

Ant Climate Project

Path analysis using PCA - Regional using conditional averaging

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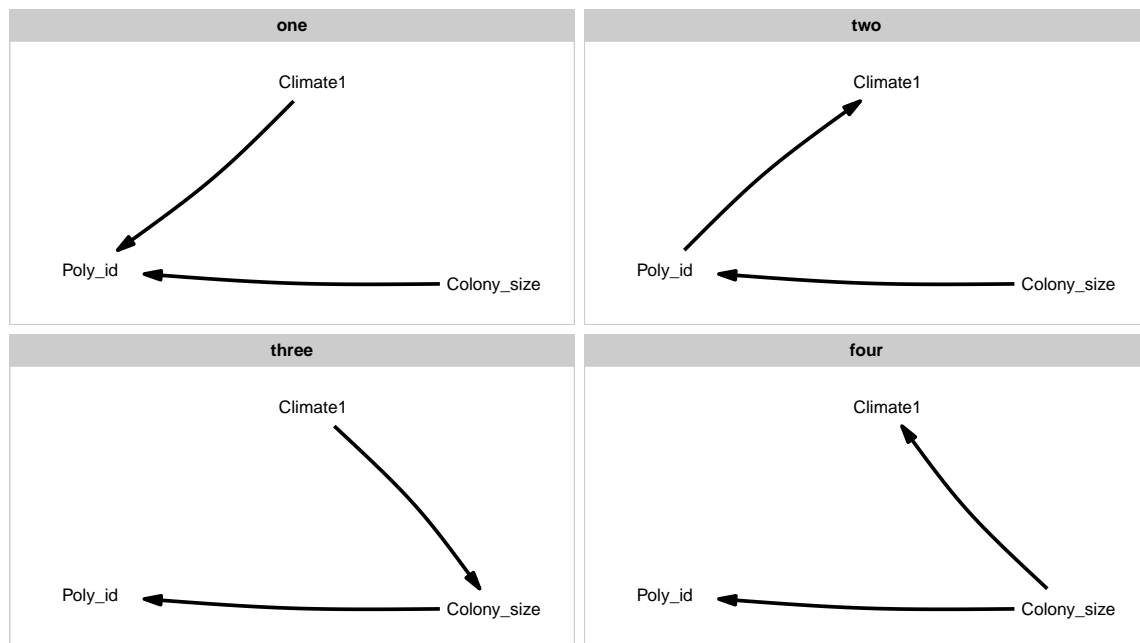
1 Initial comments

- Read in the ant data and prepare the variables for path analysis. There are 474 species for which data is available for colony size and climatic variables, excluding special ants. Process repeated on the 4 different PCA datasets created using the 4 different MCC trees.
- We use PCA for phylogenetic path analysis as path analysis with both temperature and rainfall variables in the same models were always rejected, unless causal paths were drawn between climatic variables. This is likely because of the correlation between climatic variables. Path analysis with PCA allows us to analyse both temperature and rainfall in the same causal models.
- The potential model set is reduced to just four models for each analysis, assuming that colony size has a direct effect on the number of worker castes (Bell-Roberts et al., 2023).

2 Summary

- Greater colony size favours both greater worker size variation and allows invasion into drier regions. Both path coefficients are significant.

3 Create alternative causal models

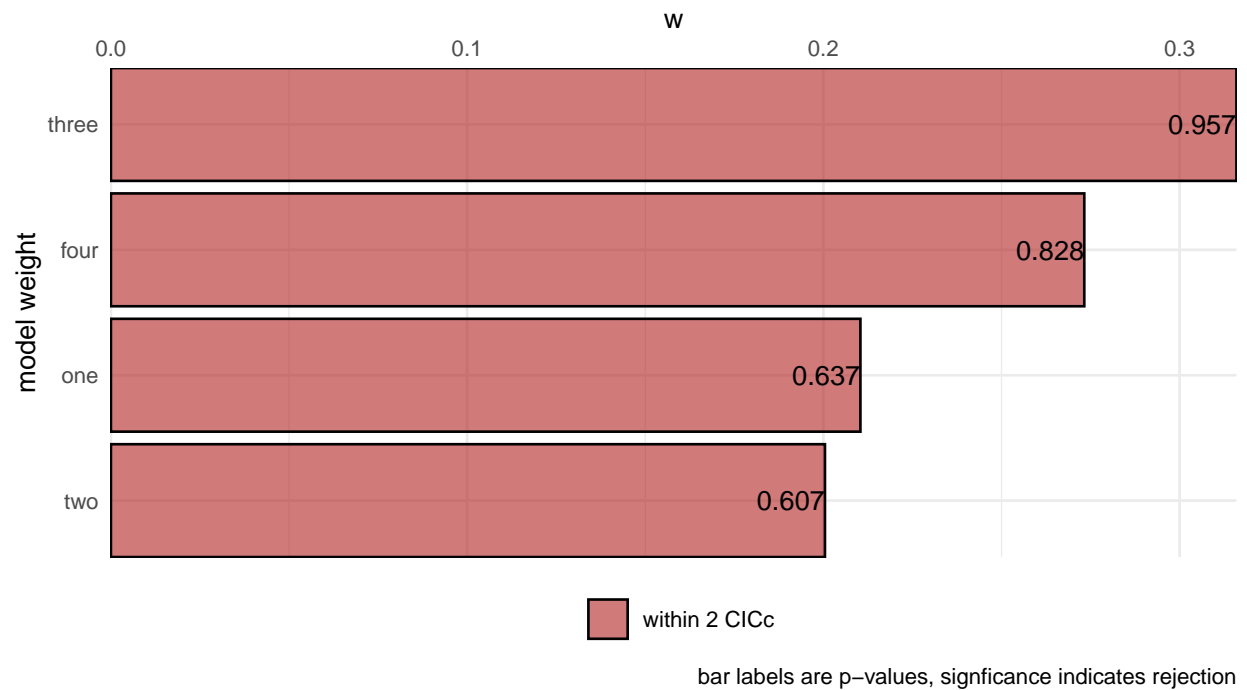


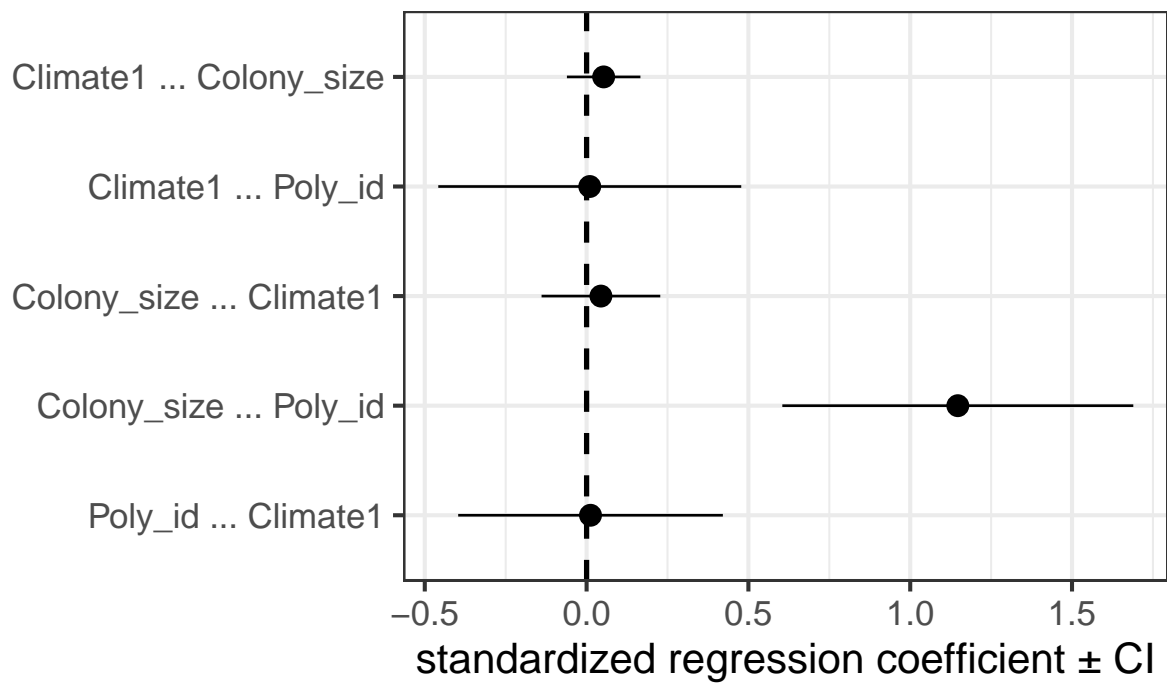
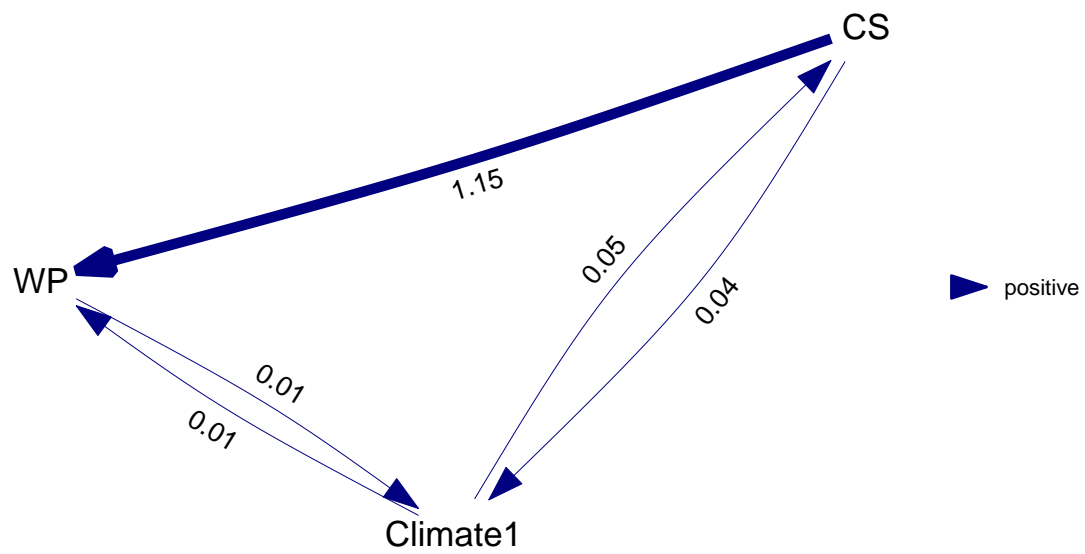
4 Path analysis

