
atlas Documentation

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Apr 29, 2020

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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).

INSTALLATION

There are two different ways to install Atlas:

1. **Install Atlas natively (Recommended).**

OR

2. **Clone the Github repository.** If you are familiar with git, Atlas can be cloned and the respective folder added to the python path. 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>

1.1 Option 1: 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` folder 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 invoke. 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.

1.2 Option 2: 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*

2.1 Metabolic Networks

Metabolic networks have four columns. The first declares a unique name for the enzyme or enzymatic complex; the second declares a unique name for the reaction; the third column lists using comma unique names for substrates; and the last row list using comma unique names for products. To declare metabolites located at the periplasm or extracellular compartments, the user should employ the prefix “PER-” and “EX-”, respectively. Use *spontaneous* for non-enzymatic reactions.

Examples:

	GENE	REACTION	SUBSTRATES	PRODUCTS	FWD_RATE	RVS_RATE
1	spontaneous	LACTOSE-MUTAROTATION		alpha-lactose	beta-	
2	↪lactose	1.0	1.0			
3	spontaneous	GALACTOSE-MUTAROTATION		alpha-GALACTOSE	beta-	
4	↪GALACTOSE	1.0	1.0			
5	spontaneous	GLUCOSE-MUTAROTATION		alpha-glucose	beta-	
6	↪glucose	1.0	1.0			
7	MEM-LACY-MONOMER	TRANS-RXN-24		PER-PROTON, PER-alpha-		
8	↪lactose	PROTON, alpha-lactose		1.0	0.0	
9	MEM-LACY-MONOMER	TRANS-RXN-24-beta		PER-PROTON, PER-beta-		
10	↪lactose	PROTON, beta-lactose		1.0	0.0	
11	MEM-LACY-MONOMER	TRANS-RXN-94		PER-PROTON, PER-MELIBIOSE		PROTON, ↪
12	↪MELIBIOSE	1.0	1.0			
13	MEM-LACY-MONOMER	RXN0-7215		PER-PROTON, PER-CPD-3561		PROTON, CPD-
14	↪3561	1.0	1.0			

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9	MEM-LACY-MONOMER	RXN0-7217	PER-PROTON, PER-CPD-3785	PROTON, CPD-
	↪3785	1.0	1.0	
10	MEM-LACY-MONOMER	RXN-17755	PER-PROTON, PER-CPD-3801	PROTON, CPD-
	↪3801	1.0	1.0	
11	BETAGALACTOSID-CPLX	BETAGALACTOSID-RXN	beta-lactose, WATER	beta-
	↪GALACTOSE, beta-glucose	1.0	0.0	
12	BETAGALACTOSID-CPLX	BETAGALACTOSID-RXN-alpha	alpha-lactose, WATER	alpha-
	↪WATER	alpha-GALACTOSE, alpha-glucose	1.0	0.0
13	BETAGALACTOSID-CPLX	RXN0-5363	alpha-lactose	alpha-
	↪ALLOLACTOSE	1.0	1.0	
14	BETAGALACTOSID-CPLX	RXN0-5363-beta	beta-lactose	beta-
	↪ALLOLACTOSE	1.0	1.0	
15	BETAGALACTOSID-CPLX	ALLOLACTOSE-DEG-alpha	alpha-	
	↪ALLOLACTOSE	alpha-GALACTOSE, alpha-glucose	1.0	0.0
16	BETAGALACTOSID-CPLX	ALLOLACTOSE-DEG-beta	beta-ALLOLACTOSE	beta-
	↪GALACTOSE, beta-glucose	1.0	0.0	
17	BETAGALACTOSID-CPLX	RXN-17726	CPD-3561, WATER	beta-GALACTOSE, WATER
	↪Fructofuranose	1.0	1.0	
18	BETAGALACTOSID-CPLX	RXN0-7219	CPD-3785, WATER	beta-GALACTOSE, D-
	↪ARABINOSE	1.0	1.0	
19	GALACTOACETYLTRAN-CPLX	GALACTOACETYLTRAN-RXN-galactose	beta-GALACTOSE, WATER	
	↪ACETYL-COA	6-Acetyl-beta-D-Galactose, CO-A	1.0	1.0

OR

1	GENE	REACTION	SUBSTRATES	PRODUCTS	FWD_RATE	RVS_RATE
2	spontaneous	LACTOSE-MUTAROTATION		alpha-lactose	beta-	
	↪lactose	1.0	1.0			
3	spontaneous	GALACTOSE-MUTAROTATION		alpha-GALACTOSE	beta-	
	↪GALACTOSE	1.0	1.0			
4	spontaneous	GLUCOSE-MUTAROTATION		alpha-glucose	beta-	
	↪glucose	1.0	1.0			
5	MEM-lacY	TRANS-RXN-24	PER-PROTON, PER-alpha-lactose		PROTON, WATER	
	↪alpha-lactose	1.0	0.0			
6	MEM-lacY	TRANS-RXN-24-beta	PER-PROTON, PER-beta-lactose		PROTON, WATER	
	↪beta-lactose	1.0	0.0			
7	MEM-lacY	TRANS-RXN-94	PER-PROTON, PER-MELIBIOSE		PROTON, WATER	
	↪MELIBIOSE	1.0	1.0			
8	MEM-lacY	RXN0-7215	PER-PROTON, PER-CPD-3561		PROTON, CPD-	
	↪3561	1.0	1.0			
9	MEM-lacY	RXN0-7217	PER-PROTON, PER-CPD-3785		PROTON, CPD-	
	↪3785	1.0	1.0			
10	MEM-lacY	RXN-17755	PER-PROTON, PER-CPD-3801		PROTON, CPD-	
	↪3801	1.0	1.0			
11	lacZ	BETAGALACTOSID-RXN	beta-lactose, WATER		beta-GALACTOSE, beta-	
	↪glucose	1.0	0.0			
12	lacZ	BETAGALACTOSID-RXN-alpha	alpha-lactose, WATER		alpha-	
	↪GALACTOSE, alpha-glucose	1.0	0.0			
13	lacZ	RXN0-5363	alpha-lactose	alpha-ALLOLACTOSE		1.
	↪0	1.0				
14	lacZ	RXN0-5363-beta	beta-lactose	beta-ALLOLACTOSE		1.
	↪0	1.0				
15	lacZ	ALLOLACTOSE-DEG-alpha	alpha-ALLOLACTOSE, WATER		alpha-	
	↪GALACTOSE, alpha-glucose	1.0	0.0			
16	lacZ	ALLOLACTOSE-DEG-beta	beta-ALLOLACTOSE, WATER		beta-GALACTOSE, WATER	
	↪beta-glucose	1.0	0.0			
17	lacZ	RXN-17726	CPD-3561, WATER	beta-GALACTOSE, WATER		
	↪Fructofuranose	1.0	1.0			

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18	lacZ	RXN0-7219	CPD-3785, WATER	beta-GALACTOSE, D-
	↪ARABINOSE	1.0	1.0	
19	lacA	GALACTOACETYLTRAN-RXN-galactose	beta-GALACTOSE, ACETYL-	
	↪COA	6-Acetyl-beta-D-Galactose, CO-A	1.0	1.0

OR

	GENE	REACTION	SUBSTRATES	PRODUCTS	FWD_RATE	RVS_RATE
1	spontaneous	LACTOSE-MUTAROTATION		alpha-lactose	beta-	
2	↪lactose	1.0	1.0			
3	spontaneous	GALACTOSE-MUTAROTATION		alpha-GALACTOSE	beta-	
	↪GALACTOSE	1.0	1.0			
4	spontaneous	GLUCOSE-MUTAROTATION		alpha-glucose	beta-	
	↪glucose	1.0	1.0			
5	MEM-lacY	TRANS-RXN-24	PER-PROTON, PER-alpha-lactose		PROTON, ↵	
	↪alpha-lactose	1.0	0.0			
6	MEM-lacY	TRANS-RXN-24-beta	PER-PROTON, PER-beta-lactose		PROTON, ↵	
	↪beta-lactose	1.0	0.0			
7	MEM-lacY	TRANS-RXN-94	PER-PROTON, PER-MELIBIOSE		PROTON, ↵	
	↪MELIBIOSE	1.0	1.0			
8	MEM-lacY	RXN0-7215	PER-PROTON, PER-CPD-3561		PROTON, CPD-	
	↪3561	1.0	1.0			
9	MEM-lacY	RXN0-7217	PER-PROTON, PER-CPD-3785		PROTON, CPD-	
	↪3785	1.0	1.0			
10	MEM-lacY	RXN-17755	PER-PROTON, PER-CPD-3801		PROTON, CPD-	
	↪3801	1.0	1.0			
11	[lacZ, lacZ, lacZ, lacZ]	BETAGALACTOSID-RXN	beta-lactose, ↵			
	↪WATER	beta-GALACTOSE, beta-glucose	1.0	0.0		
12	[lacZ, lacZ, lacZ, lacZ]	BETAGALACTOSID-RXN-alpha	alpha-lactose, ↵			
	↪WATER	alpha-GALACTOSE, alpha-glucose	1.0	0.0		
13	[lacZ, lacZ, lacZ, lacZ]	RXN0-5363	alpha-lactose	alpha-		
	↪ALLOLACTOSE	1.0	1.0			
14	[lacZ, lacZ, lacZ, lacZ]	RXN0-5363-beta	beta-lactose	beta-		
	↪ALLOLACTOSE	1.0	1.0			
15	[lacZ, lacZ, lacZ, lacZ]	ALLOLACTOSE-DEG-alpha	alpha-ALLOLACTOSE, ↵			
	↪WATER	alpha-GALACTOSE, alpha-glucose	1.0	0.0		
16	[lacZ, lacZ, lacZ, lacZ]	ALLOLACTOSE-DEG-beta	beta-ALLOLACTOSE, ↵			
	↪WATER	beta-GALACTOSE, beta-glucose	1.0	0.0		
17	[lacZ, lacZ, lacZ, lacZ]	RXN-17726	CPD-3561, WATER	beta-GALACTOSE, ↵		
	↪Fructofuranose	1.0	1.0			
18	[lacZ, lacZ, lacZ, lacZ]	RXN0-7219	CPD-3785, WATER	beta-GALACTOSE, ↵		
	↪D-ARABINOSE	1.0	1.0			
19	[lacA, lacA, lacA]	GALACTOACETYLTRAN-RXN-galactose	beta-GALACTOSE, ACETYL-			
	↪COA	6-Acetyl-beta-D-Galactose, CO-A	1.0	1.0		

Note: Visualization in Cytoscape. Transform the four-columns file into a two-columns file with the helper script “*Expand metabolic network.ipynb*”, paste the results in a new file, and import the network into Cytoscape. Colors and arrows remains to the user for customization.

