atlas Documentation

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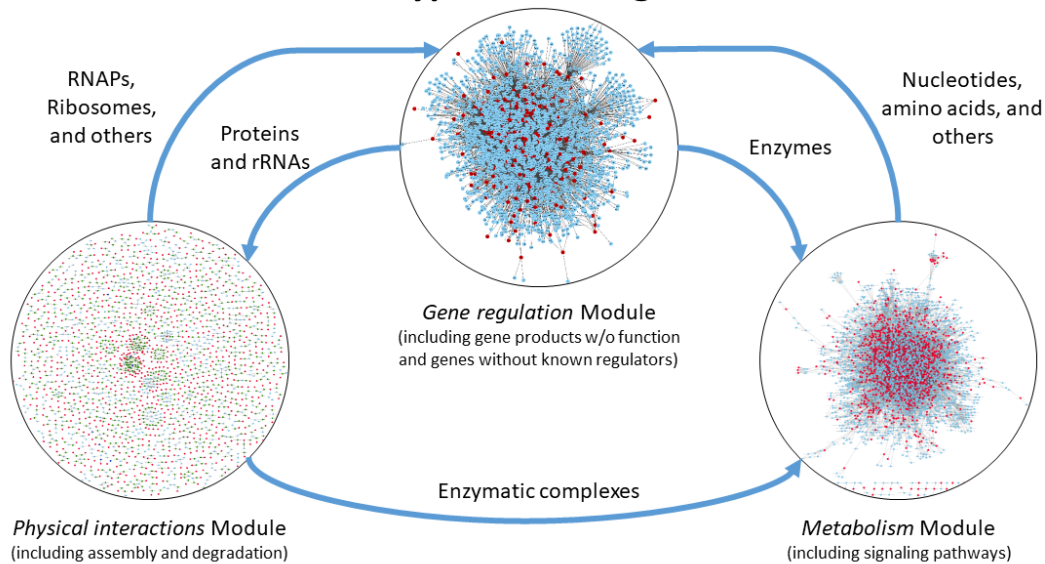
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CONTENTS

Atlas is a small software developed to use simple text files that encode biological networks and write Rule-Based Models (RBMs). Atlas writes rules and others model components for the PySB python package PySB, PMID 23423320. The RBMs could be simulated within PySB with NFsim, PMID 26556387 (within the BioNetGen2 software, PMID 27402907), KaSim (KaSim, PMID 29950016). Models could be exported to text files in *BioNetGen* (BioNetGenLanguage) or *kappa* language (Kappa) for further calibration (BioNetFit, PMID 26556387 or pleione, PMID 31641245) and analysis (sterope for parameter sensibility and alcyone for parameter uncertainty).

Atlas: Divide-and-conquer strategy to build rule-based models from diverse types of biological networks

Gene regulation Module
(including gene products w/o function
and genes without known regulators)

Physical interactions Module
(including assembly and degradation)

Metabolism Module
(including signaling pathways)

REQUIREMENTS

1. PathwayTools must be installed and running to obtain data from the BioCyc databases. Please, run `pathway-tools -lisp -python-local-only` before to obtain any data.

   (Optional) The PathwayTools software could be executed in the background, with help of `nohup pathway-tools -lisp -python-local-only > /dev/null 2> /dev/null &`. Please follow instructions at http://pathwaytools.org/ to obtain a licensed copy of the software from https://biocyc.org/download-bundle.shtml. However, data could be manually formatted using a text-based editor or a spreadsheet software.

   Note: If you ran into the `pathway-tools/ptools/24.0/exe/aclssl.so: undefined symbol: CRYPTO_set_locking_callback` error, please follow instructions here: https://github.com/networkbiolab/atlas/tree/master/PTools-Docker. Instructions will guide you to install a docker image that is able to run pathway tools, but does not include it, so you still need to obtain the software with a valid license.

2. (Highly recommended) Install Docker. Please follow instructions for a supported Operating System https://docs.docker.com/engine/install/:

   On Ubuntu, install it with `apt-get install docker.io`.

   On Win10, install Docker Desktop with WSL2 support https://docs.docker.com/docker-for-windows/wsl/.

   On MacOS, install Docker Desktop https://docs.docker.com/docker-for-mac/install/.

   The Docker `networkbiolab/pleiades` installs the python packages, the jupyter server, and the stochastic simulators.

3. (Recommended) Jupyter notebook. We recommend the use of Anaconda3 https://www.anaconda.com/products/individual because of the easier installation of the stochastic simulators from https://anaconda.org/alubbock.

4. (Optional) A stochastic simulator, supported by the pySB python package (BNG2, NFsim, KaSim or Stochkit). pySB requires BNG2 to simulate models with NFsim.

5. (Optional) Cytoscape to visualize metabolic networks and others.

6. (Optional) A deterministic simulator: pySB supports ODE integration via scipy.integrate.ode, BioNetGen ODE integration, and CUDA-accelerated ODE integration with Marco S. Nobile's cupSODA software (https://github.com/aresio/cupSODA). If the user feel comfortable with SBML models, pySB could export to SBML and deterministic simulation done with libRoadRunner (http://libroadrunner.org/), Tellurium (http://tellurium.analogmachine.org/), COPASI (http://copasi.org/), etc.

INSTALLATION

There are different ways to install Atlas:

1. **Install the docker Pleiades (Highly recommended).** The docker container is the easiest way to obtain the software Atlas, the stochastic simulators BioNetGen and KaSim, and the Jupyter notebook.

   OR

2. **Clone the Pleiades GitHub repository.** If you are familiar with git, the docker container could be obtained cloning the Pleiades repository. Further details are below.

   OR

3. **Install Atlas with pip3.**

   OR

4. **Clone the Atlas GitHub repository.** If you are familiar with git, Atlas could be obtained cloning the Atlas repository and the respective directory added to *PYTHONPATH*. Further details are below.

Note: **Need Help?** If you run into any problems with installation, please visit our chat room: https://gitter.im/glucksfall/pleiades

2.1 Option 1: Install the Pleiades docker container

Install the docker container is the easiest way to obtain the software Atlas.

Install the docker image "pleiades" using `docker pull networkbiolab/pleiades`. The container is based on the Anaconda3 software and it installs Atlas, and the stochastic simulators BNG2, NFsim, KaSim, and Stochkit. After building the image, please run the container with `docker run --detach --publish 10000:8888 networkbiolab/pleiades`, and go to `localhost:10000` in your preferred browser. The required password is `pleiades`.

2.2 Option 2: Clone the Pleiades repository

Download or clone the Github repository from https://github.com/networkbiolab/pleiades with `git clone https://github.com/networkbiolab/pleiades foo` (where `foo` is an absolute or relative path). Then, you could build the docker image with `docker build foo --tag pleiades` and run it with `docker run --detach --publish 10000:8888 pleiades`. Finally, go to `localhost:10000` in your preferred browser. The required password is `pleiades`.

2.3 Option 3: Install Atlas natively on your computer

The recommended approach is to use system tools, or install them if necessary. To install python packages, you could use pip, or download the package from the python package index.

1. **Install with system tools**

   With pip, you need to execute and Atlas will be installed on `$HOME/.local/lib/python3.6/site-packages` directory or similar.

   ```
   pip3 install atlas_rbm --user
   ```

   If you have system rights, you could install Atlas for all users with

   ```
   sudo -H pip3 install atlas_rbm
   ```

2. **Download from the python package index**

   Alternatively, you could download the package (useful when pip fails to download the package because of lack of SSL libraries) and then install with pip. For instance:

   ```
   wget https://files.pythonhosted.org/packages/ec/ed/
   ↪8b94e0a29f69a24ddb18ba4a4e6463d3ecede308576774e86baf6a84b998/atlas_rbm-1.0.2-
   ↪py3-none-any.whl
   pip3 install atlas_rbm-1.0.2-py3-none-any.whl --user
   ```

Note: Why Python3?: Atlas is intended to be used with >=python3.4 because python2.7 won't receive further development past 2020, including security updates.

Note: pip, Python, and Anaconda: Be aware which pip you invoque. You could install pip3 with `sudo apt-get install python3-pip` if you have system rights, or install python3 from source, and adding `<python3 path>/bin/pip3` to the path, or linking it in a directory like `$HOME/bin` which is commonly added to the path at login. Also be aware that, if you installed Anaconda, pip could be linked to the Anaconda specific version of pip, which will install Atlas into Anaconda's installation folder. Type `which pip` or `which pip3` to find out the source of pip, and type `python -m site` or `python3 -m site` to find out where is more likely Atlas will be installed.

2.4 Option 4: Clone the Github repository

1. **Clone with git**

   The source code is uploaded and maintained through Github at https://github.com/networkbiolab/atlas. Therefore, you could clone the repository locally, and then add the folder to the PYTHONPATH. Beware that you should install the *pysb* package (pysb) and others packages by any means, specially the Jupyter Notebook project (https://jupyter.org).

   ```
   path=/opt/atlas
   git clone https://github.com/networkbiolab/atlas $path
   echo export PYTHONPATH="\$PYTHONPATH:\$path" >> $HOME/.profile
   ```

   Note: Adding the path to $HOME/.profile allows python to find the package installation folder after each user login. Similarly, adding the path to $HOME/.bashrc allows python to find the package after each terminal invocation. Other options include setting the PYTHONPATH environmental variable in a sh file (see the example folder) or invoke python3 setup.py clean build install to install Atlas as it was downloaded from the PyPI server.

MODELING

Atlas is a modular software with each script centered in a specific biological network

1. *Metabolic Networks*

2. **Interaction Networks**

   1. *Protein-Protein Interaction Networks*

   2. *Protein-Small compounds Interaction Networks*

   3. **Protein-RNA Interaction Networks**

   4. **RNA-RNA Interaction Networks**

   5. *Transcription Factor-DNA Binding Site Interaction Networks*

   6. *Sigma Factor-Promoter Interaction Networks*

3. *Genome Graphs*

3.1 Metabolic Networks

Metabolic networks have seven columns:

1. The 1st declares a name for the enzyme, gene, or enzymatic complex. Use *spontaneous* for non-enzymatic reactions.;

2. The 2nd declares the location of the enzyme, gene, or enzymatic complex: In the case of enzymatic complexes:

   1. If the number of locations match the number of components of the complex, each location is mapped to the component.

   2. If the number of locations unmatch the number of components, the first location is used for every component

   3. If the number of locations is one, the location is used for every component.

   Valid names are: `cytosol`, `inner membrane`, `periplasmic space`, `membrane`, `outer membrane`, `extracellular space`, `bacterial nucleoid`, `cell wall`, `cell projection` and `cytoskeleton`

3. The 3rd declares a name for the reaction. If the name is not unique, Atlas drops the duplicated reaction;

4. The 4th column lists names for substrates using comma (without spaces);

5. The 5th column lists names for products using comma (without spaces); To declare metabolites located at a compartment, prefix the name of the metabolite (e.g. "PER-lactose"):

   - 'CYT-' : 'cytosol',

- 'iMEM-' : 'inner membrane',
- 'PER-' : 'periplasmic space',
- 'MEM-' : 'membrane',
- 'oMEM-' : 'outer membrane',
- 'EX-' : 'extracellular space',
- 'bNUC-' : 'bacterial nucleoid',
- 'WALL-' : 'cell wall',
- 'cPROJ-' : 'cell projection',
- 'CYTOSK-' : 'cytoskeleton'

6. The 6th declares the forward reaction rate; and finally

7. The 7th declares the reverse reaction rate.

Examples:

```
1  GENE OR COMPLEX          ENZYME␣
   →LOCATION        REACTION        SUBSTRATES        PRODUCTS        FWD␣
   →RATE        RVS_RATE
2  spontaneous        cytosol        LACTOSE-MUTAROTATION        alpha-
   →lactose        beta-lactose        1        1
3  spontaneous        cytosol        GALACTOSE-MUTAROTATION        alpha-
   →GALACTOSE        beta-GALACTOSE        1        1
4  spontaneous        cytosol        GLUCOSE-MUTAROTATION        alpha-
   →glucose        beta-glucose        1        1
5  LACY-MONOMER        inner membrane        TRANS-RXN-24        PER-PROTON,PER-alpha-
   →lactose        PROTON,alpha-lactose        1        0
6  LACY-MONOMER        inner membrane        TRANS-RXN-24-beta        PER-PROTON,PER-
   →beta-lactose        PROTON,beta-lactose        1        0
7  LACY-MONOMER        inner membrane        TRANS-RXN-94        PER-PROTON,PER-
   →MELIBIOSE        PROTON,MELIBIOSE        1        0
8  LACY-MONOMER        inner membrane        RXN0-7215        PER-PROTON,PER-CPD-
   →3561        PROTON,CPD-3561        1        0
9  LACY-MONOMER        inner membrane        RXN0-7217        PER-PROTON,PER-CPD-
   →3785        PROTON,CPD-3785        1        0
10 LACY-MONOMER        inner membrane        RXN-17755        PER-PROTON,PER-CPD-
   →3801        PROTON,CPD-3801        1        0
11 BETAGALACTOSID-CPLX        cytosol        BETAGALACTOSID-RXN        beta-lactose,
   →WATER        beta-GALACTOSE,beta-glucose        1        0
12 BETAGALACTOSID-CPLX        cytosol        BETAGALACTOSID-RXN-alpha        alpha-
   →lactose,WATER        alpha-GALACTOSE,alpha-glucose        1        0
13 BETAGALACTOSID-CPLX        cytosol        RXN0-5363        alpha-lactose        alpha-
   →ALLOLACTOSE        1        1
14 BETAGALACTOSID-CPLX        cytosol        RXN0-5363-beta        beta-
   →lactose        beta-ALLOLACTOSE        1        1
15 BETAGALACTOSID-CPLX        cytosol        ALLOLACTOSE-DEG-alpha        alpha-
   →ALLOLACTOSE        alpha-GALACTOSE,alpha-glucose        1        0
16 BETAGALACTOSID-CPLX        cytosol        ALLOLACTOSE-DEG-beta        beta-
   →ALLOLACTOSE        beta-GALACTOSE,beta-glucose        1        0
17 BETAGALACTOSID-CPLX        cytosol        RXN-17726        CPD-3561,WATER        beta-
   →GALACTOSE,Fructofuranose        1        0
18 BETAGALACTOSID-CPLX        cytosol        RXN0-7219        CPD-3785,WATER        beta-
   →GALACTOSE,D-ARABINOSE        1        0
19 GALACTOACETYLTRAN-CPLX        cytosol        GALACTOACETYLTRAN-RXN-
   →galactose        beta-GALACTOSE,ACETYL-COA        6-Acetyl-beta-D-Galactose,CO-
   →A        1        0
```

OR

```
1  GENE OR COMPLEX        ENZYME␣
   ↪LOCATION        REACTION        SUBSTRATES        PRODUCTS        FWD_
   ↪RATE        RVS_RATE
2  spontaneous        cytosol        LACTOSE-MUTAROTATION        alpha-
   ↪lactose        beta-lactose        1        1
3  spontaneous        cytosol        GALACTOSE-MUTAROTATION        alpha-
   ↪GALACTOSE        beta-GALACTOSE        1        1
4  spontaneous        cytosol        GLUCOSE-MUTAROTATION        alpha-
   ↪glucose        beta-glucose        1        1
5  lacY        inner membrane        TRANS-RXN-24        PER-PROTON,PER-alpha-
   ↪lactose        PROTON,alpha-lactose        1        0
6  lacY        inner membrane        TRANS-RXN-24-beta        PER-PROTON,PER-beta-
   ↪lactose        PROTON,beta-lactose        1        0
7  lacY        inner membrane        TRANS-RXN-94        PER-PROTON,PER-
   ↪MELIBIOSE        PROTON,MELIBIOSE        1        0
8  lacY        inner membrane        RXN0-7215        PER-PROTON,PER-CPD-
   ↪3561        PROTON,CPD-3561        1        0
9  lacY        inner membrane        RXN0-7217        PER-PROTON,PER-CPD-
   ↪3785        PROTON,CPD-3785        1        0
10 lacY        inner membrane        RXN-17755        PER-PROTON,PER-CPD-
   ↪3801        PROTON,CPD-3801        1        0
11 lacZ        cytosol        BETAGALACTOSID-RXN        beta-lactose,WATER        beta-
   ↪GALACTOSE,beta-glucose        1        0
12 lacZ        cytosol        BETAGALACTOSID-RXN-alpha        alpha-lactose,
   ↪WATER        alpha-GALACTOSE,alpha-glucose        1        0
13 lacZ        cytosol        RXN0-5363        alpha-lactose        alpha-
   ↪ALLOLACTOSE        1        1
14 lacZ        cytosol        RXN0-5363-beta        beta-lactose        beta-
   ↪ALLOLACTOSE        1        1
15 lacZ        cytosol        ALLOLACTOSE-DEG-alpha        alpha-ALLOLACTOSE,
   ↪WATER        alpha-GALACTOSE,alpha-glucose        1        0
16 lacZ        cytosol        ALLOLACTOSE-DEG-beta        beta-ALLOLACTOSE,
   ↪WATER        beta-GALACTOSE,beta-glucose        1        0
17 lacZ        cytosol        RXN-17726        CPD-3561,WATER        beta-GALACTOSE,
   ↪Fructofuranose        1        0
18 lacZ        cytosol        RXN0-7219        CPD-3785,WATER        beta-GALACTOSE,D-
   ↪ARABINOSE        1        0
19 lacA        cytosol        GALACTOACETYLTRAN-RXN-galactose        beta-GALACTOSE,
   ↪ACETYL-COA        6-Acetyl-beta-D-Galactose,CO-A        1        0
```

OR

```
1  GENE OR COMPLEX        ENZYME␣
   ↪LOCATION        REACTION        SUBSTRATES        PRODUCTS        FWD_
   ↪RATE        RVS_RATE
2  spontaneous        cytosol        LACTOSE-MUTAROTATION        alpha-
   ↪lactose        beta-lactose        1        1
3  spontaneous        cytosol        GALACTOSE-MUTAROTATION        alpha-
   ↪GALACTOSE        beta-GALACTOSE        1        1
4  spontaneous        cytosol        GLUCOSE-MUTAROTATION        alpha-
   ↪glucose        beta-glucose        1        1
5  lacY        inner membrane        TRANS-RXN-24        PER-PROTON,PER-alpha-
   ↪lactose        PROTON,alpha-lactose        1        0
```

(continued from previous page)

```
6   lacY        inner membrane        TRANS-RXN-24-beta        PER-PROTON,PER-beta-
    ↪lactose          PROTON,beta-lactose          1        0
7   lacY        inner membrane        TRANS-RXN-94        PER-PROTON,PER-
    ↪MELIBIOSE          PROTON,MELIBIOSE          1        0
8   lacY        inner membrane        RXN0-7215        PER-PROTON,PER-CPD-
    ↪3561          PROTON,CPD-3561          1        0
9   lacY        inner membrane        RXN0-7217        PER-PROTON,PER-CPD-
    ↪3785          PROTON,CPD-3785          1        0
10  lacY        inner membrane        RXN-17755        PER-PROTON,PER-CPD-
    ↪3801          PROTON,CPD-3801          1        0
11  [lacZ,lacZ,lacZ,lacZ]        [cytosol,cytosol,cytosol,cytosol]        BETAGALACTOSID-
    ↪RXN          beta-lactose,WATER        beta-GALACTOSE,beta-glucose          1        0
12  [lacZ,lacZ,lacZ,lacZ]        [cytosol,cytosol,cytosol,cytosol]        BETAGALACTOSID-
    ↪RXN-alpha        alpha-lactose,WATER        alpha-GALACTOSE,alpha-
    ↪glucose          1        0
13  [lacZ,lacZ,lacZ,lacZ]        [cytosol,cytosol,cytosol,cytosol]        RXN0-
    ↪5363        alpha-lactose          alpha-ALLOLACTOSE          1        1
14  [lacZ,lacZ,lacZ,lacZ]        [cytosol,cytosol,cytosol,cytosol]        RXN0-5363-
    ↪beta        beta-lactose          beta-ALLOLACTOSE          1        1
15  [lacZ,lacZ,lacZ,lacZ]        [cytosol,cytosol,cytosol,cytosol]        ALLOLACTOSE-DEG-
    ↪alpha        alpha-ALLOLACTOSE,WATER        alpha-GALACTOSE,alpha-
    ↪glucose          1        0
16  [lacZ,lacZ,lacZ,lacZ]        [cytosol,cytosol,cytosol,cytosol]        ALLOLACTOSE-DEG-
    ↪beta        beta-ALLOLACTOSE,WATER        beta-GALACTOSE,beta-
    ↪glucose          1        0
17  [lacZ,lacZ,lacZ,lacZ]        [cytosol,cytosol,cytosol,cytosol]        RXN-
    ↪17726        CPD-3561,WATER        beta-GALACTOSE,Fructofuranose          1        0
18  [lacZ,lacZ,lacZ,lacZ]        [cytosol,cytosol,cytosol,cytosol]        RXN0-
    ↪7219        CPD-3785,WATER        beta-GALACTOSE,D-ARABINOSE          1        0
19  [lacA,lacA,lacA]        [cytosol,cytosol,cytosol]        GALACTOACETYLTRAN-RXN-
    ↪galactose        beta-GALACTOSE,ACETYL-COA        6-Acetyl-beta-D-Galactose,CO-
    ↪A        1        0
```


Note: **Visualization in Cytoscape.** Transform the input file into a Cytoscape compatible file with `atlas_rbm.utils.metabolicNetwork.expand_network(network, 'output.txt')` and import the network into Cytoscape.

Colors and arrows remains to the user for customization: The following image was prepared from the lactose-metabolism-cytoscape-v3.txt file, and you could reproduce it with Cytoscape:

1. Click on the `Import Network from File System` icon or click on `File -> Import -> Network from File...`.

2. Navigate to the file and click on `Open`.

3. SOURCE, TARGET, and EDGE ATTRIBUTE are OK, but the 4th columns must be the SOURCE NODE ATTRIBUTE and the 5th column the TARGET NODE ATTRIBUTE. Click on the header and change it to the correct attribute. The attributes will help later to filter and to add format to nodes and edges.

4. Click on `Filter` (on the right), then on the + icon and finally on `Column Filter`:

1. On the selector, click on `Edge:   EDGE_ATTRIBUTE` and change `contains` to `is`:

   1. Write `NO_REVERSIBLE` that will select edges that correspond to irreversible reactions. Click on `Style`, then `Edge` (in the bottom), and click on the 3rd column to bypass the format of the `Target Arrow Shape` and select your favorite arrow shape.

   2. Write `REVERSIBLE` and bypass the format of the `Source Arrow Shape` AND `Target Arrow`

`Shape`, and select your favorite arrow shape.

2. On the selector, click on `Node:   SOURCE_NODE_ATTRIBUTE`:

    1. Write `RXN` that will select nodes enconding the reactions. Click on `Style`, then on `Node` and bypass the `Fill Color`. In the new window, you could set-up the color, e.g. #00AA50

    2. Write `GENE_PROD` that will select nodes encoding the gene name, protein name, or the enzyme name. Click on `Style`, then on `Node` and bypass the `Fill Color`. In the new window, you could set-up the color, e.g. #CC0033

    3. Write `MET` that will select nodes encoding substrate metabolites. Click on `Style`, then on `Node` and bypass the `Fill Color`. In the new window, you could set-up the color, e.g. #00ABDD. Also, set a shape for nodes, to differentiate substrates from products.

3. On the selector, click on `Node:   TARGET_NODE_ATTRIBUTE`:

    1. Write `MET` that will select nodes encoding product metabolites. Click on `Style`, then on `Node` and bypass the `Fill Color`. In the new window, you could set-up the color, e.g. #00ABDD
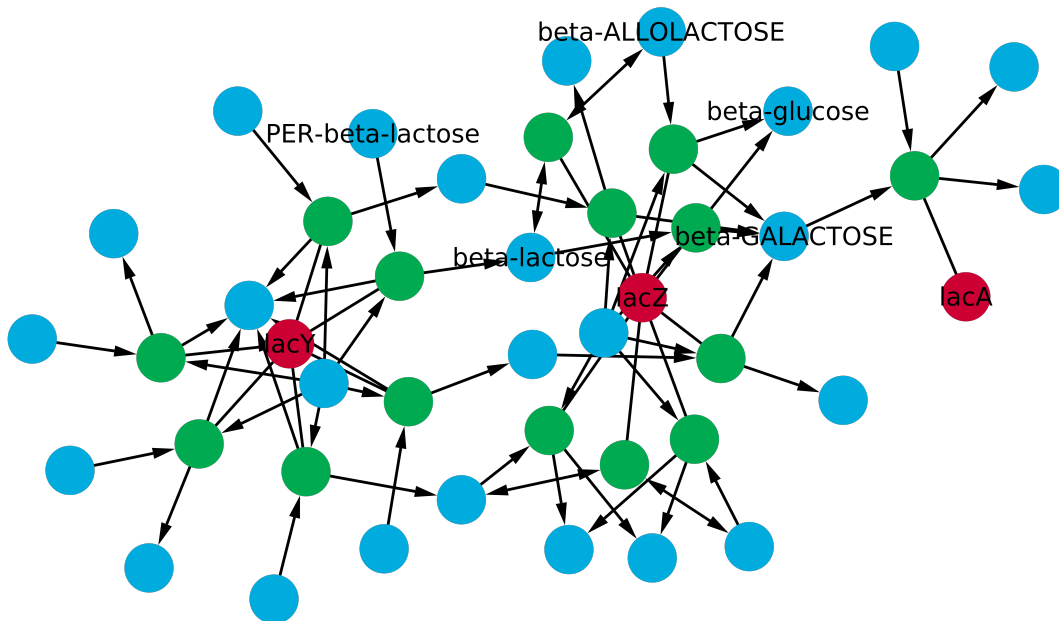
Finally, execute `atlas_rbm.construct_model_from_metabolic_network(network, verbose = False)` to obtain the model.

