

Table S1. Numerical concordance between SimpleMicrobiome GUI outputs and equivalent standalone R analyses using the HMP V3–V5 body-site cohort. All analyses were performed using the default GUI settings. For SparCC and SPIEC-EASI, the “Compare two groups” analysis mode was used. GUI and standalone R outputs were considered numerically concordant when no differences were observed through 12 decimal places. ANCOM-BC2 log fold changes and MaAsLin2 coefficients were compared at the GUI-displayed precision of two decimal places.

Module	Compared output	GUI	Standalone R script
Taxa bar plot	Relative abundance		*
Taxa comparison	CLR-transformed abundance		*
Alpha diversity	Shannon, Chao1		*
Beta diversity	PERMANOVA R ²	0.195	0.195
	PERMANOVA P value	0.001	0.001
ANCOM-BC2	log fold change, P value, q value		*
MaAsLin2	Coefficient, P value, q value		*
Random forest	Permutation importance, Accuracy, Macro-F1, One-vs-rest AUC, Confusion matrix		*
SparCC	Edge identities, Edge weights		*
SPIEC-EASI	Edge identities, Edge weights		*
Correlation heatmap	Taxon-by-group association values		*
Association biplot	PERMANOVA R ²	0.546	0.546
	PERMANOVA P value	0.001	0.001

*Taxon-specific numerical values differed among taxa but were concordant between the GUI and standalone R execution for all evaluated taxa at the reported precision.