Post-assessment InterBRC Micobiome

14 responses

Publish analytics

Please indicate your level of ABILITY with each of the following concepts, tools, or approaches.

Analysis of amplicon sequencing datasets

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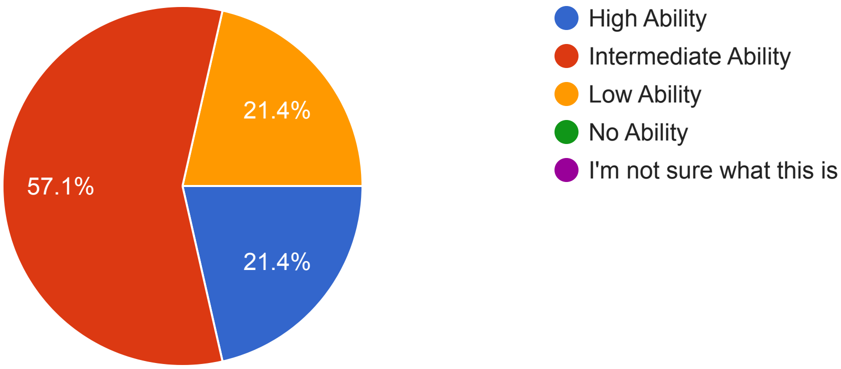

Identifying the distribution of abundance of ASVs in 1000 samples

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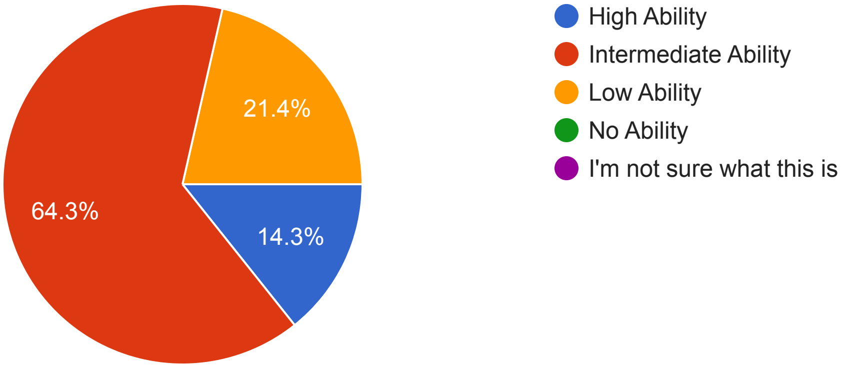

Identifying the prevalence of ASVs in 1000 samples

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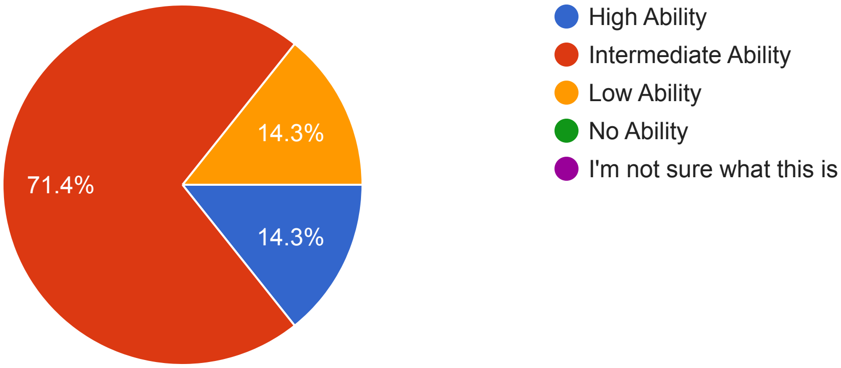

Identifying methods to define core microbiome

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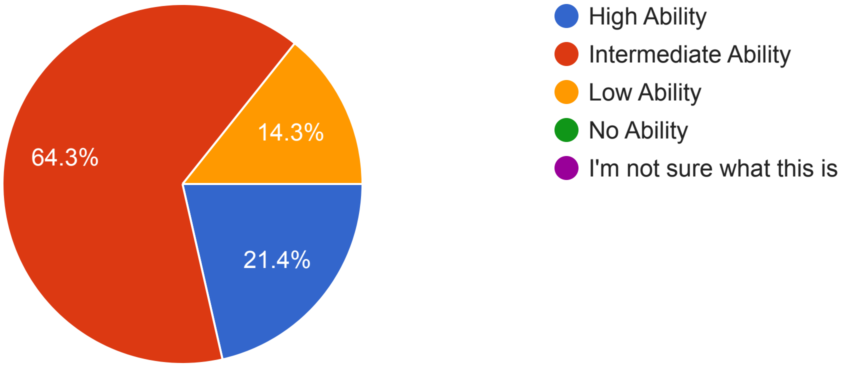

