

# Package ‘dyngen’

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**Type** Package

**Title** A Multi-Modal Simulator for Spearheading Single-Cell Omics Analyses

**Version** 1.0.3

**Description** A novel, multi-modal simulation engine for studying dynamic cellular processes at single-cell resolution. 'dyngen' is more flexible than current single-cell simulation engines. It allows better method development and benchmarking, thereby stimulating development and testing of novel computational methods. Cannoodt et al. (2021) <[doi:10.1038/s41467-021-24152-2](https://doi.org/10.1038/s41467-021-24152-2)>.

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**URL** <https://dyngen.dynverse.org>, <https://github.com/dynverse/dyngen>

**BugReports** <https://github.com/dynverse/dyngen/issues>

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## R topics documented:

as_dyno . . . . .	3
backbone . . . . .	4
bblego . . . . .	6
combine_models . . . . .	8
dyngen . . . . .	9
example_model . . . . .	12
generate_cells . . . . .	12
generate_dataset . . . . .	14
generate_experiment . . . . .	15
generate_feature_network . . . . .	17
generate_gold_standard . . . . .	18
generate_kinetics . . . . .	19
generate_tf_network . . . . .	21
get_timings . . . . .	22
initialise_model . . . . .	23
kinetics_noise_none . . . . .	24
list_backbones . . . . .	25
plot_backbone_modulenet . . . . .	27
plot_backbone_statenet . . . . .	28
plot_experiment_dimred . . . . .	28
plot_feature_network . . . . .	29
plot_gold_expression . . . . .	30
plot_gold_mappings . . . . .	30
plot_gold_simulations . . . . .	31
plot_simulations . . . . .	32
plot_simulation_expression . . . . .	33
plot_summary . . . . .	34
realcounts . . . . .	34
realnets . . . . .	35
rnorm_bounded . . . . .	35
runif_subrange . . . . .	36
simtime_from_backbone . . . . .	36

**Index**

**38**

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`as_dyno`*Convert simulation output to different formats.*

---

**Description**

For use with other packages compatible with `dyno`, `anndata`, `SingleCellExperiment`, or `Seurat`.

**Usage**

```
as_dyno(  
  model,  
  store_dimred = !is.null(model$simulations$dimred),  
  store_cellwise_grn = !is.null(model$experiment$cellwise_grn),  
  store_rna_velocity = !is.null(model$experiment$rna_velocity)  
)  
  
as_anndata(  
  model,  
  store_dimred = !is.null(model$simulations$dimred),  
  store_cellwise_grn = !is.null(model$experiment$cellwise_grn),  
  store_rna_velocity = !is.null(model$experiment$rna_velocity)  
)  
  
as_sce(  
  model,  
  store_dimred = !is.null(model$simulations$dimred),  
  store_cellwise_grn = !is.null(model$experiment$cellwise_grn),  
  store_rna_velocity = !is.null(model$experiment$rna_velocity)  
)  
  
as_seurat(  
  model,  
  store_dimred = !is.null(model$simulations$dimred),  
  store_cellwise_grn = !is.null(model$experiment$cellwise_grn),  
  store_rna_velocity = !is.null(model$experiment$rna_velocity)  
)  
  
as_list(  
  model,  
  store_dimred = !is.null(model$simulations$dimred),  
  store_cellwise_grn = !is.null(model$experiment$cellwise_grn),  
  store_rna_velocity = !is.null(model$experiment$rna_velocity)  
)  
  
wrap_dataset(  
  model,  
  format = c("list", "dyno", "sce", "seurat", "anndata", "none"),
```

```

store_dimred = !is.null(model$simulations$dimred),
store_cellwise_grn = !is.null(model$experiment$cellwise_grn),
store_rna_velocity = !is.null(model$experiment$rna_velocity)
)

```

### Arguments

<code>model</code>	A dyngen output model for which the experiment has been emulated with <code>generate_experiment()</code> .
<code>store_dimred</code>	Whether or not to store the dimensionality reduction constructed on the true counts.
<code>store_cellwise_grn</code>	Whether or not to also store cellwise GRN information.
<code>store_rna_velocity</code>	Whether or not to store the log propensity ratios.
<code>format</code>	Which output format to use, must be one of 'dyno' (requires dynwrap), 'sce' (requires SingleCellExperiment), 'seurat' (requires Seurat), 'anndata' (requires anndata), 'list' or 'none'.

### Value

A dataset object.

### Examples

```

data("example_model")
dataset <- wrap_dataset(example_model)

```

---

backbone

*Backbone of the simulation model*

---

### Description

A module is a group of genes which, to some extent, shows the same expression behaviour. Several modules are connected together such that one or more genes from one module will regulate the expression of another module. By creating chains of modules, a dynamic behaviour in gene regulation can be created.

### Usage

```
backbone(module_info, module_network, expression_patterns)
```

**Arguments**

- `module_info` A tibble containing meta information on the modules themselves.
- `module_id` (character): the name of the module
  - `basal` (numeric): basal expression level of genes in this module, must be between [0, 1]
  - `burn` (logical): whether or not outgoing edges of this module will be active during the burn in phase
  - `independence` (numeric): the independence factor between regulators of this module, must be between [0, 1]
- `module_network` A tibble describing which modules regulate which other modules.
- `from` (character): the regulating module
  - `to` (character): the target module
  - `effect` (integer): 1L if the regulating module upregulates the target module, -1L if it downregulates
  - `strength` (numeric): the strength of the interaction
  - `hill` (numeric): hill coefficient, larger than 1 for positive cooperativity, between 0 and 1 for negative cooperativity
- `expression_patterns`
- A tibble describing the expected expression pattern changes when a cell is simulated by dyngen. Each row represents one transition between two cell states.
- `from` (character): name of a cell state
  - `to` (character): name of a cell state
  - `module_progression` (character): differences in module expression between the two states. Example: "+4, -1 | +9 | -4" means the expression of module 4 will go up at the same time as module 1 goes down; afterwards module 9 expression will go up, and afterwards module 4 expression will go down again.
  - `start` (logical): Whether or not this from cell state is the start of the trajectory
  - `burn` (logical): Whether these cell states are part of the burn in phase. Cells will not get sampled from these cell states.
  - `time` (numeric): The duration of an transition.

**Value**

A dyngen backbone.

