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Interactive comment

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

Anonymous Referee #1

Received and published: 31 October 2017

The authors present a thoroughly documented manual reconstruction of Microcoleus vaginatus, a terrestrial cyanobacterium adapted to arid environments. The reconstruction is experimentally validated by comparing predicted CO2 and storage polymer production & consumption in the light and dark to measured values. The metabolic model is then exploited to predict glycogen concentration in M. vaginatus under different climate scenarios. This is solid work and I have only a few comments.

What is the number and percentage of genes with unknown functions in M. vaginatus?

How well do the predicted fluxes during light and dark agree with previous results on gene expression in M. vaginatus-dominated BSCs?

A delicate point in FBA is the definition of the objective function. The Materials &



Discussion paper



Methods part does not state clearly which function(s) is (are) optimised - is it biomass formation or flux through polymer-forming reactions or both? In case of biomass, how was the biomass formation reaction obtained? How well does the predicted light and dark growth rates (corresponding to the flux through the biomass formation reaction) agree with measured growth rates?

Is it known whether the ratio of day/night wetting events or day length influences the distribution of M. vaginatus in deserts and arid environments?

The authors should clarify whether or not upper and lower flux bounds are constrained by measurements when predicting flux through biopolymer reactions in the dark (Table 3). How well is CO2 production and biopolymer consumption predicted without constraining flux boundaries with measurements?

It is curious that M. vaginatus grows so slowly (weeks) and appears to miss vital reactions. Is it possible that it relies on near-obligate mutualistic partners in nature?

Please also share the metabolic model as an SBML file. Not everyone has access to Matlab.

I. 67: a terrestrial cyanobacteria -> a terrestrial cyanobacterium I. 249: which a possible reason -> which is a possible reason I. 264: there is either a 12-hour wetting event -> or?

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