

Identify Conserved Moieties

```
tutorial_initConservedMoietypaths
```

```
projectDir =  
'~/work/sbgCloud/programExperimental/projects/tracerBased'  
dataDir =  
'~/work/sbgCloud/programExperimental/projects/tracerBased/data/'  
softwareDir =  
'~/work/sbgCloud/programExperimental/projects/tracerBased/software/'  
visDataDir =  
'~/work/sbgCloud/programExperimental/projects/tracerBased/data/visualisation/'  
resultsDir =  
'~/work/sbgCloud/programExperimental/projects/tracerBased/results/iDopaNeuro1_ConservedMoieties/'  
rxnfileDir =  
'~/work/sbgCloud/code/fork-ctf/rxns/atomMapped'
```

```
if ~recompute || isequal(modelName,'iDopaNeuro1')  
    load([resultsDir modelName '_arm.mat'])  
    return  
end
```

1.2.3. Conserved moieties

With the atom mappings we obtained, we can compute the conserved moieties for the iDopaNeuro metabolic network using the atom transition network and the COBRA function `identifyConservedMoieties`.

```
switch modelName  
    case 'DAS'  
        load('DAS.mat')  
    otherwise  
        load([dataDir modelName '.mat'])  
end  
load([resultsDir modelName '_dATM.mat'])  
options.sanityChecks=0;  
[arm, moietyFormulae] = identifyConservedMoieties(model, dATM, options);  
save([resultsDir modelName '_arm.mat'],'arm', 'moietyFormulae','options')
```