

scanpy.pp.combat

scanpy.pp.combat(*adata*, *key*='batch', *covariates*=None, *inplace*=True)

ComBat function for batch effect correction [Johnson07] [Leek12] [Pedersen12].

Corrects for batch effects by fitting linear models, gains statistical power via an EB framework where information is borrowed across genes. This uses the implementation [combat.py](#) [Pedersen12].

Parameters:

adata : `AnnData`

Annotated data matrix

key : `str` (default: `'batch'`)

Key to a categorical annotation from `obs` that will be used for batch effect removal.

covariates : `Optional[Collection[str]]` (default: `None`)

Additional covariates besides the batch variable such as adjustment variables or biological condition. This parameter refers to the design matrix `X` in Equation 2.1 in [Johnson07] and to the `mod` argument in the original combat function in the sva R package. Note that not including covariates may introduce bias or lead to the removal of biological signal in unbalanced designs.

inplace : `bool` (default: `True`)

Whether to replace `adata.X` or to return the corrected data

Return type:

`Union[AnnData, ndarray, None]`

Returns:

: Depending on the value of `inplace`, either returns the corrected matrix or or modifies `adata.X`.