Curation and annotation for BioModels Database, a resource of published quantitative models in biology

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INTRODUCTION

BioModels Database [1] (http://www.ebi.ac.uk/biomodels) is a free resource for storing, viewing and retrieving quantitative, kinetic models described in peer reviewed publications. It uses the XML based Systems Biology Markup Language (SBML) [2] for model storage and internal representation, but allows submission and export of models in various other commonly used formats. While models can be submitted publicly, submitted models are not directly included in the database, but checked and annotated both automatically and manually by the BioModels Database curation team. The database consists of two branches - one for manually curated and annotated models and one for non-curated ones. Standards for curation and annotation of quantitative kinetic models have been developed quite recently and the BioModels.net (http://biomodels.net) project is heavily involved in these efforts. Apart from the model database it also encompasses amongst others the MIRIAM [3] and the Systems Biology Ontology (SBO) [4].

ANNOTATION

The different elements of the models are extensively annotated with references to controlled vocabularies and links to other databases to allow for identification and search. Annotation is mostly carried out manually, although we plan on using some semiautomatic support in the future. Annotations in both branches:

- model submitter and creator contacts
- reference publication data
- creation and last modification dates
- Curated branch only:
  - MIRIAM annotations of different elements of the model
  - Systems Biology Ontology (SBO) annotations (SBO v2 and above)

Annotations are saved separately as entries in the database and in the model files. MIRIAM annotations are included in SBML files using RDF in annotation elements, SBO terms are directly inserted in the corresponding sboTerm attribute of the annotated element.

MIRIAM annotations

represent information as triplets:

- annotated element: eg. reaction Notch activation
- resource and identifier in form of a URN (Uniform Resource Name)
  - resource: eg. Gene Ontology
  - identifier: eg. Notch receptor processing (GO:0007220)
- BioModels.net qualifier: eg. isVersionOf

one or more URNs identify the data-type and the data-set, the BioModels.net qualifier indicates the relation between the annotated element and the URN. URNs following the MIRIAM scheme can be resolved to URLs using the MIRIAM Resources Web Services (http://www.ebi.ac.uk/miriam)

References