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Page 7: Figure 5 General patterns of microbial β-diversity in soil samples from both (A) mangrove forest and (B) shrimp pond sites. The abscissa represents the logarithm of the distance, and the ordinate represents the similarity based on the Chao index. The equation of each line is shown along with its P-value.

Page 8: Figure 6 Null model analysis of both the deterministic and stochastic processes shaping the bacterial community assembly across both habitats.

Page 9: Figure 7 Best fit of community assembly to the neutral community model (NCM). The predicted occurrence frequencies for (A) mangrove forest and (B) shrimp pond communities. The solid blue lines indicate the best fit to the NCM (Sloan et al., 2012) and the dashed blue lines represent 95% confidence intervals around the model predictions. Operational taxonomic units (OTUs) that occur more or less frequently than predicted using the NCM are shown in different colors. Nm denotes the metacommunity size multiplied by immigration and R^2 indicates the fit to this model.

Page 10: Figure 8 Microbial co-occurrence networks for (A, C) mangrove forest and (B, D) shrimp pond communities based on correlation analysis. Each connection represents a strong (Spearman's $\rho > 0.6$) and significant ($P\text{-value} < 0.05$) correlation. Both the shrimp pond and mangrove forest communities are color-coded according to the microbial phylum or module. The interrelationships between species are shown in different colors, with red representing positive correlations and blue denoting negative correlations.

Page 11: Figure 9 Total and negative cohesion (absolute value) between each mangrove forest network and shrimp pond network (***$P < 0.001$; Wilcoxon rank-sum test). The values represent the mean ± standard error (SE).

Page 12: Figure 10. Extended error bar plot identifying significant differences between mean proportions of metabolic functions at KEGG level 2 and KEGG level 3 in mangrove habitat and shrimp pond habitat. The plot was generated in STAMP (Welch's t-test, two-sided, 95% confidence interval, $p<0.01$).

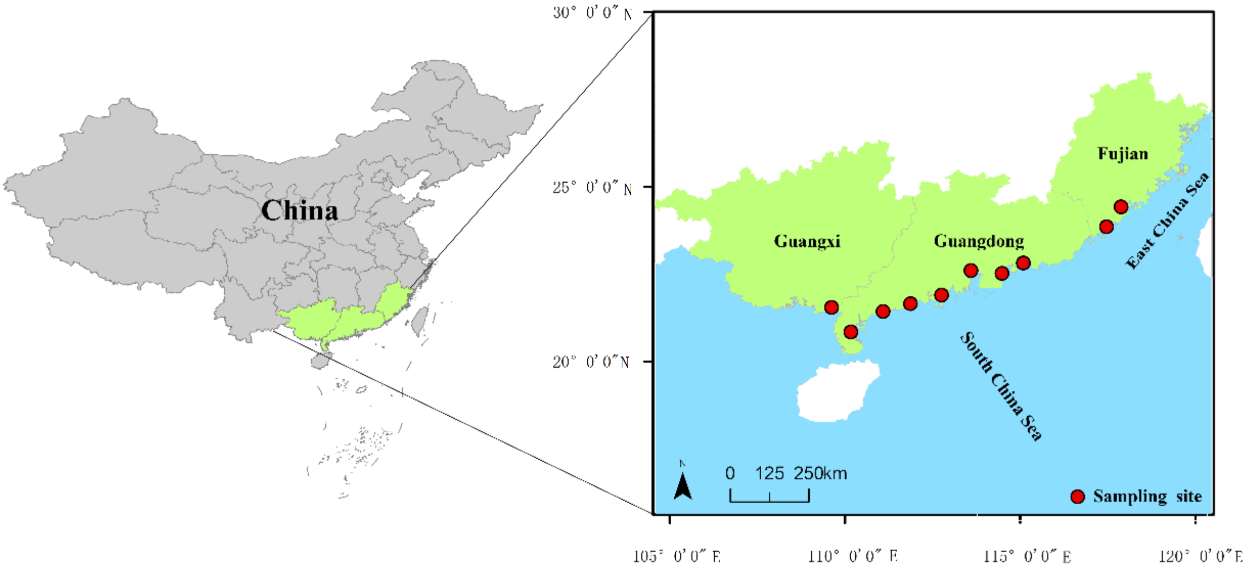


Figure 1. Locations of the 10 paired sampling sites in mangrove forests and shrimp ponds across southeastern China.

