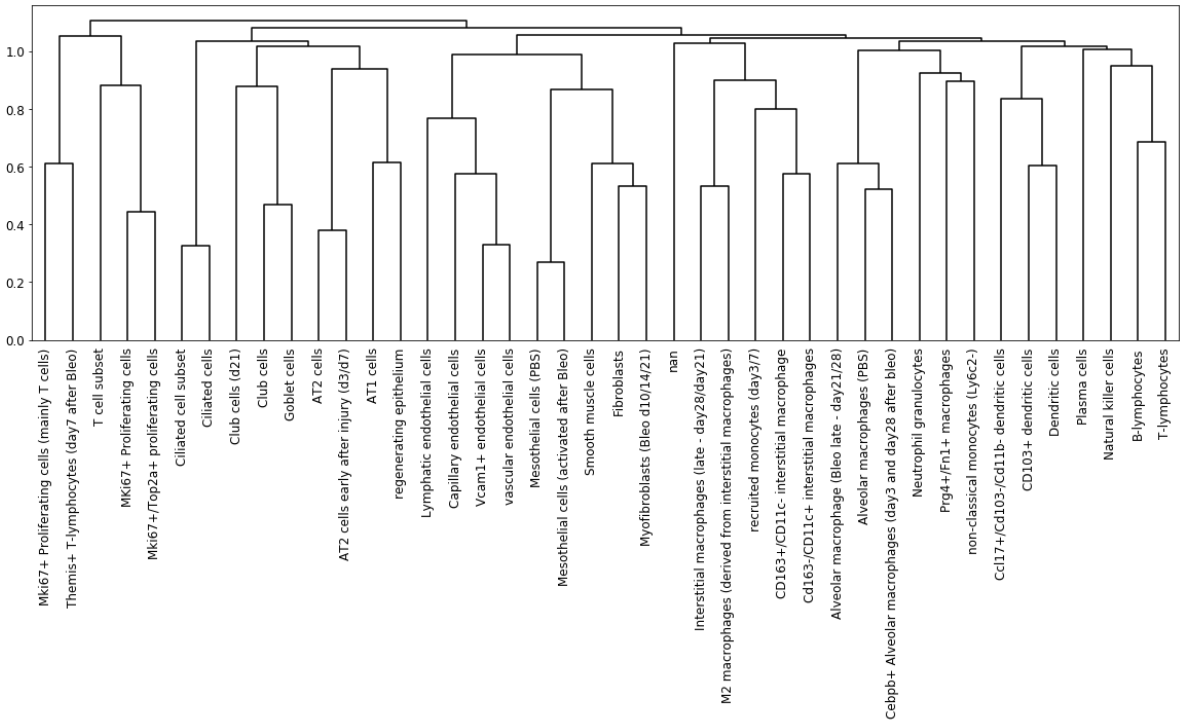
sc_toolbox.plot.**marker_dendrogram**(*marker_table*, *threshold=0.7*, *column='cluster'*, *log_fc_key='log_FC'*, *label_size=10*, *orientation='top'*, *figsize=(10, 4)*, *save=None*)

Plots a dendogram of used marker genes.

Parameters

- **marker_table** (DataFrame) – A marker table as generated by sct.calc.extended_marker_table
- **threshold** (float) – Threshold for the log fold change
- **column** (str) – Column to create pivot by; usually just the clusters
- **log_fc_key** (str) – Key for the stored log fold changes in the marker table
- **label_size** (int) – Font size of the labels
- **orientation** (str) – Orientation of the figure; Currently just 'top' or no orientation
- **figsize** (Tuple[int, int]) – Size of the figure as specified in matplotlib
- **save** (Optional[str]) – Path to save the plot to