Note: **Uniqueness of Rule names**. Atlas will write *Rules* for unique metabolic reactions. Identical names will be reported for further curation.

Note: **Simulation**. The model can be simulated only with the instantiation of `Initials`:

- `atlas_rbm.simulation.set_initial.cplx(model, complex_name, location, positive_number)`

- `atlas_rbm.simulation.set_initial.dna(model, dna_name, positive_number)`

- `atlas_rbm.simulation.set_initial.met(model, metabolite, location, positive_number)`

- `atlas_rbm.simulation.set_initial.prot(model, prot_name, location, positive_number)`

- `atlas_rbm.simulation.set_initial.rna(model, rna_name, positive_number)`

Note: For large models, the `noObservables` and the `noInitials` will make a faster compilation, while later you could add `Initials` and `Observables` to the model.

Use the keyword argument `toFile = 'name.py'` to write the model to a file (the function will return `None`):

```python
from pysb import *
Model()

Monomer('met',
        ['name', 'loc', 'dna', 'met', 'prot', 'rna'],
        { 'name' : [ 'ACETYL_COA', 'CO_A', 'CPD_3561', 'CPD_3785', 'CPD_3801', 'D_
→ARABINOSE', 'Fructofuranose', 'MELIBIOSE', 'PROTON', 'WATER', '_6_Acetyl_beta_D_
→Galactose', 'alpha_ALLOLACTOSE', 'alpha_GALACTOSE', 'alpha_glucose', 'alpha_lactose
→', 'beta_ALLOLACTOSE', 'beta_GALACTOSE', 'beta_glucose', 'beta_lactose' ],
        'loc' : ['cyt', 'cytosk', 'ex', 'mem', 'per', 'wall', 'bnuc', 'cproj', 'imem',
→ 'omem']})
Monomer('prot',
        ['name', 'loc', 'dna', 'met', 'prot', 'rna', 'up', 'dw'],
        { 'name' : [ 'LACY_MONOMER', 'spontaneous' ],
        'loc' : ['cyt', 'cytosk', 'ex', 'mem', 'per', 'wall', 'bnuc', 'cproj', 'imem',
→ 'omem']})
Monomer('cplx',
        ['name', 'loc', 'dna', 'met', 'prot', 'rna', 'up', 'dw'],
        { 'name' : [ 'BETAGALACTOSID_CPLX', 'GALACTOACETYLTRAN_CPLX' ],
        'loc' : ['cyt', 'cytosk', 'ex', 'mem', 'per', 'wall', 'bnuc', 'cproj', 'imem',
→ 'omem']})
Observable('obs_met_ACETYL_COA_cyt', met(name = 'ACETYL_COA', loc = 'cyt'))
Observable('obs_met_CO_A_cyt', met(name = 'CO_A', loc = 'cyt'))
Observable('obs_met_CPD_3561_cyt', met(name = 'CPD_3561', loc = 'cyt'))
Observable('obs_met_CPD_3785_cyt', met(name = 'CPD_3785', loc = 'cyt'))
Observable('obs_met_CPD_3801_cyt', met(name = 'CPD_3801', loc = 'cyt'))
Observable('obs_met_D_ARABINOSE_cyt', met(name = 'D_ARABINOSE', loc = 'cyt'))
Observable('obs_met_Fructofuranose_cyt', met(name = 'Fructofuranose', loc = 'cyt'))
Observable('obs_met_MELIBIOSE_cyt', met(name = 'MELIBIOSE', loc = 'cyt'))
Observable('obs_met_PROTON_cyt', met(name = 'PROTON', loc = 'cyt'))
Observable('obs_met_WATER_cyt', met(name = 'WATER', loc = 'cyt'))
Observable('obs_met__6_Acetyl_beta_D_Galactose_cyt', met(name = '_6_Acetyl_beta_D_
→Galactose', loc = 'cyt'))
Observable('obs_met_alpha_ALLOLACTOSE_cyt', met(name = 'alpha_ALLOLACTOSE', loc = 'cyt
→'))
Observable('obs_met_alpha_GALACTOSE_cyt', met(name = 'alpha_GALACTOSE', loc = 'cyt'))
Observable('obs_met_alpha_glucose_cyt', met(name = 'alpha_glucose', loc = 'cyt'))
Observable('obs_met_alpha_lactose_cyt', met(name = 'alpha_lactose', loc = 'cyt'))
Observable('obs_met_beta_ALLOLACTOSE_cyt', met(name = 'beta_ALLOLACTOSE', loc = 'cyt
→'))
Observable('obs_met_beta_GALACTOSE_cyt', met(name = 'beta_GALACTOSE', loc = 'cyt'))
Observable('obs_met_beta_glucose_cyt', met(name = 'beta_glucose', loc = 'cyt'))
Observable('obs_met_beta_lactose_cyt', met(name = 'beta_lactose', loc = 'cyt'))
Initial(met(name = 'ACETYL_COA', loc = 'cyt', dna = None, met = None, prot = None,
→rna = None), Parameter('t0_met_ACETYL_COA_cyt', 0))
Initial(met(name = 'CO_A', loc = 'cyt', dna = None, met = None, prot = None, rna =
→None), Parameter('t0_met_CO_A_cyt', 0))
```

```
37  Initial(met(name = 'CPD_3561', loc = 'cyt', dna = None, met = None, prot = None, rna
    ↪= None), Parameter('t0_met_CPD_3561_cyt', 0))
38  Initial(met(name = 'CPD_3785', loc = 'cyt', dna = None, met = None, prot = None, rna
    ↪= None), Parameter('t0_met_CPD_3785_cyt', 0))
39  Initial(met(name = 'CPD_3801', loc = 'cyt', dna = None, met = None, prot = None, rna
    ↪= None), Parameter('t0_met_CPD_3801_cyt', 0))
40  Initial(met(name = 'D_ARABINOSE', loc = 'cyt', dna = None, met = None, prot = None,
    ↪rna = None), Parameter('t0_met_D_ARABINOSE_cyt', 0))
41  Initial(met(name = 'Fructofuranose', loc = 'cyt', dna = None, met = None, prot = None,
    ↪ rna = None), Parameter('t0_met_Fructofuranose_cyt', 0))
42  Initial(met(name = 'MELIBIOSE', loc = 'cyt', dna = None, met = None, prot = None, rna
    ↪= None), Parameter('t0_met_MELIBIOSE_cyt', 0))
43  Initial(met(name = 'PROTON', loc = 'cyt', dna = None, met = None, prot = None, rna =
    ↪None), Parameter('t0_met_PROTON_cyt', 0))
44  Initial(met(name = 'WATER', loc = 'cyt', dna = None, met = None, prot = None, rna =
    ↪None), Parameter('t0_met_WATER_cyt', 0))
45  Initial(met(name = '_6_Acetyl_beta_D_Galactose', loc = 'cyt', dna = None, met = None,
    ↪prot = None, rna = None), Parameter('t0_met__6_Acetyl_beta_D_Galactose_cyt', 0))
46  Initial(met(name = 'alpha_ALLOLACTOSE', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None), Parameter('t0_met_alpha_ALLOLACTOSE_cyt', 0))
47  Initial(met(name = 'alpha_GALACTOSE', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None), Parameter('t0_met_alpha_GALACTOSE_cyt', 0))
48  Initial(met(name = 'alpha_glucose', loc = 'cyt', dna = None, met = None, prot = None,
    ↪rna = None), Parameter('t0_met_alpha_glucose_cyt', 0))
49  Initial(met(name = 'alpha_lactose', loc = 'cyt', dna = None, met = None, prot = None,
    ↪rna = None), Parameter('t0_met_alpha_lactose_cyt', 0))
50  Initial(met(name = 'beta_ALLOLACTOSE', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None), Parameter('t0_met_beta_ALLOLACTOSE_cyt', 0))
51  Initial(met(name = 'beta_GALACTOSE', loc = 'cyt', dna = None, met = None, prot = None,
    ↪ rna = None), Parameter('t0_met_beta_GALACTOSE_cyt', 0))
52  Initial(met(name = 'beta_glucose', loc = 'cyt', dna = None, met = None, prot = None,
    ↪rna = None), Parameter('t0_met_beta_glucose_cyt', 0))
53  Initial(met(name = 'beta_lactose', loc = 'cyt', dna = None, met = None, prot = None,
    ↪rna = None), Parameter('t0_met_beta_lactose_cyt', 0))
54  Initial(prot(name = 'LACY_MONOMER', loc = 'cyt', dna = None, met = None, prot = None,
    ↪rna = None, up = None, dw = None), Parameter('t0_prot_LACY_MONOMER_cyt', 0))
55  Initial(prot(name = 'spontaneous', loc = 'cyt', dna = None, met = None, prot = None,
    ↪rna = None, up = None, dw = None), Parameter('t0_prot_spontaneous_cyt', 0))
56  Initial(cplx(name = 'BETAGALACTOSID_CPLX', loc = 'cyt', dna = None, met = None, prot
    ↪= None, rna = None, up = None, dw = None), Parameter('t0_cplx_BETAGALACTOSID_CPLX_
    ↪cyt', 0))
57  Initial(cplx(name = 'GALACTOACETYLTRAN_CPLX', loc = 'cyt', dna = None, met = None,
    ↪prot = None, rna = None, up = None, dw = None), Parameter('t0_cplx_
    ↪GALACTOACETYLTRAN_CPLX_cyt', 0))
58  Rule('LACTOSE_MUTAROTATION_CYT',
59       met(name = 'alpha_lactose', loc = 'cyt', dna = None, met = None, prot = None,
    ↪rna = None) |
60       met(name = 'beta_lactose', loc = 'cyt', dna = None, met = None, prot = None,
    ↪rna = None),
61       Parameter('fwd_LACTOSE_MUTAROTATION_CYT', 1.000000),
62       Parameter('rvs_LACTOSE_MUTAROTATION_CYT', 1.000000))
63  Rule('GALACTOSE_MUTAROTATION_CYT',
64       met(name = 'alpha_GALACTOSE', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None) |
65       met(name = 'beta_GALACTOSE', loc = 'cyt', dna = None, met = None, prot = None,
    ↪ rna = None),
66       Parameter('fwd_GALACTOSE_MUTAROTATION_CYT', 1.000000),
```

```
67              Parameter('rvs_GALACTOSE_MUTAROTATION_CYT', 1.000000))
68   Rule('GLUCOSE_MUTAROTATION_CYT',
69              met(name = 'alpha_glucose', loc = 'cyt', dna = None, met = None, prot = None,
     ↪rna = None) |
70              met(name = 'beta_glucose', loc = 'cyt', dna = None, met = None, prot = None,
     ↪rna = None),
71              Parameter('fwd_GLUCOSE_MUTAROTATION_CYT', 1.000000),
72              Parameter('rvs_GLUCOSE_MUTAROTATION_CYT', 1.000000))
73   Rule('TRANS_RXN_24',
74              prot(name = 'LACY_MONOMER', loc = 'imem', dna = None, met = None, prot = None,
     ↪ rna = None, up = None, dw = None) +
75              met(name = 'PROTON', loc = 'per', dna = None, met = None, prot = None, rna =
     ↪None) +
76              met(name = 'alpha_lactose', loc = 'per', dna = None, met = None, prot = None,
     ↪rna = None) |
77              prot(name = 'LACY_MONOMER', loc = 'imem', dna = None, met = None, prot = None,
     ↪ rna = None, up = None, dw = None) +
78              met(name = 'PROTON', loc = 'cyt', dna = None, met = None, prot = None, rna =
     ↪None) +
79              met(name = 'alpha_lactose', loc = 'cyt', dna = None, met = None, prot = None,
     ↪rna = None),
80              Parameter('fwd_TRANS_RXN_24', 1.000000),
81              Parameter('rvs_TRANS_RXN_24', 0.000000))
82   Rule('TRANS_RXN_24_beta',
83              prot(name = 'LACY_MONOMER', loc = 'imem', dna = None, met = None, prot = None,
     ↪ rna = None, up = None, dw = None) +
84              met(name = 'PROTON', loc = 'per', dna = None, met = None, prot = None, rna =
     ↪None) +
85              met(name = 'beta_lactose', loc = 'per', dna = None, met = None, prot = None,
     ↪rna = None) |
86              prot(name = 'LACY_MONOMER', loc = 'imem', dna = None, met = None, prot = None,
     ↪ rna = None, up = None, dw = None) +
87              met(name = 'PROTON', loc = 'cyt', dna = None, met = None, prot = None, rna =
     ↪None) +
88              met(name = 'beta_lactose', loc = 'cyt', dna = None, met = None, prot = None,
     ↪rna = None),
89              Parameter('fwd_TRANS_RXN_24_beta', 1.000000),
90              Parameter('rvs_TRANS_RXN_24_beta', 0.000000))
91   Rule('TRANS_RXN_94',
92              prot(name = 'LACY_MONOMER', loc = 'imem', dna = None, met = None, prot = None,
     ↪ rna = None, up = None, dw = None) +
93              met(name = 'PROTON', loc = 'per', dna = None, met = None, prot = None, rna =
     ↪None) +
94              met(name = 'MELIBIOSE', loc = 'per', dna = None, met = None, prot = None, rna
     ↪= None) |
95              prot(name = 'LACY_MONOMER', loc = 'imem', dna = None, met = None, prot = None,
     ↪ rna = None, up = None, dw = None) +
96              met(name = 'PROTON', loc = 'cyt', dna = None, met = None, prot = None, rna =
     ↪None) +
97              met(name = 'MELIBIOSE', loc = 'cyt', dna = None, met = None, prot = None, rna
     ↪= None),
98              Parameter('fwd_TRANS_RXN_94', 1.000000),
99              Parameter('rvs_TRANS_RXN_94', 0.000000))
100  Rule('RXN0_7215',
101             prot(name = 'LACY_MONOMER', loc = 'imem', dna = None, met = None, prot = None,
     ↪ rna = None, up = None, dw = None) +
102             met(name = 'PROTON', loc = 'per', dna = None, met = None, prot = None, rna =
     ↪None) +
```

```
103          met(name = 'CPD_3561', loc = 'per', dna = None, met = None, prot = None, rna
    ↪= None) |
104          prot(name = 'LACY_MONOMER', loc = 'imem', dna = None, met = None, prot = None,
    ↪ rna = None, up = None, dw = None) +
105          met(name = 'PROTON', loc = 'cyt', dna = None, met = None, prot = None, rna =
    ↪None) +
106          met(name = 'CPD_3561', loc = 'cyt', dna = None, met = None, prot = None, rna
    ↪= None),
107          Parameter('fwd_RXN0_7215', 1.000000),
108          Parameter('rvs_RXN0_7215', 0.000000))
109 Rule('RXN0_7217',
110          prot(name = 'LACY_MONOMER', loc = 'imem', dna = None, met = None, prot = None,
    ↪ rna = None, up = None, dw = None) +
111          met(name = 'PROTON', loc = 'per', dna = None, met = None, prot = None, rna =
    ↪None) +
112          met(name = 'CPD_3785', loc = 'per', dna = None, met = None, prot = None, rna
    ↪= None) |
113          prot(name = 'LACY_MONOMER', loc = 'imem', dna = None, met = None, prot = None,
    ↪ rna = None, up = None, dw = None) +
114          met(name = 'PROTON', loc = 'cyt', dna = None, met = None, prot = None, rna =
    ↪None) +
115          met(name = 'CPD_3785', loc = 'cyt', dna = None, met = None, prot = None, rna
    ↪= None),
116          Parameter('fwd_RXN0_7217', 1.000000),
117          Parameter('rvs_RXN0_7217', 0.000000))
118 Rule('RXN_17755',
119          prot(name = 'LACY_MONOMER', loc = 'imem', dna = None, met = None, prot = None,
    ↪ rna = None, up = None, dw = None) +
120          met(name = 'PROTON', loc = 'per', dna = None, met = None, prot = None, rna =
    ↪None) +
121          met(name = 'CPD_3801', loc = 'per', dna = None, met = None, prot = None, rna
    ↪= None) |
122          prot(name = 'LACY_MONOMER', loc = 'imem', dna = None, met = None, prot = None,
    ↪ rna = None, up = None, dw = None) +
123          met(name = 'PROTON', loc = 'cyt', dna = None, met = None, prot = None, rna =
    ↪None) +
124          met(name = 'CPD_3801', loc = 'cyt', dna = None, met = None, prot = None, rna
    ↪= None),
125          Parameter('fwd_RXN_17755', 1.000000),
126          Parameter('rvs_RXN_17755', 0.000000))
127 Rule('BETAGALACTOSID_RXN',
128          cplx(name = 'BETAGALACTOSID_CPLX', loc = 'cyt', dna = None, met = None, prot
    ↪= None, rna = None) +
129          met(name = 'beta_lactose', loc = 'cyt', dna = None, met = None, prot = None,
    ↪rna = None) +
130          met(name = 'WATER', loc = 'cyt', dna = None, met = None, prot = None, rna =
    ↪None) |
131          cplx(name = 'BETAGALACTOSID_CPLX', loc = 'cyt', dna = None, met = None, prot
    ↪= None, rna = None) +
132          met(name = 'beta_GALACTOSE', loc = 'cyt', dna = None, met = None, prot = None,
    ↪ rna = None) +
133          met(name = 'beta_glucose', loc = 'cyt', dna = None, met = None, prot = None,
    ↪rna = None),
134          Parameter('fwd_BETAGALACTOSID_RXN', 1.000000),
135          Parameter('rvs_BETAGALACTOSID_RXN', 0.000000))
136 Rule('BETAGALACTOSID_RXN_alpha',
137          cplx(name = 'BETAGALACTOSID_CPLX', loc = 'cyt', dna = None, met = None, prot
    ↪= None, rna = None) +
```

```
138          met(name = 'alpha_lactose', loc = 'cyt', dna = None, met = None, prot = None,
     ↪rna = None) +
139          met(name = 'WATER', loc = 'cyt', dna = None, met = None, prot = None, rna =
     ↪None) |
140          cplx(name = 'BETAGALACTOSID_CPLX', loc = 'cyt', dna = None, met = None, prot
     ↪= None, rna = None) +
141          met(name = 'alpha_GALACTOSE', loc = 'cyt', dna = None, met = None, prot =
     ↪None, rna = None) +
142          met(name = 'alpha_glucose', loc = 'cyt', dna = None, met = None, prot = None,
     ↪rna = None),
143          Parameter('fwd_BETAGALACTOSID_RXN_alpha', 1.000000),
144          Parameter('rvs_BETAGALACTOSID_RXN_alpha', 0.000000))
145 Rule('RXN0_5363',
146          cplx(name = 'BETAGALACTOSID_CPLX', loc = 'cyt', dna = None, met = None, prot
     ↪= None, rna = None) +
147          met(name = 'alpha_lactose', loc = 'cyt', dna = None, met = None, prot = None,
     ↪rna = None) |
148          cplx(name = 'BETAGALACTOSID_CPLX', loc = 'cyt', dna = None, met = None, prot
     ↪= None, rna = None) +
149          met(name = 'alpha_ALLOLACTOSE', loc = 'cyt', dna = None, met = None, prot =
     ↪None, rna = None),
150          Parameter('fwd_RXN0_5363', 1.000000),
151          Parameter('rvs_RXN0_5363', 1.000000))
152 Rule('RXN0_5363_beta',
153          cplx(name = 'BETAGALACTOSID_CPLX', loc = 'cyt', dna = None, met = None, prot
     ↪= None, rna = None) +
154          met(name = 'beta_lactose', loc = 'cyt', dna = None, met = None, prot = None,
     ↪rna = None) |
155          cplx(name = 'BETAGALACTOSID_CPLX', loc = 'cyt', dna = None, met = None, prot
     ↪= None, rna = None) +
156          met(name = 'beta_ALLOLACTOSE', loc = 'cyt', dna = None, met = None, prot =
     ↪None, rna = None),
157          Parameter('fwd_RXN0_5363_beta', 1.000000),
158          Parameter('rvs_RXN0_5363_beta', 1.000000))
159 Rule('ALLOLACTOSE_DEG_alpha',
160          cplx(name = 'BETAGALACTOSID_CPLX', loc = 'cyt', dna = None, met = None, prot
     ↪= None, rna = None) +
161          met(name = 'alpha_ALLOLACTOSE', loc = 'cyt', dna = None, met = None, prot =
     ↪None, rna = None) +
162          None |
163          cplx(name = 'BETAGALACTOSID_CPLX', loc = 'cyt', dna = None, met = None, prot
     ↪= None, rna = None) +
164          met(name = 'alpha_GALACTOSE', loc = 'cyt', dna = None, met = None, prot =
     ↪None, rna = None) +
165          met(name = 'alpha_glucose', loc = 'cyt', dna = None, met = None, prot = None,
     ↪rna = None),
166          Parameter('fwd_ALLOLACTOSE_DEG_alpha', 1.000000),
167          Parameter('rvs_ALLOLACTOSE_DEG_alpha', 0.000000))
168 Rule('ALLOLACTOSE_DEG_beta',
169          cplx(name = 'BETAGALACTOSID_CPLX', loc = 'cyt', dna = None, met = None, prot
     ↪= None, rna = None) +
170          met(name = 'beta_ALLOLACTOSE', loc = 'cyt', dna = None, met = None, prot =
     ↪None, rna = None) +
171          None |
172          cplx(name = 'BETAGALACTOSID_CPLX', loc = 'cyt', dna = None, met = None, prot
     ↪= None, rna = None) +
173          met(name = 'beta_GALACTOSE', loc = 'cyt', dna = None, met = None, prot = None,
     ↪ rna = None) +
```

```
174          met(name = 'beta_glucose', loc = 'cyt', dna = None, met = None, prot = None,
    ↪rna = None),
175          Parameter('fwd_ALLOLACTOSE_DEG_beta', 1.000000),
176          Parameter('rvs_ALLOLACTOSE_DEG_beta', 0.000000))
177 Rule('RXN_17726',
178          cplx(name = 'BETAGALACTOSID_CPLX', loc = 'cyt', dna = None, met = None, prot
    ↪= None, rna = None) +
179          met(name = 'CPD_3561', loc = 'cyt', dna = None, met = None, prot = None, rna
    ↪= None) +
180          met(name = 'WATER', loc = 'cyt', dna = None, met = None, prot = None, rna =
    ↪None) |
181          cplx(name = 'BETAGALACTOSID_CPLX', loc = 'cyt', dna = None, met = None, prot
    ↪= None, rna = None) +
182          met(name = 'beta_GALACTOSE', loc = 'cyt', dna = None, met = None, prot = None,
    ↪ rna = None) +
183          met(name = 'Fructofuranose', loc = 'cyt', dna = None, met = None, prot = None,
    ↪ rna = None),
184          Parameter('fwd_RXN_17726', 1.000000),
185          Parameter('rvs_RXN_17726', 0.000000))
186 Rule('RXN0_7219',
187          cplx(name = 'BETAGALACTOSID_CPLX', loc = 'cyt', dna = None, met = None, prot
    ↪= None, rna = None) +
188          met(name = 'CPD_3785', loc = 'cyt', dna = None, met = None, prot = None, rna
    ↪= None) +
189          met(name = 'WATER', loc = 'cyt', dna = None, met = None, prot = None, rna =
    ↪None) |
190          cplx(name = 'BETAGALACTOSID_CPLX', loc = 'cyt', dna = None, met = None, prot
    ↪= None, rna = None) +
191          met(name = 'beta_GALACTOSE', loc = 'cyt', dna = None, met = None, prot = None,
    ↪ rna = None) +
192          met(name = 'D_ARABINOSE', loc = 'cyt', dna = None, met = None, prot = None,
    ↪rna = None),
193          Parameter('fwd_RXN0_7219', 1.000000),
194          Parameter('rvs_RXN0_7219', 0.000000))
195 Rule('GALACTOACETYLTRAN_RXN_galactose',
196          cplx(name = 'GALACTOACETYLTRAN_CPLX', loc = 'cyt', dna = None, met = None,
    ↪prot = None, rna = None) +
197          met(name = 'beta_GALACTOSE', loc = 'cyt', dna = None, met = None, prot = None,
    ↪ rna = None) +
198          met(name = 'ACETYL_COA', loc = 'cyt', dna = None, met = None, prot = None,
    ↪rna = None) |
199          cplx(name = 'GALACTOACETYLTRAN_CPLX', loc = 'cyt', dna = None, met = None,
    ↪prot = None, rna = None) +
200          met(name = '_6_Acetyl_beta_D_Galactose', loc = 'cyt', dna = None, met = None,
    ↪prot = None, rna = None) +
201          met(name = 'CO_A', loc = 'cyt', dna = None, met = None, prot = None, rna =
    ↪None),
202          Parameter('fwd_GALACTOACETYLTRAN_RXN_galactose', 1.000000),
203          Parameter('rvs_GALACTOACETYLTRAN_RXN_galactose', 0.000000))
```

3.2 Protein-Protein Interaction Networks

Protein-protein interaction (PPI) networks have five columns:

1. The 1st declares the `SOURCE` and the 2nd declares the `TARGET`.

   It does not matter the order, as the two columns defines a bimolecular reaction which product is the merge of all components into one complex. *Atlas* understand components inside brackets (e.g. `[lacZ,lacZ]`) as a complex, therefore, the components are internally linked.
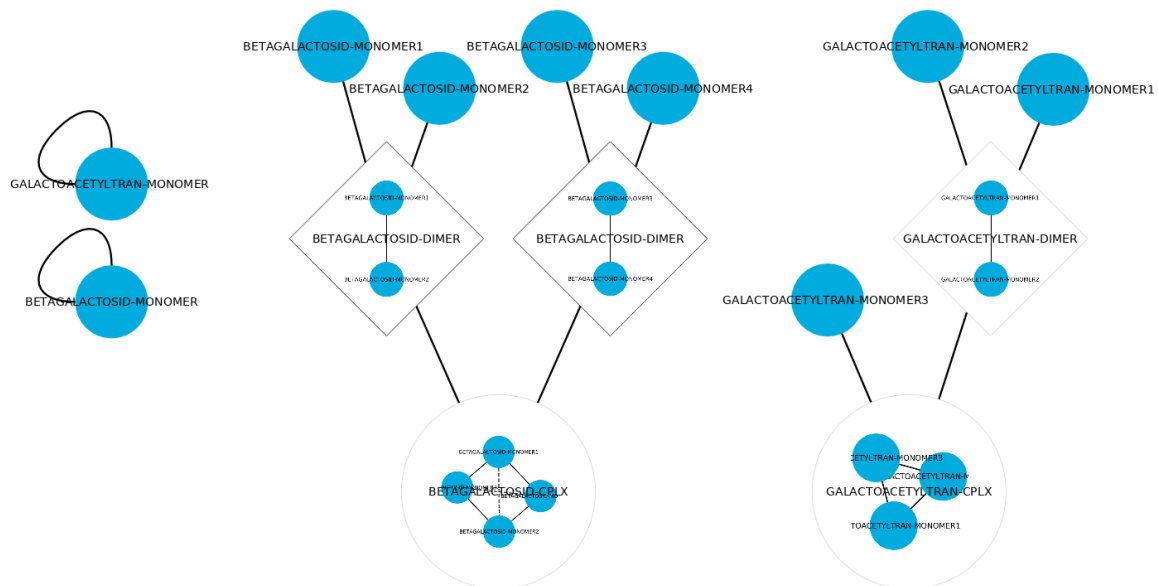
2. The 3rd and 4th columns declare the forward and the reverse reaction rates, respectively.

