Microbiome analysis

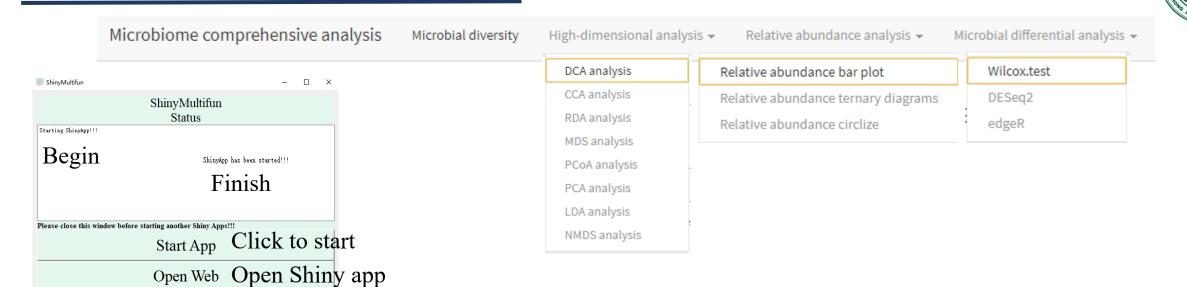


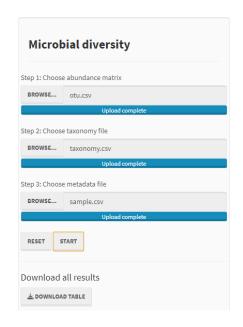
Comprehensive analysis of the microbiome

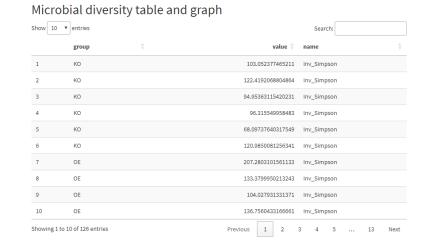
Difference analysis – NetMoss, Maaslin2

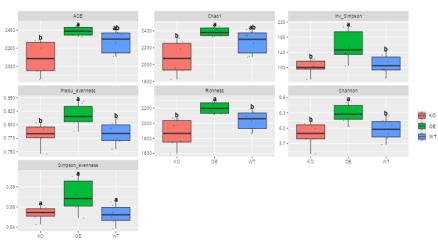
Batch effect analysis

Microbiome analysis - Microbial diversity





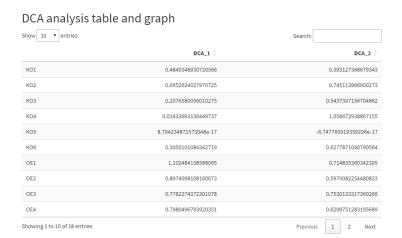


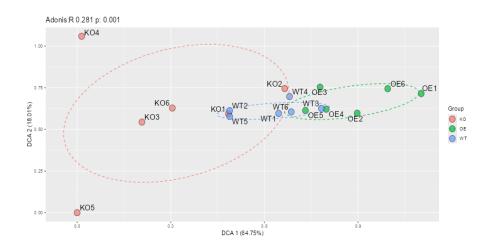


Microbiome analysis - Cluster analysis

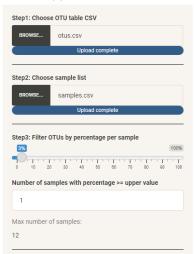






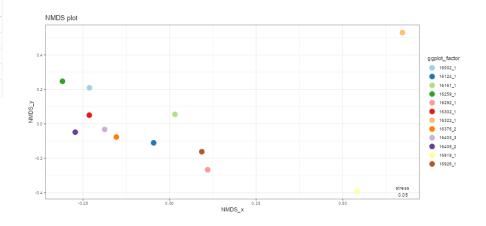


NMDS app



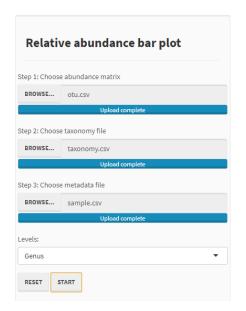
first 5 rows of OTU table are displayed												
	cluster_name	VOJ001	VOJ002	VOJ003	VOJ004	VOJ005	VOJ006	VOJ007	VOJ008	VOJ009	VOJ010	
	CL00000000002	2.63	1.20	3.27	2.08	2.31	3.30	1.26	0.21	0.99	1.86	
	CL00000000003	2.86	0.25	3.59	1.51	3.61	1.08	0.07	0.28	1.01	0.24	
	CL00000000004	2.24	0.12	2.82	1.72	4.47	0.94	0.07	0.41	2.46	1.59	
	CL00000000005	1.29	0.23	1.02	0.55	0.00	0.60	0.33	0.39	1.69	0.50	
	CL00000000008	1.65	0.04	0.79	0.20	0.20	0.71	0.02	0.09	0.84	0.06	

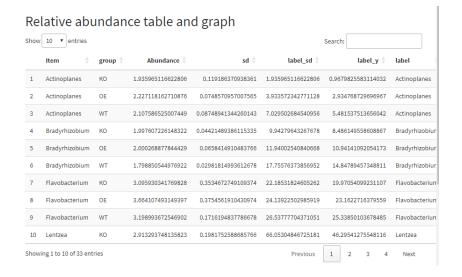
id	sample	tree	year	pН	n	С
16376_2	VOJ001	JD	2008	4.45	0.48	44.76
16292_1	V0J002	BK	2008	4.95	0.23	47.09
16302_1	VOJ003	BK	1997	3.85	0.28	47.15
16403_3	VOJ004	SM	2013	4.17	0.12	49.43
16405_2	VOJ005	SM	2013	4.00	0.13	53.33

