Relaxed Flux Balance Analysis: Recon 3

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Reviewer:

Introduction

We consider a biochemical network of m molecular species and n biochemical reactions. The biochemical network is mathematically represented by a stoichiometric matrix $S \in \mathbb{Z}^{m \times n}$. In standard notation, flux balance analysis (FBA) is the linear optimisation problem

$$\begin{aligned} \min_{v} \quad & \rho(v) \equiv c^T v \\ \text{s.t.} \quad & Sv = b, \\ & l \leq v \leq u, \end{aligned}$$

where $c \in \Re^n$ is a parameter vector that linearly combines one or more reaction fluxes to form what is termed the objective function, and where a $b_i < 0$, or $b_i > 0$, represents some fixed output, or input, of the ith molecular species.

Every FBA solution must satisfy the constraints, independent of any objective chosen to optimise over the set of constraints. It may occur that the constraints on the FBA problem are not all simultaneously feasible, i.e., the system of inequalities is infeasible. This situation might be caused by an incorrectly specified reaction bound or the absence of a reaction from the stoichiometric matrix, such that a nonzero $b \notin \mathcal{R}(S)$. To resolve the infeasiblility, we consider a cardinality optimisation problem that seeks to minimise the number of bounds to relax, the number of fixed outputs to relax, the number of fixed inputs to relax, or a combination of all three, in order to render the problem feasible. The cardinality optimisation problem, termed *relaxed flux balance analysis,* is

$$\begin{aligned} \min_{v,r,p,q} \quad & \lambda \|r\|_0 + \alpha \|p\|_0 + \alpha \|q\|_0 \\ \text{s.t.} \quad & Sv + r = b \\ & l - p \leq v \leq u + q \\ & p, q, r \geq 0 \end{aligned}$$

where $p, q \in \mathcal{R}^n$ denote the relaxations of the lower and upper bounds on reaction rates of the reaction rates vector v, and where $r \in \mathcal{R}^m$ denotes a relaxation of the mass balance constraint. Non-negative scalar parameters λ and α can be used to trade off between relaxation of mass balance or bound constraints. A non-negative vector parameter λ can be used to prioritise relaxation of one mass balance constraint over another, e.g, to avoid relaxation of a mass balance constraint on a metabolite that is not desired to be exchanged across the boundary of the system. A non-negative vector parameter α may be used to prioritise relaxation of bounds on some reactions rather than others, e.g., relaxation of bounds on exchange reactions rather than internal reactions. The optimal choice of parameters depends heavily on the biochemical context. A

relaxation of the minimum number of constraints is desirable because ideally one should be able to justify the choice of bounds or choice of metabolites to be exchanged across the boundary of the system by recourse to experimental literature. This task is magnified by the number of constraints proposed to be relaxed.

PROCEDURE: RelaxedFBA applied to Recon3.0model

TIMING: 20 seconds (computation), minutes - days (interpretation)

Recon 3D [brunk_recon_nodate] is the latest, most comprehensive, manually curated, genome-scale reconstruction of human metabolism. Recon3D is a reconstruction which currently encompasses ~3300 open reading frames, ~8000 unique metabolites, as well as ~12000 biochemical and transport reactions distributed over nine cellular compartments: cytoplasm [c], lysosome [l], nucleus [n], mitochondrion [m], mitochondrial intermembrane space [i], peroxisome [x], extracellular space [e], Golgi apparatus [g], and endoplasmic reticulum [r] [thiele_protocol_2010, brunk_recon_nodate]. Recon3.0model is a flux balance analysis model and the largest stoichiometrically and flux consistent subset of Recon3D. That is, no internal reaction in Recon3.0model is mass imbalanced and furthermore, every internal and every external reaction is admits a non-zero steady state flux. In this example, we take Recon3.0model, set the lower bound on the biomass reaction to require the synthesis of biomass yet close all of the external reactions in the model. The resulting model is therefore infeasible, that is, no steady state flux vector satisfies the steady state constraints and the bound constraints for the resulting flux balance analysis problem, irrespective of the objective coefficients, so we use relaxed flux balance analysis to identify the minimial set of external reaction bounds that are required to be relaxed in order to make biomass synthesis feasible.

Load Recon3.0model, unless it is already loaded into the workspace.

```
global CBTDIR

%Load the model if recon3 is available replace the model name.
modelFileName = 'Recon2.0model.mat';
modelDirectory = getDistributedModelFolder(modelFileName); %Look up the folder for the
modelFileName= [modelDirectory filesep modelFileName]; % Get the full path. Necessary t
model = readCbModel(modelFileName);
modelOrig = model;
```

Identify the exchange reactions and biomass reaction(s) heuristically and close (a subset) of them

```
model = findSExRxnInd(model,size(model.S,1),1);
```

```
Found biomass reaction: biomass_reaction
Found biomass reaction: biomass_maintenance
Found biomass reaction: biomass_maintenance_noTrTr
ATP demand reaction is not considered an exchange reaction by default. It should be mass balanced:
DM_atp_c_    h2o[c] + atp[c]     ->    h[c] + adp[c] + pi[c]
```

```
if ~any(model.biomassBool)
    error('Could not heuristically identify a biomass reaction')
end
```

Add a linear objective coefficient corresponding to the biomass reaction

```
model.biomassBool=strcmp(model.rxns,'biomass_reaction');
```

```
model.c(model.biomassBool)=1;
```

Check that biomass production is feasible

```
FBAsolution = optimizeCbModel(model,'max');
if FBAsolution.stat == 1
    disp('Relaxed model is feasible');
    bioMassProductionRate=FBAsolution.x(model.biomassBool);
    fprintf('%g%s\n', bioMassProductionRate, ' is the biomass production rate')
else
    disp('Relaxed model is infeasible');
end
```

```
Relaxed model is feasible
753.336 is the biomass production rate
```

Remove superflous biomass reactions and display the size of the reduced model

```
model = removeRxns(model,{'biomass_maintenance','biomass_maintenance_noTrTr'});
[m,n] = size(model.S);
fprintf('%6s\t%6s\n','#mets','#rxns'); fprintf('%6u\t%6u\t%s\n',m,n,' totals.')
```

```
 #mets     #rxns
  5835     10598     totals.
```

First close all exchange reactions, except the biomass reaction

```
model.SIntRxnBool(strcmp(model.rxns,'biomass_reaction'))=0;
model.lb(~model.SIntRxnBool)=0;
model.ub(~model.SIntRxnBool)=0;
```

Now force the biomass reaction to be active

```
model.lb(model.biomassBool) = 1;
model.ub(model.biomassBool) = 10;
```

Check if the model is feasible

```
FBAsolution = optimizeCbModel(model,'max', 0, true);
if FBAsolution.stat == 1
    disp('Model is feasible. Nothing to do.');
    return
else
    disp('Model is infeasible');
end
```

```
Model is infeasible
```

Relaxed flux balance analysis is implemented with the function relaxedFBA

```
%    [solution] = relaxedFBA(model, relaxOption)
```

The inputs are a COBRA model and an optional parameter vector

```
% INPUTS:
```

```
%    model:          COBRA model structure
%    relaxOption:    Structure containing the relaxation options:
% * internalRelax:
%  * 0 = do not allow to relax bounds on internal reactions
%  * 1 = do not allow to relax bounds on internal reactions with finite bounds
%  * 2 = allow to relax bounds on all internal reactions
%
% * exchangeRelax:
%                       * 0 = do not allow to relax bounds on exchange reactions
%                       * 1 = do not allow to relax bounds on exchange reactions of th
%                       * 2 = allow to relax bounds on all exchange reactions
%
%                     * steadyStateRelax:
%                       * 0 = do not allow to relax the steady state constraint S*v =
%                       * 1 = allow to relax the steady state constraint S*v = b
%
%                     * toBeUnblockedReactions - n x 1 vector indicating the reactions
%                       * toBeUnblockedReactions(i) = 1 : impose v(i) to be positive
%                       * toBeUnblockedReactions(i) = -1 : impose v(i) to be negative
%                       * toBeUnblockedReactions(i) = 0 : do not add any constraint
%
%                     * excludedReactions - n x 1 bool vector indicating the reactions
%                       * excludedReactions(i) = false : allow to relax bounds on reac
%                       * excludedReactions(i) = true : do not allow to relax bounds o
%
%                     * excludedMetabolites - m x 1 bool vector indicating the metabol
%                       * excludedMetabolites(i) = false : allow to relax steady state
%                       * excludedMetabolites(i) = true : do not allow to relax steady
%
%                     * lamda - trade-off parameter of relaxation on steady state cons
%                     * alpha - trade-off parameter of relaxation on bounds
%
% Note, excludedReactions and excludedMetabolites override all other relaxation options
```

