**scVelo** is a scalable toolkit for RNA velocity analysis in single cells, based on Bergen et al. (Nature Biotech, 2020). RNA velocity enables the recovery of directed dynamic information by leveraging splicing kinetics. scVelo generalizes the concept of RNA velocity (La Manno et al., Nature, 2018) by relaxing previously made assumptions with a stochastic and a dynamical model that solves the full transcriptional dynamics. It thereby adapts RNA velocity to widely varying specifications such as non-stationary populations.

scVelo is compatible with scnapy and hosts efficient implementations of all RNA velocity models.
scVelo’s key applications

• estimate RNA velocity to study cellular dynamics.
• identify putative driver genes and regimes of regulatory changes.
• infer a latent time to reconstruct the temporal sequence of transcriptomic events.
• estimate reaction rates of transcription, splicing and degradation.
• use statistical tests, e.g., to detect different kinetics regimes.

scVelo has, for instance, recently been used to study immune response in COVID-19 patients and dynamic processes in human lung regeneration. Find out more in this list of application examples.
Latest news

• Aug/2021: Perspectives paper out in MSB
• Feb/2021: scVelo goes multi-core
• Dec/2020: Cover of Nature Biotechnology
• Nov/2020: Talk at Single Cell Biology
• Oct/2020: Helmholtz Best Paper Award
• Oct/2020: Map cell fates with CellRank
• Sep/2020: Talk at Single Cell Omics
• Aug/2020: scVelo out in Nature Biotech
Bergen et al. (2020), Generalizing RNA velocity to transient cell states through dynamical modeling, *Nature Biotech*.
Bergen et al. (2021), RNA velocity - current challenges and future perspectives, *Molecular Systems Biology*. 
Chapter 3. References
Found a bug or would like to see a feature implemented? Feel free to submit an issue. Have a question or would like to start a new discussion? Head over to GitHub discussions. In either case, you can also always send us an email. Your help to improve scVelo is highly appreciated. For further information visit scvelo.org.

4.1 About scVelo

Measuring gene activity in individual cells requires destroying these cells to read out their content, making it challenging to study dynamic processes and to learn about cellular decision making. The introduction of RNA velocity by La Manno et al. (Nature, 2018) has enabled the recovery of directed dynamic information by leveraging the fact that newly transcribed, unspliced pre-mRNAs and mature, spliced mRNAs can be distinguished in common single-cell RNA-seq protocols, the former detectable by the presence of introns. This concept of measuring not only gene activity, but also their changes in individual cells (RNA velocity), has opened up new ways of studying cellular differentiation. The originally proposed framework obtains velocities as the deviation of the observed ratio of spliced and unspliced mRNA from an inferred steady state. Errors in velocity estimates arise if the central assumptions of a common splicing rate and the observation of the full splicing dynamics with steady-state mRNA levels are violated.

With scVelo, developed by Bergen et al. (Nature Biotechnology, 2020), these restrictions are addressed by solving the full transcriptional dynamics of splicing kinetics using a likelihood-based dynamical model. This generalizes RNA velocity to a wide variety of systems comprising transient cell states, which are common in development and in response to perturbations. Further, scVelo infers gene-specific rates of transcription, splicing and degradation, and recovers the latent time of the underlying cellular processes. This latent time represents the cell’s internal clock and approximates the real time experienced by cells as they differentiate, based only on its transcriptional dynamics. Moreover, scVelo identifies regimes of regulatory changes such as stages of cell fate commitment and, therein, systematically detects putative driver genes.

4.1.1 RNA velocity models

With RNA velocity, inference of directional trajectories is explored by connecting measurements to the underlying mRNA splicing kinetics: Transcriptional induction for a particular gene results in an increase of (newly transcribed) precursor unspliced mRNAs while, conversely, repression or absence of transcription results in a decrease of unspliced
mRNAs. Hence, by distinguishing unspliced from spliced mRNA, the change of mRNA abundance (RNA velocity) can be approximated. The combination of velocities across mRNAs can then be used to estimate the future state of an individual cell.

RNA velocity estimation can currently be tackled with three existing approaches:

- steady-state / deterministic model (using steady-state residuals)
- stochastic model (using second-order moments),
- dynamical model (using a likelihood-based framework).

The steady-state / deterministic model, as being used in velocyto, estimates velocities as follows: Under the assumption that transcriptional phases (induction and repression) last sufficiently long to reach a steady-state equilibrium (active and inactive), velocities are quantified as the deviation of the observed ratio from its steady-state ratio. The equilibrium mRNA levels are approximated with a linear regression on the presumed steady states in the lower and upper quantiles. This simplification makes two fundamental assumptions: a common splicing rate across genes and steady-state mRNA levels to be reflected in the data. It can lead to errors in velocity estimates and cellular states as the assumptions are often violated, in particular when a population comprises multiple heterogeneous subpopulation dynamics.

The stochastic model aims to better capture the steady states. By treating transcription, splicing and degradation as probabilistic events, the resulting Markov process is approximated by moment equations. By including second-order moments, it exploits not only the balance of unspliced to spliced mRNA levels but also their covariation. It has been demonstrated on the endocrine pancreas that stochasticity adds valuable information, overall yielding higher consistency than the deterministic model, while remaining as efficient in computation time.

The dynamical model (most powerful while computationally most expensive) solves the full dynamics of splicing kinetics for each gene. It thereby adapts RNA velocity to widely varying specifications such as non-stationary populations, as does not rely on the restrictions of a common splicing rate or steady states to be sampled.

The splicing dynamics

\[
\frac{du(t)}{dt} = \alpha_k(t) - \beta u(t), \quad (4.1)
\]

\[
\frac{ds(t)}{dt} = \beta u(t) - \gamma s(t), \quad (4.2)
\]

is solved in a likelihood-based expectation-maximization framework, by iteratively estimating the parameters of reaction rates and latent cell-specific variables, i.e. transcriptional state \( k \) and cell-internal latent time \( t \).

It thereby aims to learn the unspliced/spliced phase trajectory. Four transcriptional states are modeled to account for all possible configurations of gene activity: two dynamic transient states (induction and repression) and two steady states (active and inactive) potentially reached after each dynamic transition.

In the expectation step, for a given model estimate of the unspliced/spliced phase trajectory, a latent time is assigned to an observed mRNA value by minimizing its distance to the phase trajectory. The transcriptional states are then assigned by associating a likelihood to the respective segments on the phase trajectory (induction, repression, active and inactive steady states). In the maximization step, the overall likelihood is then optimized by updating the parameters of reaction rates.

The model yields more consistent velocity estimates and better identification of transcriptional states. It further enables the systematic identification of dynamics-driving genes in a likelihood-based way, thereby finding the key drivers that govern cell fate transitions. Moreover, the dynamical model infers a universal cell-internal latent time shared across genes that enables relating genes and identifying regimes of transcriptional changes.

For best results and above-described additional insights, we recommend using the dynamical model. If runtime is of importance, the stochastic model is advised to be used as it very efficiently approximates the dynamical model, taking few minutes on 30k cells. The dynamical yet can take up to one hour, however, enhancing efficiency is in progress.

See Bergen et al. (2020) for a detailed exposition of the methods.
4.2 Installation

scVelo requires Python 3.6 or later. We recommend to use Miniconda.

4.2.1 PyPI

Install scVelo from PyPI using:

```
pip install -U scvelo
```

-U is short for `--upgrade`. If you get a Permission denied error, use `pip install -U scvelo --user` instead.

4.2.2 Development Version

To work with the latest development version, install from GitHub using:

```
pip install git+https://github.com/theislab/scvelo@develop
```

or:

```
git clone https://github.com/theislab/scvelo && cd scvelo
git checkout --track origin/develop
pip install -e .
```

-e is short for `--editable` and links the package to the original cloned location such that pulled changes are also reflected in the environment.

To contribute to scVelo, cd into the cloned directory and install the latest packages required for development together with the pre-commit hooks:

```
pip install -r requirements-dev.txt
pre-commit install
```

4.2.3 Dependencies

- `anndata` - annotated data object.
- `scanpy` - toolkit for single-cell analysis.
- `numpy`, `scipy`, `pandas`, `scikit-learn`, `matplotlib`.

Parts of scVelo (directed PAGA and Louvain modularity) require (optional):

```
pip install python-igraph louvain
```

Using fast neighbor search via `hnswlib` further requires (optional):

```
pip install pybind11 hnswlib
```
4.2.4 Jupyter Notebook

To run the tutorials in a notebook locally, please install:

```
conda install notebook
```

and run `jupyter notebook` in the terminal. If you get the error `Not a directory: 'xdg-settings'`, use `jupyter notebook --no-browser` instead and open the url manually (or use this bugfix).

If you run into issues, do not hesitate to approach us or raise a GitHub issue. scvelo - RNA velocity generalized through dynamical modeling

4.3 API

Import scVelo as:

```
import scvelo as scv
```

After reading the data (`scv.read`) or loading an in-built dataset (`scv.datasets.*`), the typical workflow consists of subsequent calls of preprocessing (`scv.pp.*`), analysis tools (`scv.tl.*`) and plotting (`scv.pl.*`). Further, several utilities (`scv.utils.*) are provided to facilitate data analysis.

4.3.1 Read / Load

```
read(filename[, backed, sheet, ext, ...])
read_loom(filename, *[sparse, cleanup, ...])
```

Read file and return `AnnData` object.

```
scvelo.read
```

`scvelo.read` is the same as in `sc.read(filename, ...)`. To speed up reading, consider passing `cache=True`, which creates an hdf5 cache file.

Parameters

- `filename`: Path, str If the filename has no file extension, it is interpreted as a key for generating a filename via `sc.settings.writedir / (filename + sc.settings.file_format_data)`. This is the same behavior as in `sc.read(filename, ...)`.  
- `backed`: _Genericalias[r, r+], None_ If 'r', load `AnnData` in `backed` mode instead of fully loading it into memory (memory mode). If you want to modify backed attributes of the `AnnData` object, you need to choose 'r+'.  
- `sheet`: str, None Name of sheet/table in hdf5 or Excel file.  
- `ext`: str, None Extension that indicates the file type. If None, uses extension of filename.  
- `delimiter`: str, None Delimiter that separates data within text file. If None, will split at arbitrary number of white spaces, which is different from enforcing splitting at any single white space ' ']'.
**first_column_names:** bool Assume the first column stores row names. This is only necessary if these are not strings: strings in the first column are automatically assumed to be row names.

**backup_url:** str, None Retrieve the file from an URL if not present on disk.

**cache:** bool If False, read from source, if True, read from fast ‘h5ad’ cache.

**cache_compression:** _Genericalias[gzip, lzf], None, Empty See the h5py dataset_compression. (Default: settings.cache_compression)

**kwargs** Parameters passed to `read_loom()`.

Return type AnnData

Returns An AnnData object

**scvelo.read_loom**

```python
scvelo.read_loom(filename, *, sparse=True, cleanup=False, X_name='spliced', obs_names='CellID', obsm_names=None, var_names='Gene', varm_names=None, dtype='float32', obsm_mapping=mappingproxy({}), varm_mapping=mappingproxy({}), **kwargs)
```

Read .loom-formatted hdf5 file.

This reads the whole file into memory.

Beware that you have to explicitly state when you want to read the file as sparse data.

Parameters

**filename:** PathLike The filename.

**sparse:** bool Whether to read the data matrix as sparse.

**cleanup:** bool Whether to collapse all obs/var fields that only store one unique value into `.uns['loom-']`.

**X_name:** str Loompy key with which the data matrix `X` is initialized.

**obs_names:** str Loompy key where the observation/cell names are stored.

**obsm_names:** Mapping[str, Iterable[str]] Loompy keys which will be constructed into observation matrices

**var_names:** str Loompy key where the variable/gene names are stored.

**varm_names:** Mapping[str, Iterable[str]] Loompy keys which will be constructed into variable matrices

**kwargs** Arguments to loompy.connect

Example

```python
pbmc = anndata.read_loom("pbmc.loom", sparse=True, X_name="lognorm", obs_names="cell_names", var_names="gene_names", obsm_mapping="X_umap": ["umap_1", "umap_2"]
```

(continues on next page)
Return type: AnnData

### 4.3.2 Preprocessing (pp)

**Basic preprocessing** (gene selection and normalization)

<table>
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<th>Function</th>
<th>Description</th>
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<tr>
<td><code>pp.filter_genes(data[, min_counts, ...])</code></td>
<td>Filter genes based on number of cells or counts.</td>
</tr>
<tr>
<td><code>pp.filter_genes_dispersion(data[, flavor, ...])</code></td>
<td>Extract highly variable genes.</td>
</tr>
<tr>
<td><code>pp.normalize_per_cell(data[, ...])</code></td>
<td>Normalize each cell by total counts over all genes.</td>
</tr>
<tr>
<td><code>pp.log1p(data[, copy])</code></td>
<td>Logarithmize the data matrix.</td>
</tr>
<tr>
<td><code>pp.filter_and_normalize(data[, min_counts, ...])</code></td>
<td>Filtering, normalization and log transform</td>
</tr>
</tbody>
</table>

**scvelo.pp.filter_genes**

`scvelo.pp.filter_genes(data, min_counts=None, min_cells=None, max_counts=None, max_cells=None, min_counts_u=None, min_cells_u=None, max_counts_u=None, max_cells_u=None, min_shared_counts=None, min_shared_cells=None, retain_genes=None, copy=False)`

Filter genes based on number of cells or counts. Keep genes that have at least `min_counts` counts or are expressed in at least `min_cells` cells or have at most `max_counts` counts or are expressed in at most `max_cells` cells. Only provide one of the optional parameters `min_counts`, `min_cells`, `max_counts`, `max_cells` per call.

**Parameters**

- `data`: AnnData, np.ndarray, sp.spmatrix The (annotated) data matrix of shape `n_obs x n_vars`. Rows correspond to cells and columns to genes.
- `min_counts`: int, optional (default: `None`) Minimum number of counts required for a gene to pass filtering.
- `min_cells`: int, optional (default: `None`) Minimum number of cells expressed required for a gene to pass filtering.
- `max_counts`: int, optional (default: `None`) Maximum number of counts required for a gene to pass filtering.
- `max_cells`: int, optional (default: `None`) Maximum number of cells expressed required for a gene to pass filtering.
- `min_counts_u`: int, optional (default: `None`) Minimum number of unspliced counts required for a gene to pass filtering.
- `min_cells_u`: int, optional (default: `None`) Minimum number of unspliced cells expressed required to pass filtering.
- `max_counts_u`: int, optional (default: `None`) Maximum number of unspliced counts required for a gene to pass filtering.
- `max_cells_u`: int, optional (default: `None`) Maximum number of unspliced cells expressed required to pass filtering.
**min_shared_counts**: int, optional (default: None) Minimum number of counts (both unspliced and spliced) required for a gene.

**min_shared_cells**: int, optional (default: None) Minimum number of cells required to be expressed (both unspliced and spliced).

**retain_genes**: list, optional (default: None) List of gene names to be retained independent of thresholds.

**copy**: bool, optional (default: False) Determines whether a copy is returned.

**Returns** Filters the object and adds `n_counts` to `adata.var`.

### `scvelo.pp.filter_genes_dispersion`

`scvelo.pp.filter_genes_dispersion(data, flavor='seurat', min_disp=None, max_disp=None, min_mean=None, max_mean=None, n_bins=20, n_top_genes=None, retain_genes=None, log=True, subset=True, copy=False)`

Extract highly variable genes.

Expects non-logarithmized data. The normalized dispersion is obtained by scaling with the mean and standard deviation of the dispersions for genes falling into a given bin for mean expression of genes. This means that for each bin of mean expression, highly variable genes are selected.

**Parameters**

- **data**: AnnData, np.ndarray, sp.sparse The (annotated) data matrix of shape `n_obs × n_vars`. Rows correspond to cells and columns to genes.

- **flavor**: {'seurat', 'cell_ranger', 'svr'}, optional (default: 'seurat') Choose the flavor for computing normalized dispersion. If choosing 'seurat', this expects non-logarithmized data - the logarithm of mean and dispersion is taken internally when `log` is at its default value `True`. For 'cell_ranger', this is usually called for logarithmized data - in this case you should set `log` to `False`. In their default workflows, Seurat passes the cutoffs whereas Cell Ranger passes `n_top_genes`.

- **max_mean=3, min_disp=0.5, max_disp='None': min_mean=0.0125** If `n_top_genes` unequals `None`, these cutoffs for the means and the normalized dispersions are ignored.

- **n_bins**: int (default: 20) Number of bins for binning the mean gene expression. Normalization is done with respect to each bin. If just a single gene falls into a bin, the normalized dispersion is artificially set to 1. You’ll be informed about this if you set `settings.verbosity = 4`.

- **n_top_genes**: int or None (default: None) Number of highly-variable genes to keep.

- **retain_genes**: list, optional (default: None) List of gene names to be retained independent of thresholds.

- **log**: bool, optional (default: True) Use the logarithm of the mean to variance ratio.

- **subset**: bool, optional (default: True) Keep highly-variable genes only (if True) else write a bool array for highly-variable genes while keeping all genes.

- **copy**: bool, optional (default: False) If an AnnData is passed, determines whether a copy is returned.

**Returns** If an AnnData `adata` is passed, returns or updates `adata` depending on `copy`. It filters the `adata` and adds the annotations.
scvelo.pp.normalize_per_cell

`scvelo.pp.normalize_per_cell(data, counts_per_cell_after=None, counts_per_cell=None, key_n_counts=None, max_proportion_per_cell=None, use_initial_size=True, layers=None, enforce=None, copy=False)`

Normalize each cell by total counts over all genes.

**Parameters**

- **data**: AnnData, np.ndarray, sp.sparse The (annotated) data matrix of shape \( n_{\text{obs}} \times n_{\text{vars}} \). Rows correspond to cells and columns to genes.
- **counts_per_cell_after**: float or None, optional (default: None) If None, after normalization, each cell has a total count equal to the median of the `counts_per_cell` before normalization.
- **counts_per_cell**: np.array, optional (default: None) Precomputed counts per cell.
- **key_n_counts**: str, optional (default: `‘n_counts’`) Name of the field in `adata.obs` where the total counts per cell are stored.
- **max_proportion_per_cell**: int (default: None) Exclude genes counts that account for more than a specific proportion of cell size, e.g. 0.05.
- **use_initial_size**: bool (default: True) Whether to use initial cell sizes oder actual cell sizes.
- **layers**: str or list (default: [‘spliced’, ‘unspliced’]) Keys for layers to be also considered for normalization.
- **copy**: bool, optional (default: False) If an AnnData is passed, determines whether a copy is returned.

**Returns** Returns or updates `adata` with normalized counts.

scvelo.pp.log1p

`scvelo.pp.log1p(data, copy=False)`

Logarithmize the data matrix. Computes \( X = \log(X + 1) \), where \( \log \) denotes the natural logarithm.  

- **param data**: Annotated data matrix.  
- **type data**: AnnData  
- **param copy**: Return a copy of `adata` instead of updating it.  
- **type copy**: bool (default: False)

**Returns** Returns or updates `adata` depending on `copy`.

scvelo.pp.filter_and_normalize

`scvelo.pp.filter_and_normalize(data, min_counts=None, min_counts_u=None, min_cells=None, min_cells_u=None, min_shared_counts=None, min_shared_cells=None, n_top_genes=None, retain_genes=None, subset_highly_variable=True, flavor='seurat', log=True, layers_normalize=None, copy=False, **kwargs)`

Filtering, normalization and log transform

Expects non-logarithmized data. If using logarithmized data, pass `log=False`.