3. The 5th columns declares the location of the complex components:

   1. If the number of locations match the number of components of the complex, each location is mapped to the component.

   2. If the number of locations unmatch the number of components, the first location is used for every component

   3. If the number of locations is one, the location is used for every component.

   Valid names are: `cytosol`, `inner membrane`, `periplasmic space`, `membrane`, `outer membrane`, `extracellular space`, `bacterial nucleoid`, `cell wall`, `cell projection` and `cytoskeleton`

Examples:

```
1  SOURCE          TARGET          FWD_RATE          RVS_RATE          LOCATION
2  lacZ        lacZ        1.0          0.0          cytosol
3  [lacZ,lacZ]          [lacZ,lacZ]          1.0          0.0          cytosol
4  lacA        lacA        1.0          0.0          cytosol
5  lacA        [lacA,lacA]          1.0          0.0          cytosol
6  lacI        lacI        1.0          0.0          cytosol
```

Note: Visualization in Cytoscape. Cytoscape cannot import hyper-graphs. To do so, Create simple network and right-click to embed a subnetwork in the corresponding node.

Finally, execute `atlas_rbm.construct_model_from_interaction_network(network, verbose = False)` to obtain the model.

Note: **Uniqueness of Rule names**. Atlas will write *Rules* with numbered names. Merge into one the networks (`pandas.concat(list)`) or use a single file to model interactions.

Note: **Simulation**. The model can be simulated only with the instantiation of `Initials`:

- `atlas_rbm.simulation.set_initial.cplx(model, complex_name, location, positive_number)`

- `atlas_rbm.simulation.set_initial.dna(model, dna_name, positive_number)`

- `atlas_rbm.simulation.set_initial.met(model, metabolite, location, positive_number)`

- `atlas_rbm.simulation.set_initial.prot(model, prot_name, location, positive_number)`

- `atlas_rbm.simulation.set_initial.rna(model, rna_name, positive_number)`

Note: Use the keyword argument `toFile = 'name.py'` to write the model to a file (the function will return `None`):

```python
from pysb import *
Model()

Monomer('prot',
        ['name', 'loc', 'dna', 'met', 'prot', 'rna', 'up', 'dw'],
        { 'name' : [ 'lacA', 'lacI', 'lacZ' ],
        'loc' : ['cyt', 'cytosk', 'ex', 'mem', 'per', 'wall', 'bnuc', 'cproj', 'imem',
 'omem']})
Observable('obs_prot_lacA_cyt', prot(name = 'lacA', loc = 'cyt', dna = None, met =
None, prot = None, rna = None, up = None, dw = None))
Initial(prot(name = 'lacA', loc = 'cyt', dna = None, met = None, prot = None, rna =
None, up = None, dw = None), Parameter('t0_prot_lacA_cyt', 0))
Observable('obs_prot_lacI_cyt', prot(name = 'lacI', loc = 'cyt', dna = None, met =
None, prot = None, rna = None, up = None, dw = None))
Initial(prot(name = 'lacI', loc = 'cyt', dna = None, met = None, prot = None, rna =
None, up = None, dw = None), Parameter('t0_prot_lacI_cyt', 0))
Observable('obs_prot_lacZ_cyt', prot(name = 'lacZ', loc = 'cyt', dna = None, met =
None, prot = None, rna = None, up = None, dw = None))
Initial(prot(name = 'lacZ', loc = 'cyt', dna = None, met = None, prot = None, rna =
None, up = None, dw = None), Parameter('t0_prot_lacZ_cyt', 0))
Initial(prot(name = 'lacA', loc = 'cyt', dna = None, met = None, prot = None, rna =
None, up = None, dw = 1) %
        prot(name = 'lacA', loc = 'cyt', dna = None, met = None, prot = None, rna =
None, up = 1, dw = 2) %
        prot(name = 'lacA', loc = 'cyt', dna = None, met = None, prot = None, rna =
None, up = 2, dw = None),
        Parameter('t0_cplx_lacAx3_cyt', 0))
Observable('obs_cplx_lacAx3_cyt',
        prot(name = 'lacA', loc = 'cyt', dna = None, met = None, prot = None, rna =
None, up = None, dw = 1) %
        prot(name = 'lacA', loc = 'cyt', dna = None, met = None, prot = None, rna =
None, up = 1, dw = 2) %
```

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```
21          prot(name = 'lacA', loc = 'cyt', dna = None, met = None, prot = None, rna =
    ↪None, up = 2, dw = None))
22 Initial(prot(name = 'lacA', loc = 'cyt', dna = None, met = None, prot = None, rna =
    ↪None, up = None, dw = 1) %
23          prot(name = 'lacA', loc = 'cyt', dna = None, met = None, prot = None, rna =
    ↪None, up = 1, dw = None),
24          Parameter('t0_cplx_lacAx2_cyt', 0))
25 Observable('obs_cplx_lacAx2_cyt',
26          prot(name = 'lacA', loc = 'cyt', dna = None, met = None, prot = None, rna =
    ↪None, up = None, dw = 1) %
27          prot(name = 'lacA', loc = 'cyt', dna = None, met = None, prot = None, rna =
    ↪None, up = 1, dw = None))
28 Initial(prot(name = 'lacI', loc = 'cyt', dna = None, met = None, prot = None, rna =
    ↪None, up = None, dw = 1) %
29          prot(name = 'lacI', loc = 'cyt', dna = None, met = None, prot = None, rna =
    ↪None, up = 1, dw = None),
30          Parameter('t0_cplx_lacIx2_cyt', 0))
31 Observable('obs_cplx_lacIx2_cyt',
32          prot(name = 'lacI', loc = 'cyt', dna = None, met = None, prot = None, rna =
    ↪None, up = None, dw = 1) %
33          prot(name = 'lacI', loc = 'cyt', dna = None, met = None, prot = None, rna =
    ↪None, up = 1, dw = None))
34 Initial(prot(name = 'lacZ', loc = 'cyt', dna = None, met = None, prot = None, rna =
    ↪None, up = None, dw = 1) %
35          prot(name = 'lacZ', loc = 'cyt', dna = None, met = None, prot = None, rna =
    ↪None, up = 1, dw = 2) %
36          prot(name = 'lacZ', loc = 'cyt', dna = None, met = None, prot = None, rna =
    ↪None, up = 2, dw = 3) %
37          prot(name = 'lacZ', loc = 'cyt', dna = None, met = None, prot = None, rna =
    ↪None, up = 3, dw = None),
38          Parameter('t0_cplx_lacZx4_cyt', 0))
39 Observable('obs_cplx_lacZx4_cyt',
40          prot(name = 'lacZ', loc = 'cyt', dna = None, met = None, prot = None, rna =
    ↪None, up = None, dw = 1) %
41          prot(name = 'lacZ', loc = 'cyt', dna = None, met = None, prot = None, rna =
    ↪None, up = 1, dw = 2) %
42          prot(name = 'lacZ', loc = 'cyt', dna = None, met = None, prot = None, rna =
    ↪None, up = 2, dw = 3) %
43          prot(name = 'lacZ', loc = 'cyt', dna = None, met = None, prot = None, rna =
    ↪None, up = 3, dw = None))
44 Initial(prot(name = 'lacZ', loc = 'cyt', dna = None, met = None, prot = None, rna =
    ↪None, up = None, dw = 1) %
45          prot(name = 'lacZ', loc = 'cyt', dna = None, met = None, prot = None, rna =
    ↪None, up = 1, dw = None),
46          Parameter('t0_cplx_lacZx2_cyt', 0))
47 Observable('obs_cplx_lacZx2_cyt',
48          prot(name = 'lacZ', loc = 'cyt', dna = None, met = None, prot = None, rna =
    ↪None, up = None, dw = 1) %
49          prot(name = 'lacZ', loc = 'cyt', dna = None, met = None, prot = None, rna =
    ↪None, up = 1, dw = None))
50 Rule('PhysicalInteractionRule_1',
51          prot(name = 'lacZ', loc = 'cyt', dna = None, prot = None, met = None, rna =
    ↪None, up = None, dw = None) +
52          prot(name = 'lacZ', loc = 'cyt', dna = None, prot = None, met = None, rna =
    ↪None, up = None, dw = None) |
53          prot(name = 'lacZ', loc = 'cyt', dna = None, prot = None, met = None, rna =
    ↪None, up = None, dw = 1) %
```

```
54          prot(name = 'lacZ', loc = 'cyt', dna = None, prot = None, met = None, rna =␣
   ↪None, up = 1, dw = None),
55          Parameter('fwd_PhysicalInteractionRule_1', 1.000000),
56          Parameter('rvs_PhysicalInteractionRule_1', 0.000000))
57 Rule('PhysicalInteractionRule_2',
58          prot(name = 'lacZ', loc = 'cyt', dna = None, prot = None, met = None, rna =␣
   ↪None, up = None, dw = 1) %
59          prot(name = 'lacZ', loc = 'cyt', dna = None, prot = None, met = None, rna =␣
   ↪None, up = 1, dw = None) +
60          prot(name = 'lacZ', loc = 'cyt', dna = None, prot = None, met = None, rna =␣
   ↪None, up = None, dw = 2) %
61          prot(name = 'lacZ', loc = 'cyt', dna = None, prot = None, met = None, rna =␣
   ↪None, up = 2, dw = None) |
62          prot(name = 'lacZ', loc = 'cyt', dna = None, prot = None, met = None, rna =␣
   ↪None, up = None, dw = 1) %
63          prot(name = 'lacZ', loc = 'cyt', dna = None, prot = None, met = None, rna =␣
   ↪None, up = 1, dw = 2) %
64          prot(name = 'lacZ', loc = 'cyt', dna = None, prot = None, met = None, rna =␣
   ↪None, up = 2, dw = 3) %
65          prot(name = 'lacZ', loc = 'cyt', dna = None, prot = None, met = None, rna =␣
   ↪None, up = 3, dw = None),
66          Parameter('fwd_PhysicalInteractionRule_2', 1.000000),
67          Parameter('rvs_PhysicalInteractionRule_2', 0.000000))
68 Rule('PhysicalInteractionRule_3',
69          prot(name = 'lacA', loc = 'cyt', dna = None, prot = None, met = None, rna =␣
   ↪None, up = None, dw = None) +
70          prot(name = 'lacA', loc = 'cyt', dna = None, prot = None, met = None, rna =␣
   ↪None, up = None, dw = None) |
71          prot(name = 'lacA', loc = 'cyt', dna = None, prot = None, met = None, rna =␣
   ↪None, up = None, dw = 1) %
72          prot(name = 'lacA', loc = 'cyt', dna = None, prot = None, met = None, rna =␣
   ↪None, up = 1, dw = None),
73          Parameter('fwd_PhysicalInteractionRule_3', 1.000000),
74          Parameter('rvs_PhysicalInteractionRule_3', 0.000000))
75 Rule('PhysicalInteractionRule_4',
76          prot(name = 'lacA', loc = 'cyt', dna = None, prot = None, met = None, rna =␣
   ↪None, up = None, dw = None) +
77          prot(name = 'lacA', loc = 'cyt', dna = None, prot = None, met = None, rna =␣
   ↪None, up = None, dw = 1) %
78          prot(name = 'lacA', loc = 'cyt', dna = None, prot = None, met = None, rna =␣
   ↪None, up = 1, dw = None) |
79          prot(name = 'lacA', loc = 'cyt', dna = None, prot = None, met = None, rna =␣
   ↪None, up = None, dw = 1) %
80          prot(name = 'lacA', loc = 'cyt', dna = None, prot = None, met = None, rna =␣
   ↪None, up = 1, dw = 2) %
81          prot(name = 'lacA', loc = 'cyt', dna = None, prot = None, met = None, rna =␣
   ↪None, up = 2, dw = None),
82          Parameter('fwd_PhysicalInteractionRule_4', 1.000000),
83          Parameter('rvs_PhysicalInteractionRule_4', 0.000000))
84 Rule('PhysicalInteractionRule_5',
85          prot(name = 'lacI', loc = 'cyt', dna = None, prot = None, met = None, rna =␣
   ↪None, up = None, dw = None) +
86          prot(name = 'lacI', loc = 'cyt', dna = None, prot = None, met = None, rna =␣
   ↪None, up = None, dw = None) |
87          prot(name = 'lacI', loc = 'cyt', dna = None, prot = None, met = None, rna =␣
   ↪None, up = None, dw = 1) %
88          prot(name = 'lacI', loc = 'cyt', dna = None, prot = None, met = None, rna =␣
   ↪None, up = 1, dw = None),
```

```
89          Parameter('fwd_PhysicalInteractionRule_5', 1.000000),
90          Parameter('rvs_PhysicalInteractionRule_5', 0.000000))
```

3.3 Protein-Small compounds Interaction Networks

Protein-small compound interaction networks have five columns:

1. The 1st declares the `SOURCE` and the 2nd declares the `TARGET`.

   It does not matter the order, as the two columns defines a bimolecular reaction which product is the merge of all components into one complex. *Atlas* understand components inside brackets (e.g. `[lacZ, SMALL-alpha-ALLOLACTOSE]`) as a complex, therefore, the components are internally linked.

2. The 3rd and 4th columns declare the forward and the reverse reaction rates, respectively.

3. The 5th columns declares the location of the complex components:

   1. If the number of locations match the number of components of the complex, each location is mapped to the component.

   2. If the number of locations unmatch the number of components, the first location is used for every component

   3. If the number of locations is one, the location is used for every component.

   Valid names are: `cytosol, inner membrane, periplasmic space, membrane, outer membrane, extracellular space, bacterial nucleoid, cell wall, cell projection` and `cytoskeleton`

Example, and note the use of the prefix `SMALL-` to tell *Atlas* the component is a metabolite:

```
1  SOURCE          TARGET          FWD_RATE          RVS_RATE          LOCATION
2  [lacI,lacI]          SMALL-alpha-ALLOLACTOSE          10.0          0.0001          cytosol
3  [lacI,lacI,SMALL-alpha-ALLOLACTOSE]          SMALL-alpha-ALLOLACTOSE          10.
   ↪0          0.0001          cytosol
4  [lacI,lacI]          SMALL-beta-ALLOLACTOSE          10.0          0.0001          cytosol
5  [lacI,lacI,SMALL-beta-ALLOLACTOSE]          SMALL-beta-ALLOLACTOSE          10.0          0.
   ↪0001          cytosol
```

Finally, execute `atlas_rbm.construct_model_from_interaction_network(network, verbose = False)` to obtain the model.

Note: **Uniqueness of Rule names**. Atlas will write *Rules* with numbered names. Merge into one the networks (`pandas.concat(list)`) or use a single file to model interactions.

Note: Simulation. The model can be simulated only with the instantiation of `Initials`:

- `atlas_rbm.simulation.set_initial.cplx(model, complex_name, location, positive_number)`

- `atlas_rbm.simulation.set_initial.dna(model, dna_name, positive_number)`

- `atlas_rbm.simulation.set_initial.met(model, metabolite, location, positive_number)`

- atlas_rbm.simulation.set_initial.prot(model, prot_name, location, positive_number)

- atlas_rbm.simulation.set_initial.rna(model, rna_name, positive_number)

Note: Use the keyword argument `toFile = 'name.py'` to write the model to a file (the function will return `None`):

```python
from pysb import *
Model()

Monomer('met',
        ['name', 'loc', 'dna', 'met', 'prot', 'rna'],
        { 'name' : [ 'alpha_ALLOLACTOSE', 'beta_ALLOLACTOSE' ],
        'loc' : ['cyt', 'cytosk', 'ex', 'mem', 'per', 'wall', 'bnuc', 'cproj', 'imem',
 'omem']})
Monomer('prot',
        ['name', 'loc', 'dna', 'met', 'prot', 'rna', 'up', 'dw'],
        { 'name' : [ 'lacI' ],
        'loc' : ['cyt', 'cytosk', 'ex', 'mem', 'per', 'wall', 'bnuc', 'cproj', 'imem',
 'omem']})
Observable('obs_met_alpha_ALLOLACTOSE_cyt', met(name = 'alpha_ALLOLACTOSE', loc = 'cyt
'))
Initial(met(name = 'alpha_ALLOLACTOSE', loc = 'cyt', dna = None, met = None, prot =
None, rna = None), Parameter('t0_met_alpha_ALLOLACTOSE_cyt', 0))
Observable('obs_met_beta_ALLOLACTOSE_cyt', met(name = 'beta_ALLOLACTOSE', loc = 'cyt
'))
Initial(met(name = 'beta_ALLOLACTOSE', loc = 'cyt', dna = None, met = None, prot =
None, rna = None), Parameter('t0_met_beta_ALLOLACTOSE_cyt', 0))
Observable('obs_prot_lacI_cyt', prot(name = 'lacI', loc = 'cyt', dna = None, met =
None, prot = None, rna = None, up = None, dw = None))
Initial(prot(name = 'lacI', loc = 'cyt', dna = None, met = None, prot = None, rna =
None, up = None, dw = None), Parameter('t0_prot_lacI_cyt', 0))
Initial(prot(name = 'lacI', loc = 'cyt', dna = None, met = 2, prot = None, rna = None,
 up = None, dw = 1) %
        prot(name = 'lacI', loc = 'cyt', dna = None, met = 3, prot = None, rna = None,
 up = 1, dw = None) %
        met(name = 'alpha_ALLOLACTOSE', loc = 'cyt', dna = None, met = None, prot = 3,
 rna = None) %
        met(name = 'alpha_ALLOLACTOSE', loc = 'cyt', dna = None, met = None, prot = 2,
 rna = None),
        Parameter('t0_cplx_lacIx2_alpha_ALLOLACTOSEx2_cyt', 0))
Observable('obs_cplx_lacIx2_alpha_ALLOLACTOSEx2_cyt',
        prot(name = 'lacI', loc = 'cyt', dna = None, met = 2, prot = None, rna = None,
 up = None, dw = 1) %
        prot(name = 'lacI', loc = 'cyt', dna = None, met = 3, prot = None, rna = None,
 up = 1, dw = None) %
        met(name = 'alpha_ALLOLACTOSE', loc = 'cyt', dna = None, met = None, prot = 3,
 rna = None) %
        met(name = 'alpha_ALLOLACTOSE', loc = 'cyt', dna = None, met = None, prot = 2,
 rna = None))
Initial(prot(name = 'lacI', loc = 'cyt', dna = None, met = 2, prot = None, rna = None,
 up = None, dw = 1) %
        prot(name = 'lacI', loc = 'cyt', dna = None, met = None, prot = None, rna =
None, up = 1, dw = None) %
        met(name = 'alpha_ALLOLACTOSE', loc = 'cyt', dna = None, met = None, prot = 2,
 rna = None),
```

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3.3. Protein-Small compounds Interaction Networks

```
31          Parameter('t0_cplx_lacIx2_alpha_ALLOLACTOSEx1_cyt', 0))
32  Observable('obs_cplx_lacIx2_alpha_ALLOLACTOSEx1_cyt',
33          prot(name = 'lacI', loc = 'cyt', dna = None, met = 2, prot = None, rna = None,
    ↪ up = None, dw = 1) %
34          prot(name = 'lacI', loc = 'cyt', dna = None, met = None, prot = None, rna =
    ↪None, up = 1, dw = None) %
35          met(name = 'alpha_ALLOLACTOSE', loc = 'cyt', dna = None, met = None, prot = 2,
    ↪ rna = None))
36  Initial(prot(name = 'lacI', loc = 'cyt', dna = None, met = 2, prot = None, rna = None,
    ↪ up = None, dw = 1) %
37          prot(name = 'lacI', loc = 'cyt', dna = None, met = 3, prot = None, rna = None,
    ↪ up = 1, dw = None) %
38          met(name = 'beta_ALLOLACTOSE', loc = 'cyt', dna = None, met = None, prot = 3,
    ↪rna = None) %
39          met(name = 'beta_ALLOLACTOSE', loc = 'cyt', dna = None, met = None, prot = 2,
    ↪rna = None),
40          Parameter('t0_cplx_lacIx2_beta_ALLOLACTOSEx2_cyt', 0))
41  Observable('obs_cplx_lacIx2_beta_ALLOLACTOSEx2_cyt',
42          prot(name = 'lacI', loc = 'cyt', dna = None, met = 2, prot = None, rna = None,
    ↪ up = None, dw = 1) %
43          prot(name = 'lacI', loc = 'cyt', dna = None, met = 3, prot = None, rna = None,
    ↪ up = 1, dw = None) %
44          met(name = 'beta_ALLOLACTOSE', loc = 'cyt', dna = None, met = None, prot = 3,
    ↪rna = None) %
45          met(name = 'beta_ALLOLACTOSE', loc = 'cyt', dna = None, met = None, prot = 2,
    ↪rna = None))
46  Initial(prot(name = 'lacI', loc = 'cyt', dna = None, met = 2, prot = None, rna = None,
    ↪ up = None, dw = 1) %
47          prot(name = 'lacI', loc = 'cyt', dna = None, met = None, prot = None, rna =
    ↪None, up = 1, dw = None) %
48          met(name = 'beta_ALLOLACTOSE', loc = 'cyt', dna = None, met = None, prot = 2,
    ↪rna = None),
49          Parameter('t0_cplx_lacIx2_beta_ALLOLACTOSEx1_cyt', 0))
50  Observable('obs_cplx_lacIx2_beta_ALLOLACTOSEx1_cyt',
51          prot(name = 'lacI', loc = 'cyt', dna = None, met = 2, prot = None, rna = None,
    ↪ up = None, dw = 1) %
52          prot(name = 'lacI', loc = 'cyt', dna = None, met = None, prot = None, rna =
    ↪None, up = 1, dw = None) %
53          met(name = 'beta_ALLOLACTOSE', loc = 'cyt', dna = None, met = None, prot = 2,
    ↪rna = None))
54  Rule('PhysicalInteractionRule_1',
55          prot(name = 'lacI', loc = 'cyt', dna = None, prot = None, met = None, rna =
    ↪None, up = None, dw = 1) %
56          prot(name = 'lacI', loc = 'cyt', dna = None, prot = None, met = None, rna =
    ↪None, up = 1, dw = None) +
57          met(name = 'alpha_ALLOLACTOSE', loc = 'cyt', dna = None, prot = None, met =
    ↪None, rna = None) |
58          prot(name = 'lacI', loc = 'cyt', dna = None, prot = None, met = 2, rna = None,
    ↪ up = None, dw = 1) %
59          prot(name = 'lacI', loc = 'cyt', dna = None, prot = None, met = None, rna =
    ↪None, up = 1, dw = None) %
60          met(name = 'alpha_ALLOLACTOSE', loc = 'cyt', dna = None, prot = 2, met = None,
    ↪ rna = None),
61          Parameter('fwd_PhysicalInteractionRule_1', 10.000000),
62          Parameter('rvs_PhysicalInteractionRule_1', 0.000100))
63  Rule('PhysicalInteractionRule_2',
64          prot(name = 'lacI', loc = 'cyt', dna = None, prot = None, met = 2, rna = None,
    ↪ up = None, dw = 1) %
```