4.1 Tropical

4.1.1 NCuniform stem tree

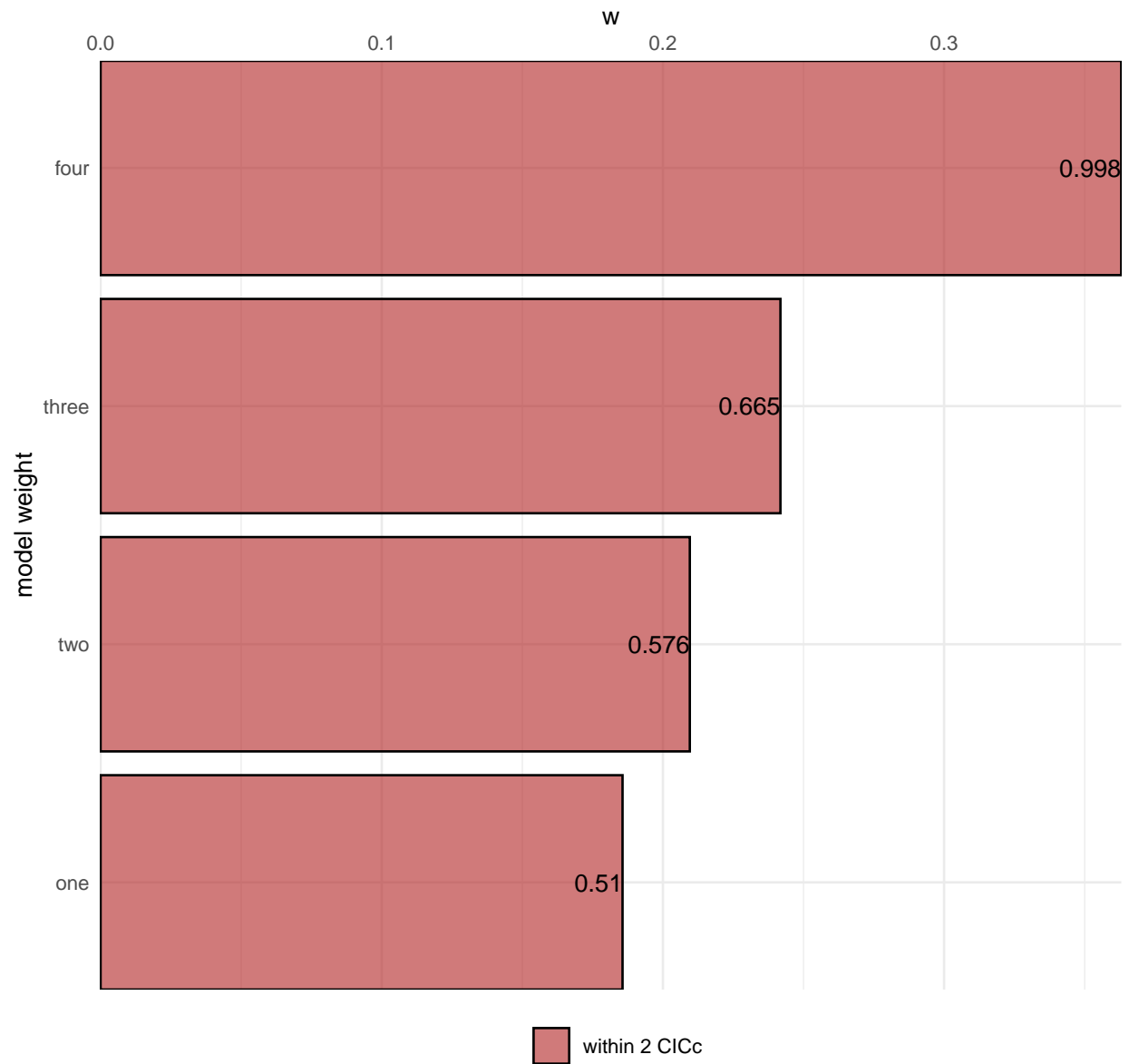
Factor loading PC1: TMP: negative; PRE: negative