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```

30     prot(name = 'LACY_MONOMER') +
31     met(name = 'PROTON', loc = 'per') +
32     met(name = 'beta_lactose', loc = 'per') |
33     prot(name = 'LACY_MONOMER') +
34     met(name = 'PROTON', loc = 'cyt') +
35     met(name = 'beta_lactose', loc = 'cyt'),
36     Parameter('fwd_TRANS_RXN_24_beta', 1),
37     Parameter('rvs_TRANS_RXN_24_beta', 1))
38
39 Rule('TRANS_RXN_94',
40     prot(name = 'LACY_MONOMER') +
41     met(name = 'PROTON', loc = 'per') +
42     met(name = 'MELIBIOSE', loc = 'per') |
43     prot(name = 'LACY_MONOMER') +
44     met(name = 'PROTON', loc = 'cyt') +
45     met(name = 'MELIBIOSE', loc = 'cyt'),
46     Parameter('fwd_TRANS_RXN_94', 1),
47     Parameter('rvs_TRANS_RXN_94', 1))
48
49 Rule('RXN0_7215', prot(name = 'LACY_MONOMER') +
50     met(name = 'PROTON', loc = 'per') +
51     met(name = 'CPD_3561', loc = 'per') |
52     prot(name = 'LACY_MONOMER') +
53     met(name = 'PROTON', loc = 'cyt') +
54     met(name = 'CPD_3561', loc = 'cyt'),
55     Parameter('fwd_RXN0_7215', 1),
56     Parameter('rvs_RXN0_7215', 1))
57
58 Rule('RXN0_7217', prot(name = 'LACY_MONOMER') +
59     met(name = 'PROTON', loc = 'per') +
60     met(name = 'CPD_3785', loc = 'per') |
61     prot(name = 'LACY_MONOMER') +
62     met(name = 'PROTON', loc = 'cyt') +
63     met(name = 'CPD_3785', loc = 'cyt'),
64     Parameter('fwd_RXN0_7217', 1),
65     Parameter('rvs_RXN0_7217', 1))
66
67 Rule('RXN_17755', prot(name = 'LACY_MONOMER') +
68     met(name = 'PROTON', loc = 'per') +
69     met(name = 'CPD_3801', loc = 'per') |
70     prot(name = 'LACY_MONOMER') +
71     met(name = 'PROTON', loc = 'cyt') +
72     met(name = 'CPD_3801', loc = 'cyt'),
73     Parameter('fwd_RXN_17755', 1),
74     Parameter('rvs_RXN_17755', 1))
75
76 Rule('BETAGALACTOSID_RXN',
77     cplx(name = 'BETAGALACTOSID_CPLX') +
78     met(name = 'beta_lactose', loc = 'cyt') +
79     met(name = 'WATER', loc = 'cyt') |
80     cplx(name = 'BETAGALACTOSID_CPLX') +
81     met(name = 'beta_GALACTOSE', loc = 'cyt') +
82     met(name = 'beta_glucose', loc = 'cyt'),
83     Parameter('fwd_BETAGALACTOSID_RXN', 1),
84     Parameter('rvs_BETAGALACTOSID_RXN', 1))
85
86 Rule('BETAGALACTOSID_RXN_alpha',

```

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```

87     cplx(name = 'BETAGALACTOSID_CPLX') +
88     met(name = 'alpha_lactose', loc = 'cyt') +
89     met(name = 'WATER', loc = 'cyt') |
90     cplx(name = 'BETAGALACTOSID_CPLX') +
91     met(name = 'alpha_GALACTOSE', loc = 'cyt') +
92     met(name = 'alpha_glucose', loc = 'cyt'),
93     Parameter('fwd_BETAGALACTOSID_RXN_alpha', 1),
94     Parameter('rvs_BETAGALACTOSID_RXN_alpha', 1))
95
96 Rule('RXN0_5363',
97     cplx(name = 'BETAGALACTOSID_CPLX') +
98     met(name = 'alpha_lactose', loc = 'cyt') |
99     cplx(name = 'BETAGALACTOSID_CPLX') +
100    met(name = 'alpha_ALLOLACTOSE', loc = 'cyt'),
101    Parameter('fwd_RXN0_5363', 1),
102    Parameter('rvs_RXN0_5363', 1))
103
104 Rule('RXN0_5363_beta',
105     cplx(name = 'BETAGALACTOSID_CPLX') +
106     met(name = 'beta_lactose', loc = 'cyt') |
107     cplx(name = 'BETAGALACTOSID_CPLX') +
108     met(name = 'beta_ALLOLACTOSE', loc = 'cyt'),
109     Parameter('fwd_RXN0_5363_beta', 1),
110     Parameter('rvs_RXN0_5363_beta', 1))
111
112 Rule('ALLOLACTOSE_DEG_alpha',
113     cplx(name = 'BETAGALACTOSID_CPLX') +
114     met(name = 'alpha_ALLOLACTOSE', loc = 'cyt') |
115     cplx(name = 'BETAGALACTOSID_CPLX') +
116     met(name = 'alpha_GALACTOSE', loc = 'cyt'),
117     Parameter('fwd_ALLOLACTOSE_DEG_alpha', 1),
118     Parameter('rvs_ALLOLACTOSE_DEG_alpha', 1))
119
120 Rule('ALLOLACTOSE_DEG_beta',
121     cplx(name = 'BETAGALACTOSID_CPLX') +
122     met(name = 'beta_ALLOLACTOSE', loc = 'cyt') |
123     cplx(name = 'BETAGALACTOSID_CPLX') +
124     met(name = 'beta_GALACTOSE', loc = 'cyt'),
125     Parameter('fwd_ALLOLACTOSE_DEG_beta', 1),
126     Parameter('rvs_ALLOLACTOSE_DEG_beta', 1))
127
128 Rule('RXN_17726',
129     cplx(name = 'BETAGALACTOSID_CPLX') +
130     met(name = 'CPD_3561', loc = 'cyt') +
131     met(name = 'WATER', loc = 'cyt') |
132     cplx(name = 'BETAGALACTOSID_CPLX') +
133     met(name = 'beta_GALACTOSE', loc = 'cyt') +
134     met(name = 'Fructofuranose', loc = 'cyt'),
135     Parameter('fwd_RXN_17726', 1),
136     Parameter('rvs_RXN_17726', 1))
137
138 Rule('RXN0_7219',
139     cplx(name = 'BETAGALACTOSID_CPLX') +
140     met(name = 'CPD_3785', loc = 'cyt') +
141     met(name = 'WATER', loc = 'cyt') |
142     cplx(name = 'BETAGALACTOSID_CPLX') +
143     met(name = 'beta_GALACTOSE', loc = 'cyt') +

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```

144     met(name = 'D_ARABINOSE', loc = 'cyt'),
145     Parameter('fwd_RXN0_7219', 1),
146     Parameter('rvs_RXN0_7219', 1))
147
148 Rule('GALACTOACETYLTRAN_RXN_galactose',
149     cplx(name = 'GALACTOACETYLTRAN_CPLX') +
150     met(name = 'beta_GALACTOSE', loc = 'cyt') +
151     met(name = 'ACETYL_COA', loc = 'cyt') |
152     cplx(name = 'GALACTOACETYLTRAN_CPLX') +
153     met(name = '_6_Acetyl_beta_D_Galactose', loc = 'cyt') +
154     met(name = 'CO_A', loc = 'cyt'),
155     Parameter('fwd_GALACTOACETYLTRAN_RXN_galactose', 1),
156     Parameter('rvs_GALACTOACETYLTRAN_RXN_galactose', 1))

```

Note: Reversibility of Rules. Atlas writes reversible *Rules* for each reaction declared in the network file. The `Parameter('rvs_RuleName', 1)` must be set to zero to define an irreversible reaction.

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 Monomers and Initials ([More here](#)). Run *Monomer+Initials+Observables from metabolic network.ipynb* to obtain automatically the necessary Monomers and Initials (including proteins and enzymatic complexes).

Plotting. The model can be observed only with the instantiation of Observables ([More here](#)). Run *Monomer+Initials+Observables from metabolic network.ipynb* to obtain automatically the all possible Observables for metabolites.

2.2 Protein-Protein Interaction Networks

Protein-protein interaction (PPI) interaction networks have two columns. In any order and for any number of components, each column lists using comma the interacting proteins or protein complexes. The user should employ brackets to enclose a list of proteins that are part of a complex.

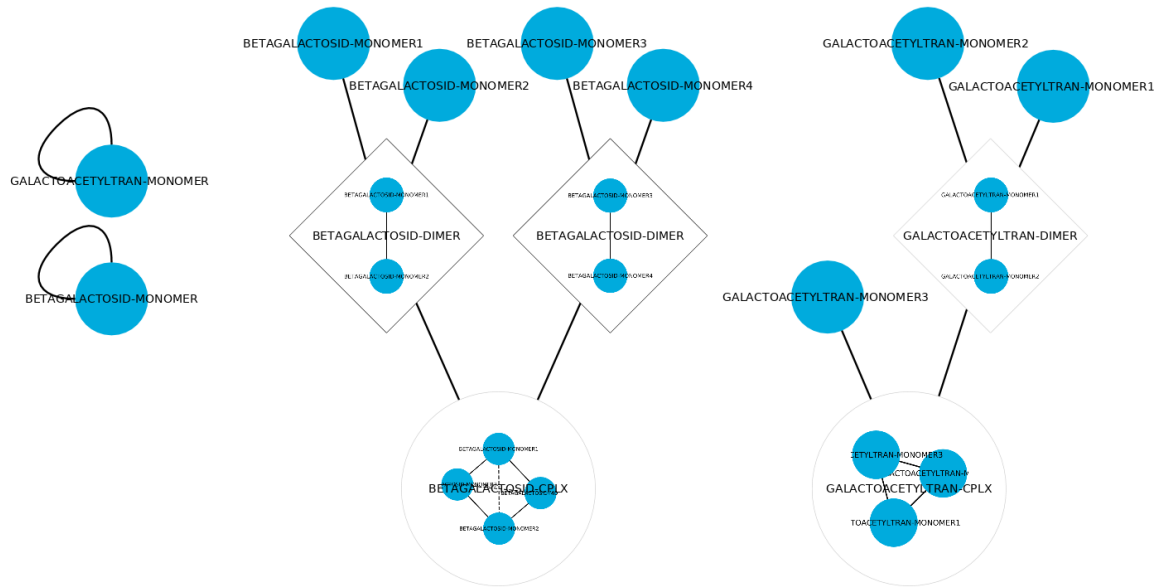
Examples:

	SOURCE	TARGET
1	BETAGALACTOSID-MONOMER	BETAGALACTOSID-MONOMER
2	GALACTOACETYLTRAN-MONOMER	GALACTOACETYLTRAN-MONOMER

OR

	SOURCE	TARGET
1	BETAGALACTOSID-MONOMER	BETAGALACTOSID-MONOMER
2	[BETAGALACTOSID-MONOMER, BETAGALACTOSID-MONOMER]	[BETAGALACTOSID-MONOMER, _
3	↔ BETAGALACTOSID-MONOMER]	
4	GALACTOACETYLTRAN-MONOMER	GALACTOACETYLTRAN-MONOMER
5	GALACTOACETYLTRAN-MONOMER	[GALACTOACETYLTRAN-MONOMER, GALACTOACETYLTRAN- ↔ MONOMER]

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 the “*Rules from protein-protein.ipynb*” to obtain the *Rules* to model the defined interaction network. The complete rule-based model can be found in the lactose folder from the Network Biology Lab GitHub repository [here](#).

```

1 Rule('complex_assembly_rule_0',
2     prot(name = 'BETAGALACTOSID_MONOMER', up = None, dw = None) +
3     prot(name = 'BETAGALACTOSID_MONOMER', up = None, dw = None) |
4     prot(name = 'BETAGALACTOSID_MONOMER', up = 1, dw = None) %
5     prot(name = 'BETAGALACTOSID_MONOMER', up = None, dw = 1),
6     Parameter('fwd_complex_assembly_rule_0', 1),
7     Parameter('rvs_complex_assembly_rule_0', 0))
8
9 Rule('complex_assembly_rule_1',
10     prot(name = 'BETAGALACTOSID_MONOMER', up = 1, dw = None) %
11     prot(name = 'BETAGALACTOSID_MONOMER', up = None, dw = 1) +
12     prot(name = 'BETAGALACTOSID_MONOMER', up = 1, dw = None) %
13     prot(name = 'BETAGALACTOSID_MONOMER', up = None, dw = 1) |
14     prot(name = 'BETAGALACTOSID_MONOMER', up = 1, dw = None) %
15     prot(name = 'BETAGALACTOSID_MONOMER', up = 2, dw = 1) %
16     prot(name = 'BETAGALACTOSID_MONOMER', up = 3, dw = 2) %
17     prot(name = 'BETAGALACTOSID_MONOMER', up = None, dw = 3),
18     Parameter('fwd_complex_assembly_rule_1', 1),
19     Parameter('rvs_complex_assembly_rule_1', 0))
20
21 Rule('complex_assembly_rule_2',
22     prot(name = 'GALACTOACETYLTRAN_MONOMER', up = None, dw = None) +
23     prot(name = 'GALACTOACETYLTRAN_MONOMER', up = None, dw = None) |
24     prot(name = 'GALACTOACETYLTRAN_MONOMER', up = 1, dw = None) %
25     prot(name = 'GALACTOACETYLTRAN_MONOMER', up = None, dw = 1),
26     Parameter('fwd_complex_assembly_rule_2', 1),
27     Parameter('rvs_complex_assembly_rule_2', 0))
28

```

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```

29 Rule('complex_assembly_rule_3',
30     prot(name = 'GALACTOACETYLTRAN_MONOMER', up = None, dw = None) +
31     prot(name = 'GALACTOACETYLTRAN_MONOMER', up = 1, dw = None) %
32     prot(name = 'GALACTOACETYLTRAN_MONOMER', up = None, dw = 1) |
33     prot(name = 'GALACTOACETYLTRAN_MONOMER', up = 1, dw = None) %
34     prot(name = 'GALACTOACETYLTRAN_MONOMER', up = 2, dw = 1) %
35     prot(name = 'GALACTOACETYLTRAN_MONOMER', up = None, dw = 2),
36     Parameter('fwd_complex_assembly_rule_3', 1),
37     Parameter('rvs_complex_assembly_rule_3', 0))

```

Note: Reversibility of Rules. Atlas writes irreversible *Rules* for each reaction declared in the network file. The `Parameter('rvs_RuleName', 0)` must be set to non-zero to define an reversible reaction.

Note: Uniqueness of Rule names. Atlas will write *Rules* with numbered names. Use only one file to model the many interactions the system has.

Note: Simulation. The model can be simulated only with the instantiation of Monomers and Initials ([More here](#)). Run *Monomer+Initials+Observables from metabolic network.ipynb* to obtain automatically the necessary Monomers and Initials (including proteins and enzymatic complexes). Manually add the necessary Monomers and Initials for non-enzymatic proteins.

Plotting. The model can be observed only with the instantiation of Observables ([More here](#)). Run *Monomer+Initials+Observables from metabolic network.ipynb* to obtain automatically the all possible Observables for enzymatic proteins. Other observables for proteins should be added manually.

2.3 Protein-Small compounds Interaction Networks

Protein-small compound interaction networks have two columns. Similar to a PPI network, but the user should add the prefix “SMALL-” to encode a small compound that interacts with the protein or protein complex.

Examples:

SOURCE	TARGET
PER-araF	SMALL-PER-alpha-L-arabinofuranose
PER-araF	SMALL-PER-beta-L-arabinofuranose
PER-araF	SMALL-PER-alpha-L-arabinopyranose
PER-araF	SMALL-PER-beta-L-arabinopyranose
[crp, crp]	SMALL-CAMP
[crp, SMALL-CAMP, crp]	SMALL-CAMP
[lacI, lacI]	SMALL-ALLOLACTOSE
[lacI, SMALL-ALLOLACTOSE, lacI]	SMALL-ALLOLACTOSE
[araG, araG]	SMALL-ATP
araC	SMALL-alpha-L-arabinopyranose
[araC, araC]	SMALL-alpha-L-arabinopyranose
[araC, SMALL-alpha-L-arabinopyranose, araC]	SMALL-alpha-L-arabinopyranose

Finally, execute the “*Rules from protein-small compounds.ipynb*” to obtain the *Rules* to model the defined interaction network. The complete rule-based model can be found in the arabinose folder from the Network Biology Lab GitHub repository [here](#).

