**metagenome\_MM\_code:**

All code using in the manuscript, ***Alterations of gut microbiome accelerate multiple myeloma progression by increasing the relative abundances of nitrogen recycling bacteria***, is presented here, including two Shell script in Linux and several R script in Windows.

1. **run\_kraken\_standard**: this script was used for taxa classification using Kraken.
2. **run\_metacv**: this script was used for function annotation using MetaCV.
3. **Code\_1\_species\_analysis.R**: this script was used to calculate alpha-diversity within the samples and beta- diversity between the two groups, as well as visualization.
4. **Code\_2\_phylum\_genus.R**: this script was used to analyze statistically taxa classification at the phylum and genus level, as well as visualization.
5. **Code\_3\_diff\_species.R**: this script was used to identify significantly differential species using R package DESeq2, as well as visualization.
6. **Code\_4\_diff\_ko.R:** this script was used to identify significantly differential KOs using R package DESeq2, and calculate beta- diversity between the two groups.
7. **Code\_5\_metabolite.R:** this script was used to screen significant metabolites which was p\_value <0.05 (two-tailed T-test) and VIP >1 (SIMCA), as well as visualization.
8. Code\_6\_interaction.R: this script was used to calculate the Spearman’s correlation between the differential species and differential metabolites, as well as visualization.
9. **Code\_7\_microbiotaViz.R:** this script was used to visualize the Cladogram of the significant species using R package microbiomeViz.
10. **Code\_RDA\_analysis.R:** this script was used to perform redundancy analysis (RDA), which presented the variation of the relative abundance of several significant strains in FMT\_HC, PBS, and FMT\_MM mice with time (week 0, week 2, week 4, week 6).
11. **sample\_group:** all samples using in this study were divided into two groups, HC and MM.