Dear Editor,

We are submitting our manuscript entitled “**PorthoMCL: Parallel orthology prediction using MCL for the realm of massive genome availability**” for the consideration of publishing in Bioinformatics.

Finding orthologous genes among multiple sequenced genomes is a primary step in comparative genomic studies. With the availability of exponentially increasing number of sequenced genomes, comparative genomics becomes more powerful than ever for genomic analysis. However, the very large number of genomes needing to be analysed makes conventional orthology prediction methods incapable for the tasks. Thus an ultrafast tool is urgently needed. He present PorthoMCL, an improved version of OrthoMCL with parallelization, for finding orthologous genes among a very large number of genomes. PorthoMCL is a platform independent, scalable and freely available package that can be run on a wide range of high performance computing clusters and cloud computing platforms. We demonstrate that PorthoMCL is capable of taking such a challenge by applying it on all the annotated bacterial genomes obtained from GenBank.

Thank you for your consideration.

Sincerely,

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