

# Preassessment InterBRC Micobiome

16 responses

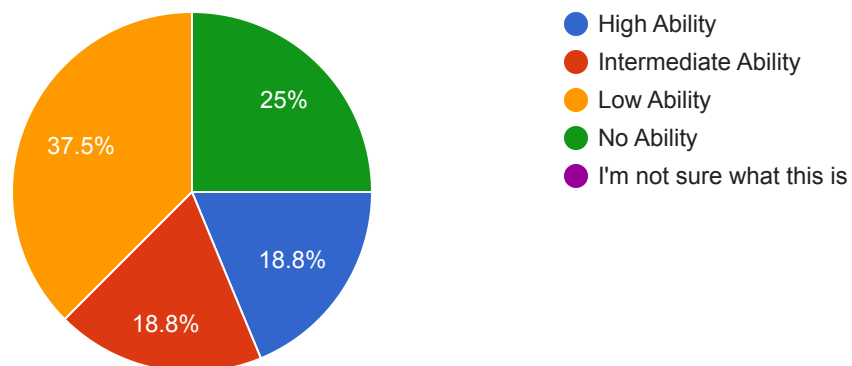
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Please indicate your level of ABILITY with each of the following concepts, tools, or approaches.

## Analysis of amplicon sequencing datasets

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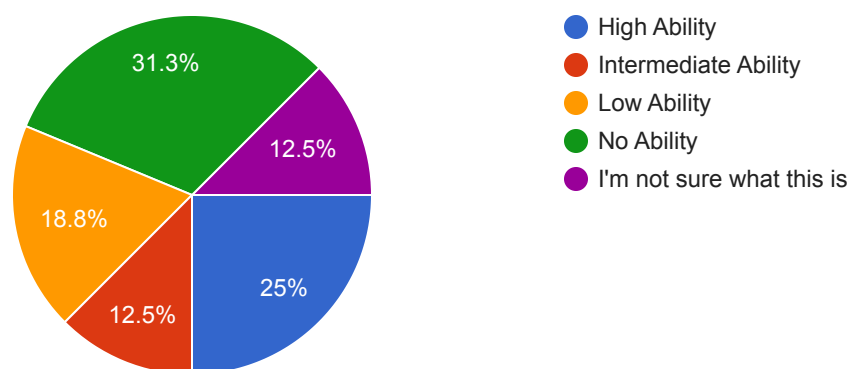
16 responses



## Identifying the distribution of abundance of ASVs in 1000 samples

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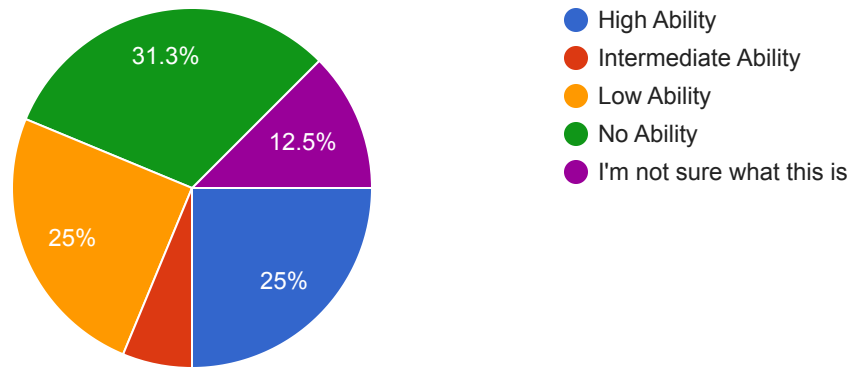
16 responses



