

November 4, 2024

Dear CIMB Editorial Board,

I am pleased to submit my manuscript entitled “*tidyplate: A Versatile R Package for Microplate Data Transformation*” for consideration for publication in *Current Issues in Molecular Biology*. In this article, I present **tidyplate**, a novel R package that streamlines the data handling of microwell plates used in high-throughput biomedical assays. Microtiter plates are ubiquitous in various experimental workflows, such as tissue culture, ELISA, PCR, and other assays integral to research and clinical diagnostics. Despite their popularity, handling and transforming the data generated from these plates into formats suitable for analysis can be time-consuming and error prone. The **tidyplate** package addresses this gap by providing an efficient, reproducible tool for transforming and exporting plate data as tidy data compatible with a wide range of analytical applications. The highlights of **tidyplate** include:

1. **Versatile Data Transformation:** tidyplate converts data from common microplate formats (6-well to 1536-well plates) into tidy data, facilitating seamless integration with downstream data analysis workflows in R and Python.
2. **Error-Checking and Data Validation:** The package’s validation functions ensure that input files adhere to necessary structural standards, reducing errors early in the analytical process.
3. **Export and Back-Transformation:** Users can back-transform tidy data into original plate layouts in CSV or Excel formats, which is particularly beneficial for researchers who need to share or archive data in its original structure.

My manuscript provides a comprehensive overview of these functionalities, with examples illustrating how **tidyplate** simplifies data management for high-throughput microplate assays. I believe that **tidyplate** can be an invaluable resource for the journal's readership, especially those working in molecular biology, bioinformatics, laboratory automation, and clinical research. By streamlining the data processing pipeline, this package aligns with the journal’s mission to publish innovations that enhance research efficiency and data integrity.

Thank you for considering our manuscript for publication in *Current Issues in Molecular Biology*. I look forward to your feedback and would be happy to make any modifications necessary to align with the journal’s standards.

Regards,
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