

Amplicon result supplementary instruction (08)

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8. Funncion_prediction 【function prediction】

1. Picrust2 [Picrust 2 function prediction]

1.1 predicted 【picrust2 (COG,EC,KO,PFAM,TIGRFAM,pathway) analysis result】

1.1.1 *_metagenome_descrip.tsv 【(COG,EC,KO,PFAM,TIGRFAM,pathway) prediction result】

1.1.2 *_seqtab_norm.tsv.gz 【Feature table based on prediction 16S copy number correction, not exist in pathways_out directory】

1.1.3 *_weighted_nsti.tsv.gz 【NSTI weight of each sample , not exist in pathways_out directory】

1.2 tables 【absolute abundance of function】

1.2.1 sample/group1/... 【absolute abundance of function】

1.2.2 picrust2. {sample,group}.*.absolute.xls 【absolute abundance of function】

Column number	Column name	Description
1	KO_Hierarchy	KO
2	Sample name	Abundance
3	KEGG_Description	Function prediction information

1.2.3 picrust2. {sample,group}.*.relative.xls 【relative abundance of function】

1.2 barplot 【barplot of relative abundance】

1.3 heatmap 【heatmap of function】

1.4 venn 【venn diagram】

1.5 flower 【flower diagram】

1.6 pca 【PCA analysis result, refer to beta_pca】

1.7 ttest 【ttest】

2. Picrust **【 Picrust function prediction 】**

2.1 predicted **【 function prediction result of KEGG database 】**

2.1.1 KEGG_metagenome_predictions. {biom,txt} **【 KEGG function prediction result 】**

2.1.2 predicted_metagenomes.KEGG_L*.txt **【 KEGG function prediction result 】**

2.2 tables **【 relative abundance of function 】**

2.2.1 sample/group1/... **【relative abundance of function in sample/group1 】**

2.2.2 picrust. {sample,group}.*.absolute.xls **【absolute abundance of function at (1,2,k) level】**

2.2.3 picrust. {sample,group}.*.relative.xls **【relative abundance of function at (1,2,k) level】**

2.3 barplot **【barplot of relative abundance of function】**

2.4 heatmap **【heatmap of function prediction】**

2.5 venn **【venn diagram】**

2.6 flower **【flower diagram】**

2.7 pca **【PCA analysis, refer to beta_pca】**

2.8 ttest **【ttest】**

3. Tax4fun 【 Tax4fun function prediction】

3.1 predicted 【 KEGG function prediction 】

3.1.1 KEGG_metagenome_predictions.txt 【 KEGG function prediction result】

3.1.2 predicted_metagenomes.KEGG_L*.txt 【 KEGG function prediction at (1,2,3) level】

3.2 tables 【relative abundance of function】

3.2.1 sample/group1/... 【relative abundance of function】

3.2.2 tax4fun. {sample,group}.*.absolute.xls 【absolute abundance of function at (1,2,3,k) level】

3.2.3 tax4fun. {sample,group}.*.relative.xls 【relative abundance of function at (1,2,3,k) level】

3.3 barplot 【barplot of relative abundance】

3.4 heatmap 【heatmap of function prediction】

3.5 venn 【venn diagram】

3.6 flower 【flower diagram】

3.7 pca 【PCA result, refer to beta_pca】

3.8 ttest 【ttest】

4. Bugbase **【 Bugbase function prediction 】**

4.1 normalized_otus **【OTU table after noemalization】**

4.2 otu_contributions **【barplot of phenotype prediction result】**

4.1.1 *. {pdf,png} **【barplot of phenotype prediction result】**

4.1.2 contributing_otus.txt **【table of phenotype prediction result】**

4.1.3 otu_table.relative.xls **【relative abundance table of phenotype prediction result】**

4.3 predicted_phenotypes **【boxplot of phenotype prediction】**

4.3.1 *. {pdf,png} **【boxplot of phenotype prediction】**

4.3.2 *_stats.txt **【data of boxplot of phenotype prediction, eg. Mean, median,standard deviation】**

4.3.3 predictions. {txt,xls} **【abundance table of phenotype prediction result】**

4.4 thresholds **【threshold】**

4.4.1 variances.txt **【result under different threshold】**

4.4.2 thresholds_used.txt **【the threshold used in phenotype prediction】**

4.4.3 *. {pdf,png} **【relative abundance change under different threshold】**

5. funguild **【 funguild prediction result 】**

5.1 predicted **【 funguild prediction result 】**

5.1.1 funguild.sample.total.absolute.xls **【 funguild prediction result 】**

5.1.2 funguild.sample.total.absolute. {guild, mode} **【 funguild (guild,mode) prediction result 】**

5.2 tables **【relative abundance of prediction result 】**

5.2.1 sample/group1/... **【relative abundance of prediction result 】**

5.2.1.1 funguild. {sample,group}.*.absolute.xls **【absolute abundance of prediction result (total,guild,mode) 】**

5.2.1.2 funguild. {sample,group}.*.relative.xls **【relative abundance of prediction result (total,guild,mode) 】**

5.3 barplot **【barplot of relative abundance 】**

5.4 heatmap **【heatmap of function prediction 】**

5.5 venn **【venn diagram 】**

5.6 flower **【flower diagram 】**

5.7 pca **【PCA result, refer to beta_pca 】**

5.8 ttest **【ttest 】**

6. faprotax 【 faprotax function prediction 】

6.1 predicted 【 faprotax function prediction 】

6.1.1 faprotax.report.txt 【 faprotax function prediction 】

6.1.2 faprotax.sample.anno.absolute.xls 【 absolute abundance of prediction result 】

6.2 tables 【relative abundance of prediction result 】

6.1.1 sample/group1/... 【 absolute abundance of prediction result 】

6.1.1.1 faprotax. {sample,group}.anno.absolute.xls 【 absolute abundance of prediction result 】

6.1.1.2 faprotax. {sample,group}.anno.relative.xls 【relative abundance of prediction result 】

6.3 barplot 【barplot of relative abundance of function 】

6.4 heatmap 【heatmap of function prediction 】

6.5 venn 【venn diagram 】

6.6 flower 【flower diagram 】

6.7 pca 【PCA analysis result, refer to beta_pca 】

6.8 ttest 【ttest 】