**Point-to-point list**

We have carefully read all reviewer comments and addressed each single one appropriately. In the following, we would like to discuss all reviewer comments in detail. Therefore, we colored the reviewer comments in red and our answers/actions in blue below.

Reviewer: 1

Comments to the Author

1) General comments

The authors describe a converter between the systems biology modeling formats of Biopax and SBML. It is good to learn that the developers of competing data formats are pooling their resources in order to simplify the modelling process. Furthermore, it appears clear that the work in developing such a conversion tool has been performed thoroughly and is described clearly in the manuscript. However, it is difficult for the lay reader to understand the necessity for the competing formats from the manuscript provided. Upon reading the paper, a number of questions remain that are listed below.

2) Specific comments for revision

a) major

Overall, it is unclear who the target audience for such a paper would be and why the converter is necessary. Without this additional contextualization, the manuscript itself reads as a rather dry technical note that would be of little interest to the general readership of the journal. Could the authors please therefore give more consideration to the following questions?

Why is a converter necessary? Are competing formats necessary?

You are absolutely correct with saying that the manuscript should point out why such a converter is necessary. SBML and BioPAX are competing formats in systems biology modeling. SBML is mostly used for quantitative modeling and BioPAX for qualitative modeling purposes. Due to this fact, many databases and programs were established for these two languages. For instance, MetaCrop or SABIO-RK exclusively provide their models with SBML but not with BioPAX. This is not so problematic because there exist several converters from SBML to BioPAX. For the other conversion direction, there exist just a few converters which deliver incomplete or wrong results. Following, the pathways from databases, like Nature Pathway Interaction Database or MetaCyc providing their models with BioPAX and not with SBML, cannot be easily used for SBML modeling. This is why a converter from BioPAX to SBML is so important. Another need for creating this converter is the development of the Qualitative Models extension which now allows the building of qualitative models with SBML, too.

We emphasized this circumstance in the introduction and changed it accordingly.

What can be done with an SBML model that could not be done with the original Biopax model? What software supports the SBML version?

The modeling language SBML allows the simulation of quantitative models while BioPAX is not able to store quantitative parameters. Following, simulations with BioPAX are not possible. Common used SBML simulators are for instance SBMLsimulator or COPASI, and a popular graphical SBML editor is CellDesigner. SBML Level 3 Version 1 is relatively new and COPASI is already able to read it. Following, it is just a matter of time that the other popular software tools will also be able to read and write SBML Level 3 Version 1.

Can the authors provide simulation results from both the Biopax version and the SBML version of one or more models to ensure that the conversion is not lossy and that the model represented by both formats is comparable?

Unfortunately, we present a converter for the translation from BioPAX into SBML and not a simulator. But the converted files can be used as a basis for further simulation experiments. We added an exemplary conversion of the ceramide signaling pathway on the official BioPAX2SBML homepage (<http://www.ra.cs.uni-tuebingen.de/software/BioPAX2SBML/>) with the original and the converted files. Additionally, we provide the conversion of the complete Nature Pathway Interaction Database on the following website: <http://www.cogsys.cs.uni-tuebingen.de/downloads/Qualitative-Models/>. This conversion is also linked in the paper. We hope this answers you question.

It is the opinion of the reviewer that without a clearly description of the context of the work, the manuscript appears to be more of a technical application note than a research article. Could the authors therefore please improve this area?

Indeed the methods part is extremely technical in contrast to all the other parts of the paper and, probably, the verbatim font emphasizes this impression. Our intention was to differentiate with this font between BioPAX instances, SBML instances and those instances used in the normal speech. For example the term ‘reaction’ can be used for a normal reaction but also for an instance in SBML. Following we use ‘reaction’ to denote a SBML instance and use ‘reaction’ if we describe a reaction.

Section 2.3.3 describes in detail the conversion of BioPAX Control elements to SBML reactions and transitions. We decided to include this detail because it is the most important part of our converter and most of the available converters do not address this problem properly.

Since, we see a deep need in shorten and facilitate our methods part we put the problem of the conversion of Control element, as well as Table 2 and Figure 2 in the supplementary part.

b) minor

The manuscript is clearly and carefully written, and as such, the only minor error appears to be the spelling mistake of “SMBL” in the final sentence of section 3.1.

Thank you, we corrected it.

Reviewer: 2

Comments to the Author

This is the best BioPAX to SBML converter available by far and clearly addresses a need in the community. I would like the thank authors for their contribution.

Thank you very much for the compliment. We are happy that we could make a contribution in this area.

