

Supplement to Memote: A community driven effort towards a standardized genome-scale metabolic model test suite

today

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To simplify interpretation the following figures are grouped by the sections of their corresponding test cases as they appear in a snapshot report. The code that was used to generate the data and figures has been deposited on GitHub <https://github.com/biosustain/memote-meta-study>.

0.1.1 Tested models

In order to respect the limited resources on the DTU high performance computing infrastructure, we set a maximum time limit for running the memote test suite. This introduced a bias against large models. Additionally, certain models failed the testing procedure. In the following we tabulate the total size of the collections as well as the final number of tested models. The results are shown in Table 1.

[[1]]

Table 1: Number of tested models.

Collection	Number of Models	Tested Models	%
AGORA	818	801	97.9
CarveMe	5587	5511	98.6
Path2Models	2641	2641	100.0
KBase	1637	1632	99.7
BiGG	36	36	100.0
Ebrahim et al.	83	80	96.4
OptFlux Models	100	79	79.0

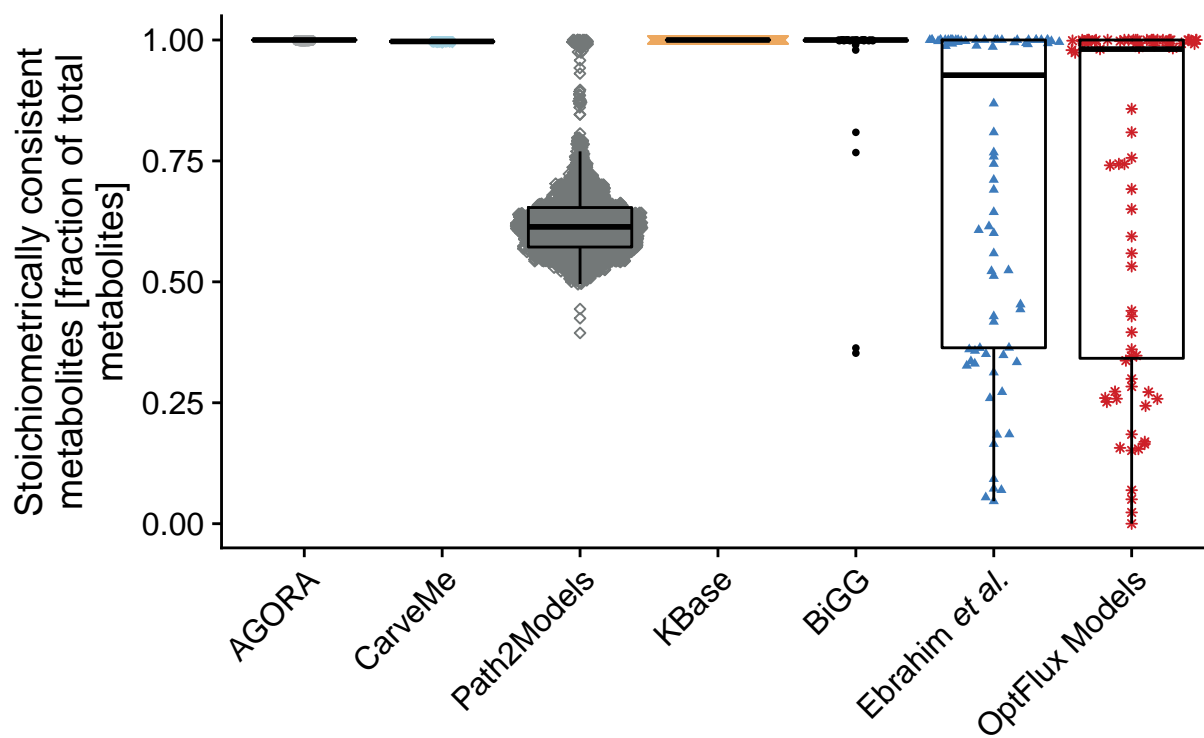


Figure 1: Stoichiometric consistency