Runs the following steps
```python
scv.pp.filter_genes(adata)
scv.pp.normalize_per_cell(adata)
if n_top_genes is not None:
    scv.pp.filter_genes_dispersion(adata)
if log:
    scv.pp.log1p(adata)

Parameters

    data : AnnData Annotated data matrix.
    min_counts : int (default: None) Minimum number of counts required for a gene to pass filtering (spliced).
    min_counts_u : int (default: None) Minimum number of counts required for a gene to pass filtering (unspliced).
    min_cells : int (default: None) Minimum number of cells expressed required to pass filtering (spliced).
    min_cells_u : int (default: None) Minimum number of cells expressed required to pass filtering (unspliced).
    min_shared_counts : int, optional (default: None) Minimum number of counts (both unspliced and spliced) required for a gene.
    min_shared_cells : int, optional (default: None) Minimum number of cells required to be expressed (both unspliced and spliced).
    n_top_genes : int (default: None) Number of genes to keep.
    retain_genes : list, optional (default: None) List of gene names to be retained independent of thresholds.
    subset_highly_variable : bool (default: True) Whether to subset highly variable genes or to store in .var[‘highly_variable’].
    log : bool (default: True) Take logarithm.
    layers_normalize : list of str (default: None) List of layers to be normalized. If set to None, the layers {‘X’, ‘spliced’, ‘unspliced’} are considered for normalization upon testing whether they have already been normalized (by checking type of entries: int -> unprocessed, float -> processed).
    copy : bool (default: False) Return a copy of adata instead of updating it.

**kwargs Keyword arguments passed to pp.normalize_per_cell (e.g. counts_per_cell).

Returns Returns or updates adata depending on copy.

Moments (across nearest neighbors in PCA space)

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>pp.pca(data[, n_comps, zero_center, ...])</code></td>
<td>Principal component analysis [Pedregosa11].</td>
</tr>
<tr>
<td><code>pp.neighbors(adata[, n_neighbors, n_pcs, ...])</code></td>
<td>Compute a neighborhood graph of observations.</td>
</tr>
<tr>
<td><code>pp.moments(data[, n_neighbors, n_pcs, mode, ...])</code></td>
<td>Computes moments for velocity estimation.</td>
</tr>
</tbody>
</table>

4.3. API
scvelo.pp.pca

scvelo.pp.pca(data, n_comps=None, zero_center=True, svd_solver='arpack', random_state=0, return_info=False, use_highly_variable=None, dtype='float32', copy=False, chunked=False, chunk_size=None)

Principal component analysis [Pedregosa11].

Computes PCA coordinates, loadings and variance decomposition. Uses the implementation of scikit-learn [Pedregosa11].

Changed in version 1.5.0: In previous versions, computing a PCA on a sparse matrix would make a dense copy of the array for mean centering. As of scanpy 1.5.0, mean centering is implicit. While results are extremely similar, they are not exactly the same. If you would like to reproduce the old results, pass a dense array.

Parameters

- **data** : AnnData, ndarray, spmatrix The (annotated) data matrix of shape n_obs × n_vars. Rows correspond to cells and columns to genes.

- **n_comps** : int, None Number of principal components to compute. Defaults to 50, or 1 - minimum dimension size of selected representation.

- **zero_center** : bool, None If True, compute standard PCA from covariance matrix. If False, omit zero-centering variables (uses TruncatedSVD), which allows to handle sparse input efficiently. Passing None decides automatically based on sparseness of the data.

- **svd_solver** : str SVD solver to use:
  - 'arpack' (the default) for the ARPACK wrapper in SciPy (svds())
  - 'randomized' for the randomized algorithm due to Halko (2009).
  - 'auto' chooses automatically depending on the size of the problem.
  - 'lobpcg' An alternative SciPy solver.
  
  Changed in version 1.4.5: Default value changed from 'auto' to 'arpack'.

- **random_state** : None, int, RandomState Change to use different initial states for the optimization.

- **return_info** : bool Only relevant when not passing an AnnData: see "Returns".

- **use_highly_variable** : bool, None Whether to use highly variable genes only, stored in .var['highly_variable']. By default uses them if they have been determined beforehand.

- **dtype** : str Numpy data type string to which to convert the result.

- **copy** : bool If an AnnData is passed, determines whether a copy is returned. Is ignored otherwise.

- **chunked** : bool If True, perform an incremental PCA on segments of chunk_size. The incremental PCA automatically zero centers and ignores settings of random_seed and svd_solver. If False, perform a full PCA.

- **chunk_size** : int, None Number of observations to include in each chunk. Required if chunked=True was passed.

Returns

AnnData, ndarray, spmatrix
• **X_pca** (spmatrix, ndarray) – If *data* is array-like and *return_info=False* was passed, this function only returns *X_pca*...

• **adata** (anndata.AnnData) – ...otherwise if *copy=True* it returns or else adds fields to *adata*:
  - .obsm['X_pca']  PCA representation of data.
  - .varm['PCs']  The principal components containing the loadings.
  - .uns['pca']['variance_ratio']  Ratio of explained variance.
  - .uns['pca']['variance']  Explained variance, equivalent to the eigenvalues of the covariance matrix.

### scvelo.pp.neighbors

**scvelo.pp.neighbors**(*adata, n_neighbors=30, n_pcs=None, use_rep=None, use_highly_variable=True, knn=True, random_state=0, method='umap', metric='euclidean', metric_kwds=None, num_threads=-1, copy=False*)

Compute a neighborhood graph of observations.

The neighbor graph methods (umap, hnsw, sklearn) only differ in runtime and yield the same result as scanpy [Wolf18]. Connectivities are computed with adaptive kernel width as proposed in Haghverdi et al. 2016 (doi:10.1038/nmeth.3971).

**Parameters**

- **adata**  Annotated data matrix.

  - **n_neighbors**  The size of local neighborhood (in terms of number of neighboring data points) used for manifold approximation. Larger values result in more global views of the manifold, while smaller values result in more local data being preserved. In general values should be in the range 2 to 100. If *knn* is True, number of nearest neighbors to be searched. If *knn* is False, a Gaussian kernel width is set to the distance of the n_neighbors neighbor.

  - **n_pcs**: int or None (default: None)  Number of principal components to use. If not specified, the full space is used of a pre-computed PCA, or 30 components are used when PCA is computed internally.

  - **use_rep**: None, ‘X’ or any key for .obsm (default: None)  Use the indicated representation. If None, the representation is chosen automatically: for n_vars < 50, X is used, otherwise ‘X_pca’ is used.

  - **use_highly_variable**: bool (default: True)  Whether to use highly variable genes only, stored in .var['highly_variable'].

  - **knn**  If True, use a hard threshold to restrict the number of neighbors to n_neighbors, that is, consider a knn graph. Otherwise, use a Gaussian Kernel to assign low weights to neighbors more distant than the n_neighbors nearest neighbor.

  - **random_state**  A numpy random seed.

  - **method**: [‘umap’, ‘hnsw’, ‘sklearn’] (default: ‘umap’)  Method to compute neighbors, only differs in runtime. The ‘hnsw’ method is most efficient and requires to pip install hnswlib. Connectivities are computed with adaptive kernel.

  - **metric**  A known metric’s name or a callable that returns a distance.

  - **metric_kwds**  Options for the metric.

  - **num_threads**  Number of threads to be used (for runtime).

  - **copy**  Return a copy instead of writing to adata.
Returns

- **connectivities** (.obsp) – Sparse weighted adjacency matrix of the neighborhood graph of data points. Weights should be interpreted as connectivities.
- **distances** (.obsp) – Sparse matrix of distances for each pair of neighbors.

### scvelo.pp.moments

**scvelo.pp.moments** *(data, n_neighbors=30, n_pcs=None, mode='connectivities', method='umap', use_rep=None, use_highly_variable=True, copy=False)*

Computes moments for velocity estimation. First-/second-order moments are computed for each cell across its nearest neighbors, where the neighbor graph is obtained from euclidean distances in PCA space.

**Parameters**

- **data**: *AnnData*  Annotated data matrix.
- **n_neighbors**: *int* (default: 30)  Number of neighbors to use.
- **n_pcs**: *int* (default: None)  Number of principal components to use. If not specified, the full space is used of a pre-computed PCA, or 30 components are used when PCA is computed internally.
- **mode**:  ‘connectivities’ or ‘distances’ (default: ‘connectivities’)  Distance metric to use for moment computation.
- **method**:  {{'umap', 'hnsw', 'sklearn', None}} (default: ‘umap’)  Method to compute neighbors, only differs in runtime. Connectivities are computed with adaptive kernel width as proposed in Haghverdi et al. 2016 (https://doi.org/10.1038/nmeth.3971).
- **use_rep**:  None, ‘X’ or any key for .obsm (default: None)  Use the indicated representation. If None, the representation is chosen automatically: for n_vars < 50, .X is used, otherwise ‘X_pca’ is used.
- **use_highly_variable**:  *bool* (default: True)  Whether to use highly variable genes only, stored in .var['highly_variable'].
- **copy**:  *bool* (default: False)  Return a copy instead of writing to adata.

**Returns**

- **Ms** (.layers) – dense matrix with first order moments of spliced counts.
- **Mu** (.layers) – dense matrix with first order moments of unspliced counts.

### 4.3.3 Tools (tl)

**Clustering and embedding** (more at scanpy-docs)

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>tl.louvain</strong> <em>(adata[, resolution, ...])</em></td>
<td>Cluster cells into subgroups [Blondel08] [Levine15] [Traag17].</td>
</tr>
<tr>
<td><strong>tl.umap</strong> <em>(adata[, min_dist, spread, ...])</em></td>
<td>Embed the neighborhood graph using UMAP [McInnes18].</td>
</tr>
</tbody>
</table>
Cluster cells into subgroups [Blondel08] [Levine15] [Traag17].
Cluster cells using the Louvain algorithm [Blondel08] in the implementation of [Traag17]. The Louvain algorithm has been proposed for single-cell analysis by [Levine15]. This requires having run `neighbors()` or `bbknn()` first, or explicitly passing a `adjacency` matrix.

**Parameters**

- `adata`: AnnData The annotated data matrix.
- `resolution`: float, None For the default flavor (`'vtraag'`), you can provide a resolution (higher resolution means finding more and smaller clusters), which defaults to 1.0. See “Time as a resolution parameter” in [Lambiotte09].
- `random_state`: None, int, RandomState Change the initialization of the optimization.
- `restrict_to`: Tuple[str, Sequence[str], None] Restrict the clustering to the categories within the key for sample annotation, tuple needs to contain `(obs_key, list_of_categories)`.
- `key_added`: str Key under which to add the cluster labels. (default: `'louvain'`)
- `adjacency`: spmatrix, None Sparse adjacency matrix of the graph, defaults to neighbors connectivities.
- `flavor`: _Genericalias[vtraag, igraph, rapids] Choose between to packages for computing the clustering. `'vtraag'` is much more powerful, and the default.
- `directed`: bool Interpret the adjacency matrix as directed graph?
- `use_weights`: bool Use weights from knn graph.
- `partition_type`: Type[MutableVertexPartition], None Type of partition to use. Only a valid argument if `flavor` is `'vtraag'`.
- `partition_kwargs`: Mapping[str, Any] Key word arguments to pass to partitioning, if `vtraag` method is being used.
- `neighbors_key`: str, None Use neighbors connectivities as adjacency. If not specified, `louvain` looks `.obsp['connectivities']` for connectivities (default storage place for `pp.neighbors`). If specified, `louvain` looks `.obsp[.uns[neighbors_key]['connectivities_key']]` for connectivities.
- `obsp`: str, None Use `.obsp[obsp]` as adjacency. You can’t specify both `obsp` and `neighbors_key` at the same time.
- `copy`: bool Copy `adata` or modify it inplace.

**Return type** AnnData, None

**Returns**

- None – By default (copy=False), updates `adata` with the following fields:
  - `adata.obs['louvain']` (pandas.Series, dtype category) Array of dim (number of samples) that stores the subgroup id (‘0’, ‘1’, . . .) for each cell.
- AnnData – When `copy=True` is set, a copy of `adata` with those fields is returned.
scvelo.tl.umap

Embed the neighborhood graph using UMAP [McInnes18].

UMAP (Uniform Manifold Approximation and Projection) is a manifold learning technique suitable for visualizing high-dimensional data. Besides tending to be faster than tSNE, it optimizes the embedding such that it best reflects the topology of the data, which we represent throughout Scanpy using a neighborhood graph. tSNE, by contrast, optimizes the distribution of nearest-neighbor distances in the embedding such that these best match the distribution of distances in the high-dimensional space. We use the implementation of umap-learn [McInnes18]. For a few comparisons of UMAP with tSNE, see this preprint.

Parameters

adata : AnnData  Annotated data matrix.

min_dist : float  The effective minimum distance between embedded points. Smaller values will result in a more clustered/clumped embedding where nearby points on the manifold are drawn closer together, while larger values will result on a more even dispersal of points. The value should be set relative to the spread value, which determines the scale at which embedded points will be spread out. The default of in the umap-learn package is 0.1.

spread : float  The effective scale of embedded points. In combination with min_dist this determines how clustered/clumped the embedded points are.

n_components : int  The number of dimensions of the embedding.

maxiter : int, None  The number of iterations (epochs) of the optimization. Called n_epochs in the original UMAP.

alpha : float  The initial learning rate for the embedding optimization.

gamma : float  Weighting applied to negative samples in low dimensional embedding optimization. Values higher than one will result in greater weight being given to negative samples.

negative_sample_rate : int  The number of negative edge/1-simplex samples to use per positive edge/1-simplex sample in optimizing the low dimensional embedding.

init_pos : _Generalias[paga, spectral, random], ndarray, None  How to initialize the low dimensional embedding. Called init in the original UMAP. Options are:

  • Any key for adata.obsm.
  • ’paga’: positions from paga().
  • ’spectral’: use a spectral embedding of the graph.
  • ‘random’: assign initial embedding positions at random.
  • A numpy array of initial embedding positions.

random_state : None, int, RandomState  If int, random_state is the seed used by the random number generator; If RandomState or Generator, random_state is the random number generator; If None, the random number generator is the RandomState instance used by np.random.

a : float, None  More specific parameters controlling the embedding. If None these values are set automatically as determined by min_dist and spread.
**b**: float, None  More specific parameters controlling the embedding. If None these values are set automatically as determined by min_dist and spread.

**copy**: bool  Return a copy instead of writing to adata.

**method**: _Genericalias[umap, rapids] Use the original ‘umap’ implementation, or ‘rapids’ (experimental, GPU only)

**neighbors_key**: str, None  If not specified, umap looks .uns[‘neighbors’] for neighbors settings and .obsp[‘connectivities’] for connectivities (default storage places for pp.neighbors). If specified, umap looks .uns[neighbors_key] for neighbors settings and .obsp[uns[neighbors_key][‘connectivities_key’]] for connectivities.

**Return type**: AnnData, None

**Returns**

- Depending on copy, returns or updates adata with the following fields.
- **X_umap** (adata.obsm field) – UMAP coordinates of data.

### Velocity estimation

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>tl.velocity(data[, vkey, mode, fit_offset,...])</code></td>
<td>Estimates velocities in a gene-specific manner.</td>
</tr>
<tr>
<td><code>tl.velocity_graph(data[, vkey, xkey, tkey,...])</code></td>
<td>Computes velocity graph based on cosine similarities.</td>
</tr>
<tr>
<td><code>tl.velocity_embedding(data[, basis, vkey,...])</code></td>
<td>Projects the single cell velocities into any embedding.</td>
</tr>
</tbody>
</table>

**scvelo.tl.velocity**

The steady-state model [Manno18] determines velocities by quantifying how observations deviate from a presumed steady-state equilibrium ratio of unspliced to spliced mRNA levels. This steady-state ratio is obtained by performing a linear regression restricting the input data to the extreme quantiles. By including second-order moments, the stochastic model [Bergen19] exploits not only the balance of unspliced to spliced mRNA levels but also their covariation. By contrast, the likelihood-based dynamical model [Bergen19] solves the full splicing kinetics and generalizes RNA velocity estimation to transient systems. It is also capable of capturing non-observed steady states.
Parameters

**data**: `AnnData` Annotated data matrix.

**vkey**: `str` (default: `velocity`) Name under which to refer to the computed velocities for `velocity_graph` and `velocity_embedding`.

**mode**: `deterministic`, `stochastic` or `dynamical` (default: `stochastic`) Whether to run the estimation using the steady-state/deterministic, stochastic or dynamical model of transcriptional dynamics. The dynamical model requires to run `tl.recover_dynamics` first.

**fit_offset**: `bool` (default: `False`) Whether to fit with offset for first order moment dynamics.

**fit_offset2**: `bool`, (default: `False`) Whether to fit with offset for second order moment dynamics.

**filter_genes**: `bool` (default: `True`) Whether to remove genes that are not used for further velocity analysis.

**groups**: `str, list` (default: `None`) Subset of groups, e.g. `['g1', 'g2', 'g3']`, to which velocity analysis shall be restricted.

**groupby**: `str, list or np.ndarray` (default: `None`) Key of observations grouping to consider.

**groups_for_fit**: `str, list or np.ndarray` (default: `None`) Subset of groups, e.g. `['g1', 'g2', 'g3']`, to which steady-state fitting shall be restricted.

**constrain_ratio**: `float` or tuple of type `float` or `None` (default: `None`) Bounds for the steady-state ratio.

**use_raw**: `bool` (default: `False`) Whether to use raw data for estimation.

**use_latent_time**: `bool` or `None` (default: `None`) Whether to use latent time as a regularization for velocity estimation.

**perc**: `float` (default: `[5, 95]`) Percentile, e.g. 98, for extreme quantile fit.

**min_r2**: `float` (default: `0.01`) Minimum threshold for coefficient of determination

**min_likelihood**: `float` (default: `None`) Minimal likelihood for velocity genes to fit the model on.
**r2_adjusted**: `bool` (default: `None`) Whether to compute coefficient of determination on full data fit (adjusted) or extreme quantile fit (None)

**use_highly_variable**: `bool` (default: `True`) Whether to use highly variable genes only, stored in `.var['highly_variable']`.

**copy**: `bool` (default: `False`) Return a copy instead of writing to `adata`.

Returns

- **velocity** (.layers) – velocity vectors for each individual cell
- **velocity_genes, velocity_beta, velocity_gamma, velocity_r2** (.var) – parameters

---

**scvelo.tl.velocity_graph**

`scvelo.tl.velocity_graph`(data, vkey='velocity', xkey='Ms', tkey=None, basis=None, n_neighbors=None, n_recursively_neighbors=None, random_neighbors_at_max=None, sqrt_transform=None, variance_stabilization=None, gene_subset=None, compute_uncertainties=None, approx=None, mode_neighbors='distances', copy=False, n_jobs=None, backend='loky')

Computes velocity graph based on cosine similarities. The cosine similarities are computed between velocities and potential cell state transitions, i.e. it measures how well a corresponding change in gene expression $\delta_{ij} = x_j - x_i$ matches the predicted change according to the velocity vector $\nu_i$.

$$\pi_{ij} = \cos \angle (\delta_{ij}, \nu_i) = \frac{\delta_{ij}^T \nu_i}{||\delta_{ij}|| ||\nu_i||}.$$ 

**Parameters**

- **data**: AnnData Annotated data matrix.
- **vkey**: str (default: ‘velocity’) Name of velocity estimates to be used.
- **xkey**: str (default: ‘Ms’) Layer key to extract count data from.
- **tkey**: str (default: None) Observation key to extract time data from.
- **basis**: str (default: None) Basis / Embedding to use.
- **n_neighbors**: int or None (default: None) Use fixed number of neighbors or do recursive neighbor search (if None).
- **n_recursively_neighbors**: int (default: None) Number of recursions for neighbors search. Defaults to 2 if mode_neighbors is ‘distances’, and 1 if mode_neighbors is ‘connectivities’.
- **random_neighbors_at_max**: int or None (default: None) If number of iterative neighbors for an individual cell is higher than this threshold, a random selection of such are chosen as reference neighbors.
- **sqrt_transform**: bool (default: False) Whether to variance-transform the cell states changes and velocities before computing cosine similarities.
- **gene_subset**: list of str, subset of adata.var_names or None‘(default: ‘None) Subset of genes to compute velocity graph on exclusively.
- **compute_uncertainties**: bool (default: None) Whether to compute uncertainties along with cosine correlation.
approx : bool or None (default: None) If True, first 30 pc’s are used instead of the full count matrix.

mode_neighbors : ‘str’ (default: ‘distances’) Determines the type of KNN graph used. Options are ‘distances’ or ‘connectivities’. The latter yields a symmetric graph.

copy : bool (default: False) Return a copy instead of writing to adata.

n_jobs : int or None (default: None) Number of parallel jobs.


Returns velocity_graph (.uns) – sparse matrix with correlations of cell state transitions with velocities.

scvelo.tl.velocity_embedding

scvelo.tl.velocity_embedding(data, basis=None, vkey='velocity', scale=10, self_transitions=True, use_negative_cosines=True, direct_pca_projection=None, retain_scale=False, autoscale=True, all_comps=True, T=None, copy=False)

Projects the single cell velocities into any embedding.

Given normalized difference of the embedding positions :math: tilde delta_{ij} = \frac{x_j-x_i}{|x_j-x_i|} the projections are obtained as expected displacements with respect to the transition matrix \tilde{\pi}_{ij} as

\tilde{\nu}_i = E_{\tilde{\pi}_i,[\tilde{\delta}_i]} = \sum_{j\neq i} \left( \tilde{\pi}_{ij} - \frac{1}{n} \right) \tilde{\delta}_{ij}.

Parameters

data : AnnData Annotated data matrix.

basis : str (default: ‘tsne’) Which embedding to use.

vkey : str (default: ‘velocity’) Name of velocity estimates to be used.

scale : int (default: 10) Scale parameter of gaussian kernel for transition matrix.

self_transitions : bool (default: True) Whether to allow self transitions, based on the confidences of transitioning to neighboring cells.

use_negative_cosines : bool (default: True) Whether to project cell-to-cell transitions with negative cosines into negative/opposite direction.

direct_pca_projection : bool (default: None) Whether to directly project the velocities into PCA space, thus skipping the velocity graph.

retain_scale : bool (default: False) Whether to retain scale from high dimensional space in embedding.

autoscale : bool (default: True) Whether to scale the embedded velocities by a scalar multiplier, which simply ensures that the arrows in the embedding are properly scaled.

all_comps : bool (default: True) Whether to compute the velocities on all embedding components.

T : csr_matrix (default: None) Allows the user to directly pass a transition matrix.

copy : bool (default: False) Return a copy instead of writing to adata.
Returns `velocity_umap` (obsm) – coordinates of velocity projection on embedding (e.g., basis='umap')

**Dynamical modeling**

```python
tl.recover_dynamics(data[, var_names, ...])  # Recovers the full splicing kinetics of specified genes.
tl.differential_kinetic_test(data[, ...])  # Test to detect cell types / lineages with different kinetics.
```

**scvelo.tl.recover_dynamics**

