Creating a Model

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INTRODUCTION

This tutorial explains the most basic functions provided by The COBRA Toolbox to create a model from scratch (i.e. define all relevant reactions and build a model from them).

MATERIALS

In this tutorial, two models are created: a small toy model and a simple model of glycolysis. The latter is also used in the model manipulation tutorial.

PROCEDURE

1. Create a simple toy model

To create a new model, there is a simple function `createModel`:

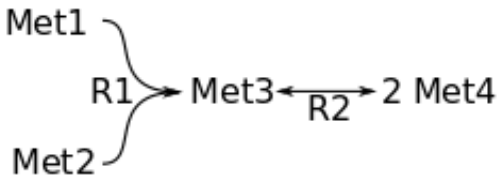
```
emptymodel = createModel()
```

```
emptymodel =
          rxns: {0×1 cell}
             S: []
            lb: [0×1 double]
            ub: [0×1 double]
             c: [0×1 double]
          mets: {0×1 cell}
             b: [0×1 double]
         rules: {0×1 cell}
         genes: {0×1 cell}
        osense: -1
        csense: ''
    rxnGeneMat: []
```

Calling it as above, yields an empty model `struct` with all required fields defined. To add reactions or metabolites please have a look at the tutorial for model manipulation.

There is also a possibility to immediately create a model with multiple reactions using `createModel`. To do so, a list of reaction identifiers, reaction names and reaction formulas has to be supplied.

Let's consider the following toy model:



The reactions are:

```
R1 = '1 Met1 + Met2 -> Met3'
```

```
R1 = 1 Met1 + Met2 -> Met3
```

```
R2 = 'Met3 <=> 2 Met4'
```

```
R2 = Met3 <=> 2 Met4
```

Reaction formulas are given as metabolites and their stoichiometric coefficient concatenated by +. Products and substrates are separated by a reversibility indicator, with `->` indicating an irreversible reaction and <=> indicating a reversible reaction.

To be able to use `createModel` to build this model, we also have to define the reaction Identifiers and the reaction names:

```
reactionIdentifiers = {'R1', 'R2'}
```

```
reactionIdentifiers =
    'R1'    'R2'
```

```
reactionNames = {'Reaction 1', 'Reaction 2'}
```

```
reactionNames =
    'Reaction 1'    'Reaction 2'
```

And we have to combine the reactions:

```
reactionFormulas = {R1, R2}
```

```
reactionFormulas =
    '1 Met1 + Met2 -> Met3'    'Met3 <=> 2 Met4'
```

now we can call

```
model1 = createModel(reactionIdentifiers, reactionNames, reactionFormulas);
```

```
Warning: Metabolite Met1[c] not in model - added to the model
Warning: Metabolite Met2[c] not in model - added to the model
Warning: Metabolite Met3[c] not in model - added to the model
R1 Met1[c] + Met2[c]  <=> Met3[c]
Warning: Metabolite Met4[c] not in model - added to the model
R2 Met3[c]  <=> 2 Met4[c]
```

to create the model including the two reactions.

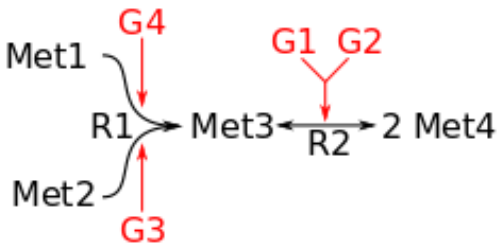
2. Explanation of options for the createModel function

`createModel` offers a couple of additional optional parameters. Those include:

- `revFlagList` - a double array of indications whether the reaction is reversible or not this will overwrite the indicator from the formula. (default: 1 for reversible formulas, 0 for irreversible formulas)
- `lowerBoundList` - a double array indicating the lower bounds of the providing reactions (again, this will overwrite both `revFlagList` and the indication from the formula). E.g. if a `revFlagList` entry indicates a reversible reaction, but the lower bound is >0, the reaction will be considered as irreversible. (The default is to assume 0 for irreversible and 1000 for irreversible reactions)
- `upperBoundList` - a double array indicating the upper bounds of the reactions. (default: 1000)
- `subSystemList` - a cell array indicating the subSystems of the reactions
- `grRuleList` - a cell array indicating the GPR rules for a formula (in textual format e.g. Gene1 and Gene2)
- `geneNameList` - a List of genes present in the `grRuleList` array
- `systNameList` - a List (of equal size as `geneNameList`), that is used to translate the genes from those used in the `geneNameList` to those used in this list.

