

Reproducibility Analysis

A comprehensive metagenomics framework to characterize organisms relevant for planetary protection

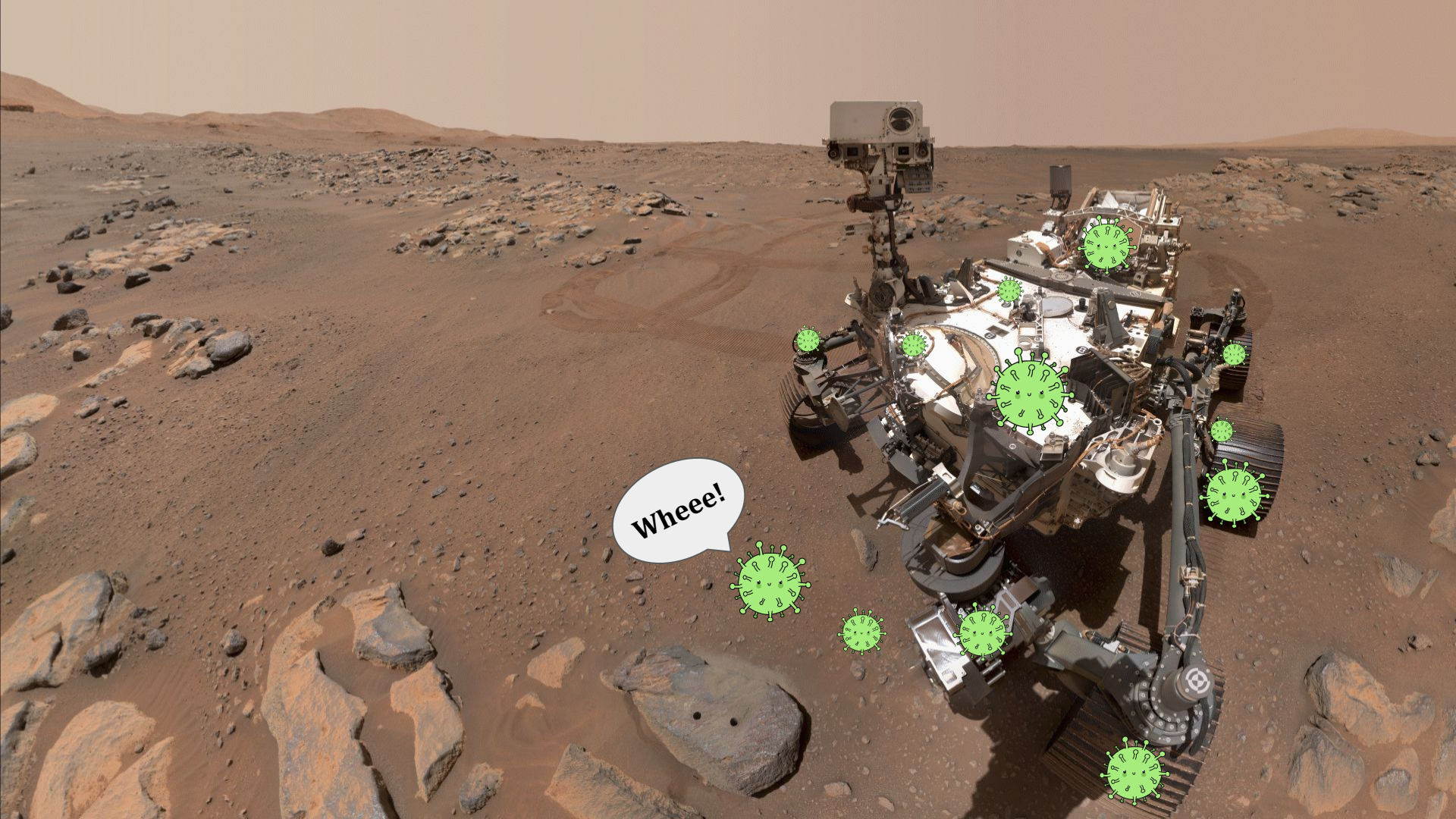
Annaliese Meyer and Matt Baldes
Environmental Bioinformatics
MIT-WHOI, 2021



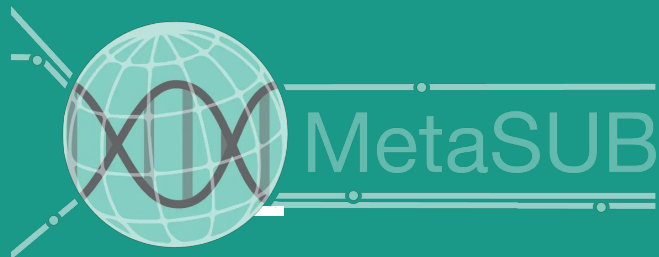
A comprehensive metagenomics framework to characterize organisms relevant for planetary protection



David C. Danko^{1,2†}, Maria A. Sierra^{1,3†}, James N. Benardini⁴, Lisa Guan⁴, Jason M. Wood⁴, Nitin Singh⁴, Arman Seuylemezian⁴, Daniel J. Butler^{2,3}, Krista Ryon^{1,3}, Katerina Kuchin^{2,3}, Dmitry Meleshko^{2,3}, Chandrima Bhattacharya^{2,3}, Kasthuri J. Venkateswaran^{4*} and Christopher E. Mason^{1,3,5,6*} 