```python
scvelo.tl.recover_dynamics(data, var_names='velocity_genes', n_top_genes=None, max_iter=10, assignment_mode='projection', t_max=None, fit_time=True, fit_scaling=True, fit_steady_states=True, fit_connected_states=None, fit_basal_transcription=None, use_raw=False, load_pars=None, return_model=None, plot_results=False, steady_state_prior=None, add_key='fit', copy=False, n_jobs=None, backend='loky', **kwargs)
```

Recovers the full splicing kinetics of specified genes.

The model infers transcription rates, splicing rates, degradation rates, as well as cell-specific latent time and transcriptional states, estimated iteratively by expectation-maximization.
Parameters

**data** : AnnData Annotated data matrix.

**var_names** : str, list of str (default: ‘velocity_genes’) Names of variables/genes to use for the fitting. If var_names=’velocity_genes’ but there is no column ‘velocity_genes’ in adata.var, velocity genes are estimated using the steady state model.

**n_top_genes** : int or None (default: None) Number of top velocity genes to use for the dynamical model.

**max_iter** : int (default: 10) Maximal iterations in the EM-Algorithm.

**assignment_mode** : str (default: projection) Determined how times are assigned to observations. If projection, observations are projected onto the model trajectory. Else uses an inverse approximating formula.

**t_max** : float, False or None (default: None) Total range for time assignments.

**fit_scaling** : bool or float or None (default: True) Whether to fit scaling between unspliced and spliced.

**fit_time** : bool or float or None (default: True) Whether to fit time or keep initially given time fixed.

**fit_steady_states** : bool or None (default: True) Whether to explicitly model and fit steady states (next to induction/repression)

**fit_connected_states** : bool or None (default: None) Restricts fitting to neighbors given by connectivities.

**fit_basal_transcription** : bool or None (default: None) Enables model to incorporate basal transcriptions.

**use_raw** : bool or None (default: None) if True, use .layers['sliced'], else use moments from .layers['Ms']

**load_pars** : bool or None (default: None) Load parameters from past fits.

**return_model** : bool or None (default: True) Whether to return the model as :DynamicRecovery: object.

**plot_results** : bool or None (default: False) Plot results after parameter inference.

**steady_state_prior** : list of bool or None (default: False) Mask for indices used for steady state regression.

**add_key** : str (default: ‘fit’) Key to add to parameter names, e.g. ‘fit_t’ for fitted time.

**copy** : bool (default: False) Return a copy instead of writing to adata.

**n_jobs** : int or None (default: None) Number of parallel jobs.

**backend** : str (default: “loky”) Backend used for multiprocessing. See joblib. Parallel for valid options.

Returns

- **fit_alpha** (.var) – inferred transcription rates
- **fit_beta** (.var) – inferred splicing rates
- **fit_gamma** (.var) – inferred degradation rates
- **fit_t** (.var) – inferred switching time points
- **fit_scaling** (.var) – internal variance scaling factor for un/spliced counts
• **fit_likelihood** (*.var*) – likelihood of model fit
• **fit_alignment_scaling** (*.var*) – scaling factor to align gene-wise latent times to a universal latent time

**scvelo.tl.differential_kinetic_test**

**scvelo.tl.differential_kinetic_test***(data, var_names='velocity_genes', groupby=None, use_raw=None, return_model=None, add_key='fit', copy=None, **kwargs)*

Test to detect cell types / lineages with different kinetics.

Likelihood ratio test for differential kinetics to detect clusters/lineages that display kinetic behavior that cannot be sufficiently explained by a single model for the overall dynamics. Each cell type is tested whether an independent fit yields a significantly improved likelihood.

![Tmsb10](image1.png) ![Fam155a](image2.png)

**Parameters**

- **data**: `AnnData` Annotated data matrix.
- **var_names**: `str, list of str` *(default: ‘velocity_genes’)* Names of variables/genes to use for the fitting.
- **groupby**: `str` *(default: None)* Key of observations grouping to consider, e.g. ‘clusters’.
- **use_raw**: `bool` *(default: False)* Whether to use raw data for estimation.
- **add_key**: `str` *(default: ‘fit’)* Key to add to parameter names, e.g. ‘fit_t’ for fitted time.
- **copy**: `bool` *(default: None)* Return a copy instead of writing to `adata`.

**Returns**

- **fit_pvals_kinetics** (*.varm*) – P-values of competing kinetic for each group and gene
- **fit_diff_kinetics** (*.var*) – Groups that have differential kinetics for each gene.

**Dynamical genes**

- **tl.rank_velocity_genes**(data[, vkey, ...]) Rank genes for velocity characterizing groups.
- **tl.rank_dynamical_genes**(data[, n_genes, ...]) Rank genes by likelihoods per cluster/ regime.

4.3. API
scvelo.tl.rank_velocity_genes

scvelo.tl.rank_velocity_genes(data, vkey='velocity', n_genes=100, groupby=None, match_with=None, resolution=None, min_counts=None, min_r2=None, min_corr=None, min_dispersion=None, min_likelihood=None, copy=False)

Rank genes for velocity characterizing groups.

This applies a differential expression test (Welch t-test with overestimated variance to be conservative) on velocity expression, to find genes in a cluster that show dynamics that is transcriptionally regulated differently compared to all other clusters (e.g. induction in that cluster and homeostasis in remaining population). If no clusters are given, it priorly computes velocity clusters by applying louvain modularity on velocity expression.

```python
csv.tl.rank_velocity_genes(adata, groupby='clusters')
csv.pl.scatter(
    adata, basis=adata.uns['rank_velocity_genes']['names']['Beta'][:3]
)
pd.DataFrame(adata.uns['rank_velocity_genes']['names']).head()
```

<table>
<thead>
<tr>
<th>Ductal</th>
<th>Ngn3 low EP</th>
<th>Ngn3 high EP</th>
<th>Pre-endocrine</th>
<th>Beta</th>
<th>Alpha</th>
<th>Delta</th>
<th>Epsilon</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>Notch2</td>
<td>Hadc1</td>
<td>Pde1c</td>
<td>Pam</td>
<td>Pax6</td>
<td>Ngn1</td>
<td>Zdbf2</td>
</tr>
<tr>
<td>1</td>
<td>Sox5</td>
<td>Hspa8</td>
<td>Polo</td>
<td>Baiap3</td>
<td>Unc5c</td>
<td>Zcchc6</td>
<td>Akr1c19</td>
</tr>
<tr>
<td>2</td>
<td>Krt19</td>
<td>Fgf12</td>
<td>Ptprs</td>
<td>Sdk1</td>
<td>Nnat</td>
<td>Prune2</td>
<td>Anik2</td>
</tr>
<tr>
<td>3</td>
<td>Hspa8</td>
<td>Trp53cor1</td>
<td>Rap1gap2</td>
<td>Abcc8</td>
<td>Tmem108</td>
<td>Ndst4</td>
<td>Cpm</td>
</tr>
<tr>
<td>4</td>
<td>Nr2f6</td>
<td>Stard10</td>
<td>Tyh2</td>
<td>Gnas</td>
<td>Ptp4</td>
<td>Ksr2</td>
<td>Ptp4</td>
</tr>
</tbody>
</table>

Parameters

- `data`: AnnData Annotated data matrix.
- `vkey`: str (default: 'velocity') Key of velocities computed in `tl.velocity`
- `n_genes`: int, optional (default: 100) The number of genes that appear in the returned tables.
- `groupby`: str, list or np.ndarray (default: None) Key of observations grouping to consider.
- `match_with`: str or None (default: None) adata.obs key to separatively rank velocities on.
- `resolution`: str or None (default: None) Resolution for louvain modularity.
- `min_counts`: float (default: None) Minimum count of genes for consideration.
- `min_r2`: float (default: None) Minimum r2 value of genes for consideration.
**min_corr**: float (default: None) Minimum Spearman's correlation coefficient between spliced and unspliced.

**min_dispersion**: float (default: None) Minimum dispersion norm value of genes for consideration.

**min_likelihood**: float between 0 and 1 or None (default: None) Only rank velocity of genes with a likelihood higher than min_likelihood.

**copy**: bool (default: False) Return a copy instead of writing to data.

Returns

- **rank_velocity_genes** (.uns) – Structured array to be indexed by group id storing the gene names. Ordered according to scores.
- **velocity_score** (.var) – Storing the score for each gene for each group. Ordered according to scores.

**scvelo.tl.rank_dynamical_genes**

**scvelo.tl.rank_dynamical_genes** (data, n_genes=100, groupby=None, copy=False)

Rank genes by likelihoods per cluster/regime.

This ranks genes by their likelihood obtained from the dynamical model grouped by clusters specified in groupby.

**Parameters**

- **data**: AnnData Annotated data matrix.
- **n_genes**: int, optional (default: 100) The number of genes that appear in the returned tables.
- **groupby**: str, list or np.ndarray (default: None) Key of observations grouping to consider.
- **copy**: bool (default: False) Return a copy instead of writing to data.

**Returns** **rank_dynamical_genes** (.uns) – Structured array to be indexed by group id storing the gene names. Ordered according to scores.

**Pseudotime and trajectory inference**

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>tl.terminal_states(data[, vkey, modalirty, ...])</td>
<td>Computes terminal states (root and end points).</td>
</tr>
<tr>
<td>tl.velocity_pseudotime(adata[, vkey, ...])</td>
<td>Computes a pseudotime based on the velocity graph.</td>
</tr>
<tr>
<td>tl.latent_time(data[, vkey, min_likelihood, ...])</td>
<td>Computes a gene-shared latent time.</td>
</tr>
<tr>
<td>tl.paga(adata[, groups, vkey, ...])</td>
<td>PAGA graph with velocity-directed edges.</td>
</tr>
</tbody>
</table>

**scvelo.tl.terminal_states**

**scvelo.tl.terminal_states** (data, vkey='velocity', modality='Ms', groupby=None, groups=None, self_transitions=False, eps=0.001, random_state=0, copy=False, **kwargs)

Computes terminal states (root and end points).

The end points and root cells are obtained as stationary states of the velocity-inferred transition matrix and its transposed, respectively, which is given by left eigenvectors corresponding to an eigenvalue of 1, i.e.

$$ \text{end} = \text{end} \pi, \quad \text{root} = \text{root} \pi^T. $$
Alternatively, we recommend to use `cellrank.tl.terminal_states()` providing an improved/generalized approach of identifying terminal states.

**Parameters**

- **data**: Anndata Annotated data matrix.
- **vkey**: str (default: `'velocity'`) Name of velocity estimates to be used.
modality : str (default: ‘Ms’) Layer used to calculate terminal states.

groupby : str, list or np.ndarray (default: None) Key of observations grouping to consider.
  Only to be set, if each group is assumed to have a distinct lineage with an independent root and end point.

groups : str, list or np.ndarray (default: None) Groups selected to find terminal states on.
  Must be an element of .obs[groupby]. To be specified only for very distinct/disconnected clusters.

self_transitions : bool (default: False) Allow transitions from one node to itself.

eps : float (default: 1e-3) Tolerance for eigenvalue selection.

random_state : int or None (default: 0) Seed used by the random number generator. If None, use the RandomState instance by np.random.

copy : bool (default: False) Return a copy instead of writing to data.

**kwargs Passed to scvelo.tl.transition_matrix(), e.g. basis, weight_diffusion.

Returns

• root_cells (.obs) – sparse matrix with transition probabilities.
• end_points (.obs) – sparse matrix with transition probabilities.

scvelo.tl.velocity_pseudotime

scvelo.tl.velocity_pseudotime (adata, vkey='velocity', groupby=None, groups=None, root_key=None, end_key=None, use_velocity_graph=True, n_dcs=10, save_diffmap=None, return_model=None, **kwargs)

Computes a pseudotime based on the velocity graph.

Velocity pseudotime is a random-walk based distance measures on the velocity graph. After computing a distribution over root cells obtained from the velocity-inferred transition matrix, it measures the average number of steps it takes to reach a cell after start walking from one of the root cells. Contrarily to diffusion pseudotime, it implicitly infers the root cells and is based on the directed velocity graph instead of the similarity-based diffusion kernel.

scv.tl.velocity_pseudotime(adata)
scv.pl.scatter(adata, color='velocity_pseudotime', color_map='gnuplot')
Parameters

adata : AnnData  Annotated data matrix

vkey : str (default: ‘velocity’)  Name of velocity estimates to be used.

groupby : str, list or np.ndarray (default: None)  Key of observations grouping to consider.

groups : str, list or np.ndarray (default: None)  Groups selected to find terminal states on. Must be an element of adata.obs[groupby]. Only to be set, if each group is assumed to have a distinct lineage with an independent root and end point.

root_key : int (default: None)  Index of root cell to be used. Computed from velocity-inferred transition matrix if not specified.

end_key : int (default: None)  Index of end point to be used. Computed from velocity-inferred transition matrix if not specified.

n_dcs : int (default: 10)  The number of diffusion components to use.

use_velocity_graph : bool (default: True)  Whether to use the velocity graph. If False, it uses the similarity-based diffusion kernel.

save_diffmap : bool (default: None)  Whether to store diffmap coordinates.

return_model : bool (default: None)  Whether to return the vpt object for further inspection.

**kwargs  Further arguments to pass to VPT (e.g. min_group_size, allow_kendall_tau_shift).

Returns velocity_pseudotime (.obs) – Velocity pseudotime obtained from velocity graph.
**scvelo.tl.latent_time**

**scvelo.tl.latent_time** *(data, vkey='velocity', min_likelihood=0.1, min_confidence=0.75, min_corr_diffusion=None, weight_diffusion=None, root_key=None, end_key=None, t_max=None, copy=False)*

Computes a gene-shared latent time.

Gene-specific latent timepoints obtained from the dynamical model are coupled to a universal gene-shared latent time, which represents the cell’s internal clock and is based only on its transcriptional dynamics.

**Parameters**

- **data**: *AnnData*  Annotated data matrix
- **vkey**: *str* (default: ‘velocity’) Name of velocity estimates to be used.
- **min_likelihood**: *float between 0 and 1 or None* (default: .1) Minimal likelihood fitness for genes to be included to the weighting.
- **min_confidence**: *float between 0 and 1* (default: .75) Parameter for local coherence selection.
- **min_corr_diffusion**: *float between 0 and 1 or None* (default: None) Only select genes that correlate with velocity pseudotime obtained from diffusion random walk on velocity graph.
- **weight_diffusion**: *float or None* (default: None) Weight applied to couple latent time with diffusion-based velocity pseudotime.
- **root_key**: *str or None* (default: ‘root_cells’) Key (.uns, .obs) of root cell to be used. If not set, it obtains root cells from velocity-inferred transition matrix.
- **end_key**: *str or None* (default: None) Key (.obs) of end points to be used.
**t_max**: float or None (default: None) Overall duration of differentiation process. If not set, an overall transcriptional timescale of 20 hours is used as prior.

**copy**: bool (default: False) Return a copy instead of writing to *adata*.

Returns latent_time (.obs) – latent time from learned dynamics for each cell

### scvelo.tl.paga

**scvelo.tl.paga**(*adata*, groups=None, vkey='velocity', use_time_prior=True, root_key=None, end_key=None, threshold_root_end_prior=None, minimum_spanning_tree=True, copy=False)

PAGA graph with velocity-directed edges.

Mapping out the coarse-grained connectivity structures of complex manifolds [Wolf19]. By quantifying the connectivity of partitions (groups, clusters) of the single-cell graph, partition-based graph abstraction (PAGA) generates a much simpler abstracted graph (PAGA graph) of partitions, in which edge weights represent confidence in the presence of connections.

**Parameters**

**adata**: AnnData An annotated data matrix.

**groups**: key for categorical in *adata.obs*, optional (default: ‘louvain’) You can pass your predefined groups by choosing any categorical annotation of observations (*adata.obs*).

**vkey**: str or None (default: None) Key for annotations of observations/cells or variables/genes.

**use_time_prior**: str or bool, optional (default: True) Obs key for pseudo-time values. If True, ‘velocity_pseudotime’ is used if available.

**root_key**: str or bool, optional (default: None) Obs key for root states.

**end_key**: str or bool, optional (default: None) Obs key for end states.

**threshold_root_end_prior**: float (default: 0.9) Threshold for root and final states priors, to be in the range of [0,1]. Values above the threshold will be considered as terminal and included as prior.

**minimum_spanning_tree**: bool, optional (default: True) Whether to prune the tree such that a path from A-to-B is removed if another more confident path exists.

**copy**: bool, optional (default: False) Copy *adata* before computation and return a copy. Otherwise, perform computation inplace and return None.

**Returns**

- **connectivities** (.uns) – The full adjacency matrix of the abstracted graph, weights correspond to confidence in the connectivities of partitions.
- **connectivities_tree** (.uns) – The adjacency matrix of the tree-like subgraph that best explains the topology.
- **transitions_confidence** (.uns) – The adjacency matrix of the abstracted directed graph, weights correspond to confidence in the transitions between partitions.

### Further tools

**tl.velocity_clusters**(data[, vkey, . . .]) Computes velocity clusters via louvain on velocities.

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<td>tl.velocity_confidence(data[, vkey, copy])</td>
<td>Computes confidences of velocities.</td>
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<td>tl.score_genes_cell_cycle(adata[, s_genes, ...])</td>
<td>Score cell cycle genes.</td>
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**scvelo.tl.velocity_clusters**

```python
scvelo.tl.velocity_clusters(data, vkey='velocity', match_with='clusters', sort_by='velocity_pseudotime', resolution=None, min_likelihood=None, copy=False)
```

Computes velocity clusters via louvain on velocities.

```python
scv.tl.velocity_clusters(adata)
scv.pl.scatter(adata, color='velocity_clusters')
```

### Parameters

- **data**: `AnnData` Annotated data matrix.
- **vkey**: `str` (default: `'velocity'`) Key of velocities computed in `tl.velocity`
- **match_with**: `str` (default: `'clusters'`) The number of genes that appear in the returned tables.
- **sort_by**: `str` or `None` (default: `'dpt_pseudotime'`) Sort velocity clusters by this key (.obs).
- **match_with** Match the names of the velocity clusters with the names of this key (.obs).
- **sort_by**: `str` or `None` (default: `'dpt_pseudotime'`) Sort velocity clusters by this key (.obs).
**scvelo.tl.velocity_confidence**

(scvelo.tl.velocity_confidence)\(\text{(data, vkey='velocity', copy=False)}\)

Computes confidences of velocities.

