This manuscript provides a valuable contribution to the field by presenting SGSEA, an R package and Shiny app that effectively integrates survival data into gene set enrichment analysis. This innovative approach enhances the ability to identify pathways associated with clinical outcomes, addressing a critical need in functional pathway analysis. The methodology is well-documented, and the comparisons with standard GSEA demonstrate the complementary insights provided by SGSEA.

While the work is strong overall, there are areas that could be improved. Highlighting the unique strengths and potential limitations of SGSEA relative to traditional GSEA would strengthen the manuscript. Additionally, refining figure captions and providing a more accessible explanation of the concepts for readers less familiar with GSEA and survival analysis would broaden its appeal. These revisions, while minor, will enhance the clarity and impact of this important work.

Thank you for the opportunity to review this thoughtful and innovative submission!