cobra Documentation

Release 0.4.0

Daniel Robert Hyduke and Ali Ebrahim

February 23, 2016

For installation instructions, please see INSTALL.md.

Many of the examples below are viewable as IPython notebooks, which can be viewed at nbviewer.

CHAPTER 1

Getting Started

To begin with, cobrapy comes with bundled models for *Salmonella* and *E. coli*, as well as a “textbook” model of *E. coli* core metabolism. To load a test model, type

```
from __future__ import print_function
import cobra.test

model = cobra.test.create_test_model("textbook")  # "ecoli" and "salmonella" are also valid argument
```

The reactions, metabolites, and genes attributes of the cobrapy model are a special type of list called a DictList, and each one is made up of Reaction, Metabolite and Gene objects respectively.

```
print(len(model.reactions))
print(len(model.metabolites))
print(len(model.genes))
```

```
95
72
137
```

Just like a regular list, objects in the DictList can be retrived by index. For example, to get the 30th reaction in the model (at index 29 because of 0-indexing):

```
model.reactions[29]
```

```
<Reaction EX_glu__L_e at 0x7fbbe05e5590>
```

Addictionally, items can be retrived by their id using the get_by_id() function. For example, to get the cytosolic atp metabolite object (the id is “atp_c”), we can do the following:

```
model.metabolites.get_by_id("atp_c")
```

```
<Metabolite atp_c at 0x7fbbe0617350>
```

As an added bonus, users with an interactive shell such as IPython will be able to tab-complete to list elements inside a list. While this is not recommended behavior for most code because of the possibility for characters like “-” inside ids, this is very useful while in an interactive prompt:

```
model.reactions.EX_glc__D_e.lower_bound
```

```
-10.0
```

1.1 Reactions

We will consider the reaction glucose 6-phosphate isomerase, which interconverts glucose 6-phosphate and fructose 6-phosphate. The reaction id for this reaction in our test model is PGI.

```
pgi = model.reactions.get_by_id("PGI")
pgi
```

```
<Reaction PGI at 0x7fbbe0611790>
```

We can view the full name and reaction catalyzed as strings

```
print(pgi.name)
print(pgi.reaction)
```

```
glucose-6-phosphate isomerase
g6p_c <=> f6p_c
```

We can also view reaction upper and lower bounds. Because the pgi.lower_bound < 0, and pgi.upper_bound > 0, pgi is reversible

```
print(pgi.lower_bound, "< pgi <", pgi.upper_bound)
print(pgi.reversibility)
```

```
-1000.0 < pgi < 1000.0
True
```

We can also ensure the reaction is mass balanced. This function will return elements which violate mass balance. If it comes back empty, then the reaction is mass balanced.

```
pgi.check_mass_balance()
```

```
{}
```

In order to add a metabolite, we pass in a dict with the metabolite object and its coefficient

```
pgi.add_metabolites({model.metabolites.get_by_id("h_c"): -1})
pgi.reaction
```

```
'g6p_c + h_c <=> f6p_c'
```

The reaction is no longer mass balanced

```
pgi.check_mass_balance()
```

```
{'H': -1.0}
```

We can remove the metabolite, and the reaction will be balanced once again.

```
pgi.pop(model.metabolites.get_by_id("h_c"))
print(pgi.reaction)
print(pgi.check_mass_balance())
```

```
g6p_c <=> f6p_c
{}
```

It is also possible to build the reaction from a string. However, care must be taken when doing this to ensure reaction id's match those in the model. The direction of the arrow is also used to update the upper and lower bounds.

```
pgi.reaction = "g6p_c --> f6p_c + h_c + green_eggs + ham"
```

```
unknown metabolite 'green_eggs' created
unknown metabolite 'ham' created
```

```
pgi.reaction
```

```
'g6p_c --> green_eggs + ham + h_c + f6p_c'
```

```
pgi.reaction = "g6p_c <=> f6p_c"
pgi.reaction
```

```
'g6p_c <=> f6p_c'
```

1.2 Metabolites

We will consider cytosolic atp as our metabolite, which has the id atp_c in our test model.

```
atp = model.metabolites.get_by_id("atp_c")
atp
```

```
<Metabolite atp_c at 0x7fbbe0617350>
```

We can print out the metabolite name and compartment (cytosol in this case).

```
print(atp.name)
print(atp.compartment)
```

```
ATP
c
```

We can see that ATP is a charged molecule in our model.

```
atp.charge
```

```
-4
```

We can see the chemical formula for the metabolite as well.

```
print(atp.formula)
```

```
C10H12N5O13P3
```

The reactions attribute gives a frozenset of all reactions using the given metabolite. We can use this to count the number of reactions which use atp.

```
len(atp.reactions)
```

```
13
```

A metabolite like glucose 6-phosphate will participate in fewer reactions.

```
model.metabolites.get_by_id("g6p_c").reactions
```

```
frozenset({<Reaction G6PDH2r at 0x7fbbe05fd050>,
           <Reaction GLCpts at 0x7fbbe05fd150>,
           <Reaction PGI at 0x7fbbe0611790>,
           <Reaction Biomass_Ecoli_core at 0x7fbbe0650ed0>})
```

1.3 Genes

The gene_reaction_rule is a boolean representation of the gene requirements for this reaction to be active as described in Schellenberger et al 2011 Nature Protocols 6(9):1290-307.

The GPR is stored as the gene_reaction_rule for a Reaction object as a string.

```
gpr = pgi.gene_reaction_rule
gpr
```

```
'b4025'
```

Corresponding gene objects also exist. These objects are tracked by the reactions itself, as well as by the model

```
pgi.genes
```

```
frozenset({<Gene b4025 at 0x7fbbe063dc90>})
```

```
pgi_gene = model.genes.get_by_id("b4025")
pgi_gene
```

```
<Gene b4025 at 0x7fbbe063dc90>
```

Each gene keeps track of the reactions it catalyzes

```
pgi_gene.reactions
```

```
frozenset({<Reaction PGI at 0x7fbbe0611790>})
```

Altering the gene_reaction_rule will create new gene objects if necessary and update all relationships.

```
pgi.gene_reaction_rule = "(spam or eggs)"
pgi.genes
```

```
frozenset({<Gene eggs at 0x7fbbe0611b50>, <Gene spam at 0x7fbbe0611e90>})
```

```
pgi_gene.reactions
```

```
frozenset()
```

Newly created genes are also added to the model

```
model.genes.get_by_id("spam")
```

```
<Gene spam at 0x7fbbe0611e90>
```

The delete_model_genes function will evaluate the gpr and set the upper and lower bounds to 0 if the reaction is knocked out. This function can preserve existing deletions or reset them using the cumulative_deletions flag.

```
cobra.manipulation.delete_model_genes(model, ["spam"], cumulative_deletions=True)
print(pgi.lower_bound, "< pgi <", pgi.upper_bound)
cobra.manipulation.delete_model_genes(model, ["eggs"], cumulative_deletions=True)
print(pgi.lower_bound, "< pgi <", pgi.upper_bound)
```

```
-1000 < pgi < 1000
0.0 < pgi < 0.0
```

The undelete_model_genes can be used to reset a gene deletion

```
cobra.manipulation.undelete_model_genes(model)
print(pgi.lower_bound, "< pgi <", pgi.upper_bound)
```

```
-1000 < pgi < 1000
```

CHAPTER 2

Building a Model

This simple example demonstrates how to create a model, create a reaction, and then add the reaction to the model.

We'll use the '3OAS140' reaction from the STM_1.0 model:

1.0 malACP[c] + 1.0 h[c] + 1.0 ddcaACP[c] $\rightarrow$ 1.0 co2[c] + 1.0 ACP[c] + 1.0 3omrsACP[c]

First, create the model and reaction.

```
from cobra import Model, Reaction, Metabolite
# Best practise: SBML compliant IDs
cobra_model = Model('example_cobra_model')

reaction = Reaction('3OAS140')
reaction.name = '3 oxoacyl acyl carrier protein synthase n C140 '
reaction.subsystem = 'Cell Envelope Biosynthesis'
reaction.lower_bound = 0.  # This is the default
reaction.upper_bound = 1000.  # This is the default
reaction.objective_coefficient = 0. # this is the default
```

We need to create metabolites as well. If we were using an existing model, we could use get_by_id to get the appropriate Metabolite objects instead.

```
ACP_c = Metabolite('ACP_c',
                   formula='C11H21N2O7PRS',
                   name='acyl-carrier-protein',
                   compartment='c')
omrsACP_c = Metabolite('3omrsACP_c',
                       formula='C25H45N2O9PRS',
                       name='3-Oxotetradecanoyl-acyl-carrier-protein',
                       compartment='c')
co2_c = Metabolite('co2_c',
                   formula='CO2',
                   name='CO2',
                   compartment='c')
malACP_c = Metabolite('malACP_c',
                      formula='C14H22N2O10PRS',
                      name='Malonyl-acyl-carrier-protein',
                      compartment='c')
h_c = Metabolite('h_c',
                 formula='H',
                 name='H',
                 compartment='c')
ddcaACP_c = Metabolite('ddcaACP_c',
                       formula='C23H43N2O8PRS',
                       name='Dodecanoyl-ACP-n-C120ACP',
                       compartment='c')
```

Adding metabolites to a reaction requires using a dictionary of the metabolites and their stoichiometric coefficients. A group of metabolites can be added all at once, or they can be added one at a time.

```
reaction.add_metabolites({malACP_c: -1.0,
                          h_c: -1.0,
                          ddcaACP_c: -1.0,
                          co2_c: 1.0,
                          ACP_c: 1.0,
                          omrsACP_c: 1.0})


reaction.reaction  # This gives a string representation of the reaction
```

```
'malACP_c + h_c + ddcaACP_c --> 3omrsACP_c + ACP_c + co2_c'
```

The gene_reaction_rule is a boolean representation of the gene requirements for this reaction to be active as described in Schellenberger et al 2011 Nature Protocols 6(9):1290-307. We will assign the gene reaction rule string, which will automatically create the corresponding gene objects.

```
reaction.gene_reaction_rule = '( STM2378 or STM1197 )'
reaction.genes
```

```
frozenset({<Gene STM1197 at 0x7feea0ae9850>, <Gene STM2378 at 0x7feea0ae9b10>})
```

At this point in time, the model is still empty

```
print('%i reactions in initial model' % len(cobra_model.reactions))
print('%i metabolites in initial model' % len(cobra_model.metabolites))
print('%i genes in initial model' % len(cobra_model.genes))
```

```
0 reactions in initial model
0 metabolites in initial model
0 genes in initial model
```

We will add the reaction to the model, which will also add all associated metabolites and genes

```
cobra_model.add_reaction(reaction)

# Now there are things in the model
print('%i reaction in model' % len(cobra_model.reactions))
print('%i metabolites in model' % len(cobra_model.metabolites))
print('%i genes in model' % len(cobra_model.genes))
```

```
1 reaction in model
6 metabolites in model
2 genes in model
```

We can iterate through the model objects to observe the contents

```
# Iterate through the the objects in the model
print("Reactions")
print("---------")
for x in cobra_model.reactions:
    print("%s : %s" % (x.id, x.reaction))
print("Metabolites")
print("-----------")
```

```
for x in cobra_model.metabolites:
    print('%s : %s' % (x.id, x.formula))
print("Genes")
print("-----")
for x in cobra_model.genes:
    reactions_list_str = "{" + ", ".join((i.id for i in x.reactions)) + "}"
    print("%s is associated with reactions: %s" % (x.id, reactions_list_str))
```

```
Reactions
---------
3OAS140 : malACP_c + h_c + ddcaACP_c --> 3omrsACP_c + ACP_c + co2_c
Metabolites
-----------
3omrsACP_c : C25H45N2O9PRS
ACP_c : C11H21N2O7PRS
co2_c : CO2
malACP_c : C14H22N2O10PRS
h_c : H
ddcaACP_c : C23H43N2O8PRS
Genes
-----
STM2378 is associated with reactions: {3OAS140}
STM1197 is associated with reactions: {3OAS140}
```

CHAPTER 3

Reading and Writing Models

Cobrapy supports reading and writing models in SBML (with and without FBC), JSON, MAT, and pickle formats. Generally, SBML with FBC version 2 is the preferred format for general use. The JSON format may be more useful for cobrapy-specific functionality.

The package also ships with test models in various formats for testing purposes.

```
import cobra.test
import os

print("mini test files: ")
print(", ".join([i for i in os.listdir(cobra.test.data_directory) if i.startswith("mini")]))

textbook_model = cobra.test.create_test_model("textbook")
ecoli_model = cobra.test.create_test_model("ecoli")
salmonella_model = cobra.test.create_test_model("salmonella")
```

```
mini test files:
mini.mat, mini_cobra.xml, mini.json, mini_fbc2.xml.gz, mini_fbc2.xml.bz2, mini_fbc2.xml, mini_fbc1.xm
```

3.1 SBML

The Systems Biology Markup Language is an XML-based standard format for distributing models which has support for COBRA models through the FBC extension version 2.

Cobrapy has native support for reading and writing SBML with FBCv2. Please note that all id's in the model must conform to the SBML SID requirements in order to generate a valid SBML file.

```
cobra.io.read_sbml_model(os.path.join(cobra.test.data_directory, "mini_fbc2.xml"))
```

```
<Model mini_textbook at 0x7f246d4e2e50>
```

```
cobra.io.write_sbml_model(textbook_model, "test_fbc2.xml")
```

There are other dialects of SBML prior to FBC 2 which have previously been use to encode COBRA models. The primary ones is the "COBRA" dialect which used the "notes" fields in SBML files.

Cobrapy can use libsbml, which must be installed separately (see installation instructions) to read and write these files. When reading in a model, it will automatically detect whether fbc was used or not. When writing a model, the use_fbc_package flag can be used can be used.

```
cobra.io.read_sbml_model(os.path.join(cobra.test.data_directory, "mini_cobra.xml"))
```

```
<Model mini_textbook at 0x7f2436c65a10>
```

```
cobra.io.write_sbml_model(textbook_model, "test_cobra.xml", use_fbc_package=False)
```

3.2 JSON

cobrapy models have a JSON (JavaScript Object Notation) representation. This format was crated for interoperability with escher.

```
cobra.io.load_json_model(os.path.join(cobra.test.data_directory, "mini.json"))
```

```
<Model mini_textbook at 0x7f2436c7c850>
```

```
cobra.io.save_json_model(textbook_model, "test.json")
```

3.3 MATLAB

Often, models may be imported and exported soley for the purposes of working with the same models in cobrapy and the MATLAB cobra toolbox. MATLAB has its own ".mat" format for storing variables. Reading and writing to these mat files from python requires scipy.

