

Conference Abstracts

Robust Circadian Transcriptomic Analytics to Reduce Bias and Disparities in Cancer Genomics Studies

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Background

Disruption of circadian regulation is increasingly implicated in cancer initiation, progression, immune evasion, and treatment response. However, most circadian transcriptomic analyses rely on statistical methods that inadequately account for complex study designs, repeated measurements, and heterogeneous populations. These limitations disproportionately affect cancer studies involving underrepresented populations, where smaller sample sizes, irregular sampling, and higher biological variability can exacerbate analytic bias and reduce reproducibility. There is a critical need for implementation-ready analytic frameworks that improve equity and reliability in cancer circadian genomics.

Methods

We developed and implemented a suite of statistically rigorous circadian and differential circadian analysis methods based on hierarchical and mixed-effects modeling frameworks, including likelihood-based and Bayesian approaches. These methods explicitly model repeated measurements, incorporate prior biological knowledge, and control false discovery rates under complex experimental designs. We applied these tools to relevant transcriptomic datasets, including tissue-related gene expression

profiles, to evaluate robustness across heterogeneous sampling schemes representative of real-world clinical and population-based cancer studies.

Results

Compared with commonly used circadian analysis approaches, our implementation demonstrated improved statistical power, superior false discovery rate control, and increased stability of circadian biomarker detection under sparse or irregular sampling. Importantly, these gains were most pronounced in scenarios mimicking under-resourced or small-cohort studies, highlighting the potential to reduce analytic bias that contributes to disparities in cancer genomics research. The framework helps identify reproducible circadian alterations in cancer-associated and immune-regulatory pathways that are missed by standard methods.

Conclusion

This work provides an implementation science framework for equitable circadian transcriptomic analysis in cancer research. By improving analytic validity in heterogeneous and resource-limited study settings, our approach supports more inclusive biomarker discovery and lays the foundation for fairer precision oncology and chronotherapy strategies.