

# External API

## ⓘ Note

More tools that integrate well with scanpy and anndata can be found on the [ecosystem page](#).

Import Scanpy's wrappers to external tools as:

```
import scanpy.external as sce
```

If you'd like to include a tool here, consider making a pull request ([instructions](#)). If the tool already uses `scanpy` or `anndata`, it may fit better in the [ecosystem page](#).

## Preprocessing: PP

### Data integration

<code>pp.bbknn</code> (adata[, batch_key, use_rep, ...])	Batch balanced kNN <a href="#">[Polanski19]</a> .
<code>pp.harmony_integrate</code> (adata, key[, basis, ...])	Use harmony <a href="#">[Korunsky19]</a> to integrate differer
<code>pp.mnn_correct</code> (*datas[, var_index, ...])	Correct batch effects by matching mutual nearest
<code>pp.scanorama_integrate</code> (adata, key[, basis, ...])	Use Scanorama <a href="#">[Hie19]</a> to integrate different expe

### Sample demultiplexing, Doublet detection

<code>pp.scrublet</code> (adata[, adata_sim, batch_key, ...])	Predict doublets using Scrublet <a href="#">[Wolock19]</a> .
<code>pp.scrublet_simulate_doublets</code> (adata[, ...])	Simulate doublets by adding the counts of random
<code>pl.scrublet_score_distribution</code> (adata[, ...])	Plot histogram of doublet scores for observed tra
<code>pp.hashsolo</code> (adata, cell_hashing_columns[, ...])	Probabilistic demultiplexing of cell hashing data u

## Imputation

Note that the fundamental limitations of imputation are still under [debate](#).

<code>pp.dca</code> (adata[, mode, ae_type, ...])	Deep count autoencoder <a href="#">[Eraslan18]</a> .
<code>pp.magic</code> (adata[, name_list, knn, decay, ...])	Markov Affinity-based Graph Imputation of Cells (MA)

## Tools: TL

### Embeddings

<code>tl.phate</code> (adata[, n_components, k, a, ...])	PHATE <a href="#">[Moon17]</a> .
<code>tl.palantir</code> (adata[, n_components, knn, ...])	Run Diffusion maps using the adaptive anisotropic l
<code>tl.trimap</code> (adata[, n_components, n_inliers, ...])	TriMap: Large-scale Dimensionality Reduction Us
<code>tl.sam</code> (adata[, max_iter, num_norm_avg, k, ...])	Self-Assembling Manifolds single-cell RNA seque

### Clustering and trajectory inference

<code>tl.phenograph</code> (adata[, clustering_algo, k, ...])	PhenoGraph clustering <a href="#">[Levine15]</a> .
<code>tl.harmony_timeseries</code> (adata, tp[, ...])	Harmony time series for data visualization with aug
<code>tl.wishbone</code> (adata, start_cell[, branch, k, ...])	Wishbone identifies bifurcating developmental traje
<code>tl.palantir</code> (adata[, n_components, knn, ...])	Run Diffusion maps using the adaptive anisotropic l
<code>tl.palantir_results</code> (adata, early_cell[, ...])	<b>Running Palantir</b>

### Gene scores, Cell cycle

<code>tl.sandbag</code> (adata[, annotation, fraction, ...])	Calculate marker pairs of genes.
<code>tl.cyclone</code> (adata[, marker_pairs, ...])	Assigns scores and predicted class to observations <a href="#">[S</a>

## Plotting: PL

<code>pl.phate</code> (adata, *[, color, gene_symbols, ...])	Scatter plot in PHATE basis.
<code>pl.trimap</code> (adata, *[, color, gene_symbols, ...])	Scatter plot in TriMap basis.
<code>pl.sam</code> (adata[, projection, c, cmap, ...])	Scatter plot using the SAM projection or another
<code>pl.wishbone_marker_trajectory</code> (adata, markers)	Plot marker trends along trajectory, and return tr

# Exporting

<code>exporting.spring_project</code> (adata, project_dir, ...)	Exports to a SPRING project directory <a href="#">[Weinberg 2016]</a>
<code>exporting.cellbrowser</code> (adata, data_dir, data_name)	Export adata to a UCSC Cell Browser project