A mat file can contain multiple MATLAB variables. Therefore, the variable name of the model in the MATLAB file can be passed into the reading function:

```
cobra.io.load_matlab_model(os.path.join(cobra.test.data_directory, "mini.mat"),
                           variable_name="mini_textbook")
```

```
<Model mini_textbook at 0x7f2436c7c810>
```

If the mat file contains only a single model, cobra can figure out which variable to read from, and the variable_name paramter is unnecessary.

```
cobra.io.load_matlab_model(os.path.join(cobra.test.data_directory, "mini.mat"))
```

```
<Model mini_textbook at 0x7f2436c65510>
```

Saving models to mat files is also relatively straightforward

```
cobra.io.save_matlab_model(textbook_model, "test.mat")
```

3.4 Pickle

Cobra models can be serialized using the python serialization format, pickle.

Please note that use of the pickle format is generally not recommended for most use cases. JSON, SBML, and MAT are generally the preferred formats.

CHAPTER 4

Simulating with FBA

Simulations using flux balance analysis can be solved using Model.optimize(). This will maximize or minimize (maximizing is the default) flux through the objective reactions.

```
import pandas
pandas.options.display.max_rows = 100

import cobra.test
model = cobra.test.create_test_model("textbook")
```

4.1 Running FBA

```
model.optimize()
```

```
<Solution 0.87 at 0x7fe558058b50>
```

The Model.optimize() function will return a Solution object, which will also be stored at model.solution. A solution object has several attributes:

- f: the objective value
- status: the status from the linear programming solver
- x_dict: a dictionary of {reaction_id: flux_value} (also called "primal")
- x: a list for x_dict
- y_dict: a dictionary of {metabolite_id: dual_value}.
- y: a list for y_dict

For example, after the last call to model.optimize(), the status should be 'optimal' if the solver returned no errors, and f should be the objective value

```
model.solution.status
```

```
'optimal'
```

```
model.solution.f
```

```
0.8739215069684305
```

4.2 Changing the Objectives

The objective function is determined from the objective_coefficient attribute of the objective reaction(s). Currently in the model, there is only one objective reaction, with an objective coefficient of 1.

```
model.objective
```

```
{<Reaction Biomass_Ecoli_core at 0x7fe526516490>: 1.0}
```

The objective function can be changed by assigning Model.objective, which can be a reaction object (or just it's name), or a dict of {Reaction: objective_coefficient}.

```
# change the objective to ATPM
# the upper bound should be 1000 so we get the actual optimal value
model.reactions.get_by_id("ATPM").upper_bound = 1000.
model.objective = "ATPM"
model.objective
```

```
{<Reaction ATPM at 0x7fe526516210>: 1}
```

```
model.optimize().f
```

```
174.99999999999997
```

The objective function can also be changed by setting Reaction.objective_coefficient directly.

```
model.reactions.get_by_id("ATPM").objective_coefficient = 0.
model.reactions.get_by_id("Biomass_Ecoli_core").objective_coefficient = 1.
model.objective
```

```
{<Reaction Biomass_Ecoli_core at 0x7fe526516490>: 1.0}
```

4.3 Running FVA

FBA will not give always give unique solution, because multiple flux states can achieve the same optimum. FVA (or flux variability analysis) finds the ranges of each metabolic flux at the optimum.

```
fva_result = cobra.flux_analysis.flux_variability_analysis(model, model.reactions[:20])
pandas.DataFrame.from_dict(fva_result).T
```

Setting parameter fraction_of_optimium=0.90 would give the flux ranges for reactions at 90% optimality.

```
fva_result = cobra.flux_analysis.flux_variability_analysis(model, model.reactions[:20], fraction_of_
pandas.DataFrame.from_dict(fva_result).T
```

4.4 Running pFBA

Parsimonious FBA (often written pFBA) finds a flux distribution which gives the optimal growth rate, but minimizes the total sum of flux. This involves solving two sequential linear programs, but is handled transparently by cobrapy. For more details on pFBA, please see Lewis et al. (2010).

```
FBA_solution = model.optimize()
pFBA_solution = cobra.flux_analysis.optimize_minimal_flux(model)
```

These functions should give approximately the same objective value

```
abs(FBA_solution.f - pFBA_solution.f)
```

```
1.1102230246251565e-16
```

CHAPTER 5

Simulating Deletions

```
import pandas
from time import time

import cobra.test

cobra_model = cobra.test.create_test_model("textbook")
ecoli_model = cobra.test.create_test_model("ecoli")
```

5.1 Single Deletions

Perform all single gene deletions on a model

```
growth_rates, statuses = cobra.flux_analysis.single_gene_deletion(cobra_model)
```

These can also be done for only a subset of genes

```
growth_rates, statuses = cobra.flux_analysis.single_gene_deletion(cobra_model, cobra_model.genes[:20]
pandas.DataFrame.from_dict({"growth_rates": growth_rates, "status": statuses})
```

This can also be done for reactions

```
growth_rates, statuses = cobra.flux_analysis.single_reaction_deletion(cobra_model, cobra_model.react
pandas.DataFrame.from_dict({"growth_rates": growth_rates, "status": statuses})
```

5.2 Double Deletions

Double deletions run in a similar way. Passing in return_frame=True will cause them to format the results as a pandas Dataframe

```
cobra.flux_analysis.double_gene_deletion(cobra_model, cobra_model.genes[-10:], return_frame=True)
```

By default, the double deletion function will automatically use multiprocessing, splitting the task over up to 4 cores if they are available. The number of cores can be manually sepcified as well. Setting use of a single core will disable use of the multiprocessing library, which often aids debuggging.

```
start = time()  # start timer()
cobra.flux_analysis.double_gene_deletion(ecoli_model, ecoli_model.genes[:100], number_of_processes=2)
t1 = time() - start
print("Double gene deletions for 100 genes completed in %.2f sec with 2 cores" % t1)
```

```
start = time()  # start timer()
cobra.flux_analysis.double_gene_deletion(ecoli_model, ecoli_model.genes[:100], number_of_processes=1)
t2 = time() - start
print("Double gene deletions for 100 genes completed in %.2f sec with 1 core" % t2)

print("Speedup of %.2fx" % (t2/t1))
```

```
Double gene deletions for 100 genes completed in 1.69 sec with 2 cores
Double gene deletions for 100 genes completed in 2.02 sec with 1 core
Speedup of 1.20x
```

Double deletions can also be run for reactions

```
cobra.flux_analysis.double_reaction_deletion(cobra_model, cobra_model.reactions[:10], return_frame=Tr
```

CHAPTER 6

Phenotype Phase Plane

Phenotype phase planes will show distinct phases of optimal growth with different use of two different substrates. For more information, see Edwards et al.

Cobrapy supports calculating and plotting (using matplotlib) these phenotype phase planes. Here, we will make one for the "textbook" *E. coli* core model.

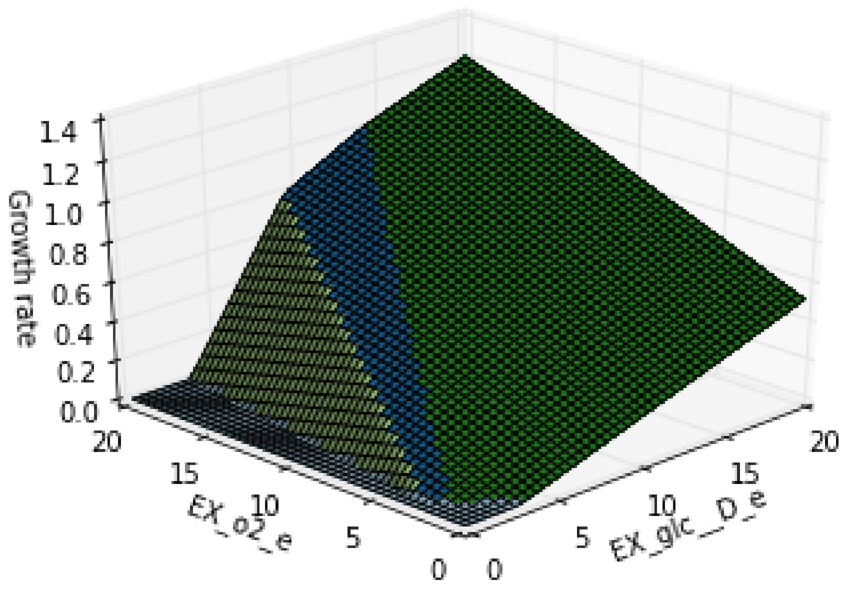
```
%matplotlib inline
from time import time

import cobra.test
from cobra.flux_analysis import calculate_phenotype_phase_plane

model = cobra.test.create_test_model("textbook")
```

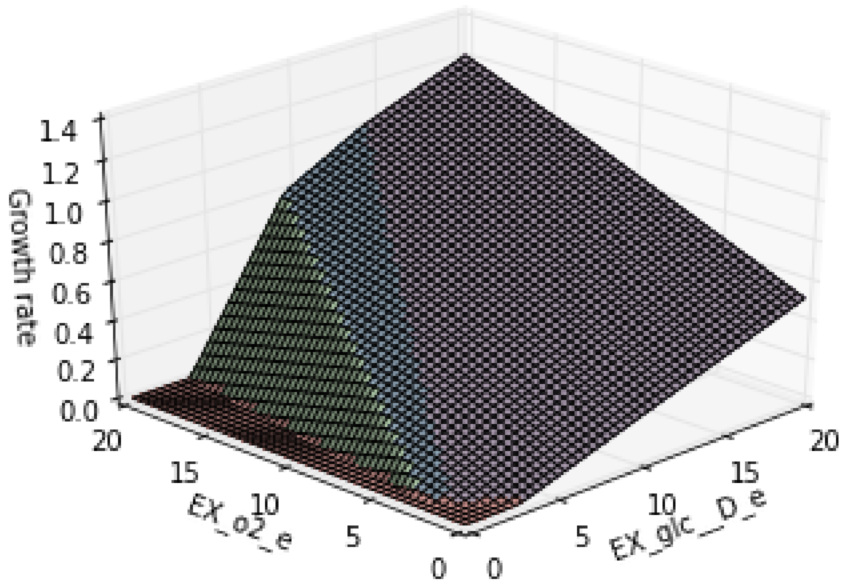
We want to make a phenotype phase plane to evaluate uptakes of Glucose and Oxygen.

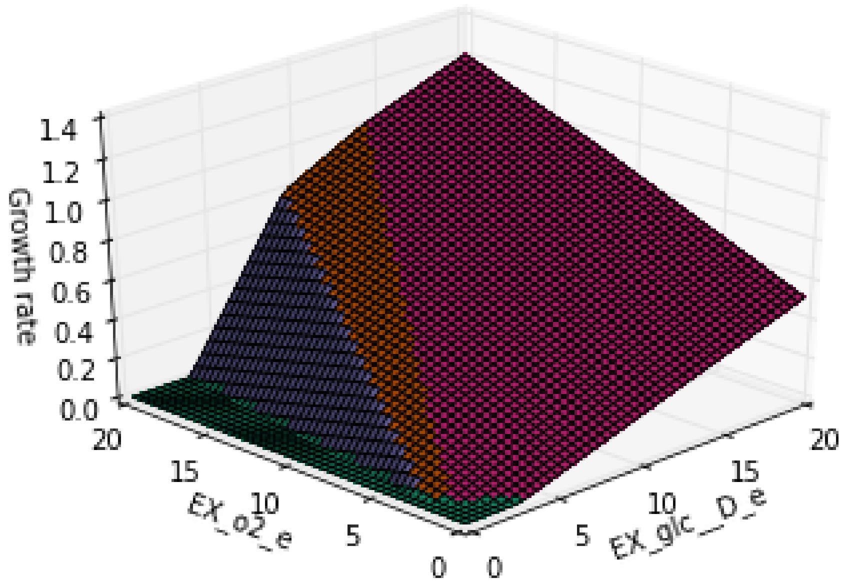
```
data = calculate_phenotype_phase_plane(model, "EX_glc__D_e", "EX_o2_e")
data.plot_matplotlib();
```



If palettable is installed, other color schemes can be used as well

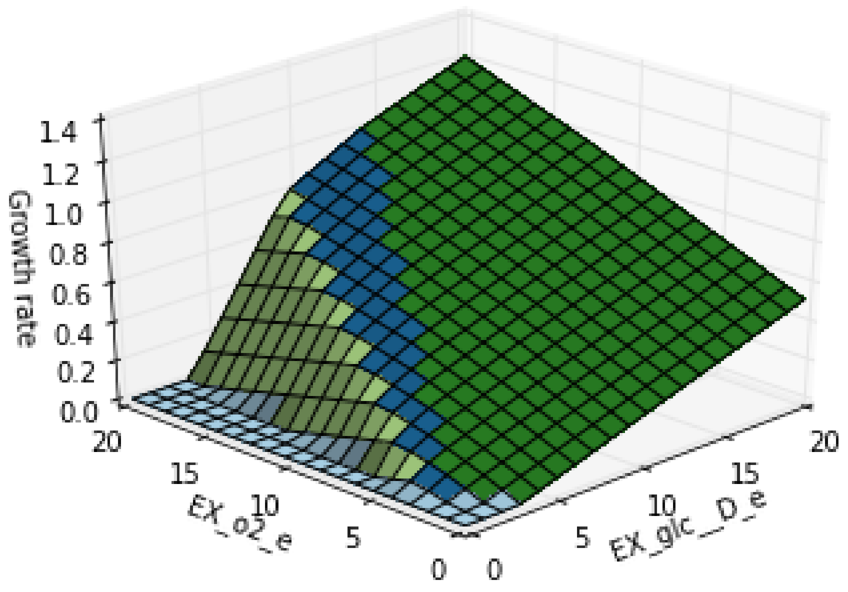
```
data.plot_matplotlib("Pastel1")
data.plot_matplotlib("Dark2");
```





The number of points which are plotted in each dimension can also be changed

```
calculate_phenotype_phase_plane(model, "EX_glc__D_e", "EX_o2_e",
                                reaction1_npoints=20,
                                reaction2_npoints=20).plot_matplotlib();
```



The code can also use multiple processes to speed up calculations

```
start_time = time()
calculate_phenotype_phase_plane(model, "EX_glc__D_e", "EX_o2_e", n_processes=1,
                                reaction1_npoints=100, reaction2_npoints=100)
print("took %.2f seconds with 1 process" % (time() - start_time))
start_time = time()
calculate_phenotype_phase_plane(model, "EX_glc__D_e", "EX_o2_e", n_processes=4,
                                reaction1_npoints=100, reaction2_npoints=100)
print("took %.2f seconds with 4 process" % (time() - start_time))
```

```
took 0.41 seconds with 1 process
took 0.29 seconds with 4 process
```

CHAPTER 7

Mixed-Integer Linear Programming

7.1 Ice Cream

This example was originally contributed by Joshua Lerman.

