

Correction

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Permutation test for periodicity in short time series data

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In our paper reporting the permuted-time test for periodicity [1], the table in Figure 4 and the text of the Discussion should be modified as follows: The % of genes detected by Tu *et al.* [2] should be reported as 57.2% rather than 38.1% as currently reported; thus the difference between the methods should be reduced (to 84.7% vs. 57.2%). The discrepancy results from the fact that the absolute number of 3552 transcripts was identified from a smaller subset of pre-selected expression profiles corresponding to known yeast genes, while the Pt-test was applied to the entire set of probesets. We would like to thank two of the co-authors of the Tu *et al.* [2] publication, Drs. Rowicka and Kudlicki (UT-Southwestern), for bringing this to our attention.

References

1. Ptitsyn AA, Zvonic S, Gimble JM: **Permutation test for periodicity in short time series data.** *BMC Bioinformatics* 2006, **7(Suppl 2)**:S10.
2. Tu BP, Kudlicki A, Rowicka M, McKnight SL: **Logic of the yeast metabolic cycle: temporal compartmentalization of cellular processes.** *Science* 2005, **310(5751)**:1152-1158.