Microbiome Scale Theta Estimate Results

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Consistent deviation across pipeline and titration from the expected θ values indicates our assumptions regarding the composition of the mixtures are not valid (Fig. 1). Overall the relationship between the inferred and mixture design θ values were consistent across pipelines but not individual whereas the size 95% CI varied by both individual and pipeline. For E01JH0004, 11, and 16 the inferred and mixture design values were in better agreement compared to E01JH0017 and 38. For E01JH0017 and E01JH00038 the inferred values were consistently less than and greater than the mixture design values, respectively. These results were consistent with the qPCR bacterial DNA concentration results(Fig. ??). The bacterial DNA concentrations for E01JH0038 was lower for titrations 5, 10, and 15 compared to titrations 1-4. Conversely, the bacterial DNA concentration was higher for titratations 5, 10, and 15 compared to titrations 1-4 for E01JH0017.

Table 1: Number of features used to estimate theta by biological replicate and pipeline.

pipe	E01JH0004	E01JH0011	E01JH0016	E01JH0017	E01JH0038
dada2	90	90	144	136	130
mothur	114	104	178	149	177
qiime	145	146	106	155	204
unclustered	346	396	466	343	472

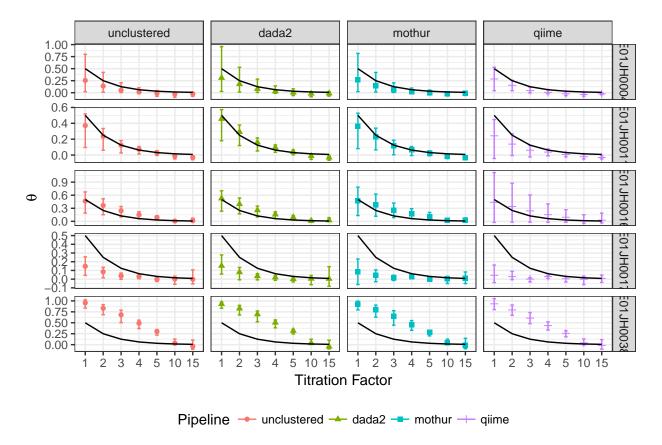


Figure 1: Theta estimates by titration, biological replicate, and bioinformatic pipeline. The points indicate mean estimate of 1000 bootstrap theta estimates and errorbars 95% confidence interval. The black line indicates the expected theta values. Theta estimates below the expected theta indicate that the titrations contains less than expected bacterial DNA from the post-treatment sample. Theta estimates greater than the expected theta indicate the titration contains more bacterial DNA from the pre-treatment sample than expected.