```

1 Rule('ProtMet_RuleAssembly_1',
2     prot(name = 'araF', loc = 'per', met = None, up = None, dw = None) +
3     met(name = 'alpha_L_arabinofuranose', loc = 'per', prot = None) |
4     prot(name = 'araF', loc = 'per', met = 1, up = None, dw = None) %
5     met(name = 'alpha_L_arabinofuranose', loc = 'per', prot = 1),
6     Parameter('fwd_ProtMet_RuleAssembly_1', 1),
7     Parameter('rvs_ProtMet_RuleAssembly_1', 1))
8
9 Rule('ProtMet_RuleAssembly_2',
10     prot(name = 'araF', loc = 'per', met = None, up = None, dw = None) +
11     met(name = 'beta_L_arabinofuranose', loc = 'per', prot = None) |
12     prot(name = 'araF', loc = 'per', met = 1, up = None, dw = None) %
13     met(name = 'beta_L_arabinofuranose', loc = 'per', prot = 1),
14     Parameter('fwd_ProtMet_RuleAssembly_2', 1),
15     Parameter('rvs_ProtMet_RuleAssembly_2', 1))
16
17 Rule('ProtMet_RuleAssembly_3',
18     prot(name = 'araF', loc = 'per', met = None, up = None, dw = None) +
19     met(name = 'alpha_L_arabinopyranose', loc = 'per', prot = None) |
20     prot(name = 'araF', loc = 'per', met = 1, up = None, dw = None) %
21     met(name = 'alpha_L_arabinopyranose', loc = 'per', prot = 1),
22     Parameter('fwd_ProtMet_RuleAssembly_3', 1),
23     Parameter('rvs_ProtMet_RuleAssembly_3', 1))
24
25 Rule('ProtMet_RuleAssembly_4',
26     prot(name = 'araF', loc = 'per', met = None, up = None, dw = None) +
27     met(name = 'beta_L_arabinopyranose', loc = 'per', prot = None) |
28     prot(name = 'araF', loc = 'per', met = 1, up = None, dw = None) %
29     met(name = 'beta_L_arabinopyranose', loc = 'per', prot = 1),
30     Parameter('fwd_ProtMet_RuleAssembly_4', 1),
31     Parameter('rvs_ProtMet_RuleAssembly_4', 1))
32
33 Rule('ProtMet_RuleAssembly_5',
34     prot(name = 'crp', loc = 'cyt', met = None, up = None, dw = 1) %
35     prot(name = 'crp', loc = 'cyt', met = None, up = 1, dw = None) +
36     met(name = 'CAMP', loc = 'cyt', prot = None) |
37     prot(name = 'crp', loc = 'cyt', met = None, up = None, dw = 1) %
38     met(name = 'crp', loc = 'cyt', met = 2, up = 1, dw = None) %
39     met(name = 'CAMP', loc = 'cyt', prot = 2),
40     Parameter('fwd_ProtMet_RuleAssembly_5', 1),
41     Parameter('rvs_ProtMet_RuleAssembly_5', 1))
42
43 Rule('ProtMet_RuleAssembly_6',
44     prot(name = 'crp', loc = 'cyt', met = 2, up = None, dw = 1) %
45     met(name = 'CAMP', loc = 'cyt', prot = 2) %
46     prot(name = 'crp', loc = 'cyt', met = None, up = 1, dw = None) +
47     met(name = 'CAMP', loc = 'cyt', prot = None) |
48     prot(name = 'crp', loc = 'cyt', met = 2, up = None, dw = 1) %
49     met(name = 'CAMP', loc = 'cyt', prot = 2) %
50     prot(name = 'crp', loc = 'cyt', met = 3, up = 1, dw = None) %
51     met(name = 'CAMP', loc = 'cyt', prot = 3),
52     Parameter('fwd_ProtMet_RuleAssembly_6', 1),
53     Parameter('rvs_ProtMet_RuleAssembly_6', 1))
54
55 Rule('ProtMet_RuleAssembly_7',
56     prot(name = 'lacI', loc = 'cyt', met = None, up = None, dw = 1) %
57     prot(name = 'lacI', loc = 'cyt', met = None, up = 1, dw = None) +

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```

58     met(name = 'ALLOLACTOSE', loc = 'cyt', prot = None) |
59     prot(name = 'lacI', loc = 'cyt', met = None, up = None, dw = 1) %
60     prot(name = 'lacI', loc = 'cyt', met = 2, up = 1, dw = None) %
61     met(name = 'ALLOLACTOSE', loc = 'cyt', prot = 2),
62     Parameter('fwd_ProtMet_RuleAssembly_7', 1),
63     Parameter('rvs_ProtMet_RuleAssembly_7', 1))
64
65 Rule('ProtMet_RuleAssembly_8',
66     prot(name = 'lacI', loc = 'cyt', met = 2, up = None, dw = 1) %
67     met(name = 'ALLOLACTOSE', loc = 'cyt', prot = 2) %
68     prot(name = 'lacI', loc = 'cyt', met = None, up = 1, dw = None) +
69     met(name = 'ALLOLACTOSE', loc = 'cyt', prot = None) |
70     prot(name = 'lacI', loc = 'cyt', met = 2, up = None, dw = 1) %
71     met(name = 'ALLOLACTOSE', loc = 'cyt', prot = 2) %
72     prot(name = 'lacI', loc = 'cyt', met = 3, up = 1, dw = None) %
73     met(name = 'ALLOLACTOSE', loc = 'cyt', prot = 3),
74     Parameter('fwd_ProtMet_RuleAssembly_8', 1),
75     Parameter('rvs_ProtMet_RuleAssembly_8', 1))
76
77 Rule('ProtMet_RuleAssembly_9',
78     prot(name = 'araG', loc = 'cyt', met = None, up = None, dw = 1) %
79     prot(name = 'araG', loc = 'cyt', met = None, up = 1, dw = None) +
80     met(name = 'ATP', loc = 'cyt', prot = None) |
81     prot(name = 'araG', loc = 'cyt', met = None, up = None, dw = 1) %
82     prot(name = 'araG', loc = 'cyt', met = 2, up = 1, dw = None) %
83     met(name = 'ATP', loc = 'cyt', prot = 2),
84     Parameter('fwd_ProtMet_RuleAssembly_9', 1),
85     Parameter('rvs_ProtMet_RuleAssembly_9', 1))
86
87 Rule('ProtMet_RuleAssembly_10',
88     prot(name = 'araC', loc = 'cyt', met = None, up = None, dw = 1) %
89     prot(name = 'araC', loc = 'cyt', met = None, up = 1, dw = None) +
90     met(name = 'alpha_L_arabinopyranose', loc = 'cyt', prot = None) |
91     prot(name = 'araC', loc = 'cyt', met = None, up = None, dw = 1) %
92     prot(name = 'araC', loc = 'cyt', met = 2, up = 1, dw = None) %
93     met(name = 'alpha_L_arabinopyranose', loc = 'cyt', prot = 2),
94     Parameter('fwd_ProtMet_RuleAssembly_10', 1),
95     Parameter('rvs_ProtMet_RuleAssembly_10', 1))
96
97 Rule('ProtMet_RuleAssembly_11',
98     prot(name = 'araC', loc = 'cyt', met = 2, up = None, dw = 1) %
99     met(name = 'alpha_L_arabinopyranose', loc = 'cyt', prot = 2) %
100    prot(name = 'araC', loc = 'cyt', met = None, up = 1, dw = None) +
101    met(name = 'alpha_L_arabinopyranose', loc = 'cyt', prot = None) |
102    prot(name = 'araC', loc = 'cyt', met = 2, up = None, dw = 1) %
103    met(name = 'alpha_L_arabinopyranose', loc = 'cyt', prot = 2) %
104    prot(name = 'araC', loc = 'cyt', met = 3, up = 1, dw = None) %
105    met(name = 'alpha_L_arabinopyranose', loc = 'cyt', prot = 3),
106    Parameter('fwd_ProtMet_RuleAssembly_11', 1),
107    Parameter('rvs_ProtMet_RuleAssembly_11', 1))

```

Note: Reversibility of Rules. Atlas writes reversible *Rules* for each reaction declared in the network file. The `Parameter('rvs_RuleName', 1)` must be set to zero to define an irreversible reaction.

Note: Uniqueness of Rule names. Atlas will write *Rules* with numbered names. Use only one file to model the many interactions the system has.

Note: Simulation. The model can be simulated only with the instantiation of *Monomers* and *Initials* ([More here](#)). Run *Monomer+Initials+Observables from metabolic network.ipynb* to obtain automatically the necessary *Monomers* and *Initials* (including proteins and enzymatic complexes). Manually add the necessary *Monomers* and *Initials* for non-enzymatic proteins.

Plotting. The model can be observed only with the instantiation of *Observables* ([More here](#)). Run *Monomer+Initials+Observables from metabolic network.ipynb* to obtain automatically the all possible *Observables* for enzymatic proteins. Other observables for proteins should be added manually.

2.4 Transcription Factor-DNA Binding Site Interaction Networks

The transcription factor-DNA binding site network represents the physical interaction between proteins and DNA. The network have two columns and for the former network, the first column lists using comma all components of a TF enclosed in brackets (optionally with small compounds) and in the second column declares the DNA binding site. Users should use the prefix “SMALL-” for small compounds and the prefix “BS-” to encode DNA binding sites using unique names. The second type of GRN shows in the first column the RNA polymerase holoenzyme complex (components in brackets) and in the second the promoter. Users should name promoters with the gene name followed by the suffix “-pro#” where # is an integer.

Examples:

```

1 SOURCE          TARGET
2 # araBAD and araC
3 [crp, SMALL-CAMP, crp, SMALL-CAMP]      BS-83-104
4 [crp, SMALL-CAMP, crp, SMALL-CAMP]      [BS-83-104, BS-araB-pro1]
5
6 araC          BS-35-51
7 araC          BS-56-72
8 araC          BS-109-125
9 araC          BS-130-146
10 araC         BS-267-283
11
12 [araC, BS-56-72]      [araC, BS-267-283, BS-araC-pro1]
13
14 [araC, SMALL-alpha-L-arabinopyranose]    BS-35-51
15 [araC, BS-56-72]      SMALL-alpha-L-arabinopyranose
16 [araC, BS-267-283]    SMALL-alpha-L-arabinopyranose
17
18 [araC, SMALL-alpha-L-arabinopyranose, BS-56-72]      [araC, SMALL-alpha-L-
19 ↪arabinopyranose, BS-35-51, BS-araB-pro1]
20 # araFGH
21 [araC, SMALL-alpha-L-arabinopyranose]    BS-158-174
22 [araC, SMALL-alpha-L-arabinopyranose]    BS-137-153
23 [araC, SMALL-alpha-L-arabinopyranose]    BS-83-99
24 [araC, SMALL-alpha-L-arabinopyranose]    BS-62-78
25
26 [araC, SMALL-alpha-L-arabinopyranose, BS-83-99]      [araC, SMALL-alpha-L-
27 ↪arabinopyranose, BS-62-78, BS-araF-pro1]

```

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```

27
28 # araE
29 [araC, SMALL-alpha-L-arabinopyranose]          BS-57-73
30 [araC, SMALL-alpha-L-arabinopyranose]          BS-36-52
31
32 [araC, SMALL-alpha-L-arabinopyranose, BS-57-73]      [araC, SMALL-alpha-L-
  ↪arabinopyranose, BS-36-52, BS-araE-pro1]

