# scanpy.tl.sim

**scanpy.tl.sim**(*model, params_file=True, tmax=None, branching=None, nrRealizations=None, noiseObs=None, noiseDyn=None, step=None, seed=None, writedir=None*)

Simulate dynamic gene expression data [Wittmann09] [Wolf18].

Sample from a stochastic differential equation model built from literature-curated boolean gene regulatory networks, as suggested by [Wittmann09]. The Scanpy implementation is due to [Wolf18].

| Parameters: | **model** : `Literal` [ `'krumsiek11'` , `'toggleswitch'` ] |
|---|---|
| | Model file in 'sim_models' directory. |
| | **params_file** : `bool` (default: `True` ) |
| | Read default params from file. |
| | **tmax** : `Optional` [ `int` ] (default: `None` ) |
| | Number of time steps per realization of time series. |
| | **branching** : `Optional` [ `bool` ] (default: `None` ) |
| | Only write realizations that contain new branches. |
| | **nrRealizations** : `Optional` [ `int` ] (default: `None` ) |
| | Number of realizations. |
| | **noiseObs** : `Optional` [ `float` ] (default: `None` ) |
| | Observatory/Measurement noise. |
| | **noiseDyn** : `Optional` [ `float` ] (default: `None` ) |
| | Dynamic noise. |
| | **step** : `Optional` [ `int` ] (default: `None` ) |
| | Interval for saving state of system. |
| | **seed** : `Optional` [ `int` ] (default: `None` ) |
| | Seed for generation of random numbers. |

**writedir** : `Union` [ `str` , `Path` , `None` ] (default: `None` )

Path to directory for writing output files.

| Return type: | `AnnData` |
|---|---|
| **Returns:** | : Annotated data matrix. |

**Examples**

See this use case