

Interactive comment on “Flux balance modelling to predict bacterial survival during pulsed activity events” by Nicholas A. Jose et al.

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Dear Referee,

Thank you for your response and apologies for the issues regarding the SBML file. Please find attached a version that should run without errors in R. Modifications were minor. The number of unique genes does not reflect the number of total genes in the model due to redundancy in annotation, where more than one gene may be associated with the same function.

Please also note the supplement to this comment:

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<https://www.biogeosciences-discuss.net/bg-2017-403/bg-2017-403-AC2-supplement.zip>

Interactive comment on Biogeosciences Discuss., <https://doi.org/10.5194/bg-2017-403>, 2017.

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