S2 Artificially reduced *B. subtilis* draft networks

We have repeated the proof of pinciple study performed for *E. coli* in the main article also for the Bacterium *B. subtilis*. We used an old version (November 10, 2006) of the Tier 3 network *bsub* from BioCyc. The target metabolites were the same generic targets as used for *E. coli*, the nutrient were taken from [1] and are listed in Supporting Text S6. In Fig. 1 the effect of including sequence information is shown.
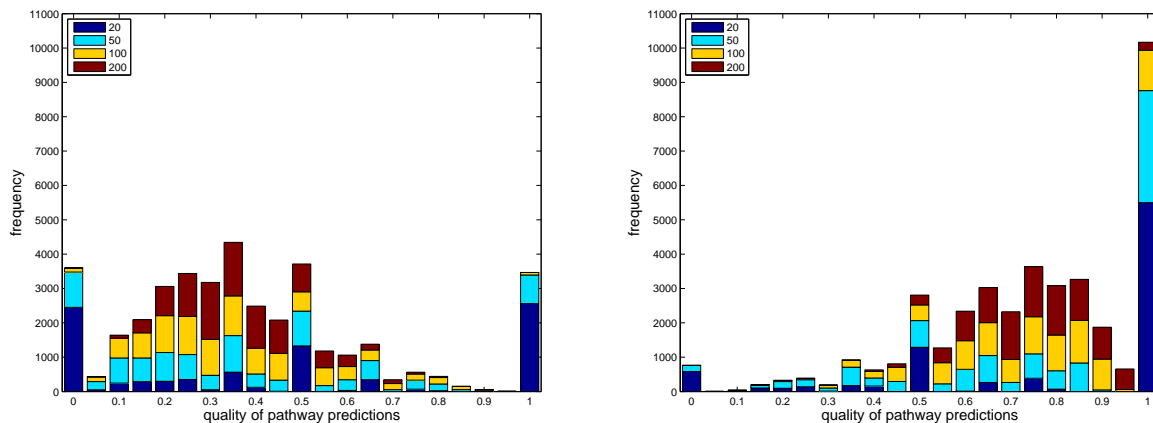

Figure 1: Histogram of the quality of predicted extensions for *B. subtilis*. (left) Extensions have been calculated without including sequence information. (right) Extensions were determined such that reactions with a high probability that coding enzymes are present in the genome of *B. subtilis* are preferentially included. The quality is measured by the fraction of correctly predicted reactions in a calculated extension. The bars are stacked indicating the contributions of pathway predictions obtained for different numbers of removed reactions.

References

[1] J. Leitch and P. Collier, *Letters in Applied Microbiology*, 1996, **22**, 18–20.