Example



2.3.12 sc_toolbox.plot.volcano_plot

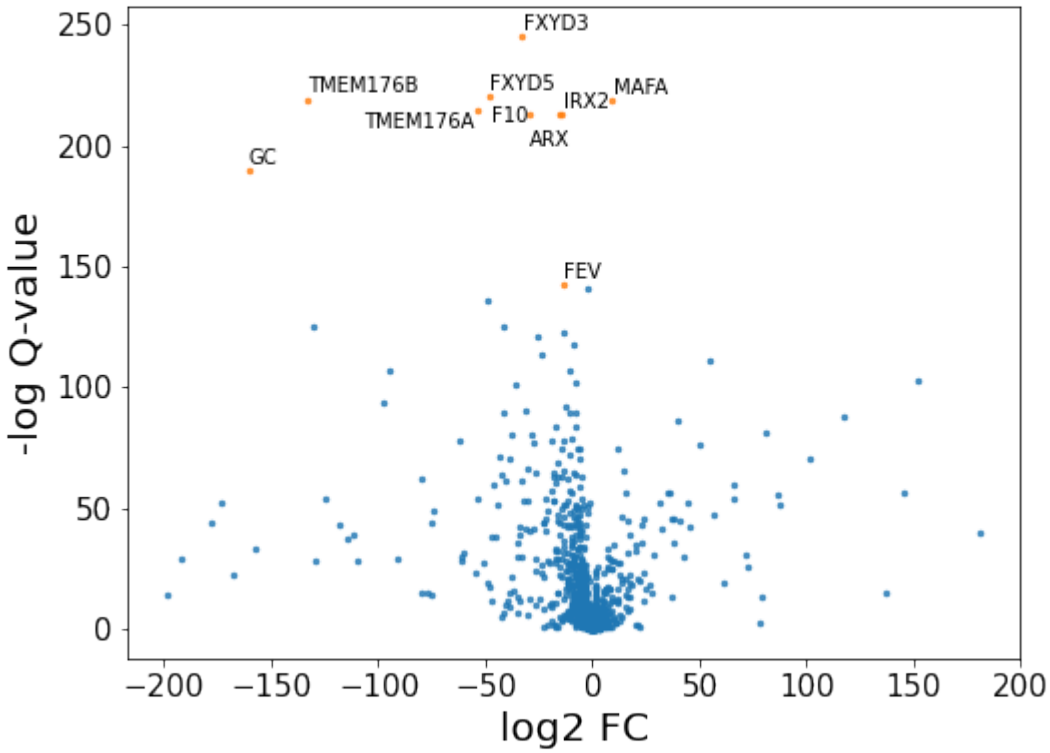
sc_toolbox.plot.**volcano_plot**(*table*, *fdr_thresh=None*, *log_fc_thresh=0*, *adj_p_val='adj_p_val'*, *log_fc='avg_logFC'*, *gene='gene'*, *sig_col='tab:orange'*, *col='tab:blue'*, *figsize=(8, 6)*, *save=None*)

Scatter plot of differential gene expression results generated by diffxpy

Parameters

- **table** – diffxpy generated table of results
- **fdr_thresh** (Optional[float]) – -log(FDR) threshold for labeling genes. If set to None, we will consider the 99th percentile of -log(FDR) values the threshold.
- **log_fc_thresh** (float) – absolute(log_fc) threshold for labeling genes.
- **adj_p_val** (str) – Label of the adjusted p value, these are considered FDRs
- **log_fc** (str) – Label of the log fold change
- **gene** (str) – Label of column with gene names
- **col** (str) – Color of dots
- **sig_col** (str) – Colour of dots surpassing defined FDR threshold
- **figsize** (Tuple[int, int]) – Size of the figure as specified in matplotlib
- **save** – Path to save the plot to

Example



2.3.13 sc_toolbox.plot.cluster_composition_stacked_barplot

sc_toolbox.plot.**cluster_composition_stacked_barplot**(*relative_frequencies*, *xlabel='name'*, *figsize=(6, 10)*, *width=0.8*, *order=None*, *error_bar=None*, *label_size=15*, *tick_size=13*, *capsize=None*, *margins=(0.02, 0.04)*, *colors=None*, *save=None*)

