Corrigendum

Identifying periodically expressed transcripts in microarray time series data

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The authors are grateful to Professor Susan R. Wilson (Australian National University, Canberra) and Professor William Dunsmuir (University of New South Wales) for bringing the following error in Equation (5) to our attention: for sample size N even the intensity of the peak belonging to the Fourier frequency π must not be included in the calculation of the g-statistic. Correspondingly, the summation in the denominator and the maximization in the numerator of Equation (5) runs through indices k=1 to k=[(N-1)/2], rather than to k=[N/2] as stated in our paper. Accordingly, we have corrected the implementation of our algorithm in the R package 'GeneCycle' (versions 1.0.4 and later), which is available from http://cran.r-project.org/web/packages/GeneCycle/.

The above change affects the evaluation of statistical significance of time series with an even number of time points only. For the readers' convenience, we provide here an update of Table 2. Note that the revised estimates of the number of periodic genes are more conservative under the correct computation of the g-statistic. This is a consequence of the implicit reduction in sample size due to the removal of the π frequency.

Table 1. Datasets analyzed in this paper and results of FDR test

Cell type	Experiment	N	G	C	C/G~%	Source
Yeast	cdc15	24	4289	221	5.2	(Spellman et al., 1998)
Yeast	cdc28	17	1365	27	2.0	
Yeast	alpha	18	4415	170	3.9	
Yeast	elution	14	5695	72	1.3	
C. crescentus	bacteria	11	1444	45	3.1	(Laub et al., 2000)
Human Fribroblasts	N2	13	4574	0	0	(Cho et al., 2001)
Human Fribroblasts	N3	12	5079	0	0	
Human HeLa	score1	12	14728	2	0	(Whitfield <i>et al.</i> , 2002)
Human HeLa	score2	26	15472	72	0.5	
Human HeLa	score3	48	39724	4250	10.7	
Human HeLa	score4	19	39192	57	0.1	
Human HeLa	score5	9	34890	0	0	

Notation: N is the sample size, G the total number of genes, C the number of periodic genes that are statistically significant for a FDR level of q = 0.05.