# Subset of a model that admits a thermodynamically consistent flux

```
[solverOK, solverInstalled]=changeCobraSolver('ibm_cplex', 'all');
> changeCobraSolver: IBM ILOG CPLEX interface added to MATLAB path.
> ibm_cplex (version 1210) is compatible and fully tested with MATLAB R2019a on your operating system.
> changeCobraSolver: Solver for LP problems has been set to ibm_cplex.
> changeCobraSolver: IBM ILOG CPLEX interface added to MATLAB path.
> ibm_cplex (version 1210) is compatible and fully tested with MATLAB R2019a on your operating system.
> changeCobraSolver: Solver for MILP problems has been set to ibm_cplex.
> changeCobraSolver: IBM ILOG CPLEX interface added to MATLAB path.
> ibm_cplex (version 1210) is compatible and fully tested with MATLAB R2019a on your operating system.
> changeCobraSolver: Solver for QP problems has been set to ibm_cplex.
> changeCobraSolver: IBM ILOG CPLEX interface added to MATLAB path.
> ibm_cplex (version 1210) is compatible and fully tested with MATLAB R2019a on your operating system.
> changeCobraSolver: Solver for MIQP problems has been set to ibm_cplex.
> changeCobraSolver: Solver ibm_cplex not supported for problems of type NLP. Currently used: matlab
%[solverOK,solverInstalled]=changeCobraSolver('gurobi','all');
%[solverOK,solverInstalled]=changeCobraSolver('ibm_cplex','QP');
```

### Load model

```
modelToLoad='circularToy';
modelToLoad='ecoli_core';
modelToLoad='modelRecon3MitoOpen';
modelToLoad='Recon3DModel';
%modelToLoad='iDopa';
```

#### Load a model

```
driver_thermoModelLoad

Model loaded: Recon3DModel
lower bounds greater than zero
Internal stochiometric nullspace computed in 0.65154 seconds.
```

### Stoichiometric consistency

```
rxnRemoveMethod='inclusive'; % maintains stoichiometric consistency
        [stoichConsistModel, rxnRemoveList] = removeMetabolites(model,
model.mets(~model.SConsistentMetBool),rxnRemoveMethod);
        SConsistentRxnBool2=~ismember(model.rxns,rxnRemoveList);
        if ~all(model.SConsistentRxnBool==SConsistentRxnBool2)
            error('inconsistent reaction removal')
        end
        try
            stoichConsistModel = removeUnusedGenes(stoichConsistModel);
        catch ME
            disp(ME.message)
        end
    else
        stoichConsistModel = model;
    end
end
[nMet,nRxn]=size(stoichConsistModel.S)
```

nMet = 5835 nRxn = 10600

## Flux consistency

```
fluxConsistentParam.method='fastcc';%can handle additional constraints
fluxConsistentParam.printLevel=1;
[~,~,~,*,*stoichConsistModel]=
findFluxConsistentSubset(stoichConsistModel,fluxConsistentParam);
```

#### Extract flux consistent submodel

nMet = 5835 nRxn = 10600

### Forced reactions

### Thermodynamic consistency

```
%save('debug_prior_to_findThermoConsistentFluxSubset.mat')
%return
param.printLevel = 1;
param.acceptRepairedFlux=1;
param.relaxBounds=1;
[thermoFluxConsistentMetBool,thermoFluxConsistentRxnBool,stoichFluxConsistMod el,stoichFluxThermoConsistModel] =
findThermoConsistentFluxSubset(stoichFluxConsistModel,param);
```

Size of the largest flux, stoich and thermo consistent submodel

```
[nMet,nRxn]=size(stoichFluxThermoConsistModel.S)
```

### **Nullspace**

Nullspace is necessary for backup check of thermodynamic consistency using thermoFlux2QNty

```
[stoichFluxThermoConsistModel,rankK,nnzK,timeTaken] =
internalNullspace(stoichFluxThermoConsistModel);
rankK
```

### Minimal thermodynamically consistent submodel

Compute the minimal thermodynamically consistent submodel

```
[minimalModel, modelThermoMetBool, modelThermoRxnBool] =
thermoKernel(stoichFluxThermoConsistModel);
[nMet,nRxn]=size(minimalModel.S)
```

## Data to define a thermodynamically consistent subnetwork

Setup random data to select a random subset

```
param.n=200;
[rankMetConnectivity,rankMetInd,rankConnectivity] =
rankMetabolicConnectivity(stoichFluxThermoConsistModel,param);
```

```
[nMet,nRxn]=size(stoichFluxThermoConsistModel.S);
rxnWeights=rand(nRxn,1)-0.5;
rxnWeights(stoichFluxThermoConsistModel.SConsistentRxnBool)=0;
coreRxnBool=rxnWeights<0.45;</pre>
removeRxnBool=rxnWeights>0.48;
rxnWeights(rxnWeights>0.4)=1;
rxnWeights(rxnWeights<-0.4)=-1;
rxnWeights(rxnWeights>=-0.4 & rxnWeights<=0.4)=0;</pre>
hist(rxnWeights)
metWeights=rand(nMet,1)-0.5;
metWeights(rankMetInd(1:200))=0;
coreMetBool=metWeights<0.45;</pre>
removeMetBool=metWeights>0.5;
metWeights(metWeights>0.4)=1;
metWeights(metWeights<-0.4)=-1;
metWeights(metWeights>=-0.4 & metWeights<=0.4)=0;</pre>
hist(metWeights)
```

### Remove inactive reactions and absent metabolites

```
param.printLevel = 1;
[solverOK,solverInstalled]=changeCobraSolver('gurobi','QP');
[thermoFluxConsistentMetBool,thermoFluxConsistentRxnBool,stoichFluxThermoConsistModel,stoichFluxThermoConsistModelRed] =
findThermoConsistentFluxSubset(stoichFluxThermoConsistModel, param,
removeMetBool, removeRxnBool);
[nMet,nRxn]=size(stoichFluxThermoConsistModelRed.S)
```