Biostatistics Statement

<p align="right">October 26, 2022</p>

Title: Comparison of genomic and transcriptional microbiome analysis in gastric cancer patients and healthy individuals

Differences in relative abundance of detected bacteria (at all taxonomic ranks) between study groups were evaluated by PERMANOVA and ANOSIM statistical tests, using 9999 permutations. Groups were considered significantly different if the p value was < 0.05, considering an estimate effect-size F values for PERMANOVA and R values for ANOSIM tests. Calculation was made by Past 3 program. The distributions of taxa abundance values were compared by Mann-Whitney test followed by Benjamini-Hochberg correction for multiple comparisons, named as false discovery rate (FDR) value. Differences were considered significant when the corrected p value (q value) was < 0.05. All statistical analysis was performed using RStudio software and respective R packages. The bacterial networks were visualized using Cytoscape program, after the Spearman correlation test with threshold of 0.2 in absolute value and p value < 0.05.

The statistical methods and techniques mentioned are appropriate for the research.

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