

iMAP: An integrative pipeline for classifying 16S rRNA gene sequences into known bacterial taxa

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Background

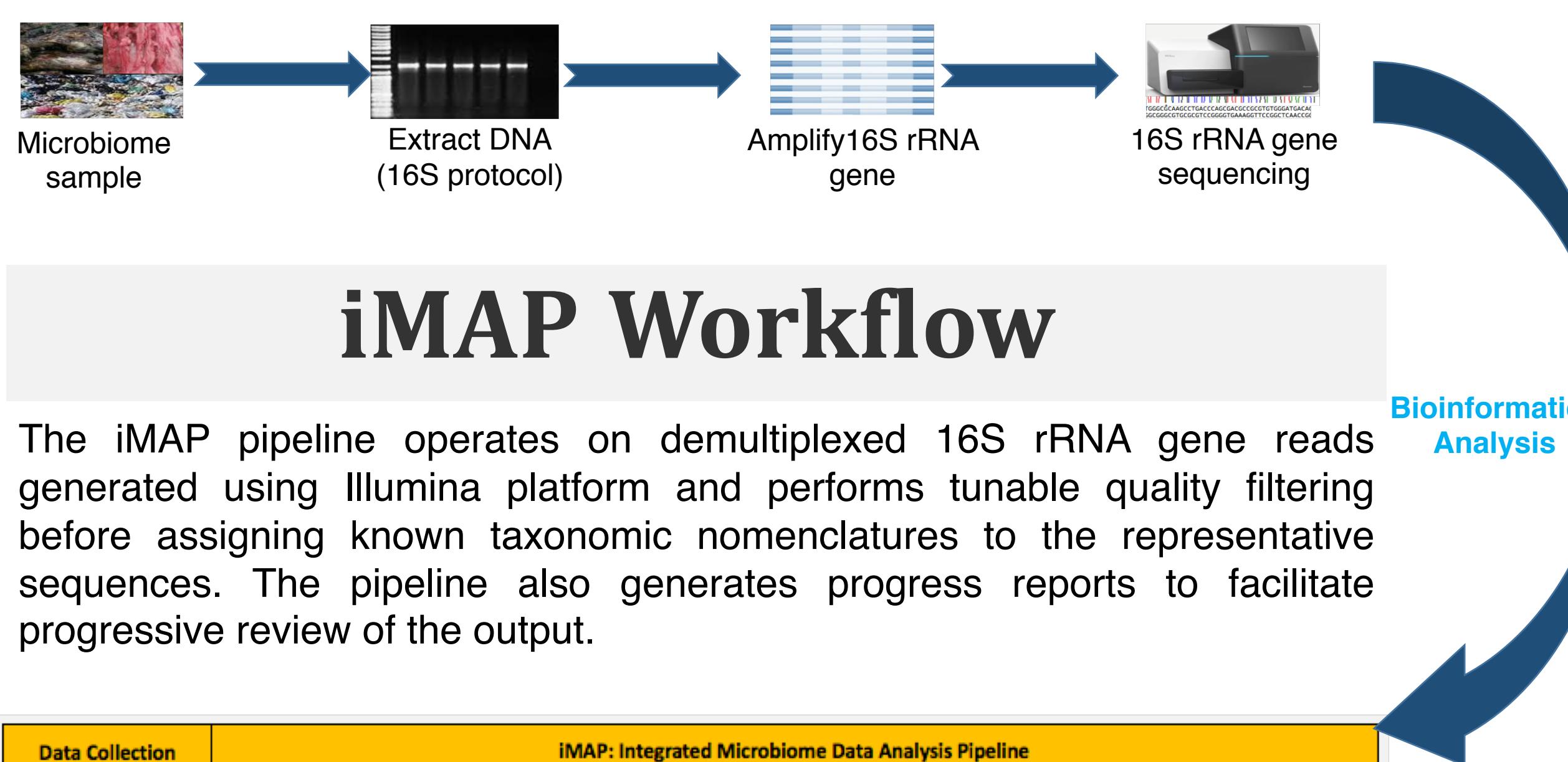
Microbiome studies present great opportunities for understanding microbial communities in diverse samples and their role in environment, health and disease. Effective analytical workflows that guarantee reproducibility, repeatability and result provenance are essential requirements for analyzing highly multidimensional microbiome data. For nearly a decade, several state-of-the-art bioinformatics tools have been developed to enable investigators gain knowledge and biological value of the microbial communities living in a given sample.