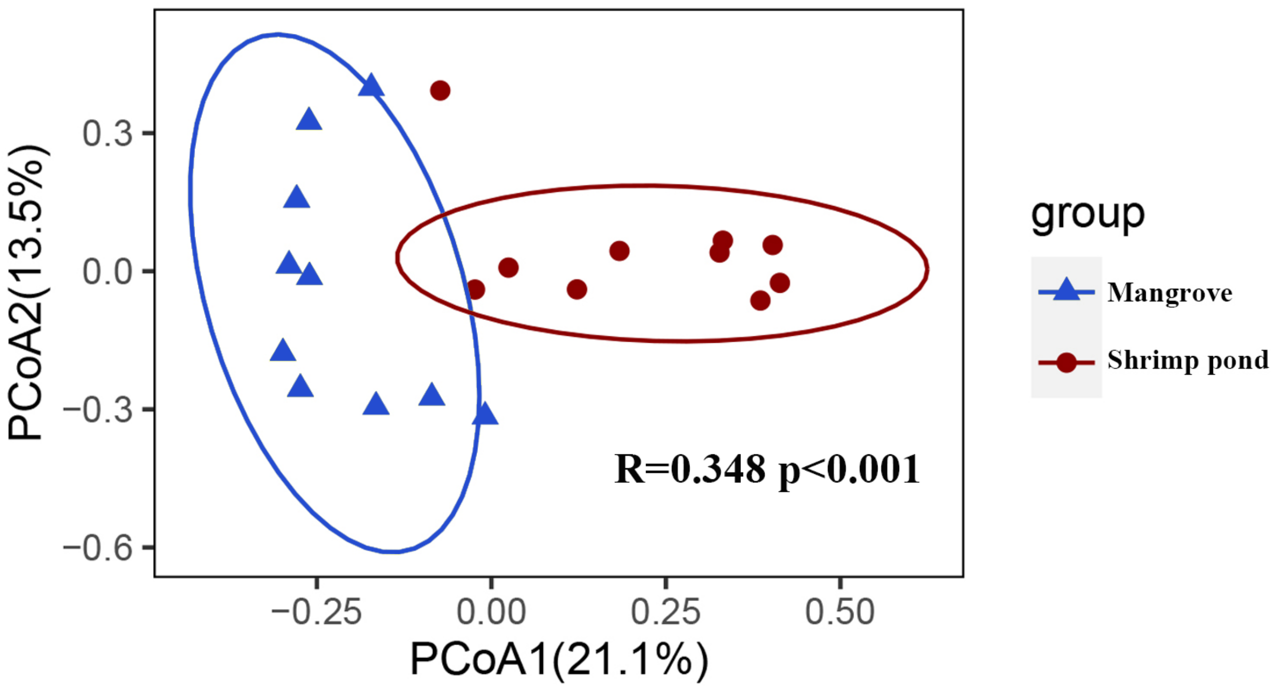
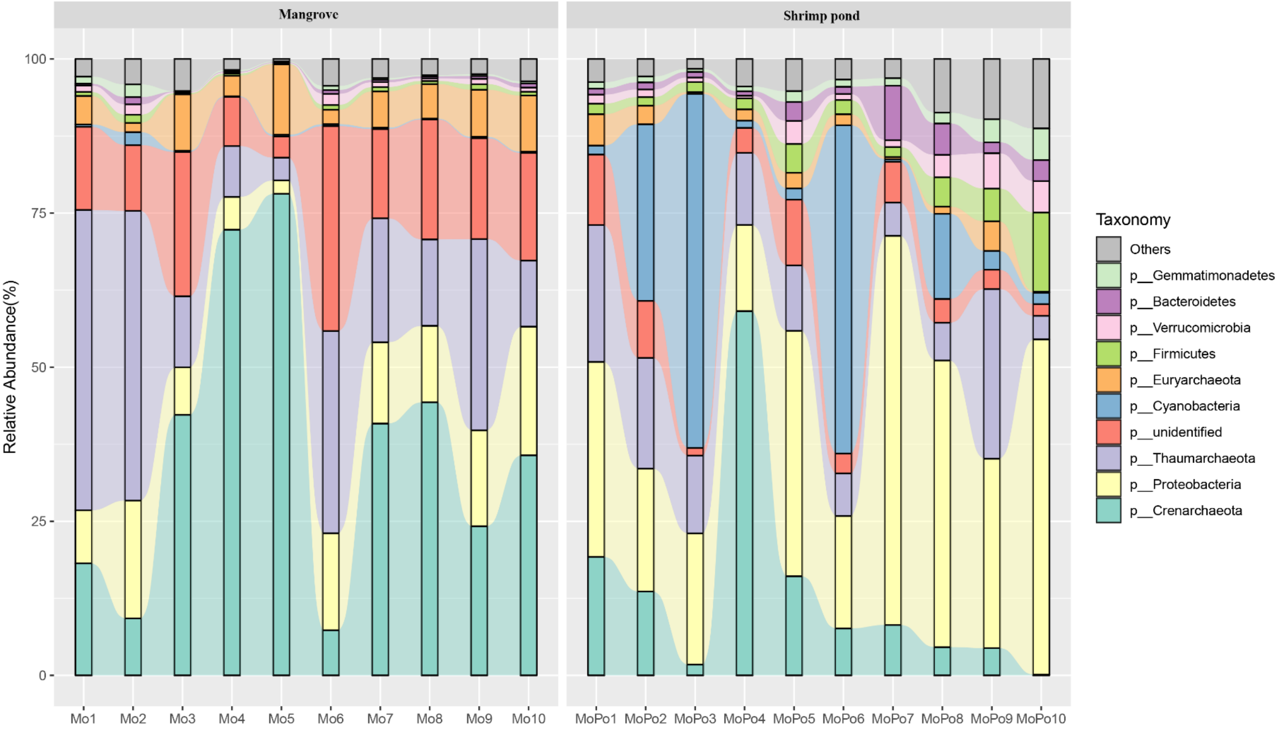