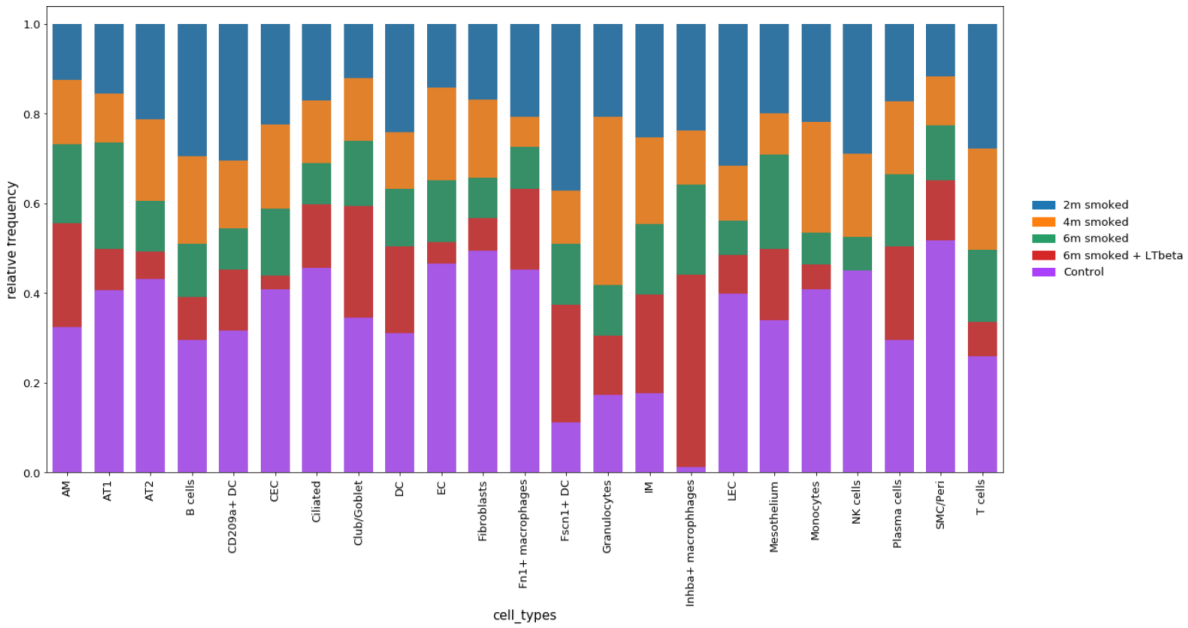
Plot relative frequencies as a stacked barplot.

Parameters

- **relative_frequencies** (DataFrame) – Data frame containing relative Frequencies as calculated by calc_relFreq()
- **xlabel** (str) – x-axis label
- **figsize** (Tuple[int, int]) – Size of the figure as specified in matplotlib
- **width** (float) – Width of the bars
- **order** – Order of x-axis labels from left to right
- **error_bar** – Set to True to add error bars (only possible when grouping the frequencies)
- **tick_size** (int) – Size of the ticks as specified in matplotlib
- **label_size** (int) – Size of the labels as specified in matplotlib

- **capsize** (Optional[int]) – Size of the horizontal lines of the error bar
- **margins** (Tuple[float, float]) – Change margins of the plot if desired
- **colors** – List of colors to use for the bands
- **save** (Optional[str]) – Path to save the plot to

Example



2.3.14 sc_toolbox.plot.gene_boxplot

sc_toolbox.plot.**gene_boxplot**(*table*, *palette*, *xlabel='cell_types'*, *hue=None*, *figsize=(10, 5)*, *legend=True*, *score='Axin2'*, *scatter=None*, *rotate=False*, *width=0.7*, *save=None*)

