

Doubs fish LCBD. %difference D

d = 50

help("LCBD comp")



Doubs fish replacement LCBD

d = 50

help("LCBD comp")

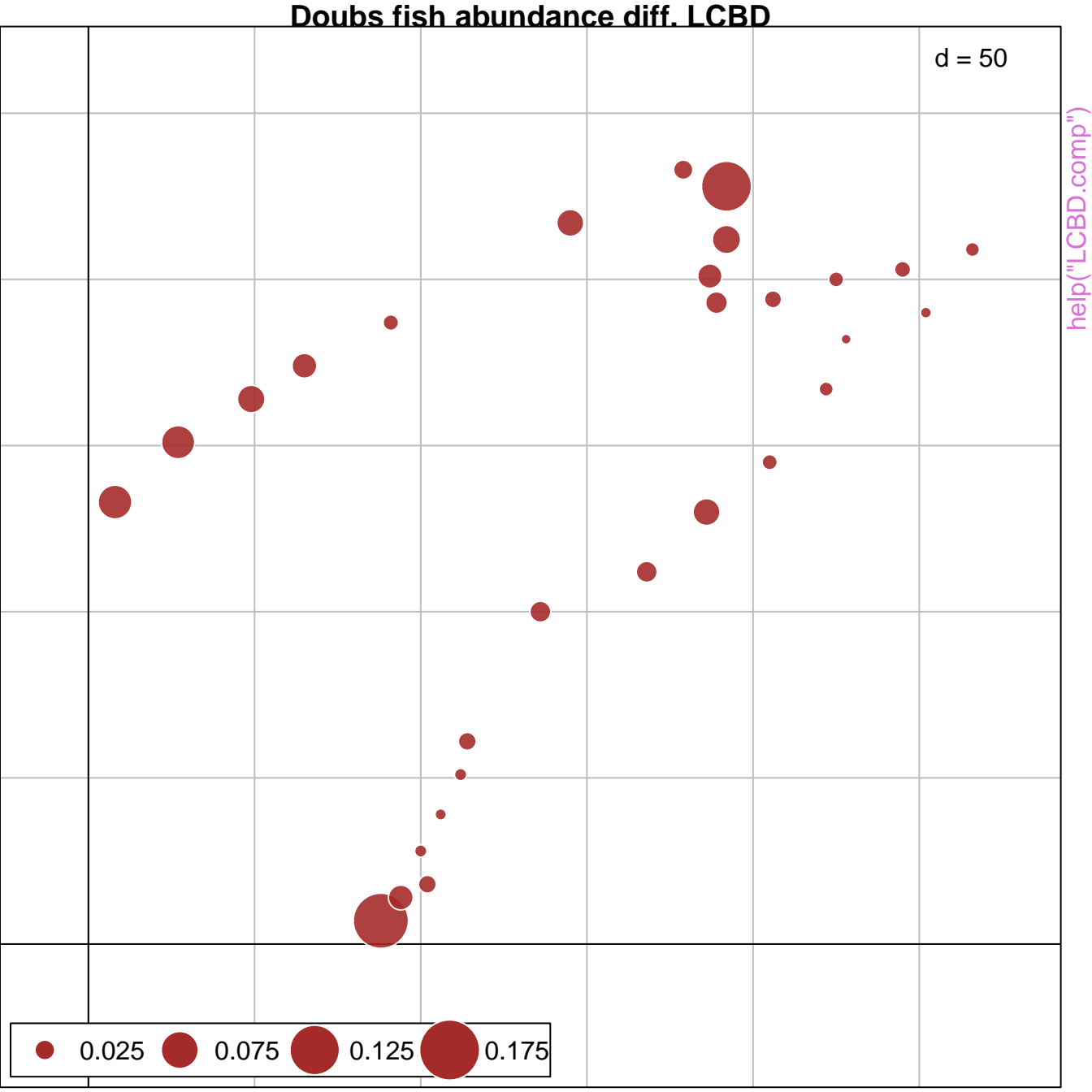


Doubs fish abundance diff. LCBD

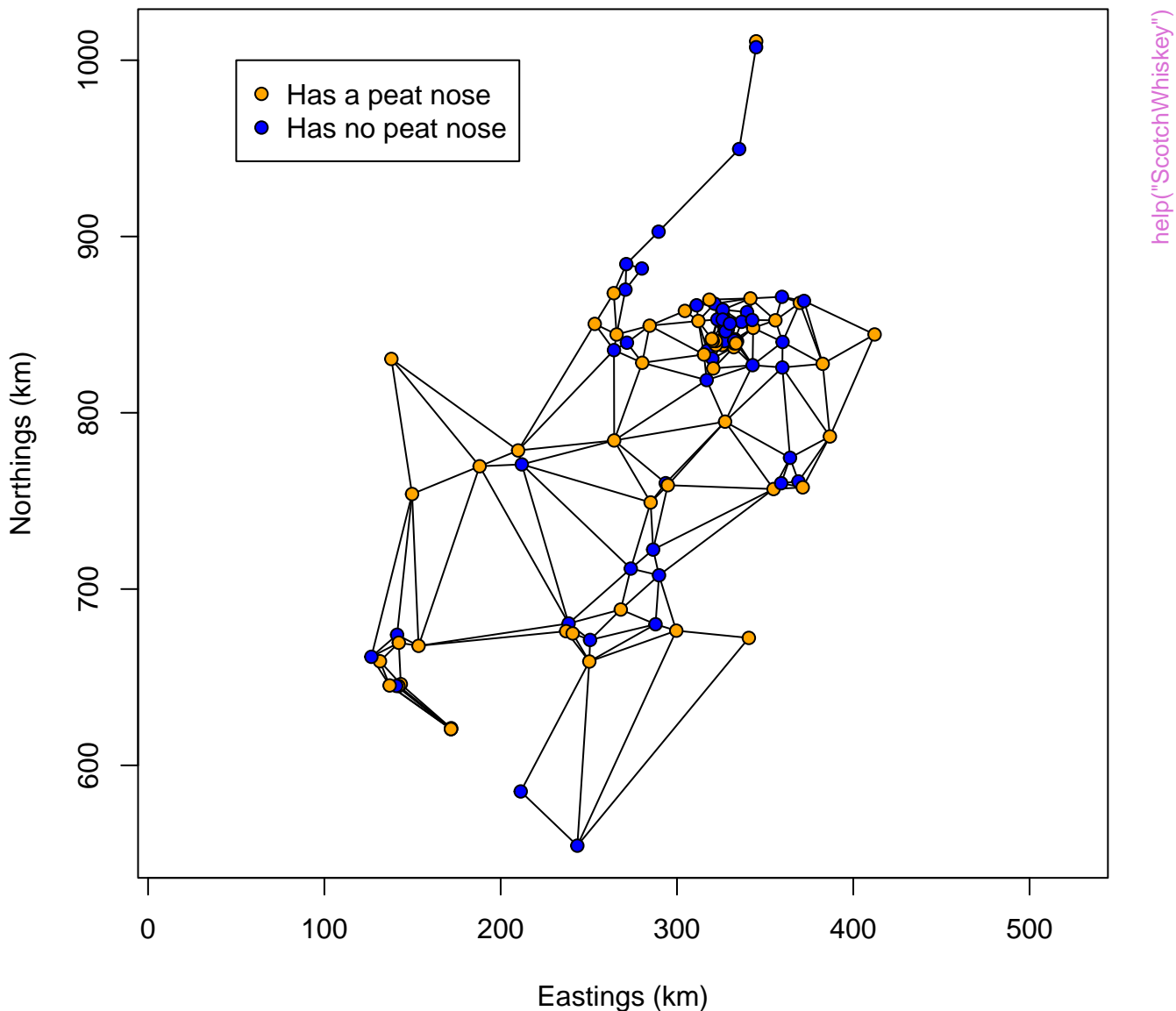
d = 50

help("LCBD comp")