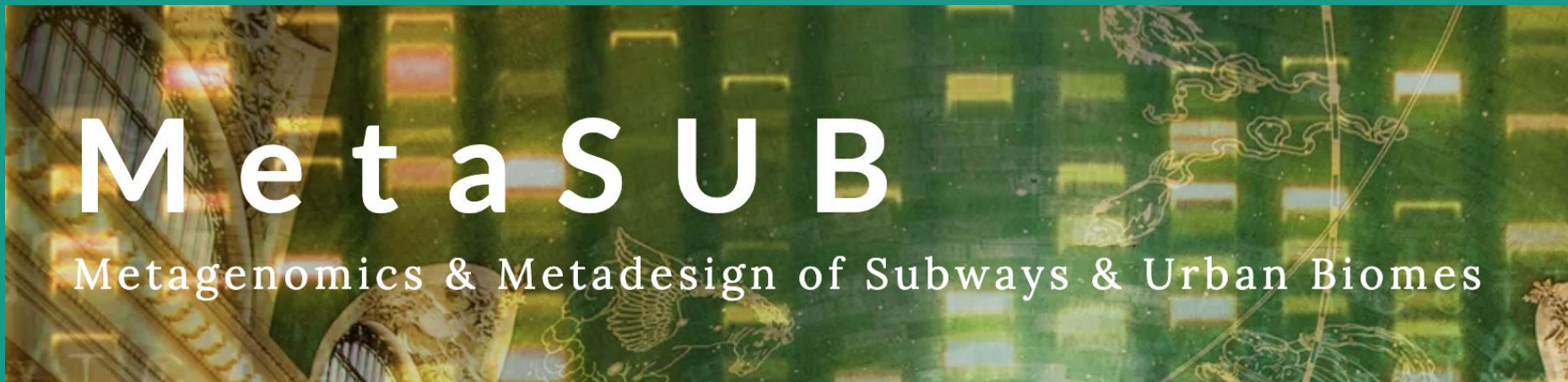
Wheee!

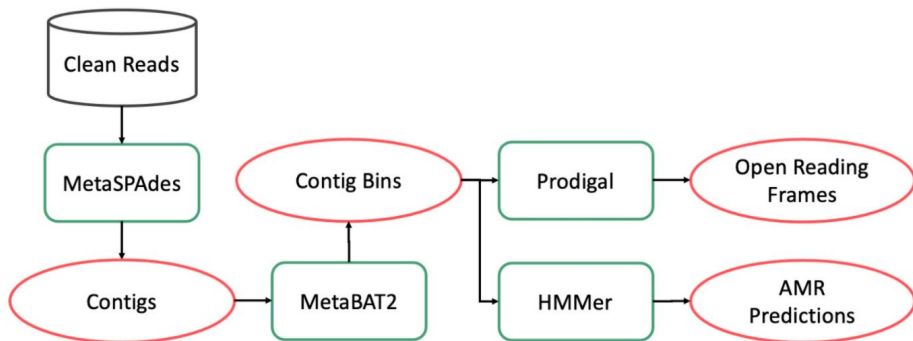
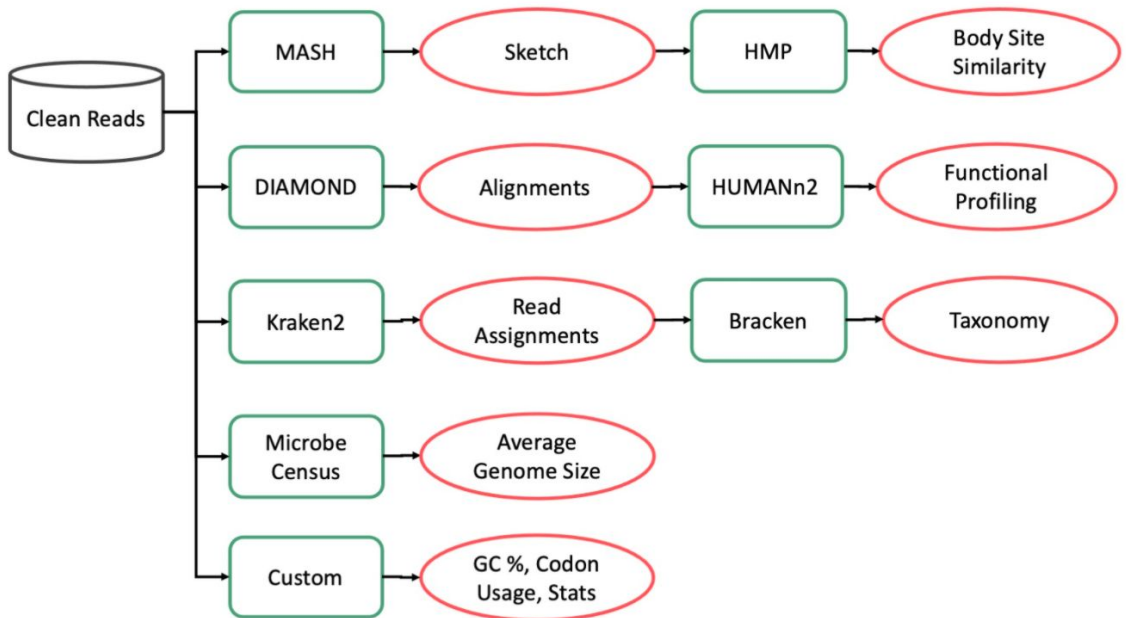
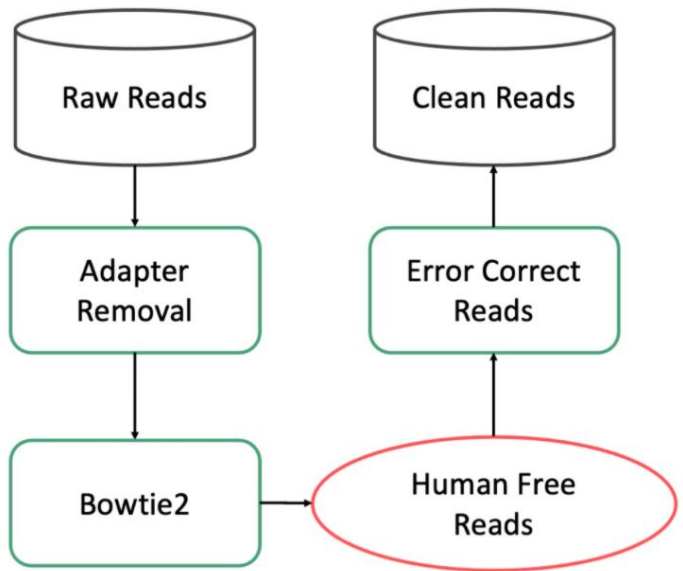