**See Also**

[dyngen](#) on how to run a dyngen simulation

**Examples**

```
library(tibble)
backbone <- backbone(
  module_info = tribble(
    ~module_id, ~basal, ~burn, ~independence,
```

```

    "M1",      1,      TRUE,  1,
    "M2",      0,      FALSE, 1,
    "M3",      0,      FALSE, 1
  ),
  module_network = tribble(
    ~from, ~to, ~effect, ~strength, ~hill,
    "M1",  "M2", 1L,      1,        2,
    "M2",  "M3", 1L,      1,        2
  ),
  expression_patterns = tribble(
    ~from, ~to, ~module_progression, ~start, ~burn, ~time,
    "s0",  "s1", "+M1",      TRUE,  TRUE,  30,
    "s1",  "s2", "+M2,+M3",  FALSE, FALSE, 80
  )
)

```

---

 bblego

*Design your own custom backbone easily*


---

## Description

You can use the bblego functions in order to create custom backbones using various components. Please note that the bblego functions currently only allow you to create tree-like backbones.

## Usage

```
bblego(..., .list = NULL)
```

```

bblego_linear(
  from,
  to,
  type = sample(c("simple", "doublerep1", "doublerep2"), 1),
  num_modules = sample(4:6, 1),
  burn = FALSE
)

```

```

bblego_branching(
  from,
  to,
  type = "simple",
  num_steps = 3,
  num_modules = 2 + length(to) * (3 + num_steps),
  burn = FALSE
)

```

```

bblego_start(
  to,
  type = sample(c("simple", "doublerep1", "doublerep2"), 1),

```

```

    num_modules = sample(4:6, 1)
  )

bblego_end(
  from,
  type = sample(c("simple", "doublerep1", "doublerep2"), 1),
  num_modules = sample(4:6, 1)
)

```

## Arguments

<code>..., .list</code>	bblego components, either as separate args or as a list.
<code>from</code>	The begin state of this component.
<code>to</code>	The end state of this component.
<code>type</code>	Some components have alternative module regulatory networks. bblego_start(), bblego_linear(), bblego_end(): <ul style="list-style-type: none"> <li>"simple": a sequence of modules in which every module upregulates the next module.</li> <li>"doublerep1": a sequence of modules in which every module downregulates the next module, and each module has positive basal expression.</li> <li>"doublerep2": a sequence of modules in which every module upregulates the next module, but downregulates the one after that.</li> <li>"flipflop": a sequence of modules in which every module upregulates the next module. In addition, the last module upregulates itself and strongly downregulates the first module.</li> </ul> bblego_branching(): <ul style="list-style-type: none"> <li>"simple": a set of <math>n</math> modules (with <math>n = \text{length}(\text{to})</math>) which all downregulate one another and upregulate themselves. This causes a branching to occur in the trajectory.</li> </ul>
<code>num_modules</code>	The number of modules this component is allowed to use. Various components might require a minimum number of components in order to work properly.
<code>burn</code>	Whether or not these components are part of the warm-up simulation.
<code>num_steps</code>	The number of branching steps to reduce the odds of double positive cells occurring.

## Details

A backbone always needs to start with a single `bblego_start()` state and needs to end with one or more `bblego_end()` states. The order of the mentioned states needs to be such that a state is never specified in the first argument (except for `bblego_start()`) before having been specified as the second argument.

## Value

A dyngen backbone.

**Examples**

```
backbone <- bblego(
  bblego_start("A", type = "simple", num_modules = 2),
  bblego_linear("A", "B", type = "simple", num_modules = 3),
  bblego_branching("B", c("C", "D"), type = "simple", num_steps = 3),
  bblego_end("C", type = "flipflop", num_modules = 4),
  bblego_end("D", type = "doublerep1", num_modules = 7)
)
```

---

combine\_models      *Combine multiple dyngen models*

---

**Description**

Assume the given models have the exact same feature ids and ran up until the `generate_cells()` step. In addition, the user is expected to run `generate_experiment()` on the combined models.

**Usage**

```
combine_models(models, duplicate_gold_standard = TRUE)
```

**Arguments**

`models`            A named list of models. The names of the list will be used to prefix the different cellular states in the combined model.

`duplicate_gold_standard`  
Whether or not the gold standards of the models are different and should be duplicated and prefixed.

**Details**

See the [vignette on simulating batch effects](#) on how to use this function.

**Examples**

```
data("example_model")
model_ab <- combine_models(list("left" = example_model, "right" = example_model))

# show a dimensionality reduction
plot_simulations(model_ab)
plot_gold_mappings(model_ab, do_facet = FALSE)
```



---

dyngen

*dyngen: A multi-modal simulator for spearheading single-cell omics analyses*

---

## Description

A toolkit for generating synthetic single cell data.

### Step 1, initialise dyngen model

- `initialise_model()`: Define and store settings for all following steps. See each of the sections below for more information.
- Use a predefined backbone:
  - `list_backbones()`
  - `backbone_bifurcating()`
  - `backbone_bifurcating_converging()`
  - `backbone_bifurcating_cycle()`
  - `backbone_bifurcating_loop()`
  - `backbone_branching()`
  - `backbone_binary_tree()`
  - `backbone_consecutive_bifurcating()`
  - `backbone_trifurcating()`
  - `backbone_converging()`
  - `backbone_cycle()`
  - `backbone_cycle_simple()`
  - `backbone_linear()`
  - `backbone_linear_simple()`
  - `backbone_disconnected()`
- Create a custom backbone:
  - `backbone()`
  - `bblego()`
  - `bblego_linear()`
  - `bblego_branching()`
  - `bblego_start()`
  - `bblego_end()`
- Visualise the backbone:
  - `plot_backbone_modulenet()`
  - `plot_backbone_statenet()`

### Step 2, generate TF network

- `generate_tf_network()`: Generate a transcription factor network from the backbone
- `tf_network_default()`: Parameters for configuring this step

**Step 3, add more genes to the gene network**

- `generate_feature_network()`: Generate a target network
- `feature_network_default()`: Parameters for configuring this step
- `plot_feature_network()`: Visualise the gene network

**Step 4, generate gene kinetics**

- `generate_kinetics()`: Generate the gene kinetics
- `kinetics_default()`, `kinetics_random_distributions()`: Parameters for configuring this step

