Microbiome Scale Qualitative Assessment Results

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There are a number of unmixed- and titration-specific features with a range of observed (titration-specific) and expected (unmix-specific) counts. (Fig. 1A-B). To determine if the observed and expected counts could be explained by sampling alone a binomial test was used for titration-specific features and a bayesian hypothesis test was used for unmixed-specific features. There were unmixed-specific features with expected counts that could not be explained by sampling alone for all biological replicates and bioinformatic pipelines (Fig. 1C). However, the proportion of unmixed-specific features that could not be explained by sampling alone varied by bioinformatic pipeline with over half of the DADA2 unmixed-specific features could not be explained by sampling alone whereas QIIME had the lowest rate of features with 0 observed counts that could not be explained by sampling alone. Consistent with the distribution of observed counts for titration-specific features more of the DADA2 features could not be explained by sampling alone compared to the other pipelines (Fig. 1D).

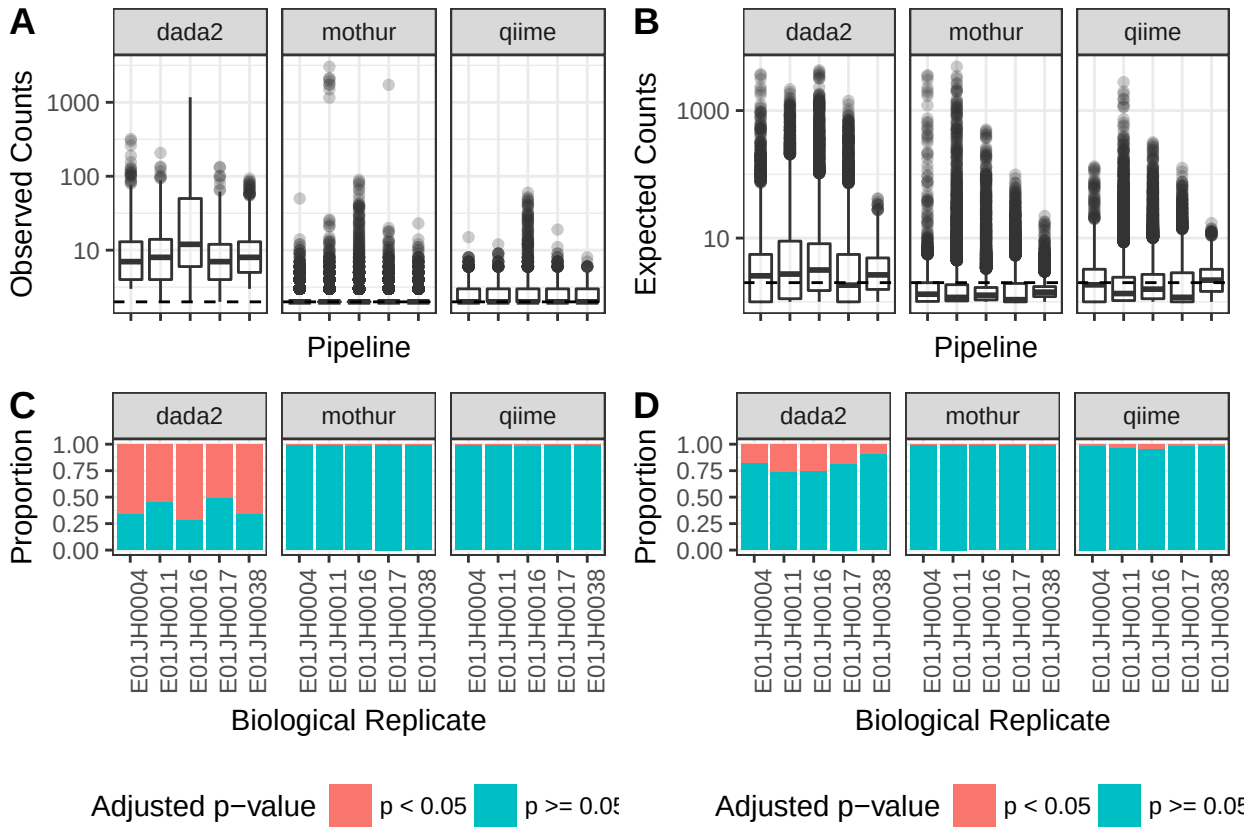

Figure 1: Distribution of (A) observed count values for titration-specific features and (B) expected count values for unmixed-specific features by pipeline and individual. The horizontal dashed line indicates a count value of 1. (C) Proportion of unmix-specific features and (D) titration-specific features with an adjusted p-value < 0.05 for the bayesian hypothesis test and binomial test respectively. We fail to accept the null hypothesis when the p-value < 0.05, indicating that for these features the discrepancy between the feature not being observed in the titration and present in the unmixed samples is not explained by sampling alone.