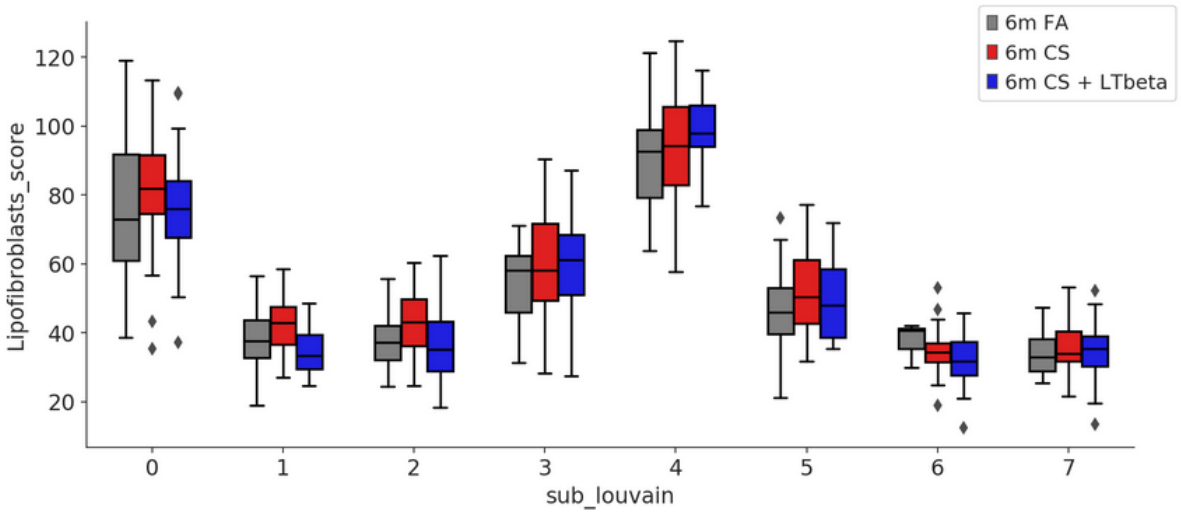
Plot gene values as split boxplots.

Parameters

- **table** – Pandas DataFrame
- **palette** (List[str]) –
- **xlabel** (str) – x-axis label
- **hue** (Optional[str]) –
- **figsize** (Tuple[int, int]) – Size of the figure as specified in matplotlib
- **legend** – Whether to draw a legend or not
- **score** –
- **scatter** –
- **rotate** –
- **width** – Width of the desired plot

- **save** – Path to save the plot to

Example



2.3.15 sc_toolbox.plot.colors_overview

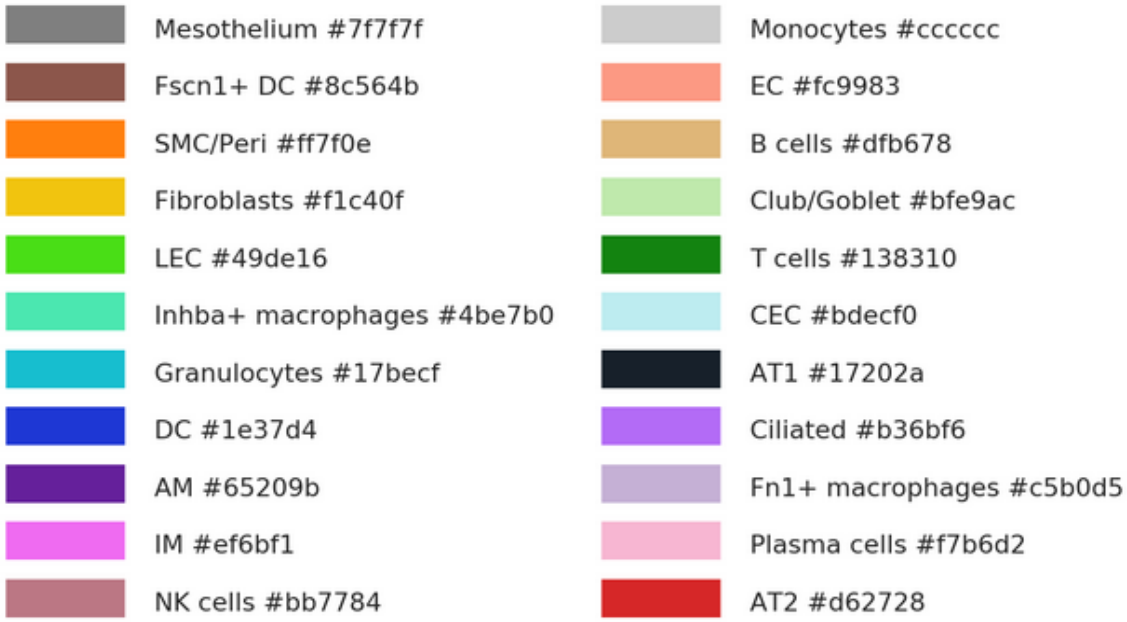
sc_toolbox.plot.**colors_overview**(*colors*, *ncols=2*, *figsize=(8, 5)*, *save=None*)

Draw an overview plot of all used colors.

