

## scanpy.pp.log1p

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**scanpy.pp.log1p**(*X*, \*, *base=None*, *copy=False*, *chunked=None*, *chunk\_size=None*, *layer=None*, *obsm=None*)

Logarithmize the data matrix.

Computes  $X = \log(X + 1)$ , where *log* denotes the natural logarithm unless a different base is given.

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**Parameters:**    **X** : Union [ AnnData , ndarray , spmatrix ]

The (annotated) data matrix of shape `n_obs` × `n_vars`. Rows correspond to cells and columns to genes.

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**base** : optional [ Number ] (default: None )

Base of the logarithm. Natural logarithm is used by default.

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**copy** : bool (default: False )

If an `AnnData` is passed, determines whether a copy is returned.

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**chunked** : optional [ bool ] (default: None )

Process the data matrix in chunks, which will save memory. Applies only to `AnnData`.

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**chunk\_size** : optional [ int ] (default: None )

`n_obs` of the chunks to process the data in.

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**layer** : optional [ str ] (default: None )

Entry of layers to tranform.

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**obsm** : optional [ str ] (default: None )

Entry of obsm to transform.

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**Returns:**    : Returns or updates `data`, depending on `copy`.