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Methodological limitations of linear parametric analysis in biological research: A critical review of NEO-Five personality traits and sleep characteristics study

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ABSTRACT

This paper critically examines the methodological approach employed in Wang et al.'s systematic review and meta-analysis of NEO-Five Personality Traits and sleep characteristics. We identify significant concerns regarding the use of linear parametric methods (Pearson's correlation and meta-regression) in analyzing potentially nonlinear and nonparametric biological data. The paper demonstrates how these analytical tools can lead to distorted results and erroneous conclusions when applied to complex biological systems. We propose alternative nonlinear nonparametric methods, including Spearman's correlation and Kendall's tau for monotonic relationships, and Mutual Information analysis and Effective Transfer Entropy for nonmonotonic interactions, to better capture the intricate relationships in biological research without restrictive assumptions about linearity or data distribution.

The relationship between personality traits and sleep characteristics was systematically reviewed and meta-analyzed by Wang et al. [1]. Their methodology primarily relied on Pearson's correlation coefficients to quantify the association strength between NEO-Five Personality Traits and sleep outcomes, particularly focusing on sleep quality and duration. The study further employed meta-regressions, which are linear parametric methods, to analyze continuous variables, such as age demographics, gender distribution, and the severity of psychological symptoms including depression and anxiety [1]. Meta-regression assumes a linear relationship between study-level covariates and effect sizes, while also assuming normal distribution of residuals, making it both a linear and parametric method.

This paper raises methodological concerns regarding the use of linear and parametric methods such as Pearson's correlation and meta-regressions. These concerns stem from the fundamental mismatch between the analytical tools chosen and the potentially nonlinear, nonparametric nature of biological data being analyzed [2–7].

Linear methods assume a straight-line relationship between variables, where changes in one variable correspond to proportional changes in another variable. Parametric methods assume data follows specific probability distributions (typically normal distribution) with fixed parameters such as mean and standard deviation. However, biological systems often exhibit nonlinear patterns, where relationships may be curved, exponential, or follow other complex patterns. Similarly, biological data frequently violates parametric assumptions, displaying asymmetric, skewed, or multimodal distributions that cannot be adequately characterized by simple parameters.

The application of linear parametric tools (both Pearson's correlation and meta-regression) to nonlinear nonparametric biological data can lead to several distortions [2–7]. Linear methods may oversimplify curved relationships, missing important patterns and underestimating or overestimating effects in different regions of the data. Parametric analyses of non-normally distributed data can produce biased estimates, incorrect confidence intervals, and invalid p-values. Meta-regression, being both linear and parametric, may particularly misrepresent relationships when the underlying associations between study-level characteristics and effect sizes are nonlinear or when effect sizes are not normally distributed. These distortions can cascade through the analysis, potentially leading to false conclusions about the strength, direction, or existence of relationships between variables.

To address these methodological limitations, this paper recommends alternative statistical approaches. For examining bivariate monotonic relationships, nonlinear nonparametric methods such as Spearman's correlation and Kendall's tau (both with p-values) are suggested [8]. For more complex, nonmonotonic interactions involving multiple variables, advanced techniques such as Mutual Information (MI) analysis [9] and Effective Transfer Entropy (ETE) are recommended [10]. These methods can better capture the intricate relationships often present in biological systems without making restrictive assumptions about linearity or data distribution.

Consent to participate

Not applicable.

Ethics approval

Not applicable.

Consent for publication

Not applicable.

Availability of data and material

Not applicable.

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Code availability

Not applicable.

AI use

Not applicable.

Authors' contributions

Yoshiyasu Takefuji completed this research and wrote this article.

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Declaration of competing interest

The author has no conflict of interest.

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