Do not allow to relax bounds on any internal reaction

```
relaxOption.internalRelax = 0;
```

Allow to relax bounds on all exchange reactions

```
relaxOption.exchangeRelax = 2;
```

Do not allow to relax the steady state constraint S*v = b

```
relaxOption.steadyStateRelax = 0;
```

Set the tolerance to distinguish between zero and non-zero flux

```
feasTol = getCobraSolverParams('LP', 'feasTol');
relaxOption.epsilon = feasTol/100;%*100;
```

Set the trade-off parameter for relaxation of bounds (advanced user). A larger value of gamma will

```
relaxOption.gamma  = 10;
```

Set the trade-off parameter for relaxation on steady state constraint (advanced user)

```
relaxOption.lambda = 10;
```

Call the relaxedFBA function, deal the solution, and set small values to zero

```
tic;
solution = relaxedFBA(model,relaxOption);
timeTaken=toc;
[v,r,p,q] = deal(solution.v,solution.r,solution.p,solution.q);
if 0
    p(p<relaxOption.epsilon) = 0;%lower bound relaxation
    q(q<relaxOption.epsilon) = 0;%upper bound relaxation
    r(r<relaxOption.epsilon) = 0;%steady state constraint relaxation
end
```

The output is a solution structure with a 'stat' field reporting the solver status and a set of fields matching the relaxation of constraints given in the mathematical formulation of the relaxed flux balance problem above.

```
% OUTPUT:
%    solution:       Structure containing the following fields:
%                      * stat - status
%                        * 1  = Solution found
%                        * 0  = Infeasible
%                        * -1 = Invalid input
%                      * r - relaxation on steady state constraints S*v = b
%                      * p - relaxation on lower bound of reactions
%                      * q - relaxation on upper bound of reactions
%                      * v - reaction rate
```

Summarise the proposed relaxation solution

```
if solution.stat == 1

   dispCutoff=relaxOption.epsilon;

    fprintf('%s\n',['Relaxed flux balance analysis problem solved in ' num2str(timeTake

    fprintf('%u%s\n',nnz(r),' steady state constraints relaxed');

    fprintf('%u%s\n',nnz(abs(p)>dispCutoff & ~abs(q)>dispCutoff & model.SIntRxnBool),'
    fprintf('%u%s\n',nnz(abs(q)>dispCutoff & ~abs(p)>dispCutoff & model.SIntRxnBool),'
    fprintf('%u%s\n',nnz(abs(p)>dispCutoff & abs(q)>dispCutoff & model.SIntRxnBool),' i

    fprintf('%u%s\n',nnz(abs(p)>dispCutoff & ~abs(q)>dispCutoff & ~model.SIntRxnBool),'
    fprintf('%u%s\n',nnz(abs(q)>dispCutoff & ~abs(p)>dispCutoff & ~model.SIntRxnBool),'
    fprintf('%u%s\n',nnz(abs(p)>dispCutoff & abs(q)>dispCutoff & ~model.SIntRxnBool),'

    fprintf('%u%s\n',nnz(abs(p)>dispCutoff | abs(q)>dispCutoff & ~model.SIntRxnBool),'

    maxUB = max(max(model.ub),-min(model.lb));
```

```
    minLB = min(-max(model.ub),min(model.lb));
    intRxnFiniteBound = ((model.ub < maxUB) & (model.lb > minLB));
    fprintf('%u%s\n',nnz(abs(p)>dispCutoff & intRxnFiniteBound),' finite lower bounds r
    fprintf('%u%s\n',nnz(abs(q)>dispCutoff & intRxnFiniteBound),' finite upper bounds r

    exRxn00 = ((model.ub == 0) & (model.lb == 0));
    fprintf('%u%s\n',nnz(abs(p)>dispCutoff & exRxn00),' lower bounds relaxed on fixed r
    fprintf('%u%s\n',nnz(abs(q)>dispCutoff & exRxn00),' upper bounds relaxed on fixed r

else
    disp('relaxedFBA problem infeasible, check relaxOption fields');
end
```

```
Relaxed flux balance analysis problem solved in 47.6492 seconds.
0 steady state constraints relaxed
0 internal only lower bounds relaxed
0 internal only upper bounds relaxed
0 internal lower and upper bounds relaxed
497 external only lower bounds relaxed
498 external only upper bounds relaxed
107 external lower and upper bounds relaxed
1102 external lower or upper bounds relaxed
604 finite lower bounds relaxed
605 finite upper bounds relaxed
603 lower bounds relaxed on fixed reactions (lb=ub=0)
605 upper bounds relaxed on fixed reactions (lb=ub=0)
```

TROUBLESHOOTING

Given an infeasible problem,

$$\begin{aligned} Sv &= b, \\ l \le v &\le u, \end{aligned}$$

the *relaxed flux balance analysis* problem

$$\begin{aligned} \min_{v,r,p,q} \quad & \lambda\|r\|_0 + \gamma\|p\|_0 + \gamma\|q\|_0 \\ \text{s.t.} \quad & Sv + r = b \\ & l - p \le v \le u + q \\ & p, q, r \ge 0 \end{aligned}$$

will always find a solution. However, relaxedFBA offers the user the option to disallow relaxation of some of the constraints. If too many constraints are not allowed to be relaxed, then relaxedFBA will report an infeasible problem. The fields of relaxOption should be reviewed. For example, if relaxation of steady state constraints is not alllowed, yet b is nonzero and not in the range of the stoichiometric matrix, then the relaxedFBA problem will be infeasible. To allow the relaxation of the steady state constraint, S*v = b, then use

```
%relaxOption.steadyStateRelax = 1;
```

If relaxedFBA does return a solution, but it is not biochemcially realistic, then again review the fields of relaxOption, to allow or disallow relaxation of certain constraints. For example, to specifically disallow relaxation of the bounds on reaction with model.rxns abbreviation 'myReaction', use

```
%relaxOption.excludedReactions=false(n,1);
```

```
%relaxOption.excludedReactions(strcmp(model.rxns,'myReaction'))=1;
```

To specifically disallow relaxation of the steady state constraint on a molecualr species with model.mets abbreviation 'myMetabolite', then use:

```
%relaxOption.excludedMetabolite=false(m,1);
%relaxOption.excludedMetabolite(strcmp(model.mets,'myMetabolite'))=1;
```

Even if the set of relaxations are properly set, in a boolean sense, tweaking of the DCA card trade off parameters can help narrow down to a biochemically realistic solution, by iterating between the biochemical literature and the numerical results from relaxedFBA after tweaking the parameters. This flexibility is provided for the expert user. See relaxFBA_cappedL1.m. A standard set of advanced parameters are:

```
%relaxOption.nbMaxIteration = 1000; %max number of iterations of the cappedL1 problem
%relaxOption.gamma0  = 0;   %trade-off parameter of l0 part of v
%relaxOption.gamma1  = 0;    %trade-off parameter of l1 part of v
%relaxOption.lambda0 = 10;   %trade-off parameter of l0 part of r
%relaxOption.lambda1 = 0;    %trade-off parameter of l1 part of r
%relaxOption.alpha0  = 10;    %trade-off parameter of l0 part of p and q
%relaxOption.alpha1  = 0;     %trade-off parameter of l1 part of p and q
%relaxOption.theta   = 2;    %parameter of capped l1 approximation
```