```
scv.tl.velocity_confidence(adata)
scv.pl.scatter(adata, color='velocity_confidence', perc=[2,98])
```

---

**Parameters**

- **data**: AnnData  
  Annotated data matrix.
- **vkey**: str (default: `'velocity'`)  
  Name of velocity estimates to be used.
- **copy**: bool (default: `False`)  
  Return a copy instead of writing to adata.

**Returns**

- **velocity_length** (.obs) – Length of the velocity vectors for each individual cell
- **velocity_confidence** (.obs) – Confidence for each cell
scvelo.tl.score_genes_cell_cycle

scvelo.tl.score_genes_cell_cycle(adata, s_genes=None, g2m_genes=None, copy=False, **kwargs)

Score cell cycle genes.

Calculates scores and assigns a cell cycle phase (G1, S, G2M) using the list of cell cycle genes defined in Tirosh et al, 2015 (https://doi.org/10.1126/science.aad0501).

Parameters

- **adata** The annotated data matrix.
- **s_genes** List of genes associated with S phase.
- **g2m_genes** List of genes associated with G2M phase.
- **copy** Copy adata or modify it inplace.
- **kwargs** Are passed to score_genes(). ctrl_size is not possible, as it’s set as min(len(s_genes), len(g2m_genes)).

Returns

- **S_score** (adata.obs, dtype object) – The score for S phase for each cell.
- **G2M_score** (adata.obs, dtype object) – The score for G2M phase for each cell.
- **phase** (adata.obs, dtype object) – The cell cycle phase (S, G2M or G1) for each cell.

4.3.4 Plotting (pl)

Base scatter plot

pl.scatter([adata, basis, x, y, vkey, ...]) Scatter plot along observations or variables axes.

scvelo.pl.scatter

scvelo.pl.scatter(adata=None, basis=None, x=None, y=None, vkey=None, use_raw=None, layer=None, color_map=None, colorbar=None, palette=None, size=None, alpha=None, linewidth=None, linecolor=None, perc=None, groups=None, sort_order=True, components=None, projection=None, legend_loc=None, legend_loc_lines=None, legend_fontsize=None, legend_fontweight=None, legend_fontoutline=None, legend_align_text=None, xlabel=None, ylabel=None, title=None, fontsize=None, figsize=None, xlim=None, ylim=None, add_density=None, add_assignments=None, add_linfit=None, add_polyfit=None, add_rug=None, add_text=None, add_text_pos=None, add_margin=None, add_outline=None, outline_width=None, outline_color=None, n_convolve=None, smooth=None, normalize_data=None, rescale_color=None, color_gradients=None, dpi=None, frameon=None, zorder=None, ncols=None, nrows=None, wspace=None, hspace=None, show=None, save=None, ax=None, **kwargs)

Scatter plot along observations or variables axes.

Parameters

- **adata** : AnnData Annotated data matrix.
- **x** : str, np.ndarray or None (default: None) x coordinate
y : str, np.ndarray or None (default: None)  y coordinate
basis : str or list of str (default: None) Key for embedding. If not specified, use ‘umap’, ‘tsne’ or ‘pca’ (ordered by preference).
vkey : str or list of str (default: None) Key for velocity / steady-state ratio to be visualized.
color : str, list of str or None (default: None) Key for annotations of observations/cells or variables/genes
use_raw : bool (default: None)  Use raw attribute of adata if present.
layer : str, list of str or None (default: None) Specify the layer for color.
color_map : str (default: matplotlib.rcParams['image.cmap']) String denoting matplotlib color map.
colorbar : bool (default: False)  Whether to show colorbar.
palette : list of str (default: None) Colors to use for plotting groups (categorical annotation).
size : float (default: 5)  Point size.
alpha : float (default: 1) Set blending - 0 transparent to 1 opaque.
linewidth : float (default: 1) Scaling factor for the width of occurring lines.
linecolor : str or list of str (default: ‘k’) Color of lines from velocity fits, linear fits and polynomial fits
perc : tuple, e.g. [2, 98] (default: None) Specify percentile for continuous coloring.
groups : str or list of str (default: all groups) Restrict to a few categories in categorical observation annotation. Multiple categories can be passed as list with [‘cluster_1’, ‘cluster_3’], or as string with ‘cluster_1, cluster_3’.
sort_order : bool (default: True) For continuous annotations used as color parameter, plot data points with higher values on top of others.
components : str or list of str (default: ‘1,2’) For instance, [‘1,2’, ‘2,3’].
legend_loc : str (default: ‘none’) Location of legend, either ‘on data’, ‘right margin’ or valid keywords for matplotlib.legend.
legend_fontsize : int (default: None) Legend font size.
legend_fontoutline : float (default: None) Line width of the legend font outline in pt. Draws a white outline using the path effect withStroke.
legend_align_text : bool or str (default: None) Aligns the positions of the legend texts. Set the axis along which the best alignment should be determined. This can be ‘y’ or True (vertically), ‘x’ (horizontally), or ‘xy’ (best alignment in both directions).
right_margin : float or list of float (default: None) Adjust the width of the space right of each plotting panel.
left_margin : float or list of float (default: None) Adjust the width of the space left of each plotting panel.
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**xlabel**: str (default: None) Label of x-axis.

**ylabel**: str (default: None) Label of y-axis.

**title**: str (default: None) Provide title for panels either as, e.g. ['title1', 'title2', ...].

**fontsize**: float (default: None) Label font size.

**figsize**: tuple (default: (7,5)) Figure size.

**xlim**: tuple, e.g. [0,1] or None (default: None) Restrict x-limits of the axis.

**ylim**: tuple, e.g. [0,1] or None (default: None) Restrict y-limits of the axis.

**add_density**: bool or str or None (default: None) Whether to show density of values along x and y axes. Color of the density plot can also be passed as str.

**add_assignments**: bool or str or None (default: None) Whether to add assignments to the model curve. Color of the assignments can also be passed as str.

**add_linfit**: bool or str or None (default: None) Whether to add linear regression fit to the data points. Color of the line can also be passed as str. Fitting with or without an intercept by passing 'intercept' or 'no_intercept'. A colored regression line with intercept is obtained with 'intercept, blue'.

**add_polyfit**: bool or str or int or None (default: None) Whether to add polynomial fit to the data points. Color of the polyfit plot can also be passed as str. The degree of the polynomial fit can be passed as int (default is 2 for quadratic fit). Fitting with or without an intercept by passing 'intercept' or 'no_intercept'. A colored regression line with intercept is obtained with 'intercept, blue'.

**add_rug**: str or None (default: None) If categorical observation annotation (e.g. ‘clusters’) is given, a rugplot is attached to the x-axis showing the data membership to each of the categories.

**add_text**: str (default: None) Text to be added to the plot, passed as str.

**add_text_pos**: tuple, e.g. [0.05, 0.95] (default: [0.05, 0.95]) Text position. Default is [0.05, 0.95], positioning the text at top right corner.

**add_margin**: float (default: None) A value between [-1, 1] to add (positive) and reduce (negative) figure margins.

**add_outline**: bool or str (default: False) Whether to show an outline around scatter plot dots. Alternatively a string of cluster names can be passed, e.g. ‘cluster_1, clusters_3’.

**outline_width**: tuple type scalar or None (default: (0.3, 0.05)) Width of the inner and outer outline

**outline_color**: tuple of type str or None (default: ('black', 'white')) Inner and outer matplotlib color of the outline

**n_convolve**: int or None (default: None) If int is given, data is smoothed by convolution along the x-axis with kernel size n_convolve.

**smooth**: bool or int (default: None) Whether to convolve/average the color values over the nearest neighbors. If int, it specifies number of neighbors.

**normalize_data**: bool (default: None) Whether to rescale values for x, y to [0,1].

**rescale_color**: tuple (default: None) Boundaries for color rescaling, e.g. [0, 1], setting min/max values of the colorbar.

**color_gradients**: str or np.ndarray (default: None) Key for .obsm or array with color gradients by categories.
dpi: int (default: 80) Figure dpi.

frameon: bool (default: True) Draw a frame around the scatter plot.

cmpols: int (default: None) Number of panels per row.

nrows: int (default: None) Number of panels per column.

wspace: float (default: None) Adjust the width of the space between multiple panels.

hspace: float (default: None) Adjust the height of the space between multiple panels.

show: bool, optional (default: None) Show the plot, do not return axis.

save: bool or str, optional (default: None) If True or a str, save the figure. A string is appended to the default filename. Infer the filetype if ending on ‘.pdf’, ‘.png’, ‘.svg’.

ax: matplotlib.Axes, optional (default: None) A matplotlib axes object. Only works if plotting a single component.

Returns If show==False a matplotlib.Axes

Velocity embeddings

pl.velocity_embedding(adata[, basis, vkey, ...]) Scatter plot of velocities on the embedding.

pl.velocity_embedding_grid(adata[, basis, ...]) Scatter plot of velocities on a grid.

pl.velocity_embedding_stream(adata[, basis, ...]) Stream plot of velocities on the embedding.

scvelo.pl.velocity_embedding

scvelo.pl.velocity_embedding (adata, basis=None, vkey='velocity', density=None, arrow_size=None, arrow_length=None, scale=None, X=None, V=None, recreate=None, color=None, use_raw=None, layer=None, color_map=None, colorbar=True, palette=None, size=None, alpha=0.2, perc=None, sort_order=True, groups=None, components=None, projection='2d', legend_loc='none', legend_fontsize=None, legend_fontweight=None, xlabel=None, ylabel=None, title=None, fontsize=None, figsize=None, dpi=None, frameon=None, show=None, save=None, ax=None, ncols=None, **kwargs)

Scatter plot of velocities on the embedding.

Parameters

adata: AnnData Annotated data matrix.

density: float (default: 1) Amount of velocities to show - 0 none to 1 all

arrow_size: float or triple headlength, headwidth, headaxislength (default: 1) Size of arrows.

arrow_length: float (default: 1) Length of arrows.

scale: float (default: 1) Length of velocities in the embedding.

basis: str or list of str (default: None) Key for embedding. If not specified, use ‘umap’, ‘tsne’ or ‘pca’ (ordered by preference).

vkey: str or list of str (default: None) Key for velocity / steady-state ratio to be visualized.
**color**: str, list of str or None (default: None) Key for annotations of observations/cells or variables/genes

**use_raw**: bool (default: None) Use raw attribute of adata if present.

**layer**: str, list of str or None (default: None) Specify the layer for color.

**color_map**: str (default: matplotlib.rcParams['image.cmap']) String denoting matplotlib color map.

**colorbar**: bool (default: False) Whether to show colorbar.

**palette**: list of str (default: None) Colors to use for plotting groups (categorical annotation).

**size**: float (default: 5) Point size.

**alpha**: float (default: 1) Set blending - 0 transparent to 1 opaque.

**linewidth**: float (default: 1) Scaling factor for the width of occurring lines.

**linecolor**: str or list of str (default: ‘k’) Color of lines from velocity fits, linear fits and polynomial fits

**perc**: tuple, e.g. [2,98] (default: None) Specify percentile for continuous coloring.

**groups**: str or list of str (default: all groups) Restrict to a few categories in categorical observation annotation. Multiple categories can be passed as list with ['cluster_1', 'cluster_3'], or as string with ‘cluster_1, cluster_3’.

**sort_order**: bool (default: True) For continuous annotations used as color parameter, plot data points with higher values on top of others.

**components**: str or list of str (default: ‘1,2’) For instance, ['1,2', '2,3'].

**projection**: {'2d', '3d'} (default: '2d') Projection of plot.

**legend_loc**: str (default: 'none') Location of legend, either ‘on data’, ‘right margin’ or valid keywords for matplotlib.legend.

**legend_fontsize**: int (default: None) Legend font size.

**legend_fontweight**: {'normal', 'bold', ...} (default: None) Legend font weight. A numeric value in range 0-1000 or a string. Defaults to ‘bold’ if legend_loc = ‘on data’, otherwise to ‘normal’. Available are ['light', 'normal', 'medium', 'semibold', 'bold', 'heavy', 'black'].

**legend_fontoutline**: float (default: None) Line width of the legend font outline in pt. Draws a white outline using the path effect withStroke.

**legend_align_text**: bool or str (default: None) Aligns the positions of the legend texts. Set the axis along which the best alignment should be determined. This can be ‘y’ or True (vertically), ‘x’ (horizontally), or ‘xy’ (best alignment in both directions).

**right_margin**: float or list of float (default: None) Adjust the width of the space right of each plotting panel.

**left_margin**: float or list of float (default: None) Adjust the width of the space left of each plotting panel.

**xlabel**: str (default: None) Label of x-axis.

**ylabel**: str (default: None) Label of y-axis.

**title**: str (default: None) Provide title for panels either as, e.g. ["title1", "title2", ...].
scVelo documentation, Release 0.2.5.dev6+g1805ab4.d20210829

**fontsize**: *float* (default: *None*) Label font size.

**figsize**: *tuple* (default: *(7, 5)*) Figure size.

**xlim**: *tuple*, e.g. *[0, 1]* or *None* (default: *None*) Restrict x-limits of the axis.

**ylim**: *tuple*, e.g. *[0, 1]* or *None* (default: *None*) Restrict y-limits of the axis.

**add_density**: *bool* or *str* or *None* (default: *None*) Whether to show density of values along x and y axes. Color of the density plot can also be passed as *str*.

**add_assignments**: *bool* or *str* or *None* (default: *None*) Whether to add assignments to the model curve. Color of the assignments can also be passed as *str*.

**add_linfit**: *bool* or *str* or *None* (default: *None*) Whether to add linear regression fit to the data points. Color of the line can also be passed as *str*. Fitting with or without an intercept by passing ‘intercept’ or ‘no_intercept’. A colored regression line with intercept is obtained with ‘intercept, blue’.

**add_polyfit**: *bool* or *str* or *int* or *None* (default: *None*) Whether to add polynomial fit to the data points. Color of the polyfit plot can also be passed as *str*. The degree of the polynomial fit can be passed as *int* (default is 2 for quadratic fit). Fitting with or without an intercept by passing ‘intercept’ or ‘no_intercept’. A colored regression line with intercept is obtained with ‘intercept, blue’.

**add_rug**: *str* or *None* (default: *None*) If categorical observation annotation (e.g. ‘clusters’) is given, a rugplot is attached to the x-axis showing the data membership to each of the categories.

**add_text**: *str* (default: *None*) Text to be added to the plot, passed as *str*.

**add_text_pos**: *tuple*, e.g. *[0.05, 0.95]* (default: *[0.05, 0.95]*) Text position. Default is *[0.05, 0.95]*, positioning the text at top right corner.

**add_margin**: *float* (default: *None*) A value between [-1, 1] to add (positive) and reduce (negative) figure margins.

**add_outline**: *bool* or *str* (default: *False*) Whether to show an outline around scatter plot dots. Alternatively a string of cluster names can be passed, e.g. ‘cluster_1, clusters_3’.

**outline_width**: *tuple type scalar or None* (default: *(0.3, 0.05)*) Width of the inner and outer outline

**outline_color**: *tuple of type str or None* (default: *(‘black’, ‘white’)*) Inner and outer matplotlib color of the outline

**n_convolve**: *int* or *None* (default: *None*) If *int* is given, data is smoothed by convolution along the x-axis with kernel size n_convolve.

**smooth**: *bool* or *int* (default: *None*) Whether to convolve/average the color values over the nearest neighbors. If *int*, it specifies number of neighbors.

**normalize_data**: *bool* (default: *None*) Whether to rescale values for x, y to [0,1].

**rescale_color**: *tuple* (default: *None*) Boundaries for color rescaling, e.g. [0, 1], setting min/max values of the colorbar.

**color_gradients**: *str* or *np.ndarray* (default: *None*) Key for .obsm or array with color gradients by categories.

**dpi**: *int* (default: 80) Figure dpi.

**frameon**: *bool* (default: *True*) Draw a frame around the scatter plot.

**ncols**: *int* (default: *None*) Number of panels per row.
nrows : int (default: None)  Number of panels per column.

wspace : float (default: None)  Adjust the width of the space between multiple panels.

hspace : float (default: None)  Adjust the height of the space between multiple panels.

show : bool, optional (default: None)  Show the plot, do not return axis.

save : bool or str, optional (default: None)  If True or a str, save the figure. A string is appended to the default filename. Infer the filetype if ending on {'.pdf', '.png', '.svg'}.

ax : matplotlib.Axes, optional (default: None)  A matplotlib axes object. Only works if plotting a single component.

Returns  matplotlib.Axis if show==False

scvelo.pl.velocity_embedding_grid

Scatter plot of velocities on a grid.

Parameters

adata : AnnData  Annotated data matrix.

density : float (default: 1)  Amount of velocities to show - 0 none to 1 all

arrow_size : float or triple headlength, headwidth, headaxislength (default: 1)  Size of arrows.

arrow_length : float (default: 1)  Length of arrows.

scale : float (default: 1)  Length of velocities in the embedding.

min_mass : float or None (default: None)  Minimum threshold for mass to be shown. It can range between 0 (all velocities) and 100 (large velocities).

smooth : bool or int (default: None)  Multiplication factor for scale in Gaussian kernel around grid point.

n_neighbors : int (default: None)  Number of neighbors to consider around grid point.

X : np.ndarray (default: None)  embedding grid point coordinates

V : np.ndarray (default: None)  embedding grid velocity coordinates

basis : str or list of str (default: None)  Key for embedding. If not specified, use ‘umap’, ‘tsne’ or ‘pca’ (ordered by preference).

vkey : str or list of str (default: None)  Key for velocity / steady-state ratio to be visualized.
color : str, list of str or None (default: None) Key for annotations of observations/cells or variables/genes

use_raw : bool (default: None) Use raw attribute of adata if present.

layer : str, list of str or None (default: None) Specify the layer for color.

color_map : str (default: matplotlib.rcParams[‘image.cmap’]) String denoting matplotlib color map.

colorbar : bool (default: False) Whether to show colorbar.

palette : list of str (default: None) Colors to use for plotting groups (categorical annotation).

size : float (default: 5) Point size.

alpha : float (default: 1) Set blending - 0 transparent to 1 opaque.

linewidth : float (default: 1) Scaling factor for the width of occurring lines.

linecolor : str or list of str (default: ‘k’) Color of lines from velocity fits, linear fits and polynomial fits

perc : tuple, e.g. [2, 98] (default: None) Specify percentile for continuous coloring.

groups : str or list of str (default: all groups) Restrict to a few categories in categorical observation annotation. Multiple categories can be passed as list with [‘cluster_1’, ‘cluster_3’], or as string with ‘cluster_1, cluster_3’.

sort_order : bool (default: True) For continuous annotations used as color parameter, plot data points with higher values on top of others.

components : str or list of str (default: ‘1,2’) For instance, [‘1,2’, ‘2,3’].


legend_loc : str (default: ’none’) Location of legend, either ‘on data’, ‘right margin’ or valid keywords for matplotlib.legend.

legend_fontsize : int (default: None) Legend font size.


legend_fontoutline : float (default: None) Line width of the legend font outline in pt. Draws a white outline using the path effect withStroke.

legend_align_text : bool or str (default: None) Aligns the positions of the legend texts. Set the axis along which the best alignment should be determined. This can be ‘y’ or True (vertically), ‘x’ (horizontally), or ‘xy’ (best alignment in both directions).

right_margin : float or list of float (default: None) Adjust the width of the space right of each plotting panel.

left_margin : float or list of float (default: None) Adjust the width of the space left of each plotting panel.

xlabel : str (default: None) Label of x-axis.

ylabel : str (default: None) Label of y-axis.

title : str (default: None) Provide title for panels either as, e.g. [“title1”, “title2”, . . . ].
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```python
fontsize: float (default: None) Label font size.

figsize: tuple (default: (7, 5)) Figure size.

xlim: tuple, e.g. [0, 1] or None (default: None) Restrict x-limits of the axis.

ylim: tuple, e.g. [0, 1] or None (default: None) Restrict y-limits of the axis.

add_density: bool or str or None (default: None) Whether to show density of values along x and y axes. Color of the density plot can also be passed as str.

add_assignments: bool or str or None (default: None) Whether to add assignments to the model curve. Color of the assignments can also be passed as str.

add_linfit: bool or str or None (default: None) Whether to add linear regression fit to the data points. Fitting with or without an intercept by passing `intercept` or `no_intercept`. A colored regression line with intercept is obtained with `intercept, blue`.

add_polyfit: bool or str or int or None (default: None) Whether to add polynomial fit to the data points. Color of the polyfit plot can also be passed as str. The degree of the polynomial fit can be passed as int (default is 2 for quadratic fit). Fitting with or without an intercept by passing `intercept` or `no_intercept`. A colored regression line with intercept is obtained with `intercept, blue`.

add_rug: str or None (default: None) If categorical observation annotation (e.g. ‘clusters’) is given, a rugplot is attached to the x-axis showing the data membership to each of the categories.

add_text: str (default: None) Text to be added to the plot, passed as str.

add_text_pos: tuple, e.g. [0.05, 0.95] (default: [0.05, 0.95]) Text position. Default is [0.05, 0.95], positioning the text at top right corner.

add_margin: float (default: None) A value between [-1, 1] to add (positive) and reduce (negative) figure margins.

add_outline: bool or str (default: False) Whether to show an outline around scatter plot dots. Alternatively a string of cluster names can be passed, e.g. ‘cluster_1, clusters_3’.

outline_width: tuple type scalar or None (default: (0.3, 0.05)) Width of the inner and outer outline

outline_color: tuple of type str or None (default: ‘black’, ‘white’)) Inner and outer matplotlib color of the outline

n_convolve: int or None (default: None) If int is given, data is smoothed by convolution along the x-axis with kernel size n_convolve.

smooth: Whether to convolve/average the color values over the nearest neighbors. If int, it specifies number of neighbors.

normalize_data: bool (default: None) Whether to rescale values for x, y to [0,1].

rescale_color: tuple (default: None) Boundaries for color rescaling, e.g. [0, 1], setting min/max values of the colorbar.

color_gradients: str or np.ndarray (default: None) Key for .obsm or array with color gradients by categories.

dpi: int (default: 80) Figure dpi.

frameon: bool (default: True) Draw a frame around the scatter plot.

ncols: int (default: None) Number of panels per row.
```
**nrows : int (default: None)** Number of panels per column.

**wspace : float (default: None)** Adjust the width of the space between multiple panels.

**hspace : float (default: None)** Adjust the height of the space between multiple panels.

**show : bool, optional (default: None)** Show the plot, do not return axis.

**save : bool or str, optional (default: None)** If True or a str, save the figure. A string is appended to the default filename. Infer the filetype if ending on ‘.pdf’, ‘.png’, ‘.svg’.

**ax : matplotlib.Axes, optional (default: None)** A matplotlib axes object. Only works if plotting a single component.

Returns `matplotlib.Axis` if `show==False`

---

**scvelo.pl.velocity_embedding_stream**

*scvelo.pl.velocity_embedding_stream*(adata, basis=None, vkey='velocity', density=2, smooth=None, min_mass=None, cutoff_perc=None, arrow_color=None, arrow_size=1, arrow_style='->', max_length=4, integration_direction='both', linewidth=None, n_neighbors=None, recompute=None, color=None, use_raw=None, layer=None, color_map=None, colorbar=True, palette=None, size=None, alpha=0.3, perc=None, X=None, V=None, X_grid=None, V_grid=None, sort_order=True, groups=None, components=None, legend_loc='on data', legend_fontsize=None, legend_fontweight=None, xlabel=None, ylabel=None, title=None, fontsize=None, figsize=None, dpi=None, frameon=None, show=None, save=None, ax=None, ncol=None, **kwargs)

Stream plot of velocities on the embedding.

**Parameters**

*adata : AnnData* Annotated data matrix.

**density : float (default: 2)** Controls the closeness of streamlines. When density = 2 (default), the domain is divided into a 60x60 grid, whereas density linearly scales this grid. Each cell in the grid can have, at most, one traversing streamline. For different densities in each direction, use a tuple (density_x, density_y).

**smooth : bool or int (default: None)** Multiplication factor for scale in Gaussian kernel around grid point.

**min_mass : float (default: 1)** Minimum threshold for mass to be shown. It can range between 0 (all velocities) and 5 (large velocities only).

**cutoff_perc : float (default: None)** If set, mask small velocities below a percentile threshold (between 0 and 100).

**linewidth : float (default: 1)** Line width for streamplot.

**arrow_color : str or 2D array (default: 'k')** The streamline color. If given an array, it must have the same shape as u and v.

**arrow_size : float (default: 1)** Scaling factor for the arrow size.

**arrow_style : str (default: '-|>')** Arrow style specification, ‘-|>’ or ‘->’.

**max_length : float (default: 4)** Maximum length of streamline in axes coordinates.
integration_direction : str (default: ‘both’) Integrate the streamline in ‘forward’, ‘backward’ or ‘both’ directions.

n_neighbors : int (default: None) Number of neighbors to consider around grid point.


