Dear Editors of BMC Biology,

Please find enclosed our manuscript entitled “Modelling with ANIMO: between Fuzzy Logic and Differential Equations” by Stefano Schivo and Jetse Scholma et al., which we would like to submit for publication as an original paper in BMC Biology.

In this manuscript, we compare our software ANIMO (Analysis of Networks with Interactive Modelling,[1-3]) with existing modelling languages and tools. The approach behind ANIMO is founded on a series of abstractions that

1. reduce the number of parameters involved, and
2. emphasize cause-and-effect relationships between molecular species.

Because of i), ANIMO is less parameter-intensive than differential equation models, and because of ii) ANIMO is more precise than logic-based models. For this reason, we position ANIMO between the two modelling approaches.

ANIMO is implemented as a plug-in to Cytoscape, which contributes to the accessibility of the tool, as Cytoscape is already widely used in biology for visualization of static network topologies. The user-input is automatically translated into an underlying formal model, which makes the tool accessible without requiring additional knowledge on the underlying formalism.

Our manuscript is interesting to the broad audience of BMC Biology for two main reasons: ANIMO allows to easily add dynamic information to normally static biological networks, and its modelling approach has the potential to be useful in a wide variety of cases. This makes us believe that our paper would be an appropriate addition to the “Beyond Mendel: modeling in biology” series.

We appreciate your consideration of reviewing our manuscript for publication in BMC Biology.

Sincerely, on behalf of all co-authors,

Rom Langerak

Formal Methods and Tools

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[1] S. Schivo, J. Scholma, B. Wanders, R.A. Urquidi Camacho, P.E. van der Vet, H.B.J. Karperien, R. Langerak, J.C. van de Pol, J.N. Post (2014) *Modelling biological pathway dynamics with Timed Automata*. IEEE Journal of Biomedical and Health Informatics, 18 (3). pp. 832-839.

[2] J. Scholma, S. Schivo, R.A. Urquidi Camacho, J.C. van de Pol, H.B.J. Karperien, J.N. Post (2014) *Biological networks 101: computational modeling for molecular biologists*. Gene, 533 (1). pp. 379-384.

[3] S. Schivo, J. Scholma, H.B.J. Karperien, J.N. Post, J.C. van de Pol, R. Langerak (2014) *Setting Parameters for Biological Models With ANIMO*. In: Proceedings 1st International Workshop on Synthesis of Continuous Parameters, 6 Apr 2014, Grenoble, France. pp. 35-47. Electronic Proceedings in Theoretical Computer Science 145.