

# scanpy.pp.subsample

---

**scanpy.pp.subsample**(*data*, *fraction=None*, *n\_obs=None*, *random\_state=0*, *copy=False*)

Subsample to a fraction of the number of observations.

---

## Parameters:

**data** : Union [ AnnData , ndarray , spmatrix ]

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

---

**fraction** : Optional [ float ] (default: None )

Subsample to this `fraction` of the number of observations.

---

**n\_obs** : Optional [ int ] (default: None )

Subsample to this number of observations.

---

**random\_state** : Union [ None , int , RandomState ] (default: 0 )

Random seed to change subsampling.

---

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

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

---

## Return type:

Optional [ AnnData ]

---

## Returns:

: Returns `X[obs_indices]`, `obs_indices` if data is array-like, otherwise subsamples the passed `AnnData` ( `copy == False` ) or returns a subsampled copy of it ( `copy == True` ).