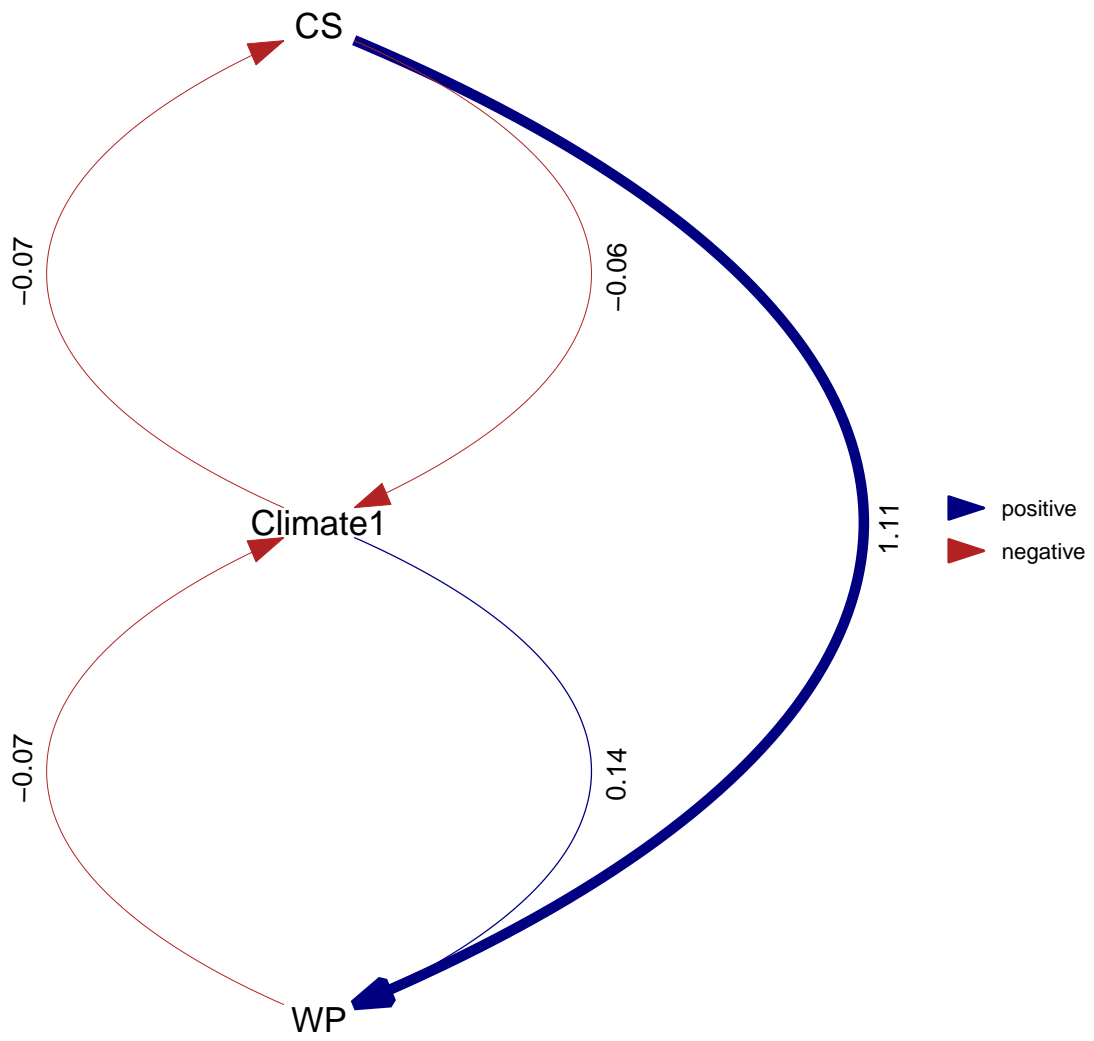


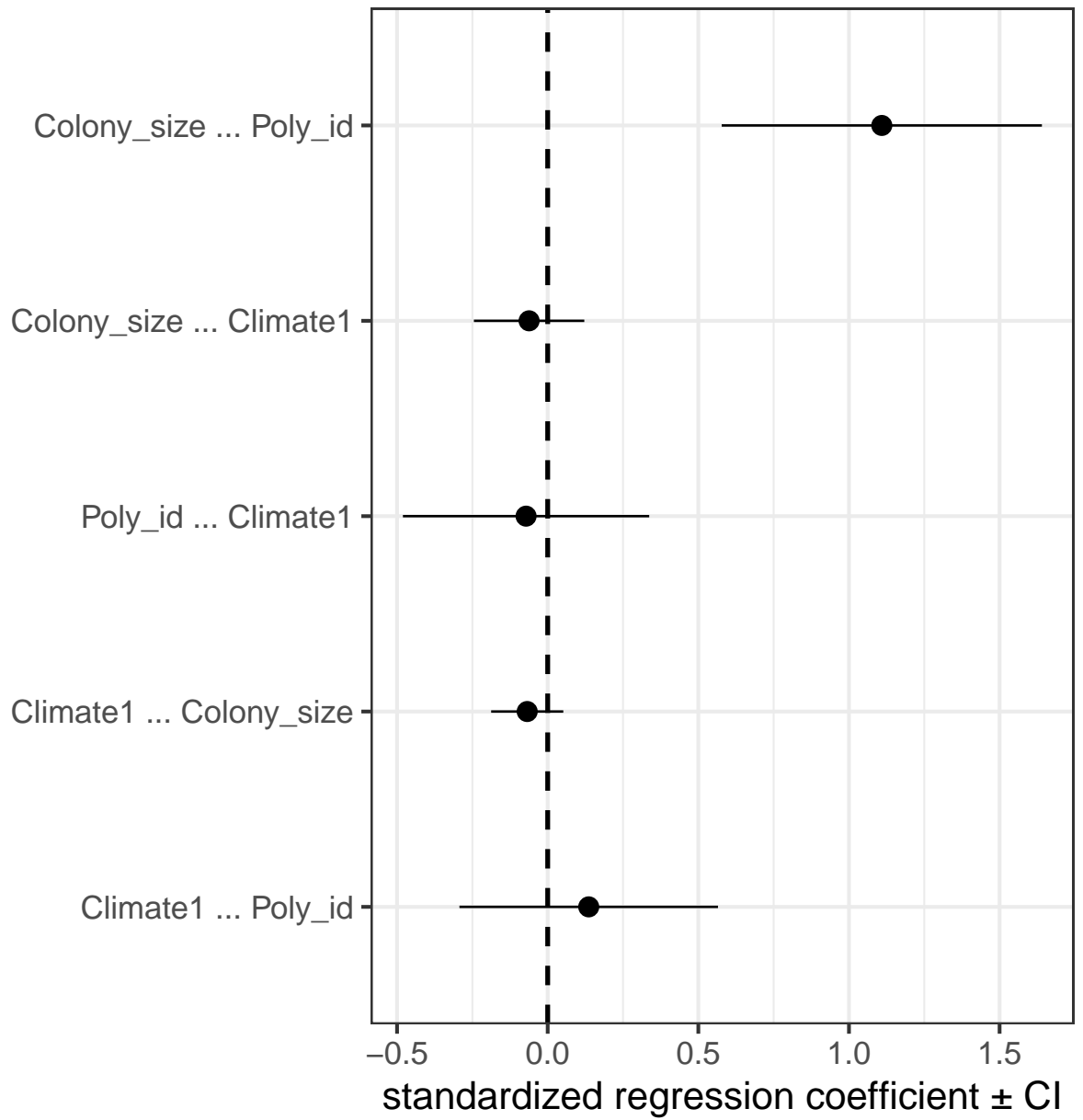
4.1.2 NCuniform crown tree

Factor loading PC1: TMP: positive; PRE: positive



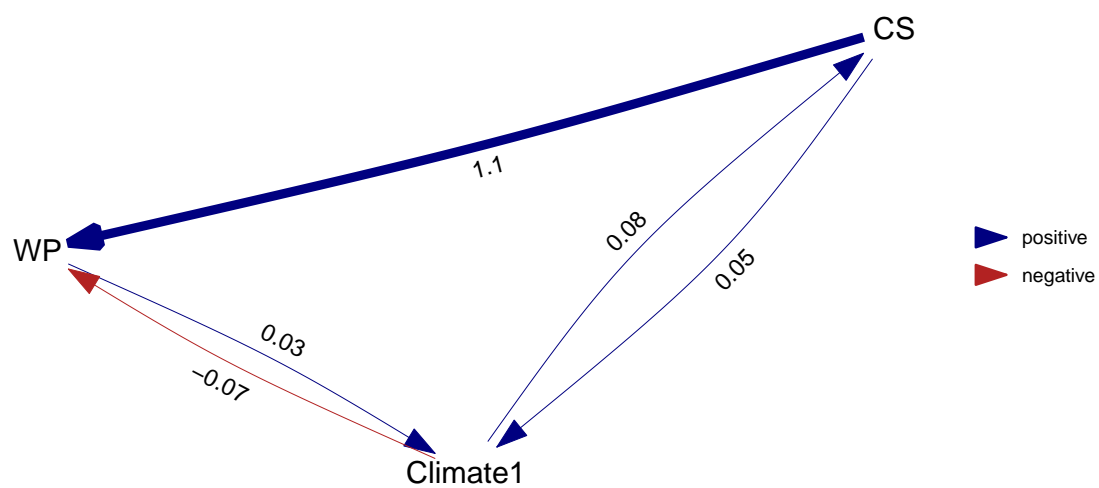
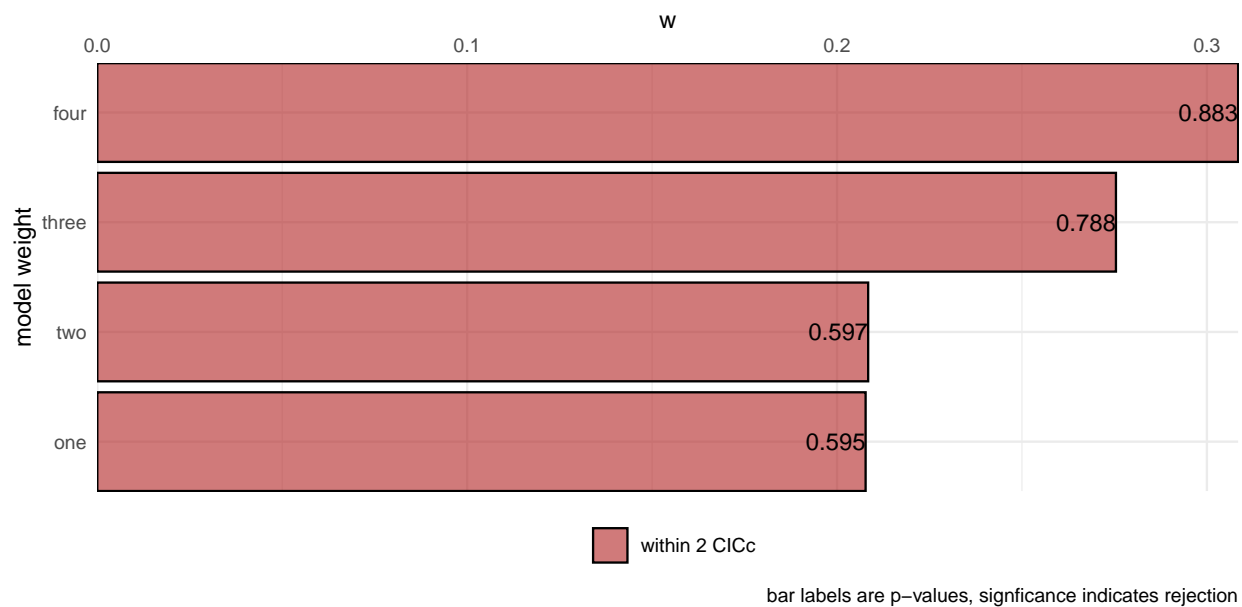
bar labels are p-values, significance indicates rejection

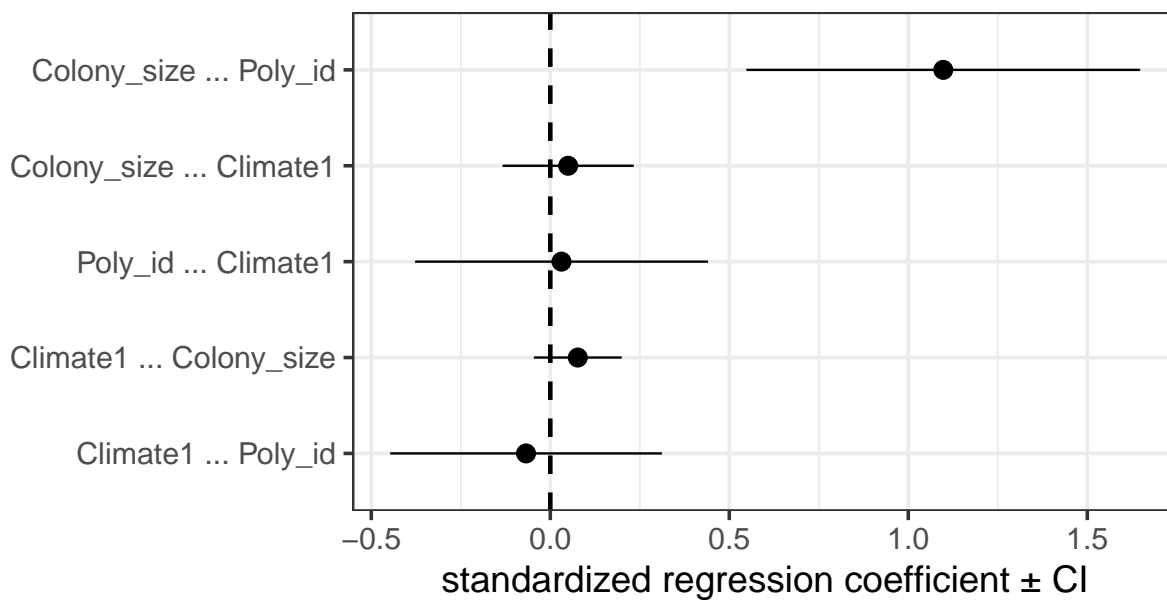




4.1.3 FBD stem tree

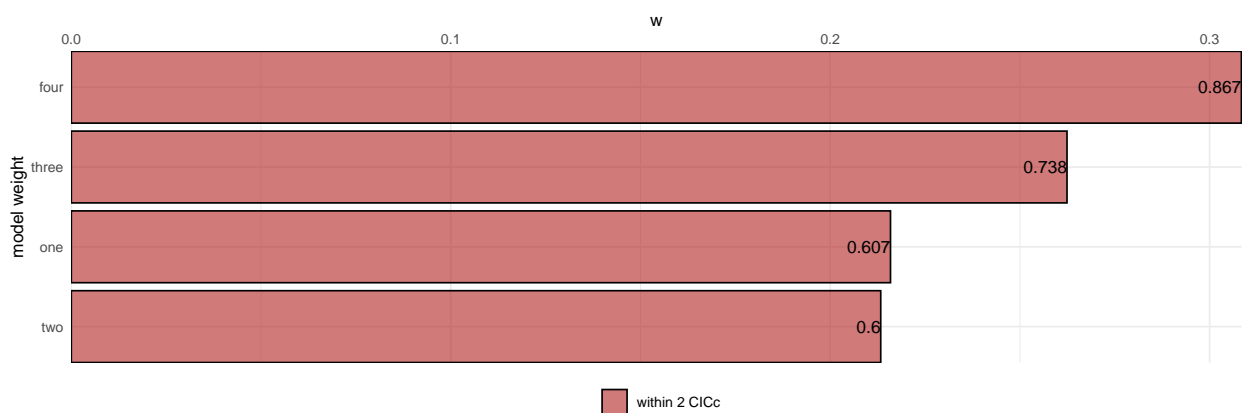
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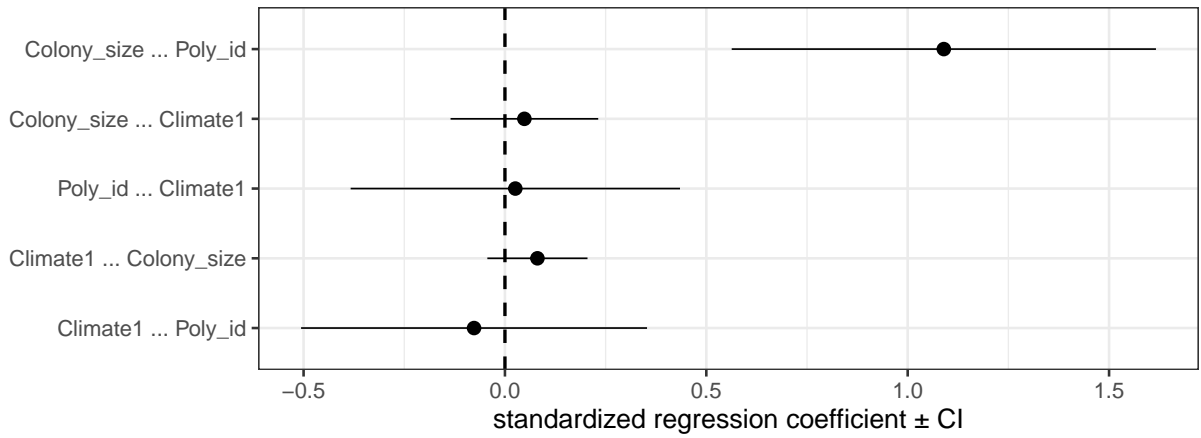
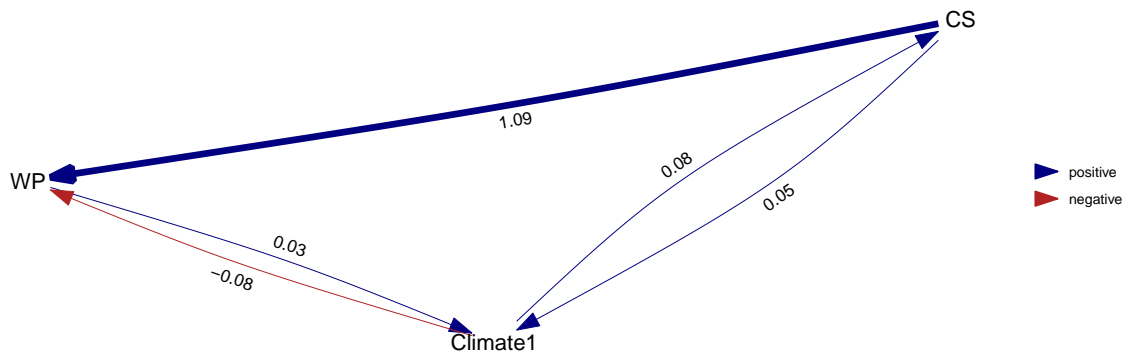