V : np.ndarray (default: None) Embedding velocity coordinates. Using `adata.obsm['velocity_umap']` per default.

basis : str or list of str (default: None) Key for embedding. If not specified, use ‘umap’, ‘tsne’ or ‘pca’ (ordered by preference).

vkey : str or list of str (default: None) Key for velocity / steady-state ratio to be visualized.

color : str, list of str or None (default: None) Key for annotations of observations/cells or variables/genes

use_raw : bool (default: None) Use raw attribute of adata if present.

layer : str, list of str or None (default: None) Specify the layer for color.

color_map : str (default: matplotlib.rcParams['image.cmap']) String denoting matplotlib color map.

colorbar : bool (default: False) Whether to show colorbar.

palette : list of str (default: None) Colors to use for plotting groups (categorical annotation).

size : float (default: 5) Point size.

alpha : float (default: 1) Set blending - 0 transparent to 1 opaque.

linewidth Scaling factor for the width of occurring lines.

linecolor : str or list of str (default: ‘k’) Color of lines from velocity fits, linear fits and polynomial fits

perc : tuple, e.g. [2,98] (default: None) Specify percentile for continuous coloring.

groups : str or list of str (default: all groups) Restrict to a few categories in categorical observation annotation. Multiple categories can be passed as list with ['cluster_1', 'cluster_3'], or as string with 'cluster_1, cluster_3'.

sort_order : bool (default: True) For continuous annotations used as color parameter, plot data points with higher values on top of others.

components : str or list of str (default: ‘1,2’) For instance, ['1,2', '2,3'].

projection: {'2d', '3d'} (default: '2d') Projection of plot.

legend_loc : str (default: 'none') Location of legend, either ‘on data’, ‘right margin’ or valid keywords for matplotlib.legend.

legend_fontsize : int (default: None) Legend font size.

legend_fontweight : {'normal', 'bold',...} (default: None) Legend font weight. A numeric value in range 0-1000 or a string. Defaults to ‘bold’ if legend_loc = ‘on data’, otherwise to ‘normal’. Available are ['light', 'normal', 'medium', 'semibold', 'bold', 'heavy', 'black'].

legend_fontoutline : float (default: None) Line width of the legend font outline in pt. Draws a white outline using the path effect withStroke.
**legend_align_text**: bool or str (default: `None`) Aligns the positions of the legend texts. Set the axis along which the best alignment should be determined. This can be ‘y’ or True (vertically), ‘x’ (horizontally), or ‘xy’ (best alignment in both directions).

**right_margin**: float or list of float (default: `None`) Adjust the width of the space right of each plotting panel.

**left_margin**: float or list of float (default: `None`) Adjust the width of the space left of each plotting panel.

**xlabel**: str (default: `None`) Label of x-axis.

**ylabel**: str (default: `None`) Label of y-axis.

**title**: str (default: `None`) Provide title for panels either as, e.g. [“title1”, “title2”, ...].

**fontsize**: float (default: `None`) Label font size.

**figsize**: tuple (default: `(7,5)`) Figure size.

**xlim**: tuple, e.g. `[0,1]` or `None` (default: `None`) Restrict x-limits of the axis.

**ylim**: tuple, e.g. `[0,1]` or `None` (default: `None`) Restrict y-limits of the axis.

**add_density**: bool or str or `None` (default: `None`) Whether to show density of values along x and y axes. Color of the density plot can also be passed as `str`.

**add_assignments**: bool or str or `None` (default: `None`) Whether to add assignments to the model curve. Color of the assignments can also be passed as `str`.

**add_linfit**: bool or str or `None` (default: `None`) Whether to add linear regression fit to the data points. Color of the line can also be passed as `str`. Fitting with or without an intercept by passing ‘intercept’ or ‘no_intercept’. A colored regression line with intercept is obtained with ‘intercept, blue’.

**add_polyfit**: bool or str or `int` or `None` (default: `None`) Whether to add polynomial fit to the data points. Color of the polyfit plot can also be passed as `str`. The degree of the polynomial fit can be passed as `int` (default is 2 for quadratic fit). Fitting with or without an intercept by passing ‘intercept’ or ‘no_intercept’. A colored regression line with intercept is obtained with ‘intercept, blue’.

**add_rug**: str or `None` (default: `None`) If categorical observation annotation (e.g. ‘clusters’) is given, a rugplot is attached to the x-axis showing the data membership to each of the categories.

**add_text**: str (default: `None`) Text to be added to the plot, passed as `str`.

**add_text_pos**: tuple, e.g. `[0.05, 0.95]` (default: `[0.05, 0.95]`) Text position. Default is `[0.05, 0.95]`, positioning the text at top right corner.

**add_margin**: float (default: `None`) A value between [-1, 1] to add (positive) and reduce (negative) figure margins.

**add_outline**: bool or str (default: `False`) Whether to show an outline around scatter plot dots. Alternatively a string of cluster names can be passed, e.g. ‘cluster_1, clusters_3’.

**outline_width**: tuple type scalar or `None` (default: `(0.3, 0.05)`) Width of the inner and outer outline

**outline_color**: tuple of type str or `None` (default: (`'black'`, `'white'`)) Inner and outer matplotlib color of the outline

**n_convolve**: int or `None` (default: `None`) If int is given, data is smoothed by convolution along the x-axis with kernel size n_convolve.
**smooth** Whether to convolve/average the color values over the nearest neighbors. If int, it specifies number of neighbors.

**normalize_data**: bool (default: None) Whether to rescale values for x, y to [0,1].

**rescale_color**: tuple (default: None) Boundaries for color rescaling, e.g. [0,1], setting min/max values of the colorbar.

**color_gradients**: str or np.ndarray (default: None) Key for .obsm or array with color gradients by categories.

**dpi**: int (default: 80) Figure dpi.

**frameon**: bool (default: True) Draw a frame around the scatter plot.

**ncols**: int (default: None) Number of panels per row.

**nrows**: int (default: None) Number of panels per column.

**wspace**: float (default: None) Adjust the width of the space between multiple panels.

**hspace**: float (default: None) Adjust the height of the space between multiple panels.

**show**: bool, optional (default: None) Show the plot, do not return axis.

**save**: bool or str, optional (default: None) If True or a str, save the figure. A string is appended to the default filename. Infer the filetype if ending on {'.pdf', '.png', '.svg'}.

**ax**: matplotlib.Axes, optional (default: None) A matplotlib axes object. Only works if plotting a single component.

**Returns** matplotlib.Axis if show==False

### Velocity graph

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### scvelo.pl.velocity

**scvelo.pl.velocity** *(adata, var_names=None, basis=None, vkey='velocity', mode=None, fits=None, layers='all', color=None, color_map=None, colorbar=True, perc=[2, 98], alpha=0.5, size=None, groupby=None, groups=None, legend_loc='none', legend_fontsize=8, use_raw=False, fontsize=None, **kwargs)*

Phase and velocity plot for set of genes.

The phase plot shows spliced against unspliced expressions with steady-state fit. Further the embedding is shown colored by velocity and expression.

**Parameters**

**adata**: AnnData Annotated data matrix.

**var_names**: str or list of str (default: None) Which variables to show.

**basis**: str (default: 'umap') Key for embedding coordinates.

**mode** : 'stochastic' or None (default: None) Whether to show show covariability phase portrait.
fits : str or list of str (default: ['velocity', 'dynamics']) Which steady-state estimates to show.

layers : str or list of str (default: 'all') Which layers to show.

color : str, list of str or None (default: None) Key for annotations of observations/cells or variables/genes

color_map : str or tuple (default: ['RdYlGn', 'gnuplot_r']) String denoting matplotlib color map. If tuple is given, first and latter color map correspond to velocity and expression, respectively.

perc : tuple, e.g. [2,98] (default: [2,98]) Specify percentile for continuous coloring.

groups : str, list (default: None) Subset of groups, e.g. ['g1', 'g2'], to which the plot shall be restricted.

groupby : str, list or np.ndarray (default: None) Key of observations grouping to consider.

legend_loc : str (default: 'none') Location of legend, either 'on data', 'right margin' or valid keywords for matplotlib.legend.

size : float (default: 5) Point size.

alpha : float (default: 1) Set blending - 0 transparent to 1 opaque.

fontsize : float (default: None) Label font size.

figsize : tuple (default: (7,5)) Figure size.

dpi : int (default: 80) Figure dpi.

show : bool, optional (default: None) Show the plot, do not return axis.

save : bool or str, optional (default: None) If True or a str, save the figure. A string is appended to the default filename. Infer the filetype if ending on {'.pdf', '.png', '.svg'}.

ax : matplotlib.Axes, optional (default: None) A matplotlib axes object. Only works if plotting a single component.

ncols : int or None (default: None) Number of columns to arrange multiplots into.

---

scvelo.pl.velocity_graph

scvelo.pl.velocity_graph (adata, basis=None, vkey='velocity', which_graph=None, n_neighbors=10, arrows=None, arrowsize=3, alpha=0.8, perc=None, threshold=None, edge_width=0.2, edge_color='grey', edges_on_top=None, color=None, layer=None, size=None, groups=None, components=None, title=None, dpi=None, show=None, save=None, ax=None, **kwargs)

Plot of the velocity graph.

Parameters

adata : AnnData Annotated data matrix.

which_graph : 'velocity_graph' or 'connectivities' (default: None) Whether to show transitions from velocity graph or neighbor connectivities.

n_neighbors : int (default: 10) Number of neighbors to be included for generating connectivity / velocity graph.

arrows : bool (default: None) Whether to display arrows instead of edges. Recommended to be used only on a cluster by setting groups parameter.
arrowsize: int (default: 3) Size of the arrow heads.

basis: str or list of str (default: None) Key for embedding. If not specified, use ‘umap’, ‘tsne’ or ‘pca’ (ordered by preference).

vkey: str or list of str (default: None) Key for velocity / steady-state ratio to be visualized.

color: str, list of str or None (default: None) Key for annotations of observations/cells or variables/genes

use_raw: bool (default: None) Use raw attribute of adata if present.

layers: str, list of str or None (default: None) Specify the layer for color.

color_map: str (default: matplotlib.rcParams[‘image.cmap’]) String denoting matplotlib color map.

colorbar: bool (default: False) Whether to show colorbar.

palette: list of str (default: None) Colors to use for plotting groups (categorical annotation).

size: float (default: 5) Point size.

alpha: float (default: 1) Set blending - 0 transparent to 1 opaque.

linewidth: float (default: 1) Scaling factor for the width of occurring lines.

linecolor: str or list of str (default: ‘k’) Color of lines from velocity fits, linear fits and polynomial fits

perc: tuple, e.g. [2,98] (default: None) Specify percentile for continuous coloring.

groups: str or list of str (default: all groups) Restrict to a few categories in categorical observation annotation. Multiple categories can be passed as list with ['cluster_1', 'cluster_3'], or as string with 'cluster_1, cluster_3'.

sort_order: bool (default: True) For continuous annotations used as color parameter, plot data points with higher values on top of others.

components: str or list of str (default: ‘1,2’) For instance, ['1,2', '2,3'].


legend_loc: str (default: 'none') Location of legend, either ‘on data’, ‘right margin’ or valid keywords for matplotlib.legend.

legend_fontsize: int (default: None) Legend font size.

legend_fontweight: ['normal', 'bold',...] (default: None) Legend font weight. A numeric value in range 0-1000 or a string. Defaults to ‘bold’ if legend_loc = ‘on data’, otherwise to ‘normal’. Available are ['light', 'normal', 'medium', 'semibold', 'bold', 'heavy', 'black'].

legend_fontoutline: float (default: None) Line width of the legend font outline in pt. Draws a white outline using the path effect withStroke.

legend_align_text: bool or str (default: None) Aligns the positions of the legend texts. Set the axis along which the best alignment should be determined. This can be ‘y’ or True (vertically), ‘x’ (horizontally), or ‘xy’ (best alignment in both directions).

right_margin: float or list of float (default: None) Adjust the width of the space right of each plotting panel.

left_margin: float or list of float (default: None) Adjust the width of the space left of each plotting panel.
xlabel : str (default: None) Label of x-axis.
ylabel : str (default: None) Label of y-axis.
title : str (default: None) Provide title for panels either as, e.g. [“title1”, “title2”, …].
fontsize : float (default: None) Label font size.
figsize : tuple (default: (7,5)) Figure size.
xlim : tuple, e.g. [0,1] or None (default: None) Restrict x-limits of the axis.
ylim : tuple, e.g. [0,1] or None (default: None) Restrict y-limits of the axis.
add_density : bool or str or None (default: None) Whether to show density of values along x and y axes. Color of the density plot can also be passed as str.
add_assignments : bool or str or None (default: None) Whether to add assignments to the model curve. Color of the assignments can also be passed as str.
add_linfit : bool or str or None (default: None) Whether to add linear regression fit to the data points. Color of the line can also be passed as str. Fitting with or without an intercept by passing ‘intercept’ or ‘no_intercept’. A colored regression line with intercept is obtained with ‘intercept, blue’.
add_polyfit : bool or str or int or None (default: None) Whether to add polynomial fit to the data points. Color of the polyfit plot can also be passed as str. The degree of the polynomial fit can be passed as int (default is 2 for quadratic fit). Fitting with or without an intercept by passing ‘intercept’ or ‘no_intercept’. A colored regression line with intercept is obtained with ‘intercept, blue’.
add_rug : str or None (default: None) If categorical observation annotation (e.g. ‘clusters’) is given, a rugplot is attached to the x-axis showing the data membership to each of the categories.
add_text : str (default: None) Text to be added to the plot, passed as str.
add_text_pos : tuple, e.g. [0.05, 0.95] (default: [0.05, 0.95]) Text position. Default is [0.05, 0.95], positioning the text at top right corner.
add_margin : float (default: None) A value between [-1, 1] to add (positive) and reduce (negative) figure margins.
add_outline : bool or str (default: False) Whether to show an outline around scatter plot dots. Alternatively a string of cluster names can be passed, e.g. ‘cluster_1, clusters_3’.
outline_width : tuple type scalar or None (default: (0.3, 0.05)) Width of the inner and outer outline
outline_color : tuple of type str or None (default: (‘black’, ‘white’)) Inner and outer matplotlib color of the outline
n_convolve : int or None (default: None) If int is given, data is smoothed by convolution along the x-axis with kernel size n_convolve.
smooth : bool or int (default: None) Whether to convolve/average the color values over the nearest neighbors. If int, it specifies number of neighbors.
normalize_data : bool (default: None) Whether to rescale values for x, y to [0,1].
rescale_color : tuple (default: None) Boundaries for color rescaling, e.g. [0, 1], setting min/max values of the colorbar.
color_gradients : str or np.ndarray (default: None) Key for .obsm or array with color gradients by categories.
dpi : int (default: 80) Figure dpi.
frameon : bool (default: True) Draw a frame around the scatter plot.
ncols : int (default: None) Number of panels per row.
nrows : int (default: None) Number of panels per column.
wspace : float (default: None) Adjust the width of the space between multiple panels.
hspace : float (default: None) Adjust the height of the space between multiple panels.
show : bool, optional (default: None) Show the plot, do not return axis.
save : bool or str, optional (default: None) If True or a str, save the figure. A string is appended to the default filename. Infer the filetype if ending on {'.pdf', '.png', '.svg'}.

Returns matplotlib.Axis if show==False

scvelo.pl.paga

scvelo.pl.paga(adata=None, basis=None, vkey='velocity', color=None, layer=None, title=None, threshold=None, layout=None, layout_kwds=None, init_pos=None, root=0, labels=None, single_component=False, dashed_edges='connectivities', solid_edges='transitions_confidence', transitions='transitions_confidence', node_size_scale=1, node_size_power=0.5, edge_width_scale=0.4, min_edge_width=None, max_edge_width=2, arrowsize=15, random_state=0, pos=None, node_colors=None, normalize_to_color=False, cmap=None, cax=None, cb_kwds=None, add_pos=True, export_to_gexf=False, plot=True, use_raw=None, size=None, groups=None, components=None, figsize=None, dpi=None, show=None, save=None, ax=None, ncols=None, scatter_flag=None, **kwargs)

Plot PAGA graph with velocity-directed edges.

PAGA graph with connectivities (dashed) and transitions (solid/arrows).

Parameters

adata Annotated data matrix.
threshold Do not draw edges for weights below this threshold. Set to 0 if you want all edges. Discarding low-connectivity edges helps in getting a much clearer picture of the graph.

color : str, list of str or None (default: None) Gene name or obs annotation defining the node colors. Also plots the degree of the abstracted graph when passing ‘degree_dashed’ or ‘degree_solid’.

labels The node labels. If None, this defaults to the group labels stored in the categorical for which paga() has been computed.
pos Two-column array-like storing the x and y coordinates for drawing. Otherwise, path to a .gdf file that has been exported from Gephi or a similar graph visualization software.

layout Plotting layout that computes positions. ‘fa’ stands for ForceAtlas2, ‘fr’ stands for Fruchterman-Reingold, ‘rt’ stands for Reingold-Tilford, ‘eq_tree’ stands for equally spaced tree. All but ‘fa’ and ‘eq_tree’ are igraph layouts. All other igraph layouts are also permitted.

layout_kwds Keywords for the layout.
init_pos Two-column array storing the x and y coordinates for initializing the layout.
random_state For layouts with random initialization like ‘fr’, change this to use different initial states for the optimization. If None, the initial state is not reproducible.

root If choosing a tree layout, this is the index of the root node or a list of root node indices. If this is a non-empty vector then the supplied node IDs are used as the roots of the trees (or a single tree if the graph is connected). If this is None or an empty list, the root vertices are automatically calculated based on topological sorting.

transitions Key for .uns['paga'] that specifies the matrix that – for instance ‘transitions_confidence’ – that specifies the matrix that stores the arrows.

dashed_edges Key for .uns['paga'] that specifies the matrix that stores the edges to be drawn dashed grey. If None, no dashed edges are drawn.

single_component Restrict to largest connected component.

solid_edges Key for .uns['paga'] that specifies the matrix that stores the edges to be drawn solid black.

fontsize: float (default: None) Font size for node labels.

fontoutline Width of the white outline around fonts.

text_kws Keywords for text().

node_size_scale Increase or decrease the size of the nodes.

node_size_power The power with which groups sizes influence the radius of the nodes.

edge_width_scale Edge with scale in units of rcParams['lines.linewidth'].

min_edge_width Min width of solid edges.

max_edge_width Max width of solid and dashed edges.

arrowsize For directed graphs, choose the size of the arrow head head’s length and width.

export_to_gexf Export to gexf format to be read by graph visualization programs such as Gephi.

normalize_to_color Whether to normalize categorical plots to color or the underlying grouping.

cmap The color map.

cax A matplotlib axes object for a potential colorbar.

cb_kws Keyword arguments for ColorbarBase, e.g., ticks.

add_pos Add the positions to adata.uns['paga'].

title: str (default: None) Provide a title.

frameon: bool (default: True) Draw a frame around the PAGA graph.

plot If False, do not create the figure, simply compute the layout.

save: bool or str, optional (default: None) Save figure under default (if set True) or specified filename (if set str). Infer the filetype if ending on ‘.pdf’, ‘.png’, or ‘.svg’.

ax: matplotlib.Axes, optional (default: None) A matplotlib axes object.

basis: str or list of str (default: None) Key for embedding. If not specified, use ‘umap’, ‘tsne’ or ‘pca’ (ordered by preference).
vkey : str or list of str (default: None) Key for velocity / steady-state ratio to be visualized.

color Key for annotations of observations/cells or variables/genes

use_raw : bool (default: None) Use raw attribute of adata if present.

layer : str, list of str or None (default: None) Specify the layer for color.

color_map : str (default: matplotlib.rcParams['image.cmap']) String denoting matplotlib color map.

colorbar : bool (default: False) Whether to show colorbar.

palette : list of str (default: None) Colors to use for plotting groups (categorical annotation).

size : float (default: 5) Point size.

alpha : float (default: 1) Set blending - 0 transparent to 1 opaque.

linewidth : float (default: 1) Scaling factor for the width of occurring lines.

linecolor : str or list of str (default: ‘k’) Color of lines from velocity fits, linear fits and polynomial fits

perc : tuple, e.g. [2,98] (default: None) Specify percentile for continuous coloring.

groups : str or list of str (default: all groups) Restrict to a few categories in categorical observation annotation. Multiple categories can be passed as list with ['cluster_1', 'cluster_3'], or as string with 'cluster_1, cluster_3'.

sort_order : bool (default: True) For continuous annotations used as color parameter, plot data points with higher values on top of others.

components : str or list of str (default: ‘1,2’) For instance, ['1,2', '2,3'].

projection : {'2d', '3d'} (default: '2d') Projection of plot.

legend_loc : str (default: 'none') Location of legend, either ‘on data’, ‘right margin’ or valid keywords for matplotlib.legend.

legend_fontsize : int (default: None) Legend font size.

legend_fontweight : {'normal', 'bold', . . . } (default: None) Legend font weight. A numeric value in range 0-1000 or a string. Defaults to ‘bold’ if legend_loc = ‘on data’, otherwise to ‘normal’. Available are ['light', 'normal', 'medium', 'semibold', 'bold', 'heavy', 'black'].

legend_fontoutline : float (default: None) Line width of the legend font outline in pt. Draws a white outline using the path effect withStroke.

legend_align_text : bool or str (default: None) Aligns the positions of the legend texts. Set the axis along which the best alignment should be determined. This can be ‘y’ or True (vertically), ‘x’ (horizontally), or ‘xy’ (best alignment in both directions).

right_margin : float or list of float (default: None) Adjust the width of the space right of each plotting panel.

left_margin : float or list of float (default: None) Adjust the width of the space left of each plotting panel.

xlabel : str (default: None) Label of x-axis.

ylabel : str (default: None) Label of y-axis.

title Provide title for panels either as, e.g. ['“title1”, “title2”, . . . ].
**fontsize** Label font size.