**Step 5, simulate the gold standard**

- `generate_gold_standard()`: Simulate the gold standard backbone, used for mapping to cell states afterwards
- `gold_standard_default()`: Parameters for configuring this step
- `plot_gold_mappings()`: Visualise the mapping of the simulations to the gold standard
- `plot_gold_simulations()`: Visualise the gold standard simulations using the dimred
- `plot_gold_expression()`: Visualise the expression of the gold standard over simulation time

**Step 6, simulate the cells**

- `generate_cells()`: Simulate the cells based on its GRN
- `simulation_default()`: Parameters for configuring this step
- `simulation_type_wild_type()`, `simulation_type_knockdown()`: Used for configuring the type of simulation
- `kinetics_noise_none()`, `kinetics_noise_simple()`: Different kinetics randomisers to apply to each simulation
- `plot_simulations()`: Visualise the simulations using the dimred
- `plot_simulation_expression()`: Visualise the expression of the simulations over simulation time

**Step 7, simulate cell and transcripting sampling**

- `generate_experiment()`: Sample cells and transcripts from experiment
- `list_experiment_samplers()`, `experiment_snapshot()`, `experiment_synchronised()`: Parameters for configuring this step
- `simtime_from_backbone()`: Determine the simulation time from the backbone
- `plot_experiment_dimred()`: Plot a dimensionality reduction of the final dataset

**Step 8, convert to dataset**

- `as_dyno()`, `wrap_dataset()`: Convert a dyngen model to a dyno dataset
- `as_anndata()`: Convert a dyngen model to an anndata dataset
- `as_sce()`: Convert a dyngen model to a SingleCellExperiment dataset
- `as_seurat()`: Convert a dyngen model to a Seurat dataset

**One-shot function**

- `generate_dataset()`: Run through steps 2 to 8 with a single function
- `plot_summary()`: Plot a summary of all dyngen simulation steps

**Data objects**

- `example_model`: A (very) small toy dyngen model, used for documentation and testing purposes
- `realcounts`: A set of real single-cell expression datasets, to be used as reference datasets
- `realnets`: A set of real gene regulatory networks, to be sampled in step 3

**Varia functions**

- `dyngen`: This help page
- `get_timings()`: Extract execution timings for each of the dyngen steps
- `combine_models()`: Combine multiple dyngen models
- `rnorm_bounded()`: A bounded version of `rnorm()`
- `runif_subrange()`: A subrange version of `runif()`

**Examples**

```

model <- initialise_model(
  backbone = backbone_bifurcating()
)

model <- model %>%
  generate_tf_network() %>%
  generate_feature_network() %>%
  generate_kinetics() %>%
  generate_gold_standard() %>%
  generate_cells() %>%
  generate_experiment()

dataset <- wrap_dataset(model, format = "dyno")
# format can also be set to "sce", "seurat", "anndata" or "list"

# library(dynplot)
# plot_dimred(dataset)

```

---

example_model	<i>A (very!) small toy dyngen model</i>
---------------	---

---

**Description**

Used for showcasing examples of functions.

**Usage**

example\_model

**Format**

An object of class list (inherits from dyngen::init) of length 19.

---

generate_cells	<i>Simulate the cells</i>
----------------	---------------------------

---

**Description**

[generate\\_cells\(\)](#) runs simulations in order to determine the gold standard of the simulations. [simulation\\_default\(\)](#) is used to configure parameters pertaining this process.

**Usage**

```
generate_cells(model)

simulation_default(
  burn_time = NULL,
  total_time = NULL,
  ssa_algorithm = ssa_etl(tau = 30/3600),
  census_interval = 4,
  experiment_params = bind_rows(simulation_type_wild_type(num_simulations = 32),
    simulation_type_knockdown(num_simulations = 0)),
  store_reaction_firings = FALSE,
  store_reaction_propensities = FALSE,
  compute_cellwise_grn = FALSE,
  compute_dimred = TRUE,
  compute_rna_velocity = FALSE,
  kinetics_noise_function = kinetics_noise_simple(mean = 1, sd = 0.005)
)

simulation_type_wild_type(
  num_simulations,
  seed = sample.int(10 * num_simulations, num_simulations)
```

```

)

simulation_type_knockdown(
  num_simulations,
  timepoint = runif(num_simulations),
  genes = "*",
  num_genes = sample(1:5, num_simulations, replace = TRUE, prob = 0.25^(1:5)),
  multiplier = runif(num_simulations, 0, 1),
  seed = sample.int(10 * num_simulations, num_simulations)
)

```

### Arguments

model	A dyngen intermediary model for which the gold standard been generated with <a href="#">generate_gold_standard()</a> .
burn_time	The burn in time of the system, used to determine an initial state vector. If NULL, the burn time will be inferred from the backbone.
total_time	The total simulation time of the system. If NULL, the simulation time will be inferred from the backbone.
ssa_algorithm	Which SSA algorithm to use for simulating the cells with <a href="#">GillespieSSA2::ssa()</a>
census_interval	A granularity parameter for the outputted simulation.
experiment_params	A tibble generated by rbinding multiple calls of <a href="#">simulation_type_wild_type()</a> and <a href="#">simulation_type_knockdown()</a> .
store_reaction_firings	Whether or not to store the number of reaction firings.
store_reaction_propensities	Whether or not to store the propensity values of the reactions.
compute_cellwise_grn	Whether or not to compute the cellwise GRN activation values.
compute_dimred	Whether to perform a dimensionality reduction after simulation.
compute_rna_velocity	Whether or not to compute the propensity ratios after simulation.
kinetics_noise_function	A function that will generate noise to the kinetics of each simulation. It takes the <code>feature_info</code> and <code>feature_network</code> as input parameters, modifies them, and returns them as a list. See <a href="#">kinetics_noise_none()</a> and <a href="#">kinetics_noise_simple()</a> .
num_simulations	The number of simulations to run.
seed	A set of seeds for each of the simulations.
timepoint	The relative time point of the knockdown
genes	Which genes to sample from. "*" for all genes.
num_genes	The number of genes to knockdown.
multiplier	The strength of the knockdown. Use 0 for a full knockout, $0 < x < 1$ for a knock-down, and $> 1$ for an overexpression.

**Value**

A dyngen model.