ANTICIPATED RESULTS

relaxedFBA will return a set of steady state constraints, lower bounds, and upper bounds, that are required to be relaxed to ensure that the FBA problem is feasible. It is necessary to analyse the solution biochemically, to see if it makes sense to relax the suggested constraints. The following code will report a summary of the results.

```
if solution.stat == 1
    printFlag=0;
    lineChangeFlag=0;
    if 1
        dispCutoffLower=relaxOption.epsilon;
        dispCutoffUpper=inf;
    else
        %useful for numerical debugging
        dispCutoffLower=-10;
        dispCutoffUpper=10;
    end
   if any(r)
        fprintf('\n%s\n','Steady state constraints relaxed');
        for i=1:m
            if abs(r(i))>dispCutoffLower && abs(r(i))<dispCutoffUpper
                fprintf('%s\n',model.mets{i});
            end
        end
   else
       fprintf('\n%s\n','No steady state constraints relaxed');
   end
    if any(p)
        fprintf('%s\n','Lower bounds relaxed');
        for j=1:n
```

```
            if abs(p(j))>dispCutoffLower && abs(p(j))<dispCutoffUpper && p(j)~=0
                rxnAbbrList=model.rxns(j);
                formulas = printRxnFormula(model, rxnAbbrList, printFlag, lineChangeFla
                fprintf('%6g\t%s',p(j),formulas{1});
            end
        end
    else
        fprintf('\n%s\n','No lower bounds relaxed');
    end
    if any(q)
        fprintf('\n%s\n','Upper bounds relaxed');
        for j=1:n
            if abs(q(j))>dispCutoffLower && abs(q(j))<dispCutoffUpper && q(j)~=0
                rxnAbbrList=model.rxns(j);
                formulas = printRxnFormula(model, rxnAbbrList, printFlag, lineChangeFla
                fprintf('%6g\t%s',q(j),formulas{1});
            end
        end
    else
        fprintf('\n%s\n','No upper bounds relaxed');
    end
end
```

```
No steady state constraints relaxed
Lower bounds relaxed
  1000    datp[m]  ->
  1000    datp[n]  ->
  1000    dctp[n]  ->
  1000    dgtp[n]  ->
  1000    dttp[n]  ->
  1000    ethamp[r]  ->
  1000    gpi_sig[r]  ->
  1000    mem2emgacpail_prot_hs[r]  ->
  1000    Ser_Gly_Ala_X_Gly[l]  ->
  1000    10fthf7glu[e]  ->
  1000    4nph[e]  ->
  1000    5adtststerone[e]  ->
  1000    7dhf[e]  ->
  1000    7thf[e]  ->
  1000    adp[e]  ->
  1000    adprbp[e]  ->
  1000    adrnl[e]  ->
  1000    ala_D[e]  ->
  1000    aqcobal[e]  ->
  1000    arachd[e]  ->
  1000    ascb_L[e]  ->
  1000    atp[e]  ->
  1000    bilglcur[e]  ->
  1000    biocyt[e]  ->
  1000    cholate[e]  ->
  1000    chsterol[e]  ->
  1000    chtn[e]  ->
  1000    cmp[e]  ->
  1000    crmp_hs[e]  ->
  1000    crn[e]  ->
  1000    crtsl[e]  ->
  1000    cspg_c[e]  ->
  1000    dag_hs[e]  ->
  1000    dheas[e]  ->
  1000    dlnlcg[e]  ->
```

```
0.15    eicostet[e]  ->
1000    estrones[e]  ->
1000    gbside_hs[e]  ->
1000    gchola[e]  ->
1000    gluala[e]  ->
1000    glygn2[e]  ->
1000    glygn4[e]  ->
1000    gthrd[e]  ->
1000    gtp[e]  ->
1000    h2o2[e]  ->
1000    ha[e]  ->
1000    hdcea[e]  ->
1000    i[e]  ->
1000    idp[e]  ->
1000    imp[e]  ->
1000    ksi[e]  ->
1000    Lcystin[e]  ->
1000    leuktrA4[e]  ->
1000    leuktrF4[e]  ->
1000    lnlc[e]  ->
1000    lnlnca[e]  ->
1000    nadp[e]  ->
1000    ncam[e]  ->
1000    o2s[e]  ->
1000    ocdca[e]  ->
1000    ocdcea[e]  ->
1000    octa[e]  ->
1000    pe_hs[e]  ->
1000    peplys[e]  ->
1000    prostgd2[e]  ->
1000    prostge1[e]  ->
1000    prostgf2[e]  ->
1000    ps_hs[e]  ->
1000    ptdca[e]  ->
1000    retinol[e]  ->
1000    s2l2fn2m2masn[e]  ->
1000    spc_hs[e]  ->
1000    sph1p[e]  ->
1000    sphs1p[e]  ->
1000    strch1[e]  ->
1000    strch2[e]  ->
1000    strdnc[e]  ->
1000    tag_hs[e]  ->
1000    tchola[e]  ->
1000    thf[e]  ->
1000    thym[e]  ->
1000    triodthy[e]  ->
1000    ttdca[e]  ->
1000    utp[e]  ->
1000    vacc[e]  ->
1000    whhdca[e]  ->
1000    xoltri27[e]  ->
1000    xylt[e]  ->
1000    pre_prot[r]  ->
1000    4abutn[e]  ->
1000    ctp[e]  ->
1000    dgmp[e]  ->
1000    dha[e]  ->
1000    dttp[e]  ->
1000    fad[e]  ->
1000    fald[e]  ->
1000    HC00250[e]  ->
1000    HC01361[e]  ->
1000    HC01446[e]  ->
```

```
1000    cpppg1[e]  ->
1000    itp[e]  ->
1000    udpg[e]  ->
1000    HC00955[e]  ->
1000    C02470[e]  ->
1000    HC00822[e]  ->
1000    HC02193[e]  ->
1000    HC02195[e]  ->
1000    HC02196[e]  ->
1000    HC02191[e]  ->
1000    HC02194[e]  ->
1000    HC02203[e]  ->
1000    HC02217[e]  ->
1000    malcoa[e]  ->
1000    arachcoa[e]  ->
1000    CE4722[e]  ->
1000    CE4723[e]  ->
1000    CE4724[e]  ->
1000    CE2839[e]  ->
1000    CE2838[e]  ->
1000    23cump[e]  ->
1000    CE5788[e]  ->
1000    CE5798[e]  ->
1000    CE5787[e]  ->
1000    CE5791[e]  ->
1000    CE5867[e]  ->
1000    CE4633[e]  ->
1000    CE5854[e]  ->
1000    udpgal[e]  ->
1000    CE0074[e]  ->
1000    CE5853[e]  ->
1001    20.6508 h2o[c] + 20.7045 atp[c] + 0.38587 glu_L[c] + 0.35261 asp_L[c] + 0.036117 gtp[c] + 0.5056
1000    c101coa[c]  ->
1000    doco13ac[e]  ->
1000    octdececoa[c]  ->
1000    tetdec2coa[c]  ->
1000    tetdece1coa[c]  ->
1000    5HPET[r]  ->
1000    taur[c]  ->
1000    pe_hs[r]  ->
1000    pmtcoa[r]  ->
1000    alaala[e]  ->
1000    bglc[e]  ->
1000    glygly[e]  ->
1000    gum[e]  ->
1000    leugly[e]  ->
1000    pect[e]  ->
1000    psyl[e]  ->
1000    slfcys[e]  ->
1000    dpcoa[e]  ->
1000    oh1[e]  ->
1000    q10[e]  ->
1000    Lcystin[c]  ->
1000    ncam[c]  ->
1000    pnto_R[c]  ->
1000    34hpp[e]  ->
1000    3mob[e]  ->
1000    3mop[e]  ->
1000    4mop[e]  ->
1000    aicar[e]  ->
1000    cbasp[e]  ->
1000    2pg[e]  ->
1000    5hoxindoa[e]  ->
1000    cholp[e]  ->
```

```
1000    cyst_L[e]  ->
1000    dmgly[e]  ->
1000    g3pc[e]  ->
1000    gudac[e]  ->
1000    hcys_L[e]  ->
1000    icit[e]  ->
1000    pep[e]  ->
1000    xtsn[e]  ->
1000    3pg[e]  ->
1000    udpglcur[e]  ->
1000    nicrnt[e]  ->
1000    orot5p[e]  ->
1000    glyc3p[e]  ->
1000    acrn[e]  ->
1000    pcrn[e]  ->
1000    lneldccrn[e]  ->
1000    odecrn[e]  ->
1000    stcrn[e]  ->
1000    pmtcrn[e]  ->
1000    hdcecrn[e]  ->
1000    15HPET[e]  ->
1000    3mhis[e]  ->
1000    5HPET[e]  ->
1000    7dhchsterol[e]  ->
1000    aclys[e]  ->
1000    adpoh[e]  ->
1000    amet[e]  ->
1000    biliverd[e]  ->
1000    C02356[e]  ->
1000    CE0955[e]  ->
1000    CE1556[e]  ->
1000    CE2176[e]  ->
1000    CE7082[e]  ->
1000    forglu[e]  ->
1000    HC00900[e]  ->
1000    hmcr[e]  ->
1000    lnlccrn[e]  ->
1000    lthstrl[e]  ->
1000    mev_R[e]  ->
1000    pe12_hs[e]  ->
1000    pe13_hs[e]  ->
1000    pe15_hs[e]  ->
1000    pe161_hs[e]  ->
1000    pe224_hs[e]  ->
1000    pe226_hs[e]  ->
1000    pedh203_hs[e]  ->
1000    pelinl_hs[e]  ->
1000    peole_hs[e]  ->
1000    pepalm_hs[e]  ->
1000    peste_hs[e]  ->
1000    saccrp_L[e]  ->
1000    xolest205_hs[e]  ->
1000    3moxtyr[e]  ->
1000    5aop[e]  ->
1000    alltn[e]  ->
1000    CE2510[e]  ->
1000    ddca[e]  ->
1000    glyc_R[e]  ->
1000    Lcyst[e]  ->
1000    oaa[e]  ->
1000    ttdcea[e]  ->
1000    bgly[e]  ->
1000    retinal[e]  ->
1000    maltttr[e]  ->
```

```
1000    progly[e]  ->
1000    dhbpt[e]  ->
1000    alaargcys[e]  ->
1000    alaasnleu[e]  ->
1000    alahisala[e]  ->
1000    alalysthr[e]  ->
1000    argalaala[e]  ->
1000    argalaphe[e]  ->
1000    argalathr[e]  ->
1000    argarglys[e]  ->
1000    argargmet[e]  ->
1000    argcysgly[e]  ->
1000    argcysser[e]  ->
1000    argglupro[e]  ->
1000    argleuphe[e]  ->
1000    argphearg[e]  ->
1000    argpromet[e]  ->
1000    argserser[e]  ->
1000    argtyrval[e]  ->
1000    argvalcys[e]  ->
1000    argvaltrp[e]  ->
1000    asnmetpro[e]  ->
1000    asnpheasp[e]  ->
1000    asnphecys[e]  ->
1000    asntyrgly[e]  ->
1000    asntyrphe[e]  ->
1000    aspalaarg[e]  ->
1000    aspasnglu[e]  ->
1000    aspglupro[e]  ->
1000    aspglutrp[e]  ->
1000    asphiscys[e]  ->
1000    asplysglu[e]  ->
1000    aspmetasp[e]  ->
1000    aspvalasn[e]  ->
1000    cysasnmet[e]  ->
1000    cysaspphe[e]  ->
1000    cysglnmet[e]  ->
1000    cysglutrp[e]  ->
1000    cysleuthr[e]  ->
1000    cystyrasn[e]  ->
1000    glnasngln[e]  ->
1000    glnlyslys[e]  ->
1000    glnproglu[e]  ->
1000    glntrpglu[e]  ->
1000    glntyrleu[e]  ->
1000    gluargleu[e]  ->
1000    gluasnleu[e]  ->
1000    glumethis[e]  ->
1000    gluthr[e]  ->
1000    gluthrlys[e]  ->
1000    glutrpala[e]  ->
1000    glyhisasn[e]  ->
