# Pathway-level, Consensus Analysis of Microbiome Profiling Data
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### PROJECT SUMMARY

The capability to detect and mitigate the adverse effects of microbiome communities exposed to Martian environments is critical to crewed missions to and from the red planet. Particularly for crewed environments, it is crucial to understand the baseline microbial communities and to detect changes or anomalies to those environments. This requires functional interpretation and comprehensive analysis of available microbiome studies that go far beyond differential abundance analyses. In this approach, we propose to develop a novel bioinformatics method, named Consensus Microbe Set Analysis (CMSA), that will allow researchers to: i) perform functional analysis to capture changes of commensal microbial communities at the systems-level, ii) perform meta-analysis of multiple related microbiome datasets, and iii) interactively and simultaneously explore the results obtained from multiple analyses, the impacted pathways, and the relationship between pathways and genes. The project has been discussed with NASA contact Dr. J Nick Benardini at Office of Planetary Protection, NASA Headquarters. Dr. Benardini has expressed his enthusiasm and approval of the proposed work. This work will be performed by Science PI Dr. Tin Nguyen and his Ph.D. student, in collaboration with NASA GeneLab Microbiom Analysis Working Group and Office of Safety and Mission Assurance. At the end of the project period, we will deliver a web-based platform implementing the proposed method.

The project fits into Emphasis 1: Microbial and Human Health Monitoring of Appendix K: Office of Safety & Mission Assurance. Indeed, the proposed work "would be the first steps on path to develop -omics based approaches (including downstream bioinformatic analyses) for planetary protection decision making with a particular emphasis on assessing perturbations in the spacecraft microbiome." Our long-term goal is to continue working with NASA to implement an automatic pipeline for microbial and human health monitoring that is capable of: i) determining the composition of microbial communities, ii) identifying the presence of unknown species of Martian origin, iii) assessing perturbation in spacecraft microbiome, and iv) predict their effect on crew and spacecraft health.