## Identifying the prevalence of ASVs in 1000 samples



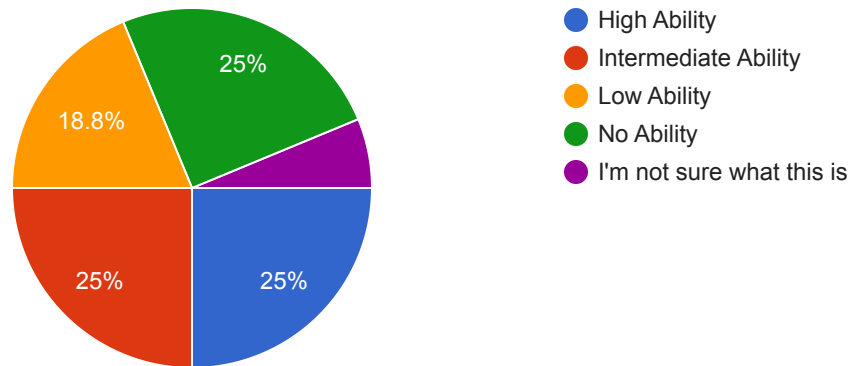
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## Identifying methods to define core microbiome



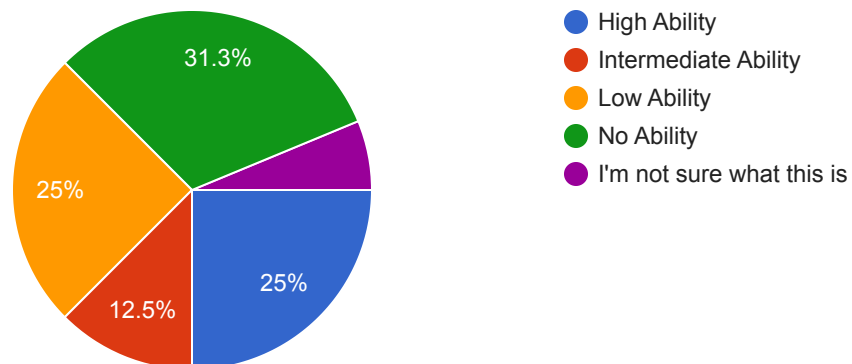
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## Implementing methods to identify core microbiome



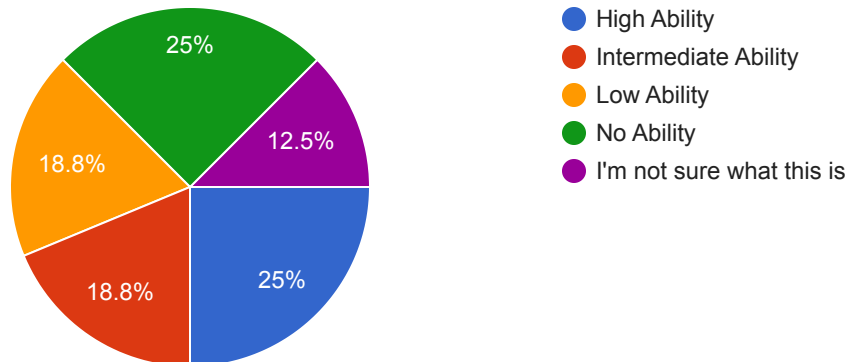
16 responses



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

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16 responses



What are topics you would like to discuss or methods you would like to learn in our tutorial (noting that it is only 3 hours long)

16 responses

The agenda looks like it's mainly focused on R processing of OTU/ASV tables, but if possible I'd also love a brief introduction on the earlier processing steps for .fasta files, like Qiime2, QC/trimming, etc.

shotgun and amplicon sequence data processing

Standardizing core microbiome(s) across datasets /w abundance-occupancy distribution(s).

How can we package the tooling for broad distribution / automation?

I have very little hands-on experience in analyzing microbiome data. I look forward to learning a lot, but the workshop should not be tailored to my needs.

How to begin working with 16S sequencing datasets using phyloseq

New methods for defining core microbiome

I am new to this field of science and open to gain any knowledge i can get from this

The importance of knowing the core microbiome

Basic R

N/A

Defining core microbiome

.

Learn basics and begin to identify important microbes for modeling



Do you have any other comments?

16 responses

No

no

N/A

Nope, looking forward to the workshop!

NA

Looking forward to the workshop

Thank you for organizing the workshop!

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I look forward to learning a lot of new things

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