Figure 2. Principle coordinate analysis (PCoA) of the Bray–Curtis dissimilarity index of the microbial community composition between the shrimp pond and mangrove forest samples. The P-value was calculated using the adonis function in R.



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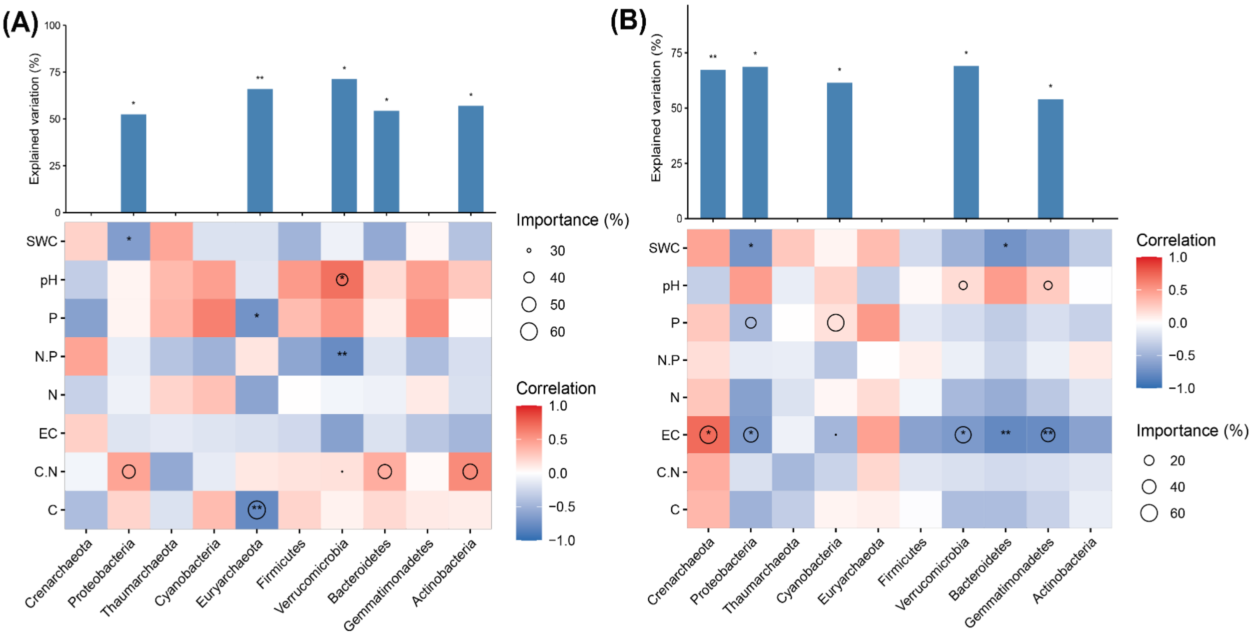