Statement of problem

Most of the available bioinformatics tools are designed with multiple functions that may require some programming skills to understand their full implementation. Microbiome data analysis is a complex process that requires thorough review of the output and graphical interpretation. The intermediate output is less frequently reviewed, which may lead to errors being propagated downstream.

Solution

We have developed a pipeline named iMAP (integrative Microbiome Analysis Pipeline) to address some of microbiome data analysis challenges including result visualization, interpretation and reporting. The development of this pipeline is guided by the need for a tool that is easily executed by a novice user, allows review of intermediate output and generates high quality images for better interpretation of the output at every major step.



The iMAP pipeline operates on demultiplexed 16S rRNA gene reads generated using Illumina platform and performs tunable quality filtering before assigning known taxonomic nomenclatures to the representative sequences. The pipeline also generates progress reports to facilitate progressive review of the output.

Data Collection		iMAP: Integrated Microbiome Data Analysis Pipeline				
Sampling & DNA Sequencing		iMAP: Integrated Microbiome Data Analysis Pipeline				
		Gathering materials & Profiling metadata	Pre-Processing & Quality control	Sequence processing & taxonomic classification	OTU clustering & taxonomy assignment	Phylogenetic annotation
Demultiplexed reads	DNA sequencing	<ul style="list-style-type: none"> Gather required materials Get demultiplexed reads (FastQ files) Get sample metadata Clone iMAP repository Install required software Download reference DBs Confirm folders and files 	<ul style="list-style-type: none"> Read inspection Review per sample read depth Review read length 	<ul style="list-style-type: none"> Merge forward & reverse reads Review, screen and filter by sequence length Pick representative sequences 	<ul style="list-style-type: none"> Cluster OTUs & assign conserved taxonomy Phylogenetic approach OTU clusters approach Phylogeny approach 	<ul style="list-style-type: none"> Phylogenetic annotation Upload trees to iTOL viewer Prepare annotation files Add annotation files to the tree Manage trees interactively Export annotated tree
Library Preparation	DNA extraction	Examine the metadata				
		<ul style="list-style-type: none"> Inspect uniformity of sample identifiers Review experimental variables Review missing data 				
Sample metadata						
Field & Wet Lab		Progress Report 1: Metadata profiling	Progress Report 2: Pre-processing	Progress Report 3: Sequence-processing	Progress Report 4: Preliminary analysis	
		Review-As-You-Go (RAYG): Progress Reports Summarizing Bioinformatics Analysis and Exploratory Visualization				

