

SEMINARIO

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CircaFMM: a flexible statistical framework for circadian rhythmicity detection in transcriptomics

Abstract: Large-scale transcriptomic datasets provide a unique challenge for detecting circadian rhythmicity when signals are weak, sampling is irregular, and genes exhibit asymmetric expression profiles. Classical Cosinor-based methods perform well under ideal conditions, but often are too rigid to accommodate these common scenarios. To address these shortcomings, we develop CircaFMM for circadian rhythmicity detection based on the single-component Frequency Modulated Möbius (FMM) model [1]. This flexible framework defines rhythmicity as time dependence induced by the Möbius phase parameter, so that the non-rhythmic null corresponds to a time-invariant mean profile. The resulting non-regular test combines regularized estimation, time-density weighting, and bootstrap calibration of a weighted likelihood-ratio-type statistic. Using simulated data with time-points mimicking common study designs, we show controlled type-I error and improved empirical power over the classical Cosinor F-test for asymmetric waveforms. When applied to the GTEx-13T postmortem transcriptomic dataset, CircaFMM identified canonical clock genes, circadian pathways, and additional rhythmic candidate genes with lower signal-to-noise ratio and non-sinusoidal temporal profiles.

Joint work with Itziar Fernández and Yolanda Larriba.

Availability and implementation:

CircaFMM is available at https://circafmm.shinyapps.io/circafmm_shinyapp/, with source code at <https://github.com/FMMGroupVa>.

[1] C. Rueda, Y. Larriba, and S. D. Peddada. Frequency-modulated Möbius model accurately predicts rhythmic signals in biological and physical sciences. *Scientific Reports*, 9(1):18701, 2019.

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