XML format for RBA models

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July 26, 2017

Contents

1 Introduction

In this document we present the XML structures used to define a RBA model. A complete RBAmodel is composed of the following files:

- metabolism.xml (definition of compartments, metabolic species and metabolic reactions).

- parameters.xml (definition of density constraints and user-defined functions).

- proteins.xml (definition of proteins).

- rnas.xml (definition of RNAs).

- dna.xml (definition of DNA).

- enzymes.xml (definition of enzymatic machineries catalyzing metabolic reactions).

- processes.xml (definition of cell processes necessary to growth and maintenance).

For every file, we present the nodes that composes the XML structure. For every node, we show a class diagram that shows the node's attributes and the children node that it may/must contain. We provide a brief description about the relevance of the node in the RBA model.

2 `metabolism.xml`