```
65          prot(name = 'lacI', loc = 'cyt', dna = None, prot = None, met = None, rna =
    ↪None, up = 1, dw = None) %
66          met(name = 'alpha_ALLOLACTOSE', loc = 'cyt', dna = None, prot = 2, met = None,
    ↪ rna = None) +
67          met(name = 'alpha_ALLOLACTOSE', loc = 'cyt', dna = None, prot = None, met =
    ↪None, rna = None) |
68          prot(name = 'lacI', loc = 'cyt', dna = None, prot = None, met = 2, rna = None,
    ↪ up = None, dw = 1) %
69          prot(name = 'lacI', loc = 'cyt', dna = None, prot = None, met = 3, rna = None,
    ↪ up = 1, dw = None) %
70          met(name = 'alpha_ALLOLACTOSE', loc = 'cyt', dna = None, prot = 3, met = None,
    ↪ rna = None) %
71          met(name = 'alpha_ALLOLACTOSE', loc = 'cyt', dna = None, prot = 2, met = None,
    ↪ rna = None),
72          Parameter('fwd_PhysicalInteractionRule_2', 10.000000),
73          Parameter('rvs_PhysicalInteractionRule_2', 0.000100))
74 Rule('PhysicalInteractionRule_3',
75          prot(name = 'lacI', loc = 'cyt', dna = None, prot = None, met = None, rna =
    ↪None, up = None, dw = 1) %
76          prot(name = 'lacI', loc = 'cyt', dna = None, prot = None, met = None, rna =
    ↪None, up = 1, dw = None) +
77          met(name = 'beta_ALLOLACTOSE', loc = 'cyt', dna = None, prot = None, met =
    ↪None, rna = None) |
78          prot(name = 'lacI', loc = 'cyt', dna = None, prot = None, met = 2, rna = None,
    ↪ up = None, dw = 1) %
79          prot(name = 'lacI', loc = 'cyt', dna = None, prot = None, met = None, rna =
    ↪None, up = 1, dw = None) %
80          met(name = 'beta_ALLOLACTOSE', loc = 'cyt', dna = None, prot = 2, met = None,
    ↪rna = None),
81          Parameter('fwd_PhysicalInteractionRule_3', 10.000000),
82          Parameter('rvs_PhysicalInteractionRule_3', 0.000100))
83 Rule('PhysicalInteractionRule_4',
84          prot(name = 'lacI', loc = 'cyt', dna = None, prot = None, met = 2, rna = None,
    ↪ up = None, dw = 1) %
85          prot(name = 'lacI', loc = 'cyt', dna = None, prot = None, met = None, rna =
    ↪None, up = 1, dw = None) %
86          met(name = 'beta_ALLOLACTOSE', loc = 'cyt', dna = None, prot = 2, met = None,
    ↪rna = None) +
87          met(name = 'beta_ALLOLACTOSE', loc = 'cyt', dna = None, prot = None, met =
    ↪None, rna = None) |
88          prot(name = 'lacI', loc = 'cyt', dna = None, prot = None, met = 2, rna = None,
    ↪ up = None, dw = 1) %
89          prot(name = 'lacI', loc = 'cyt', dna = None, prot = None, met = 3, rna = None,
    ↪ up = 1, dw = None) %
90          met(name = 'beta_ALLOLACTOSE', loc = 'cyt', dna = None, prot = 3, met = None,
    ↪rna = None) %
91          met(name = 'beta_ALLOLACTOSE', loc = 'cyt', dna = None, prot = 2, met = None,
    ↪rna = None),
92          Parameter('fwd_PhysicalInteractionRule_4', 10.000000),
93          Parameter('rvs_PhysicalInteractionRule_4', 0.000100))
```

3.4 Transcription Factor-DNA Binding Site Interaction Networks

The transcription factor-DNA binding site network represents the physical interaction bewteen proteins and DNA. The network have five columns:

1. The 1st declares the `SOURCE` and the 2nd declares the `TARGET`.

   It does not matter the order, as the two columns defines a bimolecular reaction which product is the merge of all components into one complex. *Atlas* understand components inside brackets (e.g. `[lacI,lacI]`) as a complex, therefore, the components are internally linked.

2. The 3rd and 4th columns declare the forward and the reverse reaction rates, respectively.

3. The 5th columns declares the location of the complex components:

   1. If the number of locations match the number of components of the complex, each location is mapped to the component.

   2. If the number of locations unmatch the number of components, the first location is used for every component

   3. If the number of locations is one, the location is used for every component.

   Valid name is: `cytosol`.

Example, and note the use of the prefix `BS-` to tell *Atlas* the component is a DNA binding site followed by a name and two coordinates:

```
1  SOURCE          TARGET          FWD_RATE        RVS_RATE        LOCATION
2  # lacZYA
3  [lacI,lacI]         BS-lacI-422-402       1.0         0.01         cytosol
4  [lacI,lacI]         BS-lacI-21-1      1.0       0.01        cytosol
5  [lacI,lacI]         BS-lacI-72-92       1.0         0.01         cytosol
```

Finally, execute `atlas_rbm.construct_model_from_interaction_network(network, verbose = False)` to obtain the model.

Note: **Uniqueness of Rule names**. Atlas will write *Rules* with numbered names. Merge into one the networks (`pandas.concat(list)`) or use a single file to model interactions.

Note: Simulation. The model can be simulated only with the instantiation of `Initials`:

- `atlas_rbm.simulation.set_initial.cplx(model, complex_name, location, positive_number)`

- `atlas_rbm.simulation.set_initial.dna(model, dna_name, positive_number)`

- `atlas_rbm.simulation.set_initial.met(model, metabolite, location, positive_number)`

- `atlas_rbm.simulation.set_initial.prot(model, prot_name, location, positive_number)`

- `atlas_rbm.simulation.set_initial.rna(model, rna_name, positive_number)`

Note: Use the keyword argument `toFile = 'name.py'` to write the model to a file (the function will return `None`):

```python
from pysb import *
Model()

Monomer('prot',
        ['name', 'loc', 'dna', 'met', 'prot', 'rna', 'up', 'dw'],
        { 'name' : [ 'lacI' ],
        'loc' : ['cyt', 'cytosk', 'ex', 'mem', 'per', 'wall', 'bnuc', 'cproj', 'imem',
→ 'omem']})
Monomer('dna',
        ['name', 'type', 'loc', 'dna', 'met', 'prot', 'rna', 'up', 'dw'],
        { 'name' : [ 'lacI_21_1', 'lacI_422_402', 'lacI_72_92' ],
        'type' : ['BS'],
        'loc' : ['cyt']})
Observable('obs_prot_lacI_cyt', prot(name = 'lacI', loc = 'cyt', dna = None, met =
→None, prot = None, rna = None, up = None, dw = None))
Initial(prot(name = 'lacI', loc = 'cyt', dna = None, met = None, prot = None, rna =
→None, up = None, dw = None), Parameter('t0_prot_lacI_cyt', 0))
Rule('PhysicalInteractionRule_1',
        prot(name = 'lacI', loc = 'cyt', dna = None, prot = None, met = None, rna =
→None, up = None, dw = 1) %
        prot(name = 'lacI', loc = 'cyt', dna = None, prot = None, met = None, rna =
→None, up = 1, dw = None) +
        dna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, prot = None,
→met = None, rna = None, up = WILD, dw = WILD) |
        prot(name = 'lacI', loc = 'cyt', dna = None, prot = None, met = None, rna =
→None, up = None, dw = 1) %
        prot(name = 'lacI', loc = 'cyt', dna = 2, prot = None, met = None, rna = None,
→ up = 1, dw = None) %
        dna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, prot = 2,
→met = None, rna = None, up = WILD, dw = WILD),
        Parameter('fwd_PhysicalInteractionRule_1', 1.000000),
        Parameter('rvs_PhysicalInteractionRule_1', 0.010000))
Rule('PhysicalInteractionRule_2',
        prot(name = 'lacI', loc = 'cyt', dna = None, prot = None, met = None, rna =
→None, up = None, dw = 1) %
        prot(name = 'lacI', loc = 'cyt', dna = None, prot = None, met = None, rna =
→None, up = 1, dw = None) +
        dna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', dna = None, prot = None,
→met = None, rna = None, up = WILD, dw = WILD) |
        prot(name = 'lacI', loc = 'cyt', dna = None, prot = None, met = None, rna =
→None, up = None, dw = 1) %
        prot(name = 'lacI', loc = 'cyt', dna = 2, prot = None, met = None, rna = None,
→ up = 1, dw = None) %
        dna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', dna = None, prot = 2, met =
→None, rna = None, up = WILD, dw = WILD),
        Parameter('fwd_PhysicalInteractionRule_2', 1.000000),
        Parameter('rvs_PhysicalInteractionRule_2', 0.010000))
Rule('PhysicalInteractionRule_3',
        prot(name = 'lacI', loc = 'cyt', dna = None, prot = None, met = None, rna =
→None, up = None, dw = 1) %
        prot(name = 'lacI', loc = 'cyt', dna = None, prot = None, met = None, rna =
→None, up = 1, dw = None) +
        dna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', dna = None, prot = None,
→met = None, rna = None, up = WILD, dw = WILD) |
        prot(name = 'lacI', loc = 'cyt', dna = None, prot = None, met = None, rna =
→None, up = None, dw = 1) %
        prot(name = 'lacI', loc = 'cyt', dna = 2, prot = None, met = None, rna = None,
→ up = 1, dw = None) %
```

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3.4. Transcription Factor-DNA Binding Site Interaction Networks

```
39          dna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', dna = None, prot = 2, met
   ↪= None, rna = None, up = WILD, dw = WILD),
40          Parameter('fwd_PhysicalInteractionRule_3', 1.000000),
41          Parameter('rvs_PhysicalInteractionRule_3', 0.010000))
```

3.5 Sigma Factor-Promoter Interaction Networks

The Sigma Factor-Promoter network have five columns:

1. The 1st declares the SOURCE and the 2nd declares the TARGET.

   It does not matter the order, as the two columns defines a bimolecular reaction which product is the merge of all components into one complex. *Atlas* understand components inside brackets (e.g. [rpoA, rpoA, rpoB, rpoC, rpoD]) as a complex, therefore, the components are internally linked.

2. The 3rd, 4th, and 5th columns declare rates:

   - The FWD_DOCK_RATE and the RVS_DOCK_RATE define the rates of the binding of the RNAP to the promoter and its separation, respectively.

   - The FWD_SLIDE_RATE defines the rate of the transition from the promoter to the following DNA feature declared in the genome graph.

   Note the name of the promoter: name of the gene followed by pro and a number.

Examples:

```
1  SOURCE            TARGET         FWD_DOCK_RATE        RVS_DOCK_RATE          FWD_SLIDE_RATE
2  #Docking to promoters
3  [rpoA,rpoA,rpoB,rpoC,rpoD]        lacZ-pro4         1.0        1.0          1.0
4  [rpoA,rpoA,rpoB,rpoC,rpoD]        lacZ-pro3         1.0        1.0          1.0
5  [rpoA,rpoA,rpoB,rpoC,rpoD]        lacZ-pro2         1.0        1.0          1.0
6  [rpoA,rpoA,rpoB,rpoC,rpoD]        lacZ-pro1         1.0        1.0          1.0
7  [rpoA,rpoA,rpoB,rpoC,rpoD]        lacY-pro1         1.0        1.0          1.0
```

Finally, execute atlas_rbm.construct_model_from_sigma_specificity_network(interaction_network, genome_graph, verbose = False) to obtain the model.

Note: **Simulation**. The model can be simulated only with the instantiation of Initials:

- atlas_rbm.simulation.set_initial.cplx(model, complex_name, location, positive_number)

- atlas_rbm.simulation.set_initial.dna(model, dna_name, positive_number)

- atlas_rbm.simulation.set_initial.met(model, metabolite, location, positive_number)

- atlas_rbm.simulation.set_initial.prot(model, prot_name, location, positive_number)

- atlas_rbm.simulation.set_initial.rna(model, rna_name, positive_number)

Note: Use the keyword argument toFile = 'name.py' to write the model to a file (the function will return None):

```python
from pysb import *
Model()


Monomer('dna',
        ['name', 'type', 'loc', 'dna', 'met', 'prot', 'rna', 'up', 'dw'],
        { 'name' : ['lacA', 'lacI_21_1', 'lacI_422_402', 'lacI_72_92', 'lacY', 'lacZ
↪'],
        'type' : ['BS', 'cds', 'pro1', 'pro2', 'pro3', 'pro4', 'rbs', 'ter1', 'ter2'],
        'loc' : ['cyt']})
Monomer('rna',
        ['name', 'type', 'loc', 'dna', 'met', 'prot', 'rna', 'up', 'dw'],
        { 'name' : ['lacA', 'lacI_21_1', 'lacI_422_402', 'lacI_72_92', 'lacY', 'lacZ
↪'],
        'type' : ['BS', 'cds', 'pro1', 'pro2', 'pro3', 'pro4', 'rbs', 'ter1', 'ter2'],
        'loc' : ['cyt']})
Monomer('prot',
        ['name', 'loc', 'dna', 'met', 'prot', 'rna', 'up', 'dw'],
        { 'name' : ['lacA', 'lacI_21_1', 'lacI_422_402', 'lacI_72_92', 'lacY', 'lacZ
↪'],
        'loc' : ['cyt', 'mem']})
Monomer('cplx',
        ['name', 'loc', 'dna', 'met', 'prot', 'rna'],
        { 'name' : ['RIBOSOME_CPLX'],
        'loc' : ['cyt']})
Rule('docking_1_lacZ_pro4',
        prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
        prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
        prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
        prot(name = 'rpoC', loc = 'cyt', dna = None, met = None, up = 3, dw = 4) %
        prot(name = 'rpoD', loc = 'cyt', dna = None, met = None, up = 4, dw = None) +
        dna(name = 'lacZ', type = 'pro4', loc = 'cyt', prot = None, up = WILD, dw =
↪WILD) |
        prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
        prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
        prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
        prot(name = 'rpoC', loc = 'cyt', dna = None, met = None, up = 3, dw = 4) %
        prot(name = 'rpoD', loc = 'cyt', dna = 5, met = None, up = 4, dw = None) %
        dna(name = 'lacZ', type = 'pro4', loc = 'cyt', prot = 5, up = WILD, dw =
↪WILD),
        Parameter('fwd_docking_1_lacZ_pro4', 1.000000),
        Parameter('rvs_docking_1_lacZ_pro4', 1.000000))
Rule('docking_2_lacZ_pro3',
        prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
        prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
        prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
        prot(name = 'rpoC', loc = 'cyt', dna = None, met = None, up = 3, dw = 4) %
        prot(name = 'rpoD', loc = 'cyt', dna = None, met = None, up = 4, dw = None) +
        dna(name = 'lacZ', type = 'pro3', loc = 'cyt', prot = None, up = WILD, dw =
↪WILD) |
        prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
        prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
        prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
        prot(name = 'rpoC', loc = 'cyt', dna = None, met = None, up = 3, dw = 4) %
        prot(name = 'rpoD', loc = 'cyt', dna = 5, met = None, up = 4, dw = None) %
        dna(name = 'lacZ', type = 'pro3', loc = 'cyt', prot = 5, up = WILD, dw =
↪WILD),
        Parameter('fwd_docking_2_lacZ_pro3', 1.000000),
```

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3.5. Sigma Factor-Promoter Interaction Networks

```
51          Parameter('rvs_docking_2_lacZ_pro3', 1.000000))
52   Rule('docking_3_lacZ_pro2',
53          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
54          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
55          prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
56          prot(name = 'rpoC', loc = 'cyt', dna = None, met = None, up = 3, dw = 4) %
57          prot(name = 'rpoD', loc = 'cyt', dna = None, met = None, up = 4, dw = None) +
58          dna(name = 'lacZ', type = 'pro2', loc = 'cyt', prot = None, up = WILD, dw =␣
     ↪WILD) |
59          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
60          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
61          prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
62          prot(name = 'rpoC', loc = 'cyt', dna = None, met = None, up = 3, dw = 4) %
63          prot(name = 'rpoD', loc = 'cyt', dna = 5, met = None, up = 4, dw = None) %
64          dna(name = 'lacZ', type = 'pro2', loc = 'cyt', prot = 5, up = WILD, dw =␣
     ↪WILD),
65          Parameter('fwd_docking_3_lacZ_pro2', 1.000000),
66          Parameter('rvs_docking_3_lacZ_pro2', 1.000000))
67   Rule('docking_4_lacZ_pro1',
68          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
69          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
70          prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
71          prot(name = 'rpoC', loc = 'cyt', dna = None, met = None, up = 3, dw = 4) %
72          prot(name = 'rpoD', loc = 'cyt', dna = None, met = None, up = 4, dw = None) +
73          dna(name = 'lacZ', type = 'pro1', loc = 'cyt', prot = None, up = WILD, dw =␣
     ↪WILD) |
74          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
75          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
76          prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
77          prot(name = 'rpoC', loc = 'cyt', dna = None, met = None, up = 3, dw = 4) %
78          prot(name = 'rpoD', loc = 'cyt', dna = 5, met = None, up = 4, dw = None) %
79          dna(name = 'lacZ', type = 'pro1', loc = 'cyt', prot = 5, up = WILD, dw =␣
     ↪WILD),
80          Parameter('fwd_docking_4_lacZ_pro1', 1.000000),
81          Parameter('rvs_docking_4_lacZ_pro1', 1.000000))
82   Rule('docking_5_lacY_pro1',
83          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
84          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
85          prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
86          prot(name = 'rpoC', loc = 'cyt', dna = None, met = None, up = 3, dw = 4) %
87          prot(name = 'rpoD', loc = 'cyt', dna = None, met = None, up = 4, dw = None) +
88          dna(name = 'lacY', type = 'pro1', loc = 'cyt', prot = None, up = WILD, dw =␣
     ↪WILD) |
89          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
90          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
91          prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
92          prot(name = 'rpoC', loc = 'cyt', dna = None, met = None, up = 3, dw = 4) %
93          prot(name = 'rpoD', loc = 'cyt', dna = 5, met = None, up = 4, dw = None) %
94          dna(name = 'lacY', type = 'pro1', loc = 'cyt', prot = 5, up = WILD, dw =␣
     ↪WILD),
95          Parameter('fwd_docking_5_lacY_pro1', 1.000000),
96          Parameter('rvs_docking_5_lacY_pro1', 1.000000))
97   Rule('sliding_1_lacZ_pro4_pro3_holoenzyme',
98          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
99          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
100         prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
101         prot(name = 'rpoC', loc = 'cyt', dna = None, met = None, up = 3, dw = 4) %
```

```
102        prot(name = 'rpoD', loc = 'cyt', dna = 5, met = None, up = 4, dw = None) %
103        dna(name = 'lacZ', type = 'pro4', loc = 'cyt', prot = 5, up = WILD, dw =
     ↪WILD) +
104        dna(name = 'lacZ', type = 'pro3', loc = 'cyt', prot = None, up = WILD, dw =
     ↪WILD) +
105        None >>
106        prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
107        prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
108        prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
109        prot(name = 'rpoC', loc = 'cyt', dna = 4, met = None, up = 3, dw = None) %
110        prot(name = 'rpoD', loc = 'cyt', dna = None, met = None, up = None, dw =
     ↪None) %
111        dna(name = 'lacZ', type = 'pro3', loc = 'cyt', prot = 4, up = WILD, dw =
     ↪WILD) +
112        dna(name = 'lacZ', type = 'pro4', loc = 'cyt', prot = None, up = WILD, dw =
     ↪WILD) +
113        rna(name = 'lacZ', type = 'pro3', loc = 'cyt', dna = None, met = None, prot =
     ↪None, rna = None, up = None, dw = None),
114    Parameter('fwd_sliding_1_lacZ_pro4_pro3_holoenzyme', 1.000000))
115 Rule('sliding_2_lacZ_pro3_pro2_holoenzyme',
116        prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
117        prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
118        prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
119        prot(name = 'rpoC', loc = 'cyt', dna = None, met = None, up = 3, dw = 4) %
120        prot(name = 'rpoD', loc = 'cyt', dna = 5, met = None, up = 4, dw = None) %
121        dna(name = 'lacZ', type = 'pro3', loc = 'cyt', prot = 5, up = WILD, dw =
     ↪WILD) +
122        dna(name = 'lacZ', type = 'pro2', loc = 'cyt', prot = None, up = WILD, dw =
     ↪WILD) +
123        None >>
124        prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
125        prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
126        prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
127        prot(name = 'rpoC', loc = 'cyt', dna = 4, met = None, up = 3, dw = None) %
128        prot(name = 'rpoD', loc = 'cyt', dna = None, met = None, up = None, dw =
     ↪None) %
129        dna(name = 'lacZ', type = 'pro2', loc = 'cyt', prot = 4, up = WILD, dw =
     ↪WILD) +
130        dna(name = 'lacZ', type = 'pro3', loc = 'cyt', prot = None, up = WILD, dw =
     ↪WILD) +
131        rna(name = 'lacZ', type = 'pro2', loc = 'cyt', dna = None, met = None, prot =
     ↪None, rna = None, up = None, dw = None),
132    Parameter('fwd_sliding_2_lacZ_pro3_pro2_holoenzyme', 1.000000))
133 Rule('sliding_3_lacZ_pro2_92_holoenzyme',
134        prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
135        prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
136        prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
137        prot(name = 'rpoC', loc = 'cyt', dna = None, met = None, up = 3, dw = 4) %
138        prot(name = 'rpoD', loc = 'cyt', dna = 5, met = None, up = 4, dw = None) %
139        dna(name = 'lacZ', type = 'pro2', loc = 'cyt', prot = 5, up = WILD, dw =
     ↪WILD) +
140        dna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', prot = None, up = WILD, dw
     ↪= WILD) +
141        None >>
142        prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
143        prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
144        prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
```

3.5. Sigma Factor-Promoter Interaction Networks