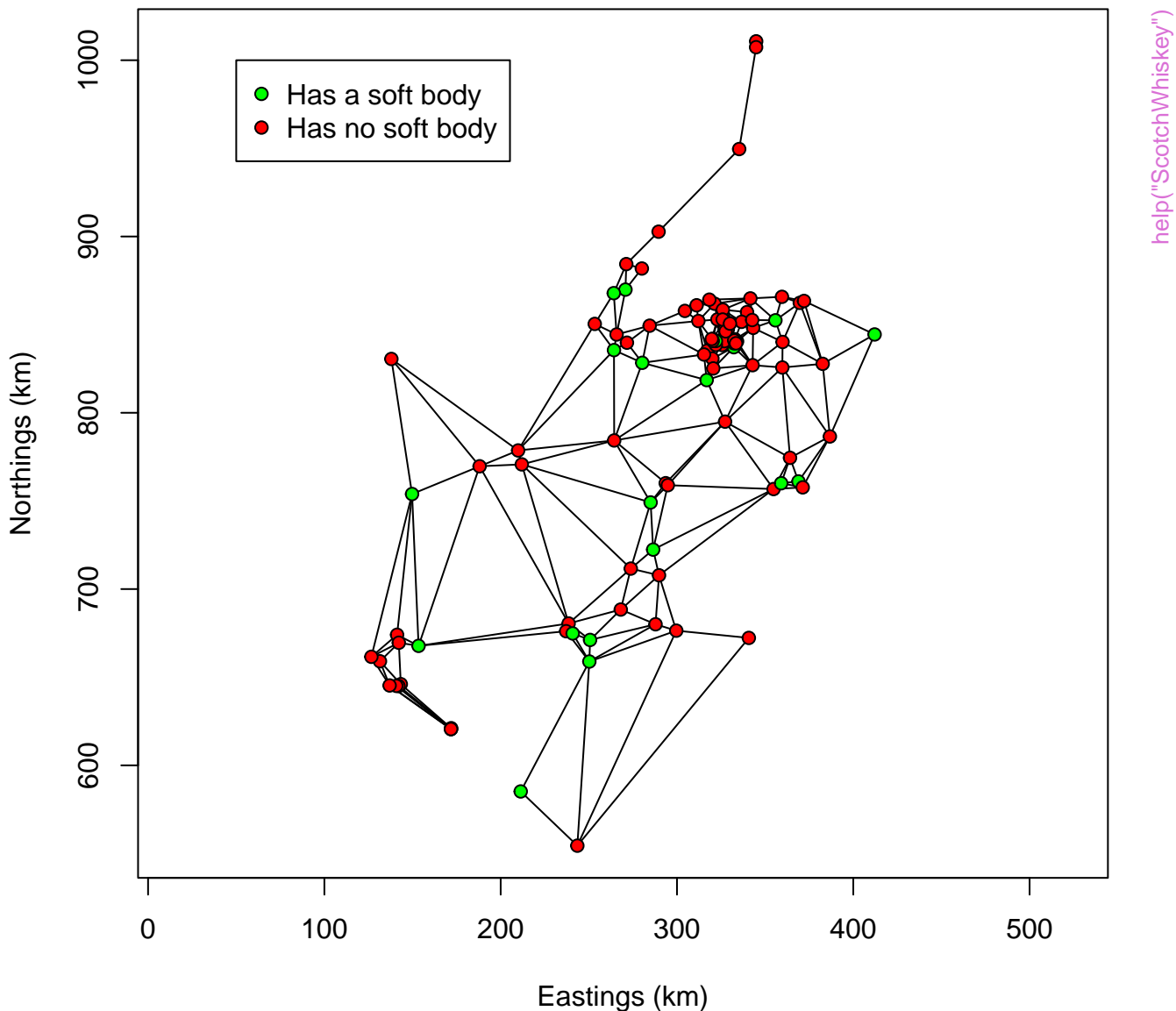
● 0.025 ● 0.075 ● 0.125 ● 0.175



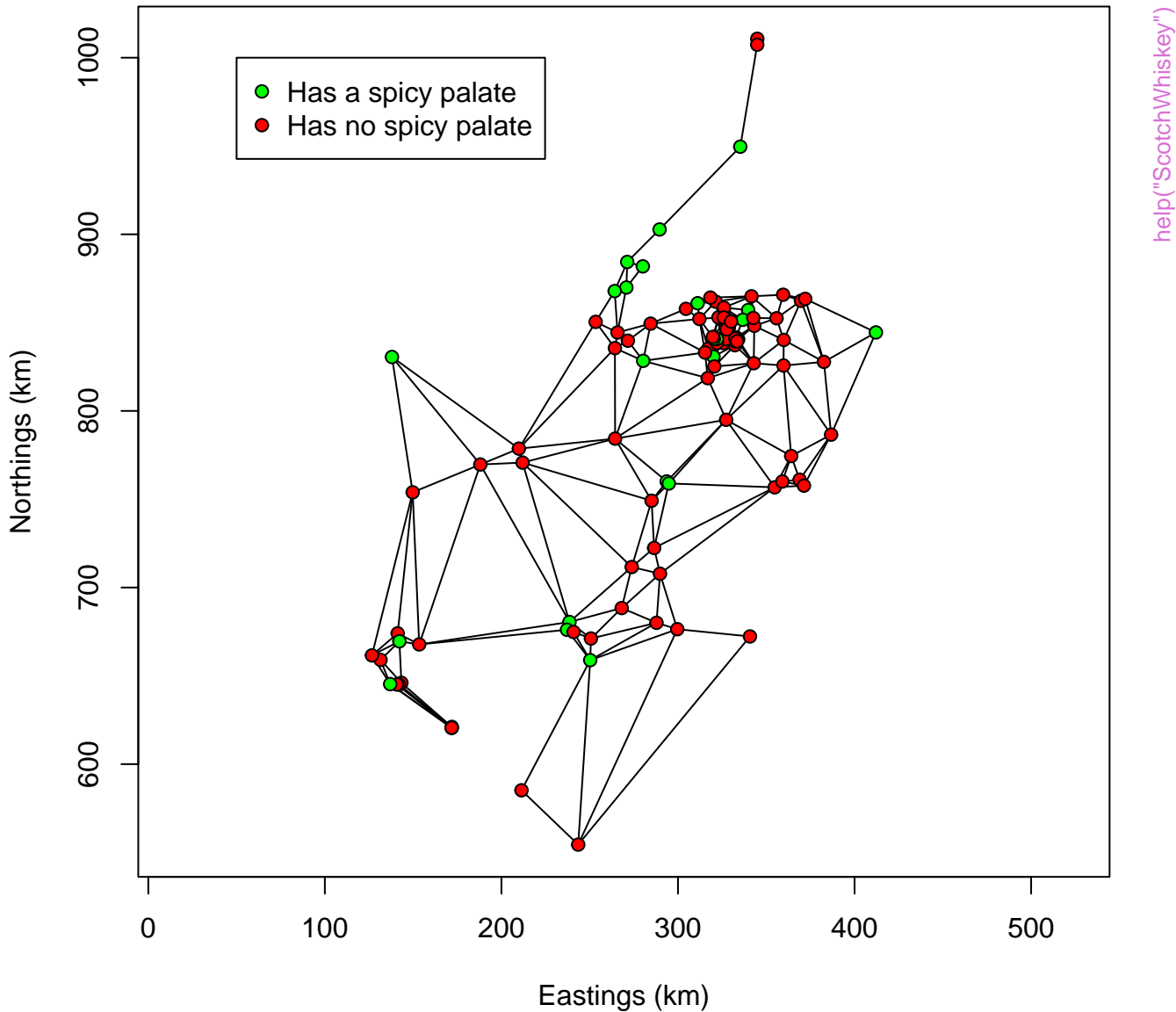
Scotch whiskey: peat nose



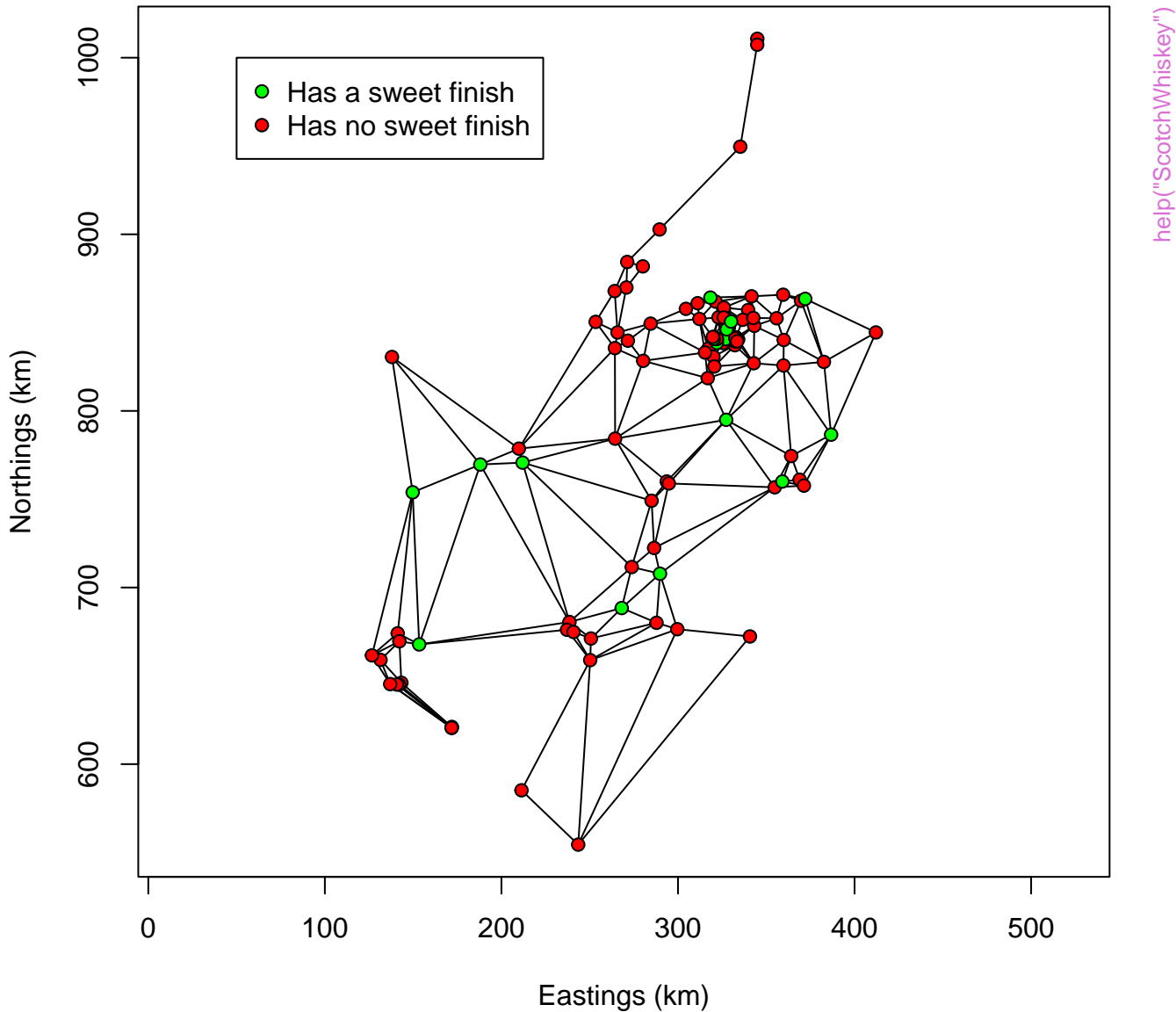