1000    glyhislys[e]  ->
1000    glylysphe[e]  ->
1000    glytyrlys[e]  ->
1000    glyvalhis[e]  ->
1000    hisargcys[e]  ->
1000    hisargser[e]  ->
1000    hiscyscys[e]  ->
1000    hisglnala[e]  ->
1000    hisglugln[e]  ->
1000    hisglylys[e]  ->
1000    hislysala[e]  ->
1000    hislysglu[e]  ->
```

```
1000    hislysile[e]  ->
1000    hislysval[e]  ->
1000    hismetgln[e]  ->
1000    hisphearg[e]  ->
1000    histrphis[e]  ->
1000    ileargile[e]  ->
1000    ileasnhis[e]  ->
1000    ileglyarg[e]  ->
1000    ileprolys[e]  ->
1000    ileserarg[e]  ->
1000    iletrptyr[e]  ->
1000    leualaarg[e]  ->
1000    leuasplys[e]  ->
1000    leusertrp[e]  ->
1000    lyscyshis[e]  ->
1000    lysglnphe[e]  ->
1000    lyslyslys[e]  ->
1000    lyspheile[e]  ->
1000    lystyrile[e]  ->
1000    lysvalphe[e]  ->
1000    lysvaltrp[e]  ->
1000    metargleu[e]  ->
1000    metasntyr[e]  ->
1000    metglntyr[e]  ->
1000    metglyarg[e]  ->
1000    metmetile[e]  ->
1000    metphearg[e]  ->
1000    mettrpphe[e]  ->
1000    pheasnmet[e]  ->
1000    pheasp[e]  ->
1000    pheglnphe[e]  ->
1000    pheleu[e]  ->
1000    pheleuasp[e]  ->
1000    pheleuhis[e]  ->
1000    phelysala[e]  ->
1000    phelyspro[e]  ->
1000    phepheasn[e]  ->
1000    phephethr[e]  ->
1000    pheproarg[e]  ->
1000    phesertrp[e]  ->
1000    phethrlys[e]  ->
1000    phetrpleu[e]  ->
1000    phetyr[e]  ->
1000    phetyrgln[e]  ->
1000    phetyrlys[e]  ->
1000    proargcys[e]  ->
1000    proasncys[e]  ->
1000    proglulys[e]  ->
1000    prophe[e]  ->
1000    proproarg[e]  ->
1000    propropro[e]  ->
1000    provalgln[e]  ->
1000    serargala[e]  ->
1000    serargtrp[e]  ->
1000    sercysarg[e]  ->
1000    serlyshis[e]  ->
1000    serphelys[e]  ->
1000    thrglnglu[e]  ->
1000    thrilearg[e]  ->
1000    thrmetarg[e]  ->
1000    thrphearg[e]  ->
1000    thrserarg[e]  ->
1000    thrtyrmet[e]  ->
1000    trpgluleu[e]  ->
```

```
1000    trpglupro[e]  ->
1000    trpglutyr[e]  ->
1000    trpglyphe[e]  ->
1000    trpglyval[e]  ->
1000    trpilelys[e]  ->
1000    trpiletrp[e]  ->
1000    trpleuval[e]  ->
1000    trpmetval[e]  ->
1000    trpphe[e]  ->
1000    trpproval[e]  ->
1000    trpsertyr[e]  ->
1000    trpthrglu[e]  ->
1000    trpthrile[e]  ->
1000    trpvalasp[e]  ->
1000    tyrala[e]  ->
1000    tyralaphe[e]  ->
1000    tyrargglu[e]  ->
1000    tyrargser[e]  ->
1000    tyrcysgly[e]  ->
1000    tyrcysthr[e]  ->
1000    tyrglu[e]  ->
1000    tyrphetyr[e]  ->
1000    tyrvalmet[e]  ->
1000    valarggly[e]  ->
1000    valhisasn[e]  ->
1000    valleuphe[e]  ->
1000    vallystyr[e]  ->
1000    valphearg[e]  ->
1000    valprotrp[e]  ->
1000    valserarg[e]  ->
1000    valtrpphe[e]  ->
1000    valtrpval[e]  ->
1000    trpglyasp[e]  ->
1000    hxa[e]  ->
1000    Lhcystin[e]  ->
1000    pe_hs[c]  ->
1000    akg[c]  ->
1000    bandmt[c]  ->
1000    for[c]  ->
1000    mi14p[c]  ->
1000    pchol_hs[c]  ->
1000    C02712[c]  ->
1000    C02528[c]  ->
1000    HC02191[c]  ->
1000    HC02192[c]  ->
1000    HC02197[c]  ->
1000    HC02198[c]  ->
1000    HC02220[c]  ->
1000    Tyr_ggn[c]  ->
1000    c226coa[c]  ->
1000    chol[c]  ->
1000    cholate[c]  ->
1000    coa[c]  ->
1000    crvnc[c]  ->
1000    gchola[c]  ->
1000    glygn2[c]  ->
1000    hdca[c]  ->
1000    lnlccoa[c]  ->
1000    retfa[c]  ->
1000    retinol[c]  ->
1000    tchola[c]  ->
1000    tdechola[c]  ->
1000    thmpp[c]  ->
1000    thmtp[c]  ->
```

```
1000    tmndnccoa[c]  ->
1000    vitd3[c]  ->
1000    dhcholestanate[c]  ->
1000    thcholstoic[c]  ->
1000    xol7ah3[c]  ->
1000    xol7aone[c]  ->
1000    7klitchol[c]  ->
1000    dchac[c]  ->
1000    CE1273[c]  ->
1000    2obut[e]  ->
1000    acac[e]  ->
1000    but[e]  ->
1000    cgly[e]  ->
1000    co2[e]  ->
1000    cytd[e]  ->
1000    dgsn[e]  ->
1000    din[e]  ->
1000    duri[e]  ->
1000    fe3[e]  ->
1000    fum[e]  ->
1000    glyleu[e]  ->
1000    glyphe[e]  ->
1000    glypro[e]  ->
1000    h[e]  ->
1000    h2o[e]  ->
1000    ins[e]  ->
1000    lac_L[e]  ->
1000    lys_L[e]  ->
1000    na1[e]  ->
1000    o2[e]  ->
1000    orn[e]  ->
1000    ppi[e]  ->
1000    pro_L[e]  ->
1000    ser_L[e]  ->
1000    so4[e]  ->
1000    thymd[e]  ->
1000    urea[e]  ->
1000    cys_L[e]  ->
1000    his_L[e]  ->
1000    thr_L[e]  ->
1000    gln_L[e]  ->
1000    phe_L[e]  ->
1000    arg_L[e]  ->
1000    nac[e]  ->
1000    cit[e]  ->
1000    etha[e]  ->
1000    fol[e]  ->
1000    glyc[e]  ->
1000    malt[e]  ->
1000    malttr[e]  ->
1000    rib_D[e]  ->
1000    trp_L[e]  ->
1000    xyl_D[e]  ->
1000    34dhpha[e]  ->
1000    ppa[e]  ->
1000    tre[e]  ->
1000    lcts[e]  ->
1000    ade[e]  ->
1000    etoh[e]  ->
1000    phpyr[e]  ->
1000    2h3mv[e]  ->
1000    2hiv[e]  ->
1000    sucsal[e]  ->
1000    3ityr_L[e]  ->
```

```
1000    35diotyr[e]  ->
1000    13_cis_retn[e]  ->
1000    CE1617[e]  ->
1000    34dhoxmand[e]  ->
1000    CE5643[e]  ->
1000    n8aspmd[e]  ->
1000    13dampp[e]  ->
1000    12ppd_R[e]  ->
1000    xylu_L[e]  ->
1000    xylu_D[e]  ->
1000    CE0737[e]  ->
1000    hdd2crn[e]  ->
1000    mlthf[e]  ->
1000    sphgn[e]  ->
1000    coke[e]  ->
1000    hdl_hs[e]  ->
1000    HC00005[e]  ->
1000    CE2172[e]  ->
1000    CE5629[e]  ->
1000    gd3_hs[e]  ->
1000    gluside_hs[e]  ->
1000    gm3_hs[e]  ->
1000    cmpacna[e]  ->
1000    34dhpac[c]  ->
1000    ts3[c]  ->
1000    gd3_hs[l]  ->
1000    k[g]  ->
1000    na1[r]  ->
1000    pail_hs[e]  ->
1000    CE1243[e]  ->
1000    CE5026[e]  ->
1000    CE1261[e]  ->
1000    gd1b_hs[e]  ->
1000    nadh[e]  ->
1000    sbt_D[e]  ->
1000    12dhchol[c]  ->
1000    3dhcdchol[c]  ->
1000    3dhchol[c]  ->
1000    3dhdchol[c]  ->
1000    3dhlchol[c]  ->
1000    7dhcdchol[c]  ->
1000    7dhchol[c]  ->
1000    ca3s[c]  ->
1000    coprost[c]  ->
1000    dca3s[c]  ->
1000    gca3s[c]  ->
1000    gcdca3s[c]  ->
1000    gdca3s[c]  ->
1000    gudca3s[c]  ->
1000    hyochol[c]  ->
1000    icdchol[c]  ->
1000    isochol[c]  ->
1000    lca3s[c]  ->
1000    tca3s[c]  ->
1000    tcdca3s[c]  ->
1000    tdca3s[c]  ->
1000    thyochol[c]  ->
1000    tudca3s[c]  ->
1000    uchol[c]  ->
1000    udca3s[c]  ->
1000    hyochol[e]  ->
1000    am1ccs[e]  ->
1000    am1csa[e]  ->
1000    am9csa[e]  ->
```

```
  1000    csa[e]  ->
  1000    fvs[e]  ->
  1000    glz[e]  ->
  1000    lvst[e]  ->
  1000    mhglz[e]  ->
  1000    nfd[e]  ->
  1000    nfdoh[e]  ->
  1000    ptvstlac[e]  ->
  1000    pvs[e]  ->
  1000    tlacfvs[e]  ->
  1000    tmdm1[e]  ->
  1000    tripvs[e]  ->
  1000    C13856[e]  ->
  1000    M02956[e]  ->
  1000    M00241[e]  ->
  1000    M00008[e]  ->
  0.05    M00017[e]  ->
  1000    M00019[e]  ->
  0.15    M00117[e]  ->
  1000    M01197[e]  ->
  0.05    M01207[e]  ->
  1000    M01235[e]  ->
  1000    M01238[e]  ->
  1000    M02560[e]  ->
  1000    h2co3[e]  ->
  1000    M02837[e]  ->
  1000    his_L[c]  ->
  1000    ile_L[c]  ->
  1000    leu_L[c]  ->
  1000    lys_L[c]  ->
  1000    met_L[c]  ->
  1000    phe_L[c]  ->
  1000    thr_L[c]  ->
  1000    trp_L[c]  ->
  1000    val_L[c]  ->
  1000    ala_L[c]  ->
  1000    arg_L[c]  ->
  1000    asn_L[c]  ->
  1000    asp_L[c]  ->
  1000    cys_L[c]  ->
  1000    gln_L[c]  ->
  1000    glu_L[c]  ->
  1000    pro_L[c]  ->
  1000    ser_L[c]  ->
  1000    tyr_L[c]  ->
  1000    gly[c]  ->
  1000    4abut[l]  ->
  1000    CE5026[c]  ->
  1000    4glu56dihdind[c]  ->
  1000    dopa[c]  ->
  1000    srtn[c]  ->
  1000    adrnl[c]  ->
  1000    ach[c]  ->
  1000    hista[c]  ->
  1000    nrpphr[c]  ->
  1000    Lkynr[c]  ->
  1000    btn[m]  ->
Upper bounds relaxed
  1000    13_cis_retn[n]  ->
  1000    datp[m]  ->
  1000    dgpi_prot_hs[r]  ->
  1000    dgtp[m]  ->
  1000    dttp[m]  ->
  1000    melanin[c]  ->
```

```
1000    mem2emgacpail_prot_hs[r]  ->
1000    10fthf[e]  ->
1000    10fthf5glu[e]  ->
1000    10fthf6glu[e]  ->
1000    13_cis_retnglc[e]  ->
1000    2hb[e]  ->
1000    34dhoxpeg[e]  ->
1000    34dhphe[e]  ->
1000    5adtststerones[e]  ->
1000    5dhf[e]  ->
1000    5mthf[e]  ->
1000    5thf[e]  ->
1000    6dhf[e]  ->
1000    6thf[e]  ->
1000    abt[e]  ->
1000    acetone[e]  ->
1000    ach[e]  ->
0.45    adrn[e]  ->
1000    amp[e]  ->
 0.1    arach[e]  ->
1000    arachd[e]  ->
1000    bhb[e]  ->
1000    bilirub[e]  ->
 0.5    clpnd[e]  ->
1000    crtstrn[e]  ->
1000    crvnc[e]  ->
1000    dag_hs[e]  ->
1000    dhdascb[e]  ->
1000    dhf[e]  ->
 0.2    dlnlcg[e]  ->
1000    dopa[e]  ->