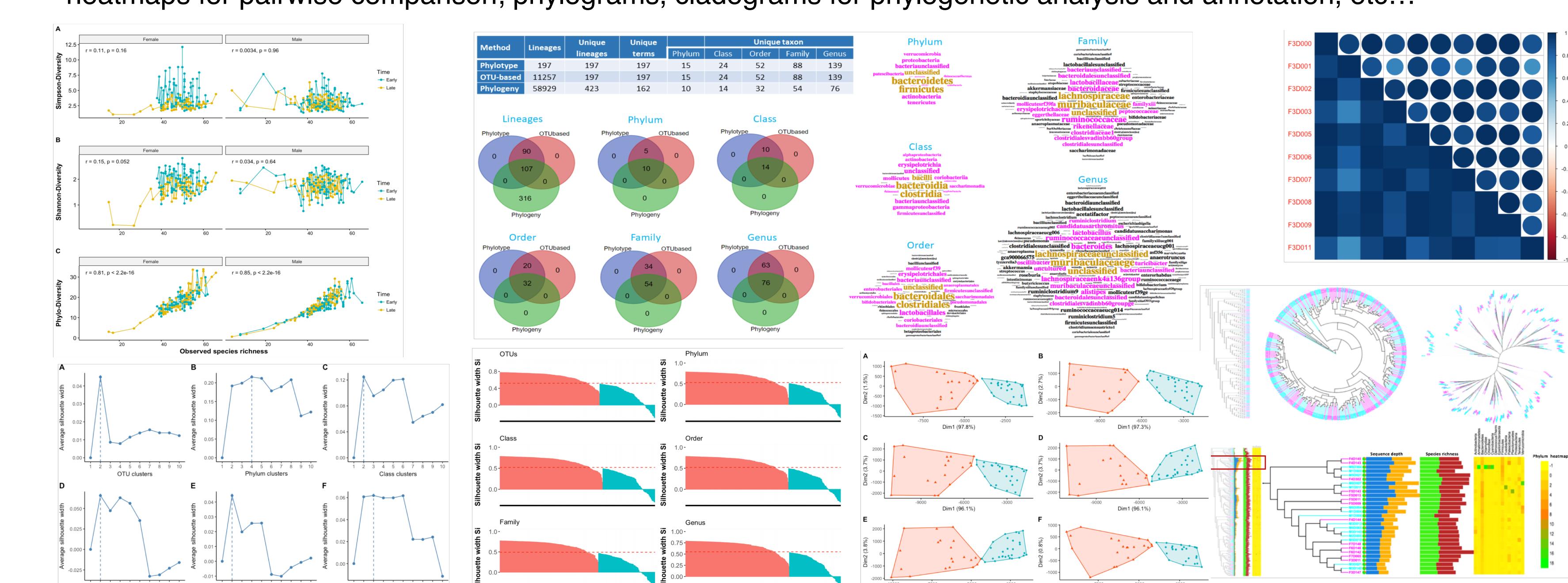
Results

The results are data tables which are transformed into structures suitable for statistical analysis and for generating publication-quality images. The progress reports facilitate communication between investigators and the analysts.



