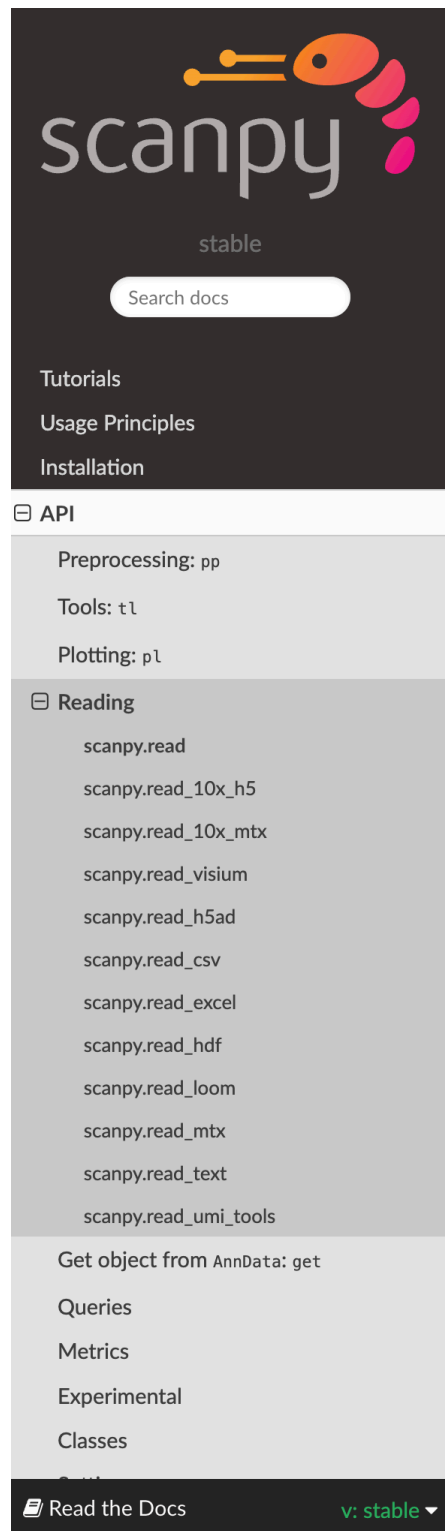


Day 4

Sphinx: Convert your docstring to a documentation website



» API » scanpy.read

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scanpy.read

scanpy.read(filename, backed=None, sheet=None, ext=None, delimiter=None, first_column_names=False, backup_url=None, cache=False, cache_compression=Empty.token, **kwargs)

Read file and return `AnnData` object.

To speed up reading, consider passing `cache=True`, which creates an hdf5 cache file.

Parameters:

filename : Union [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 : Optional [Literal ['r', 'r+']] (default: 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 : Optional [str] (default: None)

Name of sheet/table in hdf5 or Excel file.

ext : Optional [str] (default: None)

Extension that indicates the file type. If `None`, uses extension of filename.

delimiter : Optional [str] (default: 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 (default: False)

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 : Optional [str] (default: None)

Retrieve the file from an URL if not present on disk.

cache : bool (default: False)

If `False`, read from source, if `True`, read from fast 'h5ad' cache.

cache_compression : Union [Literal ['gzip', 'lzf'], None , Empty] (default: <Empty.token: 0>)

Task for Day 4:

- 1. Generate documentation website with Sphinx**
- 2. Write the README page for your repository.**
- 3. Prepare for the demo**
- 4. Optional: add capability of handling batch design following the provided example.**
- 5. Optional: visualize a new single-cell dataset**