**figsize** : tuple (default: (7,5)) Figure size.

**xlim** : tuple, e.g. [0,1] or None (default: None) Restrict x-limits of the axis.

**ylim** : tuple, e.g. [0,1] or None (default: None) Restrict y-limits of the axis.

**add_density** : bool or str or None (default: None) Whether to show density of values along x and y axes. Color of the density plot can also be passed as str.

**add_assignments** : bool or str or None (default: None) Whether to add assignments to the model curve. Color of the assignments can also be passed as str.

**add_linfit** : bool or str or None (default: None) Whether to add linear regression fit to the data points. Color of the line can also be passed as str. Fitting with or without an intercept by passing ‘intercept’ or ‘no_intercept’. A colored regression line with intercept is obtained with ‘intercept, blue’.

**add_polyfit** : bool or str or int or None (default: None) Whether to add polynomial fit to the data points. Color of the polyfit plot can also be passed as str. The degree of the polynomial fit can be passed as int (default is 2 for quadratic fit). Fitting with or without an intercept by passing ‘intercept’ or ‘no_intercept’. A colored regression line with intercept is obtained with ‘intercept, blue’.

**add_rug** : str or None (default: None) If categorical observation annotation (e.g. ‘clusters’) is given, a rugplot is attached to the x-axis showing the data membership to each of the categories.

**add_text** : str (default: None) Text to be added to the plot, passed as str.

**add_text_pos** : tuple, e.g. [0.05, 0.95] (default: [0.05, 0.95]) Text position. Default is [0.05, 0.95], positioning the text at top right corner.

**add_margin** : float (default: None) A value between [-1, 1] to add (positive) and reduce (negative) figure margins.

**add_outline** : bool or str (default: False) Whether to show an outline around scatter plot dots. Alternatively a string of cluster names can be passed, e.g. ‘cluster_1, clusters_3’.

**outline_width** : tuple type scalar or None (default: (0.3, 0.05)) Width of the inner and outer outline

**outline_color** : tuple of type str or None (default: (‘black’, ‘white’)) Inner and outer matplotlib color of the outline

**n_convolve** : int or None (default: None) If int is given, data is smoothed by convolution along the x-axis with kernel size n_convolve.

**smooth** : bool or int (default: None) Whether to convolve/average the color values over the nearest neighbors. If int, it specifies number of neighbors.

**normalize_data** : bool (default: None) Whether to rescale values for x, y to [0,1].

**rescale_color** : tuple (default: None) Boundaries for color rescaling, e.g. [0, 1], setting min/max values of the colorbar.

**color_gradients** : str or np.ndarray (default: None) Key for .obsm or array with color gradients by categories.

**dpi** : int (default: 80) Figure dpi.

**frameon** Draw a frame around the scatter plot.

**ncols** : int (default: None) Number of panels per row.
**nrows : int (default: None)** Number of panels per column.

**wspace : float (default: None)** Adjust the width of the space between multiple panels.

**hspace : float (default: None)** Adjust the height of the space between multiple panels.

**show : bool, optional (default: None)** Show the plot, do not return axis.

**save** If True or a str, save the figure. A string is appended to the default filename. Infer the filetype if ending on {'.pdf', '.png', '.svg'}.

**ax** A matplotlib axes object. Only works if plotting a single component.

**Returns**

- If `show=False`, one or more `Axes` objects.
- Adds ‘pos’ to `adata.uns[‘paga’]` if `add_pos` is True.

**Further plotting**

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**scvelo.pl.proportions**

Plot pie chart of spliced/unspliced proportions.

**Parameters**

- **adata : AnnData** Annotated data matrix.
- **groupby : str (default: ‘clusters’)** Key of observations grouping to consider.
- **layers : list of str (default: [‘spliced’, ‘unspliced’, ‘ambiguous’])** Specify the layers of count matrices for computing proportions.
- **highlight : str (default: ‘unspliced’)** Which proportions to highlight in pie chart.
- **add_labels_pie : bool (default: True)** Whether to add percentage labels in pie chart.
- **add_labels_bar : bool (default: True)** Whether to add percentage labels in bar chart.
- **fontsize : float (default: 8)** Label font size.
- **figsize : tuple (default: (10, 2))** Figure size.
- **dpi : int (default: 80)** Figure dpi.
- **use_raw : bool (default: True)** Use initial cell sizes before normalization and filtering.
- **show : bool (default: True)** Show the plot, do not return axis.
- **save : bool or str, optional (default: None)** If True or a str, save the figure. A string is appended to the default filename. Infer the filetype if ending on {’.pdf’, ‘.png’, ‘.svg’}.

**Returns** Plots the proportions of abundances as pie chart.
scvelo.pl.heatmap

scvelo.pl.heatmap(adata, var_names, sortby='latent_time', layer='Ms', color_map='viridis', col_color=None, palette='viridis', n_convolve=30, standard_scale=0, sort=True, colorbar=None, col_cluster=False, row_cluster=False, context=None, font_scale=None, figsize=(8, 4), show=None, save=None, **kwargs)

Plot time series for genes as heatmap.

Parameters

adata: AnnData  Annotated data matrix.

var_names: str, list of str  Names of variables to use for the plot.

sortby: str (default: ‘latent_time’)  Observation key to extract time data from.

layer: str (default: ‘Ms’)  Layer key to extract count data from.

color_map: str (default: ‘viridis’)  String denoting matplotlib color map.

col_color: str or list of str (default: None)  String denoting matplotlib color map to use along the columns.

palette: list of str (default: ‘viridis’)  Colors to use for plotting groups (categorical annotation).

n_convolve: int or None (default: 30)  If int is given, data is smoothed by convolution along the x-axis with kernel size n_convolve.

standard_scale: int or None (default: 0)  Either 0 (rows) or 1 (columns). Whether or not to standardize that dimension (each row or column), subtract minimum and divide each by its maximum.

sort: bool (default: True)  Whether to sort the expression values given by xkey.

colorbar: bool or None (default: None)  Whether to show colorbar.

{row, col}_cluster: bool or None  If True, cluster the {rows, columns}.

context: None, or one of {paper, notebook, talk, poster}  A dictionary of parameters or the name of a preconfigured set.

font_scale: float, optional  Scaling factor to scale the size of the font elements.

figsize: tuple (default: (8, 4))  Figure size.

show: bool, optional (default: None)  Show the plot, do not return axis.

save: bool or str, optional (default: None)  If True or a str, save the figure. A string is appended to the default filename. Infer the filetype if ending on ‘.pdf’, ‘.png’, ‘.svg’.

kwags  Arguments passed to seaborn.clustermap, e.g., set yticklabels=True to display all gene names in all rows.

Returns  If show==False a matplotlib.Axis

scvelo.pl.hist

scvelo.pl.hist(arrays, alpha=0.5, bins=50, color=None, colors=None, labels=None, hist=None, kde=None, bw_method=None, xlabel=None, ylabel=None, xlim=None, ylim=None, cutoff=None, xscale=None, yscale=None, xticks=None, yticks=None, fontsize=None, legend_fontsize=None, figsize=None, normed=None, perc=None, exclude_zeros=None, axvline=None, ashline=None, pdf=None, ax=None, dpi=None, show=True, **kwargs)

Plot a histogram.
Parameters

- **arrays**: list or array (default: ['royalblue', 'white', 'forestgreen']) List of colors, either as names or rgb values.
- **alpha**: list, np.ndarray or None (default: None) Alpha of the colors. Must be same length as colors.
- **bins**: int or sequence (default: 50) If an integer is given, bins + 1 bin edges are calculated and returned, consistent with numpy.histogram. If bins is a sequence, gives bin edges, including left edge of first bin and right edge of last bin. In this case, bins is returned unmodified.
- **colors**: list or array (default: ['royalblue', 'white', 'forestgreen']) List of colors, either as names or rgb values.
- **labels**: str or None (default: None) String, or sequence of strings to label clusters.
- **hist**: bool or None (default: None) Whether to show histogram.
- **kde**: bool or None (default: None) Whether to use kernel density estimation on data.
- **bw_method**: str, scalar or callable, (default: None) The method used to calculate the estimator bandwidth. This can be ‘scott’, ‘silverman’, a scalar constant or a callable. If a scalar, this will be used directly as kde.factor. If a callable, it should take a gaussian_kde instance as only parameter and return a scalar. If None (default), nothing happens; the current kde.covariance_factor method is kept.
- **xlabel**: str (default: None) Label of x-axis.
- **ylabel**: str (default: None) Label of y-axis.
- **xlim**: tuple, e.g. [0,1] or None (default: None) Restrict x-limits of the axis.
- **ylim**: tuple, e.g. [0,1] or None (default: None) Restrict y-limits of the axis.
- **cutoff**: tuple, e.g. [0,1] or float or None (default: None) Bins will be cut off below and above the cutoff values.
- **xscale**: log or None (default: None) Scale of the x-axis.
- **yscale**: log or None (default: None) Scale of the y-axis.
- **fontsize**: float (default: None) Label font size.
- **legend_fontsize**: int (default: None) Legend font size.
- **figsize**: tuple (default: (7,5)) Figure size.
- **normed**: bool or None (default: None) Whether to normalize data.
- **perc**: tuple, e.g. [2,98] (default: None) Specify percentile for continuous coloring.
- **exclude_zeros**: bool or None (default: None) Whether to exclude zeros in data for the kde and hist plot.
- **axvline**: float or None (default: None) Plot a vertical line at the specified x-value.
- **axhline**: float or None (default: None) Plot a horizontal line at the specified y-value.
- **pdf**: str or None (default: None) probability density function to be fitted, e.g., ‘norm’, ‘t’, ‘chi’, ‘beta’, ‘gamma’, ‘laplace’ etc.
- **ax**: matplotlib.Axes, optional (default: None) A matplotlib axes object. Only works if plotting a single component.
- **dpi**: int (default: 80) Figure dpi.
show : bool, optional (default: None)  
Show the plot, do not return axis.

Returns  
If show==False a matplotlib.Axis

4.3.5 Datasets

datasets.pancreas()  
Pancreatic endocrinogenesis.

datasets.dentategyrus([adjusted])  
Dentate Gyrus neurogenesis.

datasets.forebrain()  
Developing human forebrain.

datasets.dentategyrus_lamanno()  
Dentate Gyrus neurogenesis.

datasets.gastrulation()  
Mouse gastrulation.

datasets.gastrulation_e75()  
Mouse gastrulation subset to E7.5.

datasets.gastrulation_erythroid()  
Mouse gastrulation subset to erythroid lineage.

datasets.bonemarrow()  
Human bone marrow.

datasets.pbmc68k()  
Peripheral blood mononuclear cells.

datasets.simulation([n_obs, n_vars, alpha, ...])  
Simulation of mRNA splicing kinetics.

scvelo.datasets.pancreas

cvelo.datasets.pancreas()  
Pancreatic endocrinogenesis.

Data from Bastidas-Ponce et al. (2019).

Pancreatic epithelial and Ngn3-Venus fusion (NVF) cells during secondary transition with transcriptome profiles sampled from embryonic day 15.5.

Endocrine cells are derived from endocrine progenitors located in the pancreatic epithelium. Endocrine commitment terminates in four major fates: glucagon-producing $\alpha$-cells, insulin-producing $\beta$-cells, somatostatin-producing $\delta$-cells and ghrelin-producing $\epsilon$-cells.
**Returns**

Returns `adata` object

### `scvelo.datasets.dentategyrus`

Data from Hochgerner et al. (2018).

Dentate gyrus (DG) is part of the hippocampus involved in learning, episodic memory formation and spatial coding. The experiment from the developing DG comprises two time points (P12 and P35) measured using droplet-based scRNA-seq (10x Genomics Chromium).

The dominating structure is the granule cell lineage, in which neuroblasts develop into granule cells. Simultaneously, the remaining population forms distinct cell types that are fully differentiated (e.g. Cajal-Retzius cells) or cell types that form a sub-lineage (e.g. GABA cells).
scvelo.datasets.forebrain

scvelo.datasets.forebrain()
Developing human forebrain.
From La Manno et al. (2018).
Forebrain tissue of a human week 10 embryo, focusing on glutamatergic neuronal lineage, obtained from elective routine abortions (10 weeks post-conception).

Returns Returns adata object

scvelo.datasets.dentategyrus_lamanno

cvelo.datasets.dentategyrus_lamanno()
Dentate Gyrus neurogenesis.
From La Manno et al. (2018).
The experiment from the developing mouse hippocampus comprises two time points (P0 and P5) and reveals the complex manifold with multiple branching lineages towards astrocytes, oligodendrocyte precursors (OPCs), granule neurons and pyramidal neurons.
Returns Returns *adata* object

**scvelo.datasets.gastrulation**

```python
scvelo.datasets.gastrulation()
```

Mouse gastrulation.

Data from Pijuan-Sala et al. (2019).

Gastrulation represents a key developmental event during which embryonic pluripotent cells diversify into lineage-specific precursors that will generate the adult organism.

This data contains the erythrocyte lineage from Pijuan-Sala et al. (2019). The experiment reveals the molecular map of mouse gastrulation and early organogenesis. It comprises transcriptional profiles of 116,312 single cells from mouse embryos collected at nine sequential time points ranging from 6.5 to 8.5 days post-fertilization. It served to explore the complex events involved in the convergence of visceral and primitive streak-derived endoderm.
Returns

Returns *adata* object

**scvelo.datasets.gastrulation_e75**

`scvelo.datasets.gastrulation_e75()`  
Mouse gastrulation subset to E7.5.

Data from Pijuan-Sala et al. (2019).

Gastrulation represents a key developmental event during which embryonic pluripotent cells diversify into lineage-specific precursors that will generate the adult organism.
**Returns**

Returns `adata` object

---

**scvelo.datasets.gastrulation_erythroid**

**scvelo.datasets.gastrulation_erythroid()**

Mouse gastrulation subset to erythroid lineage.

Data from Pijuan-Sala et al. (2019).

Gastrulation represents a key developmental event during which embryonic pluripotent cells diversify into lineage-specific precursors that will generate the adult organism.
Returns

Returns *adata* object

```python
scvelo.datasets.bonemarrow()
```

*adata* object

**scvelo.datasets.bonemarrow**

**scvelo.datasets.bonemarrow()**

Human bone marrow.

Data from Setty et al. (2019).

The bone marrow is the primary site of new blood cell production or haematopoiesis. It is composed of hematopoietic cells, marrow adipose tissue, and supportive stromal cells.

This dataset served to detect important landmarks of hematopoietic differentiation, to identify key transcription factors that drive lineage fate choice and to closely track when cells lose plasticity.
Returns

Returns `adata` object

**scvelo.datasets.pbm68k**

`scvelo.datasets.pbm68k()`  
Peripheral blood mononuclear cells.  

Data from Zheng et al. (2017).  

This experiment contains 68k peripheral blood mononuclear cells (PBMC) measured using 10X.  

PBMCs are a diverse mixture of highly specialized immune cells. They originate from hematopoietic stem cells (HSCs) that reside in the bone marrow and give rise to all blood cells of the immune system (hematopoiesis). HSCs give rise to myeloid (monocytes, macrophages, granulocytes, megakaryocytes, dendritic cells, erythrocytes) and lymphoid (T cells, B cells, NK cells) lineages.
Returns

Returns `adata` object

**scvelo.datasets.simulation**

This function simulates mRNA splicing kinetics. Simulated mRNA metabolism with transcription, splicing and degradation. The parameters for each reaction are randomly sampled from a log-normal distribution and time events follow the Poisson law. The total time spent in a transcriptional state is varied between two and ten hours.
Returns

Returns *adata* object

### 4.3.6 Utils

Get data by key

```python
get_df(data[, keys, layer, index, columns, ...])
```

Get dataframe for a specified adata key.

**scvelo.get_df**

*scvelo.get_df (data, keys=None, layer=None, index=None, columns=None, sort_values=None, dropna='all', precision=None)*

Get dataframe for a specified adata key.

Return values for specified key (in obs, var, obsm, varm, obsp, varp, uns, or layers) as a dataframe.

**Parameters**

- **data** : AnnData  AnnData object or a numpy array to get values from.
- **keys** : str,List[str],None  Keys from .var_names, .obs_names, .var, .obs, .obsm, .varm, .obsp, .varp, .uns, or .layers.
- **layer** : str,None  Layer of *adata* to use as expression values.
- **index** : List[-T],None  List to set as index.
- **columns** : List[-T],None  List to set as columns names.
sort_values: bool, None  Wether to sort values by first column (sort_values=True) or a specified column.

dropna: _Generalias[all, any]  Drop columns/rows that contain NaNs in all (‘all’) or in any entry (‘any’).

precision: int, None  Set precision for pandas dataframe.

Return type DataFrame

Returns pd.DataFrame – A dataframe.

Get gene info

`utils.gene_info(name[, fields])` Retrieve gene information from biothings client.

scvelo.utils.gene_info

scvelo.utils.gene_info(name, fields='name, symbol, refseq, generif, ensembl')  Retrieve gene information from biothings client.

Data preparation

`utils.cleanup(data[, clean, keep, copy])` Delete not needed attributes.

`utils.clean_obs_names(data[, base, ...])` Clean up the obs_names.

`utils.merge(adata, ldata[, copy])` Merge two annotated data matrices.

`utils.show_proportions(adata[, layers, use_raw])` Proportions of abundances of modalities in layers.

scvelo.utils.cleanup

scvelo.utils.cleanup(data, clean='layers', keep=none, copy=False)  Delete not needed attributes.

Parameters

- **data**: AnnData  Annotated data matrix.

- **clean**: _Generalias[layers, obs, var, uns], List[_Generalias[layers, obs, var, uns]]  Which attributes to consider for freeing memory.

- **keep**: str, List[str], None  Which attributes to keep.

- **copy**: bool  Return a copy instead of writing to adata.

Return type AnnData, None

Returns Optional[AnnData] – Returns or updates adata with selection of attributes kept.

scvelo.utils.clean_obs_names

scvelo.utils.clean_obs_names(data, base=['AGTCBDHKMNRSVWY'], ID_length=12, copy=False)  Clean up the obs_names.

For example an obs_name ‘sample1_AGTCdate’ is changed to ‘AGTC’ of the sample ‘sample1_date’. The sample name is then saved in obs[‘sample_batch’]. The genetic codes are identified according to according to https://www.neb.com/tools-and-resources/usage-guidelines/the-genetic-code.
Parameters

- **data**: `AnnData` Annotated data matrix.
- **base**: `str` Genetic code letters to be identified.
- **ID_length**: `int` Length of the Genetic Codes in the samples.
- **copy**: `bool` Return a copy instead of writing to `adata`.

Return type: `AnnData, None`

Returns

`Optional[AnnData]` – Returns or updates `adata` with the attributes `obs_names: list` updated names of the observations

- **sample_batch**: `obs` names of the identified sample batches

### scvelo.utils.merge

**scvelo.utils.merge** *(adata, ldata, copy=True)*

Merge two annotated data matrices.

Parameters

- **adata**: `AnnData` Annotated data matrix (reference data set).
- **ldata**: `AnnData` Annotated data matrix (to be merged into `adata`).
- **copy**: `bool` Boolean flag to manipulate original `AnnData` or a copy of it.

Return type: `AnnData, None`

Returns

`Optional[anndata.AnnData]` – Returns a `AnnData` object

### scvelo.utils.show_proportions

**scvelo.utils.show_proportions** *(adata, layers=None, use_raw=True)*

Proportions of abundances of modalities in layers.

The proportions are printed.

Parameters

- **adata**: `AnnData` Annotated data matrix.
- **layers**: `str, None` Layers to consider.
- **use_raw**: `bool` Use initial sizes, i.e., raw data, to determine proportions.