Parameters

- **colors** (Dict) – Dictionary of color name and color
- **ncols** (int) – How many columns for the plot
- **figsize** (Tuple[int, int]) – Size of the figure as specified in matplotlib
- **save** (Optional[str]) – Path to save the plot to

Example



2.3.16 sc_toolbox.plot.relative_frequencies_lineplot

sc_toolbox.plot.**relative_frequencies_lineplot**(*relative_frequencies*, *order*, *cluster*, *xlabel='days'*, *ylabel='relative frequency'*, *hue=None*, *smooth=None*, *cols=None*, *title=None*, *rotation=None*, *figsize=(15, 5)*, *tick_size=None*, *label_size=None*, *order_smooth=3*, *conf_int=None*, *scatter=None*, *save=None*)

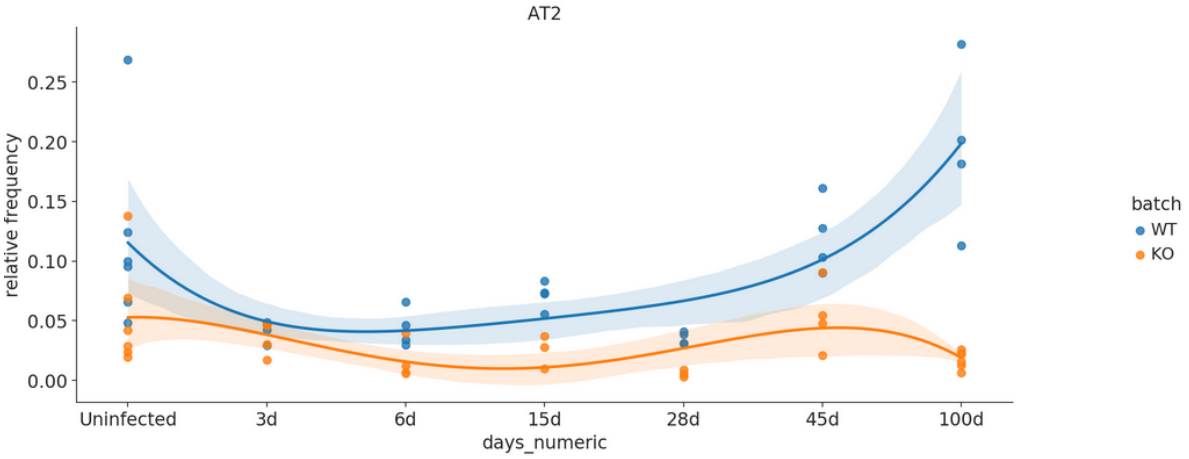
Plot relative frequencies as a line plot.

Parameters

- **relative_frequencies** (DataFrame) – Data frame containing relative Frequencies as calculated by calc_relFreq()
- **order** – Order of x-axis labels from left to right
- **cluster** – Which cluster to plot
- **xlabel** (str) – x-axis label
- **ylabel** (str) – y-axis label
- **hue** (Optional[str]) – Value to color by
- **smooth** (Optional[bool]) – Whether to smoothen the plot
- **cols** – List of colors to use for line plot
- **title** (Optional[str]) – Title of the plot
- **rotation** (Optional[int]) – Rotation of the x-axis labels
- **figsize** (Tuple[int, int]) – Size of the figure as specified in matplotlib
- **tick_size** (Optional[int]) – Size of the ticks as specified in matplotlib

- **label_size** (Optional[int]) – Size of the labels as specified in matplotlib
- **order_smooth** (int) – If greater than 1, numpy.polyfit is used to estimate a polynomial regression
- **conf_int** – Size of the confidence interval for the regression estimate
- **scatter** – Set to True to add average expression values per sample ID as dots
- **save** (Optional[str]) – Path to save the plot to