```

Finally, execute the “*Rules from tf-tfbs.ipynb*” to obtain the *Rules* to model the defined interaction network. The complete rule-based model can be found in the arabinose folder from the Network Biology Lab GitHub repository [here](#).

```

1 # [crp, SMALL_CAMP, crp, SMALL_CAMP] interacts with BS_83_104
2 Rule('TranscriptionFactorMet_AssemblyRule_1',
3     prot(name = 'crp', dna = None, met = 2, up = None, dw = 1) %
4     met(name = 'CAMP', prot = 3) %
5     prot(name = 'crp', dna = None, met = 3, up = 1, dw = None) %
6     met(name = 'CAMP', prot = 2) +
7     dna(name = 'BS_83_104', prot = None, free = 'True', up = WILD, dw = WILD) |
8     prot(name = 'crp', dna = None, met = 2, up = None, dw = 1) %
9     met(name = 'CAMP', prot = 3) %
10    prot(name = 'crp', dna = 4, met = 3, up = 1, dw = None) %
11    met(name = 'CAMP', prot = 2) %
12    dna(name = 'BS_83_104', prot = 4, free = 'False', up = WILD, dw = WILD),
13    Parameter('fwd_TranscriptionFactorMet_AssemblyRule_1', 0),
14    Parameter('rvs_TranscriptionFactorMet_AssemblyRule_1', 0))
15
16 # [crp, SMALL_CAMP, crp, SMALL_CAMP] interacts with [BS_83_104, BS_araB_pro1]
17 Rule('TranscriptionFactorMet_AssemblyRule_2',
18     prot(name = 'crp', dna = None, met = 2, up = None, dw = 1) %
19     met(name = 'CAMP', prot = 3) %
20     prot(name = 'crp', dna = None, met = 3, up = 1, dw = None) %
21     met(name = 'CAMP', prot = 2) +
22     dna(name = 'BS_83_104', prot = None, free = 'True', up = WILD, dw = WILD) %
23     dna(name = 'araB', type = 'pro1', prot = None, free = 'True', up = WILD, dw =
  ↪WILD) |
24     prot(name = 'crp', dna = None, met = 2, up = None, dw = 1) %
25     met(name = 'CAMP', prot = 3) %
26     prot(name = 'crp', dna = 4, met = 3, up = 1, dw = None) %
27     met(name = 'CAMP', prot = 2) %
28     dna(name = 'BS_83_104', prot = 4, free = 'False', up = WILD, dw = WILD) %
29     dna(name = 'araB', type = 'pro1', prot = None, free = 'False', up = WILD, dw =
  ↪WILD),
30     Parameter('fwd_TranscriptionFactorMet_AssemblyRule_2', 0),
31     Parameter('rvs_TranscriptionFactorMet_AssemblyRule_2', 0))
32
33 # araC interacts with BS_35_51
34 Rule('TranscriptionFactorMet_AssemblyRule_3',
35     prot(name = 'araC', dna = None, met = None, up = None, dw = None) +
36     dna(name = 'BS_35_51', prot = None, free = 'True', up = WILD, dw = WILD) |
37     prot(name = 'araC', dna = 1, met = None, up = None, dw = None) %
38     dna(name = 'BS_35_51', prot = 1, free = 'False', up = WILD, dw = WILD),
39     Parameter('fwd_TranscriptionFactorMet_AssemblyRule_3', 0),
40     Parameter('rvs_TranscriptionFactorMet_AssemblyRule_3', 0))
41
42 # araC interacts with BS_56_72

```

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```

43 Rule('TranscriptionFactorMet_AssemblyRule_4',
44     prot(name = 'araC', dna = None, met = None, up = None, dw = None) +
45     dna(name = 'BS_56_72', prot = None, free = 'True', up = WILD, dw = WILD) |
46     prot(name = 'araC', dna = 1, met = None, up = None, dw = None) %
47     dna(name = 'BS_56_72', prot = 1, free = 'False', up = WILD, dw = WILD),
48     Parameter('fwd_TranscriptionFactorMet_AssemblyRule_4', 0),
49     Parameter('rvs_TranscriptionFactorMet_AssemblyRule_4', 0))
50
51 # araC interacts with BS_109_125
52 Rule('TranscriptionFactorMet_AssemblyRule_5',
53     prot(name = 'araC', dna = None, met = None, up = None, dw = None) +
54     dna(name = 'BS_109_125', prot = None, free = 'True', up = WILD, dw = WILD) |
55     prot(name = 'araC', dna = 1, met = None, up = None, dw = None) %
56     dna(name = 'BS_109_125', prot = 1, free = 'False', up = WILD, dw = WILD),
57     Parameter('fwd_TranscriptionFactorMet_AssemblyRule_5', 0),
58     Parameter('rvs_TranscriptionFactorMet_AssemblyRule_5', 0))
59
60 # araC interacts with BS_130_146
61 Rule('TranscriptionFactorMet_AssemblyRule_6',
62     prot(name = 'araC', dna = None, met = None, up = None, dw = None) +
63     dna(name = 'BS_130_146', prot = None, free = 'True', up = WILD, dw = WILD) |
64     prot(name = 'araC', dna = 1, met = None, up = None, dw = None) %
65     dna(name = 'BS_130_146', prot = 1, free = 'False', up = WILD, dw = WILD),
66     Parameter('fwd_TranscriptionFactorMet_AssemblyRule_6', 0),
67     Parameter('rvs_TranscriptionFactorMet_AssemblyRule_6', 0))
68
69 # araC interacts with BS_267_283
70 Rule('TranscriptionFactorMet_AssemblyRule_7',
71     prot(name = 'araC', dna = None, met = None, up = None, dw = None) +
72     dna(name = 'BS_267_283', prot = None, free = 'True', up = WILD, dw = WILD) |
73     prot(name = 'araC', dna = 1, met = None, up = None, dw = None) %
74     dna(name = 'BS_267_283', prot = 1, free = 'False', up = WILD, dw = WILD),
75     Parameter('fwd_TranscriptionFactorMet_AssemblyRule_7', 0),
76     Parameter('rvs_TranscriptionFactorMet_AssemblyRule_7', 0))
77
78 # [araC, BS_56_72] interacts with [araC, BS_267_283, BS_araC_pro1]
79 Rule('TranscriptionFactorMet_AssemblyRule_8',
80     prot(name = 'araC', dna = 1, met = None, up = None, dw = None) %
81     dna(name = 'BS_56_72', prot = 1, free = 'False', up = WILD, dw = WILD) +
82     prot(name = 'araC', dna = 2, met = None, up = None, dw = None) %
83     dna(name = 'BS_267_283', prot = 2, free = 'False', up = WILD, dw = WILD) %
84     dna(name = 'araC', type = 'pro1', prot = None, free = 'False', up = WILD, dw_
85     ⇨= WILD) |
86     prot(name = 'araC', dna = None, met = None, up = None, dw = 1) %
87     dna(name = 'BS_56_72', prot = 2, free = 'False', up = WILD, dw = WILD) %
88     prot(name = 'araC', dna = 2, met = None, up = 1, dw = None) %
89     dna(name = 'BS_267_283', prot = None, free = 'False', up = WILD, dw = WILD) %
90     dna(name = 'araC', type = 'pro1', prot = None, free = 'False', up = WILD, dw_
91     ⇨= WILD),
92     Parameter('fwd_TranscriptionFactorMet_AssemblyRule_8', 0),
93     Parameter('rvs_TranscriptionFactorMet_AssemblyRule_8', 0))
94
95 # [araC, SMALL_alpha_L_arabinopyranose] interacts with BS_35_51
96 Rule('TranscriptionFactorMet_AssemblyRule_9',
97     prot(name = 'araC', dna = None, met = 1, up = None, dw = None) %
98     met(name = 'alpha_L_arabinopyranose', prot = 1) +
99     dna(name = 'BS_35_51', prot = None, free = 'True', up = WILD, dw = WILD) |

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```

98     prot(name = 'araC', dna = 2, met = 1, up = None, dw = None) %
99     met(name = 'alpha_L_arabinopyranose', prot = 1) %
100     dna(name = 'BS_35_51', prot = 2, free = 'False', up = WILD, dw = WILD),
101     Parameter('fwd_TranscriptionFactorMet_AssemblyRule_9', 0),
102     Parameter('rvs_TranscriptionFactorMet_AssemblyRule_9', 0))
103
104 # [araC, BS_56_72] interacts with SMALL_alpha_L_arabinopyranose
105 Rule('TranscriptionFactorMet_AssemblyRule_10',
106     prot(name = 'araC', dna = 1, met = None, up = None, dw = None) %
107     dna(name = 'BS_56_72', prot = 1, free = 'False', up = WILD, dw = WILD) +
108     met(name = 'alpha_L_arabinopyranose', prot = None) |
109     prot(name = 'araC', dna = 2, met = 1, up = None, dw = None) %
110     dna(name = 'BS_56_72', prot = 2, free = 'False', up = WILD, dw = WILD) %
111     met(name = 'alpha_L_arabinopyranose', prot = 1),
112     Parameter('fwd_TranscriptionFactorMet_AssemblyRule_10', 0),
113     Parameter('rvs_TranscriptionFactorMet_AssemblyRule_10', 0))
114
115 # [araC, BS_267_283] interacts with SMALL_alpha_L_arabinopyranose
116 Rule('TranscriptionFactorMet_AssemblyRule_11',
117     prot(name = 'araC', dna = 1, met = None, up = None, dw = None) %
118     dna(name = 'BS_267_283', prot = 1, free = 'False', up = WILD, dw = WILD) +
119     met(name = 'alpha_L_arabinopyranose', prot = None) |
120     prot(name = 'araC', dna = 2, met = 1, up = None, dw = None) %
121     dna(name = 'BS_267_283', prot = 2, free = 'False', up = WILD, dw = WILD) %
122     met(name = 'alpha_L_arabinopyranose', prot = 1),
123     Parameter('fwd_TranscriptionFactorMet_AssemblyRule_11', 0),
124     Parameter('rvs_TranscriptionFactorMet_AssemblyRule_11', 0))
125
126 # [araC, SMALL_alpha_L_arabinopyranose, BS_56_72] interacts with [araC, SMALL_alpha_L_
127 ↪ arabinopyranose, BS_35_51, BS_araB_prol]
128 Rule('TranscriptionFactorMet_AssemblyRule_12',
129     prot(name = 'araC', dna = 2, met = 1, up = None, dw = None) %
130     met(name = 'alpha_L_arabinopyranose', prot = 1) %
131     dna(name = 'BS_56_72', prot = 2, free = 'False', up = WILD, dw = WILD) +
132     prot(name = 'araC', dna = 4, met = 3, up = None, dw = None) %
133     met(name = 'alpha_L_arabinopyranose', prot = 3) %
134     dna(name = 'BS_35_51', prot = 4, free = 'False', up = WILD, dw = WILD) %
135     dna(name = 'araB', type = 'prol', prot = None, free = 'False', up = WILD, dw_
136 ↪ = WILD) |
137     prot(name = 'araC', dna = None, met = 2, up = None, dw = 1) %
138     met(name = 'alpha_L_arabinopyranose', prot = 3) %
139     dna(name = 'BS_56_72', prot = 4, free = 'False', up = WILD, dw = WILD) %
140     prot(name = 'araC', dna = 4, met = 3, up = 1, dw = None) %
141     met(name = 'alpha_L_arabinopyranose', prot = 2) %
142     dna(name = 'BS_35_51', prot = None, free = 'False', up = WILD, dw = WILD) %
143     dna(name = 'araB', type = 'prol', prot = None, free = 'False', up = WILD, dw_
144 ↪ = WILD),
145     Parameter('fwd_TranscriptionFactorMet_AssemblyRule_12', 0),
146     Parameter('rvs_TranscriptionFactorMet_AssemblyRule_12', 0))
147
148 # [araC, SMALL_alpha_L_arabinopyranose] interacts with BS_158_174
149 Rule('TranscriptionFactorMet_AssemblyRule_13',
150     prot(name = 'araC', dna = None, met = 1, up = None, dw = None) %
151     met(name = 'alpha_L_arabinopyranose', prot = 1) +
152     dna(name = 'BS_158_174', prot = None, free = 'True', up = WILD, dw = WILD) |
153     prot(name = 'araC', dna = 2, met = 1, up = None, dw = None) %
154     met(name = 'alpha_L_arabinopyranose', prot = 1) %