Return type: `None`

Returns: `None`

### Getters

- **utils.get_moments** *(adata[, layer, ...])*
  Computes moments for a specified layer.
- **utils.get_transition_matrix** *(adata[, vkey, ...])*
  Computes cell-to-cell transition probabilities
- **utils.get_cell_transitions** *(adata[, ...])*
  Simulate cell transitions

Continued on next page
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```
utils.get_extrapolated_state(adata, vkey, ...)
```

### scvelo.utils.get_moments

`scvelo.utils.get_moments(adata, layer=None, second_order=None, centered=True, mode='connectivities')`

Computes moments for a specified layer.

First and second order moments. If centered, that corresponds to means and variances across nearest neighbors.

**Parameters**

- **adata**: `AnnData` Annotated data matrix.
- **layer**: `str` (default: `None`) Key of layer with abundances to consider for moment computation.
- **second_order**: `bool` (default: `None`) Whether to compute second order moments from abundances.
- **centered**: `bool` (default: `True`) Whether to compute centered (=variance) or uncentered second order moments.
- **mode**: ‘`connectivities’` or ‘`distances’` (default: ‘`connectivities’`) Distance metric to use for moment computation.

**Returns** `Mx` (first or second order moments)

### scvelo.utils.get_transition_matrix

`scvelo.utils.get_transition_matrix(adata, vkey='velocity', basis=None, backward=False, self_transitions=True, scale=10, perc=None, threshold=None, use_negative_cosines=False, weight_diffusion=0, scale_diffusion=1, weight_indirect_neighbors=None, n_neighbors=None, vgraph=None, basis_constraint=None)`

Computes cell-to-cell transition probabilities

\[
\tilde{\pi}_{ij} = \frac{1}{z_i} \exp(\pi_{ij}/\sigma),
\]

from the velocity graph \(\pi_{ij}\), with row-normalization \(z_i\) and kernel width \(\sigma\) (scale parameter \(\lambda = \sigma^{-1}\)).

Alternatively, use `cellrank.tl.transition_matrix()` to account for uncertainty in the velocity estimates.

**Parameters**

- **adata**: `AnnData` Annotated data matrix.
- **vkey**: `str` (default: ‘velocity’) Name of velocity estimates to be used.
- **basis**: `str` or `None` (default: `None`) Restrict transition to embedding if specified
- **backward**: `bool` (default: `False`) Whether to use the transition matrix to push forward (`False`) or to pull backward (`True`)
- **self_transitions**: `bool` (default: `True`) Allow transitions from one node to itself.
scale: float (default: 10) Scale parameter of gaussian kernel.

perc: float between 0 and 100 or None (default: None) Determines threshold of transitions to include.

use_negative_cosines: bool (default: False) If True, negatively similar transitions are taken into account.

weight_diffusion: float (default: 0) Relative weight to be given to diffusion kernel (Brownian motion)

scale_diffusion: float (default: 1) Scale of diffusion kernel.

weight_indirect_neighbors: float between 0 and 1 or None (default: None) Weight to be assigned to indirect neighbors (i.e. neighbors of higher degrees).

n_neighbors: int (default: None) Number of nearest neighbors to consider around each cell.

vgraph: csr matrix or None (default: None) Velocity graph representation to use instead of adata.uns['vkey_graph'].

Returns Returns sparse matrix with transition probabilities.

scvelo.utils.get_cell_transitions

scvelo.utils.get_cell_transitions(adata, starting_cell=0, basis=None, n_steps=100, n_neighbors=30, backward=False, random_state=None, **kwargs)

Simulate cell transitions

Parameters

adata: AnnData Annotated data matrix.

starting_cell: int (default: 0) Index (int) or name (‘obs_names) of starting cell.

n_steps: int (default: 100) Number of transitions/steps to be simulated.

backward: bool (default: False) Whether to use the transition matrix to push forward (False) or to pull backward (True)

random_state: int or None (default: None) Set to int for reproducibility, otherwise None for a random seed.

**kwargs To be passed to tl.transition_matrix.

Returns

• Returns embedding coordinates (if basis is specified),
• otherwise return indices of simulated cell transitions.

scvelo.utils.get_extrapolated_state

scvelo.utils.get_extrapolated_state(adata, vkey='velocity', dt=1, use_raw=None, dropna=True)

Get extrapolated cell state.

Converters
utils.convert_to_ensembl \( ([\text{gene\_names}]) \)  Retrieve ensembl IDs from a list of gene names.

utils.convert_to_gene_names \( ([\text{ensembl\_names}]) \)  Retrieve gene names from ensembl IDs.

scvelo.utils.convert_to_ensembl

scvelo.utils.convert_to_ensembl \( (\text{gene\_names}=\text{None}) \)
   Retrieve ensembl IDs from a list of gene names.

scvelo.utils.convert_to_gene_names

scvelo.utils.convert_to_gene_names \( (\text{ensembl\_names}=\text{None}) \)
   Retrieve gene names from ensembl IDs.

Least squares and correlation

utils.leastsq \( (x, y[, \text{fit\_offset}, \text{perc}, . . .]) \)  Solves least squares \( X\cdot b=Y \) for \( b \).

utils.vcorrcoef \( (X, y[, \text{mode}, \text{axis}]) \)  Pearsons/Spearman's correlation coefficients.

utils.test_bimodality \( (x[, \text{bins}, \text{kde}, \text{plot}]) \)  Test for bimodal distribution.

scvelo.utils.leastsq

scvelo.utils.leastsq \( (x, y[, \text{fit\_offset}]=\text{False}, \text{perc}=\text{None}, \text{constraint\_positive\_offset}]=\text{True}) \)
   Solves least squares \( X\cdot b=Y \) for \( b \).

scvelo.utils.vcorrcoef

scvelo.utils.vcorrcoef \( (X, y[, \text{mode}=\text{pearsons'}, \text{axis}]=-1) \)
   Pearsons/Spearman's correlation coefficients.
   Use Pearsons / Spearman's to test for linear / monotonic relationship.

   Parameters
   
   \( X : \text{np\_ndarray} \)  Data vector or matrix
   
   \( y : \text{np\_ndarray} \)  Data vector or matrix
   
   \text{mode} : ‘pearsons’ or ‘spearmans’ (default: ‘pearsons’)  Which correlation metric to use.

scvelo.utils.test_bimodality

scvelo.utils.test_bimodality \( (x, \text{bins}=30, \text{kde}=\text{True}, \text{plot}=\text{False}) \)
   Test for bimodal distribution.

4.3.7 Settings

set_figure_params \( ([\text{style}, \text{dpi}, \text{dpi\_save}, . . .]) \)  Set resolution/size, styling and format of figures.
scvelo.set_figure_params

scvelo.set_figure_params(style='scvelo', dpi=100, dpi_save=150, frameon=None, vector_friendly=True, transparent=True, fontsize=12, figsize=None, color_map=None, facecolor=None, format='pdf', ipython_format='png2x')

Set resolution/size, styling and format of figures.

Parameters

style : str (default: None)  Init default values for matplotlib.rcParams suited for scvelo or scanpy. Use None for the default matplotlib values.

dpi : int (default: None)  Resolution of rendered figures - affects the size of figures in notebooks.

dpi_save : int (default: None)  Resolution of saved figures. This should typically be higher to achieve publication quality.

frameon : bool (default: None)  Add frames and axes labels to scatter plots.

vector_friendly : bool (default: True)  Plot scatter plots using png backend even when exporting as pdf or svg.

transparent : bool (default: True)  Save figures with transparent background. Sets rcParams['savefig.transparent'].

fontsize : int (default: 14)  Set the fontsize for several rcParams entries.

figsize : [float, float] (default: None)  Width and height for default figure size.

color_map : str (default: None)  Convenience method for setting the default color map.

facecolor : str (default: None)  Sets backgrounds rcParams['figure.facecolor'] and rcParams['axes.facecolor'] to facecolor.

format : {'png', 'pdf', 'svg', etc.} (default: 'pdf')  This sets the default format for saving figures: file_format_figs.

ipython_format : list of str (default: 'png2x')  Only concerns the notebook/IPython environment; see IPython.core.display.set_matplotlib_formats for more details.

4.4 Release Notes

4.4.1 Version 0.2.4 Aug 26, 2021

Perspectives:

• Landing page and two notebooks accompanying the perspectives manuscript at MSB.

• New datasets: Gastrulation, bone marrow, and PBMCs.

New capabilities:

• Added vignettes accompanying the NBT manuscript.

• Kinetic simulations with time-dependent rates.

• New arguments for tl.velocity_embedding_stream (PR 492).

• Introduced automated code formatting flake8 and isort (PR 360, PR 374).

• tl.velocity_graph parallelized (PR 392).
• `legend_align_text` parameter in `pl.scatter` for smart placing of labels without overlapping.
• Save option for `pl.proportions`.

Bugfixes:
• Pinned `sphinx<4.0` and `nbsphinx<0.8.7`.
• Fix IPython import at CLI.

4.4.2 Version 0.2.3 Feb 13, 2021

• `tl.recover_dynamics`: Multicore implementation thanks to M Klein, Y Schaelte, P Weiler
• CI now runs on GitHub Actions

New utility functions:
• `utils.gene_info`: Retrieve gene information from biothings client.
• `utils.convert_to_ensembl` and `utils.convert_to_gene_names`: Converting ensembl IDs into gene names and vice versa.

4.4.3 Version 0.2.2 July 22, 2020

• `tl.paga`: PAGA graph with velocity-directed edges.
• Black code style

4.4.4 Version 0.2.1 May 28, 2020

Bugfixes:
• Correct identification of root cells in `tl.latent_time` thanks to M Lange
• Correct usage of latent_time prior in `tl.paga` thanks to G Lubatti

4.4.5 Version 0.2.0 May 12, 2020

New vignettes:
• RNA velocity basics
• Dynamical Modeling
• Differential Kinetics

Tools:
• `tl.differential_kinetic_test`: introduced a statistical test to detect different kinetic regimes.
• `tl.rank_dynamical_genes`: introduced a gene ranking by cluster-wise likelihoods.
• `tl.paga`: introduced directed PAGA graph

Plotting:
• `pl.scatter` enhancements: linear and polynomial fits, gradient coloring
• `pl.proportions`: Pie and bar chart of spliced/unspliced proportions.
• *GridSpec*: multiplot environment.

### 4.4.6 Version 0.1.20 Sep 5, 2019

**Tools:**

- *tl.recover_dynamics*: introduced a dynamical model inferring the full splicing kinetics, thereby identifying all kinetic rates of transcription, splicing and degradation.
- *tl.recover_latent_time*: infers a shared latent time across all genes based on the learned splicing dynamics.

**Plotting:**

- *pl.scatter* enhancements: multiplots, rugplot, linear and polynomial fits, density plots, etc.
- *pl.heatmap*: heatmap / clustermap of genes along time coordinate sorted by expression along dynamics.

**Preprocessing:**

- New attributes in pp.filter_genes: *min_shared_counts* and *min_shared_genes*.
- Added fast neighbor search method: Hierarchical Navigable Small World graphs (HNSW)

### 4.4.7 Version 0.1.14 Dec 7, 2018

**Plotting:**

- New attributes *arrow_length* and *arrow_size* for flexible adjustment of embedded velocities.
- *pl.velocity_graph*: Scatter plot of embedding with cell-to-cell transition connectivities.
- *pl.velocity_embedding_stream*: Streamplot visualization of velocities.
- Improve visualization of embedded single cell velocities (autosize, colors etc.)

**Tools:**

- *tl.cell_fate*: compute cell-specific terminal state likelihood
- New attribute *approx=True* in *tl.velocity_graph* to enable approximate graph computation by performing cosine correlations on PCA space.

**Preprocessing:**

- Automatically detect whether data is already preprocessed.

### 4.4.8 Version 0.1.11 Oct 27, 2018

**Plotting:**

- *settings.set_figure_params()*: adjust matplotlib defaults for beautified plots
- improved default point and arrow sizes; improved quiver autoscale
- enable direct plotting of

**Tools:**

- *tl.velocity_confidence*: Added two confidence measures ‘velocity_confidence’ and ‘velocity_confidence_transition’.
- *tl.rank_velocity_genes*: Added functionality to rank genes for velocity characterizing groups using a t-test.
• New attribute `perc` in `tl.velocity` enables extreme quantile fit, e.g. set `perc=95`.
• New attribute `groups` in `tl.velocity` enables velocity estimation only on a subset of the data.
• Improved `tl.transition_matrix` by incorporating self-loops via `self_transitions=True` and state changes that have negative correlation with velocity (opposite direction) via `use_negative_cosines=True`.

Utils:
• `utils.merge` to merge to AnnData objects such as already existing AnnData and newly generated Loom File.

4.4.9 Version 0.1.8 Sep 12, 2018

Plotting:
• support saving plots as pdf, png etc.
• support multiple colors and layers
• quiver autoscaling for velocity plots
• attributes added: figsize and dpi

Preprocessing:
• `filter_and_normalize()` instead of `recipe_velocity()`
• normalization of layers is done automatically when computing moments

Tools:
• `terminal_states`: computes root and end points via eigenvalue decomposition thanks to M Lange

4.4.10 Version 0.1.5 Sep 4, 2018

• Support writing loom files
• Support both dense and sparse layers
• Plotting bugfixes
• Added `pp.recipe_velocity()`

4.4.11 Version 0.1.2 Aug 21, 2018

First alpha release of scvelo.

4.5 References

4.6 Getting Started

Here, you will be briefly guided through the basics of how to use scVelo. Once you are set, the following tutorials go straight into analysis of RNA velocity, latent time, driver identification and many more.

First of all, the input data for scVelo are two count matrices of pre-mature (unspliced) and mature (spliced) abundances, which can be obtained from standard sequencing protocols, using the `velocyto` or `loompy/kallisto` counting pipeline.
4.6.1 scVelo workflow at a glance

Import scvelo as:

```
import scvelo as scv
```

For beautified visualization you can change the matplotlib settings to our defaults with:

```
scv.set_figure_params()
```

Read your data

Read your data file (loom, h5ad, csv, ... ) using:

```
adata = scv.read(filename, cache=True)
```

which stores the data matrix (adata.X), annotation of cells / observations (adata.obs) and genes / variables (adata.var), unstructured annotation such as graphs (adata.uns) and additional data layers where spliced and unspliced counts are stored (adata.layers).

If you already have an existing preprocessed adata object you can simply merge the spliced/unspliced counts via:

```
ldata = scv.read(filename.loom, cache=True)
adat = scv.utils.merge(adata, ldata)
```

If you do not have a datasets yet, you can still play around using one of the in-built datasets, e.g.:

```
adat = scv.datasets.pancreas()
```

The typical workflow consists of subsequent calls of preprocessing (scv.pp.*), analysis tools (scv.tl.*) and plotting (scv.pl.*).

Basic preprocessing

After basic preprocessing (gene selection and normalization), we compute the first- and second-order moments (means and uncentered variances) for velocity estimation:

```
scv.pp.filter_and_normalize(adata, **params)
scv.pp.moments(adata, **params)
```

Velocity Tools

The core of the software is the efficient and robust estimation of velocities, obtained with:

```
scv.tl.velocity(adata, mode='stochastic', **params)
```

The velocities are vectors in gene expression space obtained by solving a stochastic model of transcriptional dynamics. The solution to the deterministic model is obtained by setting mode='deterministic'.

The solution to the dynamical model is obtained by setting mode='dynamical', which requires to run scv.tl.recover_dynamics(adata, **params) beforehand.

The velocities are stored in adata.layers just like the count matrices.
The velocities are projected into a lower-dimensional embedding by translating them into likely cell transitions. That is, for each velocity vector we find the likely cell transitions that are in accordance with that direction. The probabilities of one cell transitioning into another cell are computed using cosine correlation (between the potential cell transition and the velocity vector) and are stored in a matrix denoted as velocity graph:

```python
scv.tl.velocity_graph(adata, **params)
```

**Visualization**

Finally, the velocities can be projected and visualized in any embedding (e.g. UMAP) on single cell level, as gridlines, or as streamlines:

```python
scv.pl.velocity_embedding(adata, basis='umap', **params)
scv.pl.velocity_embedding_grid(adata, basis='umap', **params)
scv.pl.velocity_embedding_stream(adata, basis='umap', **params)
```

For every tool module there is a plotting counterpart, which allows you to examine your results in detail, e.g.:

```python
scv.pl.velocity(adata, var_names=['gene_A', 'gene_B'], **params)
scv.pl.velocity_graph(adata, **params)
```

### 4.7 RNA Velocity Basics

Here you will learn the basics of RNA velocity analysis.

For illustration, it is applied to endocrine development in the pancreas, with lineage commitment to four major fates: α, β, δ and ε-cells. See [here](#) for more details. It can be applied to your own data along the same lines.

The notebook is also available at [Google Colab](#) and [nbviewer](#).

```python
[ ]: # update to the latest version, if not done yet.
    !pip install scvelo --upgrade --quiet

[1]: import scvelo as scv
    scv.logging.print_version()
    Running scvelo 0.2.0 (python 3.8.2) on 2020-05-16 12:55.

[2]: scv.settings.verbosity = 3  # show errors(0), warnings(1), info(2), hints(3)
    scv.settings.presenter_view = True  # set max width size for presenter view
    scv.set_figure_params('scvelo')  # for beautified visualization

### 4.7.1 Load the Data

The analysis is based on the in-built pancreas data. To run velocity analysis on your own data, read your file (loom, h5ad, csv ...) to an AnnData object with:

```python
adata = scv.read('path/file.loom', cache=True)
```

If you want to merge your loom file into an already existing AnnData object, use:

```python
scv.utils.merge(adata, adata_loom)
```

```python
[3]: adata = scv.datasets.pancreas()
    adata
```
scVelo documentation, Release 0.2.5.dev6+g1805ab4.d20210829

scVelo is based on adata, an object that stores a data matrix adata.X, annotation of observations adata.obs, variables adata.var, and unstructured annotations adata.uns. Names of observations and variables can be accessed via adata.obs_names and adata.var_names, respectively. AnnData objects can be sliced like dataframes, for example, adata_subset = adata[:, list_of_gene_names]. For more details, see the anndata docs.

Here, the proportions of spliced/unspliced counts are displayed. Depending on the protocol used (Drop-Seq, Smart-Seq), we typically have between 10%-25% of unspliced molecules containing intronic sequences. We also advice you to examine the variations on cluster level to verify consistency in splicing efficiency. Here, we find variations as expected, with slightly lower unspliced proportions at cycling ductal cells, then higher proportion at cell fate commitment in Ngn3-high and Pre-endocrine cells where many genes start to be transcribed.

4.7.2 Preprocess the Data

Preprocessing requisites consist of gene selection by detection (with a minimum number of counts) and high variability (dispersion), normalizing every cell by its total size and logarithmizing X. Filtering and normalization is applied in the same vein to spliced/unspliced counts and X. Logarithmizing is only applied to X. If X is already preprocessed from former analysis, it will not be touched.

All of this is summarized in a single function scv.pp.filter_and_normalize, which essentially runs the following:

```python
scv.pp.filter_genes(adata, min_shared_counts=20)
scv.pp.normalize_per_cell(adata)
scv.pp.filter_genes_dispersion(adata, n_top_genes=2000)
scv.pp.log1p(adata)
```

Further, we need the first and second order moments (means and uncentered variances) computed among nearest neighbors in PCA space, summarized in scv.pp.moments, which internally computes scv.pp.pca and scv.pp.neighbors. First order is needed for deterministic velocity estimation, while stochastic estimation also requires second order moments.
[5]:
scv.pp.filter_and_normalize(adata, min_shared_counts=20, n_top_genes=2000)
scv.pp.moments(adata, n_pcs=30, n_neighbors=30)

Filtered out 20801 genes that are detected in less than 20 counts (shared).
Normalized count data: X, spliced, unspliced.
Logarithmized X.

computing neighbors
  finished (0:00:03) --> added
  'distances' and 'connectivities', weighted adjacency matrices (adata.obsp)

computing moments based on connectivities
  finished (0:00:00) --> added
  'Ms' and 'Mu', moments of spliced/unspliced abundances (adata.layers)

Further preprocessing (such as batch effect correction) may be used to remove unwanted sources of variability. See the best practices for further details. Note, that any additional preprocessing step only affects X and is not applied to spliced/unspliced counts.

### 4.7.3 Estimate RNA velocity

Velocities are vectors in gene expression space and represent the direction and speed of movement of the individual cells. The velocities are obtained by modeling transcriptional dynamics of splicing kinetics, either stochastically (default) or deterministically (by setting mode='deterministic'). For each gene, a steady-state-ratio of premature (unspliced) and mature (spliced) mRNA counts is fitted, which constitutes a constant transcriptional state. Velocities are then obtained as residuals from this ratio. Positive velocity indicates that a gene is up-regulated, which occurs for cells that show higher abundance of unspliced mRNA for that gene than expected in steady state. Conversely, negative velocity indicates that a gene is down-regulated.

The solution to the full dynamical model is obtained by setting mode='dynamical', which requires to run scv.tl.recover_dynamics(adata) beforehand. We will elaborate more on the dynamical model in the next tutorial.

[6]:
scv.tl.velocity(adata)

computing velocities
  finished (0:00:01) --> added
  'velocity', velocity vectors for each individual cell (adata.layers)

The computed velocities are stored in adata.layers just like the count matrices.

The combination of velocities across genes can then be used to estimate the future state of an individual cell. In order to project the velocities into a lower-dimensional embedding, transition probabilities of cell-to-cell transitions are estimated. That is, for each velocity vector we find the likely cell transitions that are in accordance with that direction. The transition probabilities are computed using cosine correlation between the potential cell-to-cell transitions and the velocity vector, and are stored in a matrix denoted as velocity graph. The resulting velocity graph has dimension $n_{obs} \times n_{obs}$ and summarizes the possible cell state changes that are well explained through the velocity vectors (for runtime speedup it can also be computed on reduced PCA space by setting approx=True).

[7]:
scv.tl.velocity_graph(adata)

computing velocity graph
  finished (0:00:10) --> added
  'velocity_graph', sparse matrix with cosine correlations (adata.uns)

For a variety of applications, the velocity graph can be converted to a transition matrix by applying a Gaussian kernel to transform the cosine correlations into actual transition probabilities. You can access the Markov transition matrix via scv.utils.get_transition_matrix.
As mentioned, it is internally used to project the velocities into a low-dimensional embedding by applying the mean transition with respect to the transition probabilities, obtained with `scv.tl.velocity_embedding`. Further, we can trace cells along the Markov chain to their origins and potential fates, thereby getting root cells and end points within a trajectory, obtained via `scv.tl-terminal_states`.

### 4.7.4 Project the velocities

Finally, the velocities are projected onto any embedding, specified by `basis`, and visualized in one of these ways: - on cellular level with `scv.pl.velocity_embedding`, - as gridlines with `scv.pl.velocity_embedding_grid`, - or as streamlines with `scv.pl.velocity_embedding_stream`.

Note, that the data has an already pre-computed UMAP embedding, and annotated clusters. When applying to your own data, these can be obtained with `scv.tl.umap` and `scv.tl.louvain`. For more details, see the scanpy tutorial. Further, all plotting functions are defaulted to using `basis='umap'` and `color='clusters'`, which you can set accordingly.

```
[8]: scv.pl.velocity_embedding_stream(adata, basis='umap')
```

![velocity_embedding_stream](image)

The velocity vector field displayed as streamlines yields fine-grained insights into the developmental processes. It accurately delineates the cycling population of ductal cells and endocrine progenitors. Further, it illuminates cell states of lineage commitment, cell-cycle exit, and endocrine cell differentiation.