Scotch whiskey: soft body

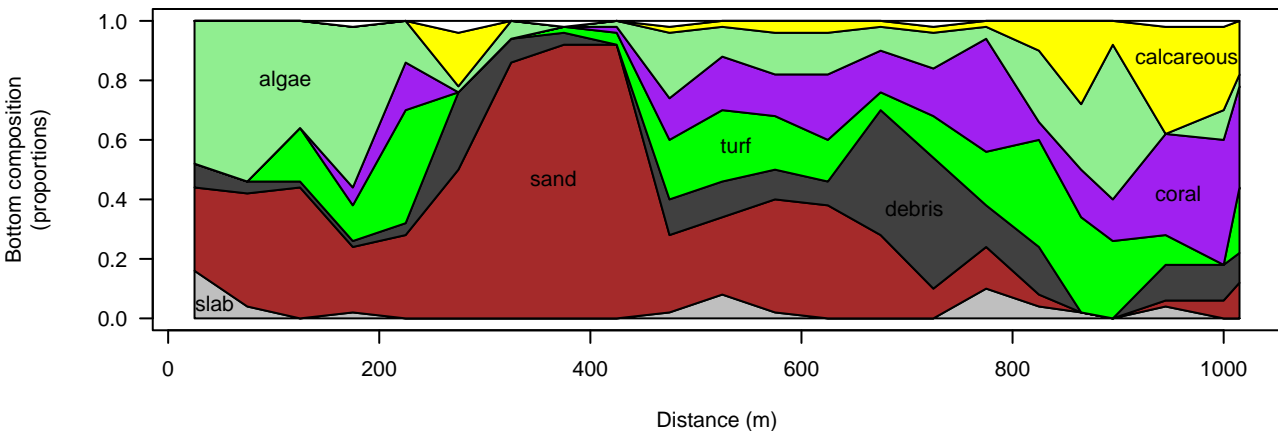
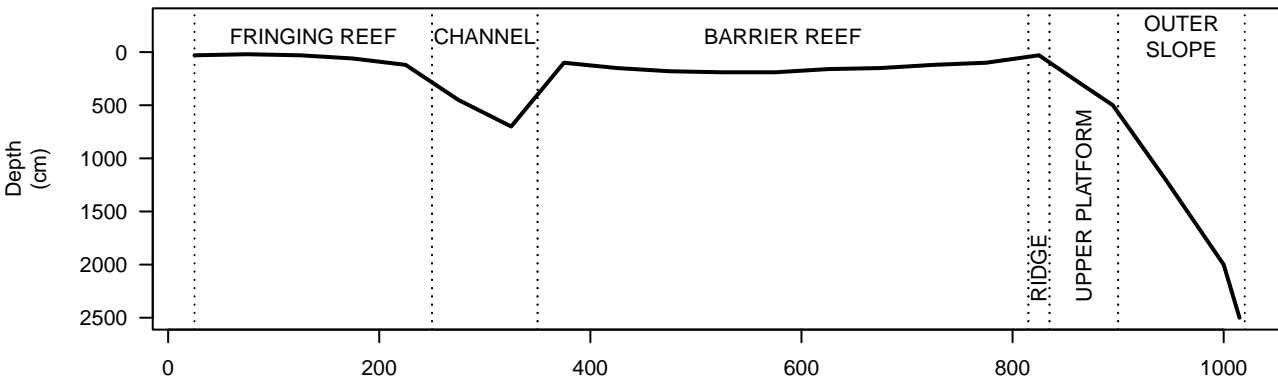
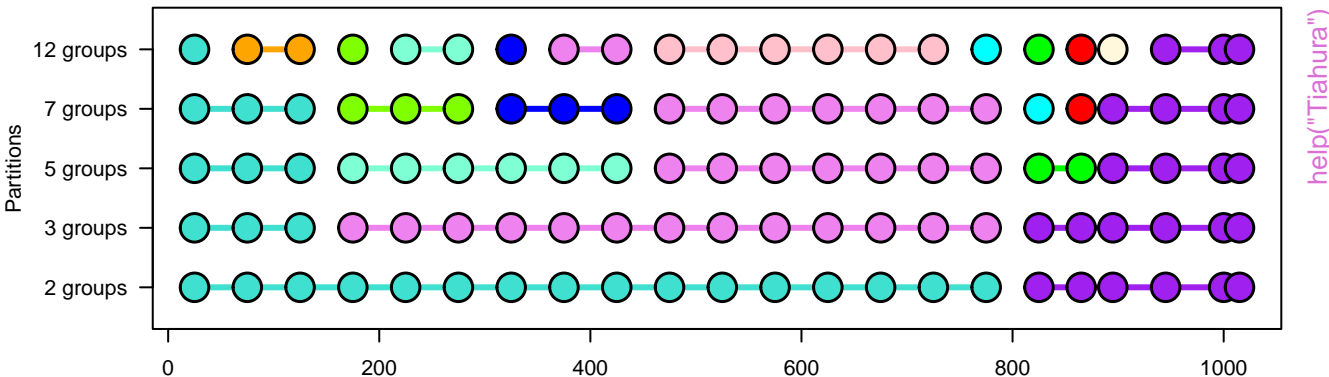