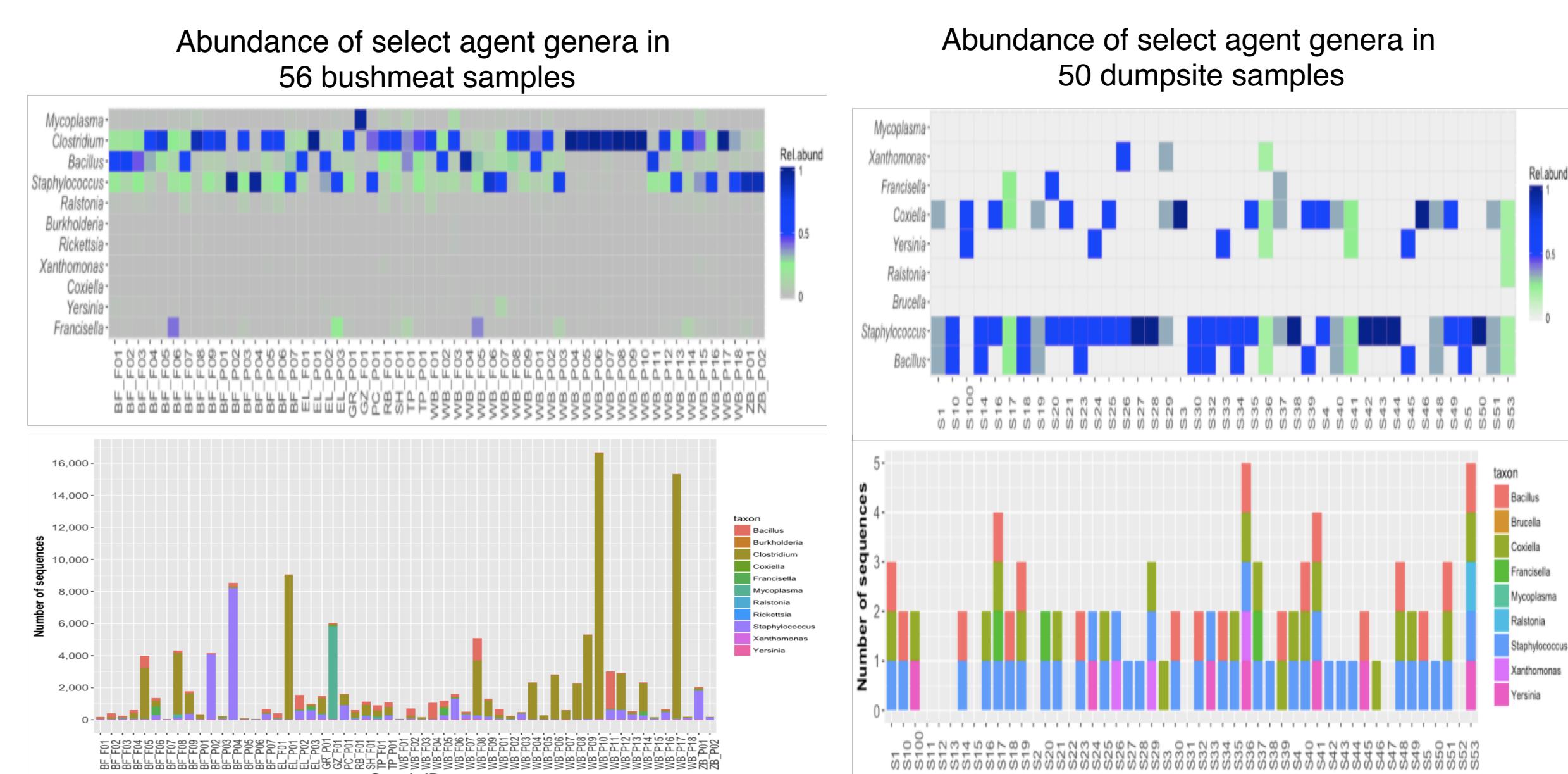
Analysis & visualization

- Metadata profiling:** Frequency of experimental variables. Any need to exclude some samples?
- Read quality:** Default threshold q=25. Poor reads are removed
- General distribution:** Histograms, barplots, boxplots, density, histograms, venn diagrams...
- Alpha diversity analysis:** Are there additional OTUs/species discovered through additional sampling? Common curves are: species accumulation, rarefaction and extrapolation, rank abundance.
- Beta diversity analysis:** Is there any similarity of data (microbial composition) between samples? Highly multidimensional OTU & taxonomic data is reduced to fewer dimensions by calculating distance matrices to specifically measure the diversity between samples. Example of visualization images: Heuristic clustering and ordination are commonly used including scree and stress plot for pre-ordination assessment; PCA, PAM, PCoA, NMDS for ordination; heatmaps for pairwise comparison; phylogenograms, cladograms for phylogenetic analysis and annotation, etc...



Reporting

- Finally, the results are summarized into HTML report using Rmarkdown for easy visualization, interpretation and sharing.
- In addition to general microbiome analysis, any hypotheses tested during bioinformatics analysis will appear in the report.
- Example: In our two training datasets (i) bushmeat and (ii) dumpsite samples we profiled 13 dangerous pathogens in the category of federal select agents.



Conclusion

The iMAP pipeline accelerates the identification of microbial communities that are present in environmental samples. The rich visuals produced by the pipeline facilitate better understanding of the multidimensional microbiome data and the reproducible HTML reports facilitate easy visualization, interpretation and quick sharing with collaborators. We anticipate that users will find this pipeline broadly useful and adaptable to their needs.

Acknowledgement

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Disclaimer

The views expressed in this poster are those of the authors and do not necessarily reflect the official policy or position of the Defense Threat Reduction Agency (DTRA), Department of Defense, or the U.S. Government.

References

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- iMAP pipeline manuscript: In preparation