

## Statistical Analysis Workflow

### 1. ANOVA Analyses

#### 1.1 Repeated-Measures ANOVA

Dependent Variables: soil temperature ( $T_{\text{soil}}$ , °C), soil salinity ( $S_{\text{soil}}$ , dS m<sup>-1</sup>), soil organic carbon content ( $\text{SOC}_{\text{content}}$ , g kg<sup>-1</sup>), SOC storage ( $\text{SOC}_{\text{storage}}$ , kg m<sup>-2</sup>), net primary productivity (NPP, kg m<sup>-2</sup>yr<sup>-1</sup>), soil heterotrophic respiration ( $R_h$ , kg C m<sup>-2</sup> yr<sup>-1</sup>), amino sugar content (mg kg<sup>-1</sup>), lignin phenol content (mg kg<sup>-1</sup>), microbial necromass C (g kg<sup>-1</sup>), plant necromass C (g kg<sup>-1</sup>), plant species diversity, and the abundance of C-degradation genes, *P. australis* biomass (kg m<sup>-2</sup> yr<sup>-1</sup>), *S. glauca* biomass (kg m<sup>-2</sup> yr<sup>-1</sup>), and the biomass of other species (kg m<sup>-2</sup> yr<sup>-1</sup>).

Factors: Warming treatment, Year, Interaction (Warming × Year).

Input File: Input\_ANNOVAs.sav

Output File: Output\_ANNOVAs.spv

#### 1.2 One-Way ANOVA (Annual Comparisons)

Dependent Variables: Same as above.

Grouping Factor: Warming treatment (analyzed separately for each year).

Input Files: Input\_ANNOVAs.sav

Output Files: Output\_ANNOVAs.spv

### 2. Redundancy Analysis with Hierarchical Partitioning (RDA-HP)

Independent Variables: Changes in plant species diversity, NPP, abundance of C-degradation genes,  $R_h$ .

Dependent Variable: Variations in microbial necromass C under warming.

Input File: Input\_RDA\_HP

R Script (using rdacca.hp package):

```
r
library(rdacca.hp)
Mydata=readxl::read_xlsx("./Data/Input_RDA_HP.xlsx")
Myrdacca=rdacca.hp(Mydata[,2],Mydata[,3:6])
write.csv(hp_contrib, "RDA_HP_Contributions.csv")
Output file: RDA_HP_Contributions.csv
```

### 3. Structural Equation Modeling (SEM)

#### 3.1 Model Hypotheses

(1) Carbon input pathways: Warming-induced shifts in plant community composition influence plant productivity, which subsequently alters microbial and plant necromass C, thereby impacting SOC. (2) Carbon output pathways: Warming directly or indirectly affects carbon decomposition by influencing carbon input and the abundance of C-degradation genes, ultimately affecting SOC through the mediation of microbial and plant necromass C.

#### 3.2 Tests of normality

We tested all variables (SOC, microbial necromass C, plant necromass C, plant species diversity, NPP, Rh, abundance of C-degradation genes) using Shapiro-Wilk tests and visual inspections (Q-Q plots, histograms). Results indicated that these variables largely adhered to univariate normality (skewness  $< |2|$ , kurtosis  $< |7|$ ; Curran et al., 1996). To further mitigate residual non-normality risks, we employed Bootstrap resampling (2,000 iterations) in AMOS, generating bias-corrected confidence intervals and standard errors. This approach reduces reliance on strict normality assumptions and enhances parameter stability. Path coefficients and model fit indices derived from Bootstrap showed high consistency with maximum likelihood estimates, supporting the robustness of our conclusions.

Output File: Tests of Normality\_SEMs

#### 3.3 AMOS Model Files:

SEM\_Input\_All.sav (Figure S14)

SEM\_Input\_PhaseI.sav (Figure 4a)

SEM\_Input\_PhaseII.sav (Figure 4b)

SEM\_ALL.amw (Figure S14)

SEM\_PhaseI.amw (Figure 4a)

SEM\_PhaseII.amw (Figure 4b)

SEM\_ALL.amp (Figure S14)

SEM\_PhaseI.amp (Figure 4a)

SEM\_PhaseII.amp (Figure 4b)

SEM\_ALL.amosoutput (Figure S14)

SEM\_PhaseI.amosoutput (Figure 4a)

SEM\_PhaseII.amosoutput (Figure 4b)