An ice cream stand sells cones and popsicles. It wants to maximize its profit, but is subject to a budget.

We can write this problem as a linear program:

$\textbf{max}\ \text{cone} \cdot \text{cone\_margin} + \text{popsicle} \cdot \text{popsicle margin}$

subject to

$\text{cone} \cdot \text{cone\_cost} + \text{popsicle} \cdot \text{popsicle\_cost} \leq \text{budget}$

```
cone_selling_price = 7.
cone_production_cost = 3.
popsicle_selling_price = 2.
popsicle_production_cost = 1.
starting_budget = 100.
```

This problem can be written as a cobra.Model

```
from cobra import Model, Metabolite, Reaction

cone = Reaction("cone")
popsicle = Reaction("popsicle")

# constrainted to a budget
budget = Metabolite("budget")
budget._constraint_sense = "L"
budget._bound = starting_budget
cone.add_metabolites({budget: cone_production_cost})
popsicle.add_metabolites({budget: popsicle_production_cost})

# objective coefficient is the profit to be made from each unit
cone.objective_coefficient = cone_selling_price - cone_production_cost
popsicle.objective_coefficient = popsicle_selling_price - \
                                 popsicle_production_cost

m = Model("lerman_ice_cream_co")
m.add_reactions((cone, popsicle))

m.optimize().x_dict
```

```
{'cone': 33.333333333333336, 'popsicle': 0.0}
```

In reality, cones and popsicles can only be sold in integer amounts. We can use the variable kind attribute of a cobra.Reaction to enforce this.

```
cone.variable_kind = "integer"
popsicle.variable_kind = "integer"
m.optimize().x_dict
```

```
{'cone': 33.0, 'popsicle': 1.0}
```

Now the model makes both popsicles and cones.

7.2 Restaurant Order

To tackle the less immediately obvious problem from the following XKCD comic:

```
from IPython.display import Image
Image(url=r"http://imgs.xkcd.com/comics/np_complete.png")
```

We want a solution satisfying the following constraints:

$$\begin{pmatrix} 2.15 & 2.75 & 3.35 & 3.55 & 4.20 & 5.80 \end{pmatrix} \cdot \vec{v} = 15.05$$

$$\vec{v}_i \geq 0$$

$$\vec{v}_i \in \mathbb{Z}$$

This problem can be written as a COBRA model as well.

```
total_cost = Metabolite("constraint")
total_cost._bound = 15.05

costs = {"mixed_fruit": 2.15, "french_fries": 2.75, "side_salad": 3.35,
         "hot_wings": 3.55, "mozarella_sticks": 4.20, "sampler_plate": 5.80}

m = Model("appetizers")

for item, cost in costs.items():
    r = Reaction(item)
    r.add_metabolites({total_cost: cost})
    r.variable_kind = "integer"
    m.add_reaction(r)

# To add to the problem, suppose we don't want to eat all mixed fruit.
m.reactions.mixed_fruit.objective_coefficient = 1

m.optimize(objective_sense="minimize").x_dict
```

```
{'french_fries': 0.0,
 'hot_wings': 2.0,
 'mixed_fruit': 1.0,
 'mozarella_sticks': 0.0,
 'sampler_plate': 1.0,
 'side_salad': 0.0}
```

There is another solution to this problem, which would have been obtained if we had maximized for mixed fruit instead of minimizing.

```
m.optimize(objective_sense="maximize").x_dict
```

```
{'french_fries': 0.0,
 'hot_wings': 0.0,
 'mixed_fruit': 7.0,
 'mozarella_sticks': 0.0,
 'sampler_plate': 0.0,
 'side_salad': 0.0}
```

7.3 Boolean Indicators

To give a COBRA-related example, we can create boolean variables as integers, which can serve as indicators for a reaction being active in a model. For a reaction flux v with lower bound -1000 and upper bound 1000, we can create a binary variable b with the following constraints:

$b \in \{0, 1\}$

$-1000 \cdot b \leq v \leq 1000 \cdot b$

To introduce the above constraints into a cobra model, we can rewrite them as follows

$v \leq b \cdot 1000 \Rightarrow v - 1000 \cdot b \leq 0$

$-1000 \cdot b \leq v \Rightarrow v + 1000 \cdot b \geq 0$

```
import cobra.test
model = cobra.test.create_test_model("textbook")

# an indicator for pgi
pgi = model.reactions.get_by_id("PGI")
# make a boolean variable
pgi_indicator = Reaction("indicator_PGI")
pgi_indicator.lower_bound = 0
pgi_indicator.upper_bound = 1
pgi_indicator.variable_kind = "integer"
# create constraint for v - 1000 b <= 0
pgi_plus = Metabolite("PGI_plus")
pgi_plus._constraint_sense = "L"
# create constraint for v + 1000 b >= 0
pgi_minus = Metabolite("PGI_minus")
pgi_minus._constraint_sense = "G"

pgi_indicator.add_metabolites({pgi_plus: -1000, pgi_minus: 1000})
pgi.add_metabolites({pgi_plus: 1, pgi_minus: 1})
model.add_reaction(pgi_indicator)


# an indicator for zwf
zwf = model.reactions.get_by_id("G6PDH2r")
zwf_indicator = Reaction("indicator_ZWF")
zwf_indicator.lower_bound = 0
zwf_indicator.upper_bound = 1
zwf_indicator.variable_kind = "integer"
# create constraint for v - 1000 b <= 0
zwf_plus = Metabolite("ZWF_plus")
zwf_plus._constraint_sense = "L"
# create constraint for v + 1000 b >= 0
```

```
zwf_minus = Metabolite("ZWF_minus")
zwf_minus._constraint_sense = "G"

zwf_indicator.add_metabolites({zwf_plus: -1000, zwf_minus: 1000})
zwf.add_metabolites({zwf_plus: 1, zwf_minus: 1})

# add the indicator reactions to the model
model.add_reaction(zwf_indicator)
```

In a model with both these reactions active, the indicators will also be active

```
solution = model.optimize()
print("PGI indicator = %d" % solution.x_dict["indicator_PGI"])
print("ZWF indicator = %d" % solution.x_dict["indicator_ZWF"])
print("PGI flux = %.2f" % solution.x_dict["PGI"])
print("ZWF flux = %.2f" % solution.x_dict["G6PDH2r"])
```

```
PGI indicator = 1
ZWF indicator = 1
PGI flux = 4.86
ZWF flux = 4.96
```

Because these boolean indicators are in the model, additional constraints can be applied on them. For example, we can prevent both reactions from being active at the same time by adding the following constraint:

$b_{\text{pgi}} + b_{\text{zwf}} = 1$

```
or_constraint = Metabolite("or")
or_constraint._bound = 1
zwf_indicator.add_metabolites({or_constraint: 1})
pgi_indicator.add_metabolites({or_constraint: 1})

solution = model.optimize()
print("PGI indicator = %d" % solution.x_dict["indicator_PGI"])
print("ZWF indicator = %d" % solution.x_dict["indicator_ZWF"])
print("PGI flux = %.2f" % solution.x_dict["PGI"])
print("ZWF flux = %.2f" % solution.x_dict["G6PDH2r"])
```

```
PGI indicator = 1
ZWF indicator = 0
PGI flux = 9.82
ZWF flux = 0.00
```

Quadratic Programming

Suppose we want to minimize the Euclidean distance of the solution to the origin while subject to linear constraints. This will require a quadratic objective function. Consider this example problem:

min $\frac{1}{2}\left(x^2 + y^2\right)$

subject to

$x + y = 2$

$x \geq 0$

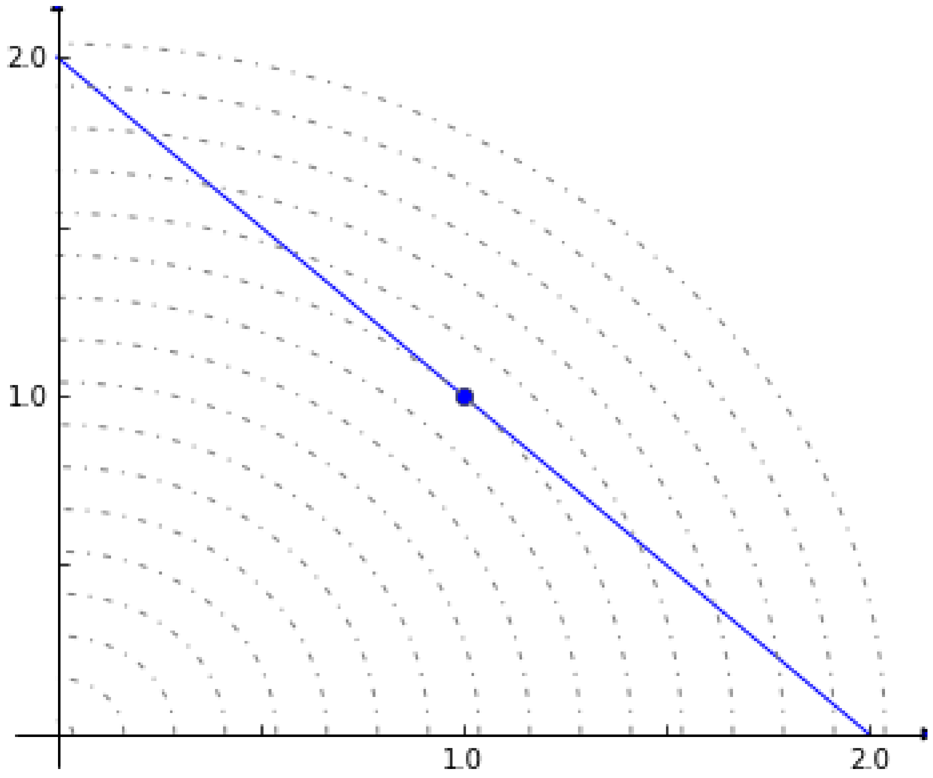
$y \geq 0$

This problem can be visualized graphically:

```
%matplotlib inline
from matplotlib.pyplot import figure, xlim, ylim
from mpl_toolkits.axes_grid.axislines import SubplotZero
from numpy import linspace, arange, sqrt, pi, sin, cos, sign
# axis style
def make_plot_ax():
    fig = figure(figsize=(6, 5));
    ax = SubplotZero(fig, 111); fig.add_subplot(ax)
    for direction in ["xzero", "yzero"]:
        ax.axis[direction].set_axisline_style("-|>")
        ax.axis[direction].set_visible(True)
    for direction in ["left", "right", "bottom", "top"]:
        ax.axis[direction].set_visible(False)
    xlim(-0.1, 2.1); ylim(xlim())
    ticks = [0.5 * i for i in range(1, 5)]
    labels = [str(i) if i == int(i) else "" for i in ticks]
    ax.set_xticks(ticks); ax.set_yticks(ticks)
    ax.set_xticklabels(labels); ax.set_yticklabels(labels)
    ax.axis["yzero"].set_axis_direction("left")
    return ax

ax = make_plot_ax()
ax.plot((0, 2), (2, 0), 'b')
ax.plot([1], [1], 'bo')

# circular grid
for r in sqrt(2.) + 0.125 * arange(-11, 6):
    t = linspace(0., pi/2., 100)
    ax.plot(r * cos(t), r * sin(t), '-.', color="gray")
```



The objective can be rewritten as $\frac{1}{2}v^T \cdot \mathbf{Q} \cdot v$, where $v = \begin{pmatrix} x \\ y \end{pmatrix}$ and $\mathbf{Q} = \begin{pmatrix} 1 & 0 \\ 0 & 1 \end{pmatrix}$

The matrix $\mathbf{Q}$ can be passed into a cobra model as the quadratic objective.

```
import scipy

from cobra import Reaction, Metabolite, Model, solvers
```

The quadratic objective $\mathbf{Q}$ should be formatted as a scipy sparse matrix.

```
Q = scipy.sparse.eye(2).todok()
Q
```

```
<2x2 sparse matrix of type '<type 'numpy.float64'>'
    with 2 stored elements in Dictionary Of Keys format>
```

In this case, the quadratic objective is simply the identity matrix

```
Q.todense()
```

```
matrix([[ 1.,  0.],
        [ 0.,  1.]])
```

We need to use a solver that supports quadratic programming, such as gurobi or cplex. If a solver which supports quadratic programming is installed, this function will return its name.

```
print(solvers.get_solver_name(qp=True))
```

```
gurobi
```

```
c = Metabolite("c")
c._bound = 2
x = Reaction("x")
y = Reaction("y")
x.add_metabolites({c: 1})
y.add_metabolites({c: 1})
m = Model()
m.add_reactions([x, y])
sol = m.optimize(quadratic_component=Q, objective_sense="minimize")
sol.x_dict
```

```
{'x': 1.0, 'y': 1.0}
```

Suppose we change the problem to have a mixed linear and quadratic objective.