Scotch whiskey: spicy palate

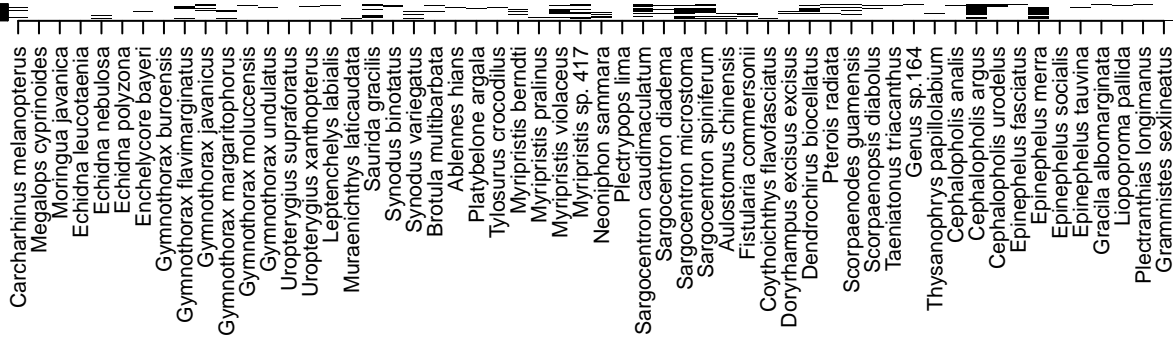


Scotch whiskey: sweet finish



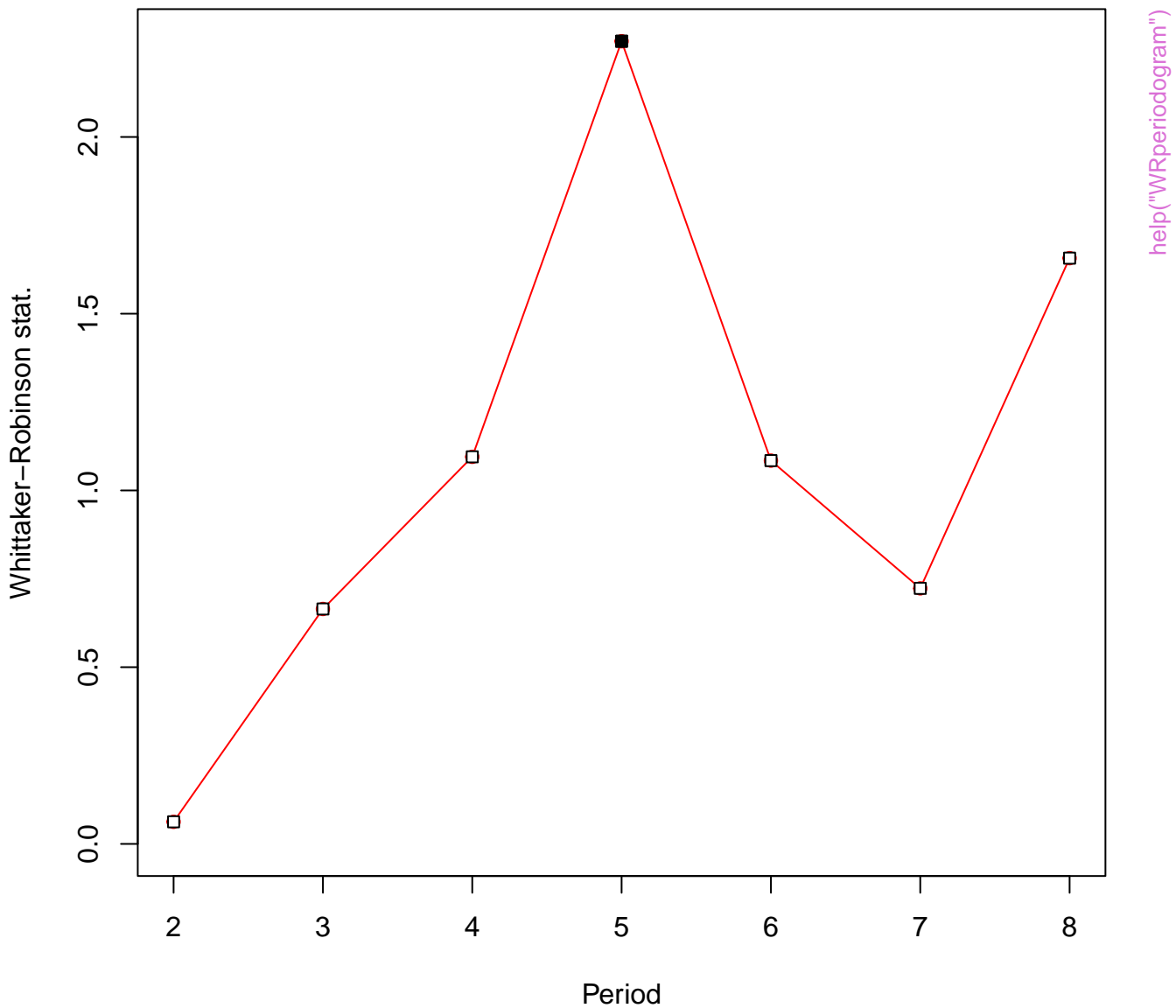


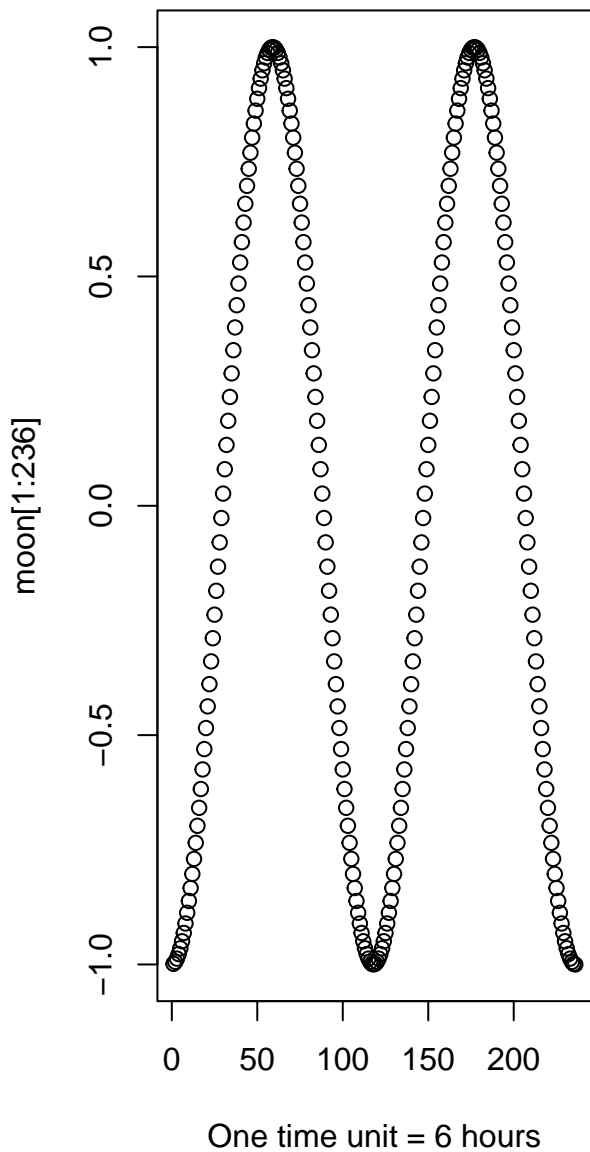
Site_1



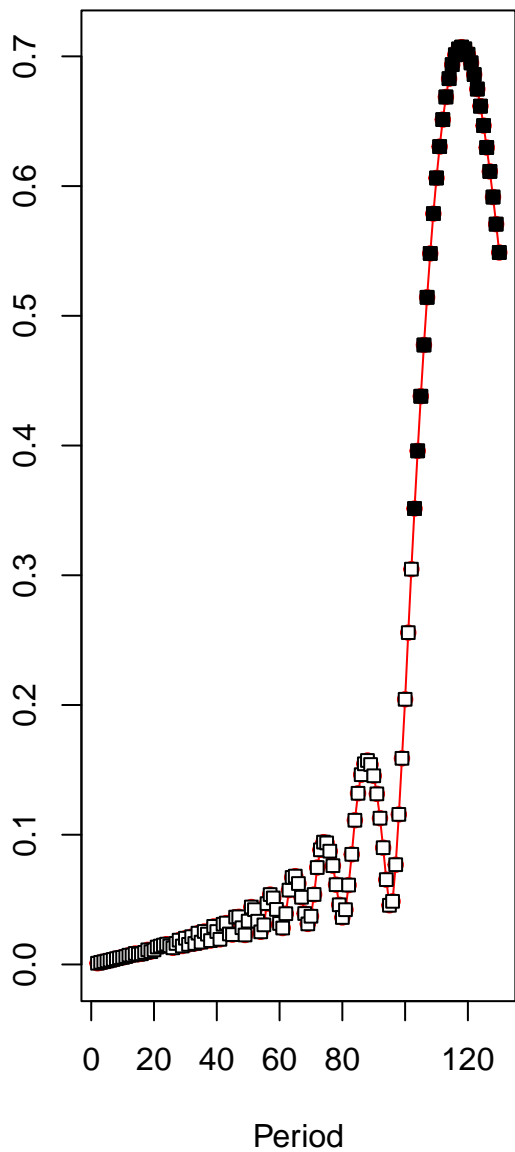
help("Tiahura")

WR Periodogram

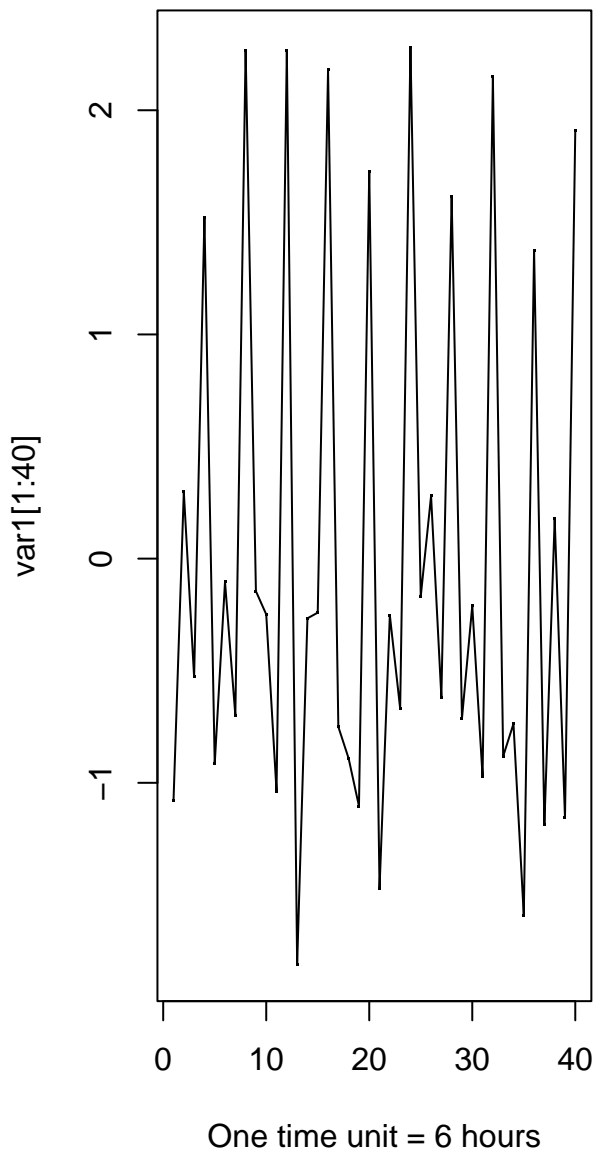




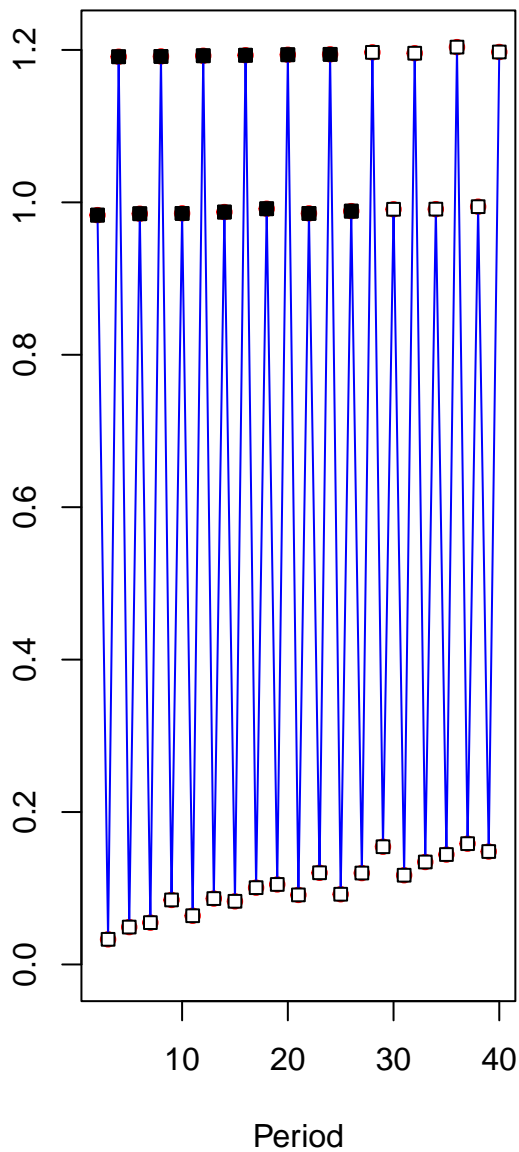
Whittaker–Robinson stat.