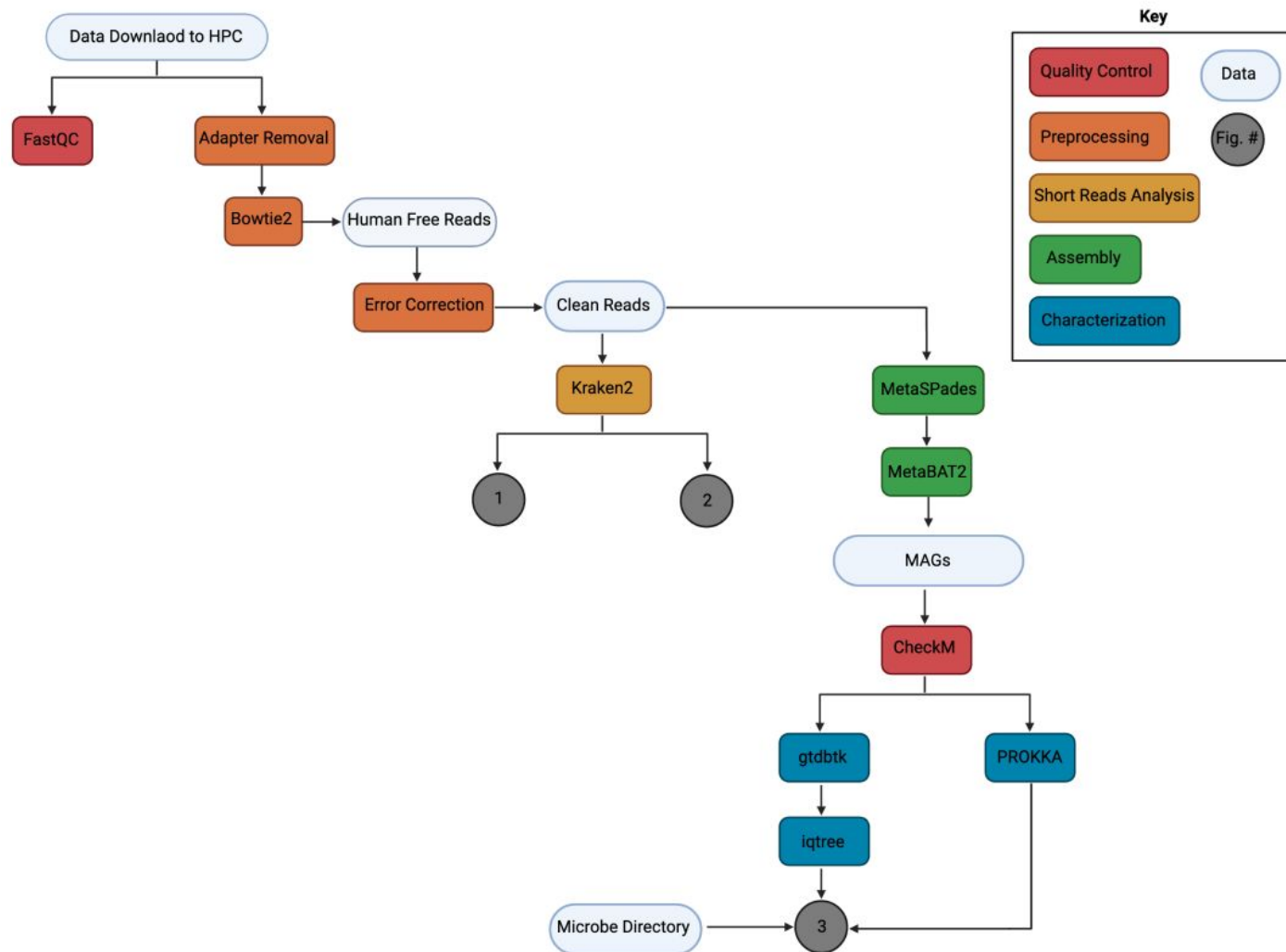
[CAP2](#)

 **FAILED**

This repository contains code for the second version of the MetaSUB Core Analysis Pipeline. This pipeline is in Beta and under development.







