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Corrigendum

MIRA: mutual information-based reporter algorithm for metabolic networks

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The authors of the above article would like the following to be noted. Results reported for the reporter algorithm (RA) in the Results section are raw z-scores per metabolite, normalized by subtracting the sample mean and dividing by the sample standard deviation. Using the background correction as described in the original scoring scheme (Ideker *et al.*, 2002; Patil and Nielsen, 2005) removes the hub metabolite bias we claim for the RA (for both normalization by k and $\sqrt{k}$). This affects only our comparisons with RA, and MIRA's results are not changed. The background correction improves the empirical significance of the RA as shown in Figure 5A and C. After the background correction, RA is among the top three permutations. MIRA still performs better but with a smaller margin than shown in Figure 5. We have updated the lists of reporter metabolites (for RA) in the supplementary file.

References

Ideker,T. *et al.* (2002) Discovering regulatory and signaling circuits in molecular interaction networks. *Bioinformatics*, **18**(Suppl. 1), 233–240.

Patil,K.R. and Nielsen,J. (2005) Uncovering transcriptional regulation of metabolism by using metabolic network topology. *Proc. Natl Acad. Sci. USA.*, **102**, 2685–2689.