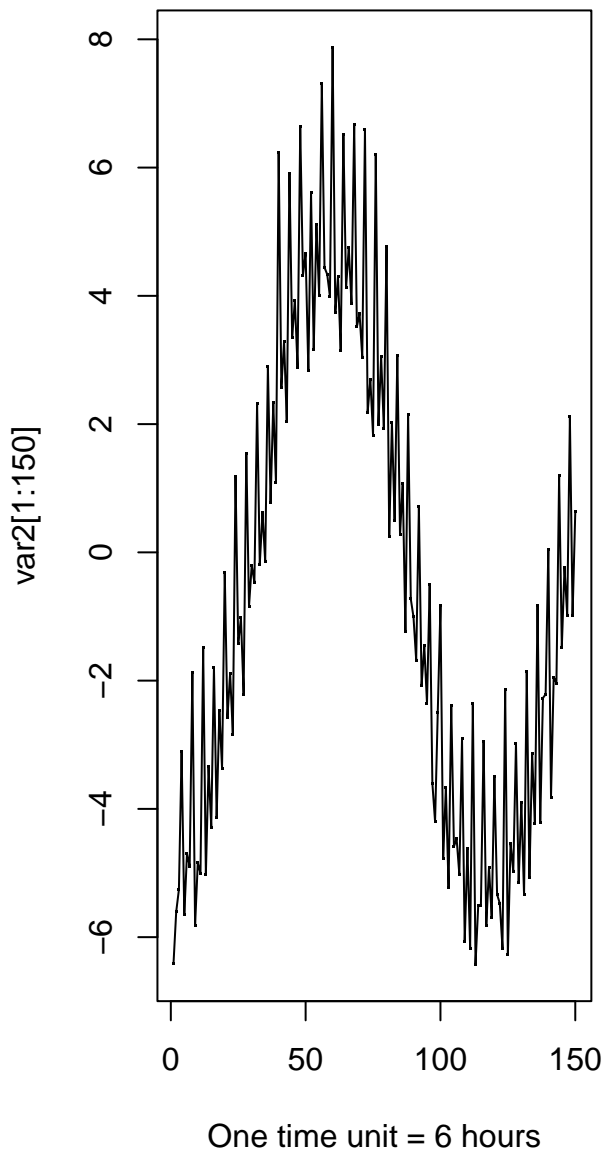
[help\("WRperiodogram"\)](#)



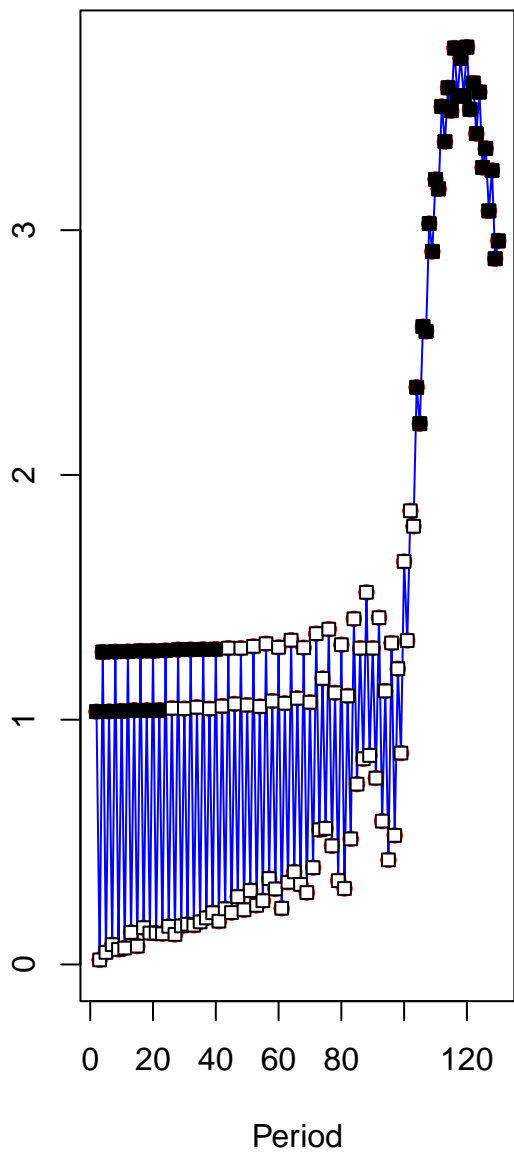
Whittaker-Robinson stat.



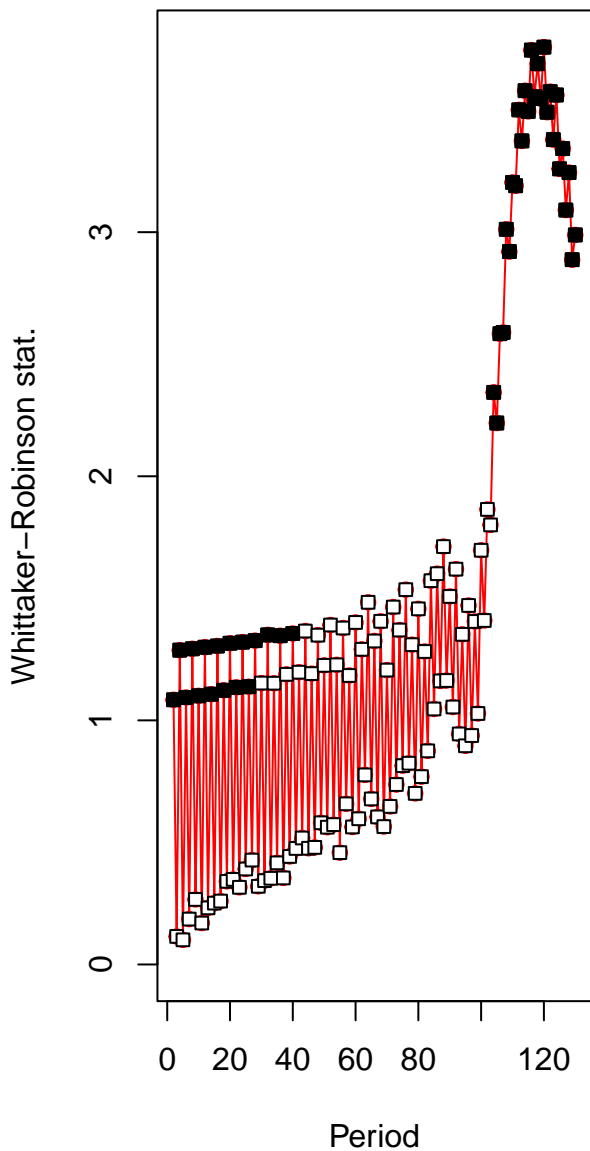
[help\("WRperiodogram"\)](#)



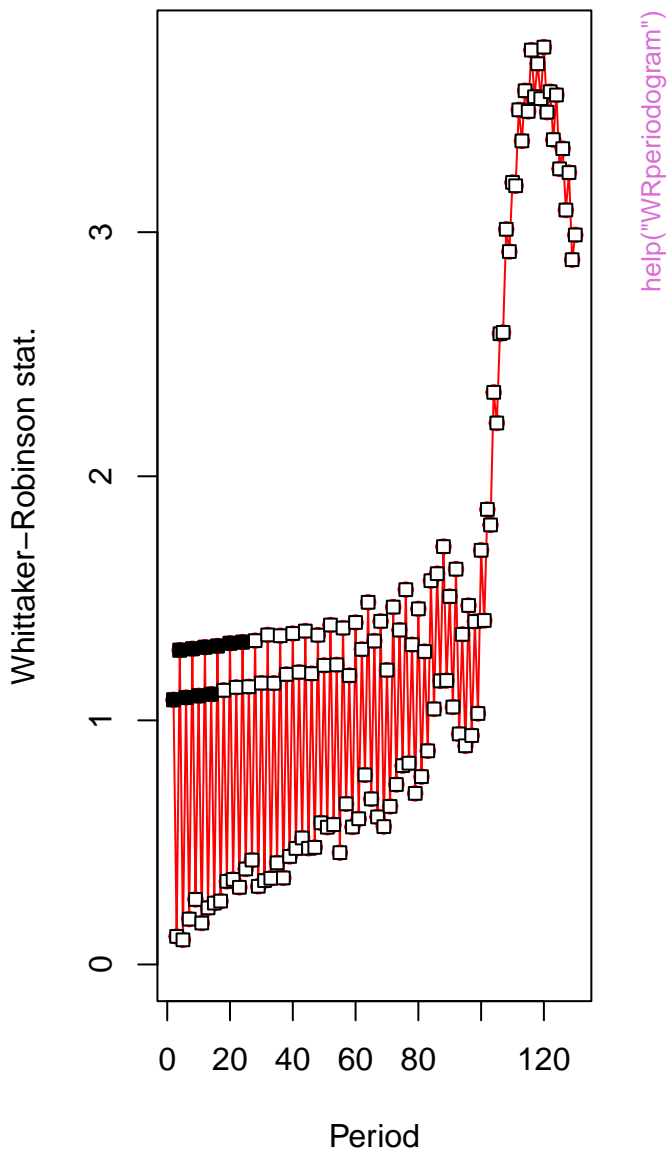
Whittaker–Robinson stat.