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152     dna(name = 'BS_158_174', prot = 2, free = 'False', up = WILD, dw = WILD),
153     Parameter('fwd_TranscriptionFactorMet_AssemblyRule_13', 0),
154     Parameter('rvs_TranscriptionFactorMet_AssemblyRule_13', 0))
155
156 # [araC, SMALL_alpha_L_arabinopyranose] interacts with BS_137_153
157 Rule('TranscriptionFactorMet_AssemblyRule_14',
158     prot(name = 'araC', dna = None, met = 1, up = None, dw = None) %
159     met(name = 'alpha_L_arabinopyranose', prot = 1) +
160     dna(name = 'BS_137_153', prot = None, free = 'True', up = WILD, dw = WILD) |
161     prot(name = 'araC', dna = 2, met = 1, up = None, dw = None) %
162     met(name = 'alpha_L_arabinopyranose', prot = 1) %
163     dna(name = 'BS_137_153', prot = 2, free = 'False', up = WILD, dw = WILD),
164     Parameter('fwd_TranscriptionFactorMet_AssemblyRule_14', 0),
165     Parameter('rvs_TranscriptionFactorMet_AssemblyRule_14', 0))
166
167 # [araC, SMALL_alpha_L_arabinopyranose] interacts with BS_83_99
168 Rule('TranscriptionFactorMet_AssemblyRule_15',
169     prot(name = 'araC', dna = None, met = 1, up = None, dw = None) %
170     met(name = 'alpha_L_arabinopyranose', prot = 1) +
171     dna(name = 'BS_83_99', prot = None, free = 'True', up = WILD, dw = WILD) |
172     prot(name = 'araC', dna = 2, met = 1, up = None, dw = None) %
173     met(name = 'alpha_L_arabinopyranose', prot = 1) %
174     dna(name = 'BS_83_99', prot = 2, free = 'False', up = WILD, dw = WILD),
175     Parameter('fwd_TranscriptionFactorMet_AssemblyRule_15', 0),
176     Parameter('rvs_TranscriptionFactorMet_AssemblyRule_15', 0))
177
178 # [araC, SMALL_alpha_L_arabinopyranose] interacts with BS_62_78
179 Rule('TranscriptionFactorMet_AssemblyRule_16',
180     prot(name = 'araC', dna = None, met = 1, up = None, dw = None) %
181     met(name = 'alpha_L_arabinopyranose', prot = 1) +
182     dna(name = 'BS_62_78', prot = None, free = 'True', up = WILD, dw = WILD) |
183     prot(name = 'araC', dna = 2, met = 1, up = None, dw = None) %
184     met(name = 'alpha_L_arabinopyranose', prot = 1) %
185     dna(name = 'BS_62_78', prot = 2, free = 'False', up = WILD, dw = WILD),
186     Parameter('fwd_TranscriptionFactorMet_AssemblyRule_16', 0),
187     Parameter('rvs_TranscriptionFactorMet_AssemblyRule_16', 0))
188
189 # [araC, SMALL_alpha_L_arabinopyranose, BS_83_99] interacts with [araC, SMALL_alpha_L_
190 ↪ arabinopyranose, BS_62_78, BS_araF_prol]
191 Rule('TranscriptionFactorMet_AssemblyRule_17',
192     prot(name = 'araC', dna = 2, met = 1, up = None, dw = None) %
193     met(name = 'alpha_L_arabinopyranose', prot = 1) %
194     dna(name = 'BS_83_99', prot = 2, free = 'False', up = WILD, dw = WILD) +
195     prot(name = 'araC', dna = 4, met = 3, up = None, dw = None) %
196     met(name = 'alpha_L_arabinopyranose', prot = 3) %
197     dna(name = 'BS_62_78', prot = 4, free = 'False', up = WILD, dw = WILD) %
198     dna(name = 'araF', type = 'prol', prot = None, free = 'False', up = WILD, dw_
199 ↪ = WILD) |
200     prot(name = 'araC', dna = None, met = 2, up = None, dw = 1) %
201     met(name = 'alpha_L_arabinopyranose', prot = 3) %
202     dna(name = 'BS_83_99', prot = 4, free = 'False', up = WILD, dw = WILD) %
203     prot(name = 'araC', dna = 4, met = 3, up = 1, dw = None) %
204     met(name = 'alpha_L_arabinopyranose', prot = 2) %
205     dna(name = 'BS_62_78', prot = None, free = 'False', up = WILD, dw = WILD) %
206     dna(name = 'araF', type = 'prol', prot = None, free = 'False', up = WILD, dw_
207 ↪ = WILD),
208     Parameter('fwd_TranscriptionFactorMet_AssemblyRule_17', 0),

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206     Parameter('rvs_TranscriptionFactorMet_AssemblyRule_17', 0))
207
208 # [araC, SMALL_alpha_L_arabinopyranose] interacts with BS_57_73
209 Rule('TranscriptionFactorMet_AssemblyRule_18',
210     prot(name = 'araC', dna = None, met = 1, up = None, dw = None) %
211     met(name = 'alpha_L_arabinopyranose', prot = 1) +
212     dna(name = 'BS_57_73', prot = None, free = 'True', up = WILD, dw = WILD) |
213     prot(name = 'araC', dna = 2, met = 1, up = None, dw = None) %
214     met(name = 'alpha_L_arabinopyranose', prot = 1) %
215     dna(name = 'BS_57_73', prot = 2, free = 'False', up = WILD, dw = WILD),
216     Parameter('fwd_TranscriptionFactorMet_AssemblyRule_18', 0),
217     Parameter('rvs_TranscriptionFactorMet_AssemblyRule_18', 0))
218
219 # [araC, SMALL_alpha_L_arabinopyranose] interacts with BS_36_52
220 Rule('TranscriptionFactorMet_AssemblyRule_19',
221     prot(name = 'araC', dna = None, met = 1, up = None, dw = None) %
222     met(name = 'alpha_L_arabinopyranose', prot = 1) +
223     dna(name = 'BS_36_52', prot = None, free = 'True', up = WILD, dw = WILD) |
224     prot(name = 'araC', dna = 2, met = 1, up = None, dw = None) %
225     met(name = 'alpha_L_arabinopyranose', prot = 1) %
226     dna(name = 'BS_36_52', prot = 2, free = 'False', up = WILD, dw = WILD),
227     Parameter('fwd_TranscriptionFactorMet_AssemblyRule_19', 0),
228     Parameter('rvs_TranscriptionFactorMet_AssemblyRule_19', 0))
229
230 # [araC, SMALL_alpha_L_arabinopyranose, BS_57_73] interacts with [araC, SMALL_alpha_L_
231 ↪ arabinopyranose, BS_36_52, BS_araE_prol]
232 Rule('TranscriptionFactorMet_AssemblyRule_20',
233     prot(name = 'araC', dna = 2, met = 1, up = None, dw = None) %
234     met(name = 'alpha_L_arabinopyranose', prot = 1) %
235     dna(name = 'BS_57_73', prot = 2, free = 'False', up = WILD, dw = WILD) +
236     prot(name = 'araC', dna = 4, met = 3, up = None, dw = None) %
237     met(name = 'alpha_L_arabinopyranose', prot = 3) %
238     dna(name = 'BS_36_52', prot = 4, free = 'False', up = WILD, dw = WILD) %
239     dna(name = 'araE', type = 'prol', prot = None, free = 'False', up = WILD, dw_
240 ↪ = WILD) |
241     prot(name = 'araC', dna = None, met = 2, up = None, dw = 1) %
242     met(name = 'alpha_L_arabinopyranose', prot = 3) %
243     dna(name = 'BS_57_73', prot = 4, free = 'False', up = WILD, dw = WILD) %
244     prot(name = 'araC', dna = 4, met = 3, up = 1, dw = None) %
245     met(name = 'alpha_L_arabinopyranose', prot = 2) %
246     dna(name = 'BS_36_52', prot = None, free = 'False', up = WILD, dw = WILD) %
247     dna(name = 'araE', type = 'prol', prot = None, free = 'False', up = WILD, dw_
248 ↪ = WILD),
249     Parameter('fwd_TranscriptionFactorMet_AssemblyRule_20', 0),
250     Parameter('rvs_TranscriptionFactorMet_AssemblyRule_20', 0))

```

Note: Reversibility of reactions. Atlas writes dead *Rules* for each reaction declared in the network file. The `Parameter('fwd_ReactionName', 0)` must be set to non-zero to activate the rule and `Parameter('rvs_ReactionName', 0)` must be set to non-zero to define a reversible reaction.

Note: Simulation. The model can be simulated only with the instantiation of Monomers and Initials ([More here](#)). Run *Monomer+Initials+Observables from metabolic network.ipynb* to obtain automatically the necessary Monomers and Initials (including proteins and enzymatic complexes).

Plotting. The model can be observed only with the instantiation of Observables ([More here](#)). Run *Monomer+Initials+Observables from metabolic network.ipynb* to obtain automatically the all possible Observables for metabolites.

2.5 Sigma Factor-Promoter Interaction Networks

The Sigma Factor-Promoter network have two columns and for the former network, the first column lists using comma all components of a TF enclosed in brackets (optionally with small compounds) and in the second column declares the DNA binding site. Users should use the prefix “SMALL-” for small compounds and the prefix “BS-” to encode DNA binding sites using unique names. The second type of GRN shows in the first column the RNA polymerase holoenzyme complex (components in brackets) and in the second the promoter. Users should name promoters with the gene name followed by the suffix “-pro#” where # is an integer.

Examples:

SOURCE	TARGET
# Docking to promoters	
[rpoA, rpoA, rpoB, rpoC, rpoD]	BS-rpoA-pro1
[rpoA, rpoA, rpoB, rpoC, rpoD]	BS-rpoB-pro1
# [rpoA, rpoA, rpoB, rpoC, rpoD]	BS-rpoC-pro1
[rpoA, rpoA, rpoB, rpoC, rpoD]	BS-rpoD-pro1
[rpoA, rpoA, rpoB, rpoC, rpoD]	BS-rpoE-pro1
[rpoA, rpoA, rpoB, rpoC, rpoD]	BS-rpoH-pro1
[rpoA, rpoA, rpoB, rpoC, rpoD]	BS-rpoN-pro1
[rpoA, rpoA, rpoB, rpoC, rpoD]	BS-rpoS-pro1
[rpoA, rpoA, rpoB, rpoC, rpoD]	BS-fliA-pro1
[rpoA, rpoA, rpoB, rpoC, rpoD]	BS-fecI-pro1
[rpoA, rpoA, rpoB, rpoC, rpoE]	BS-rpoD-pro1
[rpoA, rpoA, rpoB, rpoC, rpoE]	BS-rpoE-pro1
[rpoA, rpoA, rpoB, rpoC, rpoE]	BS-rpoH-pro1
[rpoA, rpoA, rpoB, rpoC, rpoE]	BS-rpoN-pro1
[rpoA, rpoA, rpoB, rpoC, rpoH]	BS-rpoA-pro1
[rpoA, rpoA, rpoB, rpoC, rpoH]	BS-rpoD-pro1
[rpoA, rpoA, rpoB, rpoC, rpoN]	BS-rpoA-pro1
[rpoA, rpoA, rpoB, rpoC, rpoN]	BS-rpoD-pro1
[rpoA, rpoA, rpoB, rpoC, rpoN]	BS-rpoH-pro1
[rpoA, rpoA, rpoB, rpoC, rpoS]	BS-fecI-pro1
[rpoA, rpoA, rpoB, rpoC, rpoS]	BS-rpoA-pro1
[rpoA, rpoA, rpoB, rpoC, rpoS]	BS-rpoB-pro1
# [rpoA, rpoA, rpoB, rpoC, rpoS]	BS-rpoC-pro1
[rpoA, rpoA, rpoB, rpoC, rpoS]	BS-rpoD-pro1
[rpoA, rpoA, rpoB, rpoC, rpoS]	BS-rpoE-pro1
[rpoA, rpoA, rpoB, rpoC, rpoS]	BS-rpoH-pro1
[rpoA, rpoA, rpoB, rpoC, rpoS]	BS-rpoN-pro1
[rpoA, rpoA, rpoB, rpoC, fliA]	BS-rpoD-pro1
[rpoA, rpoA, rpoB, rpoC, fliA]	BS-rpoN-pro1
[rpoA, rpoA, rpoB, rpoC, fliA]	BS-fliA-pro1

Finally, execute the “*Rules from SigmaFactors x Architecture.ipynb*” to obtain the *Rules* to model the defined interaction network. The complete rule-based model can be found in the sigma folder from the Network Biology Lab GitHub

repository [here](#).