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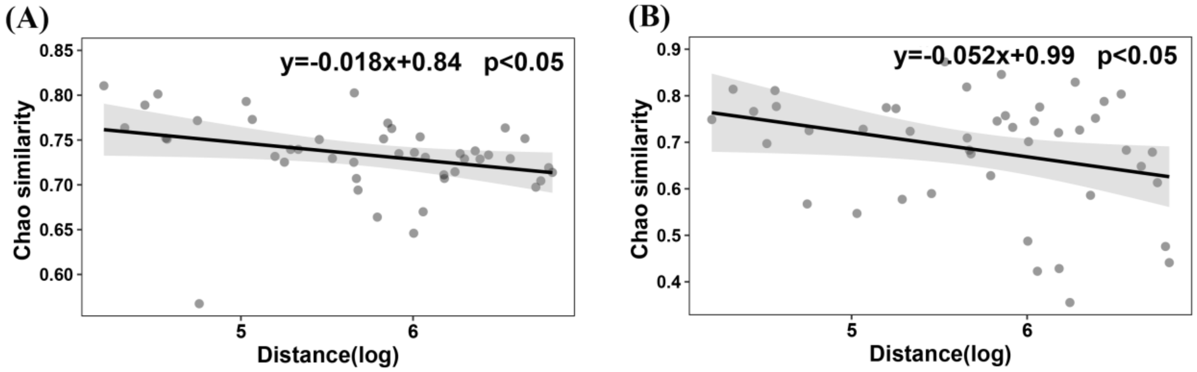


Figure 5. General patterns of microbial β-diversity in soil samples from (A) mangrove forests and (B) shrimp ponds. The abscissa represents the logarithm of the distance, and the ordinate represents the similarity based on the Chao1 index. The equation of each line is shown along with its P-value.

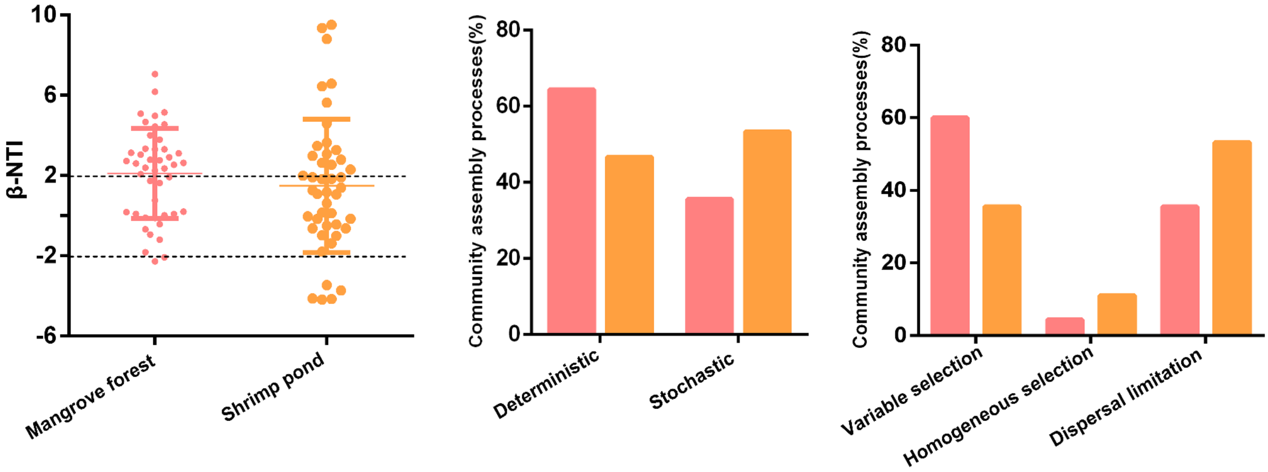


Figure 6. Null model analysis of the deterministic and stochastic processes shaping the microbial community assembly in mangrove forests and shrimp ponds.