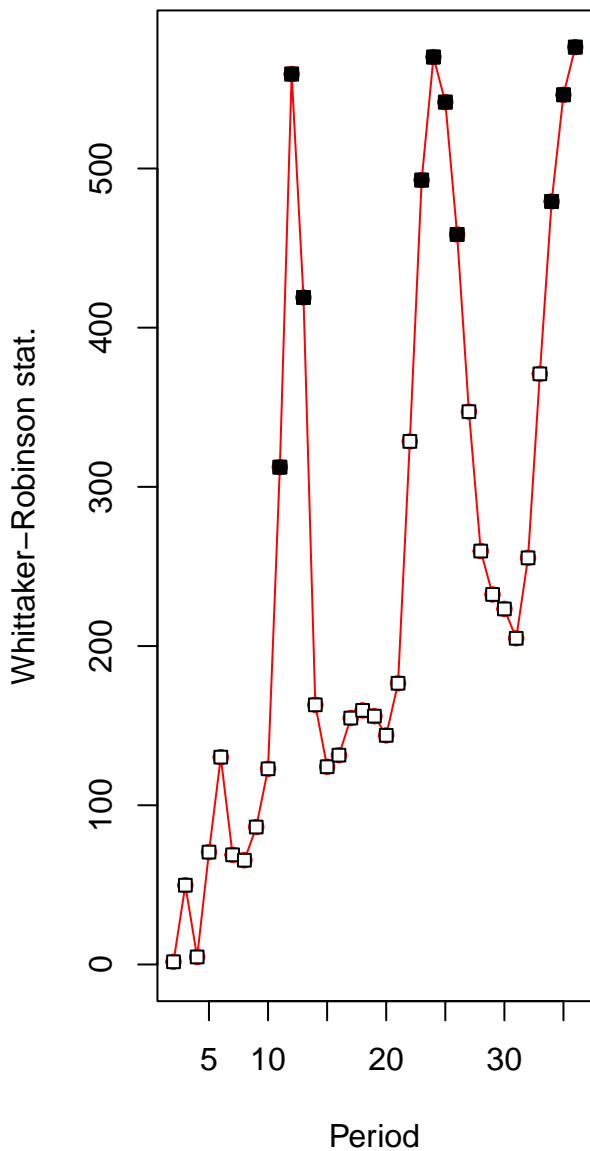
WR Periodogram



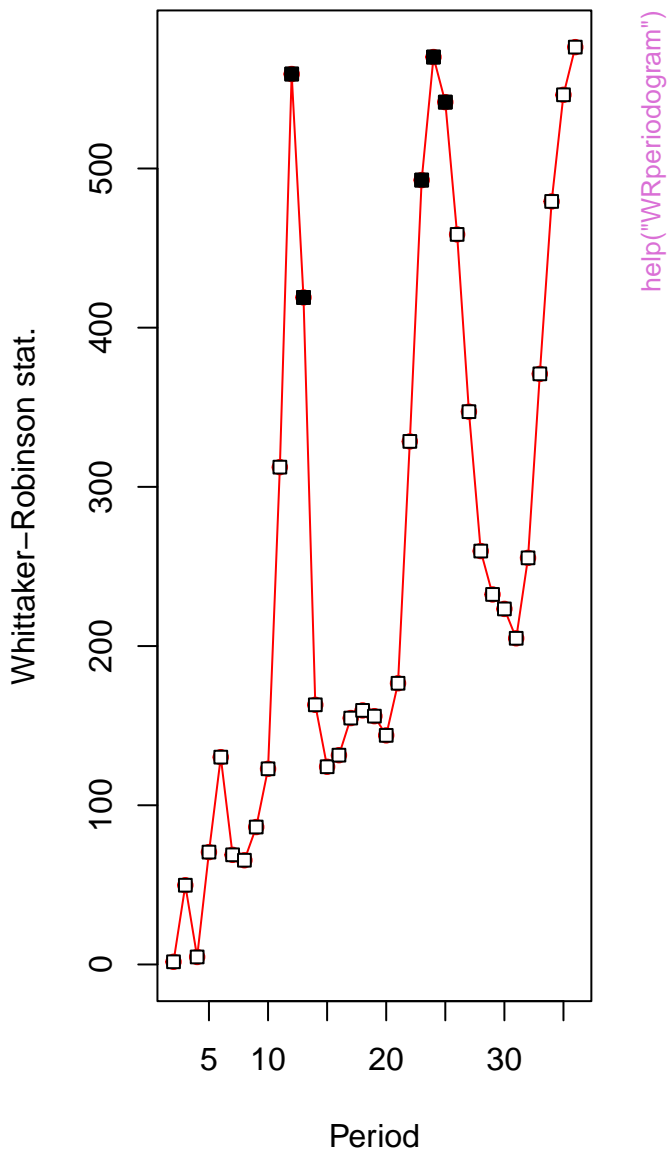
WR Periodogram



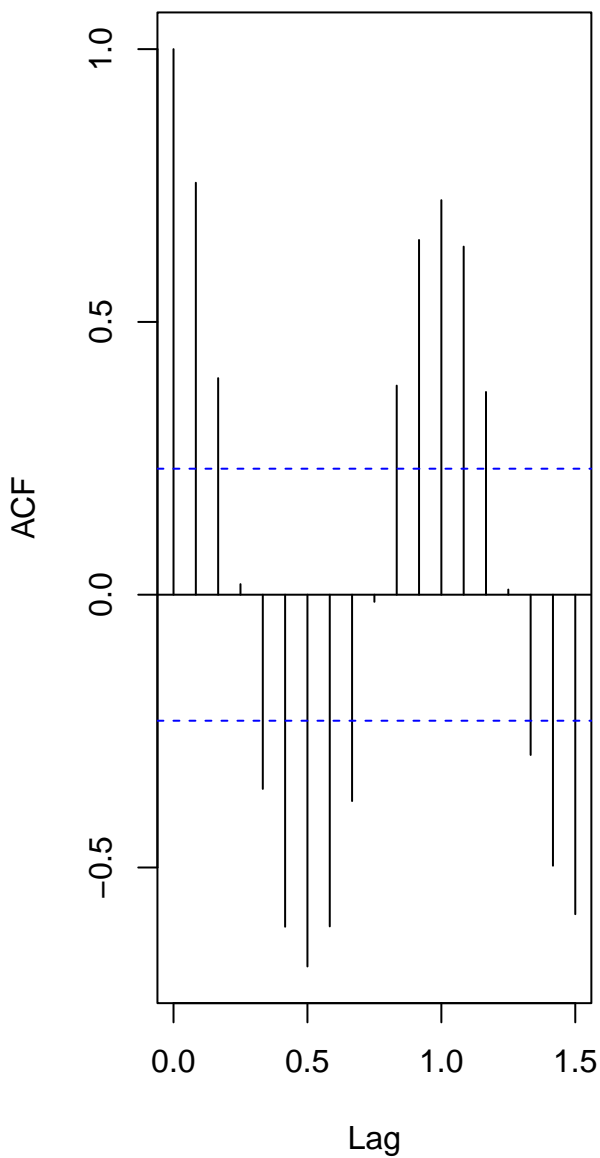
WR Periodogram

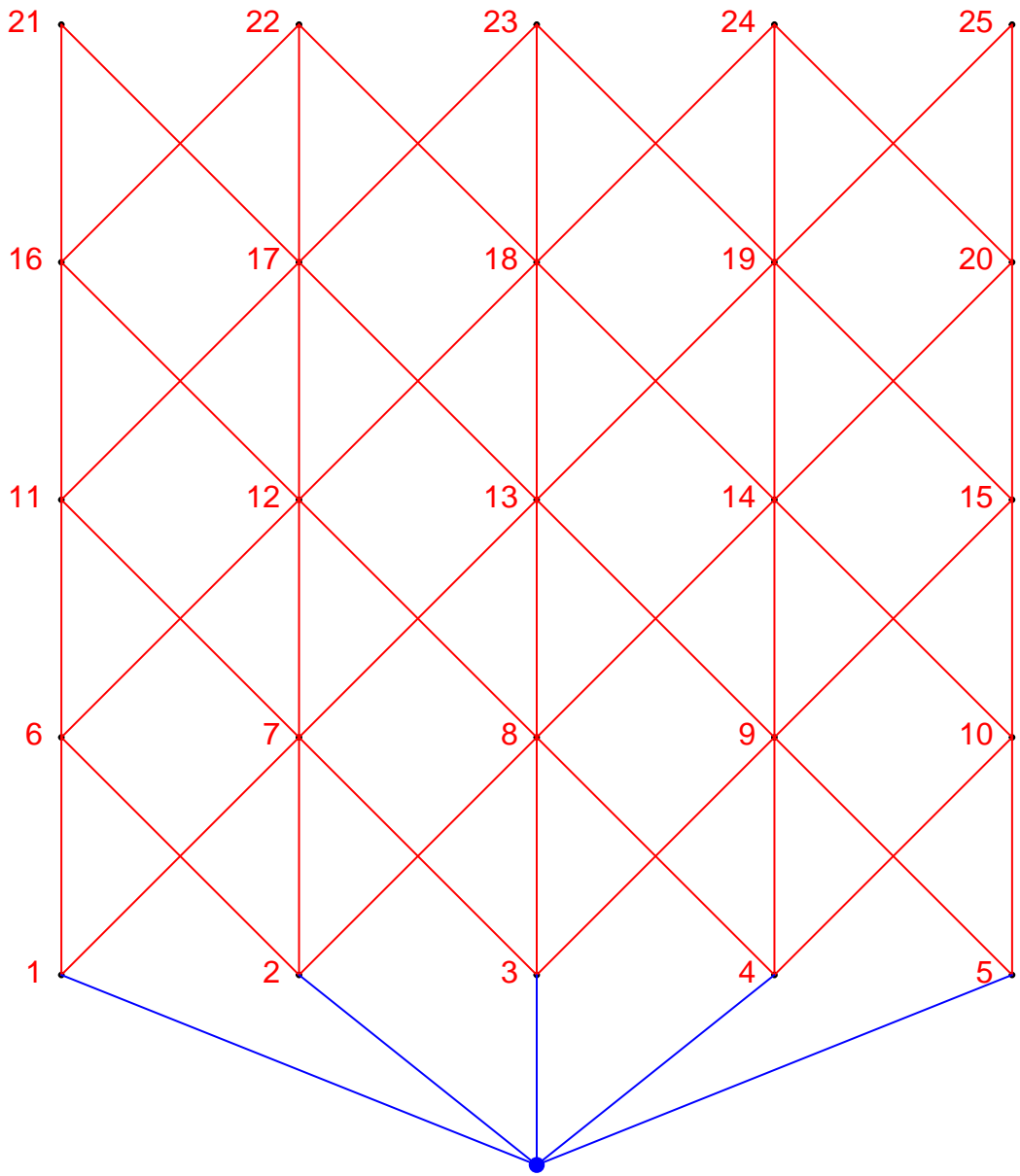


WR Periodogram