I was very interested in reading the technical details about the conversion - but I am not sure if all of them are of interest to the general audience. I suggest moving the most technical parts to an Appendix.

Thank you for this good idea. We decided to shorten section 2.3.3 and put the more detailed parts in the appendix including also Table 2 and Figure 2.

I sometimes found the wording a little bit off : For example a translator can be "sophisticated" - but I think the translation process itself should be called "complex" and/or "complicated". There are several minor cases like this and I think the article can benefit from another round of editing.

Thanks for pointing that out. We changed the corresponding parts.

Reviewer: 3

Comments to the Author

This paper presents a useful tool for converting BioPAX models into SBML models using the qualitative modeling extension. The advantages of this tool over comparable tools already available is well described in Table 3. The main advantage being the ability to minimize the loss of information by leveraging the transition construct in the qual package to represent relationships that cannot be cleanly encoded as reactions.

I do have a few minor comments that I would like to see addressed:

1) Abstract, "erroneously converted to reactions", I find this comment too harsh. While you may disagree that with this approach, it may still capture the behavior. For example, one can easily imagine a repression relationship encoded using reactions perhaps with the addition of SBO terms.

Indeed that would be possible. Howerver, due to the existence of the Qualitative Models extension this approach would not be proper. But, you are write the formulation is a bit harsh and we changed it in the document to “Before the creation of qual, relations could not be properly translated into SBML or just by adding additional SBO terms on reactions which is not so proper.”.

2) Pg 1, col 2, line 2, semantic -> semantics

Thank you, we corrected it.

3) "The SBML core specification provides no possibility to define other relationships than concrete quantitative reactions." This is not accurate. SBML has more constructs than reactions, such as events, rules, constraints, etc. While these are quantitative, they are not reactions. You should mention these additional constructs supported by core SBML but it is okay to say they are not qualitative.

In the following, we would like…

* Paper ändern.

4) I may have missed it but I could not find a reference to Table 1.

The reference was listed in brackets with a reference in section 2.3.2 Step 2. You are absolutely right, that it can be easily overseen. Therefore we split the bracket content and made and extra sentence.

5) Not sure the purpose of qualitativeModel. Can't one just ignore the parts of the model which are from the qual package.

Of course it is possible to ignore the qualitativeModel. But all relationships which are no reactions are listed in this model.

SBML Plugins define a separate model for each plugin. Therefore, when using qual, a separate qual model is defined by the qual specification that handles exclusively all qual zeugs. This has, as you correctly stated, the advantage that one can ignore those parts and simply use the metabolic (i.e., species, reactions, etc) relations of the model.

6) I'm concerned about the need to say a species is a quantitative or qualitative species. It seems that a species may actually be involved in both types of interactions in a BioPAX model. Wouldn't it make more sense to make everything be species and when a species is used in a transition, it is a qualitative relationship for that species. One could then infer that a species is qualitative if it only appears in transitions, if this is actually important. The only alternative I see is to duplicate a species as a Species and QualitatitiveSpecies which is not elegant at all.

You are absolutely right that the first idea is to combine species and qualitativeSpecies to facilitate the models. Unfortunately, the qual and SBML core specification do not allow this convenience. The reason for not extending species to qualitativeSpecies is that species is quantitative and needs values like initialConcentration or initialAmount. In contrast the qualitativeSpecies MUST NOT have these values. If we would change this basic definitions in our conversion, we would produce invalid SBML.

Zitat von Andreas aus einer Mail*: “Although it might seem to be very convenient to let qualitativeSpecies*

*extend the "regular", i.e., quantitative, species, this would actually*

*imply that there are values available for its initialConcentration or*

*initialAmount. However, if you look into the qual draft, you'll see that*

*these values MUST NOT be present in a qualitative species. A qualitative*

*speciese IS NOT quantitative and can therefore not be derived from its*

*other counterpart. The only possibility to make use of core elements was*

*described by Lucian Smith, who proposed to let qualtitativeSpecies*

*extend parameter. A parameter in SBML core has just a value, which can*

*be anything. Actually, it would be much more handy to redesign the*

*species class in SBML core so that it would also just have a value and a*

*second attribute stating what the meaning of the value is, e.g.,*

*concentration, amount, level... As this will not happen because it would*

*cause to much effort (all existing tools would have to be changed), we*

*cannot let qualitativeSpecies use its quantitative counterpart.”*

7) Pg 2, Col 2, next to last paragraph, "can not" -> "cannot" and several other places as well.

Thanks, we fixed it.

8) Please make figure 2 larger.

Thank you for pointing that out. We improved the picture and made it larger.