Category	Capability	phyloseq	QIIME	mothur	OTUbase/mcaGUI
Sequence Processing	decode barcoded reads	-	+	+	-
	cluster sequence reads into OTUs	-	+	+	-
	chimera filtering	-	+	+	-
Phylogenetics	reference alignment of OTU reps	-	+	+	-
	taxonomic classification	-	+	+	-
	store/manipulate phylogenetic trees	+	+	+	-
Ecology	multiple community distance/similarity metrics	+	+	+	+
	parallel Weighted and Unweighted UniFrac	+	+	+	-
Ordination	principal coordinates analysis (MDS/PCoA)	+	+	+	+
	nonmetric multidimensional scaling (NMDS)	+	+	+	-
	principal components analysis (PCA)	+	-	+	-
	CA, DCA, RDA, DPCoA	+	-	-	-
Graphics	ordination plot	+	P	+	P
	heat map	+	+	+	-
	quantitative abundance bar/pie plot	+	+	-	+
	multi-sample richness estimates plot	+	+	-	+
	annotated tree plot	+	-	+	-
	network plot	+	-	-	-
	integration with object oriented graphics	+	-	-	-
Validation	multiple inference correction	+	-	-	-
Reproducibility	tools for collaboration/reproduction/sharing	R	iP	S	R
Computation	language interface	R	python	C++	R
Documentation	web-based tutorials/wiki	+	+	+	-

P – PCoA-only
R – R Flavored Markdown, Sweave, etc.
iP – iPython Notebook, etc.
S – shell scripts