

This project aims to systematically analyze the effects of nuclear contamination on soil microbial community compositions such that predictors of the type and history of nuclear processes may, at some point, be predicted from composition of the microbiome. Despite a number of datasets being generated at specific sites, there is a lack of a systematic, cross-environment analyses of microbiome responses to nuclear activity. To address this gap, community metagenomes and amplicon datasets that are expected to be important with respect to nuclear processing are being identified and collated to form a database of standardized datasets re-processed from raw sequences using a common computational pipeline. The database will be used to conduct a comparative analysis to identify features that distinguish nuclear-contaminated soil samples from background samples and microbial clades and/or individual taxa that may serve as bioindicators of nuclear proliferation activity in soil samples. Initial comparison of contaminated samples to background samples suggests these do indeed cluster apart in possibly interesting ways. However, more data and deeper analysis will be necessary to confirm generalizable conclusions.