**See Also**

[dyngen](#) on how to run a complete dyngen simulation

**Examples**

```
library(dplyr)
model <-
  initialise_model(
    backbone = backbone_bifurcating(),
    simulation = simulation_default(
      ssa_algorithm = ssa_etl(tau = .1),
      experiment_params = bind_rows(
        simulation_type_wild_type(num_simulations = 4),
        simulation_type_knockdown(num_simulations = 4)
      )
    )
  )

data("example_model")
model <- example_model %>% generate_cells()

plot_simulations(model)
plot_gold_mappings(model)
plot_simulation_expression(model)
```

---

generate\_dataset

*Generate a dataset*

---

**Description**

This function contains the complete pipeline for generating a dataset with **dyngen**. In order to have more control over how the dataset is generated, run each of the steps in this function separately.

**Usage**

```
generate_dataset(
  model,
  format = c("list", "dyno", "sce", "seurat", "anndata", "none"),
  output_dir = NULL,
  make_plots = FALSE,
  store_dimred = model$simulation_params$compute_dimred,
  store_cellwise_grn = model$simulation_params$compute_cellwise_grn,
  store_rna_velocity = model$simulation_params$compute_rna_velocity
)
```

**Arguments**

model	A dyngen initial model created with <code>initialise_model()</code> .
format	Which output format to use, must be one of 'dyno' (requires dynwrap), 'sce' (requires SingleCellExperiment), 'seurat' (requires Seurat), 'anndata' (requires anndata), 'list' or 'none'.
output_dir	If not NULL, then the generated model and dynwrap dataset will be written to files in this directory.
make_plots	Whether or not to generate an overview of the dataset.
store_dimred	Whether or not to store the dimensionality reduction constructed on the true counts.
store_cellwise_grn	Whether or not to also store cellwise GRN information.
store_rna_velocity	Whether or not to store the log propensity ratios.

**Value**

A list containing a dyngen model (`li$model`) and a dynwrap dataset (`li$dataset`).

**Examples**

```

model <-
  initialise_model(
    backbone = backbone_bifurcating()
  )

out <- generate_dataset(model, format = "list")

model <- out$model
dataset <- out$dataset

# can also generate other dataset formats:
# out <- generate_dataset(model, format = "dyno")
# out <- generate_dataset(model, format = "sce")
# out <- generate_dataset(model, format = "seurat")
# out <- generate_dataset(model, format = "anndata")

```

---

generate\_experiment    *Sample cells from the simulations*

---

**Description**

`generate_experiment()` samples cells along the different simulations. Two approaches are implemented: sampling from an unsynchronised population of single cells (snapshot) or sampling at multiple time points in a synchronised population (time series).

**Usage**

```

generate_experiment(model)

list_experiment_samplers()

experiment_snapshot(
  realcount = NULL,
  map_reference_cpm = TRUE,
  map_reference_ls = TRUE,
  weight_bw = 0.1
)

experiment_synchronised(
  realcount = NULL,
  map_reference_cpm = TRUE,
  map_reference_ls = TRUE,
  num_timepoints = 8,
  pct_between = 0.75
)

```

**Arguments**

model	A dyngen intermediary model for which the simulations have been run with <a href="#">generate_cells()</a> .
realcount	The name of a dataset in <a href="#">realcounts</a> . If NULL, a random dataset will be sampled from <a href="#">realcounts</a> .
map_reference_cpm	Whether or not to try to match the CPM distribution to that of a reference dataset.
map_reference_ls	Whether or not to try to match the distribution of the library sizes to that of the reference dataset.
weight_bw	[snapshot] A bandwidth parameter for determining the distribution of cells along each edge in order to perform weighted sampling.
num_timepoints	[synchronised] The number of time points used in the experiment.
pct_between	[synchronised] The percentage of 'unused' simulation time.

**Details**

[experiment\\_snapshot\(\)](#) samples the cells using the length of each edge in the milestone network as weights. See Supplementary Figure 7A from the dyngen paper for an illustration of how these weights are computed.

[experiment\\_synchronised\(\)](#) samples the cells along the simulation timeline by binning it into `num_timepoints` groups separated by `num_timepoints-1` gaps. See Supplementary Figure 7B from the dyngen paper for an illustration of how the timepoint groups are computed.

**Value**

A dyngen model.



**Examples**

```

names(list_experiment_samplers())

model <-
  initialise_model(
    backbone = backbone_bifurcating(),
    experiment = experiment_synchronised()
  )

## Not run:
data("example_model")
model <- example_model %>% generate_experiment()

plot_experiment_dimred(model)

## End(Not run)

```

---

```
generate_feature_network
```

*Generate a target network*

---

**Description**

[generate\\_feature\\_network\(\)](#) generates a network of target genes that are regulated by the previously generated TFs, and also a separate network of housekeeping genes (HKs). [feature\\_network\\_default\(\)](#) is used to configure parameters pertaining this process.

**Usage**

```

generate_feature_network(model)

feature_network_default(
  realnet = NULL,
  damping = 0.01,
  target_resampling = Inf,
  max_in_degree = 5
)

```

**Arguments**

model	A dyngen intermediary model for which the transcription network has been generated with <a href="#">generate_tf_network()</a> .
realnet	The name of a gene regulatory network (GRN) in <a href="#">realnets</a> . If NULL, a random network will be sampled from <a href="#">realnets</a> . Alternatively, a custom GRN can be used by passing a weighted sparse matrix.
damping	A damping factor used for the page rank algorithm used to subsample the realnet.

target\_resampling      How many targets / HKs to sample from the realnet per iteration.  
 max\_in\_degree      The maximum in-degree of a target / HK.

**Value**

A dyngen model.

**See Also**

[dyngen](#) on how to run a complete dyngen simulation

**Examples**

```
model <-
  initialise_model(
    backbone = backbone_bifurcating(),
    feature_network = feature_network_default(damping = 0.1)
  )

data("example_model")
model <- example_model %>%
  generate_tf_network() %>%
  generate_feature_network()

plot_feature_network(model)
```

---

generate\_gold\_standard

*Simulate the gold standard*

---

**Description**

[generate\\_gold\\_standard\(\)](#) runs simulations in order to determine the gold standard of the simulations. [gold\\_standard\\_default\(\)](#) is used to configure parameters pertaining this process.