$$\textbf{min}\ \frac{1}{2}\left(x^2+y^2\right)-y$$

subject to

$$x+y=2$$

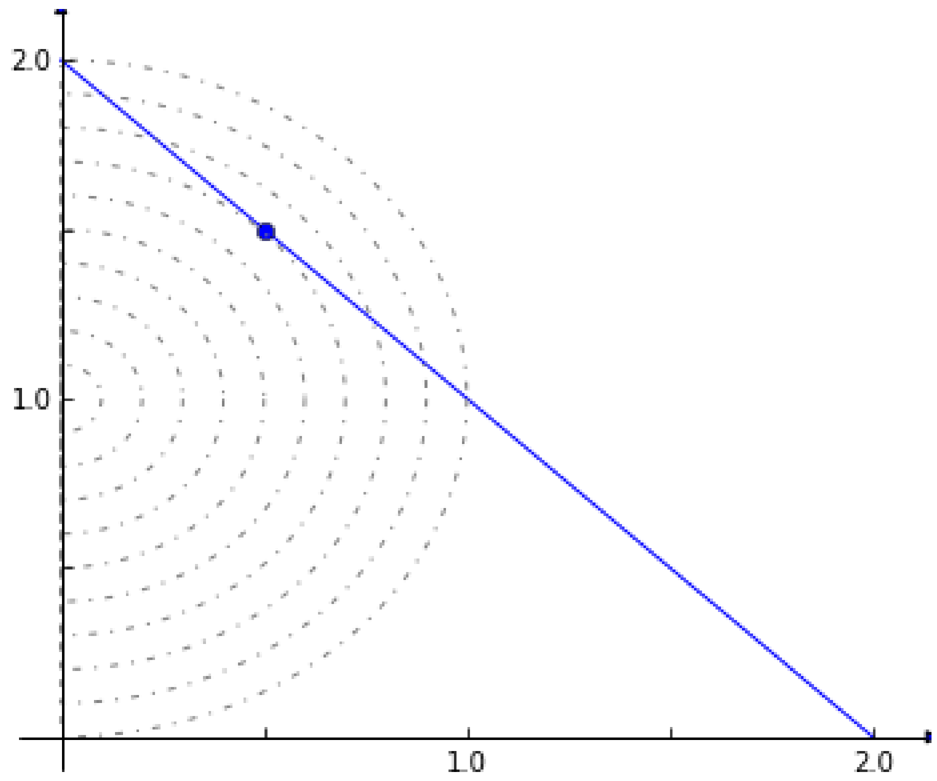
$$x\geq 0$$

$$y\geq 0$$

Graphically, this would be

```
ax = make_plot_ax()
ax.plot((0, 2), (2, 0), 'b')
ax.plot([0.5], [1.5], 'bo')

yrange = linspace(1, 2, 11)
for r in (yrange ** 2 / 2. - yrange):
    t = linspace(-sqrt(2 * r + 1) + 0.000001, sqrt(2 * r + 1) - 0.000001, 1000)
    ax.plot(abs(t), 1 + sqrt(2 * r + 1 - t ** 2) * sign(t), '-.', color="gray")
```



QP solvers in cobrapy will combine linear and quadratic coefficients. The linear portion will be obtained from the same objective_coefficient attribute used with LP's.

```
y.objective_coefficient = -1
sol = m.optimize(quadratic_component=Q, objective_sense="minimize")
sol.x_dict
```

```
{'x': 0.5, 'y': 1.5}
```

Loopless FBA

The goal of this procedure is identification of a thermodynamically consistent flux state without loops, as implied by the name.

Usually, the model has the following constraints.

$$S \cdot v = 0$$

$$lb \leq v \leq ub$$

However, this will allow for thermodynamically infeasible loops (referred to as type 3 loops) to occur, where flux flows around a cycle without any net change of metabolites. For most cases, this is not a major issue, as solutions with these loops can usually be converted to equivalent solutions without them. However, if a flux state is desired which does not exhibit any of these loops, loopless FBA can be used. The formulation used here is modified from Schellenberger et al.

We can make the model irreversible, so that all reactions will satisfy

$$0 \leq lb \leq v \leq ub \leq \max(ub)$$

We will add in boolean indicators as well, such that

$$\max(ub) \cdot i \geq v$$

$$i \in \{0, 1\}$$

We also want to ensure that an entry in the row space of S also exists with negative values wherever v is nonzero. In this expression, $1 - i$ acts as a not to indicate inactivity of a reaction.

$$S^{\mathsf{T}} x - (1 - i)(\max(ub) + 1) \leq -1$$

We will construct an LP integrating both constraints.

$$\begin{pmatrix} S & 0 & 0 \\ -I & \max(ub)I & 0 \\ 0 & (\max(ub) + 1)I & S^{\mathsf{T}} \end{pmatrix} \cdot \begin{pmatrix} v \\ i \\ x \end{pmatrix} \begin{matrix} = \\ \geq \\ \leq \end{matrix} \begin{matrix} 0 \\ 0 \\ \max(ub) \end{matrix}$$

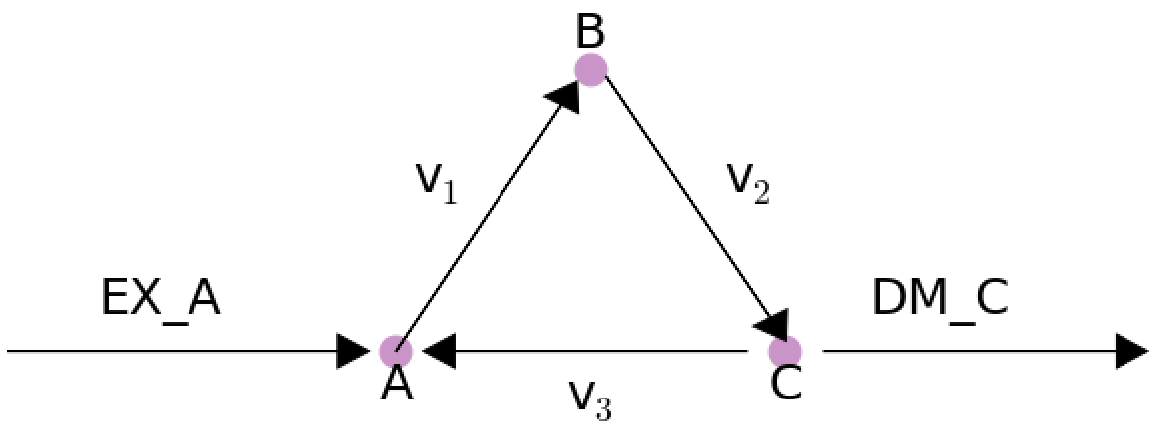
Note that these extra constraints are not applied to boundary reactions which bring metabolites in and out of the system.

```
from matplotlib.pylab import *
%matplotlib inline

import cobra.test
from cobra import Reaction, Metabolite, Model
from cobra.flux_analysis.loopless import construct_loopless_model
from cobra.solvers import get_solver_name
```

We will demonstrate with a toy model which has a simple loop cycling A -> B -> C -> A, with A allowed to enter the system and C allowed to leave. A graphical view of the system is drawn below:

```
figure(figsize=(10.5, 4.5), frameon=False)
gca().axis("off")
xlim(0.5, 3.5)
ylim(0.7, 2.2)
arrow_params = {"head_length": 0.08, "head_width": 0.1, "ec": "k", "fc": "k"}
text_params = {"fontsize": 25, "horizontalalignment": "center", "verticalalignment": "center"}
arrow(0.5, 1, 0.85, 0, **arrow_params)  # EX_A
arrow(1.5, 1, 0.425, 0.736, **arrow_params)  # v1
arrow(2.04, 1.82, 0.42, -0.72, **arrow_params)  # v2
arrow(2.4, 1, -0.75, 0, **arrow_params)  # v3
arrow(2.6, 1, 0.75, 0, **arrow_params)
# reaction labels
text(0.9, 1.15, "EX_A", **text_params)
text(1.6, 1.5, r"v$_1$", **text_params)
text(2.4, 1.5, r"v$_2$", **text_params)
text(2, 0.85, r"v$_3$", **text_params)
text(2.9, 1.15, "DM_C", **text_params)
# metabolite labels
scatter(1.5, 1, s=250, color='#c994c7')
text(1.5, 0.9, "A", **text_params)
scatter(2, 1.84, s=250, color='#c994c7')
text(2, 1.95, "B", **text_params)
scatter(2.5, 1, s=250, color='#c994c7')
text(2.5, 0.9, "C", **text_params);
```



```
test_model = Model()
test_model.add_metabolites(Metabolite("A"))
test_model.add_metabolites(Metabolite("B"))
test_model.add_metabolites(Metabolite("C"))
EX_A = Reaction("EX_A")
EX_A.add_metabolites({test_model.metabolites.A: 1})
DM_C = Reaction("DM_C")
DM_C.add_metabolites({test_model.metabolites.C: -1})
v1 = Reaction("v1")
v1.add_metabolites({test_model.metabolites.A: -1, test_model.metabolites.B: 1})
v2 = Reaction("v2")
```

```
v2.add_metabolites({test_model.metabolites.B: -1, test_model.metabolites.C: 1})
v3 = Reaction("v3")
v3.add_metabolites({test_model.metabolites.C: -1, test_model.metabolites.A: 1})
DM_C.objective_coefficient = 1
test_model.add_reactions([EX_A, DM_C, v1, v2, v3])
```

While this model contains a loop, a flux state exists which has no flux through reaction v3, and is identified by loopless FBA.

```
construct_loopless_model(test_model).optimize()
```

```
<Solution 1000.00 at 0x7f003ad82850>
```

However, if flux is forced through v3, then there is no longer a feasible loopless solution.

```
v3.lower_bound = 1
construct_loopless_model(test_model).optimize()
```

```
<Solution 'infeasible' at 0x7f003ad82f10>
```

Loopless FBA is also possible on genome scale models, but it requires a capable MILP solver.

```
salmonella = cobra.test.create_test_model("salmonella")
construct_loopless_model(salmonella).optimize(solver=get_solver_name(mip=True))
```

```
<Solution 0.38 at 0x7f003a496190>
```

```
ecoli = cobra.test.create_test_model("ecoli")
construct_loopless_model(ecoli).optimize(solver=get_solver_name(mip=True))
```

```
<Solution 0.98 at 0x7f003ae06b50>
```

CHAPTER 10

Gapfillling

GrowMatch and SMILEY are gap-filling algorithms, which try to to make the minimal number of changes to a model and allow it to simulate growth. For more information, see Kumar et al.. Please note that these algorithms are Mixed-Integer Linear Programs, which need solvers such as gurobi or cplex to function correctly.

```
import cobra.test

model = cobra.test.create_test_model("salmonella")
```

In this model D-Fructose-6-phosphate is an essential metabolite. We will remove all the reactions using it, and at them to a separate model.

```
# remove some reactions and add them to the universal reactions
Universal = cobra.Model("Universal_Reactions")
for i in [i.id for i in model.metabolites.f6p_c.reactions]:
    reaction = model.reactions.get_by_id(i)
    Universal.add_reaction(reaction.copy())
    reaction.remove_from_model()
```

Now, because of these gaps, the model won't grow.

```
model.optimize().f
```

```
3.067723590211908e-08
```

We will use GrowMatch to add back the minimal number of reactions from this set of "universal" reactions (in this case just the ones we removed) to allow it to grow.

```
cobra.flux_analysis.growMatch(model, Universal)
```

```
[[<Reaction GF6PTA at 0x7fcecddbc390>,
  <Reaction MAN6PI_reverse at 0x7fcecddbc450>,
  <Reaction F6PA_reverse at 0x7fcecddbc490>,
  <Reaction PGI_reverse at 0x7fcecddbc510>,
  <Reaction TKT2_reverse at 0x7fcecddbc590>]]
```

We can obtain multiple possible reaction sets by having the algorithm go through multiple iterations.

```
result = cobra.flux_analysis.growMatch(model, Universal, iterations=4)
for i, entries in enumerate(result):
    print("---- Run %d ----" % (i + 1))
    for e in entries:
        print(e.id)
```

```
---- Run 1 ----
FBP
GF6PTA
MAN6PI_reverse
PGI_reverse
TKT2_reverse
---- Run 2 ----
TALA
F6PP
GF6PTA
MAN6PI_reverse
F6PA_reverse
---- Run 3 ----
F6PP
GF6PTA
MAN6PI_reverse
F6PA_reverse
TKT2_reverse
---- Run 4 ----
TALA
FBP
GF6PTA
MAN6PI_reverse
PGI_reverse
```

CHAPTER 11

Solver Interface

Each cobrapy solver must expose the following API. The solvers all will have their own distinct LP object types, but each can be manipulated by these functions. This API can be used directly when implementing algorithms efficiently on linear programs because it has 2 primary benefits:

1. Avoid the overhead of creating and destroying LP's for each operation
2. Many solver objects preserve the basis between subsequent LP's, making each subsequent LP solve faster

We will walk though the API with the cglpk solver, which links the cobrapy solver API with GLPK's C API.

```
import cobra.test

model = cobra.test.create_test_model("textbook")
solver = cobra.solvers.cglpk
```

11.1 Attributes and functions

Each solver has some attributes:

11.1.1 solver_name

The name of the solver. This is the name which will be used to select the solver in cobrapy functions.

```
solver.solver_name
```

```
'cglpk'
```

```
model.optimize(solver="cglpk")
```

```
<Solution 0.87 at 0x7f9148bb2250>
```

11.1.2 _SUPPORTS_MILP

The presence of this attribute tells cobrapy that the solver supports mixed-integer linear programming

```
solver._SUPPORTS_MILP
```

```
True
```

11.1.3 solve

Model.optimize is a wrapper for each solver's solve function. It takes in a cobra model and returns a solution

```
solver.solve(model)
```

```
<Solution 0.87 at 0x7f917d50ed50>
```

11.1.4 create_problem

This creates the LP object for the solver.

```
lp = solver.create_problem(model, objective_sense="maximize")
lp
```

```
<cobra.solvers.cglpk.GLP at 0x46e8aa0>
```

11.1.5 solve_problem

Solve the LP object and return the solution status

```
solver.solve_problem(lp)
```

```
'optimal'
```

11.1.6 format_solution

Extract a cobra.Solution object from a solved LP object

```
solver.format_solution(lp, model)
```

```
<Solution 0.87 at 0x7f917d50e9d0>
```

11.1.7 get_objective_value

Extract the objective value from a solved LP object

```
solver.get_objective_value(lp)
```

```
0.8739215069684305
```