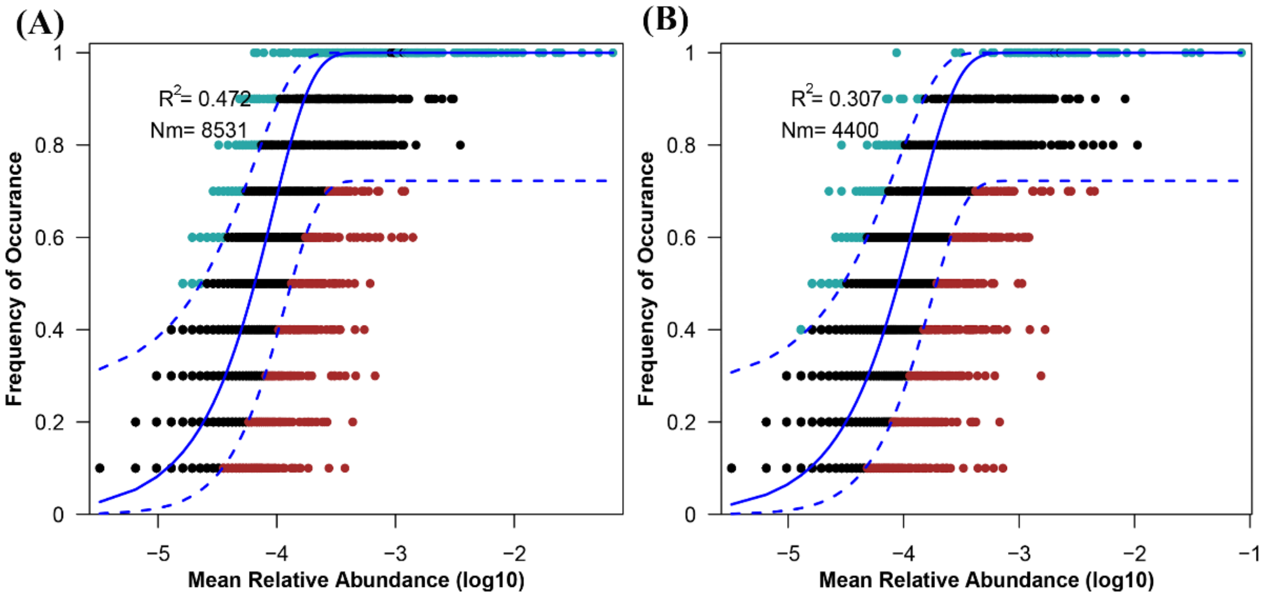