Example



2.3.17 sc_toolbox.plot.annotated_cell_type_umap

sc_toolbox.plot.**annotated_cell_type_umap**(*adata*, *primary_color*, *cell_type_color*, *legend_loc='on data'*, *legend_fontsize=8*, *title='Plot title'*, *palette=None*, *cmap=None*, *figsize=(8, 6)*, *save=None*)

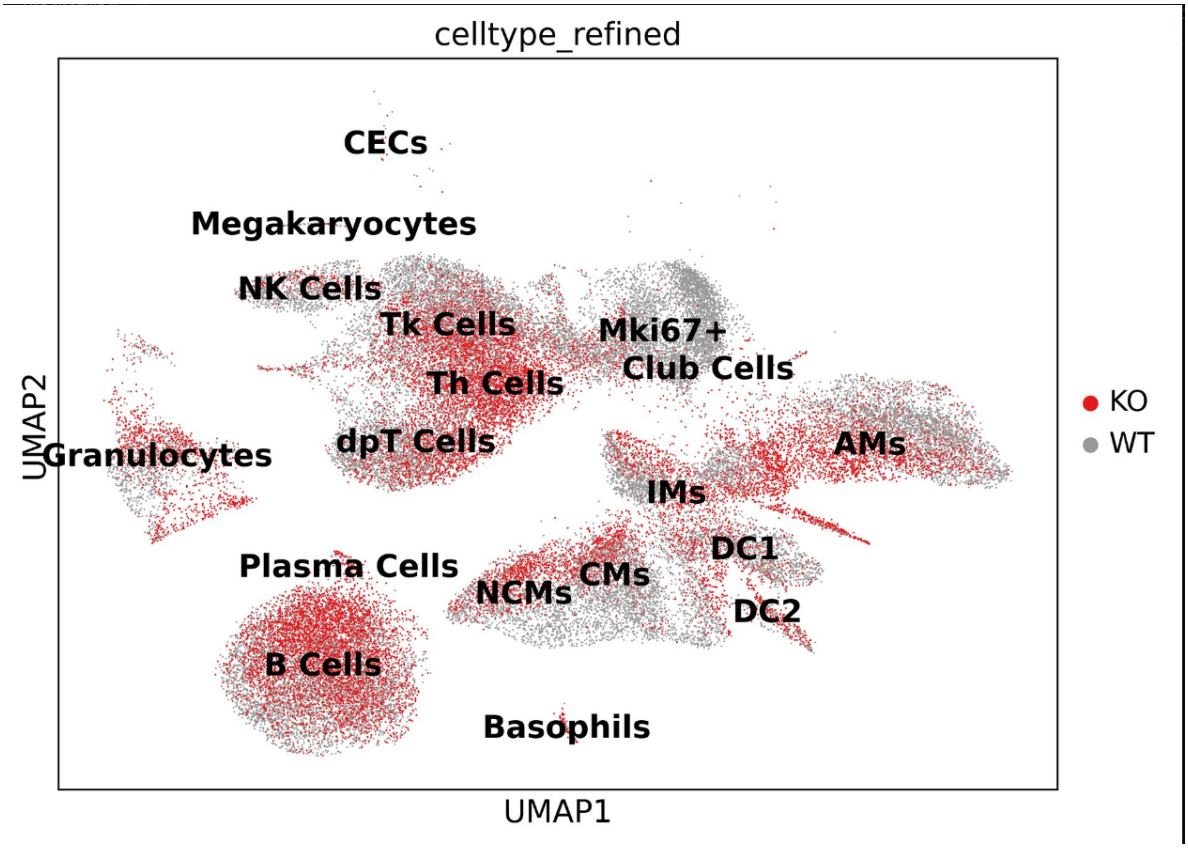
Plots a UMAP which is colored by the primary_color, but also draws all labels on top of all clusters.