1000    elaid[e]  ->
1000    estradiol[e]  ->
1000    fuc_L[e]  ->
1000    glyc_S[e]  ->
1000    glygn5[e]  ->
1000    gmp[e]  ->
1000    gsn[e]  ->
1000    hco3[e]  ->
1000    hdca[e]  ->
1000    hdcea[e]  ->
 0.2    hexc[e]  ->
1000    hista[e]  ->
1000    hpdca[e]  ->
1000    inost[e]  ->
1000    ksi_deg1[e]  ->
1000    lac_D[e]  ->
1000    leuktrC4[e]  ->
1000    leuktrD4[e]  ->
1000    leuktrE4[e]  ->
1000    lgnc[e]  ->
1000    lneldc[e]  ->
1000    lnlncg[e]  ->
1000    lpchol_hs[e]  ->
1000    mag_hs[e]  ->
1000    meoh[e]  ->
1000    mercplaccys[e]  ->
1000    mthgxl[e]  ->
1000    nad[e]  ->
1000    nrpphr[e]  ->
 0.1    nrvnc[e]  ->
1000    oagd3_hs[e]  ->
1000    ocdca[e]  ->
1000    pchol_hs[e]  ->
```

```
1000    pglyc_hs[e]  ->
1000    prostge2[e]  ->
1000    rbt[e]  ->
1000    retfa[e]  ->
1000    retn[e]  ->
1000    Rtotal[e]  ->
1000    Rtotal2[e]  ->
1000    Rtotal3[e]  ->
1000    s2l2n2m2masn[e]  ->
1000    sl_L[e]  ->
1000    tchola[e]  ->
1000    thmtp[e]  ->
1000    thyox_L[e]  ->
1000    tmndnc[e]  ->
1000    tststerone[e]  ->
1000    tsul[e]  ->
1000    udp[e]  ->
1000    ump[e]  ->
1000    urate[e]  ->
1000    vitd3[e]  ->
1000    whtststerone[e]  ->
1000    xolest_hs[e]  ->
1000    xolest2_hs[e]  ->
1000    acmana[e]  ->
1000    ahdt[e]  ->
1000    ctp[e]  ->
1000    dgtp[e]  ->
1000    dtmp[e]  ->
1000    g1p[e]  ->
1000    isomal[e]  ->
1000    HC01104[e]  ->
1000    HC01444[e]  ->
1000    HC01577[e]  ->
1000    HC01609[e]  ->
1000    HC01700[e]  ->
1000    orot[e]  ->
1000    prpp[e]  ->
1000    so3[e]  ->
1000    prostgh2[e]  ->
1000    prostgi2[e]  ->
1000    HC00004[e]  ->
1000    HC00822[e]  ->
1000    HC02192[e]  ->
1000    HC02193[e]  ->
1000    HC02220[e]  ->
1000    HC02197[e]  ->
1000    HC02198[e]  ->
1000    HC02187[e]  ->
1000    HC02202[e]  ->
1000    HC02204[e]  ->
1000    coa[e]  ->
1000    CE2250[e]  ->
1000    CE1943[e]  ->
1000    CE2915[e]  ->
1000    CE2916[e]  ->
1000    CE2917[e]  ->
1000    malthp[e]  ->
1000    CE2839[e]  ->
1000    3ump[e]  ->
1000    CE5786[e]  ->
1000    CE5789[e]  ->
1000    CE5797[e]  ->
1000    CE5868[e]  ->
1000    CE5869[e]  ->
```

```
1000    CE4881[e]  ->
1000    CE1926[e]  ->
1000    crm_hs[e]  ->
1000    galside_hs[e]  ->
1000    CE1925[e]  ->
1000    3bcrn[e]  ->
1000    3hdececrn[e]  ->
1000    3octdeccrn[e]  ->
1000    3octdece1crn[e]  ->
1000    c101crn[e]  ->
1000    c10crn[e]  ->
1000    c4dc[e]  ->
1000    c51crn[e]  ->
1000    c8crn[e]  ->
0.25    docosac[e]  ->
1000    tetdec2crn[e]  ->
1000    tetdece1crn[e]  ->
1000    4abut[n]  ->
1000    dchac[e]  ->
1000    glgchlo[e]  ->
1000    gltcho[e]  ->
1000    gumgchol[e]  ->
1000    gumtchol[e]  ->
1000    pectintchol[e]  ->
1000    psylchol[e]  ->
1000    psyltchol[e]  ->
1000    tdechola[e]  ->
1000    fmn[e]  ->
1000    pan4p[e]  ->
1000    q10h2[e]  ->
1000    5HPET[c]  ->
1000    Lcystin[c]  ->
1000    fol[c]  ->
1000    ncam[c]  ->
1000    5oxpro[e]  ->
1000    ahcys[e]  ->
1000    cholp[e]  ->
1000    cyst_L[e]  ->
1000    dcmp[e]  ->
1000    ethamp[e]  ->
1000    glyald[e]  ->
1000    icit[e]  ->
1000    L2aadp[e]  ->
1000    Lkynr[e]  ->
1000    xmp[e]  ->
1000    hLkynr[e]  ->
1000    nicrnt[e]  ->
1000    argsuc[e]  ->
1000    pcrn[e]  ->
1000    lneldccrn[e]  ->
1000    stcrn[e]  ->
1000    3mtp[e]  ->
1000    15kprostgf2[e]  ->
1000    2oxoadp[e]  ->
1000    34hpl[e]  ->
1000    3hpp[e]  ->
1000    3uib[e]  ->
1000    56dura[e]  ->
1000    acgly[e]  ->
1000    acthr_L[e]  ->
1000    C02712[e]  ->
1000    C05957[e]  ->
1000    C06314[e]  ->
1000    C06315[e]  ->
```

```
1000    C11695[e]  ->
1000    CE1273[e]  ->
1000    CE1556[e]  ->
1000    CE2176[e]  ->
1000    CE5304[e]  ->
1000    CE6031[e]  ->
1000    didecaeth[e]  ->
1000    diholineth[e]  ->
1000    docohxeth[e]  ->
1000    docteteth[e]  ->
1000    elaidcrn[e]  ->
1000    hepdeceth[e]  ->
1000    hexdeceeth[e]  ->
1000    hexdiac[e]  ->
1000    hxcoa[e]  ->
1000    lineth[e]  ->
1000    lnlccrn[e]  ->
1000    mi1p_D[e]  ->
1000    Nacasp[e]  ->
1000    oleth[e]  ->
1000    pailste_hs[e]  ->
1000    pchol2palm_hs[e]  ->
1000    pcholn261_hs[e]  ->
1000    pcholn28_hs[e]  ->
1000    pcholn281_hs[e]  ->
1000    pmeth[e]  ->
1000    sphmyln180241_hs[e]  ->
1000    sphmyln18114_hs[e]  ->
1000    sphmyln18115_hs[e]  ->
1000    sphmyln18116_hs[e]  ->
1000    sphmyln181161_hs[e]  ->
1000    sphmyln18117_hs[e]  ->
1000    sphmyln18118_hs[e]  ->
1000    sphmyln181181_hs[e]  ->
1000    sphmyln18120_hs[e]  ->
1000    sphmyln181201_hs[e]  ->
1000    sphmyln18121_hs[e]  ->
1000    sphmyln18122_hs[e]  ->
1000    sphmyln181221_hs[e]  ->
1000    sphmyln18123_hs[e]  ->
1000    sphmyln1824_hs[e]  ->
1000    sphmyln1825_hs[e]  ->
1000    steeth[e]  ->
1000    tmlys[e]  ->
1000    trideceth[e]  ->
1000    xolest183_hs[e]  ->
1000    abt_D[e]  ->
1000    glyc2p[e]  ->
1000    glyclt[e]  ->
1000    phlac[e]  ->
1000    pser_L[e]  ->
1000    bz[e]  ->
1000    mepi[e]  ->
1000    1mncam[e]  ->
1000    progly[e]  ->
1000    thbpt[e]  ->
1000    itp[n]  ->
1000    alaargcys[e]  ->
1000    alaarggly[e]  ->
1000    alaglylys[e]  ->
1000    alahisala[e]  ->
1000    argalaphe[e]  ->
1000    argarg[e]  ->
1000    argarglys[e]  ->
```

```
1000    argcysgly[e]  ->
1000    argcysser[e]  ->
1000    arggluglu[e]  ->
1000    argglygly[e]  ->
1000    arghisthr[e]  ->
1000    arglysasp[e]  ->
1000    argprothr[e]  ->
1000    argserser[e]  ->
1000    argvalcys[e]  ->
1000    asnasnarg[e]  ->
1000    asncyscys[e]  ->
1000    asnphecys[e]  ->
1000    asntyrthr[e]  ->
1000    aspasnglu[e]  ->
1000    aspglu[e]  ->
1000    asphispro[e]  ->
1000    asplysglu[e]  ->
1000    asplyshis[e]  ->
1000    aspprolys[e]  ->
1000    cysasnmet[e]  ->
1000    cysaspphe[e]  ->
1000    cyscys[e]  ->
1000    cysglnmet[e]  ->
1000    cysgluhis[e]  ->
1000    cysglutrp[e]  ->
1000    cyssermet[e]  ->
1000    glnasngln[e]  ->
1000    glnhishis[e]  ->
1000    glnhislys[e]  ->
1000    glnlyslys[e]  ->
1000    glnlystrp[e]  ->
1000    gluglu[e]  ->
1000    gluilelys[e]  ->
1000    gluleu[e]  ->
1000    glumet[e]  ->
1000    glumethis[e]  ->
1000    glutrpala[e]  ->
1000    glylyscys[e]  ->
1000    glylysphe[e]  ->
1000    glyvalhis[e]  ->
1000    hisasp[e]  ->
1000    hiscyscys[e]  ->
1000    hisglu[e]  ->
1000    hishislys[e]  ->
1000    hislysthr[e]  ->
1000    hismet[e]  ->
1000    hisprolys[e]  ->
1000    histrphis[e]  ->
1000    ileargile[e]  ->
1000    ileasp[e]  ->
1000    ileglnglu[e]  ->
1000    ileglyarg[e]  ->
1000    ileserarg[e]  ->
1000    leuasnasp[e]  ->
1000    leuleutrp[e]  ->
1000    leupro[e]  ->
1000    leuproarg[e]  ->
1000    leutrp[e]  ->
1000    leutrparg[e]  ->
1000    leutyrtyr[e]  ->
1000    leuval[e]  ->
1000    lysargleu[e]  ->
1000    lysgluglu[e]  ->
1000    lyslyslys[e]  ->
```

```
1000    lyspheile[e]  ->
1000    lystrparg[e]  ->
1000    lysvalphe[e]  ->
1000    methislys[e]  ->
1000    metmetile[e]  ->
1000    pheasnmet[e]  ->
1000    pheglnphe[e]  ->
1000    phelysala[e]  ->
1000    phephe[e]  ->
1000    phepheasn[e]  ->
1000    phephethr[e]  ->
1000    phesertrp[e]  ->
1000    proargasp[e]  ->
1000    procys[e]  ->
1000    proglnpro[e]  ->
1000    prohis[e]  ->
1000    prohistyr[e]  ->
1000    proleuarg[e]  ->
1000    prolyspro[e]  ->
1000    proproarg[e]  ->
1000    propropro[e]  ->
1000    protrplys[e]  ->
1000    protrpthr[e]  ->
1000    serargala[e]  ->
1000    sercysarg[e]  ->
1000    serglyglu[e]  ->
1000    serphelys[e]  ->
1000    sertrphis[e]  ->
1000    thrargtyr[e]  ->
1000    thrasntyr[e]  ->
1000    thrglntyr[e]  ->
1000    thrhishis[e]  ->
1000    thrthrarg[e]  ->
1000    trpalapro[e]  ->
1000    trpargala[e]  ->
1000    trpaspasp[e]  ->
1000    trpglngln[e]  ->
1000    trpglugly[e]  ->
1000    trpglyleu[e]  ->
1000    trpglyval[e]  ->
1000    trphismet[e]  ->
1000    trpiletrp[e]  ->
1000    trplys[e]  ->
1000    trpmetarg[e]  ->
1000    trpprogly[e]  ->
1000    trpproleu[e]  ->
1000    trpthrtyr[e]  ->
1000    trptyrgln[e]  ->
1000    trptyrtyr[e]  ->
1000    tyralaphe[e]  ->
1000    tyrasparg[e]  ->
1000    tyrcysgly[e]  ->
1000    tyrleuarg[e]  ->
1000    tyrthr[e]  ->
1000    tyrtrpphe[e]  ->
1000    tyrtyr[e]  ->
1000    tyrvalmet[e]  ->
1000    valarggly[e]  ->
1000    valleuphe[e]  ->
1000    valphearg[e]  ->
1000    valserarg[e]  ->
1000    valtrpphe[e]  ->
1000    valtrpval[e]  ->
1000    valval[e]  ->
```