```

1  # [rpoA, rpoA, rpoB, rpoC, rpoD] interacts with BS_rpoA_pro1
2  Rule('docking_1_rpoA_pro1',
3      prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
4      prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
5      prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
6      prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
7      prot(name = 'rpoD', dna = None, met = None, up = 4, dw = None) +
8      dna(name = 'rpoA', type = 'pro1', prot = None, free = 'True', up = WILD, dw = _
↪WILD) |
9      prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
10     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
11     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
12     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
13     prot(name = 'rpoD', dna = 5, met = None, up = 4, dw = None) %
14     dna(name = 'rpoA', type = 'pro1', prot = 5, free = 'False', up = WILD, dw = _
↪WILD),
15     Parameter('fwd_docking_1_rpoA_pro1', 0),
16     Parameter('rvs_docking_1_rpoA_pro1', 0))
17
18  # [rpoA, rpoA, rpoB, rpoC, rpoD] interacts with BS_rpoB_pro1
19  Rule('docking_2_rpoB_pro1',
20      prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
21      prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
22      prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
23      prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
24      prot(name = 'rpoD', dna = None, met = None, up = 4, dw = None) +
25      dna(name = 'rpoB', type = 'pro1', prot = None, free = 'True', up = WILD, dw = _
↪WILD) |
26      prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
27      prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
28      prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
29      prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
30      prot(name = 'rpoD', dna = 5, met = None, up = 4, dw = None) %
31      dna(name = 'rpoB', type = 'pro1', prot = 5, free = 'False', up = WILD, dw = _
↪WILD),
32      Parameter('fwd_docking_2_rpoB_pro1', 0),
33      Parameter('rvs_docking_2_rpoB_pro1', 0))
34
35  # [rpoA, rpoA, rpoB, rpoC, rpoD] interacts with BS_rpoD_pro1
36  Rule('docking_3_rpoD_pro1',
37      prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
38      prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
39      prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
40      prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
41      prot(name = 'rpoD', dna = None, met = None, up = 4, dw = None) +
42      dna(name = 'rpoD', type = 'pro1', prot = None, free = 'True', up = WILD, dw = _
↪WILD) |
43      prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
44      prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
45      prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
46      prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
47      prot(name = 'rpoD', dna = 5, met = None, up = 4, dw = None) %
48      dna(name = 'rpoD', type = 'pro1', prot = 5, free = 'False', up = WILD, dw = _
↪WILD),
49      Parameter('fwd_docking_3_rpoD_pro1', 0),
50      Parameter('rvs_docking_3_rpoD_pro1', 0))

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51
52 # [rpoA, rpoA, rpoB, rpoC, rpoD] interacts with BS_rpoE_pro1
53 Rule('docking_4_rpoE_pro1',
54     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
55     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
56     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
57     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
58     prot(name = 'rpoD', dna = None, met = None, up = 4, dw = None) +
59     dna(name = 'rpoE', type = 'pro1', prot = None, free = 'True', up = WILD, dw =
↪WILD) |
60     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
61     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
62     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
63     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
64     prot(name = 'rpoD', dna = 5, met = None, up = 4, dw = None) %
65     dna(name = 'rpoE', type = 'pro1', prot = 5, free = 'False', up = WILD, dw =
↪WILD),
66     Parameter('fwd_docking_4_rpoE_pro1', 0),
67     Parameter('rvs_docking_4_rpoE_pro1', 0))
68
69 # [rpoA, rpoA, rpoB, rpoC, rpoD] interacts with BS_rpoH_pro1
70 Rule('docking_5_rpoH_pro1',
71     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
72     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
73     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
74     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
75     prot(name = 'rpoD', dna = None, met = None, up = 4, dw = None) +
76     dna(name = 'rpoH', type = 'pro1', prot = None, free = 'True', up = WILD, dw =
↪WILD) |
77     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
78     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
79     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
80     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
81     prot(name = 'rpoD', dna = 5, met = None, up = 4, dw = None) %
82     dna(name = 'rpoH', type = 'pro1', prot = 5, free = 'False', up = WILD, dw =
↪WILD),
83     Parameter('fwd_docking_5_rpoH_pro1', 0),
84     Parameter('rvs_docking_5_rpoH_pro1', 0))
85
86 # [rpoA, rpoA, rpoB, rpoC, rpoD] interacts with BS_rpoN_pro1
87 Rule('docking_6_rpoN_pro1',
88     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
89     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
90     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
91     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
92     prot(name = 'rpoD', dna = None, met = None, up = 4, dw = None) +
93     dna(name = 'rpoN', type = 'pro1', prot = None, free = 'True', up = WILD, dw =
↪WILD) |
94     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
95     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
96     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
97     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
98     prot(name = 'rpoD', dna = 5, met = None, up = 4, dw = None) %
99     dna(name = 'rpoN', type = 'pro1', prot = 5, free = 'False', up = WILD, dw =
↪WILD),
100     Parameter('fwd_docking_6_rpoN_pro1', 0),
101     Parameter('rvs_docking_6_rpoN_pro1', 0))

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102
103 # [rpoA, rpoA, rpoB, rpoC, rpoD] interacts with BS_rpoS_prol
104 Rule('docking_7_rpoS_prol',
105     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
106     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
107     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
108     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
109     prot(name = 'rpoD', dna = None, met = None, up = 4, dw = None) +
110     dna(name = 'rpoS', type = 'prol', prot = None, free = 'True', up = WILD, dw = _
↪WILD) |
111     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
112     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
113     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
114     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
115     prot(name = 'rpoD', dna = 5, met = None, up = 4, dw = None) %
116     dna(name = 'rpoS', type = 'prol', prot = 5, free = 'False', up = WILD, dw = _
↪WILD),
117     Parameter('fwd_docking_7_rpoS_prol', 0),
118     Parameter('rvs_docking_7_rpoS_prol', 0))
119
120 # [rpoA, rpoA, rpoB, rpoC, rpoD] interacts with BS_fliA_prol
121 Rule('docking_8_fliA_prol',
122     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
123     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
124     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
125     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
126     prot(name = 'rpoD', dna = None, met = None, up = 4, dw = None) +
127     dna(name = 'fliA', type = 'prol', prot = None, free = 'True', up = WILD, dw = _
↪WILD) |
128     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
129     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
130     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
131     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
132     prot(name = 'rpoD', dna = 5, met = None, up = 4, dw = None) %
133     dna(name = 'fliA', type = 'prol', prot = 5, free = 'False', up = WILD, dw = _
↪WILD),
134     Parameter('fwd_docking_8_fliA_prol', 0),
135     Parameter('rvs_docking_8_fliA_prol', 0))
136
137 # [rpoA, rpoA, rpoB, rpoC, rpoD] interacts with BS_fecI_prol
138 Rule('docking_9_fecI_prol',
139     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
140     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
141     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
142     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
143     prot(name = 'rpoD', dna = None, met = None, up = 4, dw = None) +
144     dna(name = 'fecI', type = 'prol', prot = None, free = 'True', up = WILD, dw = _
↪WILD) |
145     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
146     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
147     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
148     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
149     prot(name = 'rpoD', dna = 5, met = None, up = 4, dw = None) %
150     dna(name = 'fecI', type = 'prol', prot = 5, free = 'False', up = WILD, dw = _
↪WILD),
151     Parameter('fwd_docking_9_fecI_prol', 0),
152     Parameter('rvs_docking_9_fecI_prol', 0))

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153
154 # [rpoA, rpoA, rpoB, rpoC, rpoE] interacts with BS_rpoD_pro1
155 Rule('docking_10_rpoD_pro1',
156     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
157     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
158     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
159     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
160     prot(name = 'rpoE', dna = None, met = None, up = 4, dw = None) +
161     dna(name = 'rpoD', type = 'pro1', prot = None, free = 'True', up = WILD, dw =
↪WILD) |
162     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
163     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
164     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
165     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
166     prot(name = 'rpoE', dna = 5, met = None, up = 4, dw = None) %
167     dna(name = 'rpoD', type = 'pro1', prot = 5, free = 'False', up = WILD, dw =
↪WILD),
168     Parameter('fwd_docking_10_rpoD_pro1', 0),
169     Parameter('rvs_docking_10_rpoD_pro1', 0))
170
171 # [rpoA, rpoA, rpoB, rpoC, rpoE] interacts with BS_rpoE_pro1
172 Rule('docking_11_rpoE_pro1',
173     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
174     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
175     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
176     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
177     prot(name = 'rpoE', dna = None, met = None, up = 4, dw = None) +
178     dna(name = 'rpoE', type = 'pro1', prot = None, free = 'True', up = WILD, dw =
↪WILD) |
179     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
180     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
181     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
182     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
183     prot(name = 'rpoE', dna = 5, met = None, up = 4, dw = None) %
184     dna(name = 'rpoE', type = 'pro1', prot = 5, free = 'False', up = WILD, dw =
↪WILD),
185     Parameter('fwd_docking_11_rpoE_pro1', 0),
186     Parameter('rvs_docking_11_rpoE_pro1', 0))
187
188 # [rpoA, rpoA, rpoB, rpoC, rpoE] interacts with BS_rpoH_pro1
189 Rule('docking_12_rpoH_pro1',
190     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
191     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
192     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
193     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
194     prot(name = 'rpoE', dna = None, met = None, up = 4, dw = None) +
195     dna(name = 'rpoH', type = 'pro1', prot = None, free = 'True', up = WILD, dw =
↪WILD) |
196     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
197     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
198     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
199     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
200     prot(name = 'rpoE', dna = 5, met = None, up = 4, dw = None) %
201     dna(name = 'rpoH', type = 'pro1', prot = 5, free = 'False', up = WILD, dw =
↪WILD),
202     Parameter('fwd_docking_12_rpoH_pro1', 0),
203     Parameter('rvs_docking_12_rpoH_pro1', 0))

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204
205 # [rpoA, rpoA, rpoB, rpoC, rpoE] interacts with BS_rpoN_pro1
206 Rule('docking_13_rpoN_pro1',
207     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
208     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
209     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
210     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
211     prot(name = 'rpoE', dna = None, met = None, up = 4, dw = None) +
212     dna(name = 'rpoN', type = 'pro1', prot = None, free = 'True', up = WILD, dw =
↪WILD) |
213     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
214     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
215     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
216     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
217     prot(name = 'rpoE', dna = 5, met = None, up = 4, dw = None) %
218     dna(name = 'rpoN', type = 'pro1', prot = 5, free = 'False', up = WILD, dw =
↪WILD),
219     Parameter('fwd_docking_13_rpoN_pro1', 0),
220     Parameter('rvs_docking_13_rpoN_pro1', 0))
221
222 # [rpoA, rpoA, rpoB, rpoC, rpoH] interacts with BS_rpoA_pro1
223 Rule('docking_14_rpoA_pro1',
224     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
225     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
226     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
227     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
228     prot(name = 'rpoH', dna = None, met = None, up = 4, dw = None) +
229     dna(name = 'rpoA', type = 'pro1', prot = None, free = 'True', up = WILD, dw =
↪WILD) |
230     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
231     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
232     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
233     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
234     prot(name = 'rpoH', dna = 5, met = None, up = 4, dw = None) %
235     dna(name = 'rpoA', type = 'pro1', prot = 5, free = 'False', up = WILD, dw =
↪WILD),
236     Parameter('fwd_docking_14_rpoA_pro1', 0),
237     Parameter('rvs_docking_14_rpoA_pro1', 0))
238
239 # [rpoA, rpoA, rpoB, rpoC, rpoH] interacts with BS_rpoD_pro1
240 Rule('docking_15_rpoD_pro1',
241     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
242     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
243     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
244     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
245     prot(name = 'rpoH', dna = None, met = None, up = 4, dw = None) +
246     dna(name = 'rpoD', type = 'pro1', prot = None, free = 'True', up = WILD, dw =
↪WILD) |
247     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
248     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
249     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
250     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
251     prot(name = 'rpoH', dna = 5, met = None, up = 4, dw = None) %
252     dna(name = 'rpoD', type = 'pro1', prot = 5, free = 'False', up = WILD, dw =
↪WILD),
253     Parameter('fwd_docking_15_rpoD_pro1', 0),
254     Parameter('rvs_docking_15_rpoD_pro1', 0))