11.1.8 get_status

Get the solution status of a solved LP object

```
solver.get_status(lp)
```

```
'optimal'
```

11.1.9 change_variable_objective

change the objective coefficient a reaction at a particular index. This does not change any of the other objectives which have already been set. This example will double and then revert the biomass coefficient.

```
model.reactions.index("Biomass_Ecoli_core")
```

```
12
```

```
solver.change_variable_objective(lp, 12, 2)
solver.solve_problem(lp)
solver.get_objective_value(lp)
```

```
1.747843013936861
```

```
solver.change_variable_objective(lp, 12, 1)
solver.solve_problem(lp)
solver.get_objective_value(lp)
```

```
0.8739215069684305
```

11.1.10 change variable_bounds

change the lower and upper bounds of a reaction at a particular index. This example will set the lower bound of the biomass to an infeasible value, then revert it.

```
solver.change_variable_bounds(lp, 12, 1000, 1000)
solver.solve_problem(lp)
```

```
'infeasible'
```

```
solver.change_variable_bounds(lp, 12, 0, 1000)
solver.solve_problem(lp)
```

```
'optimal'
```

11.1.11 change_coefficient

Change a coefficient in the stoichiometric matrix. In this example, we will set the entry for ADP in the ATMP reaction to in infeasible value, then reset it.

```
model.metabolites.index("atp_c")
```

```
16
```

```
model.reactions.index("ATPM")
```

```
10
```

```
solver.change_coefficient(lp, 16, 10, -10)
solver.solve_problem(lp)
```

```
'infeasible'
```

```
solver.change_coefficient(lp, 16, 10, -1)
solver.solve_problem(lp)
```

```
'optimal'
```

11.1.12 set_parameter

Set a solver parameter. Each solver will have its own particular set of unique paramters. However, some have unified names. For example, all solvers should accept “tolerance_feasibility.”

```
solver.set_parameter(lp, "tolerance_feasibility", 1e-9)
```

```
solver.set_parameter(lp, "objective_sense", "minimize")
solver.solve_problem(lp)
solver.get_objective_value(lp)
```

```
0.0
```

```
solver.set_parameter(lp, "objective_sense", "maximize")
solver.solve_problem(lp)
solver.get_objective_value(lp)
```

```
0.8739215069684304
```

11.2 Example with FVA

Consider flux variability analysis (FVA), which requires maximizing and minimizing every reaction with the original biomass value fixed at its optimal value. If we used the cobra Model API in a naive implementation, we would do the following:

```
%%time
# work on a copy of the model so the original is not changed
fva_model = model.copy()

# set the lower bound on the objective to be the optimal value
f = fva_model.optimize().f
for objective_reaction, coefficient in fva_model.objective.items():
    objective_reaction.lower_bound = coefficient * f

# now maximize and minimze every reaction to find its bounds
fva_result = {}
for r in fva_model.reactions:
    fva_model.change_objective(r)
    fva_result[r.id] = {}
    fva_result[r.id]["maximum"] = fva_model.optimize(objective_sense="maximize").f
    fva_result[r.id]["minimum"] = fva_model.optimize(objective_sense="minimize").f
```

```
CPU times: user 144 ms, sys: 667 µs, total: 145 ms
Wall time: 141 ms
```

Instead, we could use the solver API to do this more efficiently. This is roughly how cobrapy implementes FVA. It keeps uses the same LP object and repeatedly maximizes and minimizes it. This allows the solver to preserve the basis, and is much faster. The speed increase is even more noticeable the larger the model gets.

```
%%time
# create the LP object
lp = solver.create_problem(model)

# set the lower bound on the objective to be the optimal value
solver.solve_problem(lp)
f = solver.get_objective_value(lp)
for objective_reaction, coefficient in model.objective.items():
    objective_index = model.reactions.index(objective_reaction)
    # old objective is no longer the objective
    solver.change_variable_objective(lp, objective_index, 0.)
    solver.change_variable_bounds(lp, objective_index, f * coefficient, objective_reaction.upper_bour

# now maximize and minimze every reaction to find its bounds
fva_result = {}
for index, r in enumerate(model.reactions):
    solver.change_variable_objective(lp, index, 1.)
    fva_result[r.id] = {}
    solver.solve_problem(lp, objective_sense="maximize")
    fva_result[r.id]["maximum"] = solver.get_objective_value(lp)
    solver.solve_problem(lp, objective_sense="minimize")
    fva_result[r.id]["minimum"] = solver.get_objective_value(lp)
    solver.change_variable_objective(lp, index, 0.)
```

```
CPU times: user 9.85 ms, sys: 251 µs, total: 10.1 ms
Wall time: 9.94 ms
```

Using the COBRA toolbox with cobrapy

This example demonstrates using COBRA toolbox commands in MATLAB from python through pymatbridge.

```
%load_ext pymatbridge
```

```
Starting MATLAB on ZMQ socket ipc:///tmp/pymatbridge-39fd5b7f-475a-40d3-b831-3adf4da6edd3
Send 'exit' command to kill the server
....MATLAB started and connected!
```

```
import cobra.test
m = cobra.test.create_test_model("textbook")
```

The model_to_pymatbridge function will send the model to the workspace with the given variable name.

```
from cobra.io.mat import model_to_pymatbridge
model_to_pymatbridge(m, variable_name="model")
```

Now in the MATLAB workspace, the variable name 'model' holds a COBRA toolbox struct encoding the model.

```
%%matlab
model
```

```
model =

            rev: [95x1 double]
       metNames: {72x1 cell}
              b: [72x1 double]
              c: [95x1 double]
         csense: [72x1 char]
          genes: {137x1 cell}
    metFormulas: {72x1 cell}
           rxns: {95x1 cell}
        grRules: {95x1 cell}
       rxnNames: {95x1 cell}
    description: [8x1 char]
              S: [72x95 double]
             ub: [95x1 double]
             lb: [95x1 double]
           mets: {72x1 cell}
     subSystems: {95x1 cell}
```

First, we have to initialize the COBRA toolbox in MATLAB.

```
%%matlab --silent
warning('off'); % this works around a pymatbridge bug
```

```
addpath(genpath('~/cobratoolbox/'));
initCobraToolbox();
```

Commands from the COBRA toolbox can now be run on the model

```
%%matlab
optimizeCbModel(model)
```

```
ans =

           x: [95x1 double]
           f: 0.8739
           y: [71x1 double]
           w: [95x1 double]
        stat: 1
    origStat: 5
      solver: 'glpk'
        time: 0.2327
```

FBA in the COBRA toolbox should give the same result as cobrapy

```
%time
m.optimize().f
```

```
CPU times: user 5 µs, sys: 0 ns, total: 5 µs
Wall time: 10 µs
```

```
0.8739215069684305
```

CHAPTER 13

FAQ

This document will address frequently asked questions not addressed in other pages of the documentation.

13.1 How do I install cobrapy?

Please see the INSTALL.md file.

13.2 How do I cite cobrapy?

Please cite the 2013 publication: 10.1186/1752-0509-7-74

13.3 How do I rename reactions or metabolites?

TL;DR Use Model.repair afterwards

When renaming metabolites or reactions, there are issues because cobra indexes based off of ID's, which can cause errors. For example:

```
from __future__ import print_function
import cobra.test
model = cobra.test.create_test_model()

for metabolite in model.metabolites:
    metabolite.id = "test_" + metabolite.id

try:
    model.metabolites.get_by_id(model.metabolites[0].id)
except KeyError as e:
    print(repr(e))
```

```
KeyError('test_dcaACP_c',)
```

The Model.repair function will rebuild the necessary indexes

```
model.repair()
model.metabolites.get_by_id(model.metabolites[0].id)
```

```
<Metabolite test_dcaACP_c at 0x688b450>
```

13.4 How do I delete a gene?

That depends on what precisely you mean by delete a gene.

If you want to simulate the model with a gene knockout, use the cobra.maniupulation.delete_model_genes function. The effects of this function are reversed by cobra.manipulation.undelete_model_genes.

```
model = cobra.test.create_test_model()
PGI = model.reactions.get_by_id("PGI")
print("bounds before knockout:", (PGI.lower_bound, PGI.upper_bound))
cobra.manipulation.delete_model_genes(model, ["STM4221"])
print("bounds after knockouts", (PGI.lower_bound, PGI.upper_bound))
```

```
bounds before knockout: (-1000.0, 1000.0)
bounds after knockouts (0.0, 0.0)
```

If you want to actually remove all traces of a gene from a model, this is more difficult because this will require changing all the gene_reaction_rule strings for reactions involving the gene.

13.5 How do I change the reversibility of a Reaction?

Reaction.reversibility is a property in cobra which is computed when it is requested from the lower and upper bounds.

```
model = cobra.test.create_test_model()
model.reactions.get_by_id("PGI").reversibility
```

```
True
```

Trying to set it directly will result in an error:

```
try:
    model.reactions.get_by_id("PGI").reversibility = False
except Exception as e:
    print(repr(e))
```

```
AttributeError("can't set attribute",)
```

The way to change the reversibility is to change the bounds to make the reaction irreversible.

```
model.reactions.get_by_id("PGI").lower_bound = 10
model.reactions.get_by_id("PGI").reversibility
```

```
False
```

13.6 How do I generate an LP file from a COBRA model?

While the cobrapy does not include python code to support this feature directly, many of the bundled solvers have this capability. Create the problem with one of these solvers, and use its appropriate function.

Please note that unlike the LP file format, the MPS file format does not specify objective direction and is always a minimzation. Some (but not all) solvers will rewrite the maximization as a minimzation.

```
model = cobra.test.create_test_model()
# glpk through cglpk
glp = cobra.solvers.cglpk.create_problem(model)
glp.write("test.lp")
glp.write("test.mps")  # will not rewrite objective
# gurobi
gurobi_problem = cobra.solvers.gurobi_solver.create_problem(model)
gurobi_problem.write("test.lp")
gurobi_problem.write("test.mps")  # rewrites objective
# cplex
cplex_problem = cobra.solvers.cplex_solver.create_problem(model)
cplex_problem.write("test.lp")
cplex_problem.write("test.mps")  # rewrites objective
```

13.7 How do I visualize my flux solutions?

cobrapy works well with the escher package, which is well suited to this purpose. Consult the escher documentation for examples.

CHAPTER 14

cobra package

14.1 Subpackages

14.1.1 cobra.core package

Submodules

cobra.core.ArrayBasedModel module

class `cobra.core.ArrayBasedModel.`**`ArrayBasedModel`**(*description=None*, *deep-copy_model=False*, *matrix_type='scipy.lil_matrix'*)

Bases: `cobra.core.Model.Model`

ArrayBasedModel is a class that adds arrays and vectors to a cobra.Model to make it easier to perform linear algebra operations.

`S`

Stoichiometric matrix of the model

This will be formatted as either `lil_matrix` or `dok_matrix`

`add_metabolites`(*metabolite_list*, *expand_stoichiometric_matrix=True*)

Will add a list of metabolites to the the object, if they do not exist and then expand the stochiometric matrix

metabolite_list: A list of `Metabolite` objects

expand_stoichimetric_matrix: Boolean. If True and self.S is not None then it will add rows to self.S. self.S must be created after adding reactions and metabolites to self before it can be expanded. Trying to expand self.S when self only contains metabolites is ludacris.

`add_reactions`(*reaction_list*, *update_matrices=True*)

Will add a cobra.Reaction object to the model, if reaction.id is not in self.reactions.

reaction_list: A `Reaction` object or a list of them

update_matrices: Boolean. If true populate / update matrices S, lower_bounds, upper_bounds, ... Note this is slow to run for very large models and using this option with repeated calls will degrade performance. Better to call self.update() after adding all reactions.

> If the stoichiometric matrix is initially empty then initialize a 1x1 sparse matrix and add more rows as needed in the self.add_metabolites function

`b`

bounds for metabolites as `numpy.ndarray`

constraint_sense

copy()
Provides a partial 'deepcopy' of the Model. All of the Metabolite, Gene, and Reaction objects are created anew but in a faster fashion than deepcopy

lower_bounds

objective_coefficients

remove_reactions(*reactions*, *update_matrices=True*, ***kwargs*)
remove reactions from the model

See `cobra.core.Model.Model.remove_reactions()`

update_matrices: Boolean If true populate / update matrices S, lower_bounds, upper_bounds. Note that this is slow to run for very large models, and using this option with repeated calls will degrade performance.

update()
Regenerates the stoichiometric matrix and vectors

upper_bounds

cobra.core.DictList module

class cobra.core.DictList.**DictList**(**args*)
Bases: `list`

A combined dict and list

This object behaves like a list, but has the O(1) speed benefits of a dict when looking up elements by their id.

__add__(*other*)
x.__add__(y) <==> x + y

other: iterable other must contain only unique id's which do not intersect with self

__contains__(*object*)
DictList.__contains__(object) <==> object in DictList

object: str or `Object`

__getstate__()
gets internal state

This is only provided for backwards compatibilty so older versions of cobrapy can load pickles generated with cobrapy. In reality, the "_dict" state is ignored when loading a pickle

__iadd__(*other*)
x.__iadd__(y) <==> x += y

other: iterable other must contain only unique id's whcih do not intersect with self

__setstate__(*state*)
sets internal state

Ignore the passed in state and recalculate it. This is only for compatibility with older pickles which did not correctly specify the initialization class

append(*object*)
append object to end

extend(*iterable*)
extend list by appending elements from the iterable

get_by_id(*id*)
return the element with a matching id

has_id(*id*)

index(*id*, **args*)
Determine the position in the list

id: A string or a `Object`

insert(*index*, *object*)
insert object before index

list_attr(*attribute*)
return a list of the given attribute for every object

pop(**args*)
remove and return item at index (default last).

query(*search_function*, *attribute='id'*)
query the list

search_function: used to select which objects to return

- a string, in which case any object.attribute containing the string will be returned
- a compiled regular expression
- a function which takes one argument and returns True for desired values

attribute: the attribute to be searched for (default is 'id'). If this is None, the object itself is used.

returns: a list of objects which match the query

remove(*x*)

Warning: Internal use only

reverse()
reverse *IN PLACE*

sort(*cmp=None*, *key=None*, *reverse=False*)
stable sort *IN PLACE*

cmp(x, y) -> -1, 0, 1

union(*iterable*)
adds elements with id's not already in the model

cobra.core.Formula module

class `cobra.core.Formula.`**Formula**(*formula=None*)
Bases: `cobra.core.Object.Object`

Describes a Chemical Formula

A legal formula string contains only letters and numbers.