ISO 5

ISO 6

ISO 7

ISO 8

Figures 1a and 1b

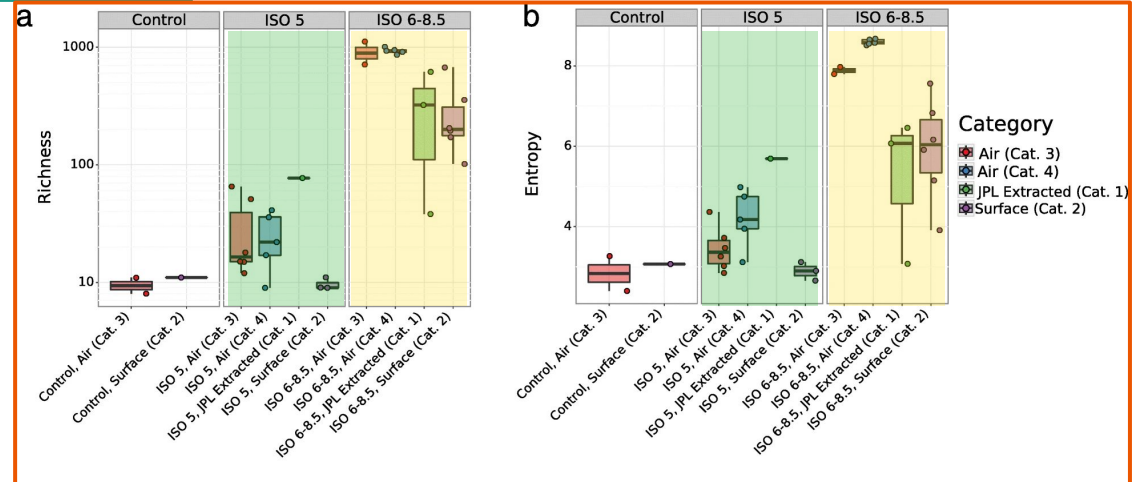
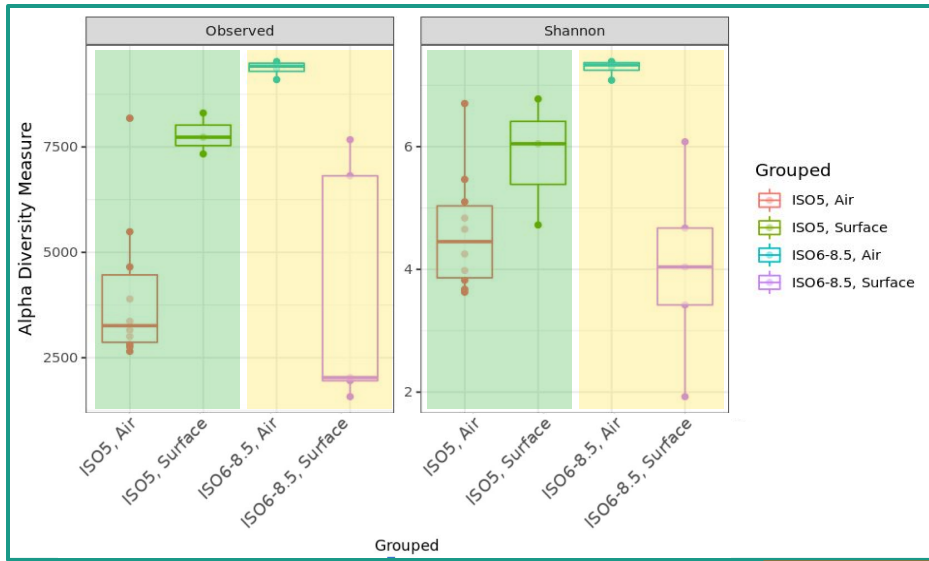