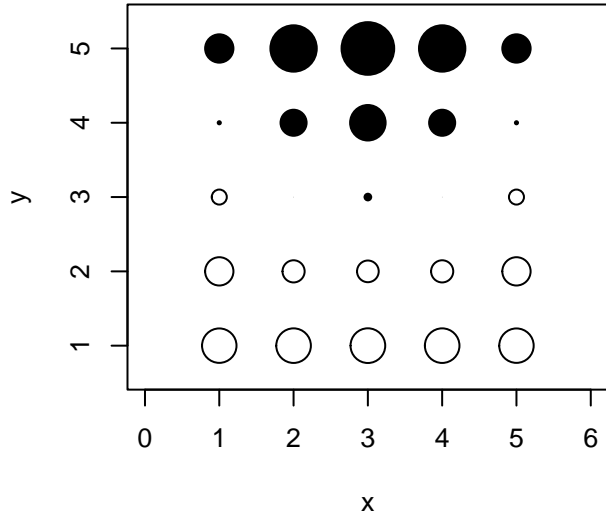
Series Ideaths



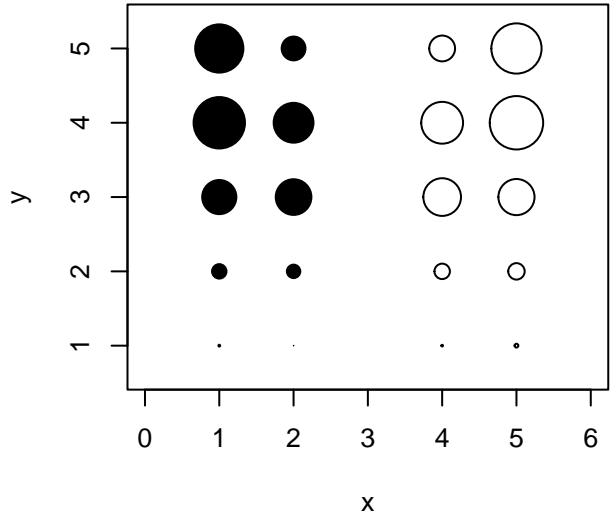


help("aem")

AEM 1

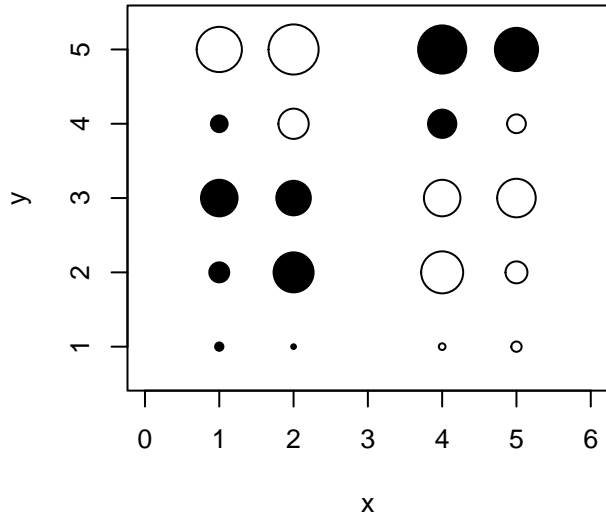


AEM 2

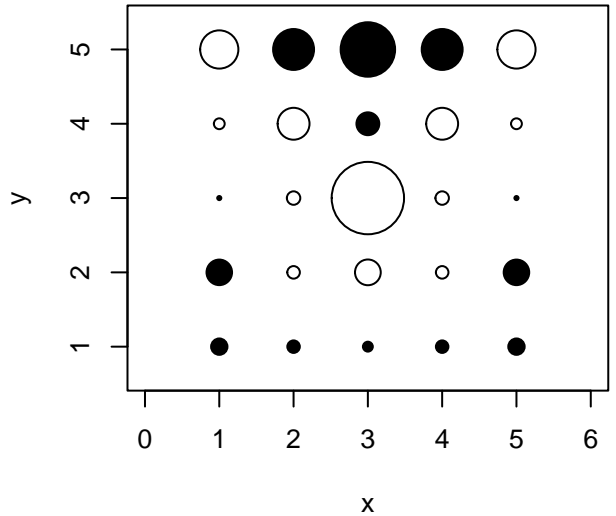


help("aem")

