Dear Sir or Madam,

We enclose a manuscript titled *“Toward standards for tomorrow’s whole-cell models”* for consideration for publication in your special issue on *Reproducibility in Biomedical Modeling*  in *Transactions on Biomedical Engineering*. The manuscript at hand discusses the path toward standards for whole-cell models, based on the experiences gained at this year's summer school on Whole-Cell modeling in Rostock, Germany.

In this manuscript, we motivate the importance of whole-cell modeling as a tool for biomedical research. In March 2015, we organised a summer school devoted to encoding the whole-cell model by Jonathan Karr et al in open standards and software tools. One goal of the summer school was the education of young scientists. A second, equally important goal, was the identification of shortcomings in current standards and tools for whole-cell modeling. We evaluated standards for modeling (Systems Biology Markup Language and its extensions), standards for simulation description (Simulation Experiment Description Markup Language), standards for graphical representation of networks (Systems Biology Graphical Notation), and standards for semantic annotation, and open software tools.

In summary, we believe that whole-cell modeling is a state-of-the-art technique that will benefit from greater support by open standards and software tools. In our manuscript, we summarise the shortcomings identified in a summer school dedicated to a specific whole-cell model, and we show paths towards future improvements. The manuscript is co-authored by the participants of the summer school.

Yours sincerely,

Dagmar Waltemath, University of Rostock, Germany

Jonathan Karr, Icahn School of Medicine at Mount Sinai, US

Falk Schreiber, Monash University, Australia

on behalf of the participants of the 2015 Summer School on Whole Cell modeling.