3. Creating a model with Gene-Protein-Reaction Association (GPR) rules

Let's assume, our network has the following GPR associations:



i.e. a complex of G1 and G2 catalyses R2 and either G3 or G4 catalyse R1. We further assume, that the flux maximum through R1 is 10 and 30 through R2

```
upperBounds = [10, 30];
grRuleR1 = 'G3 or G4';
grRuleR2 = 'G1 and G2';
grRuleList = {grRuleR1, grRuleR2};
```

The model creation call would then be:

```
model2 = createModel(reactionIdentifiers, reactionNames, reactionFormulas, ...
                     'upperBoundList', upperBounds, 'grRuleList', grRuleList);
```

```
Warning: Metabolite Met1[c] not in model - added to the model
Warning: Metabolite Met2[c] not in model - added to the model
Warning: Metabolite Met3[c] not in model - added to the model
New gene G3 added to model
New gene G4 added to model
R1 Met1[c] + Met2[c]  <=> Met3[c]
Warning: Metabolite Met4[c] not in model - added to the model
New gene G1 added to model
New gene G2 added to model
R2 Met3[c]  <=> 2 Met4[c]
```

If we now compare the reactions, printing the GPR rules in both models

```
printRxnFormula(model1, 'gprFlag', 1);
```

```
R1 Met1[c] + Met2[c]  <=> Met3[c]
R2 Met3[c]  <=> 2 Met4[c]
```

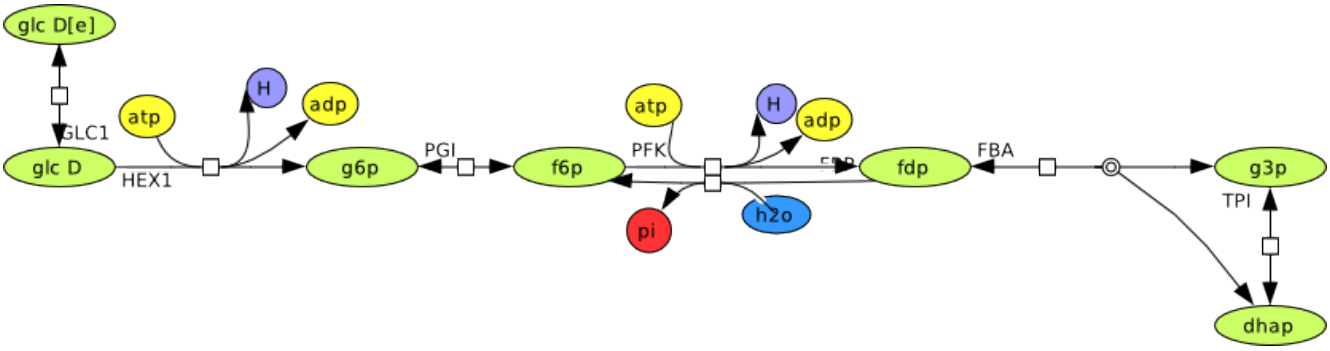
```
printRxnFormula(model2, 'gprFlag', 1);
```

```
R1 Met1[c] + Met2[c]  <=> Met3[c]  G3 or G4
R2 Met3[c]  <=> 2 Met4[c]  G1 and G2
```

we see, that `model2` has assigned GPR rules, while `model1` does not have those.

4. Create a model of the upper part of glycolysis

We will now create a slightly more complex model (essentially, the upper part of the glycolysis) which will be used in other tutorials (e.g. ModelManipulation)



To create this model, we have to define the reactions:

```
reactionFormulas = {'glc-D[e]  -> glc-D',...
    'glc-D + atp  -> H + adp + g6p',...
    'g6p  <=> f6p',...
    'atp + f6p  -> H + adp + fdp',...
    'fdp + h2o  -> f6p + pi',...
    'fdp  -> g3p + dhap',...
    'dhap  -> g3p'};
reactionNames = {'GLCt1', 'HEX1', 'PGI', 'PFK', 'FBP', 'FBA', 'TPI'};
lowerBounds = [-20, 0, -20, 0, 0, -20, -20];
upperBounds = [20, 20, 20, 20, 20, 20, 20];
glycolysisModel = createModel(reactionNames, reactionNames, reactionFormulas,...
                              'lowerBoundList', lowerBounds, 'upperBoundList', upperBounds);
```

```
Warning: Metabolite glc-D[e] not in model - added to the model
Warning: Metabolite glc-D[c] not in model - added to the model
GLCt1 glc-D[e]  <=> glc-D[c]
Warning: Metabolite atp[c] not in model - added to the model
Warning: Metabolite H[c] not in model - added to the model
Warning: Metabolite adp[c] not in model - added to the model
Warning: Metabolite g6p[c] not in model - added to the model
HEX1 glc-D[c] + atp[c]  -> H[c] + adp[c] + g6p[c]
Warning: Metabolite f6p[c] not in model - added to the model
PGI g6p[c]  <=> f6p[c]
Warning: Metabolite fdp[c] not in model - added to the model
PFK atp[c] + f6p[c]  -> H[c] + adp[c] + fdp[c]
Warning: Metabolite h2o[c] not in model - added to the model
Warning: Metabolite pi[c] not in model - added to the model
```

```
FBP fdp[c] + h2o[c]  -> f6p[c] + pi[c]
Warning: Metabolite g3p[c] not in model - added to the model
Warning: Metabolite dhap[c] not in model - added to the model
FBA fdp[c]  <=> g3p[c] + dhap[c]
TPI dhap[c]  <=> g3p[c]
```