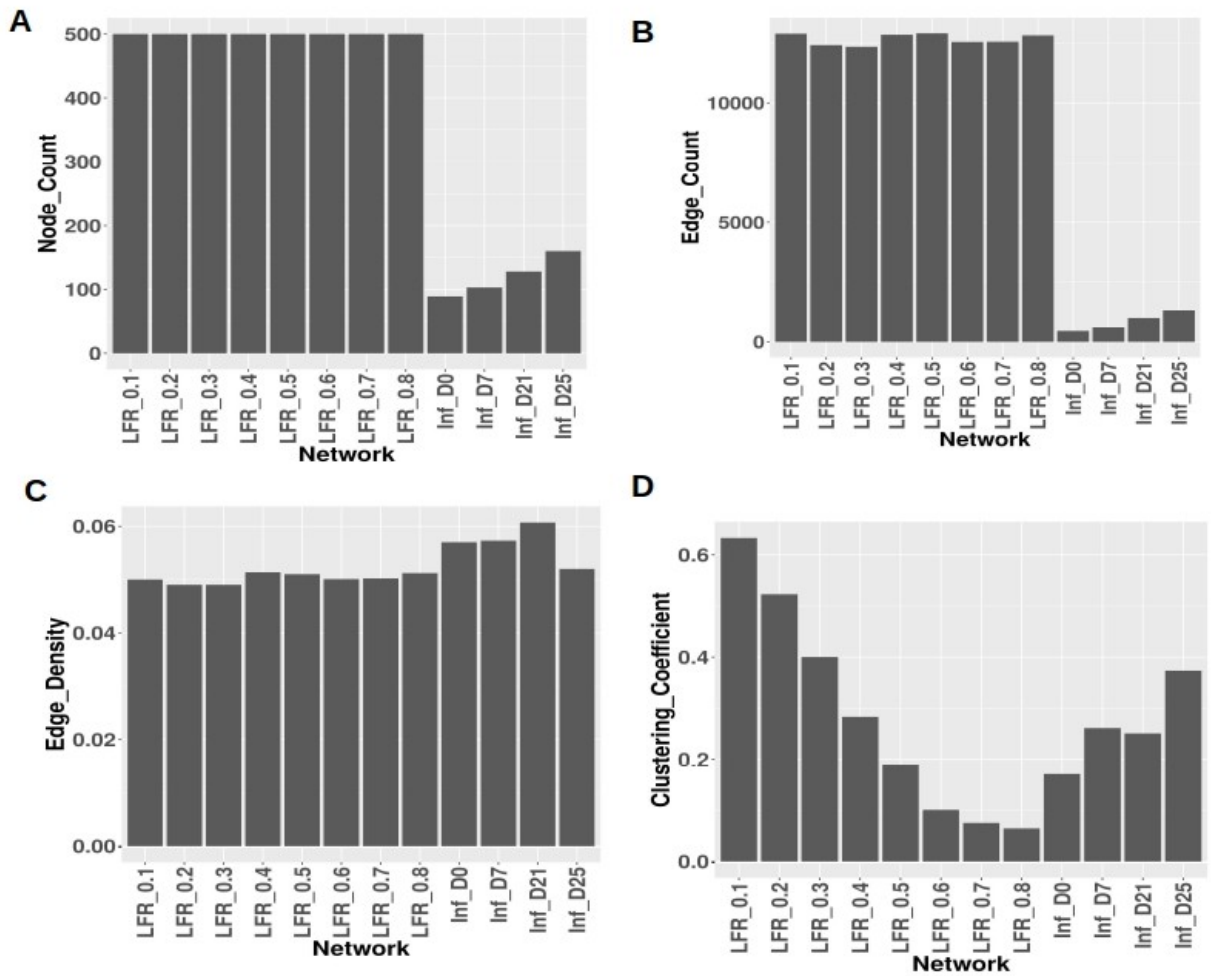
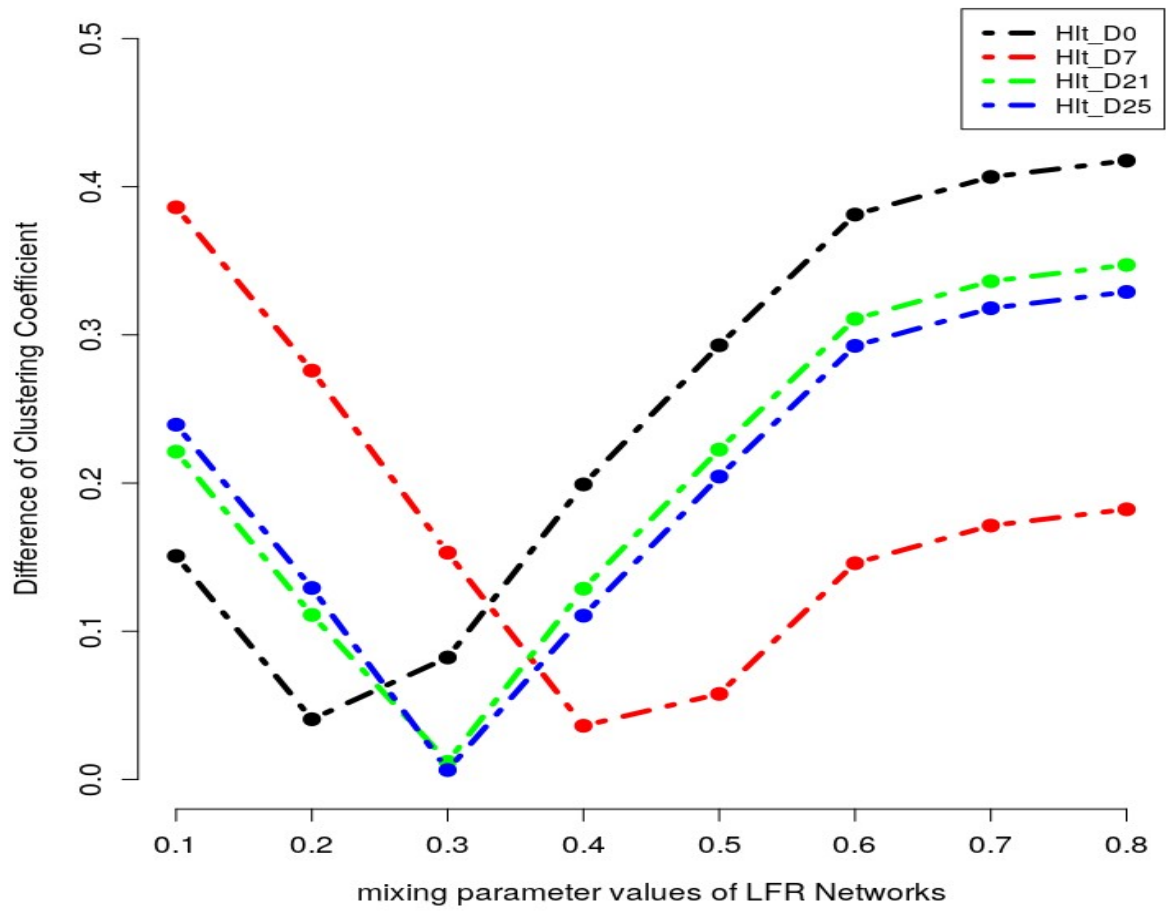


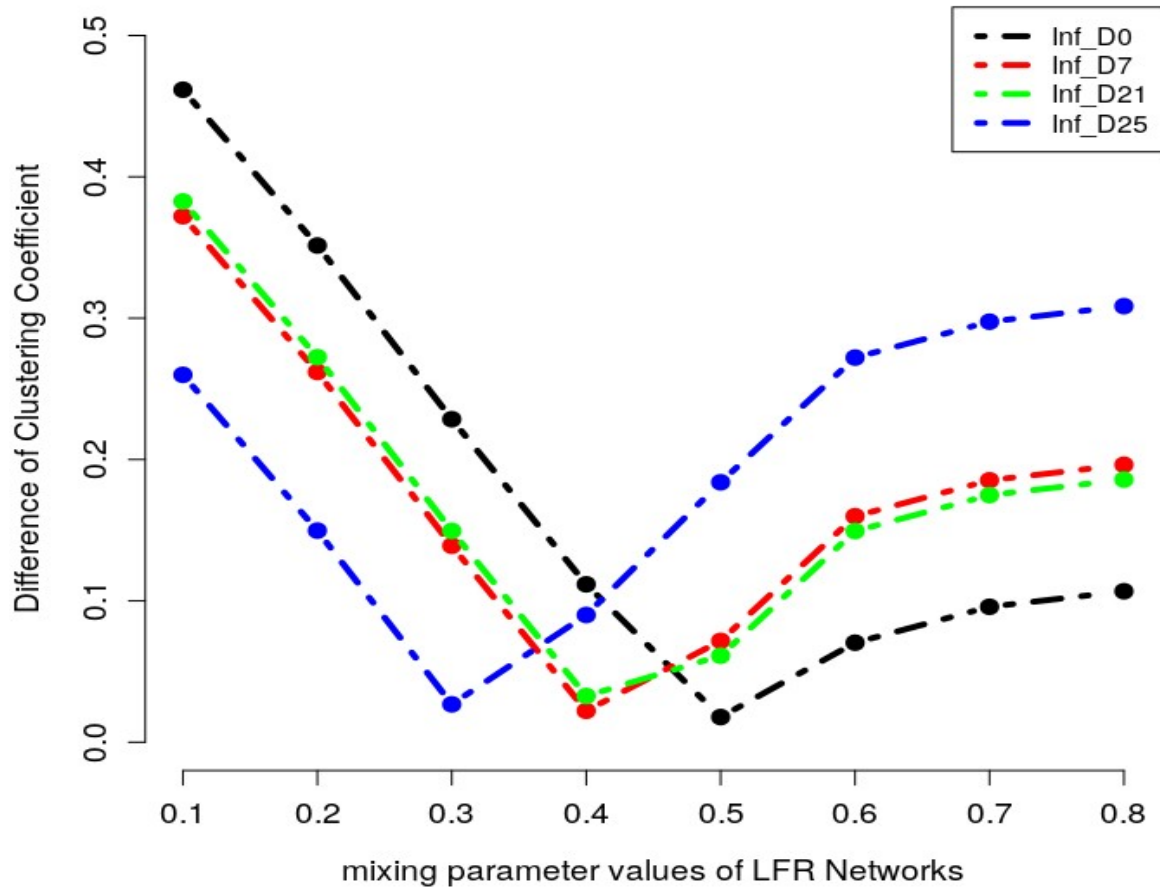
Supplementary Figure 1: Comparison between LFR benchmark networks (AN_1) and the healthy co-abundance networks in terms of **(A)** number of nodes, **(B)** number