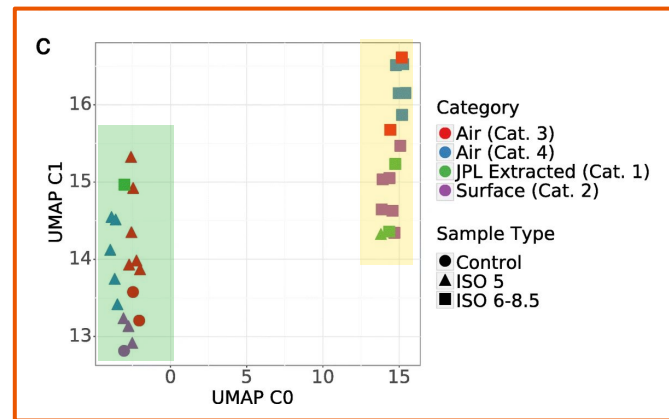
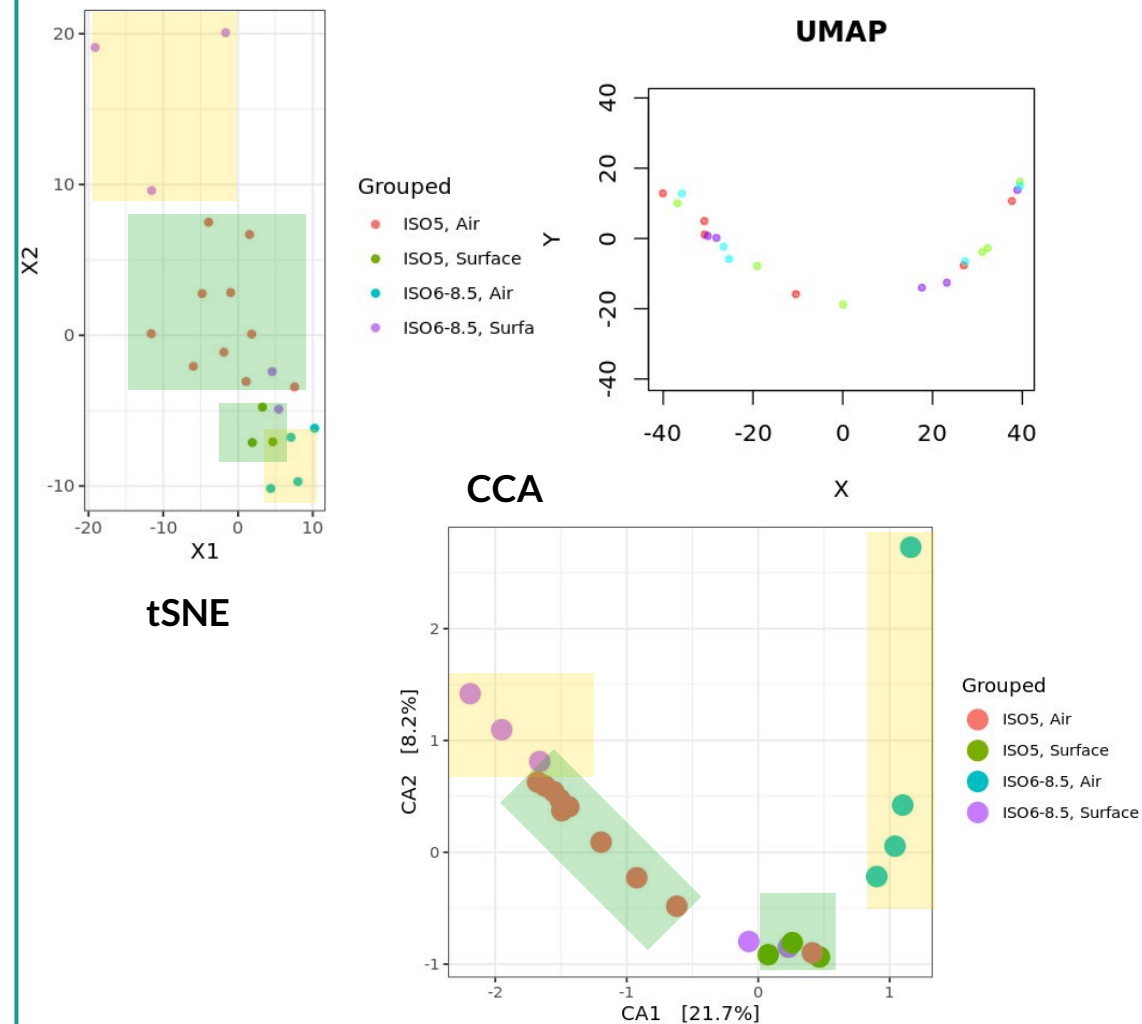
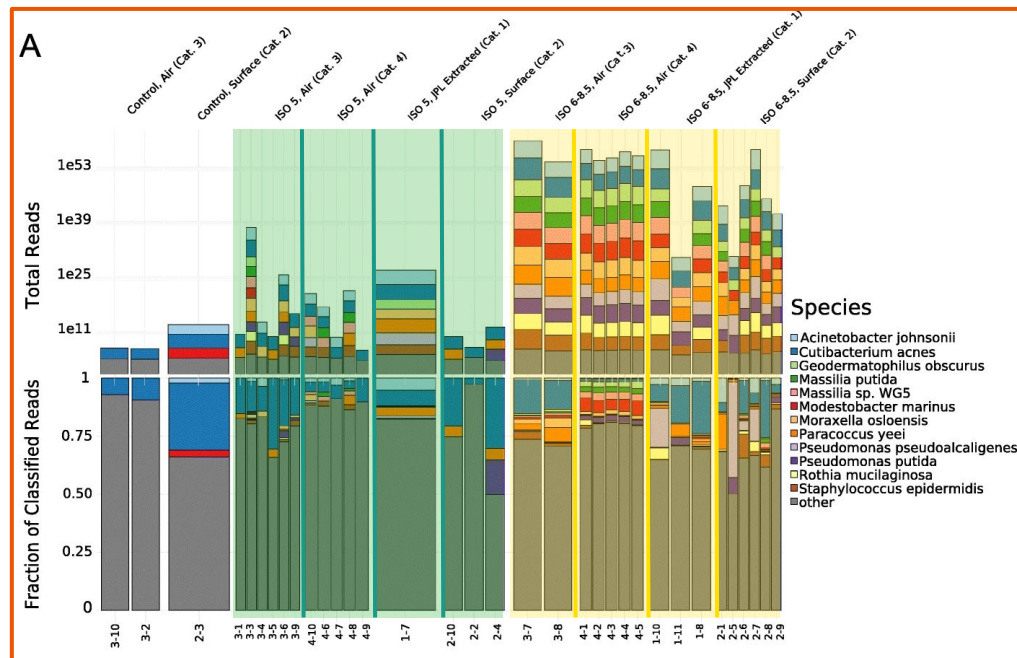
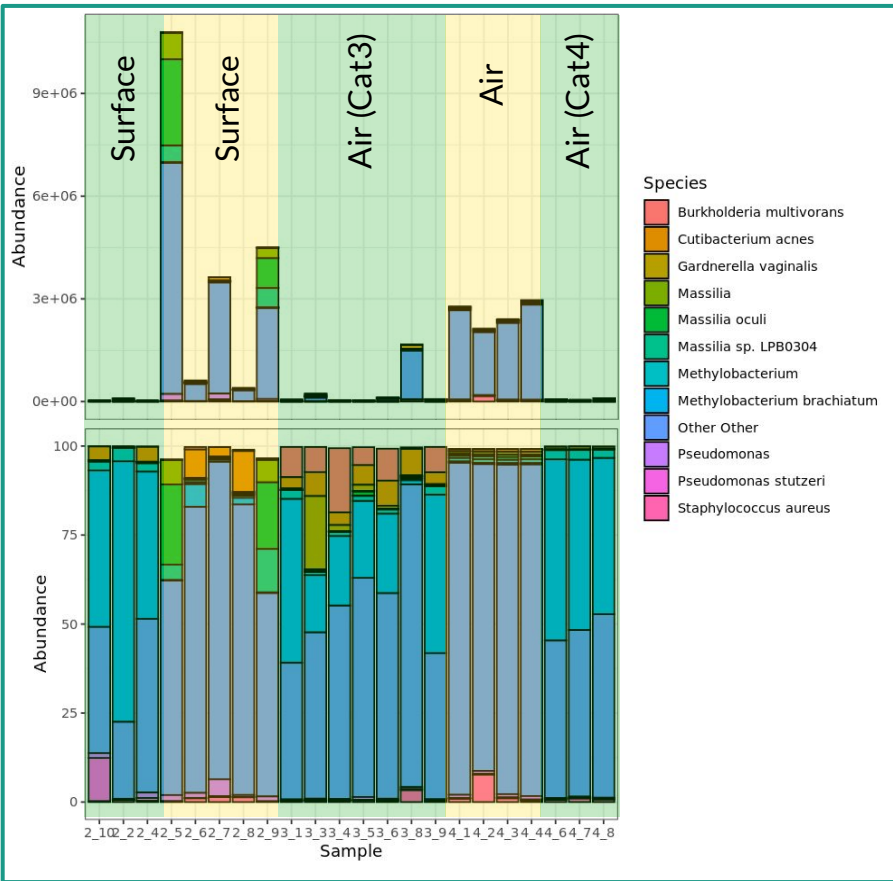