4.1.4 FBD crown tree

Factor loading PC1: TMP: negative; PRE: negative



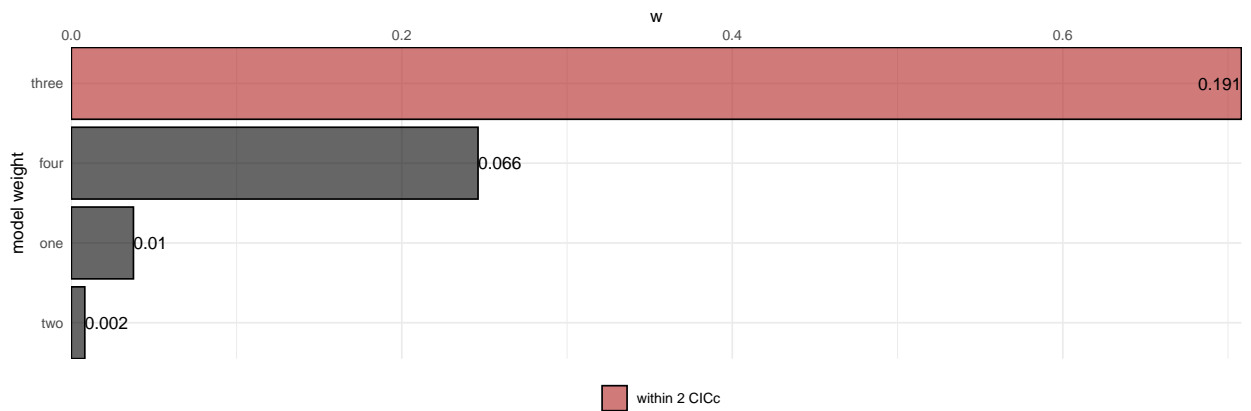
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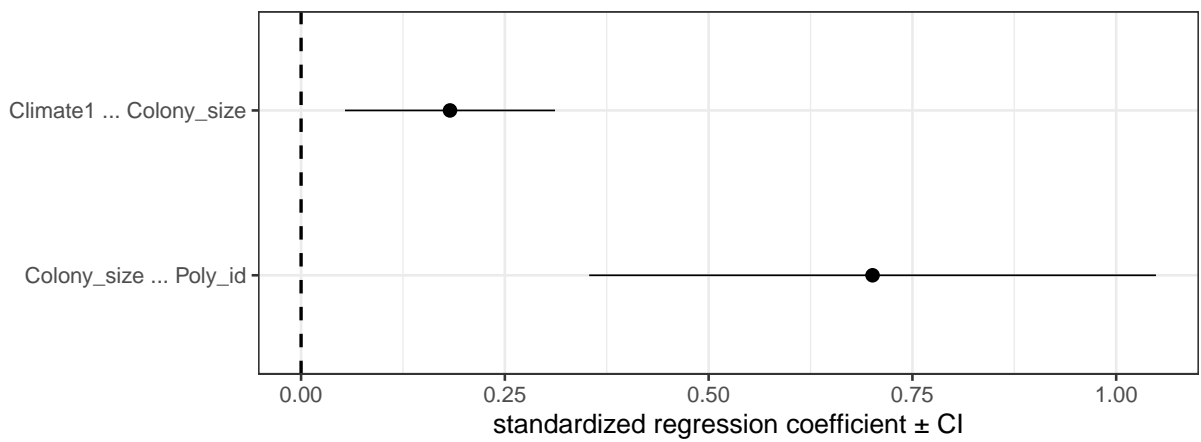
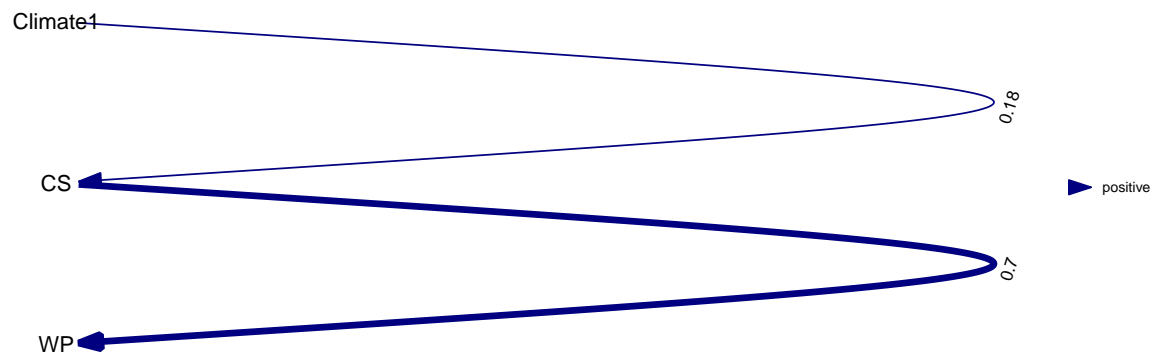
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4.2.1 NCuniform stem tree

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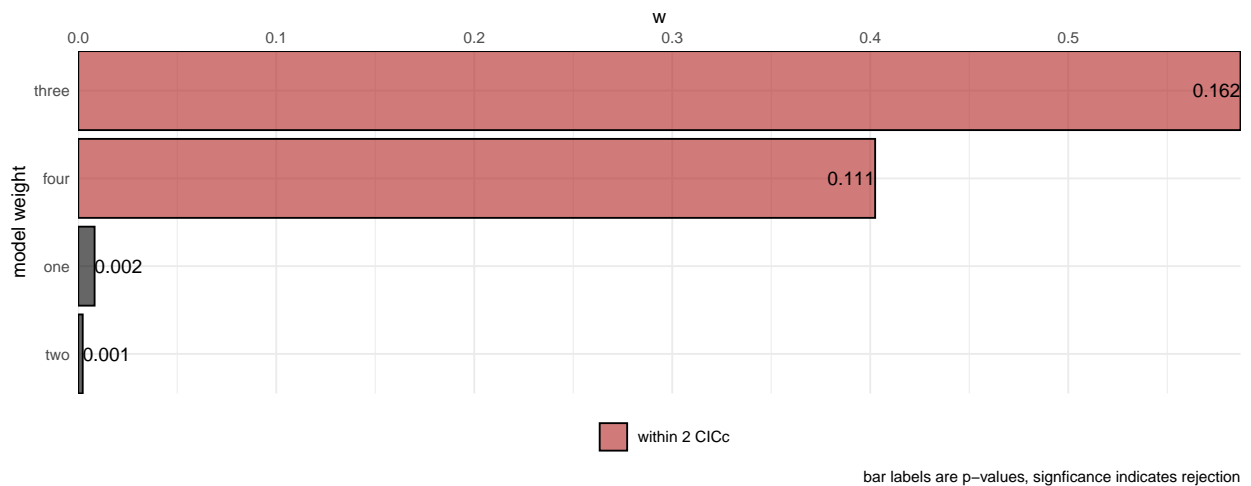


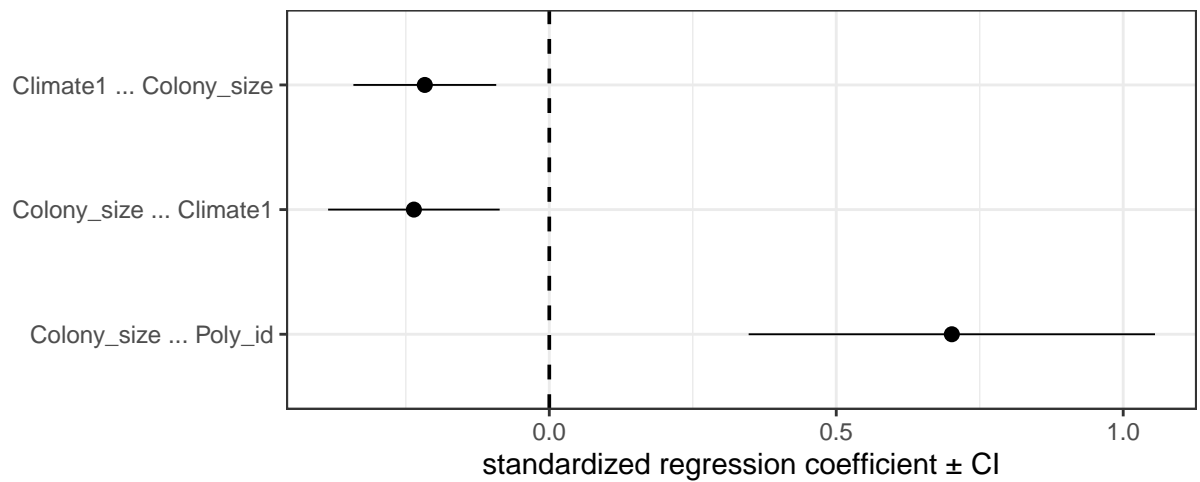
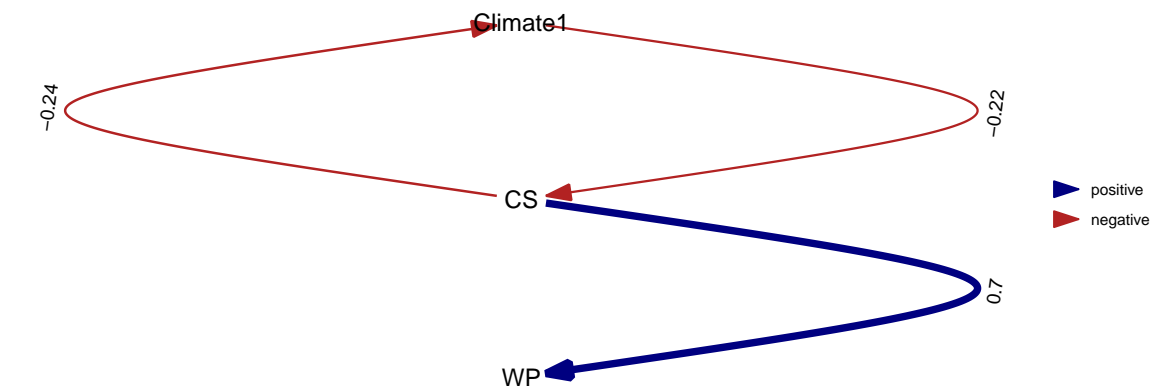
bar labels are p-values, significance indicates rejection



