# Fathi Camel Microbiome Project (MS Repo)

This repository contains files needed to reproduce the analysis found in the submitted manuscript "Extensive novel diversity and phenotypic associations in the dromedary camel microbiome are revealed through deep metagenomics and machine learning" by Fathi A. Mubaraki.

## Contents

The main script needed to reproduce the analysis is found in camel2.r. This file draws upon other files (metadata, microbial abundances table) which are also included in the same relative hierarchy. To run, download all files in the repo (either by cloning or downloading a zip archive of the repo), extract them a single directory, and modify the "setwd()" command in R accordingly to step through the code.