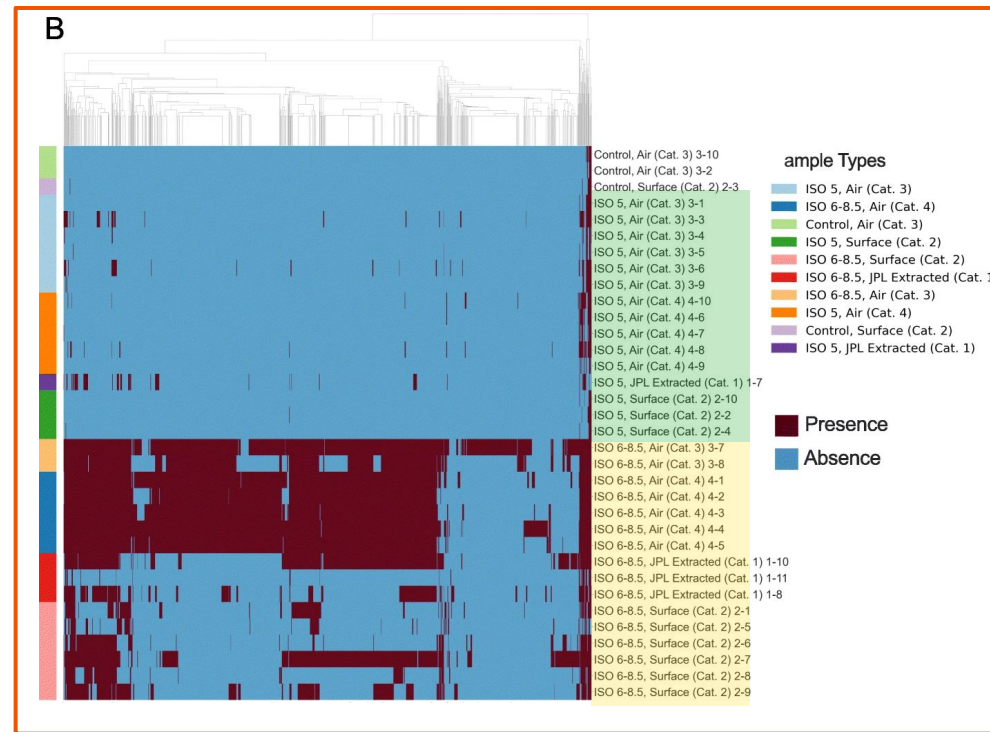
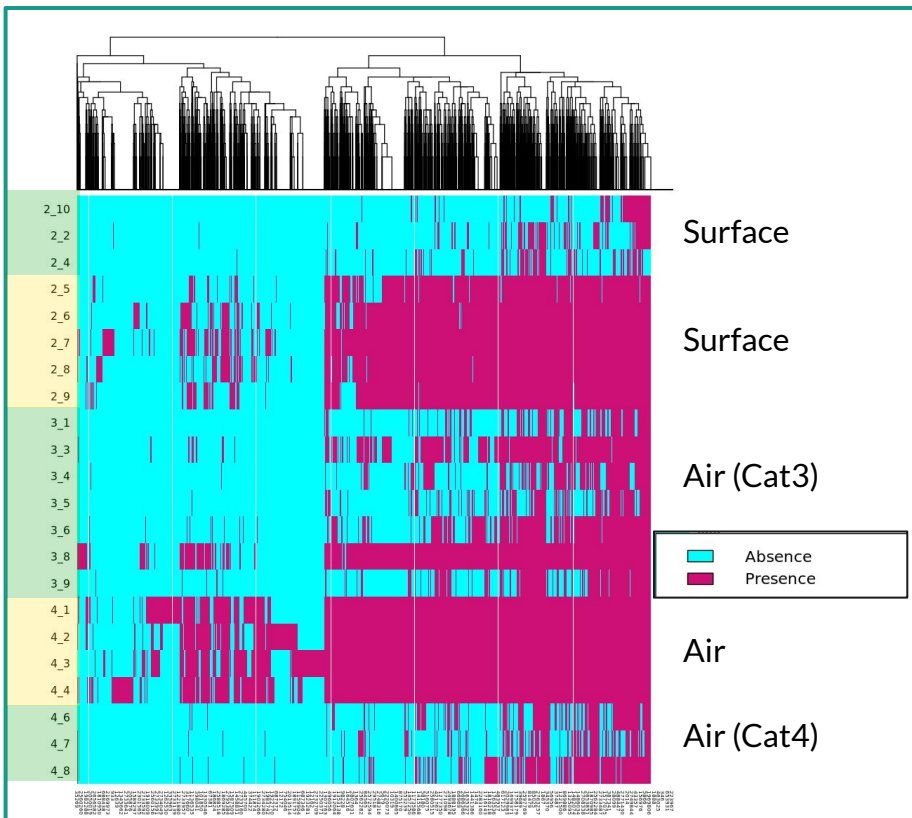
Figure 1c