Parameters

- **adata** – AnnData object
- **primary_color** (Union[str, Sequence[str]]) – Primary color to color all cells by, e.g. 'genotype'
- **cell_type_color** (str) – Key containing all cell types, e.g. 'cell_type'
- **legend_loc** (str) – Location of the legend (default: 'on data')
- **legend_fontsize** (int) – Font size of the legend (default: 8)
- **title** (str) – Title of the plot
- **palette** – Color
- **cmap** – Color map of the UMAP
- **figsize** – Size of the figure
- **save** – Path to save the plot to

Returns
fig and axs Matplotlib objects

Example



2.3.18 sc_toolbox.plot.genotype_vs_genotype_umaps

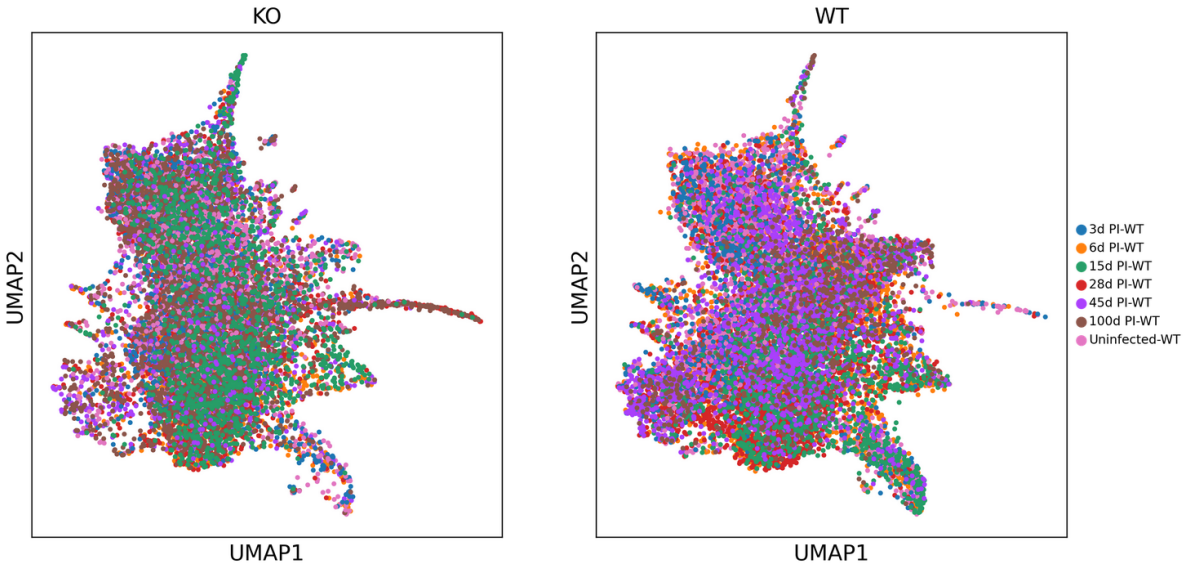
sc_toolbox.plot.**genotype_vs_genotype_umaps**(*adata*, *genotype_key*, *genotype_label_1*, *genotype_label_2*, *color*, *hide_one_legend=True*, *figsize=(12, 6)*)

Plots a two UMAPs of genotypes next to each other displaying only the colors of the second UMAP.

Parameters

- **adata** – AnnData object
- **genotype_key** (str) – Key of the genotypes
- **genotype_label_1** (str) – Name of the first genotype; Must be contained in the genotypes
- **genotype_label_2** (str) – Name of the second genotype; Must be contained in the genotypes
- **color** (str) – Key to color by
- **hide_one_legend** (bool) – Whether to hide the legend of the genotype_label_1
- **figsize** (Tuple[int, int]) – Size of the figure

Example


KO
WT
UMAP2
UMAP1
UMAP2
UMAP1
3d PI-WT
6d PI-WT
15d PI-WT
28d PI-WT
45d PI-WT
100d PI-WT
Uninfected-WT

CHAPTER

THREE

CONTRIBUTOR GUIDE

Thank you for your interest in improving this project. This project is open-source under the Apache2.0 license and highly welcomes contributions in the form of bug reports, feature requests, and pull requests.

Here is a list of important resources for contributors:

- Source Code
- Documentation
- Issue Tracker
- Code of Conduct

3.1 How to report a bug

Report bugs on the Issue Tracker.

3.2 How to request a feature

Request features on the Issue Tracker.

