

# scanpy.tl.score\_genes\_cell\_cycle

**scanpy.tl.score\_genes\_cell\_cycle**(adata, s\_genes, g2m\_genes, copy=False, \*\*kwargs)

Score cell cycle genes [Satija15].

Given two lists of genes associated to S phase and G2M phase, calculates scores and assigns a cell cycle phase (G1, S or G2M). See `score_genes()` for more explanation.

## Parameters:

**adata** : `AnnData`

The annotated data matrix.

**s\_genes** : `Sequence` [ `str` ]

List of genes associated with S phase.

**g2m\_genes** : `Sequence` [ `str` ]

List of genes associated with G2M phase.

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

Copy `adata` or modify it inplace.

**\*\*kwargs**

Are passed to `score_genes()`. `ctrl_size` is not possible, as it's set as `min(len(s_genes), len(g2m_genes))`.

## Return type:

`Optional` [ `AnnData` ]

## Returns:

: Depending on `copy`, returns or updates `adata` with the following fields.

**S\_score** : `adata.obs`, dtype `object`

The score for S phase for each cell.

**G2M\_score** : `adata.obs`, dtype `object`

The score for G2M phase for each cell.

**phase** : `adata.obs`, dtype `object`

The cell cycle phase ( `s`, `G2M` or `G1` ) for each cell.

! See also

score\_genes

## Examples

See this [notebook](#).