

```
sfischer@randompc:~/rba/depot/trunk/rba$ ls data/example/  
data params.in  
sfischer@randompc:~/rba/depot/trunk/rba$ ls data/example/data  
chaperones.fasta iJ01366.xml ribosome.fasta trnas.fasta  
  
sfischer@randompc:~/rba/depot/trunk/rba$ python generate_xml_files.py data/example/params.in  
Importing default data...  
Importing SBML data...  
Importing Uniprot data and manual annotation...  
Could not find uniprot file. Downloading most recent version...  
Helper file data/example/data/locations.tsv not found.  
Helper file data/example/data/cofactors.tsv not found.  
Helper file data/example/data/subunits.tsv not found.  
Helper file data/example/data/unknown_proteins.tsv not found.  
Helper file data/example/data/location_map.tsv not found.  
WARNING: ambiguous uniprot locations have been added to file data/example/data/locations.tsv. Execution will continue with default values.  
WARNING: uniprot locations with no user-defined counterpart have been added to data/example/data/location_map.tsv.  
WARNING: ambiguous uniprot cofactor notes have been added to file data/example/data/cofactors.tsv. Execution will continue with default values.  
WARNING: ambiguous subunit notes have been added to file data/example/data/subunits.tsv. Execution will continue with default values.  
WARNING: SBML genes not referenced in uniprot have been added to file data/example/data/unknown_proteins.tsv. Execution will continue with default values.  
Helper file data/example/data/macrocomponents.tsv not found.  
Helper file data/example/data/metabolites.tsv not found.  
WARNING: unidentified key metabolites have been added to file data/example/data/metabolites.tsv. Unknown metabolites will be removed from production targets.  
Building model...  
Done.
```

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sfischer@randompc:~/rba/depot/trunk/rba$ ls data/example/  
data enzymes.xml metabolism.xml params.in proteins.xml  
dna.xml medium.tsv parameters.xml processes.xml rnas.xml  
sfischer@randompc:~/rba/depot/trunk/rba$ ls data/example/data/  
chaperones.fasta location_map.tsv protein_summary.tsv trnas.fasta  
cofactors.tsv locations.tsv ribosome.fasta uniprot.csv  
iJ01366.xml metabolites.tsv subunits.tsv unknown_proteins.tsv  
  
sfischer@randompc:~/rba/depot/trunk/rba$ python solve_model.py data/example/  
2.5 infeasible  
1.25 optimal  
1.875 optimal  
2.1875 infeasible  
2.03125 infeasible  
1.953125 optimal  
1.9921875 infeasible  
1.97265625 infeasible  
1.962890625 infeasible  
1.9580078125 optimal  
1.96044921875 infeasible  
1.95922851562 infeasible  
1.95861816406 optimal  
1.95892333984 infeasible  
1.95877075195 infeasible  
1.95869445801 infeasible  
1.95861816406
```