4.2.2 NCuniform crown tree

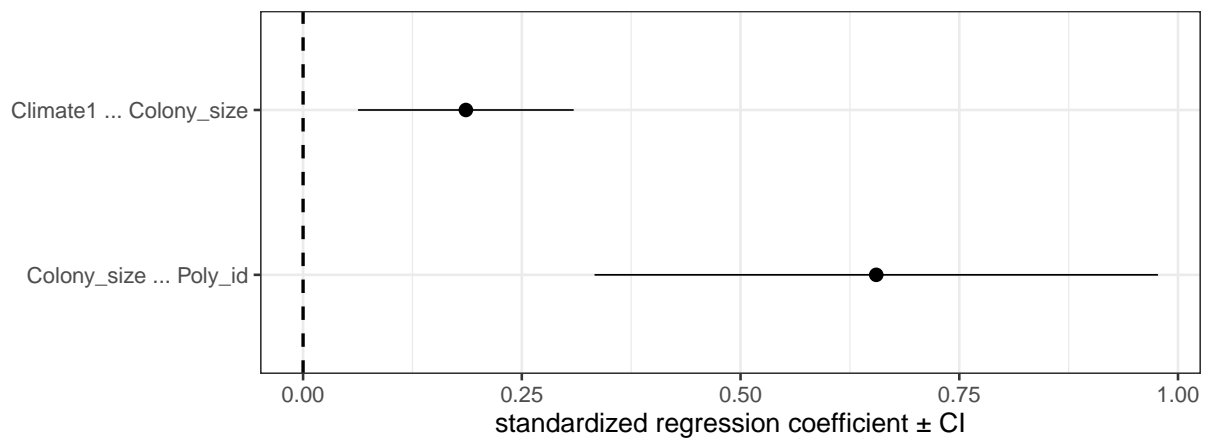
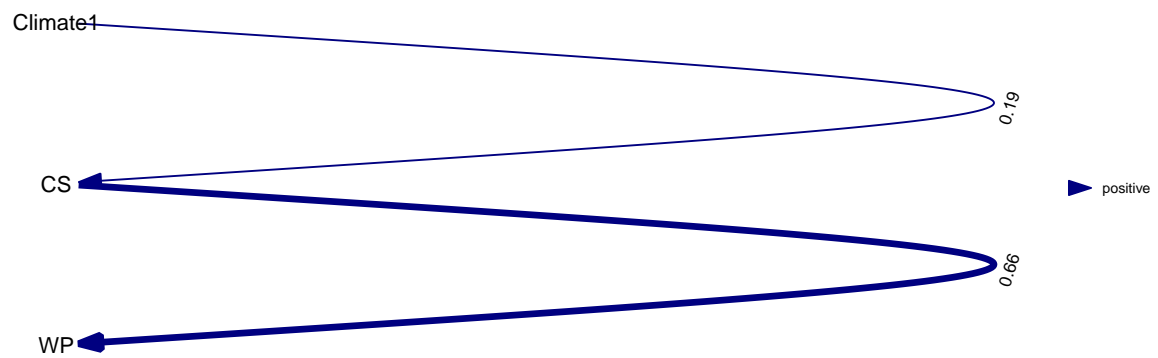
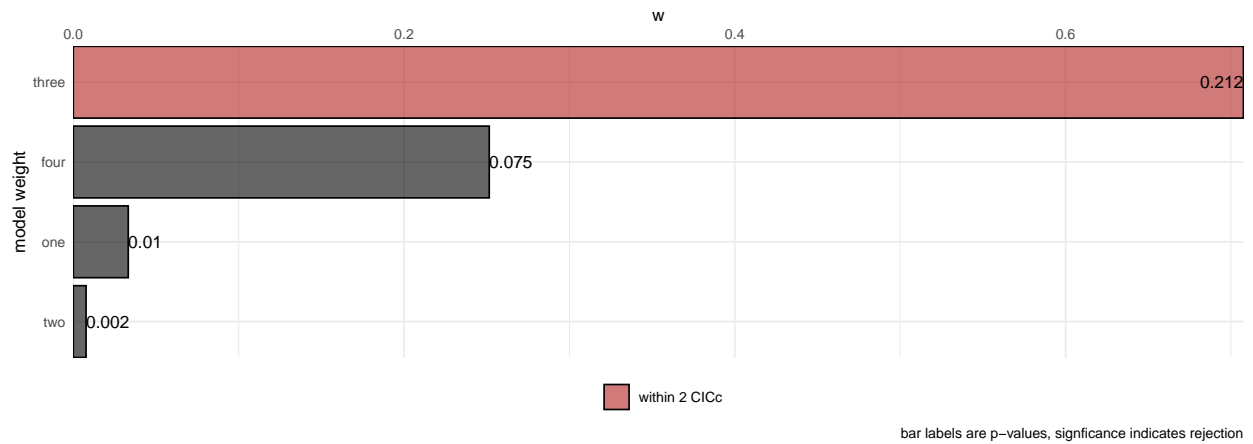
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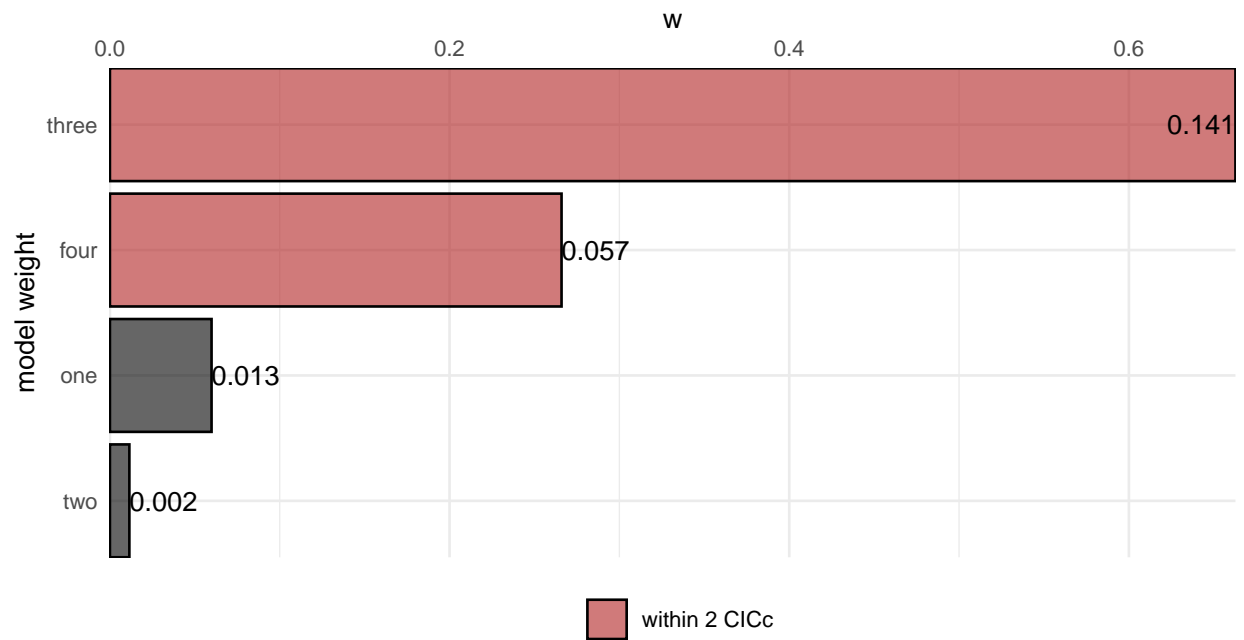
4.2.3 FBD stem tree