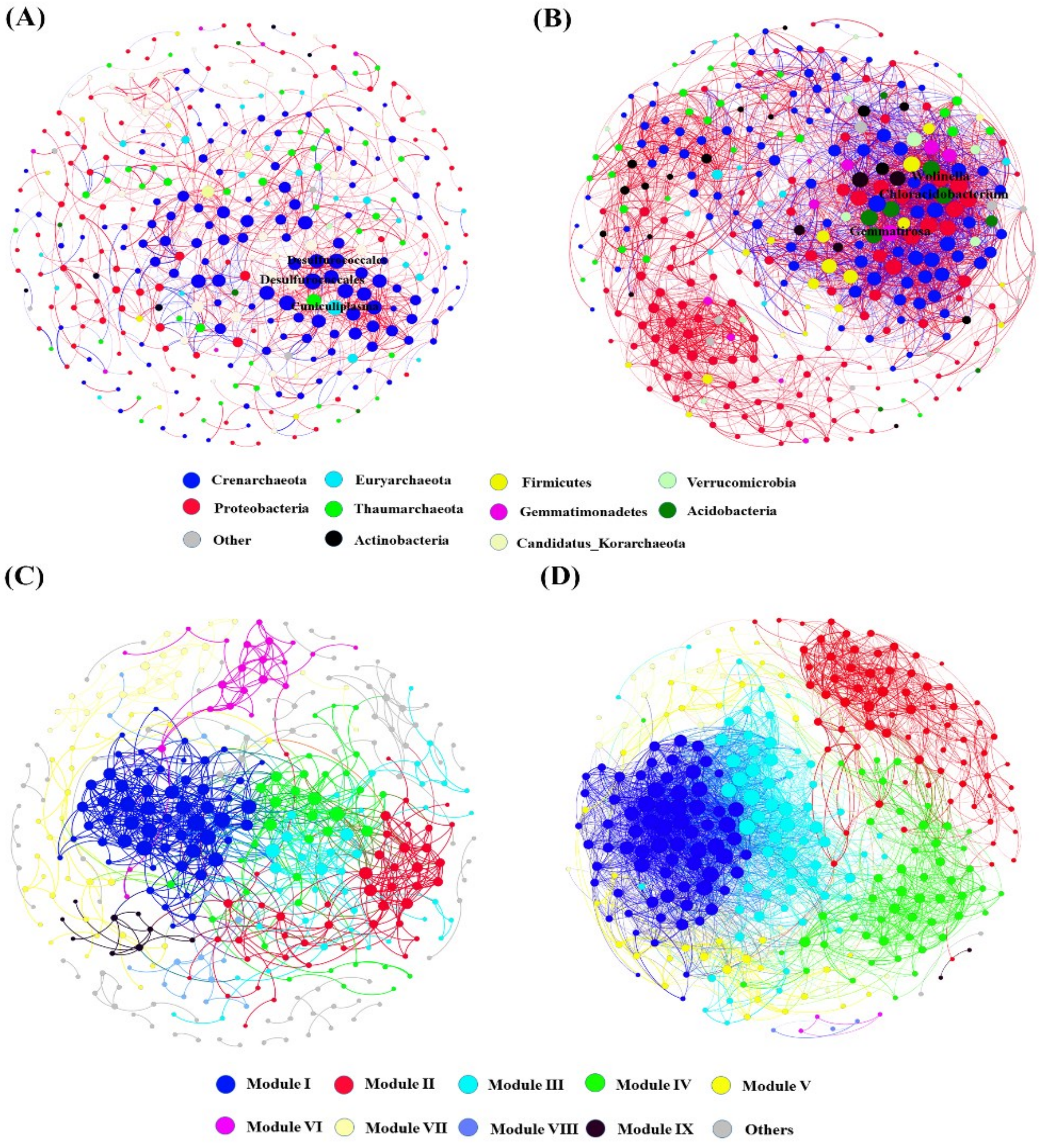


