 San Sebastian, April 21nd 2023

Dear Editor,

We are pleased to submit our manuscript entitled "GPUmatrix: Seamlessly harness the power of GPU computing in R" for publication in Bioinformatics.

Our team developed GPUmatrix to address the lack of transparent and well-maintained packages that harness the power of GPU computing using R, the most widely used programming language in the field of bioinformatics. We have successfully developed an R package hosted on CRAN (https://cran.r-project.org/web/packages/GPUmatrix) that connects R to the GPU to efficiently perform statistical and linear algebra calculations. GPUmatrix mimics the behavior of the Matrix package and extends R to use the GPU in computations. As a result, users with little or no experience with computational data structures can perform algebraic calculations using the GPU without extensive training. GPUmatrix relies on R's Tensorflow or Torch packages to perform operations on the GPU thanks to their use of tensors.

In this manuscript, we provide a detailed description of the features and functionalities of GPUmatrix, as well as a tutorial on how to use it effectively (package documentation).

We believe that our manuscript will be of great interest to bioinformatics readers interested in using GPU computing for efficient statistical and linear algebra calculations. Our package fills a gap in current computational biology research by providing an easy-to-use tool that can significantly accelerate data analysis processes. We show how it provides a computational advantage over the basic methods implemented by R for certain operations.

Moreover, this work has broader implications than just computational biology research. The ability to use GPUs for efficient computation is becoming increasingly important in many fields, including machine learning, data science, and high-performance computing. Our package makes a valuable contribution to this goal by enabling researchers with little experience in GPU programming to take advantage of its benefits.

We hope that you will find our manuscript suitable for publication in Bioinformatics.

Thank you for your consideration.

Sincerely,

Prof. Angel Rubio and all the authors.

Vice-head of the Department of Bioengineering and Sciences.

TECNUN. University of Navarra.