```
145            prot(name = 'rpoC', loc = 'cyt', dna = 4, met = None, up = 3, dw = None) %
146            prot(name = 'rpoD', loc = 'cyt', dna = None, met = None, up = None, dw =
      →None) %
147            dna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', prot = 4, up = WILD, dw =
      →WILD) +
148            dna(name = 'lacZ', type = 'pro2', loc = 'cyt', prot = None, up = WILD, dw =
      →WILD) +
149            rna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', dna = None, met = None,
      →prot = None, rna = None, up = None, dw = None),
150            Parameter('fwd_sliding_3_lacZ_pro2_92_holoenzyme', 1.000000))
151   Rule('sliding_4_lacZ_pro1_rbs_holoenzyme',
152            prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
153            prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
154            prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
155            prot(name = 'rpoC', loc = 'cyt', dna = None, met = None, up = 3, dw = 4) %
156            prot(name = 'rpoD', loc = 'cyt', dna = 5, met = None, up = 4, dw = None) %
157            dna(name = 'lacZ', type = 'pro1', loc = 'cyt', prot = 5, up = WILD, dw =
      →WILD) +
158            dna(name = 'lacZ', type = 'rbs', loc = 'cyt', prot = None, up = WILD, dw =
      →WILD) +
159            None >>
160            prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
161            prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
162            prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
163            prot(name = 'rpoC', loc = 'cyt', dna = 4, met = None, up = 3, dw = None) %
164            prot(name = 'rpoD', loc = 'cyt', dna = None, met = None, up = None, dw =
      →None) %
165            dna(name = 'lacZ', type = 'rbs', loc = 'cyt', prot = 4, up = WILD, dw = WILD)
      →+
166            dna(name = 'lacZ', type = 'pro1', loc = 'cyt', prot = None, up = WILD, dw =
      →WILD) +
167            rna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
      →None, rna = None, up = None, dw = None),
168            Parameter('fwd_sliding_4_lacZ_pro1_rbs_holoenzyme', 1.000000))
169   Rule('sliding_5_lacY_pro1_rbs_holoenzyme',
170            prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
171            prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
172            prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
173            prot(name = 'rpoC', loc = 'cyt', dna = None, met = None, up = 3, dw = 4) %
174            prot(name = 'rpoD', loc = 'cyt', dna = 5, met = None, up = 4, dw = None) %
175            dna(name = 'lacY', type = 'pro1', loc = 'cyt', prot = 5, up = WILD, dw =
      →WILD) +
176            dna(name = 'lacY', type = 'rbs', loc = 'cyt', prot = None, up = WILD, dw =
      →WILD) +
177            None >>
178            prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
179            prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
180            prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
181            prot(name = 'rpoC', loc = 'cyt', dna = 4, met = None, up = 3, dw = None) %
182            prot(name = 'rpoD', loc = 'cyt', dna = None, met = None, up = None, dw =
      →None) %
183            dna(name = 'lacY', type = 'rbs', loc = 'cyt', prot = 4, up = WILD, dw = WILD)
      →+
184            dna(name = 'lacY', type = 'pro1', loc = 'cyt', prot = None, up = WILD, dw =
      →WILD) +
185            rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
      →None, rna = None, up = None, dw = None),
```

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186          Parameter('fwd_sliding_5_lacY_pro1_rbs_holoenzyme', 1.000000))
187  Rule('sliding_1_lacZ_pro3_to_lacZ_pro2',
188          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
189          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
190          prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
191          prot(name = 'rpoC', loc = 'cyt', dna = 4, met = None, up = 3, dw = None) %
192          dna(name = 'lacZ', type = 'pro3', loc = 'cyt', prot = 4, up = WILD, dw =
     ↪WILD) +
193          dna(name = 'lacZ', type = 'pro2', loc = 'cyt', prot = None, up = WILD, dw =
     ↪WILD) +
194          None >>
195          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
196          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
197          prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
198          prot(name = 'rpoC', loc = 'cyt', dna = 4, met = None, up = 3, dw = None) %
199          dna(name = 'lacZ', type = 'pro2', loc = 'cyt', prot = 4, up = WILD, dw =
     ↪WILD) +
200          dna(name = 'lacZ', type = 'pro3', loc = 'cyt', prot = None, up = WILD, dw =
     ↪WILD) +
201          rna(name = 'lacZ', type = 'pro2', loc = 'cyt', dna = None, met = None, prot =
     ↪None, rna = None, up = None, dw = None),
202          Parameter('fwd_sliding_1_lacZ_pro3_to_lacZ_pro2', 1.000000))
203  Rule('sliding_2_lacZ_pro2_to_BS_lacI_72_92',
204          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
205          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
206          prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
207          prot(name = 'rpoC', loc = 'cyt', dna = 4, met = None, up = 3, dw = None) %
208          dna(name = 'lacZ', type = 'pro2', loc = 'cyt', prot = 4, up = WILD, dw =
     ↪WILD) +
209          dna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', prot = None, up = WILD, dw
     ↪= WILD) +
210          None >>
211          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
212          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
213          prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
214          prot(name = 'rpoC', loc = 'cyt', dna = 4, met = None, up = 3, dw = None) %
215          dna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', prot = 4, up = WILD, dw =
     ↪WILD) +
216          dna(name = 'lacZ', type = 'pro2', loc = 'cyt', prot = None, up = WILD, dw =
     ↪WILD) +
217          rna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', dna = None, met = None,
     ↪prot = None, rna = None, up = None, dw = None),
218          Parameter('fwd_sliding_2_lacZ_pro2_to_BS_lacI_72_92', 1.000000))
219  Rule('sliding_3_BS_lacI_72_92_to_BS_lacI_21_1',
220          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
221          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
222          prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
223          prot(name = 'rpoC', loc = 'cyt', dna = 4, met = None, up = 3, dw = None) %
224          dna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', prot = 4, up = WILD, dw =
     ↪WILD) +
225          dna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', prot = None, up = WILD, dw
     ↪= WILD) +
226          None >>
227          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
228          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
229          prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
230          prot(name = 'rpoC', loc = 'cyt', dna = 4, met = None, up = 3, dw = None) %
```

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231            dna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', prot = 4, up = WILD, dw =
    ↪WILD) +
232            dna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', prot = None, up = WILD, dw
    ↪= WILD) +
233            rna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', dna = None, met = None,
    ↪prot = None, rna = None, up = None, dw = None),
234            Parameter('fwd_sliding_3_BS_lacI_72_92_to_BS_lacI_21_1', 1.000000))
235   Rule('sliding_4_BS_lacI_21_1_to_lacZ_pro1',
236            prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
237            prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
238            prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
239            prot(name = 'rpoC', loc = 'cyt', dna = 4, met = None, up = 3, dw = None) %
240            dna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', prot = 4, up = WILD, dw =
    ↪WILD) +
241            dna(name = 'lacZ', type = 'pro1', loc = 'cyt', prot = None, up = WILD, dw =
    ↪WILD) +
242            None >>
243            prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
244            prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
245            prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
246            prot(name = 'rpoC', loc = 'cyt', dna = 4, met = None, up = 3, dw = None) %
247            dna(name = 'lacZ', type = 'pro1', loc = 'cyt', prot = 4, up = WILD, dw =
    ↪WILD) +
248            dna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', prot = None, up = WILD, dw
    ↪= WILD) +
249            rna(name = 'lacZ', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = None, dw = None),
250            Parameter('fwd_sliding_4_BS_lacI_21_1_to_lacZ_pro1', 1.000000))
251   Rule('sliding_5_lacZ_pro1_to_lacZ_rbs',
252            prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
253            prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
254            prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
255            prot(name = 'rpoC', loc = 'cyt', dna = 4, met = None, up = 3, dw = None) %
256            dna(name = 'lacZ', type = 'pro1', loc = 'cyt', prot = 4, up = WILD, dw =
    ↪WILD) +
257            dna(name = 'lacZ', type = 'rbs', loc = 'cyt', prot = None, up = WILD, dw =
    ↪WILD) +
258            None >>
259            prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
260            prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
261            prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
262            prot(name = 'rpoC', loc = 'cyt', dna = 4, met = None, up = 3, dw = None) %
263            dna(name = 'lacZ', type = 'rbs', loc = 'cyt', prot = 4, up = WILD, dw = WILD)
    ↪+
264            dna(name = 'lacZ', type = 'pro1', loc = 'cyt', prot = None, up = WILD, dw =
    ↪WILD) +
265            rna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = None, dw = None),
266            Parameter('fwd_sliding_5_lacZ_pro1_to_lacZ_rbs', 1.000000))
267   Rule('sliding_6_lacZ_rbs_to_lacZ_cds',
268            prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
269            prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
270            prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
271            prot(name = 'rpoC', loc = 'cyt', dna = 4, met = None, up = 3, dw = None) %
272            dna(name = 'lacZ', type = 'rbs', loc = 'cyt', prot = 4, up = WILD, dw = WILD)
    ↪+
273            dna(name = 'lacZ', type = 'cds', loc = 'cyt', prot = None, up = WILD, dw =
    ↪WILD) +
```

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274          None >>
275          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
276          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
277          prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
278          prot(name = 'rpoC', loc = 'cyt', dna = 4, met = None, up = 3, dw = None) %
279          dna(name = 'lacZ', type = 'cds', loc = 'cyt', prot = 4, up = WILD, dw = WILD)␣
    ↪+
280          dna(name = 'lacZ', type = 'rbs', loc = 'cyt', prot = None, up = WILD, dw =␣
    ↪WILD) +
281          rna(name = 'lacZ', type = 'cds', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = None, dw = None),
282          Parameter('fwd_sliding_6_lacZ_rbs_to_lacZ_cds', 1.000000))
283  Rule('sliding_7_lacZ_cds_to_BS_lacI_422_402',
284          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
285          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
286          prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
287          prot(name = 'rpoC', loc = 'cyt', dna = 4, met = None, up = 3, dw = None) %
288          dna(name = 'lacZ', type = 'cds', loc = 'cyt', prot = 4, up = WILD, dw = WILD)␣
    ↪+
289          dna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', prot = None, up = WILD,␣
    ↪dw = WILD) +
290          None >>
291          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
292          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
293          prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
294          prot(name = 'rpoC', loc = 'cyt', dna = 4, met = None, up = 3, dw = None) %
295          dna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', prot = 4, up = WILD, dw␣
    ↪= WILD) +
296          dna(name = 'lacZ', type = 'cds', loc = 'cyt', prot = None, up = WILD, dw =␣
    ↪WILD) +
297          rna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, met = None,␣
    ↪prot = None, rna = None, up = None, dw = None),
298          Parameter('fwd_sliding_7_lacZ_cds_to_BS_lacI_422_402', 1.000000))
299  Rule('sliding_8_BS_lacI_422_402_to_lacY_pro1',
300          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
301          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
302          prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
303          prot(name = 'rpoC', loc = 'cyt', dna = 4, met = None, up = 3, dw = None) %
304          dna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', prot = 4, up = WILD, dw␣
    ↪= WILD) +
305          dna(name = 'lacY', type = 'pro1', loc = 'cyt', prot = None, up = WILD, dw =␣
    ↪WILD) +
306          None >>
307          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
308          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
309          prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
310          prot(name = 'rpoC', loc = 'cyt', dna = 4, met = None, up = 3, dw = None) %
311          dna(name = 'lacY', type = 'pro1', loc = 'cyt', prot = 4, up = WILD, dw =␣
    ↪WILD) +
312          dna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', prot = None, up = WILD,␣
    ↪dw = WILD) +
313          rna(name = 'lacY', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = None, dw = None),
314          Parameter('fwd_sliding_8_BS_lacI_422_402_to_lacY_pro1', 1.000000))
315  Rule('sliding_9_lacY_pro1_to_lacY_rbs',
316          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
317          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
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318        prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
319        prot(name = 'rpoC', loc = 'cyt', dna = 4, met = None, up = 3, dw = None) %
320        dna(name = 'lacY', type = 'pro1', loc = 'cyt', prot = 4, up = WILD, dw =
    ↪WILD) +
321        dna(name = 'lacY', type = 'rbs', loc = 'cyt', prot = None, up = WILD, dw =
    ↪WILD) +
322        None >>
323        prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
324        prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
325        prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
326        prot(name = 'rpoC', loc = 'cyt', dna = 4, met = None, up = 3, dw = None) %
327        dna(name = 'lacY', type = 'rbs', loc = 'cyt', prot = 4, up = WILD, dw = WILD)
    ↪+
328        dna(name = 'lacY', type = 'pro1', loc = 'cyt', prot = None, up = WILD, dw =
    ↪WILD) +
329        rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = None, dw = None),
330        Parameter('fwd_sliding_9_lacY_pro1_to_lacY_rbs', 1.000000))
331 Rule('sliding_10_lacY_rbs_to_lacY_cds',
332        prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
333        prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
334        prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
335        prot(name = 'rpoC', loc = 'cyt', dna = 4, met = None, up = 3, dw = None) %
336        dna(name = 'lacY', type = 'rbs', loc = 'cyt', prot = 4, up = WILD, dw = WILD)
    ↪+
337        dna(name = 'lacY', type = 'cds', loc = 'cyt', prot = None, up = WILD, dw =
    ↪WILD) +
338        None >>
339        prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
340        prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
341        prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
342        prot(name = 'rpoC', loc = 'cyt', dna = 4, met = None, up = 3, dw = None) %
343        dna(name = 'lacY', type = 'cds', loc = 'cyt', prot = 4, up = WILD, dw = WILD)
    ↪+
344        dna(name = 'lacY', type = 'rbs', loc = 'cyt', prot = None, up = WILD, dw =
    ↪WILD) +
345        rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = None, dw = None),
346        Parameter('fwd_sliding_10_lacY_rbs_to_lacY_cds', 1.000000))
347 Rule('sliding_11_lacY_cds_to_lacA_rbs',
348        prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
349        prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
350        prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
351        prot(name = 'rpoC', loc = 'cyt', dna = 4, met = None, up = 3, dw = None) %
352        dna(name = 'lacY', type = 'cds', loc = 'cyt', prot = 4, up = WILD, dw = WILD)
    ↪+
353        dna(name = 'lacA', type = 'rbs', loc = 'cyt', prot = None, up = WILD, dw =
    ↪WILD) +
354        None >>
355        prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
356        prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
357        prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
358        prot(name = 'rpoC', loc = 'cyt', dna = 4, met = None, up = 3, dw = None) %
359        dna(name = 'lacA', type = 'rbs', loc = 'cyt', prot = 4, up = WILD, dw = WILD)
    ↪+
360        dna(name = 'lacY', type = 'cds', loc = 'cyt', prot = None, up = WILD, dw =
    ↪WILD) +
```

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361          rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =␣
     →None, rna = None, up = None, dw = None),
362          Parameter('fwd_sliding_11_lacY_cds_to_lacA_rbs', 1.000000))
363 Rule('sliding_12_lacA_rbs_to_lacA_cds',
364          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
365          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
366          prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
367          prot(name = 'rpoC', loc = 'cyt', dna = 4, met = None, up = 3, dw = None) %
368          dna(name = 'lacA', type = 'rbs', loc = 'cyt', prot = 4, up = WILD, dw = WILD)␣
     →+
369          dna(name = 'lacA', type = 'cds', loc = 'cyt', prot = None, up = WILD, dw =␣
     →WILD) +
370          None >>
371          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
372          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
373          prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
374          prot(name = 'rpoC', loc = 'cyt', dna = 4, met = None, up = 3, dw = None) %
375          dna(name = 'lacA', type = 'cds', loc = 'cyt', prot = 4, up = WILD, dw = WILD)␣
     →+
376          dna(name = 'lacA', type = 'rbs', loc = 'cyt', prot = None, up = WILD, dw =␣
     →WILD) +
377          rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =␣
     →None, rna = None, up = None, dw = None),
378          Parameter('fwd_sliding_12_lacA_rbs_to_lacA_cds', 1.000000))
379 Rule('sliding_13_lacA_cds_to_lacA_ter1',
380          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
381          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
382          prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
383          prot(name = 'rpoC', loc = 'cyt', dna = 4, met = None, up = 3, dw = None) %
384          dna(name = 'lacA', type = 'cds', loc = 'cyt', prot = 4, up = WILD, dw = WILD)␣
     →+
385          dna(name = 'lacA', type = 'ter1', loc = 'cyt', prot = None, up = WILD, dw =␣
     →WILD) >>
386          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
387          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
388          prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
389          prot(name = 'rpoC', loc = 'cyt', dna = 4, met = None, up = 3, dw = None) %
390          dna(name = 'lacA', type = 'ter1', loc = 'cyt', prot = 4, up = WILD, dw =␣
     →WILD) +
391          dna(name = 'lacA', type = 'cds', loc = 'cyt', prot = None, up = WILD, dw =␣
     →WILD),
392          Parameter('fwd_sliding_13_lacA_cds_to_lacA_ter1', 1.000000))
393 Rule('sliding_14_lacA_ter1_to_lacA_ter2',
394          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
395          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
396          prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
397          prot(name = 'rpoC', loc = 'cyt', dna = 4, met = None, up = 3, dw = None) %
398          dna(name = 'lacA', type = 'ter1', loc = 'cyt', prot = 4, up = WILD, dw =␣
     →WILD) +
399          dna(name = 'lacA', type = 'ter2', loc = 'cyt', prot = None, up = WILD, dw =␣
     →WILD) >>
400          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
401          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
402          prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
403          prot(name = 'rpoC', loc = 'cyt', dna = 4, met = None, up = 3, dw = None) %
404          dna(name = 'lacA', type = 'ter2', loc = 'cyt', prot = 4, up = WILD, dw =␣
     →WILD) +
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405          dna(name = 'lacA', type = 'ter1', loc = 'cyt', prot = None, up = WILD, dw =␣
    ↪WILD),
406          Parameter('fwd_sliding_14_lacA_ter1_to_lacA_ter2', 1.000000))
407  Rule('falloff_from_lacA_ter1',
408          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
409          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
410          prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
411          prot(name = 'rpoC', loc = 'cyt', dna = 4, met = None, up = 3, dw = None) %
412          dna(name = 'lacA', type = 'ter1', loc = 'cyt', prot = 4, up = WILD, dw =␣
    ↪WILD) >>
413          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
414          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
415          prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
416          prot(name = 'rpoC', loc = 'cyt', dna = None, met = None, up = 3, dw = None) +
417          dna(name = 'lacA', type = 'ter1', loc = 'cyt', prot = None, up = WILD, dw =␣
    ↪WILD),
418          Parameter('fwd_falloff_from_lacA_ter1', 1.000000))
419  Rule('falloff_from_lacA_ter2',
420          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
421          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
422          prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
423          prot(name = 'rpoC', loc = 'cyt', dna = 4, met = None, up = 3, dw = None) %
424          dna(name = 'lacA', type = 'ter2', loc = 'cyt', prot = 4, up = WILD, dw =␣
    ↪WILD) >>
425          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = None, dw = 1) %
426          prot(name = 'rpoA', loc = 'cyt', dna = None, met = None, up = 1, dw = 2) %
427          prot(name = 'rpoB', loc = 'cyt', dna = None, met = None, up = 2, dw = 3) %
428          prot(name = 'rpoC', loc = 'cyt', dna = None, met = None, up = 3, dw = None) +
429          dna(name = 'lacA', type = 'ter2', loc = 'cyt', prot = None, up = WILD, dw =␣
    ↪WILD),
430          Parameter('fwd_falloff_from_lacA_ter2', 1.000000))
431  Rule('dr_lacZ_rbs',
432          cplx(name = 'RIBOSOME_CPLX', loc = 'cyt', rna = None) +
433          rna(name = 'lacZ', type = 'rbs', loc = 'cyt', prot = None) |
434          cplx(name = 'RIBOSOME_CPLX', loc = 'cyt', rna = 1) %
435          rna(name = 'lacZ', type = 'rbs', loc = 'cyt', prot = 1),
436          Parameter('fwd_dr_lacZ_rbs', 1.000000),
437          Parameter('rvs_dr_lacZ_rbs', 1.000000))
438  Rule('dr_lacY_rbs',
439          cplx(name = 'RIBOSOME_CPLX', loc = 'cyt', rna = None) +
440          rna(name = 'lacY', type = 'rbs', loc = 'cyt', prot = None) |
441          cplx(name = 'RIBOSOME_CPLX', loc = 'cyt', rna = 1) %
442          rna(name = 'lacY', type = 'rbs', loc = 'cyt', prot = 1),
443          Parameter('fwd_dr_lacY_rbs', 1.000000),
444          Parameter('rvs_dr_lacY_rbs', 1.000000))
445  Rule('dr_lacA_rbs',
446          cplx(name = 'RIBOSOME_CPLX', loc = 'cyt', rna = None) +
447          rna(name = 'lacA', type = 'rbs', loc = 'cyt', prot = None) |
448          cplx(name = 'RIBOSOME_CPLX', loc = 'cyt', rna = 1) %
449          rna(name = 'lacA', type = 'rbs', loc = 'cyt', prot = 1),
450          Parameter('fwd_dr_lacA_rbs', 1.000000),
451          Parameter('rvs_dr_lacA_rbs', 1.000000))
452  Rule('sr_lacZ_rbs',
453          cplx(name = 'RIBOSOME_CPLX', loc = 'cyt', rna = 1) %
454          rna(name = 'lacZ', type = 'rbs', loc = 'cyt', prot = 1) +
455          rna(name = 'lacZ', type = 'cds', loc = 'cyt', prot = None) +
456          None >>
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457          cplx(name = 'RIBOSOME_CPLX', loc = 'cyt', rna = 1) %
458          rna(name = 'lacZ', type = 'cds', loc = 'cyt', prot = 1) +
459          rna(name = 'lacZ', type = 'rbs', loc = 'cyt', prot = None) +
460          prot(name = 'lacZ', loc = 'cyt', dna = None, met = None, prot = None, rna =
     →None, up = None, dw = None),
461          Parameter('fwd_sr_lacZ_rbs', 1.000000))
462  Rule('sr_lacY_rbs',
463          cplx(name = 'RIBOSOME_CPLX', loc = 'cyt', rna = 1) %
464          rna(name = 'lacY', type = 'rbs', loc = 'cyt', prot = 1) +
465          rna(name = 'lacY', type = 'cds', loc = 'cyt', prot = None) +
466          None >>
467          cplx(name = 'RIBOSOME_CPLX', loc = 'cyt', rna = 1) %
468          rna(name = 'lacY', type = 'cds', loc = 'cyt', prot = 1) +
469          rna(name = 'lacY', type = 'rbs', loc = 'cyt', prot = None) +
470          prot(name = 'lacY', loc = 'cyt', dna = None, met = None, prot = None, rna =
     →None, up = None, dw = None),
471          Parameter('fwd_sr_lacY_rbs', 1.000000))
472  Rule('sr_lacA_rbs',
473          cplx(name = 'RIBOSOME_CPLX', loc = 'cyt', rna = 1) %
474          rna(name = 'lacA', type = 'rbs', loc = 'cyt', prot = 1) +
475          rna(name = 'lacA', type = 'cds', loc = 'cyt', prot = None) +
476          None >>
477          cplx(name = 'RIBOSOME_CPLX', loc = 'cyt', rna = 1) %
478          rna(name = 'lacA', type = 'cds', loc = 'cyt', prot = 1) +
479          rna(name = 'lacA', type = 'rbs', loc = 'cyt', prot = None) +
480          prot(name = 'lacA', loc = 'cyt', dna = None, met = None, prot = None, rna =
     →None, up = None, dw = None),
481          Parameter('fwd_sr_lacA_rbs', 1.000000))
482  Rule('fr_lacZ_cds',
483          cplx(name = 'RIBOSOME_CPLX', loc = 'cyt', rna = 1) %
484          rna(name = 'lacZ', type = 'cds', loc = 'cyt', prot = 1) >>
485          cplx(name = 'RIBOSOME_CPLX', loc = 'cyt', rna = None) +
486          rna(name = 'lacZ', type = 'cds', loc = 'cyt', prot = None),
487          Parameter('fwd_fr_lacZ_cds', 1.000000))
488  Rule('fr_lacY_cds',
489          cplx(name = 'RIBOSOME_CPLX', loc = 'cyt', rna = 1) %
490          rna(name = 'lacY', type = 'cds', loc = 'cyt', prot = 1) >>
491          cplx(name = 'RIBOSOME_CPLX', loc = 'cyt', rna = None) +
492          rna(name = 'lacY', type = 'cds', loc = 'cyt', prot = None),
493          Parameter('fwd_fr_lacY_cds', 1.000000))
494  Rule('fr_lacA_cds',
495          cplx(name = 'RIBOSOME_CPLX', loc = 'cyt', rna = 1) %
496          rna(name = 'lacA', type = 'cds', loc = 'cyt', prot = 1) >>
497          cplx(name = 'RIBOSOME_CPLX', loc = 'cyt', rna = None) +
498          rna(name = 'lacA', type = 'cds', loc = 'cyt', prot = None),
499          Parameter('fwd_fr_lacA_cds', 1.000000))
500  Initial(prot(name = 'lacZ', loc = 'cyt', dna = None, met = None, prot = None, rna =
     →None, up = None, dw = None),
501          Parameter('t0_prot_lacZ_cyt', 0))
502  Observable('obs_prot_lacZ_cyt',
503          prot(name = 'lacZ', loc = 'cyt', dna = None, met = None, prot = None, rna =
     →None, up = None, dw = None))
504  Initial(prot(name = 'lacY', loc = 'cyt', dna = None, met = None, prot = None, rna =
     →None, up = None, dw = None),
505          Parameter('t0_prot_lacY_cyt', 0))
506  Observable('obs_prot_lacY_cyt',
507          prot(name = 'lacY', loc = 'cyt', dna = None, met = None, prot = None, rna =
     →None, up = None, dw = None))
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508  Initial(prot(name = 'lacA', loc = 'cyt', dna = None, met = None, prot = None, rna =_
     →None, up = None, dw = None),
509          Parameter('t0_prot_lacA_cyt', 0))
510  Observable('obs_prot_lacA_cyt',
511          prot(name = 'lacA', loc = 'cyt', dna = None, met = None, prot = None, rna =_
     →None, up = None, dw = None))
512  Initial(dna(name = 'lacZ', type = 'pro4', loc = 'cyt', dna = None, met = None, prot =_
     →None, rna = None, up = None, dw = 1) %
513          dna(name = 'lacZ', type = 'pro3', loc = 'cyt', dna = None, met = None, prot =_
     →None, rna = None, up = 1, dw = 2) %
514          dna(name = 'lacZ', type = 'pro2', loc = 'cyt', dna = None, met = None, prot =_
     →None, rna = None, up = 2, dw = 3) %
515          dna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', dna = None, met = None,_
     →prot = None, rna = None, up = 3, dw = 4) %
516          dna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', dna = None, met = None,_
     →prot = None, rna = None, up = 4, dw = 5) %
517          dna(name = 'lacZ', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =_
     →None, rna = None, up = 5, dw = 6) %
518          dna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =_
     →None, rna = None, up = 6, dw = 7) %
519          dna(name = 'lacZ', type = 'cds', loc = 'cyt', dna = None, met = None, prot =_
     →None, rna = None, up = 7, dw = 8) %
520          dna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, met = None,_
     →prot = None, rna = None, up = 8, dw = 9) %
521          dna(name = 'lacY', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =_
     →None, rna = None, up = 9, dw = 10) %
522          dna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =_
     →None, rna = None, up = 10, dw = 11) %
523          dna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =_
     →None, rna = None, up = 11, dw = 12) %
524          dna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =_
     →None, rna = None, up = 12, dw = 13) %
525          dna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =_
     →None, rna = None, up = 13, dw = 14) %
526          dna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =_
     →None, rna = None, up = 14, dw = 15) %
527          dna(name = 'lacA', type = 'ter2', loc = 'cyt', dna = None, met = None, prot =_
     →None, rna = None, up = 15, dw = None),
528          Parameter('t0_dna_lacZlacYlacA', 0))
529  Observable('obs_dna_lacZlacYlacA',
530          dna(name = 'lacZ', type = 'pro4', loc = 'cyt', dna = None, met = None, prot =_
     →None, rna = None, up = None, dw = 1) %
531          dna(name = 'lacZ', type = 'pro3', loc = 'cyt', dna = None, met = None, prot =_
     →None, rna = None, up = 1, dw = 2) %
532          dna(name = 'lacZ', type = 'pro2', loc = 'cyt', dna = None, met = None, prot =_
     →None, rna = None, up = 2, dw = 3) %
533          dna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', dna = None, met = None,_
     →prot = None, rna = None, up = 3, dw = 4) %
534          dna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', dna = None, met = None,_
     →prot = None, rna = None, up = 4, dw = 5) %
535          dna(name = 'lacZ', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =_
     →None, rna = None, up = 5, dw = 6) %
536          dna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =_
     →None, rna = None, up = 6, dw = 7) %
537          dna(name = 'lacZ', type = 'cds', loc = 'cyt', dna = None, met = None, prot =_
     →None, rna = None, up = 7, dw = 8) %
538          dna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, met = None,_
     →prot = None, rna = None, up = 8, dw = 9) %
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539          dna(name = 'lacY', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 9, dw = 10) %
540          dna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 10, dw = 11) %
541          dna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 11, dw = 12) %
542          dna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 12, dw = 13) %
543          dna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 13, dw = 14) %
544          dna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 14, dw = 15) %
545          dna(name = 'lacA', type = 'ter2', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 15, dw = None))
546 Initial(rna(name = 'lacZ', type = 'pro3', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = None, dw = 1) %
547          rna(name = 'lacZ', type = 'pro2', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 1, dw = 2) %
548          rna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = 2, dw = 3) %
549          rna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = 3, dw = 4) %
550          rna(name = 'lacZ', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 4, dw = 5) %
551          rna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 5, dw = 6) %
552          rna(name = 'lacZ', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 6, dw = 7) %
553          rna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = 7, dw = 8) %
554          rna(name = 'lacY', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 8, dw = 9) %
555          rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 9, dw = 10) %
556          rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 10, dw = 11) %
557          rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 11, dw = 12) %
558          rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 12, dw = 13) %
559          rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 13, dw = None),
560          Parameter('t0_rna_lacZlacYlacA_form1', 0))
561 Observable('obs_rna_lacZlacYlacA_form1',
562          rna(name = 'lacZ', type = 'pro3', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = None, dw = 1) %
563          rna(name = 'lacZ', type = 'pro2', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 1, dw = 2) %
564          rna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = 2, dw = 3) %
565          rna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = 3, dw = 4) %
566          rna(name = 'lacZ', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 4, dw = 5) %
567          rna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 5, dw = 6) %
568          rna(name = 'lacZ', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 6, dw = 7) %
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569         rna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, met = None,
    →prot = None, rna = None, up = 7, dw = 8) %
570         rna(name = 'lacY', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 8, dw = 9) %
571         rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 9, dw = 10) %
572         rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 10, dw = 11) %
573         rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 11, dw = 12) %
574         rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 12, dw = 13) %
575         rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 13, dw = None))
576 Initial(rna(name = 'lacZ', type = 'pro3', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = None, dw = 1) %
577         rna(name = 'lacZ', type = 'pro2', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 1, dw = 2) %
578         rna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', dna = None, met = None,
    →prot = None, rna = None, up = 2, dw = 3) %
579         rna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', dna = None, met = None,
    →prot = None, rna = None, up = 3, dw = 4) %
580         rna(name = 'lacZ', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 4, dw = 5) %
581         rna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 5, dw = 6) %
582         rna(name = 'lacZ', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 6, dw = 7) %
583         rna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, met = None,
    →prot = None, rna = None, up = 7, dw = 8) %
584         rna(name = 'lacY', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 8, dw = 9) %
585         rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 9, dw = 10) %
586         rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 10, dw = 11) %
587         rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 11, dw = 12) %
588         rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 12, dw = 13) %
589         rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 13, dw = 14) %
590         rna(name = 'lacA', type = 'ter2', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 14, dw = None),
591         Parameter('t0_rna_lacZlacYlacA_form2', 0))
592 Observable('obs_rna_lacZlacYlacA_form2',
593         rna(name = 'lacZ', type = 'pro3', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = None, dw = 1) %
594         rna(name = 'lacZ', type = 'pro2', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 1, dw = 2) %
595         rna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', dna = None, met = None,
    →prot = None, rna = None, up = 2, dw = 3) %
596         rna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', dna = None, met = None,
    →prot = None, rna = None, up = 3, dw = 4) %
597         rna(name = 'lacZ', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 4, dw = 5) %
598         rna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 5, dw = 6) %
```