Note: Coloured boxes do not indicate statistically significant groupings





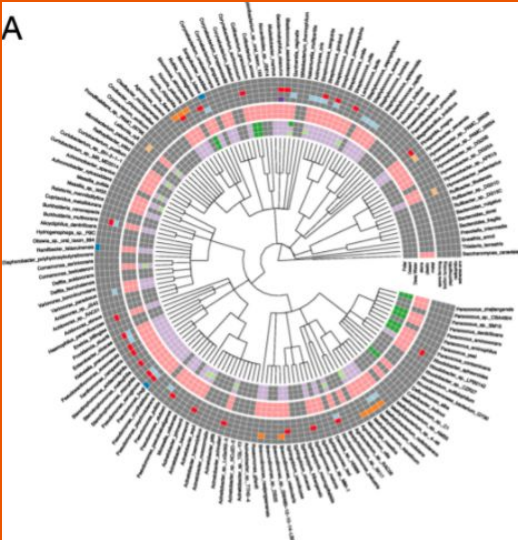


The Microbe Directory: An annotated, searchable inventory of microbes' characteristics

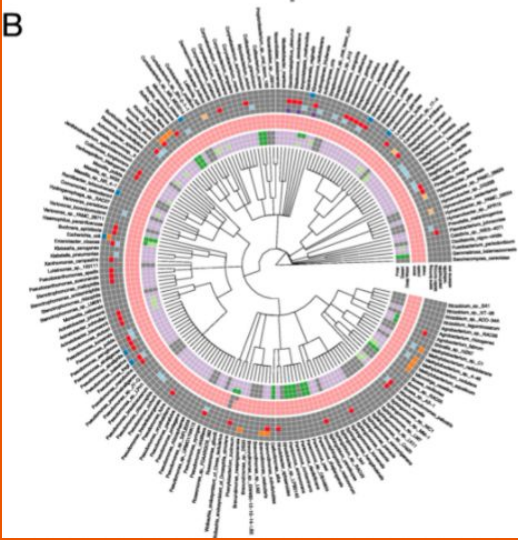
Heba Shaaban ^{# 1 2 3}, David A Westfall ^{# 1 2 4}, Rawhi Mohammad ^{1 2 5}, David Danko ^{1 2}, Daniela Bezdan ^{1 2}, Ebrahim Afshinnkoo ^{1 2 6}, Nicola Segata ⁷, Christopher E Mason ^{1 2 8}

