## rba.parameters

functions: user-defined functions
density: maximal density values

1. readXMLParameters

## rba.metabolism

metaboliteId: id of metabolites
externalId: id of external metabolites
initialInternalConcentration: vector
initialExternalConcentration: vector
reactionId: id of reactions
reversibility: boolean vector
S: stoichiometry matrix
compartmentId: id of compartments

2. readSBMLMetabolism

## rba.enzymes

efficiency: arrays of efficiency functions
(one array per efficiency model)
proteinIndex: vector mapping each
reaction to the protein catalyzing it
importEfficiency: vector of factors
modulating efficiency for transporter
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modulating efficiency for transporter

3. readXMLProtein

## rba.processes (structure array)

id: process id
machine: array containing
 - composition: machinery composition
 - processingCost: machinery processing cost
 - weight: machinery density
capacity: processing capacity
target: array containing
 - composition: target composition
 - processingCost: target processing cost
 - weight: target density
 - value: target production value
 - dilution: true if target production value is
compensation dilution (scales with mu), false
if it is an absolute target.
 - function: mu-dependent function used to
recompute target value (optional)
targetReaction: array containing
 - id: reaction id
 - value: target flux value
 - function: mu-dependent function used to
recompute target value (optional)

4. readXMLRna
5. readXMLDna

6. readXMLProcess

## rba.macromolecules (structure array)

setName: protein, rna or dna
componentId: ids of components used to build
a macromolecule (e.g. amino acids)
componentMatrix: composition matrix in terms
of components (NOT metabolites)
weight: vector of densities
zeroCost: vector

composition: compositon matrix in terms of
metabolites
degradation: decomposition matrix in terms
of metabolites
processingCost: matrix containing the price each
process has to pay to produce/degrade a molecule