**Usage**

```
generate_gold_standard(model)

gold_standard_default(
  tau = 30/3600,
  census_interval = 10/60,
  simulate_targets = FALSE
)
```

**Arguments**

model	A dyngen intermediary model for which the kinetics of the feature network has been generated with <code>generate_kinetics()</code> .
tau	The time step of the ODE algorithm used to generate the gold standard.
census_interval	A granularity parameter of the gold standard time steps. Should be larger than or equal to tau.
simulate_targets	Also simulate the targets during the gold standard simulation

**Value**

A dyngen model.

**See Also**

[dyngen](#) on how to run a complete dyngen simulation

**Examples**

```
model <-  
  initialise_model(  
    backbone = backbone_bifurcating(),  
    gold_standard = gold_standard_default(tau = .01, census_interval = 1)  
  )  
  
data("example_model")  
model <- example_model %>% generate_gold_standard()  
  
plot_gold_simulations(model)  
plot_gold_mappings(model)  
plot_gold_expression(model)
```

---

generate\_kinetics      *Determine the kinetics of the feature network*

---

**Description**

`generate_kinetics()` samples the kinetics of genes in the feature network for which the kinetics have not yet been defined. `kinetics_default()` is used to configure parameters pertaining this process. `kinetics_random_distributions()` will do the same, but the distributions are also randomised.

**Usage**

```
generate_kinetics(model)

kinetics_default()

kinetics_random_distributions()
```

**Arguments**

`model` A dyngen intermediary model for which the feature network has been generated with `generate_feature_network()`.

**Details**

To write different kinetics settings, you need to write three functions with interface function(`feature_info`, `feature_network`, `cache_dir`, `verbose`). Described below are the default kinetics samplers.

`sampler_tfs()` mutates the `feature_info` data frame by adding the following columns:

- `transcription_rate`: the rate at which pre-mRNAs are transcribed, in pre-mRNA / hour. Default distribution:  $U(1, 2)$ .
- `translation_rate`: the rate at which mRNAs are translated into proteins, in protein / mRNA / hour. Default distribution:  $U(100, 150)$ .
- `mrna_half-life`: the half-life of (pre-)mRNA molecules, in hours. Default distribution:  $U(2.5, 5)$ .
- `protein_half-life`: the half-life of proteins, in hours. Default distribution:  $U(5, 10)$ .
- `splicing_rate`: the rate at which pre-mRNAs are spliced into mRNAs, in reactions / hour. Default value:  $\log(2) / (10/60)$ , which corresponds to a half-life of 10 minutes.
- `independence`: the degree to which all regulators need to be bound for transcription to occur (0), or whether transcription can occur if only one of the regulators is bound (1).

`sampler_nontfs()` samples the `transcription_rate`, `translation_rate`, `mrna_half-life` and `protein_half-life` from a supplementary file of Schwannhäusser et al., 2011, doi.org/10.1038/nature10098. `splicing_rate` is by default the same as in `sampler_tfs()`. `independence` is sampled from  $U(0, 1)$ .

`sampler_interactions()` mutates the `feature_network` data frame by adding the following columns.

- `effect`: the effect of the interaction; upregulating = +1, downregulating = -1. By default, sampled from -1, 1 with probabilities .25, .75.
- `strength`: the strength of the interaction. Default distribution:  $10^U(0, 2)$ .
- `hill`: the hill coefficient. Default distribution:  $N(2, 2)$  with a minimum of 1 and a maximum of 10.

**Value**

A dyngen model.

**See Also**

[dyngen](#) on how to run a complete dyngen simulation

**Examples**

```
model <-  
  initialise_model(  
    backbone = backbone_bifurcating(),  
    kinetics_params = kinetics_default()  
  )
```

```
data("example_model")  
model <- example_model %>%  
  generate_kinetics()
```

---

generate\_tf\_network    *Generate a transcription factor network from the backbone*

---

**Description**

`generate_tf_network()` generates the transcription factors (TFs) that drive the dynamic process a cell undergoes. `tf_network_default()` is used to configure parameters pertaining this process.

**Usage**

```
generate_tf_network(model)  
  
tf_network_default(  
  min_tfs_per_module = 1L,  
  sample_num_regulators = function() 2,  
  weighted_sampling = FALSE  
)
```

**Arguments**

model	A dyngen initial model created with <code>initialise_model()</code> .
min_tfs_per_module	The number of TFs to generate per module in the backbone.
sample_num_regulators	A function to generate the number of TFs per module each TF will be regulated by.
weighted_sampling	When determining what TFs another TF is regulated by, whether to perform weighted sampling (by rank) or not.

**Value**

A dyngen model.

**See Also**

[dyngen](#) on how to run a complete dyngen simulation

**Examples**

```
model <-  
  initialise_model(  
    backbone = backbone_bifurcating()  
  )  
model <- model %>%  
  generate_tf_network()  
  
plot_feature_network(model)
```

---

get\_timings

*Return the timings of each of the dyngen steps*

---

**Description**

Return the timings of each of the dyngen steps

**Usage**

```
get_timings(model)
```

**Arguments**

model            A dyngen object

**Examples**

```
data("example_model")  
timings <- get_timings(example_model)
```

---

initialise_model	<i>Initial settings for simulating a dyngen dataset</i>
------------------	---

---

## Description

Initial settings for simulating a dyngen dataset

## Usage

```
initialise_model(
  backbone,
  num_cells = 1000,
  num_tfs = nrow(backbone$module_info),
  num_targets = 100,
  num_hks = 50,
  distance_metric = c("pearson", "spearman", "cosine", "euclidean", "manhattan"),
  tf_network_params = tf_network_default(),
  feature_network_params = feature_network_default(),
  kinetics_params = kinetics_default(),
  gold_standard_params = gold_standard_default(),
  simulation_params = simulation_default(),
  experiment_params = experiment_snapshot(),
  verbose = TRUE,
  download_cache_dir = getOption("dyngen_download_cache_dir"),
  num_cores = getOption("Ncpus") %||% 1L,
  id = NULL
)
```

## Arguments

backbone	The gene module configuration that determines the type of dynamic process being simulated. See <a href="#">list_backbones()</a> for a full list of different backbones available in this package.
num_cells	The number of cells to sample.
num_tfs	The number of transcription factors (TFs) to generate. TFs are the main drivers of the changes that occur in a cell. TFs are regulated only by other TFs.
num_targets	The number of target genes to generate. Target genes are regulated by TFs and sometimes by other target genes.
num_hks	The number of housekeeping genes (HKs) to generate. HKs are typically highly expressed, and are not regulated by the TFs or targets.
distance_metric	The distance metric to be used to calculate the distance between cells. See <a href="#">dynutils::calculate_distance()</a> for a list of possible distance metrics.
tf_network_params	Settings for generating the TF network with <a href="#">generate_tf_network()</a> , see <a href="#">tf_network_default()</a> .