__add__(*other_formula*)
Combine two molecular formulas.

other_formula: cobra.Formula or str of a chemical Formula.

parse_composition()
Breaks the chemical formula down by element.

weight
Calculate the formula weight

cobra.core.Gene module

class cobra.core.Gene.**GPRCleaner**
Bases: ast.NodeTransformer

Parses compiled ast of a gene_reaction_rule and identifies genes

Parts of the tree are rewritten to allow periods in gene ID's and bitwise boolean operations

visit_BinOp(*node*)

visit_Name(*node*)

class cobra.core.Gene.**Gene**(*id=None*, *name='‘*, *functional=True*)
Bases: *cobra.core.Species.Species*

remove_from_model(*model=None*, *make_dependent_reactions_nonfunctional=True*)
Removes the association

make_dependent_reactions_nonfunctional: Boolean. If True then replace the gene with 'False' in the gene association, else replace the gene with 'True'

Deprecated since version 0.4: Use cobra.manipulation.delete_model_genes to simulate knockouts and cobra.manipulation.remove_genes to remove genes from the model.

cobra.core.Gene.**ast2str**(*expr*, *level=0*, *names=None*)
convert compiled ast to gene_reaction_rule str

expr: str of a gene reaction rule

level: internal use only

names: optional dict of {Gene.id: Gene.name} Use this to get a rule str which uses names instead. This should be done for display purposes only. All gene_reaction_rule strings which are computed with should use the id.

cobra.core.Gene.**eval_gpr**(*expr*, *knockouts*)
evaluate compiled ast of gene_reaction_rule with knockouts

cobra.core.Gene.**parse_gpr**(*str_expr*)
parse gpr into AST

returns: (ast_tree, {gene_ids})

cobra.core.Metabolite module

class cobra.core.Metabolite.**Metabolite**(*id=None*, *formula=None*, *name='‘*, *compartment=None*)
Bases: *cobra.core.Species.Species*

Metabolite is a class for holding information regarding a metabolite in a cobra.Reaction object.

elements

formula_weight
Calculate the formula weight

remove_from_model(*method='subtractive'*, ***kwargs*)
Removes the association from self.model

method: 'subtractive' or 'destructive'. If 'subtractive' then the metabolite is removed from all associated reactions. If 'destructive' then all associated reactions are removed from the Model.

y
The shadow price for the metabolite in the most recent solution

Shadow prices are computed from the dual values of the bounds in the solution.

cobra.core.Model module

class cobra.core.Model.**Model**(*id_or_model=None*, *name=None*)
Bases: `cobra.core.Object.Object`

Metabolic Model

Refers to Metabolite, Reaction, and Gene Objects.

__add__(*other_model*)
Adds two models. +

The issue of reactions being able to exists in multiple Models now arises, the same for metabolites and such. This might be a little difficult as a reaction with the same name / id in two models might have different coefficients for their metabolites due to pH and whatnot making them different reactions.

__iadd__(*other_model*)
Adds a Model to this model +=

The issue of reactions being able to exists in multiple Models now arises, the same for metabolites and such. This might be a little difficult as a reaction with the same name / id in two models might have different coefficients for their metabolites due to pH and whatnot making them different reactions.

__setstate__(*state*)
Make sure all cobra.Objects in the model point to the model

add_metabolites(*metabolite_list*)
Will add a list of metabolites to the the object, if they do not exist and then expand the stochiometric matrix

metabolite_list: A list of `Metabolite` objects

add_reaction(*reaction*)
Will add a cobra.Reaction object to the model, if reaction.id is not in self.reactions.

reaction: A `Reaction` object

add_reactions(*reaction_list*)
Will add a cobra.Reaction object to the model, if reaction.id is not in self.reactions.

reaction_list: A list of `Reaction` objects

change_objective(*objectives*)
Change the model objective

copy()
Provides a partial 'deepcopy' of the Model. All of the Metabolite, Gene, and Reaction objects are created anew but in a faster fashion than deepcopy

description

objective

optimize(*objective_sense='maximize'*, ***kwargs*)

Optimize model using flux balance analysis

objective_sense: 'maximize' or 'minimize'

solver: 'glpk', 'cglpk', 'gurobi', 'cplex' or None

quadratic_component: None or `scipy.sparse.dok_matrix` The dimensions should be (n, n) where n is the number of reactions.

This sets the quadratic component (Q) of the objective coefficient, adding $frac12v^T \cdot Q \cdot v$ to the objective.

tolerance_feasibility: Solver tolerance for feasibility.

tolerance_markowitz: Solver threshold during pivot

time_limit: Maximum solver time (in seconds)

Note: Only the most commonly used parameters are presented here. Additional parameters for cobra.solvers may be available and specified with the appropriate keyword argument.

remove_reactions(*reactions*, *delete=True*, *remove_orphans=False*)

remove reactions from the model

reactions: [*Reaction*] or [str] The reactions (or their id's) to remove

delete: Boolean Whether or not the reactions should be deleted after removal. If the reactions are not deleted, those objects will be recreated with new metabolite and gene objects.

remove_orphans: Boolean Remove orphaned genes and metabolites from the model as well

repair(*rebuild_index=True*, *rebuild_relationships=True*)

Update all indexes and pointers in a model

to_array_based_model(*deepcopy_model=False*, ***kwargs*)

Makes a *ArrayBasedModel* from a cobra.Model which may be used to perform linear algebra operations with the stoichiomatric matrix.

deepcopy_model: Boolean. If False then the ArrayBasedModel points to the Model

cobra.core.Object module

class cobra.core.Object.**Object**(*id=None*, *name=''*)

Bases: `object`

Defines common behavior of object in cobra.core

__getstate__()

To prevent excessive replication during deepcopy.

cobra.core.Reaction module

class cobra.core.Reaction.**Frozendict**

Bases: `dict`

Read-only dictionary view

pop(*key*, *value*)

popitem()

class cobra.core.Reaction.**Reaction**(*id=None*, *name=''*, *subsystem=''*, *lower_bound=0.0*, *upper_bound=1000.0*, *objective_coefficient=0.0*)

Bases: `cobra.core.Object.Object`

Reaction is a class for holding information regarding a biochemical reaction in a cobra.Model object

__add__(*other_reaction*)
Adds two reactions to each other. Default behavior is to combine the metabolites but only use the remaining parameters from the first object.

TODO: Either clean up metabolite associations or remove function

TODO: Deal with gene association logic from adding reactions.

TODO: Simplify and add in an __iadd__

__imul__(*the_coefficient*)
Allows the reaction coefficients to be rapidly scaled.

__mul__(*the_coefficient*)
Allows a reaction to be multiplied by a coefficient.

TODO: this should return a new reaction.

__setstate__(*state*)
Probably not necessary to set _model as the cobra.Model that contains self sets the _model attribute for all metabolites and genes in the reaction.

However, to increase performance speed we do want to let the metabolite and gene know that they are employed in this reaction

__sub__(*other_reaction*)
Subtracts two reactions. Default behavior is to combine the metabolites but only use the remaining parameters from the first object.

Note: This is equivalent to adding reactions after changing the sign of the metabolites in other_reaction

add_metabolites(*metabolites*, *combine=True*, *add_to_container_model=True*)
Add metabolites and stoichiometric coefficients to the reaction. If the final coefficient for a metabolite is 0 then it is removed from the reaction.

metabolites: dict {str or `Metabolite`: coefficient}

combine: Boolean. Describes behavior a metabolite already exists in the reaction. True causes the coefficients to be added. False causes the coefficient to be replaced. True and a metabolite already exists in the

add_to_container_model: Boolean. Add the metabolite to the `Model` the reaction is associated with (i.e. self.model)

boundary

build_reaction_from_string(*reaction_str*, *verbose=True*, *fwd_arrow=None*, *rev_arrow=None*, *reversible_arrow=None*, *term_split='+'*)
Builds reaction from reaction equation reaction_str using parser

Takes a string and using the specifications supplied in the optional arguments infers a set of metabolites, metabolite compartments and stoichiometries for the reaction. It also infers the reversibility of the reaction from the reaction arrow.

Parameters

- **reaction_str** – a string containing a reaction formula (equation)

- **verbose** – Boolean setting verbosity of function (optional, default=True)
- **fwd_arrow** – re.compile for forward irreversible reaction arrows (optional, default=_forward_arrow_finder)
- **reverse_arrow** – re.compile for backward irreversible reaction arrows (optional, default=_reverse_arrow_finder)
- **fwd_arrow** – re.compile for reversible reaction arrows (optional, default=_reversible_arrow_finder)
- **term_split** – String dividing individual metabolite entries (optional, default='+')

build_reaction_string(*use_metabolite_names=False*)
Generate a human readable reaction string

check_mass_balance()
Compute mass and charge balance for the reaction

returns a dict of {element: amount} for unbalanced elements. "charge" is treated as an element in this dict This should be empty for balanced reactions.

clear_metabolites()
Remove all metabolites from the reaction

copy()
When copying a reaction, it is necessary to deepcopy the components so the list references aren't carried over.

Additionally, a copy of a reaction is no longer in a cobra.Model.

This should be fixed with self.__deecopy__ if possible

delete(*remove_orphans=False*)
Completely delete a reaction

This removes all associations between a reaction the associated model, metabolites and genes (unlike remove_from_model which only dissociates the reaction from the model).

remove_orphans: Boolean Remove orphaned genes and metabolites from the model as well

gene_name_reaction_rule
Display gene_reaction_rule with names intead.

Do NOT use this string for computation. It is intended to give a representation of the rule using more familiar gene names instead of the often cryptic ids.

gene_reaction_rule

genes

get_coefficient(*metabolite_id*)
Return the stoichiometric coefficient for a metabolite in the reaction.

metabolite_id: str or *Metabolite*

get_coefficients(*metabolite_ids*)
Return the stoichiometric coefficients for a list of metabolites in the reaction.

metabolite_ids: iterable Containing str or *Metabolite*

get_compartments()
lists compartments the metabolites are in

knock_out()
Change the upper and lower bounds of the reaction to 0.

metabolites

model
returns the model the reaction is a part of

pop(*metabolite_id*)
Remove a metabolite from the reaction and return the stoichiometric coefficient.

metabolite_id: str or `Metabolite`

products
Return a list of products for the reaction

reactants
Return a list of reactants for the reaction.

reaction
Human readable reaction string

remove_from_model(*model=None*, *remove_orphans=False*)
Removes the reaction from the model while keeping it intact

remove_orphans: Boolean Remove orphaned genes and metabolites from the model as well

model: deprecated argument, must be None

reversibility
Whether the reaction can proceed in both directions (reversible)

This is computed from the current upper and lower bounds.

subtract_metabolites(*metabolites*)
This function will 'subtract' metabolites from a reaction, which means add the metabolites with -1*coefficient. If the final coefficient for a metabolite is 0 then the metabolite is removed from the reaction.

metabolites: dict of {`Metabolite`: coefficient} These metabolites will be added to the reaction

Note: A final coefficient < 0 implies a reactant.

x
The flux through the reaction in the most recent solution

Flux values are computed from the primal values of the variables in the solution.

cobra.core.Solution module

class cobra.core.Solution.**Solution**(*f*, *x=None*, *x_dict=None*, *y=None*, *y_dict=None*, *solver=None*, *the_time=0*, *status='NA'*)
Bases: `object`

Stores the solution from optimizing a cobra.Model. This is used to provide a single interface to results from different solvers that store their values in different ways.

f: The objective value

solver: A string indicating which solver package was used.

x: List or Array of the values from the primal.

x_dict: A dictionary of reaction ids that maps to the primal values.

y: List or Array of the values from the dual.

y_dict: A dictionary of reaction ids that maps to the dual values.

dress_results(*model*)

> **Warning:** deprecated

cobra.core.Species module

class `cobra.core.Species.`**Species**(*id=None*, *name=None*)

Bases: `cobra.core.Object.Object`

Species is a class for holding information regarding a chemical Species

__getstate__()

Remove the references to container reactions when serializing to avoid problems associated with recursion.

copy()

When copying a reaction, it is necessary to deepcopy the components so the list references aren't carried over.

Additionally, a copy of a reaction is no longer in a cobra.Model.

This should be fixed with self.__deecopy__ if possible

model

reactions

Module contents

14.1.2 cobra.flux_analysis package

Submodules

cobra.flux_analysis.deletion_worker module

class `cobra.flux_analysis.deletion_worker.`**CobraDeletionMockPool**(*cobra_model*, *n_processes=1*, *solver=None*, ***kwargs*)

Bases: `object`

Mock pool solves LP's in the same process

receive_all()

receive_one()

start()

submit(*indexes*, *label=None*)

terminate()

class `cobra.flux_analysis.deletion_worker.`**CobraDeletionPool**(*cobra_model*, *n_processes=None*, *solver=None*, ***kwargs*)

Bases: `object`

A pool of workers for solving deletions

submit jobs to the pool using submit and recieve results using receive_all

pids

receive_all()

receive_one()
This function blocks

start()

submit(*indexes*, *label=None*)

terminate()

cobra.flux_analysis.deletion_worker.**compute_fba_deletion**(*lp*, *solver_object*, *model*, *indexes*, ***kwargs*)

cobra.flux_analysis.deletion_worker.**compute_fba_deletion_worker**(*cobra_model*, *solver*, *job_queue*, *output_queue*, ***kwargs*)

cobra.flux_analysis.double_deletion module

cobra.flux_analysis.double_deletion.**double_deletion**(*cobra_model*, *element_list_1=None*, *element_list_2=None*, *element_type='gene'*, ***kwargs*)

Wrapper for double_gene_deletion and double_reaction_deletion

Deprecated since version 0.4: Use double_reaction_deletion and double_gene_deletion

cobra.flux_analysis.double_deletion.**double_gene_deletion**(*cobra_model*, *gene_list1=None*, *gene_list2=None*, *method='fba'*, *return_frame=False*, *solver=None*, *zero_cutoff=1e-12*, ***kwargs*)

sequentially knocks out pairs of genes in a model

cobra_model [`Model`] cobra model in which to perform deletions

gene_list1 [[`Gene`:] (or their id's)] Genes to be deleted. These will be the rows in the result. If not provided, all reactions will be used.

gene_list1 [[`Gene`:] (or their id's)] Genes to be deleted. These will be the rows in the result. If not provided, reaction_list1 will be used.

method: "fba" or "moma" Procedure used to predict the growth rate

solver: str for solver name This must be a QP-capable solver for MOMA. If left unspecified, a suitable solver will be automatically chosen.

zero_cutoff: float When checking to see if a value is 0, this threshold is used.

number_of_processes: int for number of processes to use. If unspecified, the number of parallel processes to use will be automatically determined. Setting this to 1 explicitly disables used of the multiprocessing library.

