Convert a reconstruction into a flux balance analysis model Author: Ronan Fleming, Inse Thiele, University of Luxembourg

Reviewers:

INTERCOLLE

INTRODUCTION

Siver with quality control during the reconstruction process, it is not appropriate to assume that any reconstruction can be converted directly into a model and used to make

predictions. A model must statify cetted in immunification for our level to real work to prediction. Depending on the type of model model, the assumption will be defined. Each assumption will be model to deministing in registration of present an examination accurate and primately in the midway and retainmentation. Furthermore, assigns in a medicination information of the second of the second

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tables repetitions are from institution and many contractions are the contraction of the contraction and the contraction of the contraction and the contraction of th

Select reconstruction to convert into a model and enter parameters Load the PeconX reconstruction and save the original reconstruction in the workspace, urless it is already loaded into the workspace.

General Control Contro

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Choose the directory to place the results

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Optionally create a diary to save the output in case it is very time, this makes it easier to search, especially when debugging the process during the early stages.

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Overview some of the key properties of the reconstruction

Overview some or the key properties or the reconstruction.

Noting the initial size of the reconstruction is useful for comparisons later with subsets derived according to mathematical specifications.

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Check in case the reconstruction is a model that is already ready for flux balance analysis

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Manually remove certain reactions from the reconstruction
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	actions reactions that offer only in the number of protons involved as substitutes or products. Also remove exclusively involved reactants.
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8 5 deficate reactions upto protons removed.

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Heuristically identify exchange reactions and metabolites exclusively involved in exchange reactions

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EXPECTED RESULTS In the returned model, model distribusion, is a boolean of readdons hausistically though to be made bistanced, while model distribution is a boolean of metabolites.

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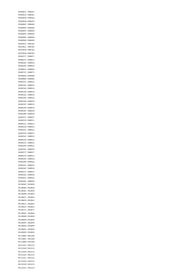
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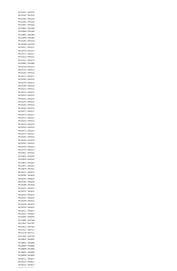
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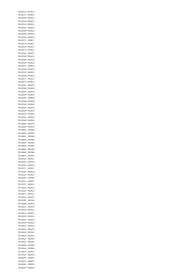
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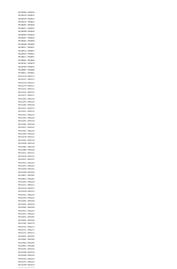
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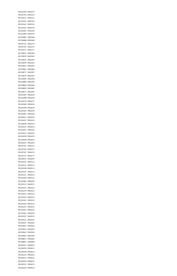
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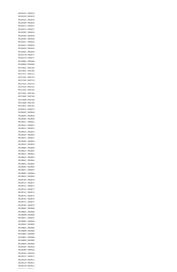




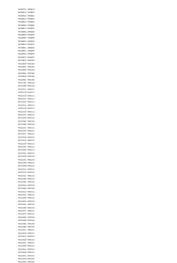


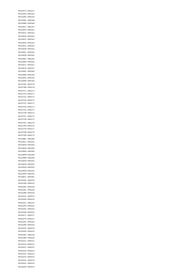






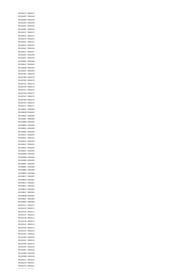


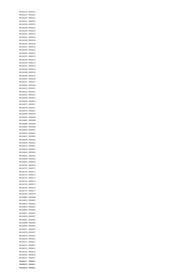












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