feature_network_params	Settings for generating the feature network with <a href="#">generate_feature_network()</a> , see <a href="#">feature_network_default()</a> .
kinetics_params	Settings for determining the kinetics of the feature network with <a href="#">generate_kinetics()</a> , see <a href="#">kinetics_default()</a> .
gold_standard_params	Settings pertaining simulating the gold standard with <a href="#">generate_gold_standard()</a> , see <a href="#">gold_standard_default()</a> .
simulation_params	Settings pertaining the simulation itself with <a href="#">generate_cells()</a> , see <a href="#">simulation_default()</a> .
experiment_params	Settings related to how the experiment is simulated with <a href="#">generate_experiment()</a> , see <a href="#">experiment_snapshot()</a> or <a href="#">experiment_synchronised()</a> .
verbose	Whether or not to print messages during the simulation.
download_cache_dir	If not NULL, temporary downloaded files will be cached in this directory.
num_cores	Parallellisation parameter for various steps in the pipeline.
id	An identifier for the model.

**Value**

A dyngen model.

**See Also**

[dyngen](#) on how to run a complete dyngen simulation

**Examples**

```
model <- initialise_model(
  backbone = backbone_bifurcating(),
  num_cells = 555,
  verbose = FALSE,
  download_cache_dir = "~/cache/dyngen"
)
```

---

kinetics\_noise\_none    *Add small noise to the kinetics of each simulation*

---

**Description**

Add small noise to the kinetics of each simulation



**Usage**

```
kinetics_noise_none()

kinetics_noise_simple(mean = 1, sd = 0.005)
```

**Arguments**

mean	The mean level of noise (should be 1)
sd	The sd of the noise (should be a relatively small value)

**Value**

A list of noise generators for the kinetics.

---

list_backbones	<i>List of all predefined backbone models</i>
----------------	---

---

**Description**

A module is a group of genes which, to some extent, shows the same expression behaviour. Several modules are connected together such that one or more genes from one module will regulate the expression of another module. By creating chains of modules, a dynamic behaviour in gene regulation can be created.

**Usage**

```
list_backbones()

backbone_bifurcating()

backbone_bifurcating_converging()

backbone_bifurcating_cycle()

backbone_bifurcating_loop()

backbone_branching(
  num_modifications = rbinom(1, size = 6, 0.25) + 1,
  min_degree = 3,
  max_degree = sample(min_degree:5, 1)
)

backbone_binary_tree(num_modifications = rbinom(1, size = 6, 0.25) + 1)

backbone_consecutive_bifurcating()
```

```

backbone_trifurcating()

backbone_converging()

backbone_cycle()

backbone_cycle_simple()

backbone_linear()

backbone_linear_simple()

backbone_disconnected(
  left_backbone = list_backbones() %>% keep(., names(.) != "disconnected") %>%
    sample(1) %>% first(),
  right_backbone = list_backbones() %>% keep(., names(.) != "disconnected") %>%
    sample(1) %>% first(),
  num_common_modules = 10
)

```

### Arguments

`num_modifications` The number of branch points in the generated backbone.

`min_degree` The minimum degree of each node in the backbone.

`max_degree` The maximum degree of each node in the backbone.

`left_backbone` A backbone (other than a disconnected backbone), see [list\\_backbones\(\)](#).

`right_backbone` A backbone (other than a disconnected backbone), see [list\\_backbones\(\)](#).

`num_common_modules` The number of modules which are regulated by either backbone.

### Value

A list of all the available backbone generators.

### See Also

[dyngen](#) on how to run a dyngen simulation

### Examples

```

names(list_backbones())

bb <- backbone_bifurcating()
bb <- backbone_bifurcating_converging()
bb <- backbone_bifurcating_cycle()
bb <- backbone_bifurcating_loop()
bb <- backbone_binary_tree()
bb <- backbone_branching()

```

```
bb <- backbone_consecutive_bifurcating()
bb <- backbone_converging()
bb <- backbone_cycle()
bb <- backbone_cycle_simple()
bb <- backbone_disconnected()
bb <- backbone_linear()
bb <- backbone_linear_simple()
bb <- backbone_trifurcating()

model <- initialise_model(
  backbone = bb
)
```

---

plot\_backbone\_modulenet

*Visualise the backbone of a model*

---

### Description

Visualise the backbone of a model

### Usage

```
plot_backbone_modulenet(model)
```

### Arguments

model            A dynngen initial model created with `initialise_model()`.

### Value

A ggplot2 object.

### Examples

```
data("example_model")
plot_backbone_modulenet(example_model)
```

---

plot\_backbone\_statenet

*Visualise the backbone state network of a model*

---

### Description

Visualise the backbone state network of a model

### Usage

```
plot_backbone_statenet(model, detailed = FALSE)
```

### Arguments

model	A dyngen initial model created with <code>initialise_model()</code> .
detailed	Whether or not to also plot the substates of transitions.

### Value

A ggplot2 object.

### Examples

```
data("example_model")  
plot_backbone_statenet(example_model)
```

---

plot\_experiment\_dimred

*Plot a dimensionality reduction of the final dataset*

---

### Description

Plot a dimensionality reduction of the final dataset

### Usage

```
plot_experiment_dimred(model, mapping = aes_string("comp_1", "comp_2"))
```

### Arguments

model	A dyngen intermediary model for which the simulations have been run with <code>generate_experiment()</code> .
mapping	Which components to plot.

**Value**

A ggplot2 object.

**Examples**

```
data("example_model")
plot_experiment_dimred(example_model)
```

---

plot\_feature\_network *Visualise the feature network of a model*

---

**Description**

Visualise the feature network of a model

**Usage**

```
plot_feature_network(  
  model,  
  show_tfs = TRUE,  
  show_targets = TRUE,  
  show_hks = FALSE  
)
```

**Arguments**

model	A dyngen intermediary model for which the feature network has been generated with <a href="#">generate_feature_network()</a> .
show_tfs	Whether or not to show the transcription factors.
show_targets	Whether or not to show the targets.
show_hks	Whether or not to show the housekeeping genes.

