# Code and Data for " Biodegradable plastic exposure enhances microbial functional diversity while reducing taxonomic diversity across multi–kingdom soil microbiota in cherry tomato fields "

This document describes the correspondence between code lines and figure panels for reproducibility.

## Repository Structure

All figures were generated using the R script main\_plot.R, and the corresponding source data files located in the /data folder.

## Figure–Code Correspondence

|  |  |  |  |
| --- | --- | --- | --- |
| Figure | Panel | Code Lines in main\_plot.R | Description |
| Fig. 1 | a | L436–L998 | Beta diversity of microbiome |
| Fig. 1 | b | L386–L427 | Alpha diversity of microbiome |
| Fig. 2 | a | L10838–L10947 | Phylogenetic diversity |
| Fig. 2 | b | L10950–L11498 | LDA analyze |
| Fig. 3 | — | L5018–L7642 | The neutral community model |
| Fig. 4 | a | L7747–L9011 | Co-occurrence network |
| Fig. 4 | b-d | L9016–L9231 | Topological characteristics of network |
| Fig. 5 | a | L2895–L3429 | Alpha diversity of function |
| Fig. 5 | b | L2895–L3429 | Beta diversity of function |
| Fig. 5 | c-d | L4147–L4348 | Carbon function lefse |
| Fig. 5 | e-f | L3073–L3096 | Barplot of Xenobiotics Biodegradation and Metabolism pathways |

## Software Environment

R version 4.4.2

## Version Information

Zenodo DOI: 10.5281/zenodo.16902958  
Version 2 (Oct 2025): Added figure–code correspondence by line numbers for reproducibility.  
Version 1 (Apr 2024): Initial release.