Factor loading PC1: TMP: negative; PRE: negative

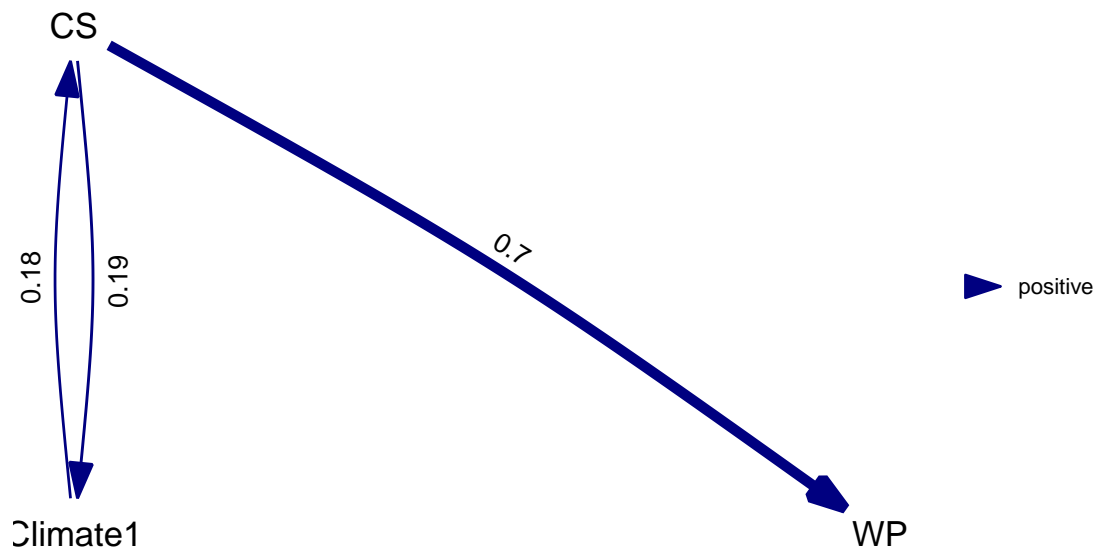


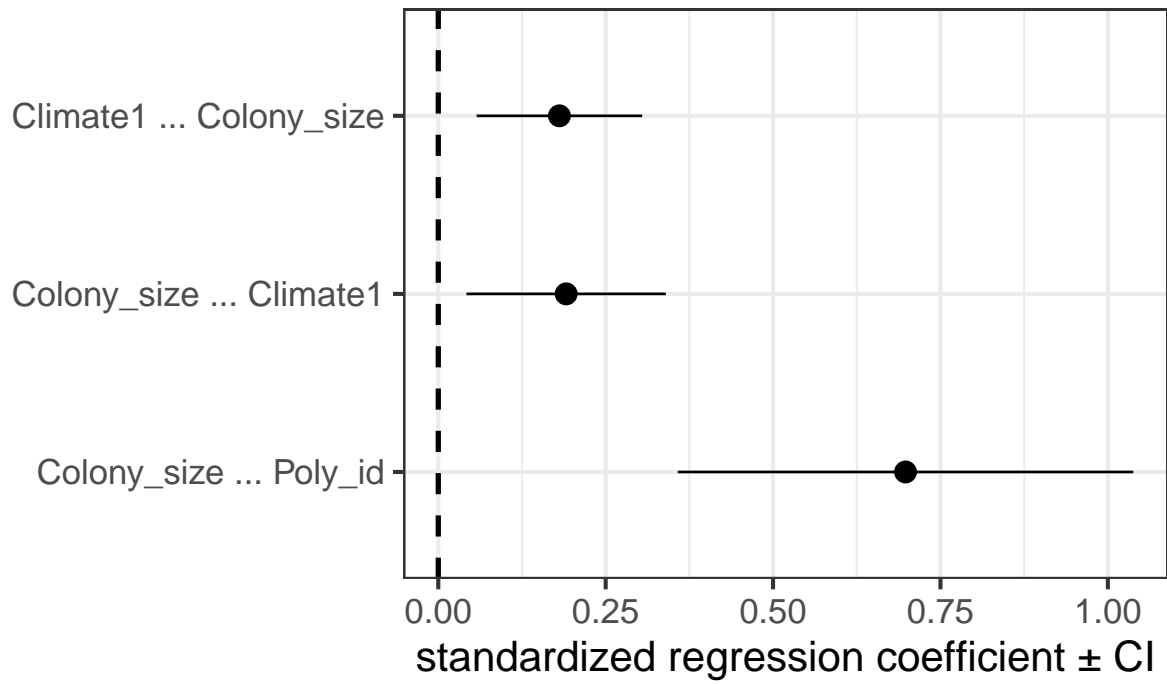
4.2.4 FBD crown tree

Factor loading PC1: TMP: negative; PRE: negative



bar labels are p-values, significance indicates rejection

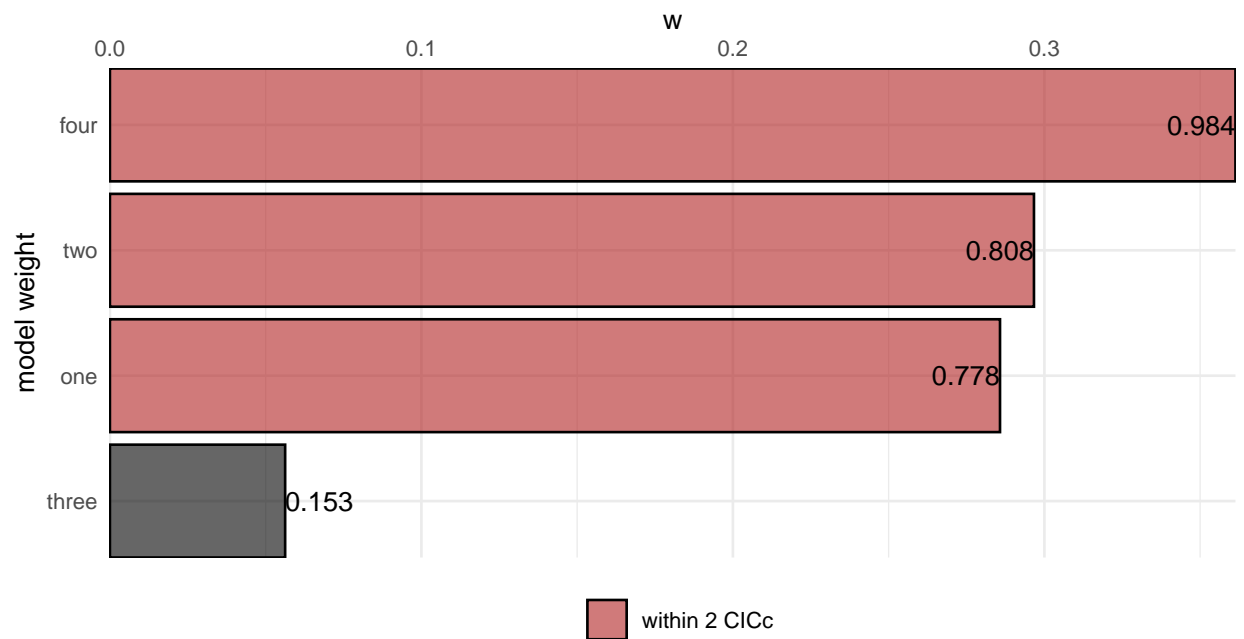




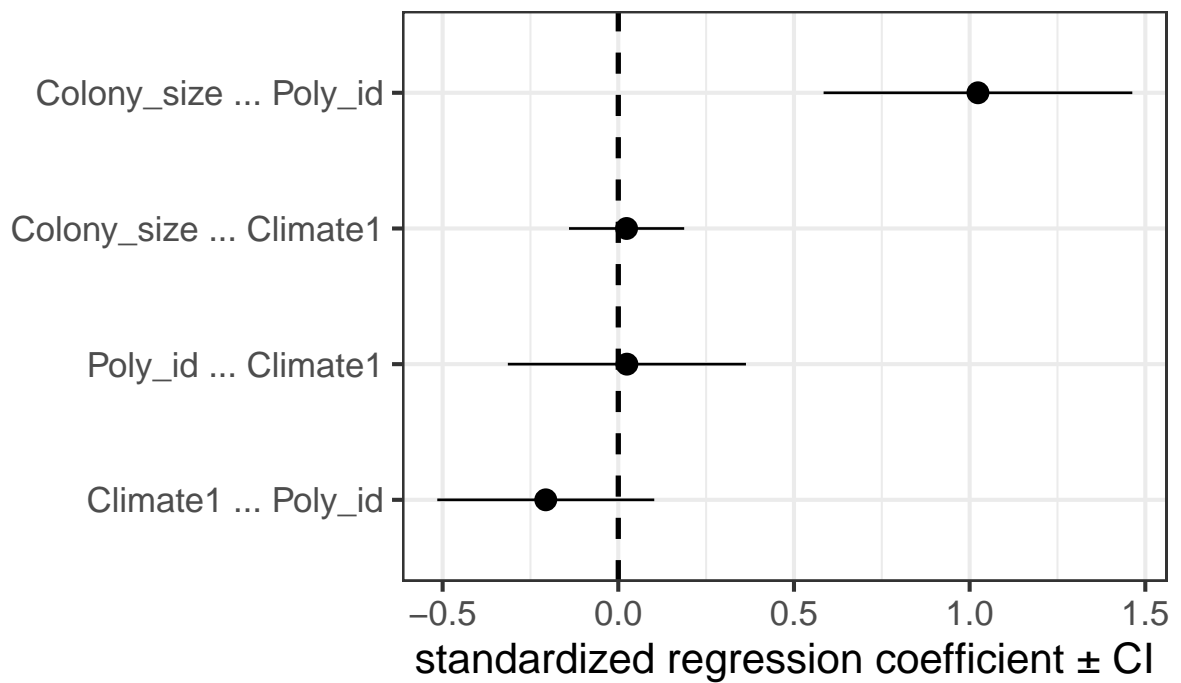
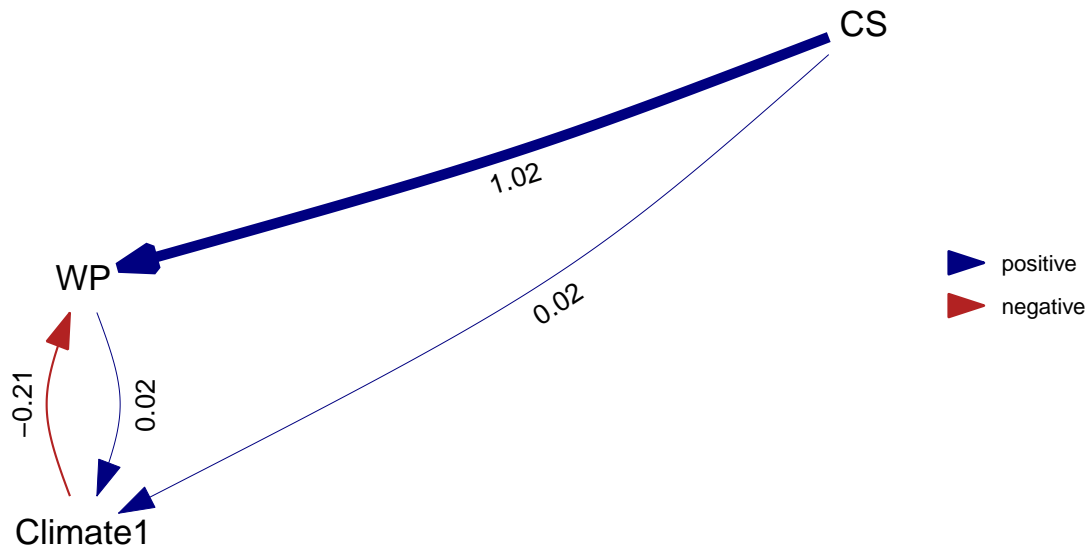
4.3 Both