**Value**

A ggplot2 object.

**Examples**

```
data("example_model")
plot_feature_network(example_model)
```

---

plot\_gold\_expression *Visualise the expression of the gold standard over simulation time*

---

### Description

Visualise the expression of the gold standard over simulation time

### Usage

```
plot_gold_expression(  
  model,  
  what = c("mol_premrna", "mol_mrna", "mol_protein"),  
  label_changing = TRUE  
)
```

### Arguments

**model** A dyngen intermediary model for which the simulations have been run with [generate\\_gold\\_standard\(\)](#).

**what** Which molecule types to visualise.

**label\_changing** Whether or not to add a label next to changing molecules.

### Value

A ggplot2 object.

### Examples

```
data("example_model")  
plot_gold_expression(example_model, what = "mol_mrna", label_changing = FALSE)
```

---

plot\_gold\_mappings *Visualise the mapping of the simulations to the gold standard*

---

### Description

Visualise the mapping of the simulations to the gold standard

### Usage

```
plot_gold_mappings(  
  model,  
  selected_simulations = NULL,  
  do_facet = TRUE,  
  mapping = aes_string("comp_1", "comp_2")  
)
```

**Arguments**

model	A dyngen intermediary model for which the simulations have been run with <code>generate_cells()</code> .
selected_simulations	Which simulation indices to visualise.
do_facet	Whether or not to facet according to simulation index.
mapping	Which components to plot.

**Value**

A ggplot2 object.

**Examples**

```
data("example_model")
plot_gold_mappings(example_model)
```

---

plot\_gold\_simulations *Visualise the simulations using the dimred*

---

**Description**

Visualise the simulations using the dimred

**Usage**

```
plot_gold_simulations(  
  model,  
  detailed = FALSE,  
  mapping = aes_string("comp_1", "comp_2"),  
  highlight = 0  
)
```

**Arguments**

model	A dyngen intermediary model for which the simulations have been run with <code>generate_cells()</code> .
detailed	Whether or not to colour according to each separate sub-edge in the gold standard.
mapping	Which components to plot.
highlight	Which simulation to highlight. If <code>highlight == 0</code> then the gold simulation will be highlighted.

**Value**

A ggplot2 object.

**Examples**

```
data("example_model")
plot_gold_simulations(example_model)
```

---

plot_simulations	<i>Visualise the simulations using the dimred</i>
------------------	---

---

**Description**

Visualise the simulations using the dimred

**Usage**

```
plot_simulations(model, mapping = aes_string("comp_1", "comp_2"))
```

**Arguments**

model	A dyngen intermediary model for which the simulations have been run with <a href="#">generate_cells()</a> .
mapping	Which components to plot.

**Value**

A ggplot2 object.

**Examples**

```
data("example_model")
plot_simulations(example_model)
```



---

`plot_simulation_expression`*Visualise the expression of the simulations over simulation time*

---

## Description

Visualise the expression of the simulations over simulation time

## Usage

```
plot_simulation_expression(  
  model,  
  simulation_i = 1:4,  
  what = c("mol_premrna", "mol_mrna", "mol_protein"),  
  facet = c("simulation", "module_group", "module_id", "none"),  
  label_nonzero = FALSE  
)
```

## Arguments

<code>model</code>	A dyngen intermediary model for which the simulations have been run with <a href="#">generate_cells()</a> .
<code>simulation_i</code>	Which simulation to visualise.
<code>what</code>	Which molecule types to visualise.
<code>facet</code>	What to facet on.
<code>label_nonzero</code>	Plot labels for non-zero molecules.

## Value

A ggplot2 object.

## Examples

```
data("example_model")  
plot_simulation_expression(example_model)
```

---

plot_summary	<i>Plot a summary of all dyngen simulation steps.</i>
--------------	---

---

**Description**

Plot a summary of all dyngen simulation steps.

**Usage**

```
plot_summary(model)
```

**Arguments**

model	A dyngen intermediary model for which the simulations have been run with <code>generate_experiment()</code> .
-------	---

**Value**

A ggplot2 object.

**Examples**

```
data("example_model")  
plot_summary(example_model)
```

---

realcounts	<i>A set of real single cell expression datasets</i>
------------	--

---

**Description**

Statistics are derived from these datasets in order to simulate single cell experiments.

**Usage**

```
realcounts
```

**Format**

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 111 rows and 9 columns.

---

realnets	<i>A set of gold standard gene regulatory networks</i>
----------	--

---

**Description**

These networks are subsampled in order to generate realistic feature and housekeeping networks.

**Usage**

```
realnets
```

**Format**

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 32 rows and 2 columns.

---

<code>rnorm_bounded</code>	<i>A bounded version of <code>rnorm</code></i>
----------------------------	--

---

**Description**

A bounded version of `rnorm`

**Usage**

```
rnorm_bounded(n, mean = 0, sd = 1, min = -Inf, max = Inf)
```

**Arguments**

<code>n</code>	number of observations. If <code>length(n) &gt; 1</code> , the length is taken to be the number required.
<code>mean</code>	vector of means.
<code>sd</code>	vector of standard deviations.
<code>min</code>	lower limits of the distribution.
<code>max</code>	upper limits of the distribution.

**Value**

Generates values with `rnorm`, bounded by `[min, max]`

**Examples**

```
rnorm_bounded(10)
```

---

runif_subrange	<i>A subrange version of runif</i>
----------------	------------------------------------

---

**Description**

Will generate numbers from a random subrange within the given range. For example, if [min, max] is set to [0, 10], this function could decide to generate numbers between 2 and 6.

**Usage**

```
runif_subrange(n, min, max)
```

**Arguments**

n	Number of observations
min	Lower limits of the distribution.
max	Upper limits of the distribution.

**Value**

Generates values with runif, bounded by a range drawn from `sort(runif(2, min, max))`.