Note: multiprocessing is not supported with method=moma

---

return_frame: bool If true, formats the results as a pandas.Dataframe. Otherwise returns a dict of the form: {"x": row_labels, "y": column_labels", "data": 2D matrix}

`cobra.flux_analysis.double_deletion.`**`double_reaction_deletion`**(*cobra_model*, *reaction_list1=None*, *reaction_list2=None*, *method='fba'*, *return_frame=False*, *solver=None*, *zero_cutoff=1e-12*, ***kwargs*)

sequentially knocks out pairs of reactions in a model

cobra_model [`Model`] cobra model in which to perform deletions

reaction_list1 [[`Reaction`:] (or their id's)] Reactions to be deleted. These will be the rows in the result. If not provided, all reactions will be used.

reaction_list2 [[`Reaction`:] (or their id's)] Reactions to be deleted. These will be the rows in the result. If not provided, reaction_list1 will be used.

method: "fba" or "moma" Procedure used to predict the growth rate

solver: str for solver name This must be a QP-capable solver for MOMA. If left unspecified, a suitable solver will be automatically chosen.

zero_cutoff: float When checking to see if a value is 0, this threshold is used.

return_frame: bool If true, formats the results as a pandas.Dataframe. Otherwise returns a dict of the form: {"x": row_labels, "y": column_labels", "data": 2D matrix}

`cobra.flux_analysis.double_deletion.`**`format_results_frame`**(*row_ids*, *column_ids*, *matrix*, *return_frame=False*)

format results as a pandas.DataFrame if desired/possible

Otherwise returns a dict of {"x": row_ids, "y": column_ids", "data": result_matrx}

`cobra.flux_analysis.double_deletion.`**`generate_matrix_indexes`**(*ids1*, *ids2*)

map an identifier to an entry in the square result matrix

`cobra.flux_analysis.double_deletion.`**`yield_upper_tria_indexes`**(*ids1*, *ids2*, *id_to_index*)

gives the necessary indexes in the upper triangle

ids1 and ids2 are lists of the identifiers i.e. gene id's or reaction indexes to be knocked out. id_to_index maps each identifier to its index in the result matrix.

Note that this does not return indexes for the diagonal. Those have to be computed separately.

cobra.flux_analysis.essentiality module

`cobra.flux_analysis.essentiality.`**`assess_medium_component_essentiality`**(*cobra_model*, *the_components=None*, *the_medium=None*, *medium_compartment='e'*, *solver='glpk'*, *the_problem='return'*, *the_condition=None*, *method='fba'*)

Determines which components in an in silico medium are essential for growth in the context of the remaining components.

cobra_model: A Model object.

the_components: None or a list of external boundary reactions that will be sequentially disabled.

the_medium: Is None, a string, or a dictionary. If a string then the initialize_growth_medium function expects that the_model has an attribute dictionary called media_compositions, which is a dictionary of dictionaries for various medium compositions. Where a medium composition is a dictionary of external boundary reaction ids for the medium components and the external boundary fluxes for each medium component.

medium_compartment: the compartment in which the boundary reactions supplying the medium components exist

NOTE: that these fluxes must be negative because the convention is backwards means something is feed into the system.

solver: 'glpk', 'gurobi', or 'cplex'

the_problem: Is None, 'return', or an LP model object for the solver.

Returns A dictionary providing the maximum growth rate accessible when the respective component is removed from the medium.

Return type essentiality_dict

cobra.flux_analysis.gapfilling module

`cobra.flux_analysis.gapfilling.`**`SMILEY`**(*model*, *metabolite_id*, *Universal*, *dm_rxns=False*, *ex_rxns=False*, *panalties=None*, ***solver_parameters*)

runs the SMILEY algorithm to determine which gaps should be filled in order for the model to create the metabolite with the given metabolite_id.

This function is good for running the algorithm once. For more fine- grained control, create a SUXModelMILP object, add a demand reaction for the given metabolite_id, and call the solve function on the SUXModelMILP object.

class `cobra.flux_analysis.gapfilling.`**`SUXModelMILP`**(*model*, *Universal=None*, *threshold=0.05*, *penalties=None*, *dm_rxns=True*, *ex_rxns=False*)

Bases: `cobra.core.Model.Model`

Model with additional Universal and Exchange reactions. Adds corresponding dummy reactions and dummy metabolites for each added reaction which are used to impose MILP constraints to minimize the total number of added reactions. See the figure for more information on the structure of the matrix.

`add_reactions`(*reactions*)

solve (*solver=None*, *iterations=1*, *debug=False*, *time_limit=100*, ***solver_parameters*)
solve the MILP problem

`cobra.flux_analysis.gapfilling.`**growMatch** (*model*, *Universal*, *dm_rxns=False*, *ex_rxns=False*, *penalties=None*, ***solver_parameters*)
runs growMatch

cobra.flux_analysis.loopless module

`cobra.flux_analysis.loopless.`**construct_loopless_model** (*cobra_model*)
construct a loopless model

This adds MILP constraints to prevent flux from proceeding in a loop, as done in http://dx.doi.org/10.1016/j.bpj.2010.12.3707 Please see the documentation for an explanation of the algorithm.

This must be solved with an MILP capable solver.

cobra.flux_analysis.moma module

`cobra.flux_analysis.moma.`**create_euclidian_distance_lp** (*moma_model*, *solver*)

`cobra.flux_analysis.moma.`**create_euclidian_distance_objective** (*n_moma_reactions*)
returns a matrix which will minimze the euclidian distance

This matrix has the structure [I -I] [-I I] where I is the identity matrix the same size as the number of reactions in the original model.

n_moma_reactions: int This is the number of reactions in the MOMA model, which should be twice the number of reactions in the original model

`cobra.flux_analysis.moma.`**create_euclidian_moma_model** (*cobra_model*, *wt_model=None*, ***solver_args*)

`cobra.flux_analysis.moma.`**moma** (*wt_model*, *mutant_model*, *solver=None*, ***solver_args*)

`cobra.flux_analysis.moma.`**moma_knockout** (*moma_model*, *moma_objective*, *reaction_indexes*, ***moma_args*)
computes result of reaction_knockouts using moma

`cobra.flux_analysis.moma.`**solve_moma_model** (*moma_model*, *objective_id*, *solver=None*, ***solver_args*)

cobra.flux_analysis.parsimonious module

`cobra.flux_analysis.parsimonious.`**optimize_minimal_flux** (*model*, *already_irreversible=False*, ***optimize_kwargs*)
Perform basic pFBA (parsimonius FBA) and minimize total flux.

The function attempts to act as a drop-in replacement for optimize. It will make the reaction reversible and perform an optimization, then force the objective value to remain the same and minimize the total flux. Finally, it will convert the reaction back to the irreversible form it was in before. See http://dx.doi.org/10.1038/msb.2010.47

model : `Model` object

already_irreversible [bool, optional] By default, the model is converted to an irreversible one. However, if the model is already irreversible, this step can be skipped.

cobra.flux_analysis.phenotype_phase_plane module

`cobra.flux_analysis.phenotype_phase_plane.`**`calculate_phenotype_phase_plane`**(*model*, *reaction1_name*, *reaction2_name*, *reaction1_range_max=20*, *reaction2_range_max=20*, *reaction1_npoints=50*, *reaction2_npoints=50*, *solver=None*, *n_processes=1*, *tolerance=1e-06*)

calculates the growth rates while varying the uptake rates for two reactions.

returns: an object containing the growth rates for the uptake rates. To plot the result, call the plot function of the returned object.

Example: data = calculate_phenotype_phase_plane(my_model, “EX_foo”, “EX_bar”) data.plot()

class `cobra.flux_analysis.phenotype_phase_plane.`**`phenotypePhasePlaneData`**(*reaction1_name*, *reaction2_name*, *reaction1_range_max*, *reaction2_range_max*, *reaction1_npoints*, *reaction2_npoints*)

class to hold results of a phenotype phase plane analysis

`plot`()

plot the phenotype phase plane in 3D using any available backend

`plot_matplotlib`(*theme='Paired'*, *scale_grid=False*)

Use matplotlib to plot a phenotype phase plane in 3D.

theme: color theme to use (requires palettable)

returns: maptlotlib 3d subplot object

plot_mayavi()
Use mayavi to plot a phenotype phase plane in 3D. The resulting figure will be quick to interact with in real time, but might be difficult to save as a vector figure. returns: mlab figure object

segment(*threshold=0.01*)
attempt to segment the data and identify the various phases

cobra.flux_analysis.reaction module

cobra.flux_analysis.reaction.**assess**(*model*, *reaction*, *flux_coefficient_cutoff=0.001*)
Assesses the capacity of the model to produce the precursors for the reaction and absorb the production of the reaction while the reaction is operating at, or above, the specified cutoff.

model: A *Model* object

reaction: A *Reaction* object

flux_coefficient_cutoff: Float. The minimum flux that reaction must carry to be considered active.

returns: True if the model can produce the precursors and absorb the products for the reaction operating at, or above, flux_coefficient_cutoff. Otherwise, a dictionary of {'precursor': Status, 'product': Status}. Where Status is the results from assess_precursors and assess_products, respectively.

cobra.flux_analysis.reaction.**assess_precursors**(*model*, *reaction*, *flux_coefficient_cutoff=0.001*)
Assesses the ability of the model to provide sufficient precursors for a reaction operating at, or beyond, the specified cutoff.

model: A *Model* object

reaction: A *Reaction* object

flux_coefficient_cutoff: Float. The minimum flux that reaction must carry to be considered active.

returns: True if the precursors can be simultaneously produced at the specified cutoff. False, if the model has the capacity to produce each individual precursor at the specified threshold but not all precursors at the required level simultaneously. Otherwise a dictionary of the required and the produced fluxes for each reactant that is not produced in sufficient quantities.

cobra.flux_analysis.reaction.**assess_products**(*model*, *reaction*, *flux_coefficient_cutoff=0.001*)
Assesses whether the model has the capacity to absorb the products of a reaction at a given flux rate. Useful for identifying which components might be blocking a reaction from achieving a specific flux rate.

model: A *Model* object

reaction: A *Reaction* object

flux_coefficient_cutoff: Float. The minimum flux that reaction must carry to be considered active.

returns: True if the model has the capacity to absorb all the reaction products being simultaneously given the specified cutoff. False, if the model has the capacity to absorb each individual product but not all products at the required level simultaneously. Otherwise a dictionary of the required and the capacity fluxes for each product that is not absorbed in sufficient quantities.

cobra.flux_analysis.single_deletion module

cobra.flux_analysis.single_deletion.**single_deletion**(*cobra_model*, *element_list=None*, *element_type='gene'*, ***kwargs*)
Wrapper for single_gene_deletion and single_reaction_deletion

Deprecated since version 0.4: Use single_reaction_deletion and single_gene_deletion

`cobra.flux_analysis.single_deletion.`**`single_gene_deletion`**(*cobra_model*, *gene_list=None*, *solver=None*, *method='fba'*, ***solver_args*)

sequentially knocks out each gene in a model

gene_list: list of gene_ids or cobra.Gene

method: "fba" or "moma"

returns ({gene_id: growth_rate}, {gene_id: status})

`cobra.flux_analysis.single_deletion.`**`single_gene_deletion_fba`**(*cobra_model*, *gene_list*, *solver=None*, ***solver_args*)

`cobra.flux_analysis.single_deletion.`**`single_gene_deletion_moma`**(*cobra_model*, *gene_list*, *solver=None*, ***solver_args*)

`cobra.flux_analysis.single_deletion.`**`single_reaction_deletion`**(*cobra_model*, *reaction_list=None*, *solver=None*, *method='fba'*, ***solver_args*)

sequentially knocks out each reaction in a model

reaction_list: list of reaction_ids or cobra.Reaction

method: "fba" or "moma"

returns ({reaction_id: growth_rate}, {reaction_id: status})

`cobra.flux_analysis.single_deletion.`**`single_reaction_deletion_fba`**(*cobra_model*, *reaction_list*, *solver=None*, ***solver_args*)

sequentially knocks out each reaction in a model using FBA

reaction_list: list of reaction_ids or cobra.Reaction

method: "fba" or "moma"

returns ({reaction_id: growth_rate}, {reaction_id: status})

`cobra.flux_analysis.single_deletion.`**`single_reaction_deletion_moma`**(*cobra_model*, *reaction_list*, *solver=None*, ***solver_args*)

sequentially knocks out each reaction in a model using MOMA

reaction_list: list of reaction_ids or cobra.Reaction

returns ({reaction_id: growth_rate}, {reaction_id: status})

cobra.flux_analysis.variability module

`cobra.flux_analysis.variability.`**`calculate_lp_variability`**(*lp*, *solver*, *cobra_model*, *reaction_list*, ***solver_args*)

calculate max and min of selected variables in an LP

`cobra.flux_analysis.variability.`**`find_blocked_reactions`**(*cobra_model*, *reaction_list=None*, *solver=None*, *zero_cutoff=1e-09*, *open_exchanges=False*, ***solver_args*)

Finds reactions that cannot carry a flux with the current exchange reaction settings for cobra_model, using flux variability analysis.