```
599          rna(name = 'lacZ', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 6, dw = 7) %
600          rna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = 7, dw = 8) %
601          rna(name = 'lacY', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 8, dw = 9) %
602          rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 9, dw = 10) %
603          rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 10, dw = 11) %
604          rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 11, dw = 12) %
605          rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 12, dw = 13) %
606          rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 13, dw = 14) %
607          rna(name = 'lacA', type = 'ter2', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 14, dw = None))
608 Initial(rna(name = 'lacZ', type = 'pro2', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = None, dw = 1) %
609          rna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = 1, dw = 2) %
610          rna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = 2, dw = 3) %
611          rna(name = 'lacZ', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 3, dw = 4) %
612          rna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 4, dw = 5) %
613          rna(name = 'lacZ', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 5, dw = 6) %
614          rna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = 6, dw = 7) %
615          rna(name = 'lacY', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 7, dw = 8) %
616          rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 8, dw = 9) %
617          rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 9, dw = 10) %
618          rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 10, dw = 11) %
619          rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 11, dw = 12) %
620          rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 12, dw = None),
621          Parameter('t0_rna_lacZlacYlacA_form3', 0))
622 Observable('obs_rna_lacZlacYlacA_form3',
623          rna(name = 'lacZ', type = 'pro2', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = None, dw = 1) %
624          rna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = 1, dw = 2) %
625          rna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = 2, dw = 3) %
626          rna(name = 'lacZ', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 3, dw = 4) %
627          rna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 4, dw = 5) %
628          rna(name = 'lacZ', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 5, dw = 6) %
```

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629          rna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, met = None,
    ↪prot = None, rna = None, up = 6, dw = 7) %
630          rna(name = 'lacY', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 7, dw = 8) %
631          rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 8, dw = 9) %
632          rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 9, dw = 10) %
633          rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 10, dw = 11) %
634          rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 11, dw = 12) %
635          rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 12, dw = None))
636 Initial(rna(name = 'lacZ', type = 'pro2', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = None, dw = 1) %
637          rna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', dna = None, met = None,
    ↪prot = None, rna = None, up = 1, dw = 2) %
638          rna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', dna = None, met = None,
    ↪prot = None, rna = None, up = 2, dw = 3) %
639          rna(name = 'lacZ', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 3, dw = 4) %
640          rna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 4, dw = 5) %
641          rna(name = 'lacZ', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 5, dw = 6) %
642          rna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, met = None,
    ↪prot = None, rna = None, up = 6, dw = 7) %
643          rna(name = 'lacY', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 7, dw = 8) %
644          rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 8, dw = 9) %
645          rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 9, dw = 10) %
646          rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 10, dw = 11) %
647          rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 11, dw = 12) %
648          rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 12, dw = 13) %
649          rna(name = 'lacA', type = 'ter2', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 13, dw = None),
650          Parameter('t0_rna_lacZlacYlacA_form4', 0))
651 Observable('obs_rna_lacZlacYlacA_form4',
652          rna(name = 'lacZ', type = 'pro2', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = None, dw = 1) %
653          rna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', dna = None, met = None,
    ↪prot = None, rna = None, up = 1, dw = 2) %
654          rna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', dna = None, met = None,
    ↪prot = None, rna = None, up = 2, dw = 3) %
655          rna(name = 'lacZ', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 3, dw = 4) %
656          rna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 4, dw = 5) %
657          rna(name = 'lacZ', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 5, dw = 6) %
658          rna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, met = None,
    ↪prot = None, rna = None, up = 6, dw = 7) %
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659        rna(name = 'lacY', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 7, dw = 8) %
660        rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 8, dw = 9) %
661        rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 9, dw = 10) %
662        rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 10, dw = 11) %
663        rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 11, dw = 12) %
664        rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 12, dw = 13) %
665        rna(name = 'lacA', type = 'ter2', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 13, dw = None))
666 Initial(rna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', dna = None, met = None,␣
    ↪prot = None, rna = None, up = None, dw = 1) %
667        rna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', dna = None, met = None,␣
    ↪prot = None, rna = None, up = 1, dw = 2) %
668        rna(name = 'lacZ', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 2, dw = 3) %
669        rna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 3, dw = 4) %
670        rna(name = 'lacZ', type = 'cds', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 4, dw = 5) %
671        rna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, met = None,␣
    ↪prot = None, rna = None, up = 5, dw = 6) %
672        rna(name = 'lacY', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 6, dw = 7) %
673        rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 7, dw = 8) %
674        rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 8, dw = 9) %
675        rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 9, dw = 10) %
676        rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 10, dw = 11) %
677        rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 11, dw = None),
678        Parameter('t0_rna_lacZlacYlacA_form5', 0))
679 Observable('obs_rna_lacZlacYlacA_form5',
680        rna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', dna = None, met = None,␣
    ↪prot = None, rna = None, up = None, dw = 1) %
681        rna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', dna = None, met = None,␣
    ↪prot = None, rna = None, up = 1, dw = 2) %
682        rna(name = 'lacZ', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 2, dw = 3) %
683        rna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 3, dw = 4) %
684        rna(name = 'lacZ', type = 'cds', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 4, dw = 5) %
685        rna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, met = None,␣
    ↪prot = None, rna = None, up = 5, dw = 6) %
686        rna(name = 'lacY', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 6, dw = 7) %
687        rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 7, dw = 8) %
688        rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 8, dw = 9) %
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689          rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 9, dw = 10) %
690          rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 10, dw = 11) %
691          rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 11, dw = None))
692 Initial(rna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = None, dw = 1) %
693          rna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = 1, dw = 2) %
694          rna(name = 'lacZ', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 2, dw = 3) %
695          rna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 3, dw = 4) %
696          rna(name = 'lacZ', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 4, dw = 5) %
697          rna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = 5, dw = 6) %
698          rna(name = 'lacY', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 6, dw = 7) %
699          rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 7, dw = 8) %
700          rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 8, dw = 9) %
701          rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 9, dw = 10) %
702          rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 10, dw = 11) %
703          rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 11, dw = 12) %
704          rna(name = 'lacA', type = 'ter2', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 12, dw = None),
705          Parameter('t0_rna_lacZlacYlacA_form6', 0))
706 Observable('obs_rna_lacZlacYlacA_form6',
707          rna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = None, dw = 1) %
708          rna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = 1, dw = 2) %
709          rna(name = 'lacZ', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 2, dw = 3) %
710          rna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 3, dw = 4) %
711          rna(name = 'lacZ', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 4, dw = 5) %
712          rna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = 5, dw = 6) %
713          rna(name = 'lacY', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 6, dw = 7) %
714          rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 7, dw = 8) %
715          rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 8, dw = 9) %
716          rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 9, dw = 10) %
717          rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 10, dw = 11) %
718          rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 11, dw = 12) %
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719          rna(name = 'lacA', type = 'ter2', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 12, dw = None))
720 Initial(rna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = None, dw = 1) %
721          rna(name = 'lacZ', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 1, dw = 2) %
722          rna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = 2, dw = 3) %
723          rna(name = 'lacY', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 3, dw = 4) %
724          rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 4, dw = 5) %
725          rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 5, dw = 6) %
726          rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 6, dw = 7) %
727          rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 7, dw = 8) %
728          rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 8, dw = None),
729          Parameter('t0_rna_lacZlacYlacA_form7', 0))
730 Observable('obs_rna_lacZlacYlacA_form7',
731          rna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = None, dw = 1) %
732          rna(name = 'lacZ', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 1, dw = 2) %
733          rna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = 2, dw = 3) %
734          rna(name = 'lacY', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 3, dw = 4) %
735          rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 4, dw = 5) %
736          rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 5, dw = 6) %
737          rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 6, dw = 7) %
738          rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 7, dw = 8) %
739          rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 8, dw = None))
740 Initial(rna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = None, dw = 1) %
741          rna(name = 'lacZ', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 1, dw = 2) %
742          rna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = 2, dw = 3) %
743          rna(name = 'lacY', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 3, dw = 4) %
744          rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 4, dw = 5) %
745          rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 5, dw = 6) %
746          rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 6, dw = 7) %
747          rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 7, dw = 8) %
748          rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 8, dw = 9) %
```

```
749          rna(name = 'lacA', type = 'ter2', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 9, dw = None),
750          Parameter('t0_rna_lacZlacYlacA_form8', 0))
751 Observable('obs_rna_lacZlacYlacA_form8',
752          rna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = None, dw = 1) %
753          rna(name = 'lacZ', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 1, dw = 2) %
754          rna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, met = None,
    ↪prot = None, rna = None, up = 2, dw = 3) %
755          rna(name = 'lacY', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 3, dw = 4) %
756          rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 4, dw = 5) %
757          rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 5, dw = 6) %
758          rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 6, dw = 7) %
759          rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 7, dw = 8) %
760          rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 8, dw = 9) %
761          rna(name = 'lacA', type = 'ter2', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 9, dw = None))
762 Initial(rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = None, dw = 1) %
763          rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 1, dw = 2) %
764          rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 2, dw = 3) %
765          rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 3, dw = 4) %
766          rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 4, dw = None),
767          Parameter('t0_rna_lacZlacYlacA_form9', 0))
768 Observable('obs_rna_lacZlacYlacA_form9',
769          rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = None, dw = 1) %
770          rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 1, dw = 2) %
771          rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 2, dw = 3) %
772          rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 3, dw = 4) %
773          rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 4, dw = None))
774 Initial(rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = None, dw = 1) %
775          rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 1, dw = 2) %
776          rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 2, dw = 3) %
777          rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 3, dw = 4) %
778          rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 4, dw = 5) %
779          rna(name = 'lacA', type = 'ter2', loc = 'cyt', dna = None, met = None, prot =
    ↪None, rna = None, up = 5, dw = None),
```

```
780         Parameter('t0_rna_lacZlacYlacA_form10', 0))
781 Observable('obs_rna_lacZlacYlacA_form10',
782         rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =␣
    →None, rna = None, up = None, dw = 1) %
783         rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =␣
    →None, rna = None, up = 1, dw = 2) %
784         rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =␣
    →None, rna = None, up = 2, dw = 3) %
785         rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =␣
    →None, rna = None, up = 3, dw = 4) %
786         rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =␣
    →None, rna = None, up = 4, dw = 5) %
787         rna(name = 'lacA', type = 'ter2', loc = 'cyt', dna = None, met = None, prot =␣
    →None, rna = None, up = 5, dw = None))
```

3.6 Genome Graphs

The Genome Graphs have ten columns:

1. The 1st declares the UPSTREAM and the 2nd declares the DOWNSTREAM DNA feature.

   The DNA features are five: pro followed by a number, rbs, cds, ter followed by a number, and BS- to define DNA binding sites.

2. The next columns declare rates:

   - RNAP_FWD_DOCK_RATE and RNAP_RVS_DOCK_RATE are valid values only for the description of the reversible interaction of the RNA Polymerase to the promoters.

   - RNAP_FWD_SLIDE_RATE are valid values for the transition of the RNA Polymerase from the UPSTREAM to the DOWNSTREAM DNA parts. We describe rules where the RNA Polymerase could not move back.

   - RNAP_FWD_FALL_RATE are valid values only for the description of the unbinding of the RNA Polymerase and the UPSTREAM identifiying a DNA terminator.

   - RIB_FWD_DOCK_RATE and RIB_RVS_DOCK_RATE are valid values only for the description of the reversible interaction of the bacterial Ribosome to the RBS.

   - RIB_FWD_SLIDE_RATE are valid values for the transition of the Ribosome from the UPSTREAM to the DOWNSTREAM RNA parts. We describe rules where the Ribosome could not move back.

   - RIB_FWD_FALL_RATE are valid values only for the description of the unbinding of the Ribosome and the UPSTREAM identifiying a CDS.

Example, and note the use of the prefix BS- to tell *Atlas* the component is a DNA binding site followed by a name and two coordinates:

```
1 UPSTREAM          DOWNSTREAM        RNAP_FWD_DOCK_RATE         RNAP_RVS_DOCK_
  →RATE           RNAP_FWD_SLIDE_RATE        RNAP_FWD_FALL_RATE        RIB_FWD_DOCK_
  →RATE           RIB_RVS_DOCK_RATE         RIB_FWD_SLIDE_RATE        RIB_FWD_FALL_RATE
2 [lacZ-pro4        lacZ-pro3         1        1         1
3 lacZ-pro3         lacZ-pro2         1        1         1
4 lacZ-pro2         BS-lacI-72-92     1        1         1
5 BS-lacI-72-92        BS-lacI-21-1                      1
6 BS-lacI-21-1         lacZ-pro1                     1
```

```
 7  lacZ-pro1        lacZ-rbs         1       1       1
 8  lacZ-rbs         lacZ-
    →cds                              1               1       1       1       1
 9  lacZ-cds         BS-lacI-422-402                  1
10  BS-lacI-422-402        lacY-pro1                          1
11  lacY-pro1        lacY-rbs         0       0       1
12  lacY-rbs         lacY-
    →cds                              1               1       1       1       1
13  lacY-cds         lacA-rbs                         1
14  lacA-rbs         lacA-
    →cds                              1               1       1       1       1
15  lacA-cds         lacA-ter1                        1       1
16  lacA-ter1         lacA-ter2]                      1       1
```

OR

```
 1  UPSTREAM         DOWNSTREAM      RNAP_FWD_DOCK_RATE       RNAP_RVS_DOCK_
    →RATE    RNAP_FWD_SLIDE_RATE      RNAP_FWD_FALL_RATE       RIB_FWD_DOCK_
    →RATE    RIB_RVS_DOCK_RATE       RIB_FWD_SLIDE_RATE       RIB_FWD_FALL_RATE
 2  [rpoA-pro1       rpoA-rbs         1       1       1
 3  rpoA-rbs         rpoA-
    →cds                              1               1       1       1       1
 4  rpoA-cds         rpoA-ter1]                       1       1
 5
 6  [rpoB-pro1       rpoB-rbs         1       1       1
 7  rpoB-rbs         rpoB-
    →cds                              1               1       1       1       1
 8  rpoB-cds         rpoC-rbs                 1
 9  rpoC-rbs         rpoC-
    →cds                              1               1       1       1       1
10  rpoC-cds         rpoC-ter1]                       1       1
11
12  [rpoD-pro1       rpoD-rbs         1       1       1
13  rpoD-rbs         rpoD-
    →cds                              1               1       1       1       1
14  rpoD-cds         rpoD-ter1]                       1       1
15
16  [rpoE-pro1       rpoE-rbs         1       1       1
17  rpoE-rbs         rpoE-
    →cds                              1               1       1       1       1
18  rpoE-cds         rpoE-ter1]                       1       1
19
20  [rpoH-pro1       rpoH-rbs         1       1       1
21  rpoH-rbs         rpoH-
    →cds                              1               1       1       1       1
22  rpoH-cds         rpoH-ter1]                       1       1
23
24  [rpoN-pro1       rpoN-rbs         1       1       1
25  rpoN-rbs         rpoN-
    →cds                              1               1       1       1       1
26  rpoN-cds         rpoN-ter1]                       1       1
27
28  [rpoS-pro1       rpoS-rbs         1       1       1
29  rpoS-rbs         rpoS-
    →cds                              1               1       1       1       1
30  rpoS-cds         rpoS-ter1]                       1       1
31
```

```
32  [fliA-pro1        fliA-rbs        1        1          1
33  fliA-rbs       fliA-
    ↪cds                            1                1          1          1          1
34  fliA-cds       fliA-ter1]                       1          1
35
36  [fecI-pro1       fecI-rbs        1        1          1
37  fecI-rbs       fecI-
    ↪cds                            1                1          1          1          1
38  fecI-cds       fecI-ter1]                       1          1
```

Note: Visualization in Cytoscape. Colors and arrows remains to the user for customization. The network could be complemented with a description of sigma factor specifity for promoter, as the following network
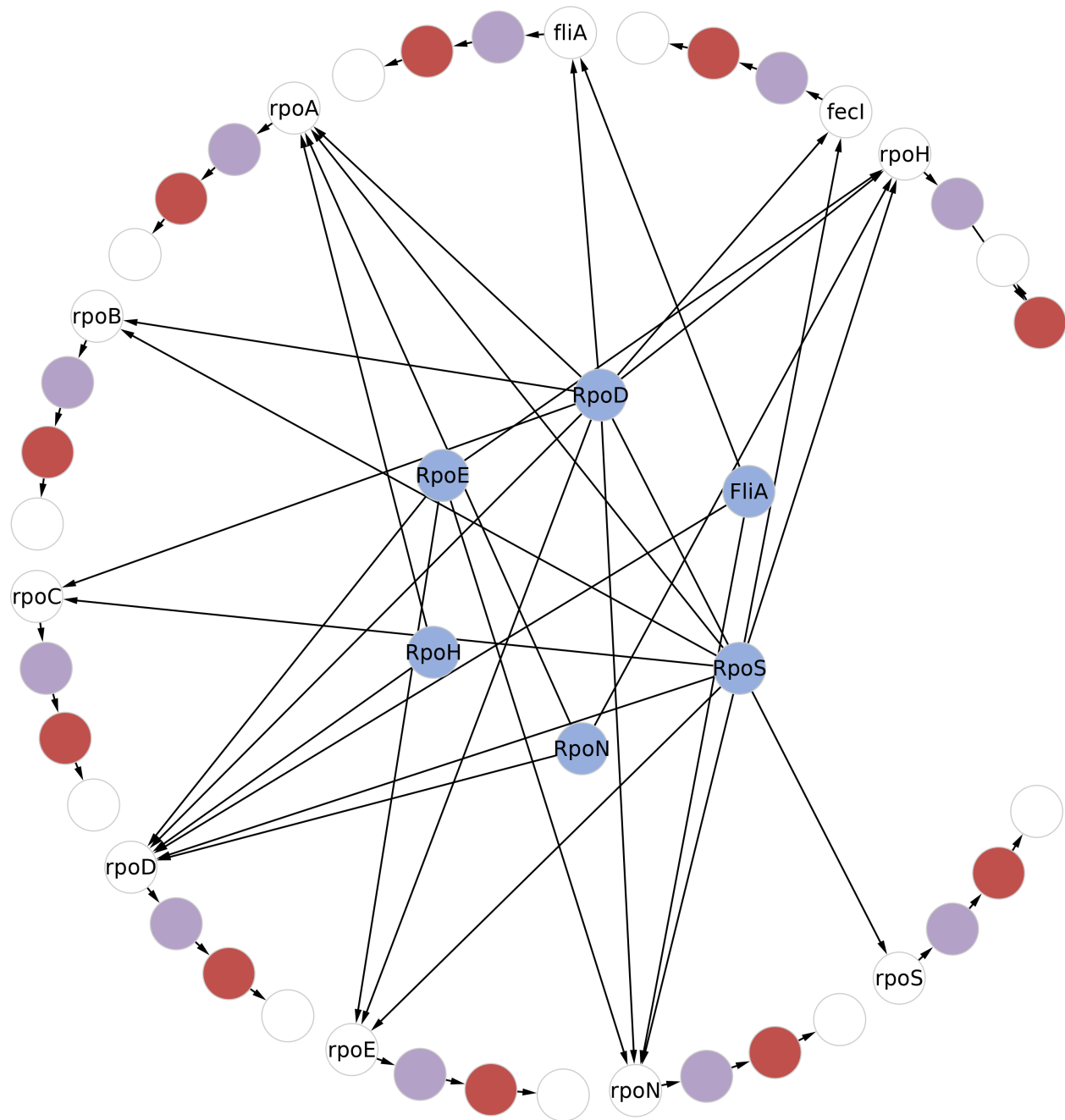
Finally, execute `atlas_rbm.construct_model_from_genome_graph(network, verbose = False)` to obtain the model.

