scanpy.pp.scale 🔗

`scanpy.pp.scale`*(X, zero_center=True, max_value=None, copy=False, layer=None, obsm=None)*

Scale data to unit variance and zero mean.

> ℹ **Note**
>
> Variables (genes) that do not display any variation (are constant across all observations) are retained and (for zero_center==True) set to 0 during this operation. In the future, they might be set to NaNs.

Parameters:	**X** : `Union` [`AnnData` , `spmatrix` , `ndarray`]
	The (annotated) data matrix of shape `n_obs` × `n_vars` . Rows correspond to cells and columns to genes.
	zero_center : `bool` (default: `True`)
	If `False` , omit zero-centering variables, which allows to handle sparse input efficiently.
	max_value : `Optional` [`float`] (default: `None`)
	Clip (truncate) to this value after scaling. If `None` , do not clip.
	copy : `bool` (default: `False`)
	Whether this function should be performed inplace. If an AnnData object is passed, this also determines if a copy is returned.
	layer : `Optional` [`str`] (default: `None`)
	If provided, which element of layers to scale.
	obsm : `Optional` [`str`] (default: `None`)
	If provided, which element of obsm to scale.
Returns:	: Depending on `copy` returns or updates `adata` with a scaled `adata.X` , annotated with `'mean'` and `'std'` in `adata.var` .