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1000    homoval[e]  ->
1000    pe_hs[c]  ->
1000    adprbp[c]  ->
1000    mi145p[c]  ->
1000    band[c]  ->
1000    acgal[e]  ->
1000    acnam[e]  ->
1000    HC00342[e]  ->
1000    pa_hs[e]  ->
1000    CE2934[e]  ->
1000    HC02191[c]  ->
1000    HC02193[c]  ->
1000    HC02194[c]  ->
1000    HC02195[c]  ->
1000    HC02196[c]  ->
1000    Tyr_ggn[c]  ->
1000    btn[c]  ->
1000    coa[c]  ->
1000    fad[c]  ->
1000    lnlc[c]  ->
1000    lnlccoa[c]  ->
1000    nad[c]  ->
1000    odecoa[c]  ->
1000    pmtcoa[c]  ->
1000    retinol[c]  ->
1000    stcoa[c]  ->
1000    tag_hs[c]  ->
1000    thf[c]  ->
1000    tmndnc[c]  ->
1000    dxtrn[e]  ->
1000    dhcholestanate[e]  ->
1000    thcholstoic[e]  ->
1000    xol7ah3[e]  ->
1000    xol7ah3[c]  ->
1000    xol7aone[e]  ->
1000    7klitchol[e]  ->
1000    glcn[e]  ->
1000    acac[e]  ->
1000    adn[e]  ->
1000    akg[e]  ->
1000    asn_L[e]  ->
1000    asp_L[e]  ->
1000    co2[e]  ->
1000    dad_2[e]  ->
1000    dcyt[e]  ->
1000    fe2[e]  ->
1000    gal[e]  ->
1000    glu_L[e]  ->
1000    glyb[e]  ->
1000    glypro[e]  ->
1000    ile_L[e]  ->
1000    ins[e]  ->
1000    k[e]  ->
1000    lac_L[e]  ->
1000    leu_L[e]  ->
1000    mal_L[e]  ->
1000    met_L[e]  ->
1000    no2[e]  ->
1000    pi[e]  ->
1000    pro_L[e]  ->
1000    ser_L[e]  ->
1000    succ[e]  ->
1000    urea[e]  ->
1000    uri[e]  ->
```