3.3 Getting the code

```
$ git clone --recurse-submodules https://github.com/schillerlab/sc-toolbox
```

3.4 How to set up your development environment

You need Python 3.8+ and the following tools:

- Poetry
- Nox
- nox-poetry

You can install them with:

```
$ pip install poetry nox nox-poetry
```

Install the package with development requirements:

```
$ make install
```

You can now run an interactive Python session, or the command-line interface:

```
$ poetry run python
$ poetry run sc_toolbox
```

3.5 How to test the project

Run the full test suite:

```
$ nox
```

List the available Nox sessions:

```
$ nox --list-sessions
```

You can also run a specific Nox session. For example, invoke the unit test suite like this:

```
$ nox --session=tests
```

Unit tests are located in the `tests` directory, and are written using the pytest testing framework.

3.6 How to build and view the documentation

This project uses [Sphinx] together with several extensions to build the documentation. It further requires [Pandoc] to translate various formats.

To install all required dependencies for the documentation run:

```
$ pip install -r docs/requirements.txt
```

Please note that ehrapy itself must also be installed. To build the documentation run:

```
$ make html
```

from inside the docs folder. The generated static HTML files can be found in the `_build/html` folder. Simply open them with your favorite browser.

3.7 How to submit changes

Open a pull request to submit changes to this project against the `development` branch.

Your pull request needs to meet the following guidelines for acceptance:

- The Nox test suite must pass without errors and warnings.
- Include unit tests. This project maintains a high code coverage.
- If your changes add functionality, update the documentation accordingly.

To run linting and code formatting checks before committing your change, you can install pre-commit as a Git hook by running the following command:

```
$ nox --session=pre-commit -- install
```

It is recommended to open an issue before starting work on anything. This will allow a chance to talk it over with the owners and validate your approach.

CHAPTER

FOUR

CONTRIBUTOR COVENANT CODE OF CONDUCT

4.1 Our Pledge

In the interest of fostering an open and welcoming environment, we as contributors and maintainers pledge to making participation in our project and our community a harassment-free experience for everyone, regardless of age, body size, disability, ethnicity, gender identity and expression, level of experience, nationality, personal appearance, race, religion, or sexual identity and orientation.

4.2 Our Standards

Examples of behavior that contributes to creating a positive environment include:

- Using welcoming and inclusive language
- Being respectful of differing viewpoints and experiences
- Gracefully accepting constructive criticism
- Focusing on what is best for the community
- Showing empathy towards other community members

Examples of unacceptable behavior by participants include:

- The use of sexualized language or imagery and unwelcome sexual attention or advances
- Trolling, insulting/derogatory comments, and personal or political attacks
- Public or private harassment
- Publishing others' private information, such as a physical or electronic address, without explicit permission
- Other conduct which could reasonably be considered inappropriate in a professional setting

4.3 Our Responsibilities

Project maintainers are responsible for clarifying the standards of acceptable behavior and are expected to take appropriate and fair corrective action in response to any instances of unacceptable behavior.

Project maintainers have the right and responsibility to remove, edit, or reject comments, commits, code, wiki edits, issues, and other contributions that are not aligned to this Code of Conduct, or to ban temporarily or permanently any contributor for other behaviors that they deem inappropriate, threatening, offensive, or harmful.

4.4 Scope

This Code of Conduct applies both within project spaces and in public spaces when an individual is representing the project or its community. Examples of representing a project or community include using an official project e-mail address, posting via an official social media account, or acting as an appointed representative at an online or offline event. Representation of a project may be further defined and clarified by project maintainers.

4.5 Enforcement

Instances of abusive, harassing, or otherwise unacceptable behavior may be reported by opening an issue. The project team will review and investigate all complaints, and will respond in a way that it deems appropriate to the circumstances. The project team is obligated to maintain confidentiality with regard to the reporter of an incident. Further details of specific enforcement policies may be posted separately.

Project maintainers who do not follow or enforce the Code of Conduct in good faith may face temporary or permanent repercussions as determined by other members of the project's leadership.

4.6 Attribution

This Code of Conduct is adapted from the Contributor Covenant, version 1.4, available at https://www.contributor-covenant.org/version/1/4/code-of-conduct.html

CHAPTER

FIVE

CREDITS

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CHAPTER

SIX

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