Note: Simulation. The model can be simulated only with the instantiation of `Initials`:

- `atlas_rbm.simulation.set_initial.cplx(model, complex_name, location, positive_number)`

- `atlas_rbm.simulation.set_initial.dna(model, dna_name, positive_number)`

- `atlas_rbm.simulation.set_initial.met(model, metabolite, location, positive_number)`

- `atlas_rbm.simulation.set_initial.prot(model, prot_name, location, positive_number)`

- `atlas_rbm.simulation.set_initial.rna(model, rna_name, positive_number)`

Note: Kappa BioBrick Framework. The *Rules* for transcription and translation come from the work of Stewart and Wilson-Kanamori (See more here). A "pure" genome graph uses the originally defined rules, while a genome graph + sigma factor specifity uses a modified *rules* to model the release of the sigma factor from the RNA Polymerase at the transcription initiation.

```python
from pysb import *
Model()

Monomer('dna',
        ['name', 'type', 'loc', 'dna', 'met', 'prot', 'rna', 'up', 'dw'],
        { 'name' : ['lacI_21_1', 'lacI_422_402', 'lacI_72_92', 'lacA', 'lacY', 'lacZ
        ↪'],
        'type' : ['BS', 'cds', 'pro1', 'pro2', 'pro3', 'pro4', 'rbs', 'ter1', 'ter2'],
        'loc' : ['cyt']})
Monomer('rna',
        ['name', 'type', 'loc', 'dna', 'met', 'prot', 'rna', 'up', 'dw'],
        { 'name' : ['lacI_21_1', 'lacI_422_402', 'lacI_72_92', 'lacA', 'lacY', 'lacZ
        ↪'],
        'type' : ['BS', 'cds', 'pro1', 'pro2', 'pro3', 'pro4', 'rbs', 'ter1', 'ter2'],
        'loc' : ['cyt']})
Monomer('prot',
        ['name', 'loc', 'dna', 'met', 'prot', 'rna', 'up', 'dw'],
        { 'name' : ['lacA', 'lacY', 'lacZ'],
        'loc' : ['cyt', 'cytosk', 'ex', 'mem', 'per', 'wall', 'bnuc', 'cproj', 'imem',
        ↪ 'omem']})
Monomer('cplx',
        ['name', 'loc', 'dna', 'met', 'prot', 'rna'],
        { 'name' : ['RNAP_CPLX', 'RIBOSOME_CPLX'],
        'loc' : ['cyt']})
Rule('docking_lacZ_pro4',
        cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = None) +
        dna(name = 'lacZ', type = 'pro4', loc = 'cyt', prot = None) |
        cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = 1) %
        dna(name = 'lacZ', type = 'pro4', loc = 'cyt', prot = 1),
        Parameter('fwd_docking_lacZ_pro4', 1.000000),
        Parameter('rvs_docking_lacZ_pro4', 1.000000))
Rule('docking_lacZ_pro3',
        cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = None) +
        dna(name = 'lacZ', type = 'pro3', loc = 'cyt', prot = None) |
        cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = 1) %
        dna(name = 'lacZ', type = 'pro3', loc = 'cyt', prot = 1),
        Parameter('fwd_docking_lacZ_pro3', 1.000000),
        Parameter('rvs_docking_lacZ_pro3', 1.000000))
Rule('docking_lacZ_pro2',
        cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = None) +
        dna(name = 'lacZ', type = 'pro2', loc = 'cyt', prot = None) |
        cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = 1) %
        dna(name = 'lacZ', type = 'pro2', loc = 'cyt', prot = 1),
        Parameter('fwd_docking_lacZ_pro2', 1.000000),
        Parameter('rvs_docking_lacZ_pro2', 1.000000))
Rule('docking_lacZ_pro1',
```

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```
44          cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = None) +
45          dna(name = 'lacZ', type = 'pro1', loc = 'cyt', prot = None) |
46          cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = 1) %
47          dna(name = 'lacZ', type = 'pro1', loc = 'cyt', prot = 1),
48          Parameter('fwd_docking_lacZ_pro1', 1.000000),
49          Parameter('rvs_docking_lacZ_pro1', 1.000000))
50   Rule('docking_lacY_pro1',
51          cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = None) +
52          dna(name = 'lacY', type = 'pro1', loc = 'cyt', prot = None) |
53          cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = 1) %
54          dna(name = 'lacY', type = 'pro1', loc = 'cyt', prot = 1),
55          Parameter('fwd_docking_lacY_pro1', 0.000000),
56          Parameter('rvs_docking_lacY_pro1', 0.000000))
57   Rule('sliding_lacZ_pro4',
58          cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = 1) %
59          dna(name = 'lacZ', type = 'pro4', loc = 'cyt', prot = 1) +
60          dna(name = 'lacZ', type = 'pro3', loc = 'cyt', prot = None) +
61          None >>
62          cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = 1) %
63          dna(name = 'lacZ', type = 'pro3', loc = 'cyt', prot = 1) +
64          dna(name = 'lacZ', type = 'pro4', loc = 'cyt', prot = None) +
65          rna(name = 'lacZ', type = 'pro3', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = None, dw = None),
66          Parameter('fwd_sliding_lacZ_pro4', 1.000000))
67   Rule('sliding_lacZ_pro3',
68          cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = 1) %
69          dna(name = 'lacZ', type = 'pro3', loc = 'cyt', prot = 1) +
70          dna(name = 'lacZ', type = 'pro2', loc = 'cyt', prot = None) +
71          None >>
72          cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = 1) %
73          dna(name = 'lacZ', type = 'pro2', loc = 'cyt', prot = 1) +
74          dna(name = 'lacZ', type = 'pro3', loc = 'cyt', prot = None) +
75          rna(name = 'lacZ', type = 'pro2', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = None, dw = None),
76          Parameter('fwd_sliding_lacZ_pro3', 1.000000))
77   Rule('sliding_lacZ_pro2',
78          cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = 1) %
79          dna(name = 'lacZ', type = 'pro2', loc = 'cyt', prot = 1) +
80          dna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', prot = None) +
81          None >>
82          cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = 1) %
83          dna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', prot = 1) +
84          dna(name = 'lacZ', type = 'pro2', loc = 'cyt', prot = None) +
85          rna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = None, dw = None),
86          Parameter('fwd_sliding_lacZ_pro2', 1.000000))
87   Rule('sliding_BS_lacI_72_92',
88          cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = 1) %
89          dna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', prot = 1) +
90          dna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', prot = None) +
91          None >>
92          cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = 1) %
93          dna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', prot = 1) +
94          dna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', prot = None) +
95          rna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = None, dw = None),
96          Parameter('fwd_sliding_BS_lacI_72_92', 1.000000))
```

```
97   Rule('sliding_BS_lacI_21_1',
98         cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = 1) %
99         dna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', prot = 1) +
100        dna(name = 'lacZ', type = 'pro1', loc = 'cyt', prot = None) +
101        None >>
102        cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = 1) %
103        dna(name = 'lacZ', type = 'pro1', loc = 'cyt', prot = 1) +
104        dna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', prot = None) +
105        rna(name = 'lacZ', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = None, dw = None),
106        Parameter('fwd_sliding_BS_lacI_21_1', 1.000000))
107  Rule('sliding_lacZ_pro1',
108        cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = 1) %
109        dna(name = 'lacZ', type = 'pro1', loc = 'cyt', prot = 1) +
110        dna(name = 'lacZ', type = 'rbs', loc = 'cyt', prot = None) +
111        None >>
112        cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = 1) %
113        dna(name = 'lacZ', type = 'rbs', loc = 'cyt', prot = 1) +
114        dna(name = 'lacZ', type = 'pro1', loc = 'cyt', prot = None) +
115        rna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = None, dw = None),
116        Parameter('fwd_sliding_lacZ_pro1', 1.000000))
117  Rule('sliding_lacZ_rbs',
118        cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = 1) %
119        dna(name = 'lacZ', type = 'rbs', loc = 'cyt', prot = 1) +
120        dna(name = 'lacZ', type = 'cds', loc = 'cyt', prot = None) +
121        None >>
122        cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = 1) %
123        dna(name = 'lacZ', type = 'cds', loc = 'cyt', prot = 1) +
124        dna(name = 'lacZ', type = 'rbs', loc = 'cyt', prot = None) +
125        rna(name = 'lacZ', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = None, dw = None),
126        Parameter('fwd_sliding_lacZ_rbs', 1.000000))
127  Rule('sliding_lacZ_cds',
128        cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = 1) %
129        dna(name = 'lacZ', type = 'cds', loc = 'cyt', prot = 1) +
130        dna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', prot = None) +
131        None >>
132        cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = 1) %
133        dna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', prot = 1) +
134        dna(name = 'lacZ', type = 'cds', loc = 'cyt', prot = None) +
135        rna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = None, dw = None),
136        Parameter('fwd_sliding_lacZ_cds', 1.000000))
137  Rule('sliding_BS_lacI_422_402',
138        cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = 1) %
139        dna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', prot = 1) +
140        dna(name = 'lacY', type = 'pro1', loc = 'cyt', prot = None) +
141        None >>
142        cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = 1) %
143        dna(name = 'lacY', type = 'pro1', loc = 'cyt', prot = 1) +
144        dna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', prot = None) +
145        rna(name = 'lacY', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = None, dw = None),
146        Parameter('fwd_sliding_BS_lacI_422_402', 1.000000))
147  Rule('sliding_lacY_pro1',
148        cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = 1) %
```

```
149          dna(name = 'lacY', type = 'pro1', loc = 'cyt', prot = 1) +
150          dna(name = 'lacY', type = 'rbs', loc = 'cyt', prot = None) +
151          None >>
152          cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = 1) %
153          dna(name = 'lacY', type = 'rbs', loc = 'cyt', prot = 1) +
154          dna(name = 'lacY', type = 'pro1', loc = 'cyt', prot = None) +
155          rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = None, dw = None),
156          Parameter('fwd_sliding_lacY_pro1', 1.000000))
157 Rule('sliding_lacY_rbs',
158          cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = 1) %
159          dna(name = 'lacY', type = 'rbs', loc = 'cyt', prot = 1) +
160          dna(name = 'lacY', type = 'cds', loc = 'cyt', prot = None) +
161          None >>
162          cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = 1) %
163          dna(name = 'lacY', type = 'cds', loc = 'cyt', prot = 1) +
164          dna(name = 'lacY', type = 'rbs', loc = 'cyt', prot = None) +
165          rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = None, dw = None),
166          Parameter('fwd_sliding_lacY_rbs', 1.000000))
167 Rule('sliding_lacY_cds',
168          cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = 1) %
169          dna(name = 'lacY', type = 'cds', loc = 'cyt', prot = 1) +
170          dna(name = 'lacA', type = 'rbs', loc = 'cyt', prot = None) +
171          None >>
172          cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = 1) %
173          dna(name = 'lacA', type = 'rbs', loc = 'cyt', prot = 1) +
174          dna(name = 'lacY', type = 'cds', loc = 'cyt', prot = None) +
175          rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = None, dw = None),
176          Parameter('fwd_sliding_lacY_cds', 1.000000))
177 Rule('sliding_lacA_rbs',
178          cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = 1) %
179          dna(name = 'lacA', type = 'rbs', loc = 'cyt', prot = 1) +
180          dna(name = 'lacA', type = 'cds', loc = 'cyt', prot = None) +
181          None >>
182          cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = 1) %
183          dna(name = 'lacA', type = 'cds', loc = 'cyt', prot = 1) +
184          dna(name = 'lacA', type = 'rbs', loc = 'cyt', prot = None) +
185          rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = None, dw = None),
186          Parameter('fwd_sliding_lacA_rbs', 1.000000))
187 Rule('sliding_lacA_cds',
188          cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = 1) %
189          dna(name = 'lacA', type = 'cds', loc = 'cyt', prot = 1) +
190          dna(name = 'lacA', type = 'ter1', loc = 'cyt', prot = None) +
191          None >>
192          cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = 1) %
193          dna(name = 'lacA', type = 'ter1', loc = 'cyt', prot = 1) +
194          dna(name = 'lacA', type = 'cds', loc = 'cyt', prot = None) +
195          rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = None, dw = None),
196          Parameter('fwd_sliding_lacA_cds', 1.000000))
197 Rule('sliding_lacA_ter1',
198          cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = 1) %
199          dna(name = 'lacA', type = 'ter1', loc = 'cyt', prot = 1) +
200          dna(name = 'lacA', type = 'ter2', loc = 'cyt', prot = None) +
```

```
201          None >>
202          cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = 1) %
203          dna(name = 'lacA', type = 'ter2', loc = 'cyt', prot = 1) +
204          dna(name = 'lacA', type = 'ter1', loc = 'cyt', prot = None) +
205          rna(name = 'lacA', type = 'ter2', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = None, dw = None),
206          Parameter('fwd_sliding_lacA_ter1', 1.000000))
207   Rule('falloff_lacA_ter1',
208          cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = 1) %
209          dna(name = 'lacA', type = 'ter1', loc = 'cyt', prot = 1) >>
210          cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = None) +
211          dna(name = 'lacA', type = 'ter1', loc = 'cyt', prot = None),
212          Parameter('fwd_falloff_lacA_ter1', 1.000000))
213   Rule('falloff_lacA_ter2',
214          cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = 1) %
215          dna(name = 'lacA', type = 'ter2', loc = 'cyt', prot = 1) >>
216          cplx(name = 'RNAP_CPLX', loc = 'cyt', dna = None) +
217          dna(name = 'lacA', type = 'ter2', loc = 'cyt', prot = None),
218          Parameter('fwd_falloff_lacA_ter2', 1.000000))
219   Rule('dr_lacZ_rbs',
220          cplx(name = 'RIBOSOME_CPLX', loc = 'cyt', rna = None) +
221          rna(name = 'lacZ', type = 'rbs', loc = 'cyt', prot = None) |
222          cplx(name = 'RIBOSOME_CPLX', loc = 'cyt', rna = 1) %
223          rna(name = 'lacZ', type = 'rbs', loc = 'cyt', prot = 1),
224          Parameter('fwd_dr_lacZ_rbs', 1.000000),
225          Parameter('rvs_dr_lacZ_rbs', 1.000000))
226   Rule('dr_lacY_rbs',
227          cplx(name = 'RIBOSOME_CPLX', loc = 'cyt', rna = None) +
228          rna(name = 'lacY', type = 'rbs', loc = 'cyt', prot = None) |
229          cplx(name = 'RIBOSOME_CPLX', loc = 'cyt', rna = 1) %
230          rna(name = 'lacY', type = 'rbs', loc = 'cyt', prot = 1),
231          Parameter('fwd_dr_lacY_rbs', 1.000000),
232          Parameter('rvs_dr_lacY_rbs', 1.000000))
233   Rule('dr_lacA_rbs',
234          cplx(name = 'RIBOSOME_CPLX', loc = 'cyt', rna = None) +
235          rna(name = 'lacA', type = 'rbs', loc = 'cyt', prot = None) |
236          cplx(name = 'RIBOSOME_CPLX', loc = 'cyt', rna = 1) %
237          rna(name = 'lacA', type = 'rbs', loc = 'cyt', prot = 1),
238          Parameter('fwd_dr_lacA_rbs', 1.000000),
239          Parameter('rvs_dr_lacA_rbs', 1.000000))
240   Rule('sr_lacZ_rbs',
241          cplx(name = 'RIBOSOME_CPLX', loc = 'cyt', rna = 1) %
242          rna(name = 'lacZ', type = 'rbs', loc = 'cyt', prot = 1) +
243          rna(name = 'lacZ', type = 'cds', loc = 'cyt', prot = None) +
244          None >>
245          cplx(name = 'RIBOSOME_CPLX', loc = 'cyt', rna = 1) %
246          rna(name = 'lacZ', type = 'cds', loc = 'cyt', prot = 1) +
247          rna(name = 'lacZ', type = 'rbs', loc = 'cyt', prot = None) +
248          prot(name = 'lacZ', loc = 'cyt', dna = None, met = None, prot = None, rna =
    →None, up = None, dw = None),
249          Parameter('fwd_sr_lacZ_rbs', 1.000000))
250   Rule('sr_lacY_rbs',
251          cplx(name = 'RIBOSOME_CPLX', loc = 'cyt', rna = 1) %
252          rna(name = 'lacY', type = 'rbs', loc = 'cyt', prot = 1) +
253          rna(name = 'lacY', type = 'cds', loc = 'cyt', prot = None) +
254          None >>
255          cplx(name = 'RIBOSOME_CPLX', loc = 'cyt', rna = 1) %
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256          rna(name = 'lacY', type = 'cds', loc = 'cyt', prot = 1) +
257          rna(name = 'lacY', type = 'rbs', loc = 'cyt', prot = None) +
258          prot(name = 'lacY', loc = 'cyt', dna = None, met = None, prot = None, rna =
     →None, up = None, dw = None),
259          Parameter('fwd_sr_lacY_rbs', 1.000000))
260 Rule('sr_lacA_rbs',
261          cplx(name = 'RIBOSOME_CPLX', loc = 'cyt', rna = 1) %
262          rna(name = 'lacA', type = 'rbs', loc = 'cyt', prot = 1) +
263          rna(name = 'lacA', type = 'cds', loc = 'cyt', prot = None) +
264          None >>
265          cplx(name = 'RIBOSOME_CPLX', loc = 'cyt', rna = 1) %
266          rna(name = 'lacA', type = 'cds', loc = 'cyt', prot = 1) +
267          rna(name = 'lacA', type = 'rbs', loc = 'cyt', prot = None) +
268          prot(name = 'lacA', loc = 'cyt', dna = None, met = None, prot = None, rna =
     →None, up = None, dw = None),
269          Parameter('fwd_sr_lacA_rbs', 1.000000))
270 Rule('fr_lacZ_cds',
271          cplx(name = 'RIBOSOME_CPLX', loc = 'cyt', rna = 1) %
272          rna(name = 'lacZ', type = 'cds', loc = 'cyt', prot = 1) >>
273          cplx(name = 'RIBOSOME_CPLX', loc = 'cyt', rna = None) +
274          rna(name = 'lacZ', type = 'cds', loc = 'cyt', prot = None),
275          Parameter('fwd_fr_lacZ_cds', 1.000000))
276 Rule('fr_lacY_cds',
277          cplx(name = 'RIBOSOME_CPLX', loc = 'cyt', rna = 1) %
278          rna(name = 'lacY', type = 'cds', loc = 'cyt', prot = 1) >>
279          cplx(name = 'RIBOSOME_CPLX', loc = 'cyt', rna = None) +
280          rna(name = 'lacY', type = 'cds', loc = 'cyt', prot = None),
281          Parameter('fwd_fr_lacY_cds', 1.000000))
282 Rule('fr_lacA_cds',
283          cplx(name = 'RIBOSOME_CPLX', loc = 'cyt', rna = 1) %
284          rna(name = 'lacA', type = 'cds', loc = 'cyt', prot = 1) >>
285          cplx(name = 'RIBOSOME_CPLX', loc = 'cyt', rna = None) +
286          rna(name = 'lacA', type = 'cds', loc = 'cyt', prot = None),
287          Parameter('fwd_fr_lacA_cds', 1.000000))
288 Initial(prot(name = 'lacZ', loc = 'cyt', dna = None, met = None, prot = None, rna =
     →None, up = None, dw = None),
289          Parameter('t0_prot_lacZ_cyt', 0))
290 Observable('obs_prot_lacZ_cyt',
291          prot(name = 'lacZ', loc = 'cyt', dna = None, met = None, prot = None, rna =
     →None, up = None, dw = None))
292 Initial(prot(name = 'lacY', loc = 'cyt', dna = None, met = None, prot = None, rna =
     →None, up = None, dw = None),
293          Parameter('t0_prot_lacY_cyt', 0))
294 Observable('obs_prot_lacY_cyt',
295          prot(name = 'lacY', loc = 'cyt', dna = None, met = None, prot = None, rna =
     →None, up = None, dw = None))
296 Initial(prot(name = 'lacA', loc = 'cyt', dna = None, met = None, prot = None, rna =
     →None, up = None, dw = None),
297          Parameter('t0_prot_lacA_cyt', 0))
298 Observable('obs_prot_lacA_cyt',
299          prot(name = 'lacA', loc = 'cyt', dna = None, met = None, prot = None, rna =
     →None, up = None, dw = None))
300 Initial(dna(name = 'lacZ', type = 'pro4', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = None, dw = 1) %
301          dna(name = 'lacZ', type = 'pro3', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 1, dw = 2) %
302          dna(name = 'lacZ', type = 'pro2', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 2, dw = 3) %
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303          dna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', dna = None, met = None,
    →prot = None, rna = None, up = 3, dw = 4) %
304          dna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', dna = None, met = None,
    →prot = None, rna = None, up = 4, dw = 5) %
305          dna(name = 'lacZ', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 5, dw = 6) %
306          dna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 6, dw = 7) %
307          dna(name = 'lacZ', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 7, dw = 8) %
308          dna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, met = None,
    →prot = None, rna = None, up = 8, dw = 9) %
309          dna(name = 'lacY', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 9, dw = 10) %
310          dna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 10, dw = 11) %
311          dna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 11, dw = 12) %
312          dna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 12, dw = 13) %
313          dna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 13, dw = 14) %
314          dna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 14, dw = 15) %
315          dna(name = 'lacA', type = 'ter2', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 15, dw = None),
316          Parameter('t0_dna_lacZlacYlacA', 0))
317 Observable('obs_dna_lacZlacYlacA',
318          dna(name = 'lacZ', type = 'pro4', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = None, dw = 1) %
319          dna(name = 'lacZ', type = 'pro3', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 1, dw = 2) %
320          dna(name = 'lacZ', type = 'pro2', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 2, dw = 3) %
321          dna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', dna = None, met = None,
    →prot = None, rna = None, up = 3, dw = 4) %
322          dna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', dna = None, met = None,
    →prot = None, rna = None, up = 4, dw = 5) %
323          dna(name = 'lacZ', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 5, dw = 6) %
324          dna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 6, dw = 7) %
325          dna(name = 'lacZ', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 7, dw = 8) %
326          dna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, met = None,
    →prot = None, rna = None, up = 8, dw = 9) %
327          dna(name = 'lacY', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 9, dw = 10) %
328          dna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 10, dw = 11) %
329          dna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 11, dw = 12) %
330          dna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 12, dw = 13) %
331          dna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 13, dw = 14) %
332          dna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 14, dw = 15) %
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333          dna(name = 'lacA', type = 'ter2', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 15, dw = None))
334  Initial(rna(name = 'lacZ', type = 'pro3', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = None, dw = 1) %
335          rna(name = 'lacZ', type = 'pro2', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 1, dw = 2) %
336          rna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', dna = None, met = None,
    →prot = None, rna = None, up = 2, dw = 3) %
337          rna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', dna = None, met = None,
    →prot = None, rna = None, up = 3, dw = 4) %
338          rna(name = 'lacZ', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 4, dw = 5) %
339          rna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 5, dw = 6) %
340          rna(name = 'lacZ', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 6, dw = 7) %
341          rna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, met = None,
    →prot = None, rna = None, up = 7, dw = 8) %
342          rna(name = 'lacY', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 8, dw = 9) %
343          rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 9, dw = 10) %
344          rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 10, dw = 11) %
345          rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 11, dw = 12) %
346          rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 12, dw = 13) %
347          rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 13, dw = None),
348          Parameter('t0_rna_lacZlacYlacA_form1', 0))
349  Observable('obs_rna_lacZlacYlacA_form1',
350          rna(name = 'lacZ', type = 'pro3', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = None, dw = 1) %
351          rna(name = 'lacZ', type = 'pro2', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 1, dw = 2) %
352          rna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', dna = None, met = None,
    →prot = None, rna = None, up = 2, dw = 3) %
353          rna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', dna = None, met = None,
    →prot = None, rna = None, up = 3, dw = 4) %
354          rna(name = 'lacZ', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 4, dw = 5) %
355          rna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 5, dw = 6) %
356          rna(name = 'lacZ', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 6, dw = 7) %
357          rna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, met = None,
    →prot = None, rna = None, up = 7, dw = 8) %
358          rna(name = 'lacY', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 8, dw = 9) %
359          rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 9, dw = 10) %
360          rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 10, dw = 11) %
361          rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 11, dw = 12) %
362          rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 12, dw = 13) %
```

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363          rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 13, dw = None))
364 Initial(rna(name = 'lacZ', type = 'pro3', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = None, dw = 1) %
365          rna(name = 'lacZ', type = 'pro2', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 1, dw = 2) %
366          rna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = 2, dw = 3) %
367          rna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = 3, dw = 4) %
368          rna(name = 'lacZ', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 4, dw = 5) %
369          rna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 5, dw = 6) %
370          rna(name = 'lacZ', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 6, dw = 7) %
371          rna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = 7, dw = 8) %
372          rna(name = 'lacY', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 8, dw = 9) %
373          rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 9, dw = 10) %
374          rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 10, dw = 11) %
375          rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 11, dw = 12) %
376          rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 12, dw = 13) %
377          rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 13, dw = 14) %
378          rna(name = 'lacA', type = 'ter2', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 14, dw = None),
379          Parameter('t0_rna_lacZlacYlacA_form2', 0))
380 Observable('obs_rna_lacZlacYlacA_form2',
381          rna(name = 'lacZ', type = 'pro3', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = None, dw = 1) %
382          rna(name = 'lacZ', type = 'pro2', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 1, dw = 2) %
383          rna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = 2, dw = 3) %
384          rna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = 3, dw = 4) %
385          rna(name = 'lacZ', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 4, dw = 5) %
386          rna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 5, dw = 6) %
387          rna(name = 'lacZ', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 6, dw = 7) %
388          rna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = 7, dw = 8) %
389          rna(name = 'lacY', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 8, dw = 9) %
390          rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 9, dw = 10) %
391          rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 10, dw = 11) %
392          rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 11, dw = 12) %
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393         rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =␣
     ↪None, rna = None, up = 12, dw = 13) %
394         rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =␣
     ↪None, rna = None, up = 13, dw = 14) %
395         rna(name = 'lacA', type = 'ter2', loc = 'cyt', dna = None, met = None, prot =␣
     ↪None, rna = None, up = 14, dw = None))
396 Initial(rna(name = 'lacZ', type = 'pro2', loc = 'cyt', dna = None, met = None, prot =␣
     ↪None, rna = None, up = None, dw = 1) %
397         rna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', dna = None, met = None,␣
     ↪prot = None, rna = None, up = 1, dw = 2) %
398         rna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', dna = None, met = None,␣
     ↪prot = None, rna = None, up = 2, dw = 3) %
399         rna(name = 'lacZ', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =␣
     ↪None, rna = None, up = 3, dw = 4) %
400         rna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =␣
     ↪None, rna = None, up = 4, dw = 5) %
401         rna(name = 'lacZ', type = 'cds', loc = 'cyt', dna = None, met = None, prot =␣
     ↪None, rna = None, up = 5, dw = 6) %
402         rna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, met = None,␣
     ↪prot = None, rna = None, up = 6, dw = 7) %
403         rna(name = 'lacY', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =␣
     ↪None, rna = None, up = 7, dw = 8) %
404         rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =␣
     ↪None, rna = None, up = 8, dw = 9) %
405         rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =␣
     ↪None, rna = None, up = 9, dw = 10) %
406         rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =␣
     ↪None, rna = None, up = 10, dw = 11) %
407         rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =␣
     ↪None, rna = None, up = 11, dw = 12) %
408         rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =␣
     ↪None, rna = None, up = 12, dw = None),
409         Parameter('t0_rna_lacZlacYlacA_form3', 0))
410 Observable('obs_rna_lacZlacYlacA_form3',
411         rna(name = 'lacZ', type = 'pro2', loc = 'cyt', dna = None, met = None, prot =␣
     ↪None, rna = None, up = None, dw = 1) %
412         rna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', dna = None, met = None,␣
     ↪prot = None, rna = None, up = 1, dw = 2) %
413         rna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', dna = None, met = None,␣
     ↪prot = None, rna = None, up = 2, dw = 3) %
414         rna(name = 'lacZ', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =␣
     ↪None, rna = None, up = 3, dw = 4) %
415         rna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =␣
     ↪None, rna = None, up = 4, dw = 5) %
416         rna(name = 'lacZ', type = 'cds', loc = 'cyt', dna = None, met = None, prot =␣
     ↪None, rna = None, up = 5, dw = 6) %
417         rna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, met = None,␣
     ↪prot = None, rna = None, up = 6, dw = 7) %
418         rna(name = 'lacY', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =␣
     ↪None, rna = None, up = 7, dw = 8) %
419         rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =␣
     ↪None, rna = None, up = 8, dw = 9) %
420         rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =␣
     ↪None, rna = None, up = 9, dw = 10) %
421         rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =␣
     ↪None, rna = None, up = 10, dw = 11) %
422         rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =␣
     ↪None, rna = None, up = 11, dw = 12) %
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423          rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 12, dw = None))
424  Initial(rna(name = 'lacZ', type = 'pro2', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = None, dw = 1) %
425          rna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = 1, dw = 2) %
426          rna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = 2, dw = 3) %
427          rna(name = 'lacZ', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 3, dw = 4) %
428          rna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 4, dw = 5) %
429          rna(name = 'lacZ', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 5, dw = 6) %
430          rna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = 6, dw = 7) %
431          rna(name = 'lacY', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 7, dw = 8) %
432          rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 8, dw = 9) %
433          rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 9, dw = 10) %
434          rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 10, dw = 11) %
435          rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 11, dw = 12) %
436          rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 12, dw = 13) %
437          rna(name = 'lacA', type = 'ter2', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 13, dw = None),
438          Parameter('t0_rna_lacZlacYlacA_form4', 0))
439  Observable('obs_rna_lacZlacYlacA_form4',
440          rna(name = 'lacZ', type = 'pro2', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = None, dw = 1) %
441          rna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = 1, dw = 2) %
442          rna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = 2, dw = 3) %
443          rna(name = 'lacZ', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 3, dw = 4) %
444          rna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 4, dw = 5) %
445          rna(name = 'lacZ', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 5, dw = 6) %
446          rna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = 6, dw = 7) %
447          rna(name = 'lacY', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 7, dw = 8) %
448          rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 8, dw = 9) %
449          rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 9, dw = 10) %
450          rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 10, dw = 11) %
451          rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 11, dw = 12) %
452          rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 12, dw = 13) %
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453          rna(name = 'lacA', type = 'ter2', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 13, dw = None))
454  Initial(rna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', dna = None, met = None,␣
    ↪prot = None, rna = None, up = None, dw = 1) %
455          rna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', dna = None, met = None,␣
    ↪prot = None, rna = None, up = 1, dw = 2) %
456          rna(name = 'lacZ', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 2, dw = 3) %
457          rna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 3, dw = 4) %
458          rna(name = 'lacZ', type = 'cds', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 4, dw = 5) %
459          rna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, met = None,␣
    ↪prot = None, rna = None, up = 5, dw = 6) %
460          rna(name = 'lacY', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 6, dw = 7) %
461          rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 7, dw = 8) %
462          rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 8, dw = 9) %
463          rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 9, dw = 10) %
464          rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 10, dw = 11) %
465          rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 11, dw = None),
466          Parameter('t0_rna_lacZlacYlacA_form5', 0))
467  Observable('obs_rna_lacZlacYlacA_form5',
468          rna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', dna = None, met = None,␣
    ↪prot = None, rna = None, up = None, dw = 1) %
469          rna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', dna = None, met = None,␣
    ↪prot = None, rna = None, up = 1, dw = 2) %
470          rna(name = 'lacZ', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 2, dw = 3) %
471          rna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 3, dw = 4) %
472          rna(name = 'lacZ', type = 'cds', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 4, dw = 5) %
473          rna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, met = None,␣
    ↪prot = None, rna = None, up = 5, dw = 6) %
474          rna(name = 'lacY', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 6, dw = 7) %
475          rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 7, dw = 8) %
476          rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 8, dw = 9) %
477          rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 9, dw = 10) %
478          rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 10, dw = 11) %
479          rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 11, dw = None))
480  Initial(rna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', dna = None, met = None,␣
    ↪prot = None, rna = None, up = None, dw = 1) %
481          rna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', dna = None, met = None,␣
    ↪prot = None, rna = None, up = 1, dw = 2) %
482          rna(name = 'lacZ', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =␣
    ↪None, rna = None, up = 2, dw = 3) %
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483              rna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 3, dw = 4) %
484              rna(name = 'lacZ', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 4, dw = 5) %
485              rna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = 5, dw = 6) %
486              rna(name = 'lacY', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 6, dw = 7) %
487              rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 7, dw = 8) %
488              rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 8, dw = 9) %
489              rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 9, dw = 10) %
490              rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 10, dw = 11) %
491              rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 11, dw = 12) %
492              rna(name = 'lacA', type = 'ter2', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 12, dw = None),
493          Parameter('t0_rna_lacZlacYlacA_form6', 0))
494  Observable('obs_rna_lacZlacYlacA_form6',
495              rna(name = 'lacI_72_92', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = None, dw = 1) %
496              rna(name = 'lacI_21_1', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = 1, dw = 2) %
497              rna(name = 'lacZ', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 2, dw = 3) %
498              rna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 3, dw = 4) %
499              rna(name = 'lacZ', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 4, dw = 5) %
500              rna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = 5, dw = 6) %
501              rna(name = 'lacY', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 6, dw = 7) %
502              rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 7, dw = 8) %
503              rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 8, dw = 9) %
504              rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 9, dw = 10) %
505              rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 10, dw = 11) %
506              rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 11, dw = 12) %
507              rna(name = 'lacA', type = 'ter2', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 12, dw = None))
508  Initial(rna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = None, dw = 1) %
509              rna(name = 'lacZ', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 1, dw = 2) %
510              rna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, met = None,
     →prot = None, rna = None, up = 2, dw = 3) %
511              rna(name = 'lacY', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 3, dw = 4) %
512              rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 4, dw = 5) %
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513          rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 5, dw = 6) %
514          rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 6, dw = 7) %
515          rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 7, dw = 8) %
516          rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 8, dw = None),
517          Parameter('t0_rna_lacZlacYlacA_form7', 0))
518  Observable('obs_rna_lacZlacYlacA_form7',
519          rna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = None, dw = 1) %
520          rna(name = 'lacZ', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 1, dw = 2) %
521          rna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, met = None,
    →prot = None, rna = None, up = 2, dw = 3) %
522          rna(name = 'lacY', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 3, dw = 4) %
523          rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 4, dw = 5) %
524          rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 5, dw = 6) %
525          rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 6, dw = 7) %
526          rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 7, dw = 8) %
527          rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 8, dw = None))
528  Initial(rna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = None, dw = 1) %
529          rna(name = 'lacZ', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 1, dw = 2) %
530          rna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, met = None,
    →prot = None, rna = None, up = 2, dw = 3) %
531          rna(name = 'lacY', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 3, dw = 4) %
532          rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 4, dw = 5) %
533          rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 5, dw = 6) %
534          rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 6, dw = 7) %
535          rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 7, dw = 8) %
536          rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 8, dw = 9) %
537          rna(name = 'lacA', type = 'ter2', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 9, dw = None),
538          Parameter('t0_rna_lacZlacYlacA_form8', 0))
539  Observable('obs_rna_lacZlacYlacA_form8',
540          rna(name = 'lacZ', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = None, dw = 1) %
541          rna(name = 'lacZ', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 1, dw = 2) %
542          rna(name = 'lacI_422_402', type = 'BS', loc = 'cyt', dna = None, met = None,
    →prot = None, rna = None, up = 2, dw = 3) %
543          rna(name = 'lacY', type = 'pro1', loc = 'cyt', dna = None, met = None, prot =
    →None, rna = None, up = 3, dw = 4) %
```

```
544          rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 4, dw = 5) %
545          rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 5, dw = 6) %
546          rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 6, dw = 7) %
547          rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 7, dw = 8) %
548          rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 8, dw = 9) %
549          rna(name = 'lacA', type = 'ter2', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 9, dw = None))
550 Initial(rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = None, dw = 1) %
551          rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 1, dw = 2) %
552          rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 2, dw = 3) %
553          rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 3, dw = 4) %
554          rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 4, dw = None),
555          Parameter('t0_rna_lacZlacYlacA_form9', 0))
556 Observable('obs_rna_lacZlacYlacA_form9',
557          rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = None, dw = 1) %
558          rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 1, dw = 2) %
559          rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 2, dw = 3) %
560          rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 3, dw = 4) %
561          rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 4, dw = None))
562 Initial(rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = None, dw = 1) %
563          rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 1, dw = 2) %
564          rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 2, dw = 3) %
565          rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 3, dw = 4) %
566          rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 4, dw = 5) %
567          rna(name = 'lacA', type = 'ter2', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 5, dw = None),
568          Parameter('t0_rna_lacZlacYlacA_form10', 0))
569 Observable('obs_rna_lacZlacYlacA_form10',
570          rna(name = 'lacY', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = None, dw = 1) %
571          rna(name = 'lacY', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 1, dw = 2) %
572          rna(name = 'lacA', type = 'rbs', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 2, dw = 3) %
573          rna(name = 'lacA', type = 'cds', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 3, dw = 4) %
574          rna(name = 'lacA', type = 'ter1', loc = 'cyt', dna = None, met = None, prot =
     →None, rna = None, up = 4, dw = 5) %
```

```
575          rna(name = 'lacA', type = 'ter2', loc = 'cyt', dna = None, met = None, prot =␣
     ↪None, rna = None, up = 5, dw = None))
```