4.3.1 NCuniform stem tree

Factor loading PC1: TMP: negative; PRE: negative

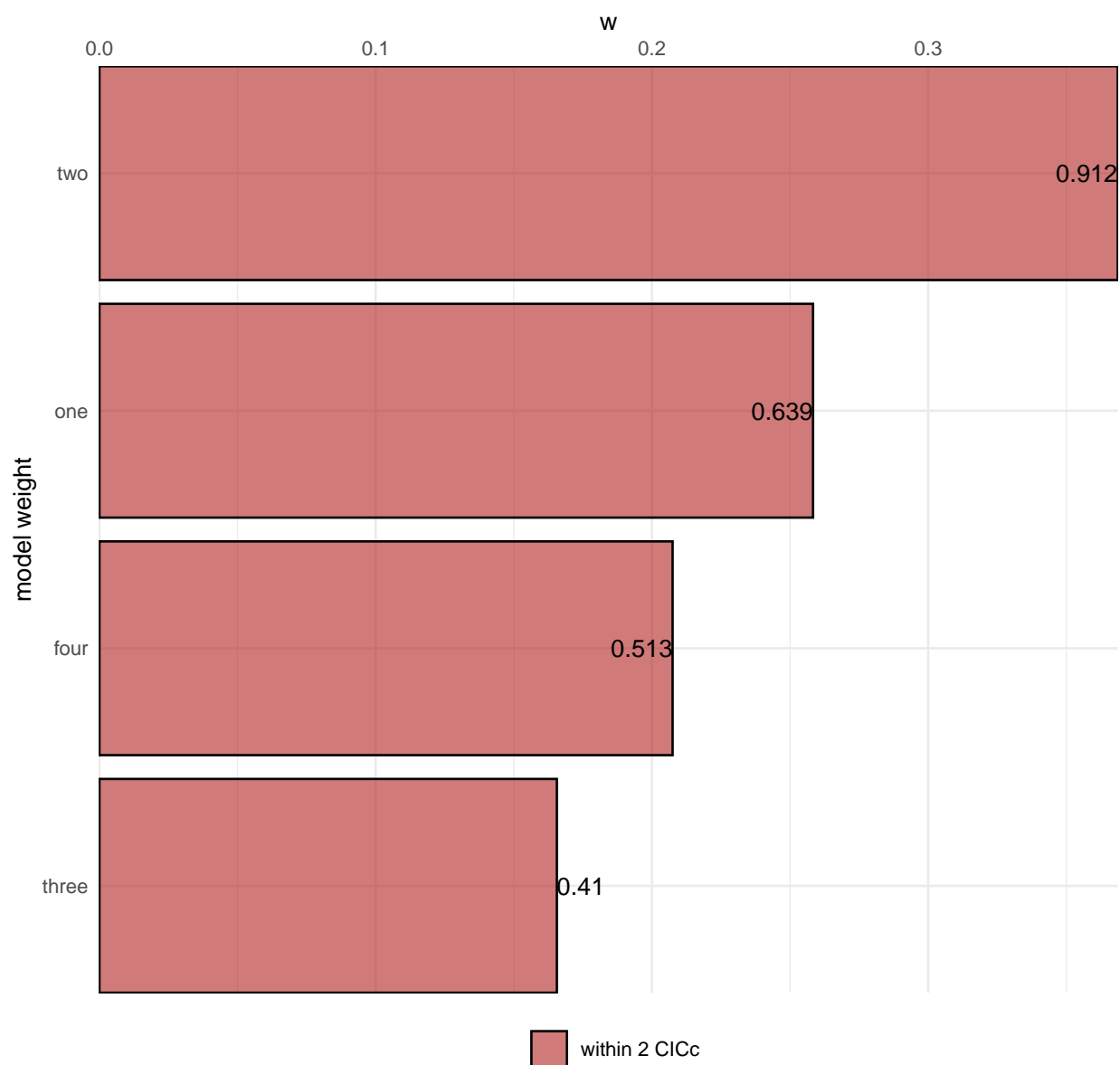


bar labels are p-values, significance indicates rejection

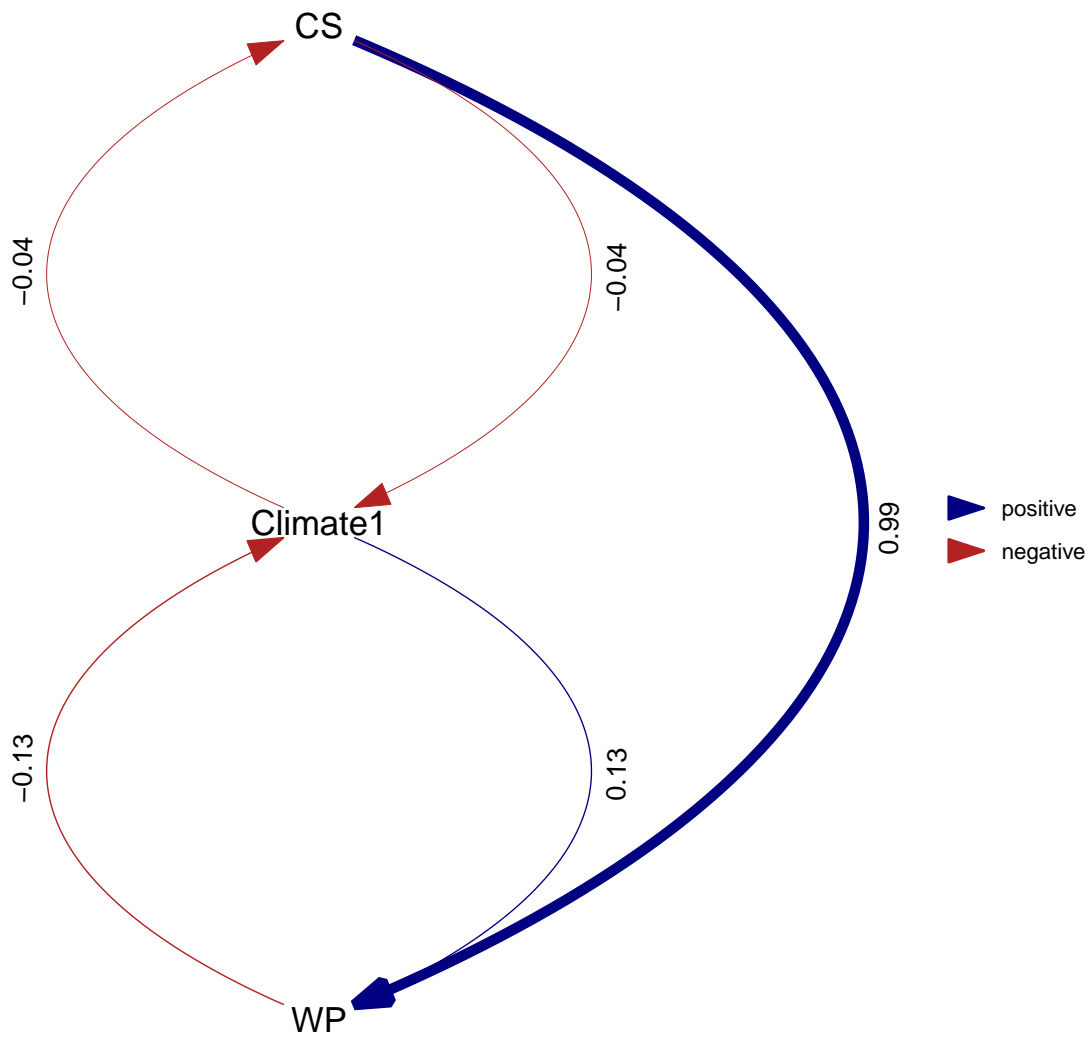


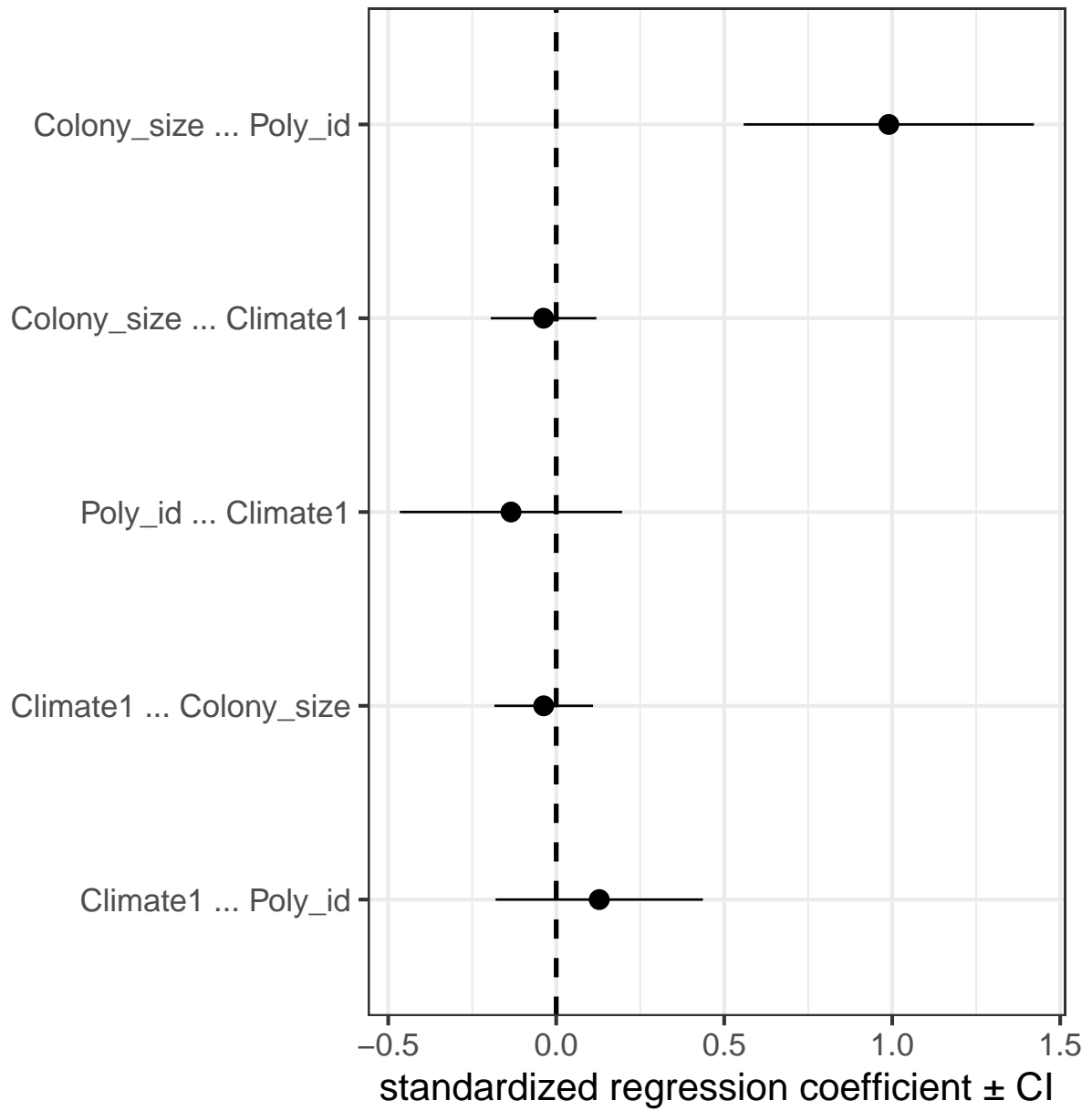
4.3.2 NCuniform crown tree

Factor loading PC1: TMP: positive; PRE: positive



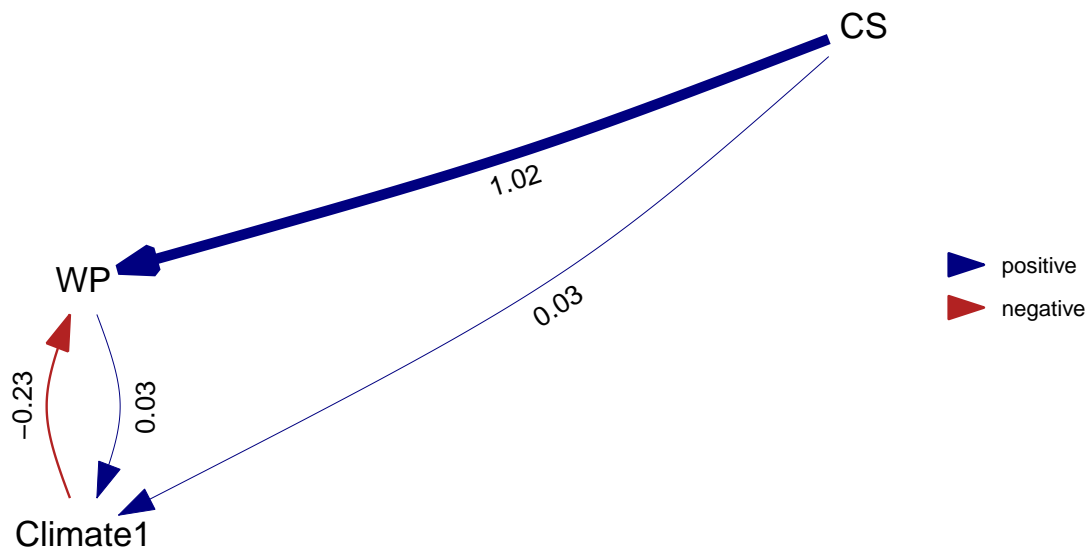
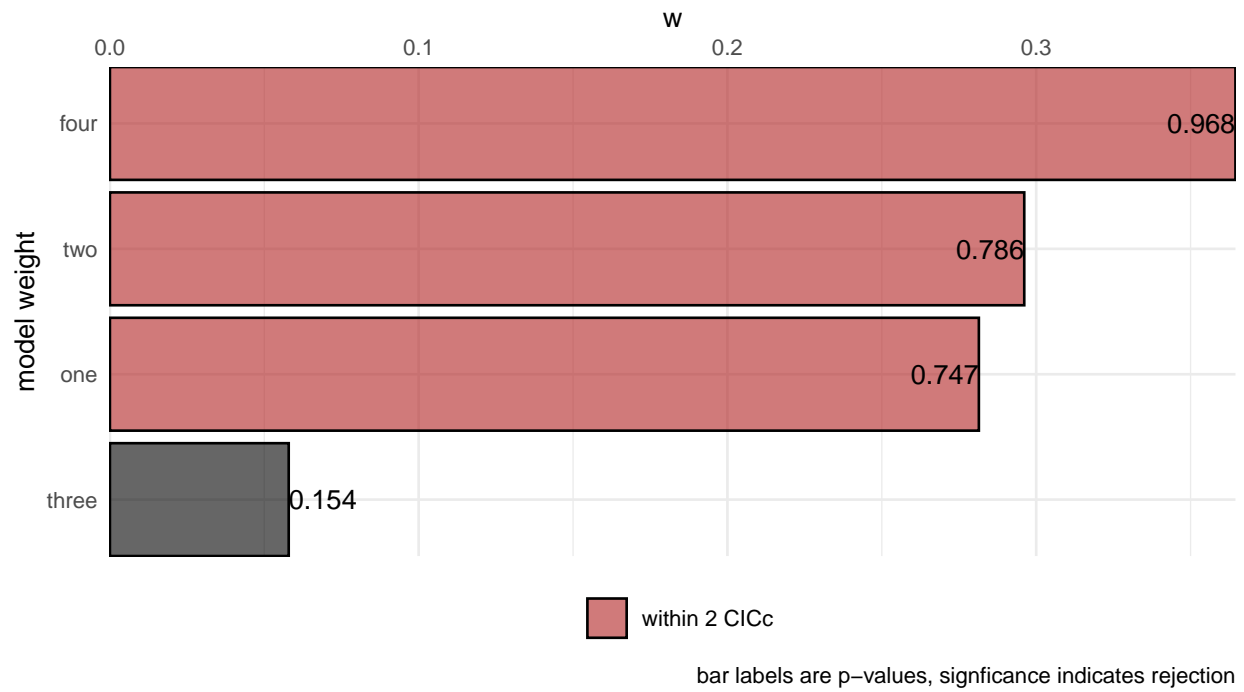
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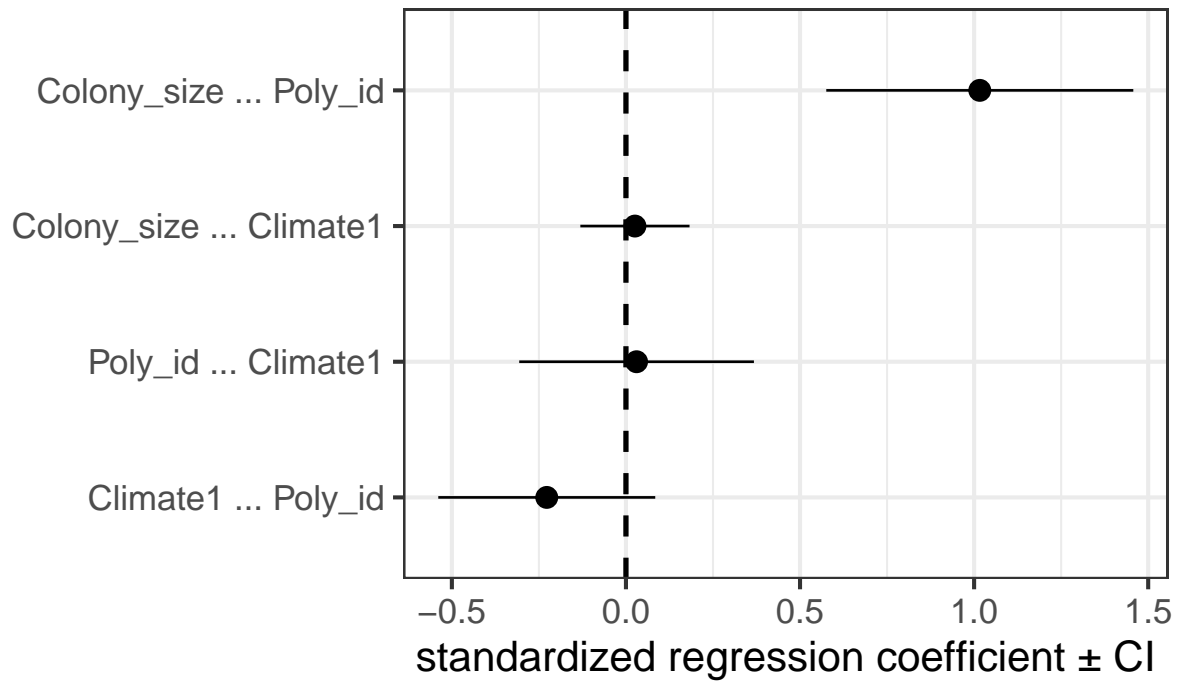




