

**Kinetic model:** Select the kinetic mass-action model from the drop-down menu.

**Input profile:** Choose whether you want to use a temporal input profile (e.g., measured TF-abundance).

**Load input data:** Press button to select and load an input data file.

**Parameter table:** Adjust priors for reaction rates by changing  $a$  and  $b$ . One reaction can be assumed to be depending on extrinsic factors by choosing *Heterogeneous* in the column *Type*.

**Hyperparameters:** Set mean and covariance of the log-normal prior distribution of the extrinsic statistics  $a$  and  $b$ .

**Measurement model:** (a) Specify the species that was measured in the experiment. (b) Select measurement noise density. (c) The measurement noise is estimated from the data. Provide parameters for the inverse-Gamma prior distribution.

**Select cells to consider:** You can specify which cells shall be used for inference. Enter integer-numbers between 1 and the number of cells separated by comma.

**Load measurements:** Press button to select and load the single-cell measurements.

**Algorithm configuration:** Choose number of particles and the fraction of discarded particles at each time-step (*Burn-In*). Check Swap data to HD in order to save intermediate results to hard drive. This will reduce the amount of memory needed during computation.

**Input data plot:** Visualizes the loaded input data. In case no input data is selected, a constant value of 1 will be displayed.

**Measurement plot:** Plots the imported single-cell trajectories.

**Run / Stop DPP:** Starts the inference algorithm with the given configuration. Once running, the algorithm can be stopped by pressing the button again.

**DPP**

**Model Configuration**

Kinetic Model: Simple Expression Model

	Name	Type	a	b
	Transc.	Homogeneous	3	3
	Deg. (mRNA)	Homogeneous	3	600
	Transl.	Heterogeneous	3	300
	Deg. (Protein)	Homogeneous	3	3000

**Hyperparameters**

Position

	a	b
a	1	
b	1000	

Shape

	a	b
a	2	0
b	0	2

**Measurement Model**

Measured Species: Protein

Error Model: Log-Normal

Prior Shape: 2

Prior Scaling: 0.03

**Data Configuration**

**Transcriptional Activation (Input)**

Type: Temporal

Filename: GEVInput\_50nm.mat

Load Data

**Input data plot:** A line plot showing input data over time. The x-axis is 'Time in min' (0 to 250) and the y-axis is 'Input' (0 to 0.2). A green curve starts at 0, peaks at approximately 0.18 at 50 minutes, and then decays towards 0.

**Protein Measurements (Output)**

Filename: YVenus\_50nm.mat

Load Data

Number of Cells: 10

Use cells: 1,2,3,4,5,6,7,8,9,10

**Measurement plot:** A line plot showing multiple single-cell trajectories over time. The x-axis is 'Time in min' (0 to 200) and the y-axis is 'Abundance' (0 to 8000). Multiple blue lines with square markers show individual cell trajectories, all peaking around 100 minutes.

**Algorithm Configuration**

Number of Particles: 10000

Swap data to HD: ☐

Burn-In: 30 %

Run!

Export