```
1000    val_L[e]  ->
1000    pnto_R[e]  ->
1000    gly[e]  ->
1000    cys_L[e]  ->
1000    ala_L[e]  ->
1000    thr_L[e]  ->
1000    gln_L[e]  ->
1000    phe_L[e]  ->
1000    tyr_L[e]  ->
1000    for[e]  ->
1000    nh4[e]  ->
1000    ac[e]  ->
1000    acgam[e]  ->
1000    cit[e]  ->
1000    drib[e]  ->
1000    fru[e]  ->
1000    galt[e]  ->
1000    glcr[e]  ->
1000    glcur[e]  ->
1000    glyc[e]  ->
1000    hxan[e]  ->
1000    malt[e]  ->
1000    ptrc[e]  ->
1000    spmd[e]  ->
1000    trp_L[e]  ->
1000    ura[e]  ->
1000    xan[e]  ->
1000    ppa[e]  ->
1000    pyr[e]  ->
1000    btn[e]  ->
1000    ade[e]  ->
1000    acald[e]  ->
1000    gua[e]  ->
1000    4abut[e]  ->
1000    taur[e]  ->
1000    phpyr[e]  ->
1000    CE4970[e]  ->
1000    CE4968[e]  ->
1000    vanillac[e]  ->
1000    2m3hvac[e]  ->
1000    3h3mglt[e]  ->
1000    3mglutac[e]  ->
1000    3mglutr[e]  ->
1000    mvlac[e]  ->
1000    ethmalac[e]  ->
1000    methsucc[e]  ->
1000    4ohbut[e]  ->
1000    agm[e]  ->
1000    T4hcinnm[e]  ->
1000    egme[e]  ->
1000    HC02020[e]  ->
1000    chsterols[e]  ->
1000    CE1401[e]  ->
1000    melatn[e]  ->
1000    CE4890[e]  ->
1000    C09642[e]  ->
1000    mhista[e]  ->
1000    ppbng[e]  ->
1000    sphings[e]  ->
1000    CE1918[e]  ->
1000    aact[e]  ->
1000    N1aspmd[e]  ->
1000    fdp[e]  ->
1000    ldl_hs[e]  ->
```