Figure 7. Best fit of community assembly to the neutral community model (NCM). The predicted occurrence frequencies for (A) mangrove forest and (B) shrimp pond communities. Solid blue lines indicate the best fit to the NCM (Sloan et al., 2012), and dashed blue lines represent the 95% confidence intervals around the model predictions. Operational taxonomic units (OTUs) occurring more or less frequently than predicted using the NCM are shown in different colors. Nm indicates the metacommunity size multiplied by migration, and R^2 indicates the fit to the model.



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representing the respectively positive and negative correlations.

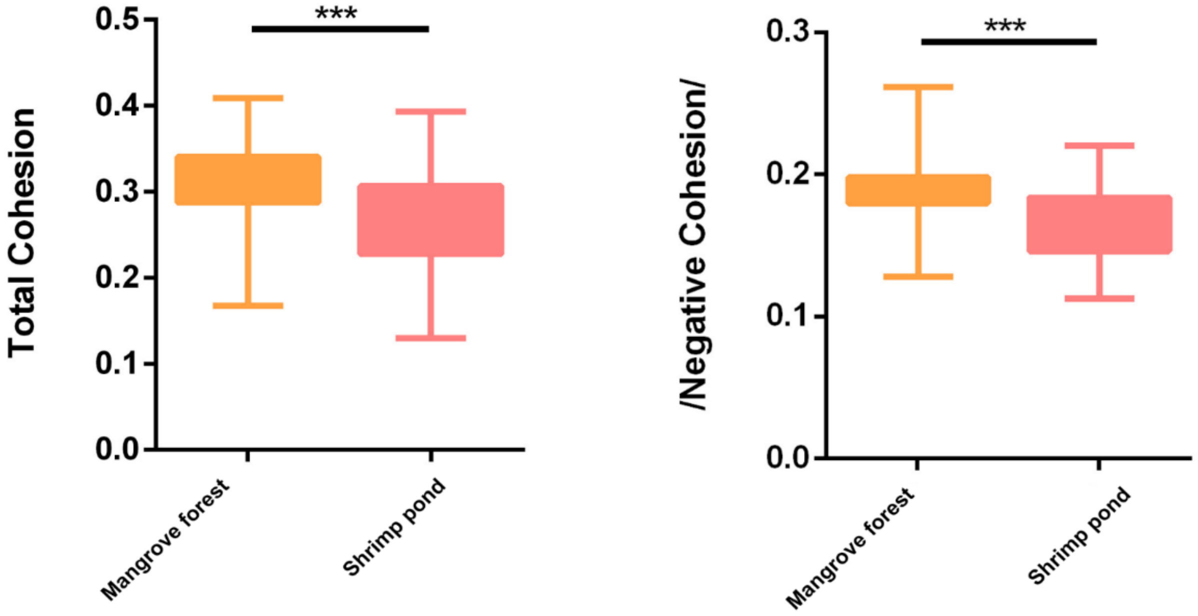
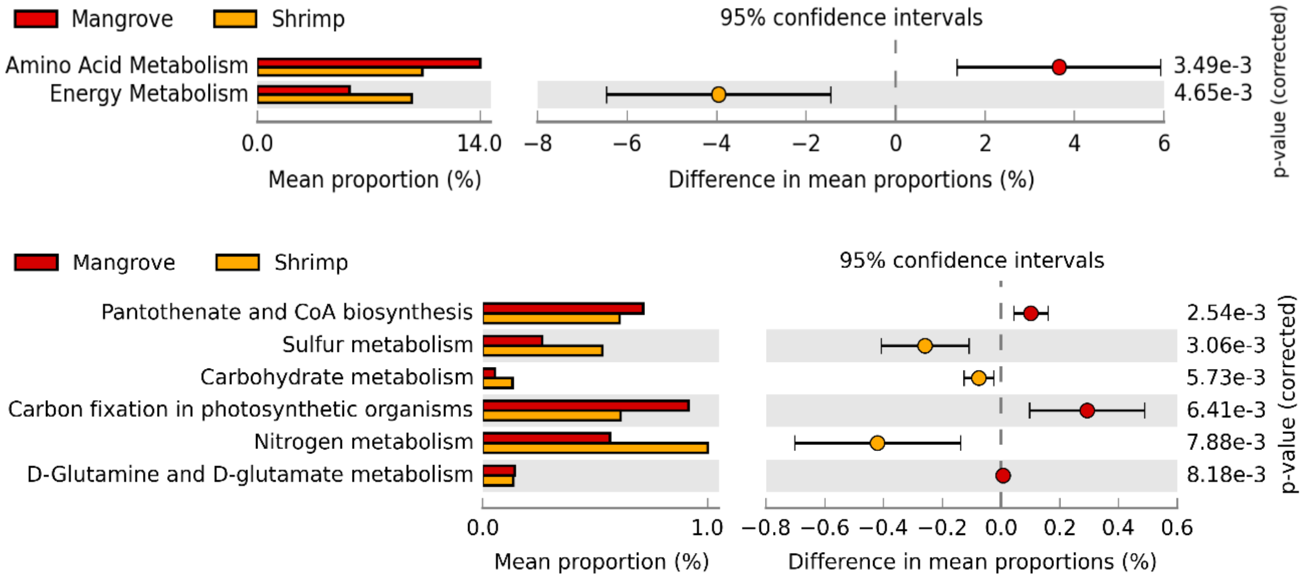


Figure 9. Total and negative cohesion (absolute value) between each mangrove forest and shrimp pond (***P < 0.001; Wilcoxon rank-sum test) network. The values are presented as the mean ± standard error (SE).



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