`cobra.flux_analysis.variability.`**`flux_variability_analysis`**(*cobra_model*, *reaction_list=None*, *fraction_of_optimum=1.0*, *solver=None*, *objective_sense='maximize'*, ***solver_args*)

Runs flux variability analysis to find max/min flux values

cobra_model : *`Model`*:

reaction_list [list of *`Reaction`*: or their id's] The id's for which FVA should be run. If this is None, the bounds will be comptued for all reactions in the model.

fraction_of_optimum [fraction of optimum which must be maintained.] The original objective reaction is constrained to be greater than maximal_value * fraction_of_optimum

solver [string of solver name] If None is given, the default solver will be used.

Module contents

14.1.3 cobra.io package

Submodules

cobra.io.json module

`cobra.io.json.`**`from_json`**(*jsons*)

Load cobra model from a json string

`cobra.io.json.`**`load_json_model`**(*file_name*)

Load a cobra model stored as a json file

file_name : str or file-like object

`cobra.io.json.`**`save_json_model`**(*model*, *file_name*, *pretty=False*)

Save the cobra model as a json file.

model : *`Model`* object

file_name : str or file-like object

`cobra.io.json.`**`to_json`**(*model*)

Save the cobra model as a json string

cobra.io.mat module

`cobra.io.mat.`**`create_mat_dict`**(*model*)
create a dict mapping model attributes to arrays

`cobra.io.mat.`**`from_mat_struct`**(*mat_struct*, *model_id=None*)
create a model from the COBRA toolbox struct

The struct will be a dict read in by scipy.io.loadmat

`cobra.io.mat.`**`load_matlab_model`**(*infile_path*, *variable_name=None*)
Load a cobra model stored as a .mat file

infile_path : str

variable_name [str, optional] The variable name of the model in the .mat file. If this is not specified, then the first MATLAB variable which looks like a COBRA model will be used

`cobra.io.mat.`**`model_to_pymatbridge`**(*model*, *variable_name='model'*, *matlab=None*)
send the model to a MATLAB workspace through pymatbridge

This model can then be manipulated through the COBRA toolbox

variable_name: str The variable name to which the model will be assigned in the MATLAB workspace

matlab: None or pymatbridge.Matlab instance The MATLAB workspace to which the variable will be sent. If this is None, then this will be sent to the same environment used in IPython magics.

`cobra.io.mat.`**`save_matlab_model`**(*model*, *file_name*, *varname=None*)
Save the cobra model as a .mat file.

This .mat file can be used directly in the MATLAB version of COBRA.

model : `Model` object

file_name : str or file-like object

cobra.io.sbml module

`cobra.io.sbml.`**`add_sbml_species`**(*sbml_model*, *cobra_metabolite*, *note_start_tag*, *note_end_tag*, *boundary_metabolite=False*)
A helper function for adding cobra metabolites to an sbml model.

sbml_model: sbml_model object

cobra_metabolite: a cobra.Metabolite object

note_start_tag: the start tag for parsing cobra notes. this will eventually be supplanted when COBRA is worked into sbml.

note_end_tag: the end tag for parsing cobra notes. this will eventually be supplanted when COBRA is worked into sbml.

`cobra.io.sbml.`**`create_cobra_model_from_sbml_file`**(*sbml_filename*, *old_sbml=False*, *legacy_metabolite=False*, *print_time=False*, *use_hyphens=False*)
convert an SBML XML file into a cobra.Model object. Supports SBML Level 2 Versions 1 and 4. The function will detect if the SBML fbc package is used in the file and run the converter if the fbc package is used.

sbml_filename: String.

old_sbml: Boolean. Set to True if the XML file has metabolite formula appended to metabolite names. This was a poorly designed artifact that persists in some models.

legacy_metabolite: Boolean. If True then assume that the metabolite id has the compartment id appended after an underscore (e.g. _c for cytosol). This has not been implemented but will be soon.

print_time: deprecated

use_hyphens: Boolean. If True, double underscores (__) in an SBML ID will be converted to hyphens

`cobra.io.sbml.`**`fix_legacy_id`**(*id*, *use_hyphens=False*, *fix_compartments=False*)

`cobra.io.sbml.`**`get_libsbml_document`**(*cobra_model*, *sbml_level=2*, *sbml_version=1*, *print_time=False*, *use_fbc_package=True*)

Return a libsbml document object for writing to a file. This function is used by write_cobra_model_to_sbml_file().

`cobra.io.sbml.`**`parse_legacy_id`**(*the_id*, *the_compartment=None*, *the_type='metabolite'*, *use_hyphens=False*)

Deals with a bunch of problems due to bigg.ucsd.edu not following SBML standards

the_id: String.

the_compartment: String.

the_type: String. Currently only 'metabolite' is supported

use_hyphens: Boolean. If True, double underscores (__) in an SBML ID will be converted to hyphens

`cobra.io.sbml.`**`parse_legacy_sbml_notes`**(*note_string*, *note_delimiter=':'*)

Deal with legacy SBML format issues arising from the COBRA Toolbox for MATLAB and BiGG.ucsd.edu developers.

`cobra.io.sbml.`**`read_legacy_sbml`**(*filename*, *use_hyphens=False*)

read in an sbml file and fix the sbml id's

`cobra.io.sbml.`**`write_cobra_model_to_sbml_file`**(*cobra_model*, *sbml_filename*, *sbml_level=2*, *sbml_version=1*, *print_time=False*, *use_fbc_package=True*)

Write a cobra.Model object to an SBML XML file.

cobra_model: `Model` object

sbml_filename: The file to write the SBML XML to.

sbml_level: 2 is the only level supported at the moment.

sbml_version: 1 is the only version supported at the moment.

use_fbc_package: Boolean. Convert the model to the FBC package format to improve portability.
http://sbml.org/Documents/Specifications/SBML_Level_3/Packages/Flux_Balance_Constraints_(flux)

TODO: Update the NOTES to match the SBML standard and provide support for Level 2 Version 4

cobra.io.sbml3 module

class `cobra.io.sbml3.`**`Basic`**

exception `cobra.io.sbml3.`**`CobraSBMLError`**

Bases: `exceptions.Exception`

`cobra.io.sbml3.`**`annotate_cobra_from_sbml`**(*cobra_element*, *sbml_element*)

`cobra.io.sbml3.`**`annotate_sbml_from_cobra`**(*sbml_element*, *cobra_element*)

`cobra.io.sbml3.`**`clip`**(*string*, *prefix*)

clips a prefix from the beginning of a string if it exists

```
>>> clip("R_pgi", "R_")
"pgi"
```

cobra.io.sbml3.**construct_gpr_xml**(*parent*, *expression*)
create gpr xml under parent node

cobra.io.sbml3.**extract_rdf_annotation**(*sbml_element*, *metaid*)

cobra.io.sbml3.**get_attrib**(*tag*, *attribute*, *type=<function <lambda>>*, *require=False*)

cobra.io.sbml3.**indent_xml**(*elem*, *level=0*)
indent xml for pretty printing

cobra.io.sbml3.**model_to_xml**(*cobra_model*, *units=True*)

cobra.io.sbml3.**ns**(*query*)
replace prefixes with namespace

cobra.io.sbml3.**parse**(*source*, *parser=None*)

cobra.io.sbml3.**parse_stream**(*filename*)
parses filename or compressed stream to xml

cobra.io.sbml3.**parse_xml_into_model**(*xml*, *number=<type 'float'>*)

cobra.io.sbml3.**read_sbml_model**(*filename*, *number=<type 'float'>*, ***kwargs*)

cobra.io.sbml3.**set_attrib**(*xml*, *attribute_name*, *value*)

cobra.io.sbml3.**strnum**(*number*)
Utility function to convert a number to a string

cobra.io.sbml3.**validate_sbml_model**(*filename*, *check_model=True*)
returns the model along with a list of errors

cobra.io.sbml3.**write_sbml_model**(*cobra_model*, *filename*, *use_fbc_package=True*, ***kwargs*)

Module contents

14.1.4 cobra.manipulation package

Submodules

cobra.manipulation.delete module

cobra.manipulation.delete.**delete_model_genes**(*cobra_model*, *gene_list*, *cumulative_deletions=True*, *disable_orphans=False*)
delete_model_genes will set the upper and lower bounds for reactions catalysed by the genes in gene_list if deleting the genes means that the reaction cannot proceed according to cobra_model.reactions[:].gene_reaction_rule

cumulative_deletions: False or True. If True then any previous deletions will be maintained in the model.

cobra.manipulation.delete.**find_gene_knockout_reactions**(*cobra_model*, *gene_list*, *compiled_gene_reaction_rules=None*)
identify reactions which will be disabled when the genes are knocked out

cobra_model: `Model`

gene_list: iterable of `Gene`

compiled_gene_reaction_rules: dict of {reaction_id: compiled_string} If provided, this gives pre-compiled gene_reaction_rule strings. The compiled rule strings can be evaluated much faster. If a rule is not provided, the regular expression evaluation will be used. Because not all gene_reaction_rule strings can be evaluated, this dict must exclude any rules which can not be used with eval.

`cobra.manipulation.delete.`**`get_compiled_gene_reaction_rules`**`(`*cobra_model*`)`

Generates a dict of compiled gene_reaction_rules

Any gene_reaction_rule expressions which cannot be compiled or do not evaluate after compiling will be excluded. The result can be used in the find_gene_knockout_reactions function to speed up evaluation of these rules.

`cobra.manipulation.delete.`**`prune_unused_metabolites`**`(`*cobra_model*`)`

Removes metabolites that aren't involved in any reactions in the model

cobra_model: A Model object.

`cobra.manipulation.delete.`**`prune_unused_reactions`**`(`*cobra_model*`)`

Removes reactions from cobra_model.

cobra_model: A Model object.

reactions_to_prune: None, a string matching a reaction.id, a cobra.Reaction, or as list of the ids / Reactions to remove from cobra_model. If None then the function will delete reactions that have no active metabolites in the model.

`cobra.manipulation.delete.`**`remove_genes`**`(`*cobra_model*, *gene_list*, *remove_reactions=True*`)`

remove genes entirely from the model

This will also simplify all gene_reaction_rules with this gene inactivated.

`cobra.manipulation.delete.`**`undelete_model_genes`**`(`*cobra_model*`)`

Undoes the effects of a call to delete_model_genes in place.

cobra_model: A cobra.Model which will be modified in place

cobra.manipulation.modify module

`cobra.manipulation.modify.`**`canonical_form`**`(`*model*, *objective_sense='maximize'*, *already_irreversible=False*, *copy=True*`)`

Return a model (problem in canonical_form).

Converts a minimization problem to a maximization, makes all variables positive by making reactions irreversible, and converts all constraints to <= constraints.

model: class:~*cobra.core.Model*. The model/problem to convert.

objective_sense: str. The objective sense of the starting problem, either 'maximize' or 'minimize'. A minimization problems will be converted to a maximization.

already_irreversible: bool. If the model is already irreversible, then pass True.

copy: bool. Copy the model before making any modifications.

`cobra.manipulation.modify.`**`convert_to_irreversible`**`(`*cobra_model*`)`

Split reversible reactions into two irreversible reactions

These two reactions will proceed in opposite directions. This guarentees that all reactions in the model will only allow positive flux values, which is useful for some modeling problems.

cobra_model: A Model object which will be modified in place.

`cobra.manipulation.modify.`**`escape_ID`**(*cobra_model*)

makes all ids SBML compliant

`cobra.manipulation.modify.`**`initialize_growth_medium`**(*cobra_model*, *the_medium='MgM'*, *external_boundary_compartment='e'*, *external_boundary_reactions=None*, *reaction_lower_bound=0.0*, *reaction_upper_bound=1000.0*, *irreversible=False*, *reactions_to_disable=None*)

Sets all of the input fluxes to the model to zero and then will initialize the input fluxes to the values specified in the_medium if it is a dict or will see if the model has a composition dict and use that to do the initialization.

cobra_model: A cobra.Model object.

the_medium: A string, or a dictionary. If a string then the initialize_growth_medium function expects that the_model has an attribute dictionary called media_compositions, which is a dictionary of dictionaries for various medium compositions. Where a medium composition is a dictionary of external boundary reaction ids for the medium components and the external boundary fluxes for each medium component.

external_boundary_compartment: None or a string. If not None then it specifies the compartment in which to disable all of the external systems boundaries.

external_boundary_reactions: None or a list of external_boundaries that are to have their bounds reset. This acts in conjunction with external_boundary_compartment.

reaction_lower_bound: Float. The default value to use for the lower bound for the boundary reactions.

reaction_upper_bound: Float. The default value to use for the upper bound for the boundary.

irreversible: Boolean. If the model is irreversible then the medium composition is taken as the upper bound

reactions_to_disable: List of reactions for which the upper and lower bounds are disabled. This is superceded by the contents of media_composition

`cobra.manipulation.modify.`**`revert_to_reversible`**(*cobra_model*, *update_solution=True*)

This function will convert a reversible model made by convert_to_irreversible into a reversible model.

cobra_model: A cobra.Model which will be modified in place.

Module contents

14.1.5 cobra.topology package

Submodules

cobra.topology.reporter_metabolites module

`cobra.topology.reporter_metabolites.`**`identify_reporter_metabolites`**(*cobra_model*, *reaction_scores_dict*, *number_of_randomizations=1000*, *number_of_layers=1*, *scoring_metric='default'*, *score_type='p'*, *entire_network=False*, *background_correction=True*, *ignore_external_boundary_reactions=*

Calculate the aggregate Z-score for the metabolites in the model. Ignore reactions that are solely spontaneous or orphan. Allow the scores to have multiple columns / experiments. This will change the way the output is represented.

cobra_model: A cobra.Model object

TODO: CHANGE TO USING DICTIONARIES for the_reactions: the_scores

reaction_scores_dict: A dictionary where the keys are reactions in cobra_model.reactions and the values are the scores. Currently, only supports a single numeric value as the value; however, this will be updated to allow for lists

number_of_randomizations: Integer. Number of random shuffles of the scores to assess which are significant.

number_of_layers: 1 is the only option supported

scoring_metric: default means divide by k**0.5

score_type: 'p' Is the only option at the moment and indicates p-value.

entire_network: Boolean. Currently, only compares scores calculated from the_reactions

background_correction: Boolean. If True apply background correction to the aggreagate Z-score

ignore_external_boundary_reactions: Not yet implemented. Boolean. If True do not count exchange reactions when calculating the score.

Module contents

14.2 Module contents

CHAPTER 15

Indices and tables

- genindex
- modindex
- search