**Examples**

```
runif_subrange(20, 0, 10)
```

---

simtime_from_backbone	<i>Determine simulation time from backbone</i>
-----------------------	--

---

**Description**

Determine simulation time from backbone

**Usage**

```
simtime_from_backbone(backbone, burn = FALSE)
```

**Arguments**

backbone	A valid dyngen backbone object
burn	Whether or not to compute the simtime for only the burn phase

**Value**

An estimation of the required simulation time

**Examples**

```
backbone <- backbone_linear()

simtime_from_backbone(backbone)

model <- initialise_model(
  backbone = backbone,
  simulation_params = simulation_default(
    burn_time = simtime_from_backbone(backbone, burn = TRUE),
    total_time = simtime_from_backbone(backbone, burn = FALSE)
  )
)
```

# Index

- \* **datasets**
  - example\_model, 12
  - realcounts, 34
  - realnets, 35
- as\_anndata (as\_dyno), 3
- as\_anndata(), 11
- as\_dyno, 3
- as\_dyno(), 11
- as\_list (as\_dyno), 3
- as\_sce (as\_dyno), 3
- as\_sce(), 11
- as\_seurat (as\_dyno), 3
- as\_seurat(), 11
  
- backbone, 4
- backbone(), 9
- backbone\_bifurcating (list\_backbones), 25
- backbone\_bifurcating(), 9
- backbone\_bifurcating\_converging (list\_backbones), 25
- backbone\_bifurcating\_converging(), 9
- backbone\_bifurcating\_cycle (list\_backbones), 25
- backbone\_bifurcating\_cycle(), 9
- backbone\_bifurcating\_loop (list\_backbones), 25
- backbone\_bifurcating\_loop(), 9
- backbone\_binary\_tree (list\_backbones), 25
- backbone\_binary\_tree(), 9
- backbone\_branching (list\_backbones), 25
- backbone\_branching(), 9
- backbone\_consecutive\_bifurcating (list\_backbones), 25
- backbone\_consecutive\_bifurcating(), 9
- backbone\_converging (list\_backbones), 25
- backbone\_converging(), 9
- backbone\_cycle (list\_backbones), 25
- backbone\_cycle(), 9
- backbone\_cycle\_simple (list\_backbones), 25
- backbone\_cycle\_simple(), 9
- backbone\_disconnected (list\_backbones), 25
- backbone\_disconnected(), 9
- backbone\_linear (list\_backbones), 25
- backbone\_linear(), 9
- backbone\_linear\_simple (list\_backbones), 25
- backbone\_linear\_simple(), 9
- backbone\_trifurcating (list\_backbones), 25
- backbone\_trifurcating(), 9
- bblego, 6
- bblego(), 9
- bblego\_branching (bblego), 6
- bblego\_branching(), 9
- bblego\_end (bblego), 6
- bblego\_end(), 9
- bblego\_linear (bblego), 6
- bblego\_linear(), 9
- bblego\_start (bblego), 6
- bblego\_start(), 9
  
- combine\_models, 8
- combine\_models(), 11
  
- dyngen, 5, 9, 11, 14, 18, 19, 21, 22, 24, 26
- dynutils::calculate\_distance(), 23
  
- example\_model, 11, 12
- experiment\_snapshot (generate\_experiment), 15
- experiment\_snapshot(), 10, 16, 24
- experiment\_synchronised (generate\_experiment), 15
- experiment\_synchronised(), 10, 16, 24

- feature\_network\_default
  - (generate\_feature\_network), 17
- feature\_network\_default(), 10, 17, 24
- generate\_cells, 12
- generate\_cells(), 10, 12, 16, 24, 31–33
- generate\_dataset, 14
- generate\_dataset(), 11
- generate\_experiment, 15
- generate\_experiment(), 4, 10, 15, 24, 28, 34
- generate\_feature\_network, 17
- generate\_feature\_network(), 10, 17, 20, 24, 29
- generate\_gold\_standard, 18
- generate\_gold\_standard(), 10, 13, 18, 24, 30
- generate\_kinetics, 19
- generate\_kinetics(), 10, 19, 24
- generate\_tf\_network, 21
- generate\_tf\_network(), 9, 17, 21, 23
- get\_timings, 22
- get\_timings(), 11
- GillespieSSA2::ssa(), 13
- gold\_standard\_default
  - (generate\_gold\_standard), 18
- gold\_standard\_default(), 10, 18, 24
- initialise\_model, 23
- initialise\_model(), 9, 15, 21, 27, 28
- kinetics\_default (generate\_kinetics), 19
- kinetics\_default(), 10, 19, 24
- kinetics\_noise\_none, 24
- kinetics\_noise\_none(), 10, 13
- kinetics\_noise\_simple
  - (kinetics\_noise\_none), 24
- kinetics\_noise\_simple(), 10, 13
- kinetics\_random\_distributions
  - (generate\_kinetics), 19
- kinetics\_random\_distributions(), 10, 19
- list\_backbones, 25
- list\_backbones(), 9, 23, 26
- list\_experiment\_samplers
  - (generate\_experiment), 15
- list\_experiment\_samplers(), 10
- plot\_backbone\_modulenet, 27
- plot\_backbone\_modulenet(), 9
- plot\_backbone\_statenet, 28
- plot\_backbone\_statenet(), 9
- plot\_experiment\_dimred, 28
- plot\_experiment\_dimred(), 10
- plot\_feature\_network, 29
- plot\_feature\_network(), 10
- plot\_gold\_expression, 30
- plot\_gold\_expression(), 10
- plot\_gold\_mappings, 30
- plot\_gold\_mappings(), 10
- plot\_gold\_simulations, 31
- plot\_gold\_simulations(), 10
- plot\_simulation\_expression, 33
- plot\_simulation\_expression(), 10
- plot\_simulations, 32
- plot\_simulations(), 10
- plot\_summary, 34
- plot\_summary(), 11
- realcounts, 11, 16, 34
- realnets, 11, 17, 35
- rnorm(), 11
- rnorm\_bounded, 35
- rnorm\_bounded(), 11
- runif(), 11
- runif\_subrange, 36
- runif\_subrange(), 11
- simtime\_from\_backbone, 36
- simtime\_from\_backbone(), 10
- simulation\_default (generate\_cells), 12
- simulation\_default(), 10, 12, 24
- simulation\_type\_knockdown
  - (generate\_cells), 12
- simulation\_type\_knockdown(), 10, 13
- simulation\_type\_wild\_type
  - (generate\_cells), 12
- simulation\_type\_wild\_type(), 10, 13
- tf\_network\_default
  - (generate\_tf\_network), 21
- tf\_network\_default(), 9, 21, 23
- wrap\_dataset (as\_dyno), 3
- wrap\_dataset(), 11