4.3.3 FBD stem tree

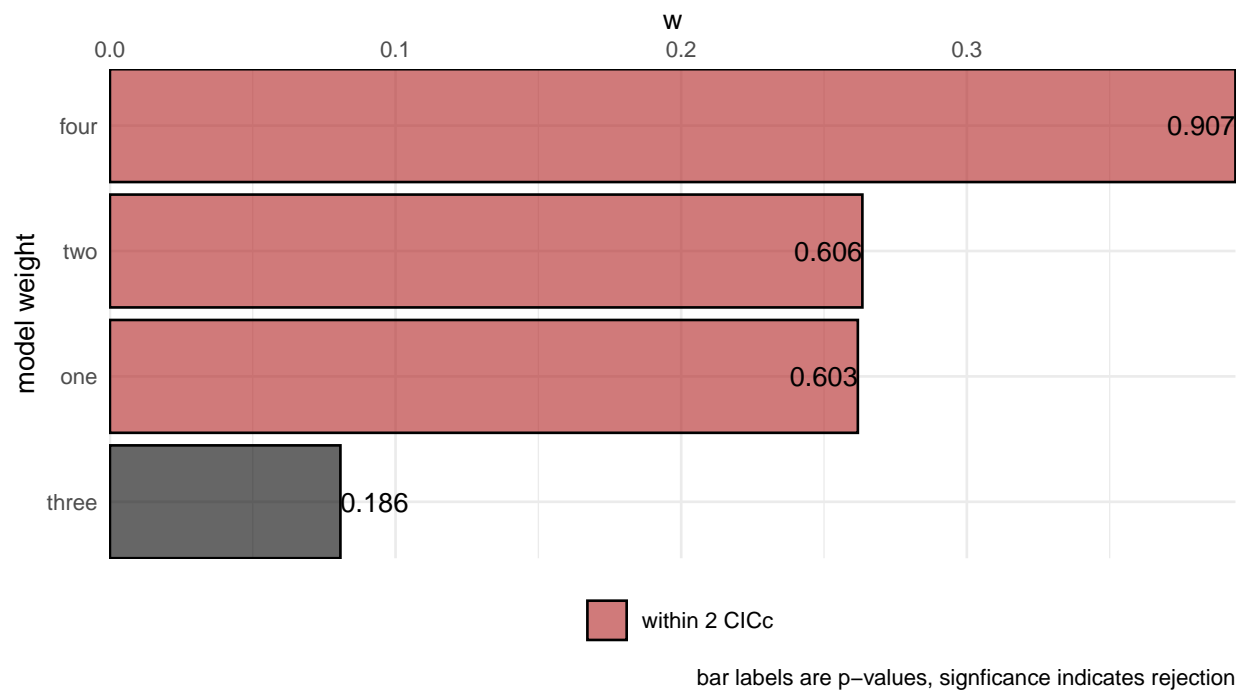
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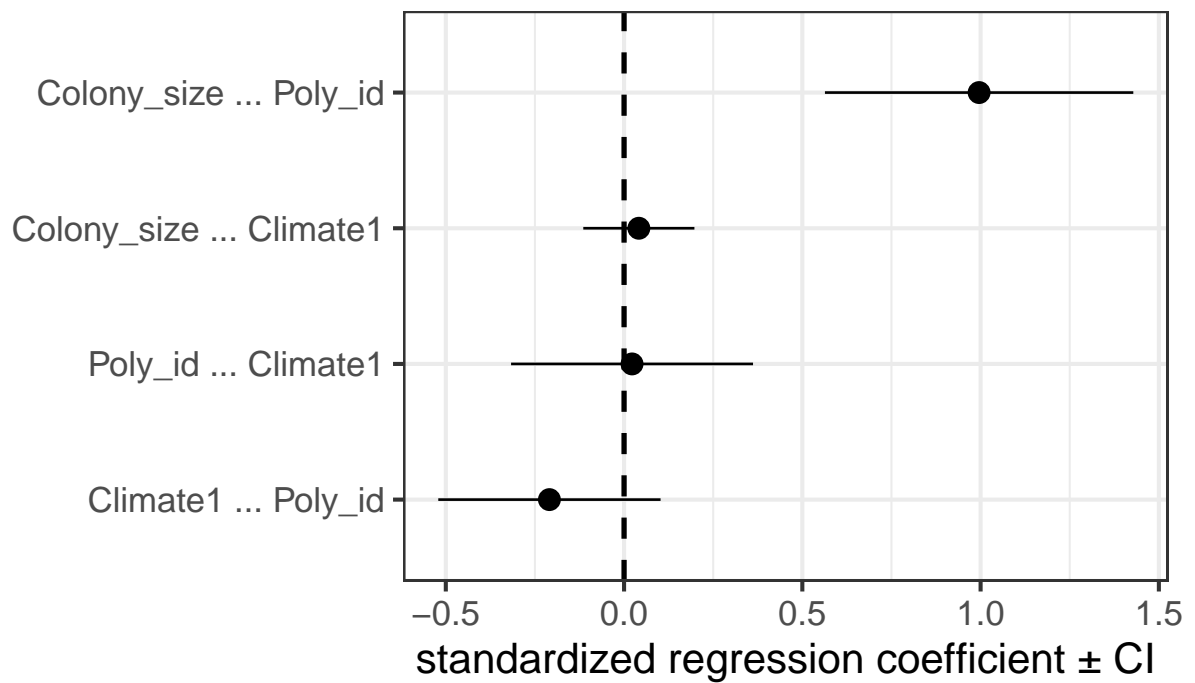
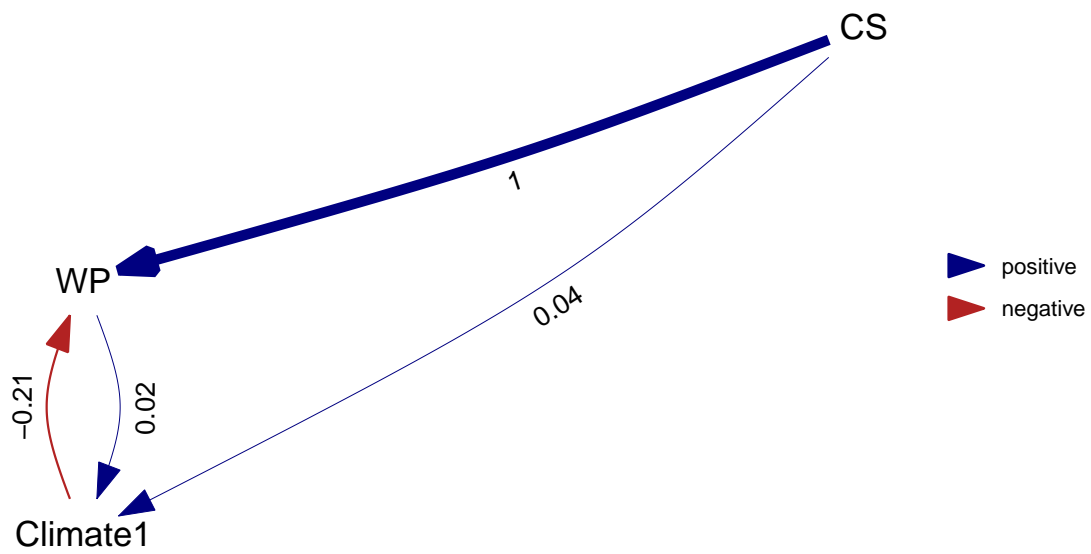




4.3.4 FBD crown tree

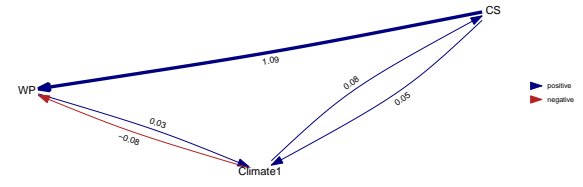
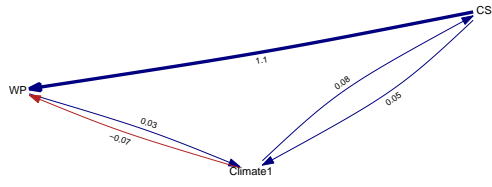
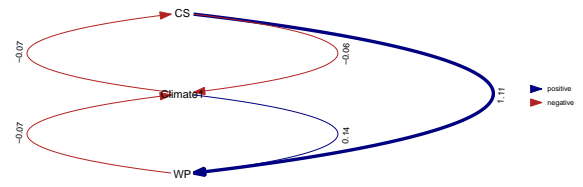
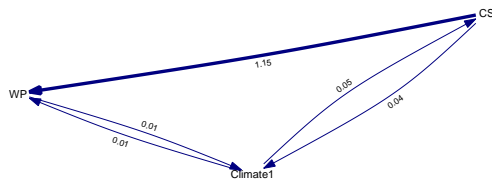
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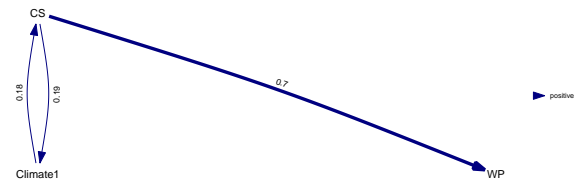
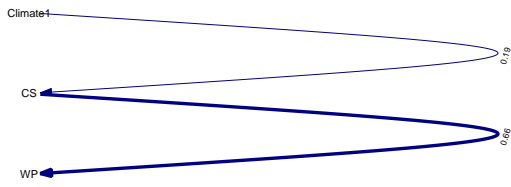
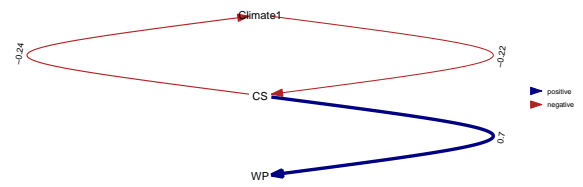
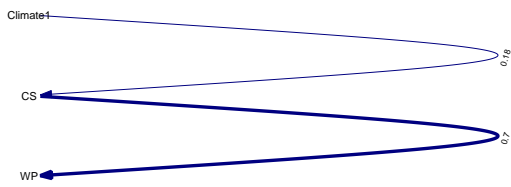


5 Panel plots

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## pdf
## 2
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pdf
2



pdf
2