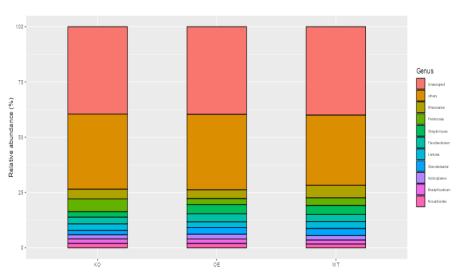


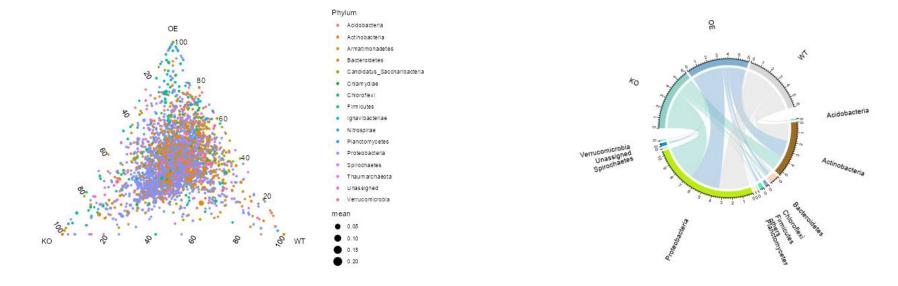
Microbiome analysis - Relative abundance analysis





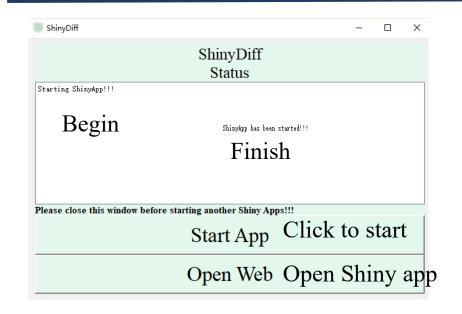


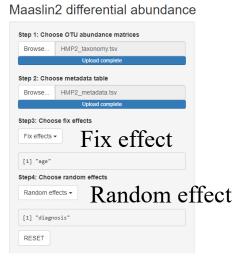




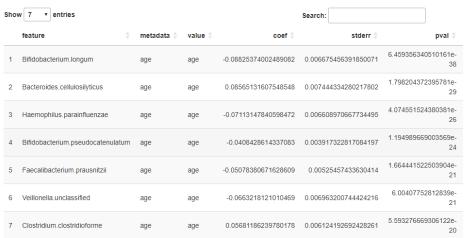
Microbiome analysis - Relative abundance analysis

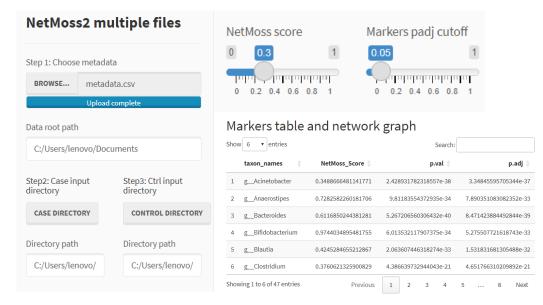


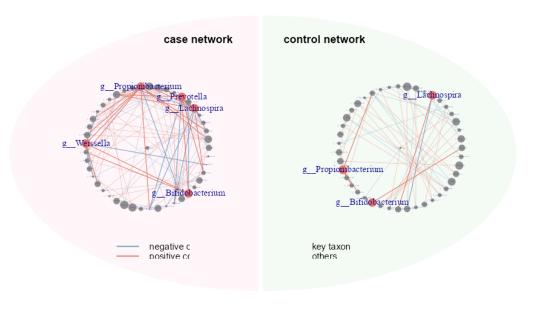




Differential abundance table

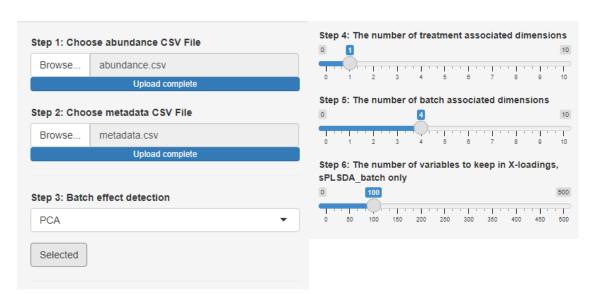






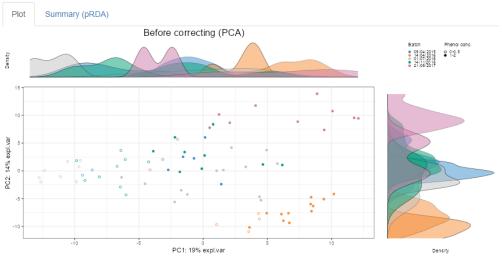
Microbiome analysis - Batch effect analysis







Before correcting



After correcting