Figure 3

A

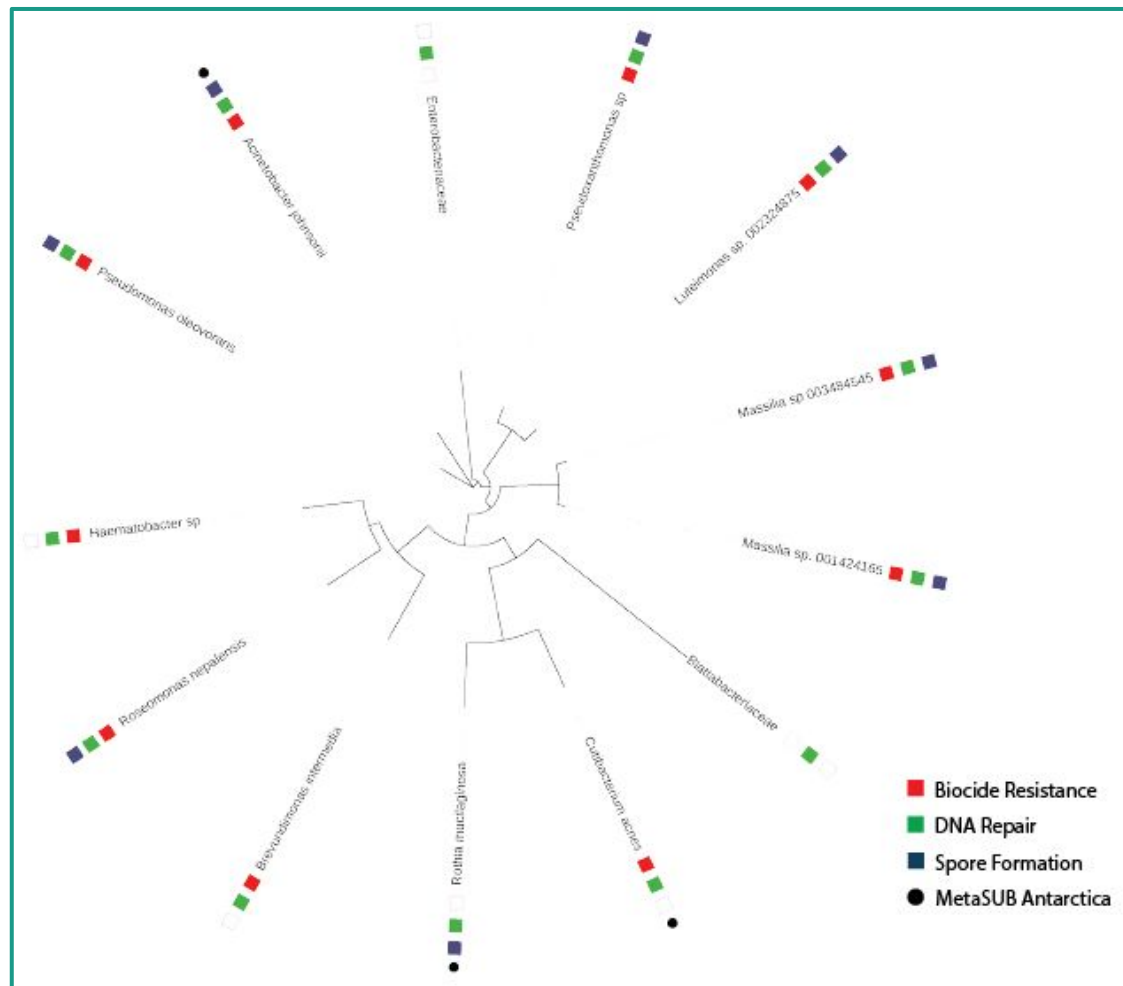


B



Value

- Biofilm Forming
- Extremophile
- Never Observed
- Observed in some
- Often Present
- Psychrophilic
- Psychrophilic Genus
- Radiophilic Genus
- Rarely Observed
- Spore Forming



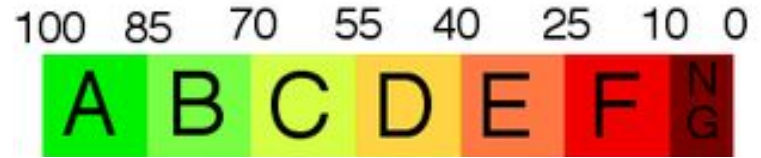


Quantification of Reproducibility: Ease of use

Starting 'grade' of 100

Penalties:

- -1 per missing version number
- -2 per tool setting/flag not specified
- -5 per paid tool
- -8 per step/tool not outlined in manuscript or pipeline





Reproducibility Issues

- Non-standard repository
- Pipeline failed - both versions and many install parameters
 - Poorly designed custom workflow manager (v1)
- No version numbers specified outside of the source code
- No flags specified outside of the source code except in an isolated case
- Kmer length not specified
- Microbe Directory datasets not specified
- No figure documentation

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(generously)