Implementing methods to identify core microbiome

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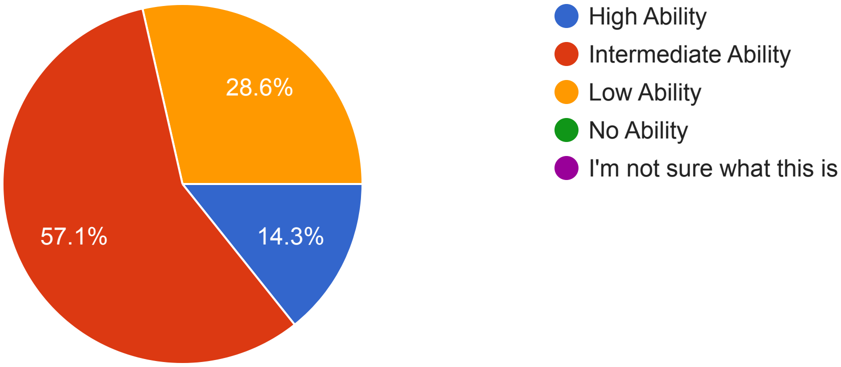

Characterizing the core microbiome and comparing it to the non-core microbiome

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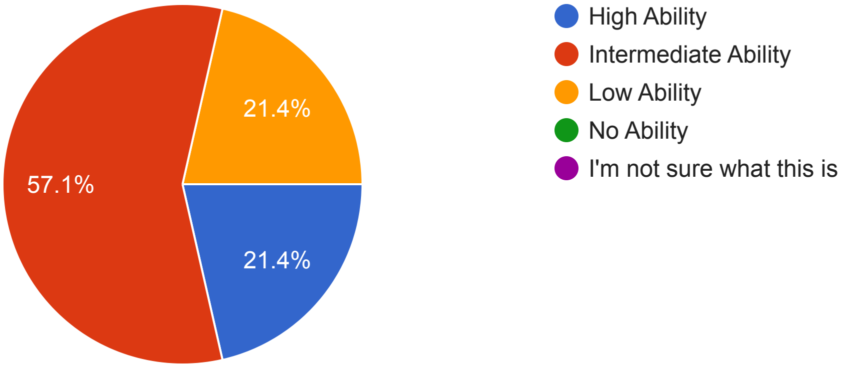

What topics would you like to learn about in our next collaboration?

14 responses

NA

New directions and experiments.

Core analysis of BRC's feedstocks

It was great! Thank you!

Would like to dive into "functional microbiome" topics

functional aspect

More about basic R script

the isolates

n/a

Discussions about data generation (such as primer choice), handling unknowns, and extensions to eurkaryotes

Standardizing sampling/sequencing methods to make the data easier to compare. Also the steps before getting to R, like Qiime or DADA.

Overall gaps in InterBRC research.

Would you recommend this workshop to a colleague?

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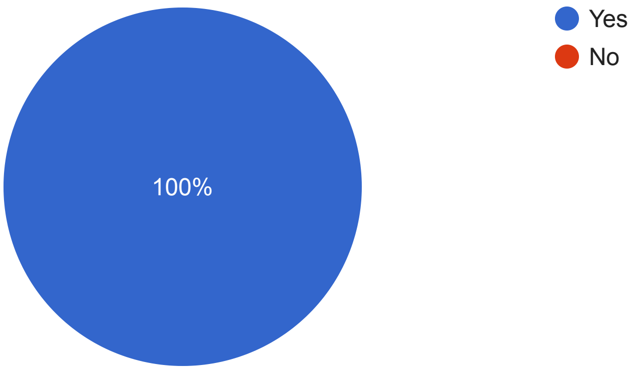

Do you have any other comments?

14 responses

NA

This workshop was great for building relationships across BRCs and developing new collaborations going forward.

More days for the workshop

Thank you!

Very well done. I greatly enjoyed this workshop

na

I loved the workshop! Good Job!

No!

n/a

Tutorial code was easy to follow, even for someone less familiar with R, and introduced the topic well

Great workshop, I had a lot of fun!

N/A