```
1000    HC00006[e]  ->
1000    HC00007[e]  ->
1000    HC00008[e]  ->
1000    HC00009[e]  ->
1000    gluside_hs[e]  ->
1000    34dhpe[e]  ->
1000    sph1p[n]  ->
1000    sphs1p[n]  ->
1000    gd3_hs[g]  ->
1000    na1[g]  ->
1000    na1[c]  ->
1000    retn[n]  ->
1000    Ser_Gly_Ala_X_Gly[r]  ->
1000    5cysgly34dhphe[e]  ->
1000    galgluside_hs[e]  ->
1000    mem2emgacpail_prot_hs[e]  ->
1000    glc_D[e]  ->
1000    cdca24g[c]  ->
1000    cdca3g[c]  ->
1000    dca24g[c]  ->
1000    hca24g[c]  ->
1000    hca6g[c]  ->
1000    hyochol[c]  ->
1000    lca24g[c]  ->
1000    lca3g[c]  ->
1000    12dhchol[e]  ->
1000    3dhcdchol[e]  ->
1000    3dhchol[e]  ->
1000    3dhdchol[e]  ->
1000    3dhlchol[e]  ->
1000    7dhcdchol[e]  ->
1000    7dhchol[e]  ->
1000    ca3s[e]  ->
1000    coprost[e]  ->
1000    dca3s[e]  ->
1000    gca3s[e]  ->
1000    gcdca3s[e]  ->
1000    gdca3s[e]  ->
1000    gudca3s[e]  ->
1000    icdchol[e]  ->
1000    isochol[e]  ->
1000    lca3s[e]  ->
1000    tca3s[e]  ->
1000    tcdca3s[e]  ->
1000    tdca3s[e]  ->
1000    thyochol[e]  ->
1000    tudca3s[e]  ->
1000    uchol[e]  ->
1000    udca3s[e]  ->
1000    3ispvs[e]  ->
1000    56dhpvs[e]  ->
1000    6epvs[e]  ->
1000    6melvst[e]  ->
1000    am1accs[e]  ->
1000    am1alcs[e]  ->
1000    am4n9cs[e]  ->
1000    am4ncs[e]  ->
1000    crglz[e]  ->
1000    deoxfvs[e]  ->
1000    dhglz[e]  ->
1000    dspvs[e]  ->
1000    nfdlac[e]  ->
1000    nfdnpy[e]  ->
1000    ptvst[e]  ->
```

```
  1000    thrfvs[e]  ->
  1000    tmdm5[e]  ->
  1000    M01807[e]  ->
  1000    M00503[e]  ->
  1000    M01820[e]  ->
  1000    M00510[e]  ->
  1000    M00003[e]  ->
  1000    M00010[e]  ->
   0.2    M02457[e]  ->
  0.05    M03045[e]  ->
  1000    M02561[e]  ->
  1000    M01111[e]  ->
  1000    M01966[e]  ->
  1000    M01989[e]  ->
  1000    gpi_sig[e]  ->
  1000    glu_L[c]  ->
  1000    tyr_L[c]  ->
  1000    CE4888[c]  ->
  1000    4abut[c]  ->
  1000    kynate[c]  ->
  1000    tym[c]  ->
  1000    cbl2[m]  ->
  1000    protein[c]  ->
```

Generate a relaxed model and test if it is feasible.

```
if solution.stat == 1
    modelRelaxed=model;
    delta=0;%can be used for debugging, in case more relaxation is necessary
    modelRelaxed.lb = model.lb - p - delta;
    modelRelaxed.ub = model.ub + q + delta;
    modelRelaxed.b  = model.b  - r;

    FBAsolution = optimizeCbModel(modelRelaxed,'max', 0, true);
    if FBAsolution.stat == 1
        disp('Relaxed model is feasible');
    else
        disp('Relaxed model is infeasible');
        solutionRelaxed = relaxedFBA(modelRelaxed,relaxOption);
    end
end
```

```
Relaxed model is feasible
```

EXPECTED RESULTS

The relaxed model should be feasible. Indicated by 'Relaxed model is feasible'

TROUBLESHOOTING

If the relaxed model is not feasible. If not, there could be a numerical issue due to the numerical tolerance of the linear optimisation solutions or due to the numerical tolerance on the relaxedFBA algorithm, both of which are by default set to the feasibility tolerance for the currently installed solver (typically 1e-6 for a double precision

solver like Gurobi). If problems persist, examine the numerical properties of the constraints, esp wrt scaling, or try the dqqMinos solver.

```
%changeCobraSolver('dqqMinos','LP')
```

REFERENCES

Fleming, R.M.T., et al., Cardinality optimisation in constraint-based modelling: Application to Recon 3D (submitted), 2017.

Brunk, E. et al. Recon 3D: A resource enabling a three-dimensional view of gene variation in human metabolism. (submitted) 2017.