SIMULATION

Simulation could be done within the PySB python package (See more at PySB documentation) . Here is the relevant code that able the simulation of any PySB model, albeit PySB exports the model, calls the simulator, and imports the results under the hood. See *Plotting* for a simple example on how to plot simulation results.

```
1  # simulation
2  bng = '/opt/git-repositories/bionetgen.RuleWorld/bng2/'
3  kasim = '/opt/git-repositories/KaSim4.Kappa-Dev/'
4  cupsoda = '/opt/git-repositories/cupSODA.aresio/'
5  stochkit = '/opt/git-repositories/StochKit.StochSS' # not the bin folder
6
7  data0 = simulation.scipy(model, start = 0, finish = 10, points = 2000)
8  data1 = simulation.cupsoda(model, start = 0, finish = 10, points = 2000, path =
   →cupsoda) # only if you have a GPU NVIDIA; comment if not.
9  data2 = simulation.bngODE(model, start = 0, finish = 10, points = 2000, path = bng)
10 data3 = simulation.bngSSA(model, start = 0, finish = 10, points = 2000, n_runs = 20,
   →path = bng)
11 data4 = simulation.bngPLA(model, start = 0, finish = 10, points = 2000, n_runs = 20,
   →path = bng)
12 data5 = simulation.bngNF(model, start = 0, finish = 10, points = 2000, n_runs = 20,
   →path = bng)
13 data6 = simulation.kasim(model, start = 0, finish = 10, points = 2000, n_runs = 20,
   →path = kasim)
14 data7 = simulation.stochkit(model, start = 0, finish = 10, points = 2000, n_runs = 20,
   → path = stochkit)
```

Note: Please follow the instructions at BioNetGen and at KaSim documentations to install the stochactic simulators. Also, you could install the simulators from here if you have anaconda or conda installed on your system.

In the case of the cupSODA, modify the compile.sh file to match the compute architecture of your NVIDIA GPU and compile the executable as `cupSODA`.

For network-based simulations (Ordinary Differential Equations and Gillespie's algorithm), BioNetGen is required to perform the network generation. Change the corresponding paths (lines 2-5) to match the parent folder for the BNG2.pl or KaSim executable.

PLOTTING

The simulation functions returns a dataframe in the case of deterministic simulations and a dictionary in the case of stochastic simulations:

- The `sims` key of the dictionary is a list of dataframes, one for each simulation.
- The `avrg` key is a dataframe with the average of all simulations.
- The `stdv` key is a dataframe with the standard deviation of all simulations.

We provide three kind of plots: `plot` (continuous line), `scatter`, and `fill_between` (avrg $\pm$ weight * stdv).

The `plt_kws` is a dictionary that aids to pass arguments to the matplotlib functions used to plot the results.

To plot an `observable`, please execute one of the following functions:

- dna: `atlas_rbm.simulation.plot.dna(data, dna_name, plt_kws, **kwargs)`
- rna: `atlas_rbm.simulation.plot.rna(data, rna_name, plt_kws, **kwargs)`
- complexes: `atlas_rbm.simulation.plot.cplx(data, complex_name, location, plt_kws, **kwargs)`
- metabolites: `atlas_rbm.simulation.plot.metabolite(data, metabolite, location, plt_kws, **kwargs)`
- proteins: `atlas_rbm.simulation.plot.protein(data, protein_name, location, plt_kws, **kwargs)`

You could explore the available observables with `model.observable.observables._map.keys()` and use the name of the observable:

- observable: `atlas_rbm.simulation.plot.monomer(data, observable_name, plt_kws, **kwargs)`

```python
import seaborn
import matplotlib.pyplot as plt

palette = seaborn.color_palette('colorblind')

for kind in ['scatter', 'plot']:
    # first plot, periplasmic concentration
    fig, ax = plt.subplots(1, 2, figsize = (4*2, 3*1), dpi = 100)

    simulation.plot.metabolite(data3['avrg'], 'Alpha_lactose', 'per', ax = ax[0], **{
'kind' : kind},
        plt_kws = {'s' : 2, 'color' : palette[0], 'label' : r'$\alpha$-lactose [PER]',
 'alpha' : .5})

```

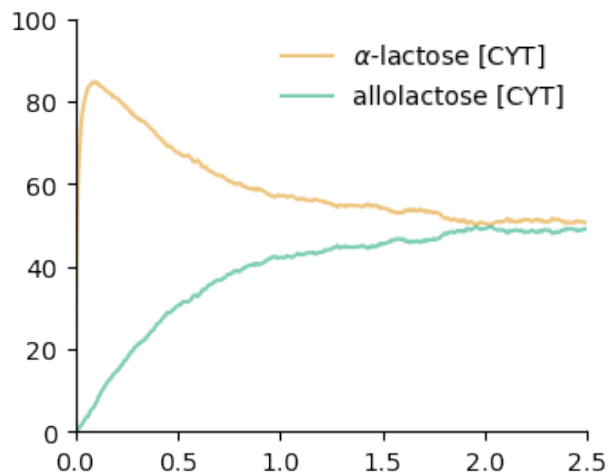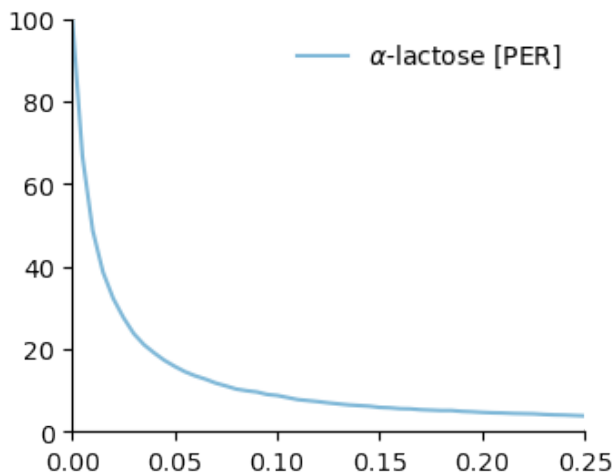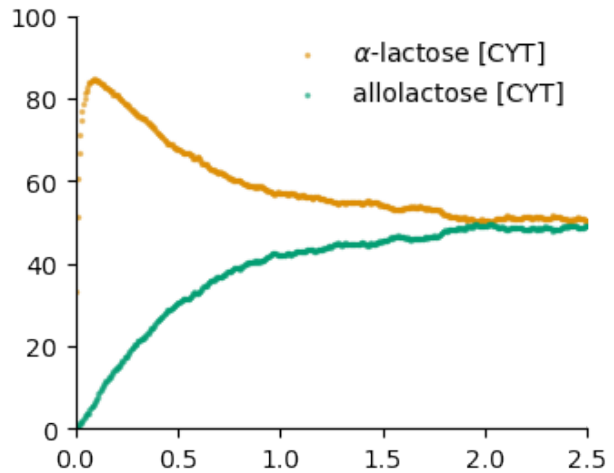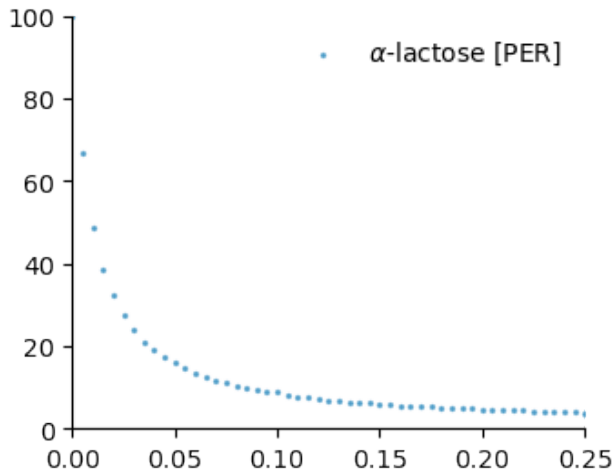(continues on next page)

```
13      simulation.plot.metabolite(data3['avrg'], 'Alpha_lactose', 'cyt', ax = ax[1], **{
    ↪'kind' : kind},
14          plt_kws = {'s' : 2, 'color' : palette[1], 'label' : r'$\alpha$-lactose [CYT]',
    ↪ 'alpha' : .5})
15
16      simulation.plot.metabolite(data3['avrg'], 'ALLOLACTOSE', 'cyt', ax = ax[1], **{
    ↪'kind' : kind},
17          plt_kws = {'s' : 2, 'color' : palette[2], 'label' : r'allolactose [CYT]',
    ↪'alpha' : .5})
18
19      ax[0].set_xlim((0,.25))
20      ax[1].set_xlim((0,2.5))
21      ax[0].set_ylim((0,100))
22      ax[1].set_ylim((0,100))
23
24      seaborn.despine()
```



```
1  import seaborn
2  import matplotlib.pyplot as plt
3
4  palette = seaborn.color_palette('colorblind')
```

Chapter 5. Plotting

```
5
6   # first plot, periplasmic concentration
7   fig, ax = plt.subplots(1, 2, figsize = (4*2, 3*1), dpi = 100)
8   simulation.plot.metabolite(data3, 'Alpha_lactose', 'per', ax = ax[0], **{'kind' :
    →'fill_between', 'weight' : .5},
9     plt_kws = {'s' : 2, 'color' : palette[0], 'label' : r'$\alpha$-lactose [PER]',
    →'alpha' : .5})
10
11  # second plot, cytoplasmic concentration
12  simulation.plot.metabolite(data3, 'Alpha_lactose', 'cyt', ax = ax[1], **{'kind' :
    →'fill_between', 'weight' : .5},
13    plt_kws = {'s' : 2, 'color' : palette[1], 'label' : r'$\alpha$-lactose [CYT]',
    →'alpha' : .5})
14
15  # second plot, cytoplasmic concentration
16  simulation.plot.metabolite(data3, 'ALLOLACTOSE', 'cyt', ax = ax[1], **{'kind' : 'fill_
    →between', 'weight' : .5},
17    plt_kws = {'s' : 2, 'color' : palette[2], 'label' : r'allolactose [CYT]', 'alpha'␣
    →: .5})
18
19  # first plot, periplasmic concentration
20  simulation.plot.metabolite(data0, 'Alpha_lactose', 'per', ax = ax[0], **{'kind' :
    →'plot'},
21    plt_kws = {'s' : 2, 'color' : palette[0], 'label' : r'ODE'})
22
23  # second plot, cytoplasmic concentration
24  simulation.plot.metabolite(data0, 'Alpha_lactose', 'cyt', ax = ax[1], **{'kind' :
    →'plot'},
25    plt_kws = {'s' : 2, 'color' : palette[1], 'label' : r'ODE'})
26
27  # second plot, cytoplasmic concentration
28  simulation.plot.metabolite(data0, 'ALLOLACTOSE', 'cyt', ax = ax[1], **{'kind' : 'plot
    →'},
29    plt_kws = {'s' : 2, 'color' : palette[2], 'label' : r'ODE'})
30
31  ax[0].set_xlim((0,.25))
32  ax[1].set_xlim((0,2.5))
33  ax[0].set_ylim((0,100))
34  ax[1].set_ylim((0,100))
35
36  seaborn.despine()
```
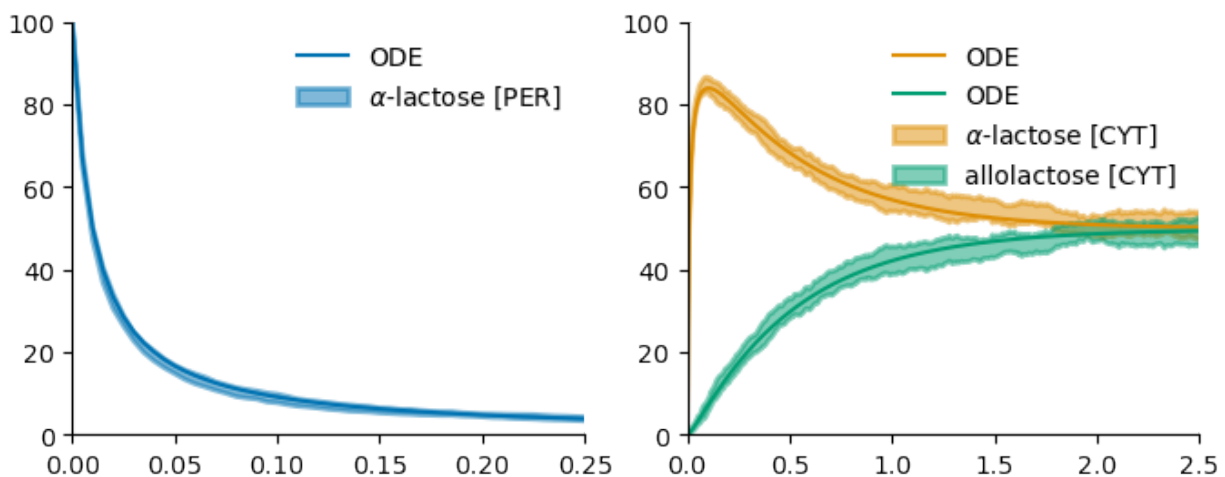
Note: *Atlas* produces automatically `Observables` for metabolites and other components. However, *Atlas* do not produce `Observables` for every possible component and the user could add observables with `atlas_rbm.` `simulation.set_observable(model, pattern, alias)`.

EXPORT TO

The PySB python package could export to different languages (See more here). Use the following code to export to the supported formats:

```
1   # export to
2   export.to_sbml(model, 'export-to-sbml.sbml')
3   export.to_matlab(model, 'export-to-matlab.m')
4   export.to_mathematica(model, 'export-to-mathematica.wl')
5   export.to_potterswheel(model, 'export-to-potterswheel.m')
6   export.to_bngl(model, 'export-to-bngl.bngl')
7   export.to_bngnet(model, 'export-to-bngnet.net')
8   export.to_kappa(model, 'export-to-kappa.kappa')
9   export.to_python(model, 'export-to-python.py')
10  export.to_pysb(model, 'export-to-pysb.py')
11  export.to_stochkit(model, 'export-to-stochkit.xml')
12  export.to_json(model, 'export-to-json.json')
```

Note: In the case of matlab, mathematica, potterswheel, python, and stochkit, PySB requires to expand the rules to determine all mass-balances to write ODE-based models, a proccess call network generation and could take excessive time to finish.

INDICES AND TABLES

- genindex
- modindex
- search