

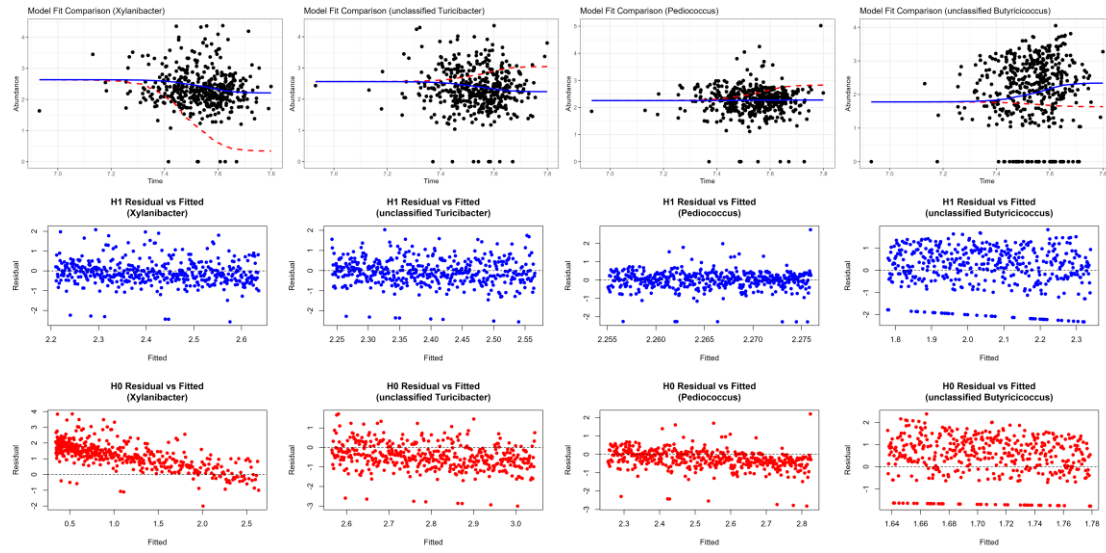


Figure S4. Model fitting and residual diagnostics for representative microbial taxa under models with and without interaction effects. For each selected taxon, observed abundance trajectories (black points) are compared with fitted curves from the null model H_0 (red dashed lines, without interaction terms) and the full model H_1 (blue solid lines, including interaction effects). Residuals versus fitted values are shown below to assess systematic deviations and model adequacy. Across all taxa, the H_1 model demonstrates improved agreement with observed quasi-dynamics and reduced structured residual patterns.