The most fine-grained resolution of the velocity vector field we get at single-cell level, with each arrow showing the direction and speed of movement of an individual cell. That reveals, e.g., the early endocrine commitment of Ngn3-cells (yellow) and a clear-cut difference between near-terminal α-cells (blue) and transient β-cells (green).

```
[9]: scv.pl.velocity_embedding(adata, arrow_length=3, arrow_size=2, dpi=120)
```

![velocity_embedding](image)
4.7.5 Interpret the velocities

This is perhaps the most important part as we advise the user not to limit biological conclusions to the projected velocities, but to examine individual gene dynamics via phase portraits to understand how inferred directions are supported by particular genes.

See the gif here to get an idea of how to interpret a spliced vs. unspliced phase portrait. Gene activity is orchestrated by transcriptional regulation. Transcriptional induction for a particular gene results in an increase of (newly transcribed) precursor unspliced mRNAs while, conversely, repression or absence of transcription results in a decrease of unspliced mRNAs. Spliced mRNAs is produced from unspliced mRNA and follows the same trend with a time lag. Time is a hidden/latent variable. Thus, the dynamics needs to be inferred from what is actually measured: spliced and unspliced mRNAs as displayed in the phase portrait.

Now, let us examine the phase portraits of some marker genes, visualized with `scv.pl.velocity(adata, gene_names)` or `scv.pl.scatter(adata, gene_names)`.

```
[10]: scv.pl.velocity(adata, ['Cpe', 'Gnao1', 'Ins2', 'Adk'], ncols=2)
```
The black line corresponds to the estimated ‘steady-state’ ratio, i.e. the ratio of unspliced to spliced mRNA abundance which is in a constant transcriptional state. RNA velocity for a particular gene is determined as the residual, i.e. how much an observation deviates from that steady-state line. Positive velocity indicates that a gene is up-regulated, which occurs for cells that show higher abundance of unspliced mRNA for that gene than expected in steady state. Conversely, negative velocity indicates that a gene is down-regulated.

For instance, *Cpe* explains the directionality in the up-regulated Ngn3 (yellow) to Pre-endocrine (orange) to β-cells (green), while *Adk* explains the directionality in the down-regulated Ductal (dark green) to Ngn3 (yellow) to the remaining endocrine cells.

4.7.6 Identify important genes

We need a systematic way to identify genes that may help explain the resulting vector field and inferred lineages. To do so, we can test which genes have cluster-specific differential velocity expression, being significantly higher/lower compared to the remaining population. The module `scv.tl.rank_velocity_genes` runs a differential velocity t-test and outputs a gene ranking for each cluster. Thresholds can be set (e.g. `min_corr`) to restrict the test on a selection of gene candidates.

```
[12]: scv.tl.rank_velocity_genes(adata, groupby='clusters', min_corr=.3)
```

```
df = scv.DataFrame(adata.uns['rank_velocity_genes']['names'])
df.head()
```
The genes *Ptprs*, *Pclo*, *Pam*, *Abcc8*, *Gnas*, for instance, support the directionality from *Ngn3 high EP* (yellow) to *Pre-endocrine* (orange) to *Beta* (green).

### 4.7.7 Velocities in cycling progenitors

The cell cycle detected by RNA velocity, is biologically affirmed by cell cycle scores (standardized scores of mean expression levels of phase marker genes).
For the cycling Ductal cells, we may screen through S and G2M phase markers. The previous module also computed a spearman's correlation score, which we can use to rank/sort the phase marker genes to then display their phase portraits.

```python
s_genes, g2m_genes = scv.utils.get_phase_marker_genes(adata)
s_genes = scv.get_df(adata[:, s_genes], 'spearmans_score', sort_values=True).index
g2m_genes = scv.get_df(adata[:, g2m_genes], 'spearmans_score', sort_values=True).index

kwargs = dict(frameon=False, ylabel='cell cycle genes')
scv.pl.scatter(adata, list(s_genes[:2]) + list(g2m_genes[:3]), **kwargs)
```

Particularly Hells and Top2a are well-suited to explain the vector field in the cycling progenitors. Top2a gets assigned a high velocity shortly before it actually peaks in the G2M phase. There, the negative velocity then perfectly matches the immediately following down-regulation.

```python
scv.pl.velocity(adata, ['Hells', 'Top2a'], ncols=2, addoutline=True)
```

4.7. RNA Velocity Basics
### 4.7.8 Speed and coherence

Two more useful stats: - The speed or rate of differentiation is given by the length of the velocity vector. - The coherence of the vector field (i.e., how a velocity vector correlates with its neighboring velocities) provides a measure of confidence.

```
[17]: scv.tl.velocity_confidence(adata)
    keys = 'velocity_length', 'velocity_confidence'
    scv.pl.scatter(adata, c=keys, cmap='coolwarm', perc=[5, 95])
```

These provide insights where cells differentiate at a slower/faster pace, and where the direction is un-/determined.

On cluster-level, we find that differentiation substantially speeds up after cell cycle exit (Ngn3 low EP), keeping the pace during Beta cell production while slowing down during Alpha cell production.

```
[18]: df = adata.obs.groupby('clusters')[keys].mean().T
    df.style.background_gradient(cmap='coolwarm', axis=1)
```

```
[18]: <pandas.io.formats.style.Styler at 0x1293e3550>
```

### 4.7.9 Velocity graph and pseudotime

We can visualize the velocity graph to portray all velocity-inferred cell-to-cell connections/transitions. It can be confined to high-probability transitions by setting a threshold. The graph, for instance, indicates two phases of Epsilon cell production, coming from early and late Pre-endocrine cells.

```
[19]: scv.pl.velocity_graph(adata, threshold=.1)
```
Further, the graph can be used to draw descendents/ancestors coming from a specified cell. Here, a pre-endocrine cell is traced to its potential fate.

```
x, y = scv.utils.get_cell_transitions(adata, basis='umap', starting_cell=70)
ax = scv.pl.velocity_graph(adata, c='lightgrey', edge_width=.05, show=False)
ax = scv.pl.scatter(adata, x=x, y=y, s=120, c='ascending', cmap='gnuplot', ax=ax)
```

Finally, based on the velocity graph, a *velocity pseudotime* can be computed. After inferring a distribution over root cells from the graph, it measures the average number of steps it takes to reach a cell after walking along the graph.
starting from the root cells.
Contrarily to diffusion pseudotime, it implicitly infers the root cells and is based on the directed velocity graph instead of the similarity-based diffusion kernel.

```
[21]: scv.tl.velocity_pseudotime(adata)
scv.pl.scatter(adata, color='velocity_pseudotime', cmap='gnuplot')
```

computing terminal states
identified 2 regions of root cells and 1 region of end points
finished (0:00:00) --> added
'root_cells', root cells of Markov diffusion process (adata.obs)
'end_points', end points of Markov diffusion process (adata.obs)

4.7.10 PAGA velocity graph

PAGA graph abstraction has benchmarked as top-performing method for trajectory inference. It provides a graph-like map of the data topology with weighted edges corresponding to the connectivity between two clusters. Here, PAGA is extended by velocity-inferred directionality.

```
[ ]: # PAGA requires to install igraph, if not done yet.
!pip install python-igraph --upgrade --quiet

[22]: # this is needed due to a current bug - bugfix is coming soon.
adata.uns['neighbors']['distances'] = adata.obsp['distances']
adata.uns['neighbors']['connectivities'] = adata.obsp['connectivities']

csv.tl.paga(adata, groups='clusters')
df = scv.get_df(adata, 'paga/transitions_confidence', precision=2).T
df.style.background_gradient(cmap='Blues').format('{:2g}')
```
running PAGA
finished (0:00:01) --> added
'paga/transitions_confidence', connectivities adjacency (adata.uns)
'paga/connectivities', connectivities adjacency (adata.uns)
'paga/connectivities_tree', connectivities subtree (adata.uns)

[22]: <pandas.io.formats.style.Styler at 0x12b7abbb0>

This reads from left/row to right/column, thus e.g. assigning a confident transition from Ductal to Ngn3 low EP.
This table can be summarized by a directed graph superimposed onto the UMAP embedding.

[23]: scv.pl.paga(adata, basis='umap', size=50, alpha=.1, min_edge_width=2, node_size_scale=1.5)

4.8 Dynamical Modeling

Here, we use the generalized dynamical model to solve the full transcriptional dynamics.
That yields several additional insights such as latent time and identification of putative driver genes.
As in the previous tutorial, it is illustratively applied to endocrine development in the pancreas.

[ ]: # update to the latest version, if not done yet.
!pip install scvelo --upgrade --quiet

[1]: import scvelo as scv
scv.logging.print_version()

Running scvelo 0.2.0 (python 3.8.2) on 2020-05-15 00:27.
4.8.1 Prepare the Data

Processing consists of gene selection, normalizing by total size, logarithmizing X, and computing moments for velocity estimation. See the previous tutorial for further explanation.

```python
[3]: adata = scv.datasets.pancreas()

[4]: scv.pp.filter_and_normalize(adata, min_shared_counts=20, n_top_genes=2000)
   scv.pp.moments(adata, n_pcs=30, n_neighbors=30)
```

Filtered out 20801 genes that are detected in less than 20 counts (shared).
Normalized count data: X, spliced, unspliced.
Logarithmized X.

```
        computing neighbors
          finished (0:00:03) --> added
            'distances' and 'connectivities', weighted adjacency matrices (adata.obsp)
        computing moments based on connectivities
          finished (0:00:00) --> added
            'Ms' and 'Mu', moments of spliced/unspliced abundances (adata.layers)
```

4.8.2 Dynamical Model

We run the dynamical model to learn the full transcriptional dynamics of splicing kinetics.

It is solved in a likelihood-based expectation-maximization framework, by iteratively estimating the parameters of reaction rates and latent cell-specific variables, i.e. transcriptional state and cell-internal latent time. It thereby aims to learn the unspliced/spliced phase trajectory for each gene.

```python
[5]: scv.tl.recover_dynamics(adata)
```

```
        recovering dynamics
          finished (0:13:31) --> added
            'fit_pars', fitted parameters for splicing dynamics (adata.var)
```

```python
[6]: scv.tl.velocity(adata, mode='dynamical')
   scv.tl.velocity_graph(adata)
```

```
        computing velocities
          finished (0:00:04) --> added
            'velocity', velocity vectors for each individual cell (adata.layers)
        computing velocity graph
          finished (0:00:08) --> added
            'velocity_graph', sparse matrix with cosine correlations (adata.uns)
```

Running the dynamical model can take a while. Hence, you may want to store the results for re-use, with `adata.write('data/pancreas.h5ad', which can later be read with `adata = scv.read('data/pancreas.h5ad').`
4.8.3 Kinetic rate parameters

The rates of RNA transcription, splicing and degradation are estimated without the need of any experimental data. They can be useful to better understand the cell identity and phenotypic heterogeneity.

```python
[9]: df = adata.var
    df = df[(df['fit_likelihood'] > .1) & df['velocity_genes'] == True]

    kwargs = dict(xscale='log', fontsize=16)
    with scv.GridSpec(ncols=3) as pl:
        pl.hist(df['fit_alpha'], xlabel='transcription rate', **kwargs)
        pl.hist(df['fit_beta'] * df['fit_scaling'], xlabel='splicing rate', xticks=[.1, .4, 1], **kwargs)
        pl.hist(df['fit_gamma'], xlabel='degradation rate', xticks=[.1, .4, 1], **kwargs)

    scv.get_df(adata, 'fit*', dropna=True).head()
```

4.8. Dynamical Modeling
The estimated gene-specific parameters comprise rates of transcription (\( \text{fit\_alpha} \)), splicing (\( \text{fit\_beta} \)), degradation (\( \text{fit\_gamma} \)), switching time point (\( \text{fit\_t} \)), a scaling parameter to adjust for under-represented unspliced reads (\( \text{fit\_scaling} \)), standard deviation of unspliced and spliced reads (\( \text{fit\_std\_u}, \text{fit\_std\_s} \)), the gene likelihood (\( \text{fit\_likelihood} \)), inferred steady-state levels (\( \text{fit\_steady\_u}, \text{fit\_steady\_s} \)) with their corresponding p-values (\( \text{fit\_pval\_steady\_u}, \text{fit\_pval\_steady\_s} \)), the overall model variance (\( \text{fit\_variance} \)), and a scaling factor to align the gene-wise latent times to a universal, gene-shared latent time (\( \text{fit\_alignment\_scaling} \)).

4.8.4 Latent time

The dynamical model recovers the latent time of the underlying cellular processes. This latent time represents the cell’s internal clock and approximates the real time experienced by cells as they differentiate, based only on its transcriptional...
dynamics.

[10]: `scv.tl.latent_time(adata)`
    `scv.pl.scatter(adata, color='latent_time', color_map='gnuplot', size=80)`

    computing terminal states
    identified 2 regions of root cells and 1 region of end points
    finished (0:00:00) --> added
    'root_cells', root cells of Markov diffusion process (adata.obs)
    'end_points', end points of Markov diffusion process (adata.obs)

    computing latent time
    finished (0:00:02) --> added
    'latent_time', shared time (adata.obs)

[11]: `top_genes = adata.var['fit_likelihood'].sort_values(ascending=False).index[:300]`
    `scv.pl.heatmap(adata, var_names=top_genes, sortby='latent_time', col_color='clusters', n_convolve=100)`
4.8.5 Top-likelihood genes

Driver genes display pronounced dynamic behavior and are systematically detected via their characterization by high likelihoods in the dynamic model.

[12]: top_genes = adata.var['fit_likelihood'].sort_values(ascending=False).index
cnv.pl.scatter(adata, basis=top_genes[:15], ncols=5, frameon=False)

[13]: var_names = ['Actn4', 'Ppp3ca', 'Cpe', 'Nnat']
cnv.pl.scatter(adata, var_names, frameon=False)
cnv.pl.scatter(adata, x='latent_time', y=var_names, frameon=False)
4.8.6 Cluster-specific top-likelihood genes

Moreover, partial gene likelihoods can be computed for each cluster of cells to enable cluster-specific identification of potential drivers.

```python
[14]: scv.tl.rank_dynamical_genes(adata, groupby='clusters')
df = scv.get_df(adata, 'rank_dynamical_genes/names')
df.head(5)
```

```
ranking genes by cluster-specific likelihoods
finished (0:00:03) --> added
'rank_dynamical_genes', sorted scores by group ids (adata.uns)
```

```python
[15]: for cluster in ['Ductal', 'Ngn3 high EP', 'Pre-endocrine', 'Beta']:
   scv.pl.scatter(adata, df[cluster][:5], ylabel=cluster, frameon=False)
```

4.8. Dynamical Modeling
4.9 Differential Kinetics

One important concern is dealing with systems that represent multiple lineages and processes, where genes are likely to show different kinetic regimes across subpopulations. Distinct cell states and lineages are typically governed by different variations in the gene regulatory networks and may hence exhibit different splicing kinetics. This gives rise to genes that display multiple trajectories in phase space.

To address this, the dynamical model can be used to perform a likelihood-ratio test for differential kinetics. This way, we can detect clusters that display kinetic behavior that cannot be well explained by a single model of the overall dynamics. Clustering cell types into their different kinetic regimes then allows fitting each regime separately.

For illustration, we apply differential kinetic analysis to dentate gyrus neurogenesis, which comprises multiple heterogeneous subpopulations.

```
[ ]: # update to the latest version, if not done yet.
    !pip install scvelo --upgrade --quiet

[1]: import scvelo as scv
    scv.logging.print_version()
    Running scvelo 0.2.0 (python 3.8.2) on 2020-05-15 00:57.

[2]: scv.settings.verbosity = 3  # show errors(0), warnings(1), info(2), hints(3)
    scv.settings.presenter_view = True  # set max width size for presenter view
    scv.settings.set_figure_params('scvelo')  # for beautified visualization
```

4.9.1 Prepare the Data

Processing consists of gene selection, log-normalizing, and computing moments. See the previous tutorials for further explanation.
4.9.2 Basic Velocity Estimation

[5]: scv.tl.velocity(adata)
    scv.tl.velocity_graph(adata)
    computing velocities
    finished (0:00:00) --> added
    'velocity', velocity vectors for each individual cell (adata.layers)
    computing velocity graph
    finished (0:00:05) --> added
    'velocity_graph', sparse matrix with cosine correlations (adata.uns)

[6]: scv.pl.velocity_embedding_stream(adata, basis='umap')
    computing velocity embedding
    finished (0:00:00) --> added
    'velocity_umap', embedded velocity vectors (adata.obsm)
4.9.3 Differential Kinetic Test

Distinct cell types and lineages may exhibit different kinetics regimes as these can be governed by a different network structure. Even if cell types or lineages are related, kinetics can be differential due to alternative splicing, alternative polyadenylation and modulations in degradation.

The dynamical model allows us to address this issue with a likelihood ratio test for differential kinetics to detect clusters/lineages that display kinetic behavior that cannot be sufficiently explained by a single model for the overall dynamics. Each cell type is tested whether an independent fit yields a significantly improved likelihood.

The likelihood ratio, following an asymptotic chi-squared distribution, can be tested for significance. Note that for efficiency reasons, by default an orthogonal regression is used instead of a full phase trajectory to test whether a cluster is well explained by the overall kinetic or exhibits a different kinetic.

```
[7]: var_names = ['Tmsb10', 'Fam155a', 'Hn1', 'Rp16']
scv.tl.differential_kinetic_test(adata, var_names=var_names, groupby='clusters')
```

recovering dynamics
finished (0:00:02) --> added
'fit_pars', fitted parameters for splicing dynamics (adata.var)

outputs model fit of gene: Rp16

testing for differential kinetics
finished (0:00:00) --> added
'fit_diff_kinetics', clusters displaying differential kinetics (adata.var)
'fit_pval_kinetics', p-values of differential kinetics (adata.var)

outputs model fit of gene: Rp16

```
[7]: <scvelo.tools.dynamical_model.DynamicsRecovery at 0x12390f4a8>
```
In Tmsb10, for instance, Endothelial display a kinetic behaviour (outlined, with the black line fitted through), that cannot be well explained by the overall dynamics (purple curve).
### 4.9.4 Testing top-likelihood genes

Screening through the top-likelihood genes, we find some gene-wise dynamics that display multiple kinetic regimes.

```python
[11]: scv.tl.recover_dynamics(adata)
#adata.write('data/pancreas.h5ad', compression='gzip')
#adata = scv.read('data/pancreas.h5ad')
recovering dynamics
   finished (0:06:39) --> added
      'fit_pars', fitted parameters for splicing dynamics (adata.var)

[12]: top_genes = adata.var['fit_likelihood'].sort_values(ascending=False).index[:100]
scv.tl.differential_kinetic_test(adata, var_names=top_genes, groupby='clusters')
testing for differential kinetics
   finished (0:00:21) --> added
      'fit_diff_kinetics', clusters displaying differential kinetics (adata.var)
      'fit_pval_kinetics', p-values of differential kinetics (adata.var)
```

Particularly, cell types that are distinct from the main granule - such as Cck/Tox, GABA, Endothelial, and Microglia - occur frequently.

```python
[13]: scv.pl.scatter(adata, basis=top_genes[:15], ncols=5, add_outline='fit_diff_kinetics', **kwargs)
[14]: scv.pl.scatter(adata, basis=top_genes[15:30], ncols=5, add_outline='fit_diff_kinetics', **kwargs)
```
4.9.5 Recompute velocities

Finally, velocities can be recomputed leveraging the information of multiple competing kinetic regimes.

```
[15]: scv.tl.velocity(adata, diff_kinetics=True)
scv.tl.velocity_graph(adata)
```

- computing velocities
  - finished (0:00:00) --> added
    - 'velocity', velocity vectors for each individual cell (adata.layers)
- computing velocity graph
  - finished (0:00:05) --> added
    - 'velocity_graph', sparse matrix with cosine correlations (adata.uns)

```
[16]: scv.pl.velocity_embedding(adata, dpi=120, arrow_size=2, arrow_length=2)
```

- computing velocity embedding
  - finished (0:00:00) --> added
    - 'velocity_umap', embedded velocity vectors (adata.obsm)
4.10 Other Vignettes

4.10.1 Example Datasets

- Dentate Gyrus
- Pancreas

4.10.2 Nature Biotech Figures

- NBT Cover | cover | notebook
- Fig.1 Concept | figure | notebook
- Fig.2 Dentate Gyrus | figure | notebook
- Fig.3 Pancreas | figure | notebook
- Suppl. Figures | figure | notebook | runtime

All notebooks are deposited at GitHub. Found a bug? Feel free to submit an issue.
4.11 Challenges and Perspectives

This page complements our manuscript Bergen et al. (MSB, 2021) RNA velocity - Current challenges and future perspectives

We provide several examples to discuss potential pitfalls of current RNA velocity modeling approaches, and provide guidance on how the ensuing challenges may be addressed. Our aspiration is to suggest promising future directions and to stimulate a communities effort on further model extensions.

In the following, you find two vignettes with several use cases, as well as an in-depth analysis of time-dependent kinetic rate parameters.

4.11.1 Potential pitfalls

![Image of potential pitfalls](image)

This notebook reproduces Fig. 2 with several use cases, including multiple kinetics in Dentate Gyrus, transcriptional boost in erythroid lineage, and misleading arrow projections in mature PBMCs.

Notebook: Perspectives

4.11.2 Kinetic parameter analysis

![Image of kinetic parameter analysis](image)

This notebook reproduces Fig. 3, where we demonstrate how time-variable kinetic rates shape the curvature patterns of gene activation.

Notebook: Kinetic parameter analysis
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