of edges, **(C)** edge density and **(D)** clustering coefficient



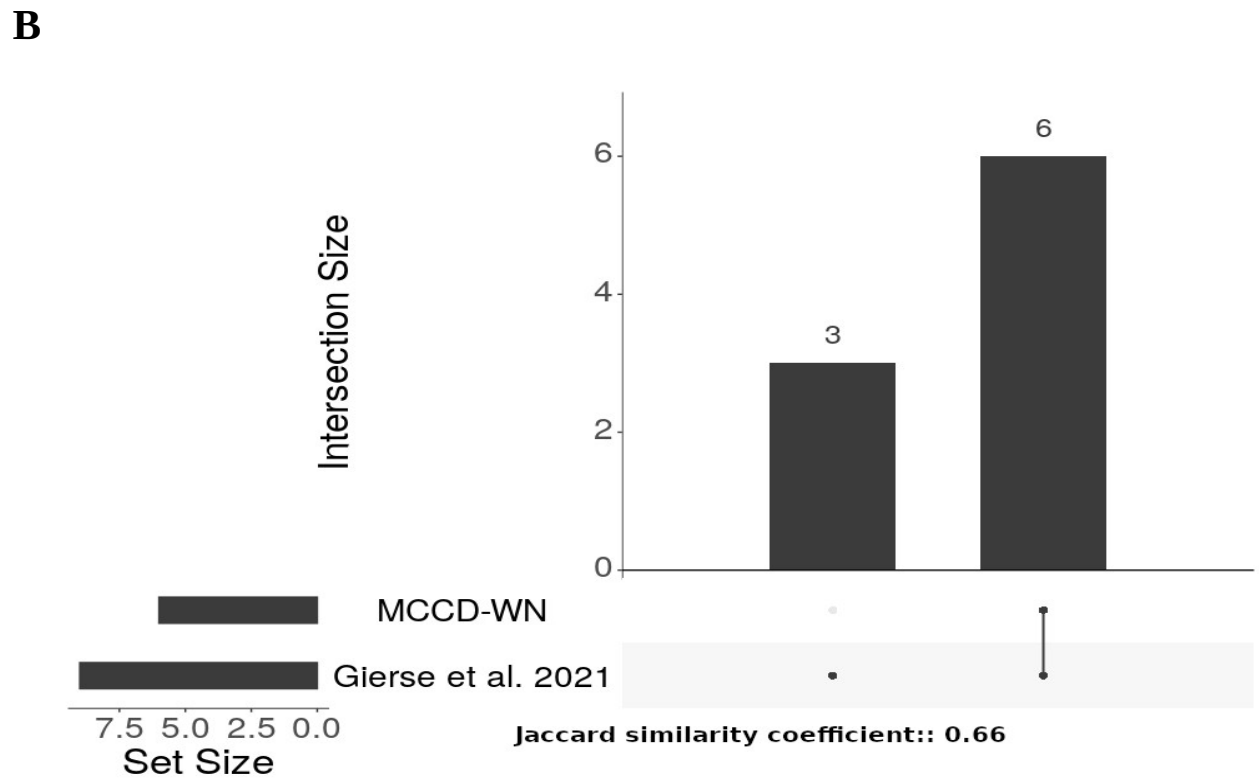
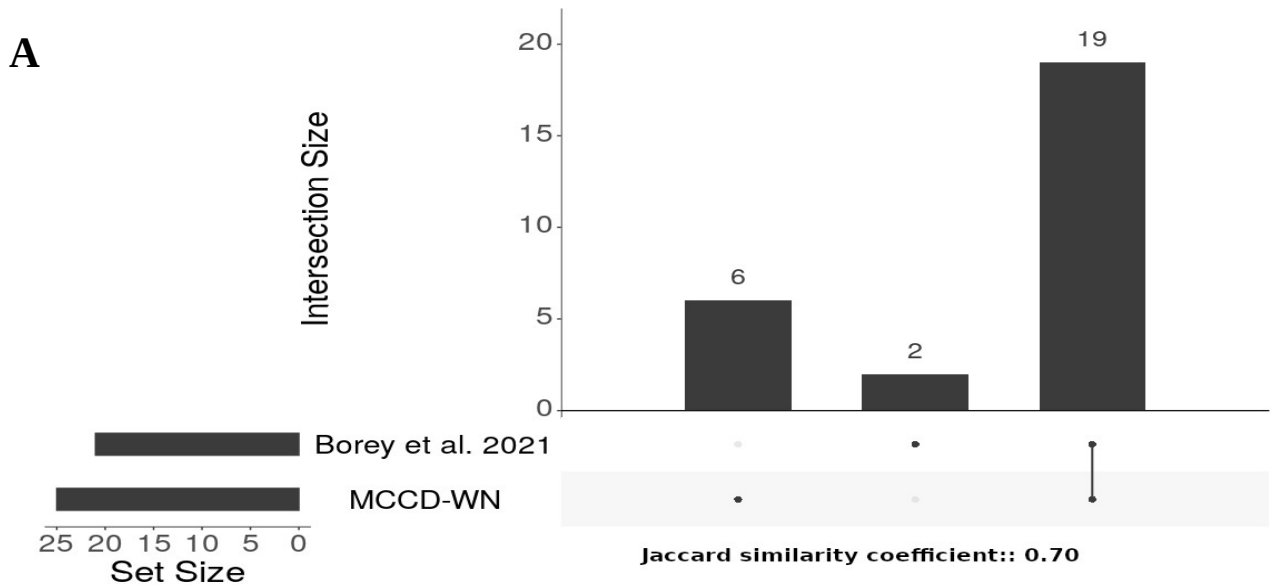
Supplementary Figure 2: Comparison between LFR benchmark networks (AN_1) and the infected co-abundance networks in terms of **(A)** number of nodes, **(B)** number of edges, **(C)** edge density and **(D)** clustering coefficient



Supplementary Figure 3: Absolute difference between clustering coefficients of healthy co-abundance network and LFR benchmark networks (AN_1)



Supplementary Figure 4: Absolute difference between clustering coefficients of infected co-abundance network and LFR benchmark networks (AN_1).



Supplementary Figure 5: Intersection between the microbiome families found by the proposed workflow and (A) reported to be important in Borey, M et al., 2021 and (B) Gierse, LC et al., 2021.