Methods	Pros	Cons
LS	Can effectively handle missing values	 Loses its detectability when applied to datasets with low sampling resolution. U-shaped p-values distribution Sensitive to outliers and non-sinusoidal shapes [1] Assumption of Gaussian noise on the error term [1]
ARSER	High reproducibility	 Limited to datasets with no replicates, uneven samplings, or missing values Sensitive to noise (citation)
JTK_CYCLE	 Effective in controlling for false positives Robust to outliers [2] 	 Ineffective to asymmetric waveforms U-shaped p-values distribution Base on simulation, very sensitive to low sampling resolution Sensitive to noise High false negatives Low reproducibility
RAIN	 High recall Effective in detecting asymmetric waveforms High reproducibility 	 High false positives in detection U-shaped p-values distribution Underpowered in detecting datasets with replicates Computationally intensive with increasing sampling resolution
eJTK_CYCLE	 uniform distribution of nominal p-values Can effectively detect data with low sampling resolution or replicates Most effective in detecting asymmetric waveforms Robust to noises 	 Unable to test different periods simultaneously Cannot handle missing values and uneven samplings
MetaCycle	 Not restricted by data type High recall Offset the disadvantages of one method by the other two methods. Self-select one or multiple methods for analysis. 	 U-shaped p-values distribution Results are integrated from different methods, thus it is easily influenced by the poor performance of one method.
BIO_CYCLE	 The most effective in detection while controlling for false positives Most robust to data with high noise, uneven sampling, and low sampling resolutions. High performance with replicates High and stable precision High computational efficiency by reusable fitted models. 	 Require extensive time to train the DNN model Handle missing values only if data have replicates and the missingness only pertains to part of the replicates. Low reproducibility

^[1] Glynn EF, Chen J, Mushegian AR: Detecting periodic patterns in unevenly spaced gene expression time series using Lomb-Scargle periodograms. *Bioinformatics* 2006, **22:**310-316.
[2] Wu G, Zhu J, Yu J, Zhou L, Huang JZ, Zhang Z: Evaluation of five methods for genome-wide circadian gene

identification. J Biol Rhythms 2014, 29:231-242.