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255
256 # [rpoA, rpoA, rpoB, rpoC, rpoN] interacts with BS_rpoA_pro1
257 Rule('docking_16_rpoA_pro1',
258     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
259     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
260     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
261     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
262     prot(name = 'rpoN', dna = None, met = None, up = 4, dw = None) +
263     dna(name = 'rpoA', type = 'pro1', prot = None, free = 'True', up = WILD, dw = _
↪WILD) |
264     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
265     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
266     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
267     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
268     prot(name = 'rpoN', dna = 5, met = None, up = 4, dw = None) %
269     dna(name = 'rpoA', type = 'pro1', prot = 5, free = 'False', up = WILD, dw = _
↪WILD),
270     Parameter('fwd_docking_16_rpoA_pro1', 0),
271     Parameter('rvs_docking_16_rpoA_pro1', 0))
272
273 # [rpoA, rpoA, rpoB, rpoC, rpoN] interacts with BS_rpoD_pro1
274 Rule('docking_17_rpoD_pro1',
275     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
276     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
277     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
278     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
279     prot(name = 'rpoN', dna = None, met = None, up = 4, dw = None) +
280     dna(name = 'rpoD', type = 'pro1', prot = None, free = 'True', up = WILD, dw = _
↪WILD) |
281     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
282     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
283     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
284     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
285     prot(name = 'rpoN', dna = 5, met = None, up = 4, dw = None) %
286     dna(name = 'rpoD', type = 'pro1', prot = 5, free = 'False', up = WILD, dw = _
↪WILD),
287     Parameter('fwd_docking_17_rpoD_pro1', 0),
288     Parameter('rvs_docking_17_rpoD_pro1', 0))
289
290 # [rpoA, rpoA, rpoB, rpoC, rpoN] interacts with BS_rpoH_pro1
291 Rule('docking_18_rpoH_pro1',
292     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
293     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
294     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
295     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
296     prot(name = 'rpoN', dna = None, met = None, up = 4, dw = None) +
297     dna(name = 'rpoH', type = 'pro1', prot = None, free = 'True', up = WILD, dw = _
↪WILD) |
298     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
299     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
300     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
301     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
302     prot(name = 'rpoN', dna = 5, met = None, up = 4, dw = None) %
303     dna(name = 'rpoH', type = 'pro1', prot = 5, free = 'False', up = WILD, dw = _
↪WILD),
304     Parameter('fwd_docking_18_rpoH_pro1', 0),
305     Parameter('rvs_docking_18_rpoH_pro1', 0))

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306
307 # [rpoA, rpoA, rpoB, rpoC, rpoS] interacts with BS_fecI_prol
308 Rule('docking_19_fecI_prol',
309     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
310     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
311     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
312     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
313     prot(name = 'rpoS', dna = None, met = None, up = 4, dw = None) +
314     dna(name = 'fecI', type = 'prol', prot = None, free = 'True', up = WILD, dw = _
↪WILD) |
315     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
316     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
317     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
318     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
319     prot(name = 'rpoS', dna = 5, met = None, up = 4, dw = None) %
320     dna(name = 'fecI', type = 'prol', prot = 5, free = 'False', up = WILD, dw = _
↪WILD),
321     Parameter('fwd_docking_19_fecI_prol', 0),
322     Parameter('rvs_docking_19_fecI_prol', 0))
323
324 # [rpoA, rpoA, rpoB, rpoC, rpoS] interacts with BS_rpoA_prol
325 Rule('docking_20_rpoA_prol',
326     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
327     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
328     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
329     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
330     prot(name = 'rpoS', dna = None, met = None, up = 4, dw = None) +
331     dna(name = 'rpoA', type = 'prol', prot = None, free = 'True', up = WILD, dw = _
↪WILD) |
332     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
333     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
334     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
335     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
336     prot(name = 'rpoS', dna = 5, met = None, up = 4, dw = None) %
337     dna(name = 'rpoA', type = 'prol', prot = 5, free = 'False', up = WILD, dw = _
↪WILD),
338     Parameter('fwd_docking_20_rpoA_prol', 0),
339     Parameter('rvs_docking_20_rpoA_prol', 0))
340
341 # [rpoA, rpoA, rpoB, rpoC, rpoS] interacts with BS_rpoB_prol
342 Rule('docking_21_rpoB_prol',
343     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
344     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
345     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
346     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
347     prot(name = 'rpoS', dna = None, met = None, up = 4, dw = None) +
348     dna(name = 'rpoB', type = 'prol', prot = None, free = 'True', up = WILD, dw = _
↪WILD) |
349     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
350     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
351     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
352     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
353     prot(name = 'rpoS', dna = 5, met = None, up = 4, dw = None) %
354     dna(name = 'rpoB', type = 'prol', prot = 5, free = 'False', up = WILD, dw = _
↪WILD),
355     Parameter('fwd_docking_21_rpoB_prol', 0),
356     Parameter('rvs_docking_21_rpoB_prol', 0))

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357
358 # [rpoA, rpoA, rpoB, rpoC, rpoS] interacts with BS_rpoD_pro1
359 Rule('docking_22_rpoD_pro1',
360     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
361     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
362     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
363     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
364     prot(name = 'rpoS', dna = None, met = None, up = 4, dw = None) +
365     dna(name = 'rpoD', type = 'pro1', prot = None, free = 'True', up = WILD, dw = _
↪WILD) |
366     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
367     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
368     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
369     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
370     prot(name = 'rpoS', dna = 5, met = None, up = 4, dw = None) %
371     dna(name = 'rpoD', type = 'pro1', prot = 5, free = 'False', up = WILD, dw = _
↪WILD),
372     Parameter('fwd_docking_22_rpoD_pro1', 0),
373     Parameter('rvs_docking_22_rpoD_pro1', 0))
374
375 # [rpoA, rpoA, rpoB, rpoC, rpoS] interacts with BS_rpoE_pro1
376 Rule('docking_23_rpoE_pro1',
377     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
378     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
379     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
380     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
381     prot(name = 'rpoS', dna = None, met = None, up = 4, dw = None) +
382     dna(name = 'rpoE', type = 'pro1', prot = None, free = 'True', up = WILD, dw = _
↪WILD) |
383     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
384     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
385     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
386     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
387     prot(name = 'rpoS', dna = 5, met = None, up = 4, dw = None) %
388     dna(name = 'rpoE', type = 'pro1', prot = 5, free = 'False', up = WILD, dw = _
↪WILD),
389     Parameter('fwd_docking_23_rpoE_pro1', 0),
390     Parameter('rvs_docking_23_rpoE_pro1', 0))
391
392 # [rpoA, rpoA, rpoB, rpoC, rpoS] interacts with BS_rpoH_pro1
393 Rule('docking_24_rpoH_pro1',
394     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
395     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
396     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
397     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
398     prot(name = 'rpoS', dna = None, met = None, up = 4, dw = None) +
399     dna(name = 'rpoH', type = 'pro1', prot = None, free = 'True', up = WILD, dw = _
↪WILD) |
400     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
401     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
402     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
403     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
404     prot(name = 'rpoS', dna = 5, met = None, up = 4, dw = None) %
405     dna(name = 'rpoH', type = 'pro1', prot = 5, free = 'False', up = WILD, dw = _
↪WILD),
406     Parameter('fwd_docking_24_rpoH_pro1', 0),
407     Parameter('rvs_docking_24_rpoH_pro1', 0))

```

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```

408
409 # [rpoA, rpoA, rpoB, rpoC, rpoS] interacts with BS_rpoN_prol
410 Rule('docking_25_rpoN_prol',
411     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
412     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
413     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
414     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
415     prot(name = 'rpoS', dna = None, met = None, up = 4, dw = None) +
416     dna(name = 'rpoN', type = 'prol', prot = None, free = 'True', up = WILD, dw =
↪WILD) |
417     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
418     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
419     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
420     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
421     prot(name = 'rpoS', dna = 5, met = None, up = 4, dw = None) %
422     dna(name = 'rpoN', type = 'prol', prot = 5, free = 'False', up = WILD, dw =
↪WILD),
423     Parameter('fwd_docking_25_rpoN_prol', 0),
424     Parameter('rvs_docking_25_rpoN_prol', 0))
425
426 # [rpoA, rpoA, rpoB, rpoC, fliA] interacts with BS_rpoD_prol
427 Rule('docking_26_rpoD_prol',
428     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
429     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
430     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
431     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
432     prot(name = 'fliA', dna = None, met = None, up = 4, dw = None) +
433     dna(name = 'rpoD', type = 'prol', prot = None, free = 'True', up = WILD, dw =
↪WILD) |
434     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
435     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
436     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
437     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
438     prot(name = 'fliA', dna = 5, met = None, up = 4, dw = None) %
439     dna(name = 'rpoD', type = 'prol', prot = 5, free = 'False', up = WILD, dw =
↪WILD),
440     Parameter('fwd_docking_26_rpoD_prol', 0),
441     Parameter('rvs_docking_26_rpoD_prol', 0))
442
443 # [rpoA, rpoA, rpoB, rpoC, fliA] interacts with BS_rpoN_prol
444 Rule('docking_27_rpoN_prol',
445     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
446     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
447     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
448     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
449     prot(name = 'fliA', dna = None, met = None, up = 4, dw = None) +
450     dna(name = 'rpoN', type = 'prol', prot = None, free = 'True', up = WILD, dw =
↪WILD) |
451     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
452     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
453     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
454     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
455     prot(name = 'fliA', dna = 5, met = None, up = 4, dw = None) %
456     dna(name = 'rpoN', type = 'prol', prot = 5, free = 'False', up = WILD, dw =
↪WILD),
457     Parameter('fwd_docking_27_rpoN_prol', 0),
458     Parameter('rvs_docking_27_rpoN_prol', 0))

```

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```

459 # [rpoA, rpoA, rpoB, rpoC, fliA] interacts with BS_fliA_pro1
460 Rule('docking_28_fliA_pro1',
461     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
462     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
463     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
464     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
465     prot(name = 'fliA', dna = None, met = None, up = 4, dw = None) +
466     dna(name = 'fliA', type = 'pro1', prot = None, free = 'True', up = WILD, dw =
↪WILD) |
468     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
469     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
470     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
471     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
472     prot(name = 'fliA', dna = 5, met = None, up = 4, dw = None) %
473     dna(name = 'fliA', type = 'pro1', prot = 5, free = 'False', up = WILD, dw =
↪WILD),
474     Parameter('fwd_docking_28_fliA_pro1', 0),
475     Parameter('rvs_docking_28_fliA_pro1', 0))

```

Note: Reversibility of reactions. Atlas writes dead *Rules* for each reaction declared in the network file. The `Parameter('fwd_ReactionName', 0)` must be set to non-zero to activate the rule and `Parameter('rvs_ReactionName', 0)` must be set to non-zero to define a reversible reaction.

Note: Simulation. The model can be simulated only with the instantiation of Monomers and Initials ([More here](#)). Run *Monomer+Initials+Observables from metabolic network.ipynb* to obtain automatically the necessary Monomers and Initials (including proteins and enzymatic complexes).

Plotting. The model can be observed only with the instantiation of Observables ([More here](#)). Run *Monomer+Initials+Observables from metabolic network.ipynb* to obtain automatically the all possible Observables for metabolites.

2.6 Genome Graphs

Metabolic networks have four columns. The first declares a unique name for the enzyme or enzymatic complex; the second declares a unique name for the reaction; the third column lists using comma unique names for substrates; and the last row list using comma unique names for products. To declare metabolites located at the periplasm or extracellular compartments, the user should employ the prefix “PER-” and “EX-”, respectively. Use *spontaneous* for non-enzymatic reactions.

Examples:

	SOURCE	TARGET
1	araB-pro1	araB-rbs
2	araB-rbs	araB-cds
3	araB-cds	araA-rbs
4	araA-rbs	araA-cds
5	araA-cds	araD-rbs
6	araD-rbs	araD-cds
7	araD-cds	araD-ter1
8		

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```

9
10 araC-pro1      araC-BS-56-72
11 araC-BS-56-72      araC-rbs
12 araC-rbs      araC-cds
13 araC-cds      araC-ter1
14
15 araE-pro1      araE-rbs
16 araE-rbs      araE-cds
17 araE-cds      araE-ter1
18
19 araF-pro1      araF-rbs
20 araF-rbs      araF-cds
21 araF-cds      araG-rbs
22 araG-rbs      araG-cds
23 araG-cds      araH-rbs
24 araH-rbs      araH-cds
25 araH-cds      araH-ter1

```

OR

```

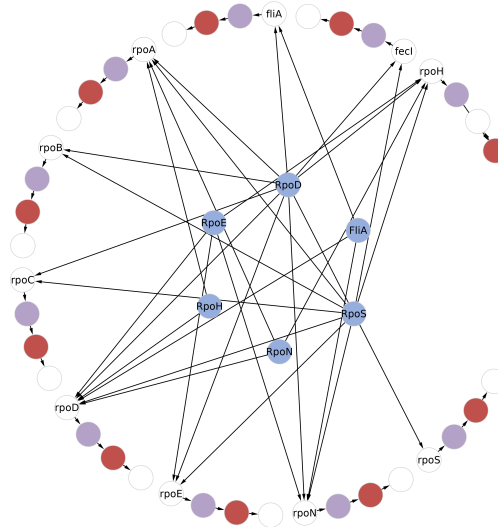
1 SOURCE      TARGET
2 rpoA-pro1      rpoA-rbs
3 rpoA-rbs      rpoA-cds
4 rpoA-cds      rpoA-ter1
5
6 rpoB-pro1      rpoB-rbs
7 rpoB-rbs      rpoB-cds
8 rpoB-cds      rpoC-rbs
9 rpoC-rbs      rpoC-cds
10 rpoC-cds      rpoC-ter1
11
12 rpoD-pro1      rpoD-rbs
13 rpoD-rbs      rpoD-cds
14 rpoD-cds      rpoD-ter1
15
16 rpoE-pro1      rpoE-rbs
17 rpoE-rbs      rpoE-cds
18 rpoE-cds      rpoE-ter1
19
20 rpoH-pro1      rpoH-rbs
21 rpoH-rbs      rpoH-cds
22 rpoH-cds      rpoH-ter1
23
24 rpoN-pro1      rpoN-rbs
25 rpoN-rbs      rpoN-cds
26 rpoN-cds      rpoN-ter1
27
28 rpoS-pro1      rpoS-rbs
29 rpoS-rbs      rpoS-cds
30 rpoS-cds      rpoS-ter1
31
32 fliA-pro1      fliA-rbs
33 fliA-rbs      fliA-cds
34 fliA-cds      fliA-ter1
35
36 fecI-pro1      fecI-rbs
37 fecI-rbs      fecI-cds

```

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fecI-cds fecI-ter1

Note: Visualization in Cytoscape. Colors and arrows remains to the user for customization. The network could be complemented with a description of sigma factor specificity for promoter, as the following network



Finally, execute the “*Rules from metabolic network.ipynb*” to obtain the *Rules* to model the defined network. If using a Sigma Factor-Promoter Interaction Network, the user could use “*Rules from SigmaFactors x Architecture*” to obtain the *Rules* to model both network at once. The complete rule-based model can be found in the arabinose folder (1st example) and in the sigma folder (2nd example) from the Network Biology Lab GitHub repository [here](#).

