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I am pleased to submit an original article entitled “Mothulity facilitates 16S/ITS amplicon diversity analysis” by Dariusz Izak, Agnieszka Gromadka and Szymon Kaczanowski for your consideration for publication in the Current Protocols in Bioinformatics. All the authors have run a number of analyses of 16S/ITS amplicon supporting bacterial/fungal biodiversity research. Our work responds to the need for rapid delivery of publication-quality results. In this manuscript, we describe the ease of installation and set-up of our software. Thanks to Mothulity, a complete analysis can be run with a single short command. Few projects in our institution have benefited from using it (manuscripts on this topic are in progress). We believe that this manuscript is appropriate for inclusion in Current Protocols in Bioinformatics because Mothulity is a novel interface, that significantly reduces hands-on time while ensuring best operational procedures. This manuscript has not been published and is not under consideration for publication elsewhere. We have no conflicts of interest to disclose.

Thank you for your time and consideration.

Sincerely,

Dariusz Izak

We would like to suggest potential reviewers who are the Mothur users in their daily scientific work.

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