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 specificity uses a modified *rules* to model the release of the sigma factor from the RNA Polymerase at the transcription initiation. Please note the explicit modeling of the RNA Polymerase complex in the second example.

```
1 Rule('docking_araB_prol',
2     cplx(name = 'RNAP', dna = None) + dna(name = 'araB', type = 'prol', prot =
3     ↪None, free = 'True') |
4     cplx(name = 'RNAP', dna = 1) % dna(name = 'araB', type = 'prol', prot = 1,
5     ↪free = 'False'),
6     Parameter('fwd_docking_araB_prol', 1), Parameter('rvs_docking_araB_prol', 1))
```

OR

```
1 # [rpoA, rpoA, rpoB, rpoC, rpoD] interacts with BS_rpoA_prol
2 Rule('docking_1_rpoA_prol',
3     prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
4     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
5     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
6     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
7     prot(name = 'rpoD', dna = None, met = None, up = 4, dw = None) +
8     dna(name = 'rpoA', type = 'prol', prot = None, free = 'True', up = WILD, dw =
9     ↪WILD) |
10    prot(name = 'rpoA', dna = None, met = None, up = None, dw = 1) %
```

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```

10     prot(name = 'rpoA', dna = None, met = None, up = 1, dw = 2) %
11     prot(name = 'rpoB', dna = None, met = None, up = 2, dw = 3) %
12     prot(name = 'rpoC', dna = None, met = None, up = 3, dw = 4) %
13     prot(name = 'rpoD', dna = 5, met = None, up = 4, dw = None) %
14     dna(name = 'rpoA', type = 'pro1', prot = 5, free = 'False', up = WILD, dw =
↪WILD),
15     Parameter('fwd_docking_1_rpoA_rbs', 1),
16     Parameter('rvs_docking_1_rpoA_pro1', 0))

```

Note: Reversibility of reactions. Atlas writes irreversible *Rules* for each interaction between the RNA Polymerase and a promoter. The `Parameter('rvs_ReactionName', 0)` must be set to non-zero to define a reversible reaction. The remaining *Rules* are irreversible without a way to define reversible reactions.

Note: Simulation. The model can be simulated only with the instantiation of Monomers and Initials ([More here](#)). Run *Monomer+Initials+Observables from metabolic network.ipynb* to obtain automatically the necessary Monomers and Initials (including proteins and enzymatic complexes). For initial genes, please refer to the following example:

Plotting. The model can be observed only with the instantiation of Observables ([More here](#)). Run *Monomer+Initials+Observables from metabolic network.ipynb* to obtain automatically the all possible Observables for metabolites.

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 from numpy import linspace
2 from pysb.bng import generate_network, generate_equations
3 from pysb.simulator import ScipyOdeSimulator, BngSimulator, KappaSimulator
4
5 # modify accordingly
6 from pysb.pathfinder import set_path
7 set_path('bng', '/opt/git-repositories/bionetgen.RuleWorld/bng2/')
8 set_path('kasim', '/opt/git-repositories/KaSim4.Kappa-Dev/')
9
10 ## for network-based simulations:
11 ## ScipyOdeSimulator and BngSimulator ode and ssa methods
12 # generate_network(model)
13 # generate_equations(model)
14
15 ## set the number of stochastic simulations
16 runs = 100
17 # data1 = ScipyOdeSimulator(model, linspace(0, 100, 200)).run().dataframe
18 # data1 = BngSimulator(model, linspace(0, 200, 201)).run(method = 'ode').dataframe
19 # data2 = BngSimulator(model, linspace(0, 200, 201)).run(method = 'ssa', n_runs =
20 ↪ runs).dataframe
21 # data2 = BngSimulator(model, linspace(0, 200, 201)).run(method = 'nf', n_runs =
22 ↪ runs).dataframe
23 data2 = KappaSimulator(model, linspace(0, 100, 101)).run(n_runs = runs).dataframe
24
25 ## process simulations
26 data = []
27 for i in range(0, runs):
28     data.append(data2.xs(i))
29
30 avrg = 0
31 for i in range(0, runs):
32     avrg += data[i]
33 avrg = avrg / runs
34
35 stdv = 0
36 for i in range(0, runs):
37     stdv += (data[i] - avrg)**2
38 stdv = (stdv / (runs-1))*0.5
```

Note: Please follow the instructions at [BioNetGen](#) and at [KaSim](#) documentations to install the stochastic simulators. For network-based simulations (Ordinary Differential Equations and Gillespie`s algorithm), BioNetGen is required to perform the network generation. Change the corresponding paths (lines 7-8) to match the parent folder for the BNG2.pl or KaSim executable.

PLOTTING

PySB could inform the results of a simulation to dataframes (See [Simulation](#)) and visualization of results could be done with matplotlib or seaborn even (See [more here](#)). To access the data, the dataframes columns reproduce the names of the Observables. The following example could be adapted to show the dynamics of any Observable.

Note: Importantly, PySB allows the inspection of the model to find which Monomers (and complexes of monomers) exists in the model, but as the simulation is network-free, the possible formed complexes are up to the user concern.

Note: Atlas produces automatically Observables for metabolites, and other components and complexes could also be observed and plotted, but their declaration in the model is entirely up to the user.

```

1 fig, ax = plt.subplots(1, 2, figsize = (4*2, 3*1), dpi = 100)
2
3 # ax[0].plot(data1.index, data1['obs_alpha_L_arabinopyranose_cyt'], label = '__
  ↳NOLABEL__', color = palette[0])
4 # ax[0].plot(data1.index, data1['obs_ATP_cyt'], label = '__NOLABEL__', color =
  ↳palette[3])
5 ax[0].fill_between(avrg.index,
6                    avrg['obs_alpha_L_arabinopyranose_cyt'] + stdv['obs_alpha_L_arabinopyranose_
  ↳cyt'],
7                    avrg['obs_alpha_L_arabinopyranose_cyt'] - stdv['obs_alpha_L_arabinopyranose_
  ↳cyt'],
8                    label = r'$\alpha$-arabinopyranose', **{'color' : palette[0], 'alpha' : 0.5})
9 ax[0].fill_between(avrg.index,
10                   avrg['obs_ATP_cyt'] + stdv['obs_ATP_cyt'],
11                   avrg['obs_ATP_cyt'] - stdv['obs_ATP_cyt'],
12                   label = r'ATP', **{'color' : palette[3], 'alpha' : 0.5})
13
14 # ax[1].plot(data1.index, data1['obs_PROTON_cyt'], label = '__NOLABEL__', color =
  ↳palette[0])
15 # ax[1].plot(data1.index, data1['obs_XYLULOSE_5_PHOSPHATE_cyt'], label = '__NOLABEL__
  ↳', color = palette[3])
16 ax[1].fill_between(avrg.index,
17                   avrg['obs_PROTON_cyt'] + stdv['obs_PROTON_cyt'],
18                   avrg['obs_PROTON_cyt'] - stdv['obs_PROTON_cyt'],
19                   label = r'H$^+$', **{'color' : palette[0], 'alpha' : 0.5})
20 ax[1].fill_between(avrg.index,
21                   avrg['obs_WATER_cyt'] + stdv['obs_WATER_cyt'],
22                   avrg['obs_WATER_cyt'] - stdv['obs_WATER_cyt'],
23                   label = 'WATER', **{'color' : palette[1], 'alpha' : 0.5})
24 ax[1].fill_between(avrg.index,

```

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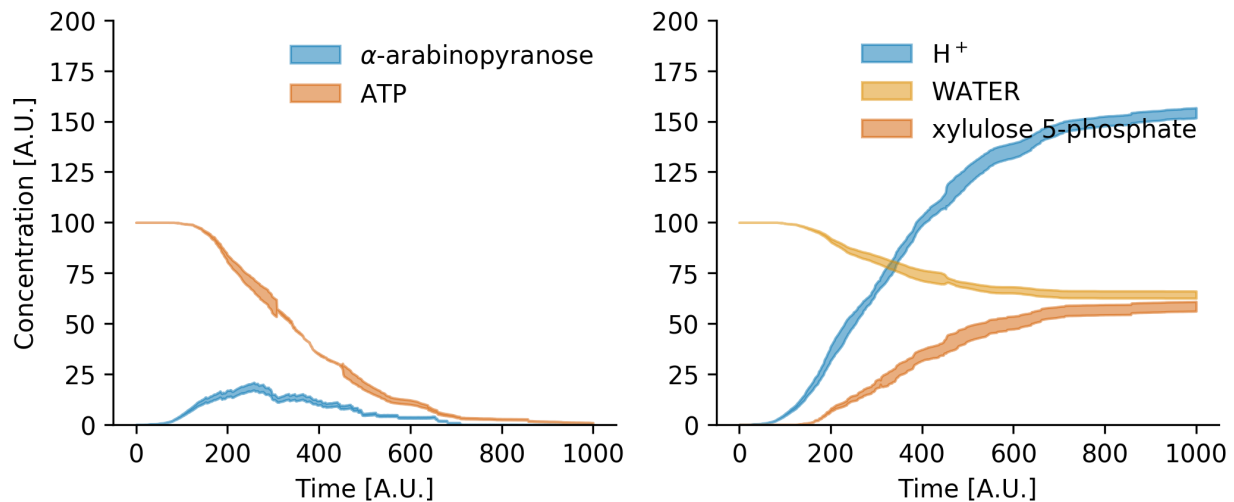
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```

25     avrg['obs_XYLULOSE_5_PHOSPHATE_cyt'] + stdv['obs_XYLULOSE_5_PHOSPHATE_cyt'],
26     avrg['obs_XYLULOSE_5_PHOSPHATE_cyt'] - stdv['obs_XYLULOSE_5_PHOSPHATE_cyt'],
27     label = r'xylulose 5-phosphate', **{'color' : palette[3], 'alpha' : 0.5})
28
29 ax[0].set_xlabel('Time [A.U.]')
30 ax[0].set_ylabel('Concentration [A.U.]')
31 # ax[0].set_xlim(left = 0, right = 100)
32 ax[0].set_ylim(bottom = 0, top = 200)
33
34 ax[1].set_xlabel('Time [A.U.]')
35 # ax[1].set_xlim(left = 0, right = 100)
36 ax[1].set_ylim(bottom = 0, top = 200)
37
38 ax[0].legend(frameon = False)
39 ax[1].legend(frameon = False)
40
41 seaborn.despine()
42 plt.savefig('Fig_Arabinose.png', format = 'png', bbox_inches = 'tight', dpi = 350)
43 # for publication
44 # plt.savefig('Fig_Arabinose.pdf', format = 'pdf', bbox_inches = 'tight', dpi = 350)
45
46 plt.show()

```

And the results is



Note: See the [Arabinose Model](#) to inspect the rules and reproduce (at some extent because of stochasticity) the plot showed in this Manual.

EXPORT TO

The PySB python package could export to different languages (See more [here](#)). Use the following code to export to BioNetGen and *kappa* languages, putting the code at the end of the model.

```
1 from pysb.export import export
2 with open('model.kappa', 'w') as outfile:
3     outfile.write(export(model, 'kappa'))
4 with open('model.bngl', 'w') as outfile:
5     outfile.write(export(model, 'bngl'))
```

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

INDICES AND TABLES

- `genindex`
- `modindex`
- `search`