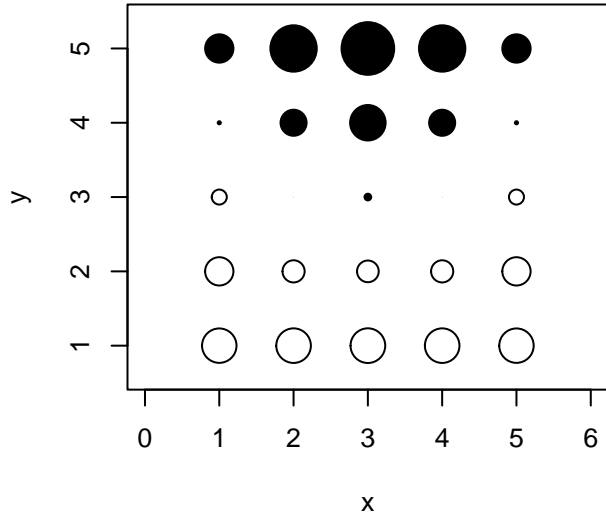
AEM 3



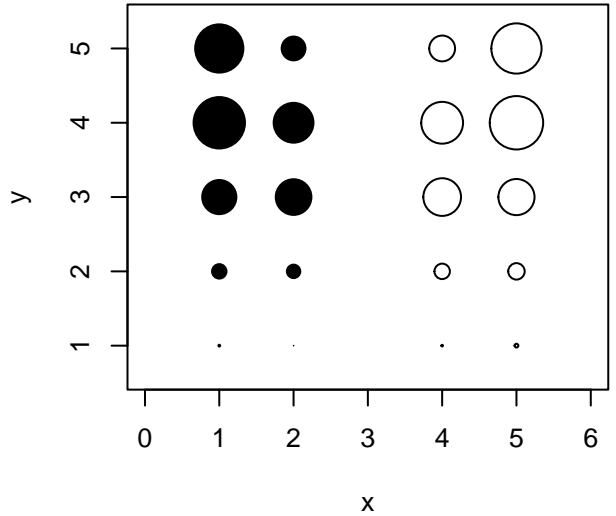
AEM 4



AEM 1

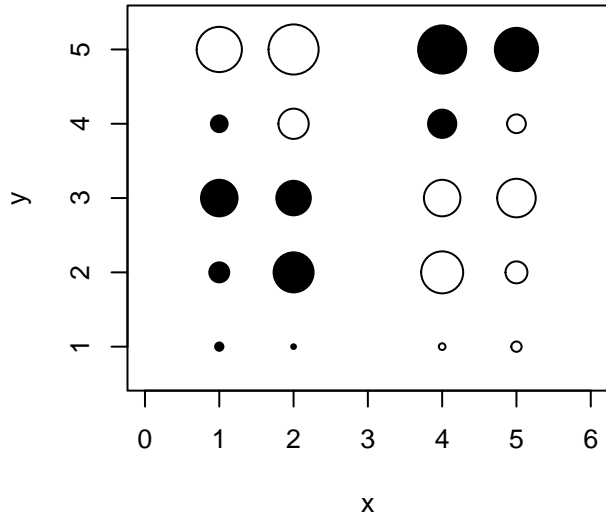


AEM 2

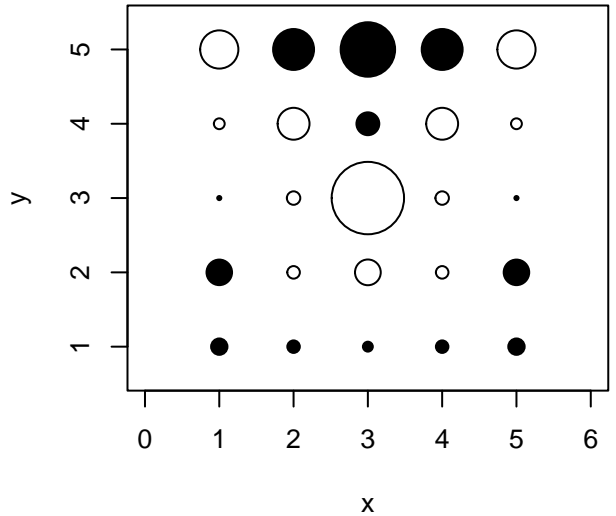


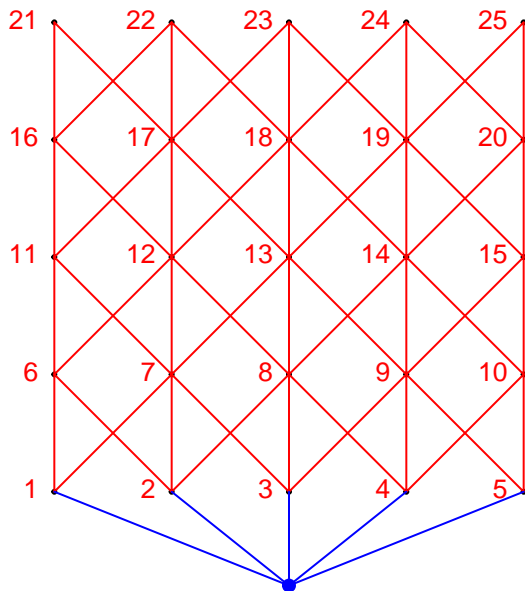
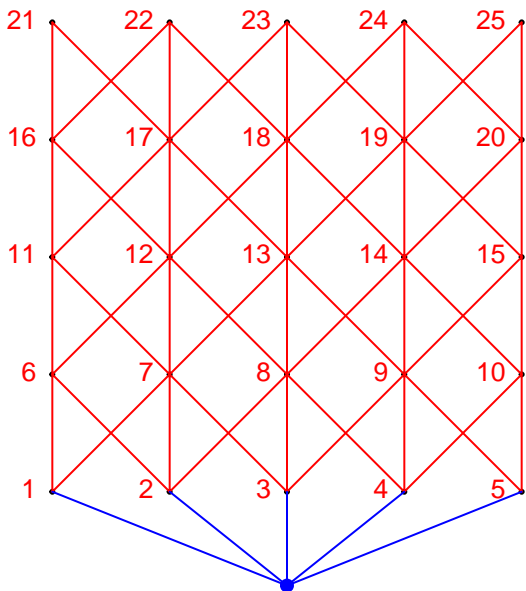
help("aem")

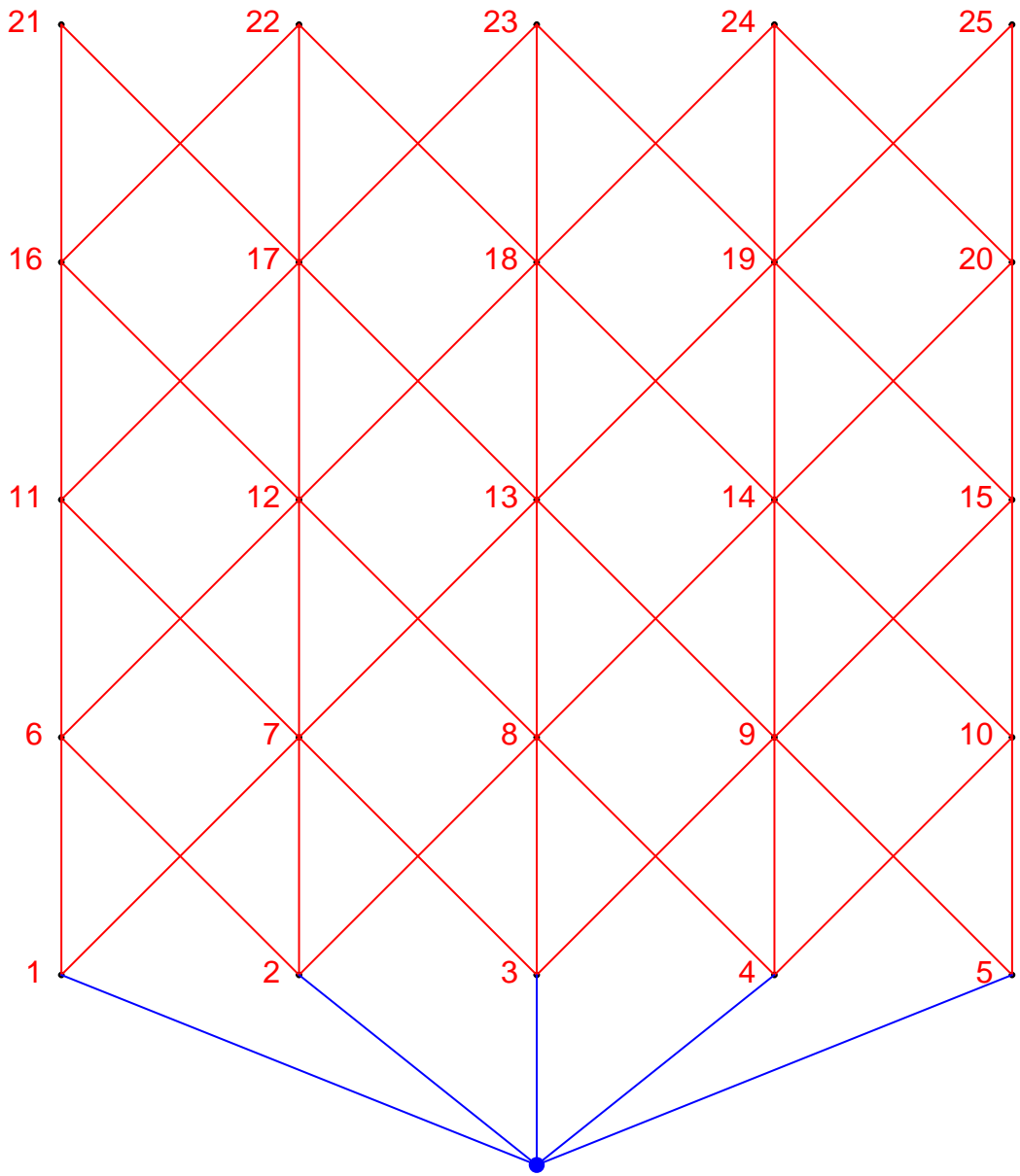
AEM 3

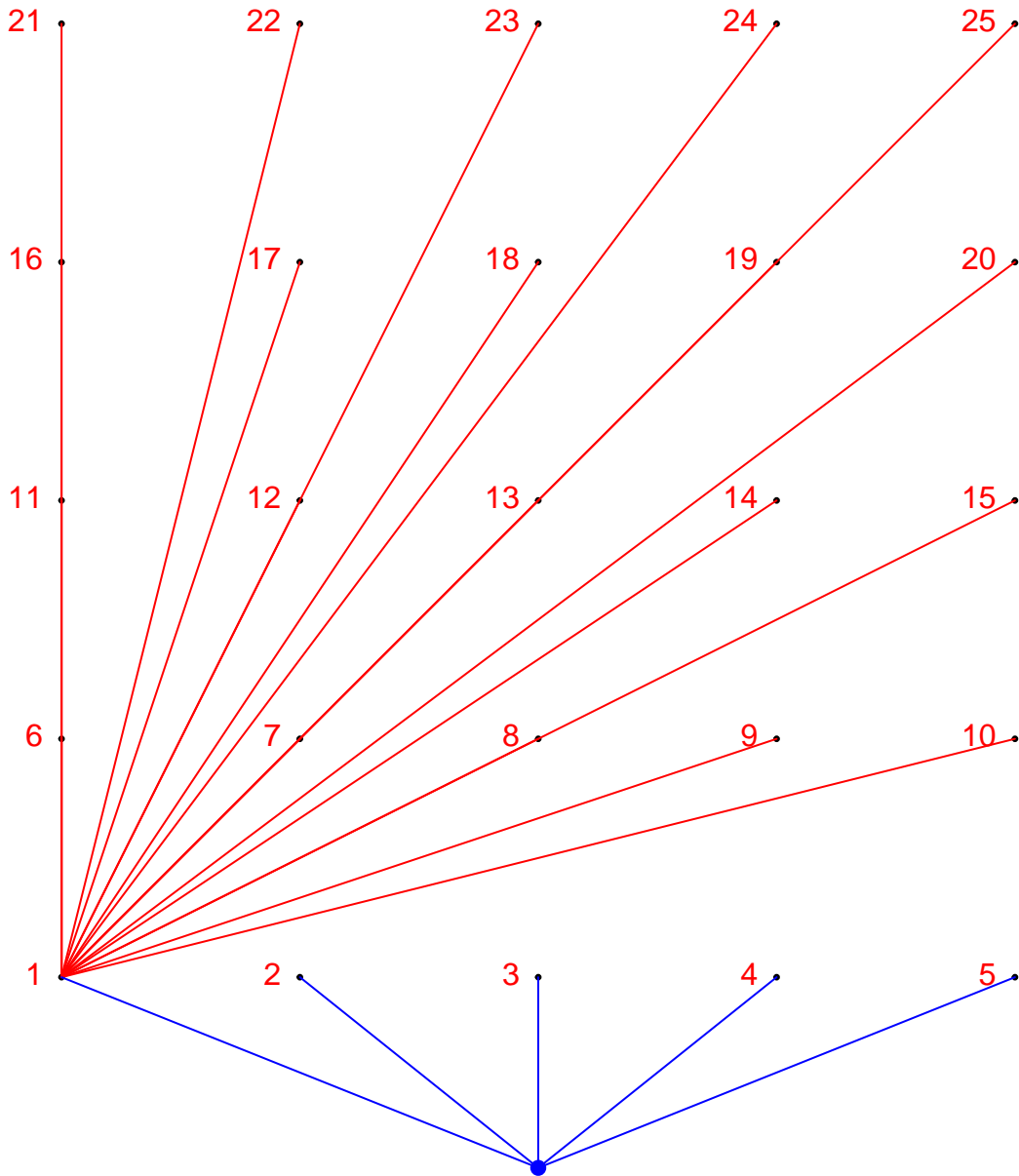


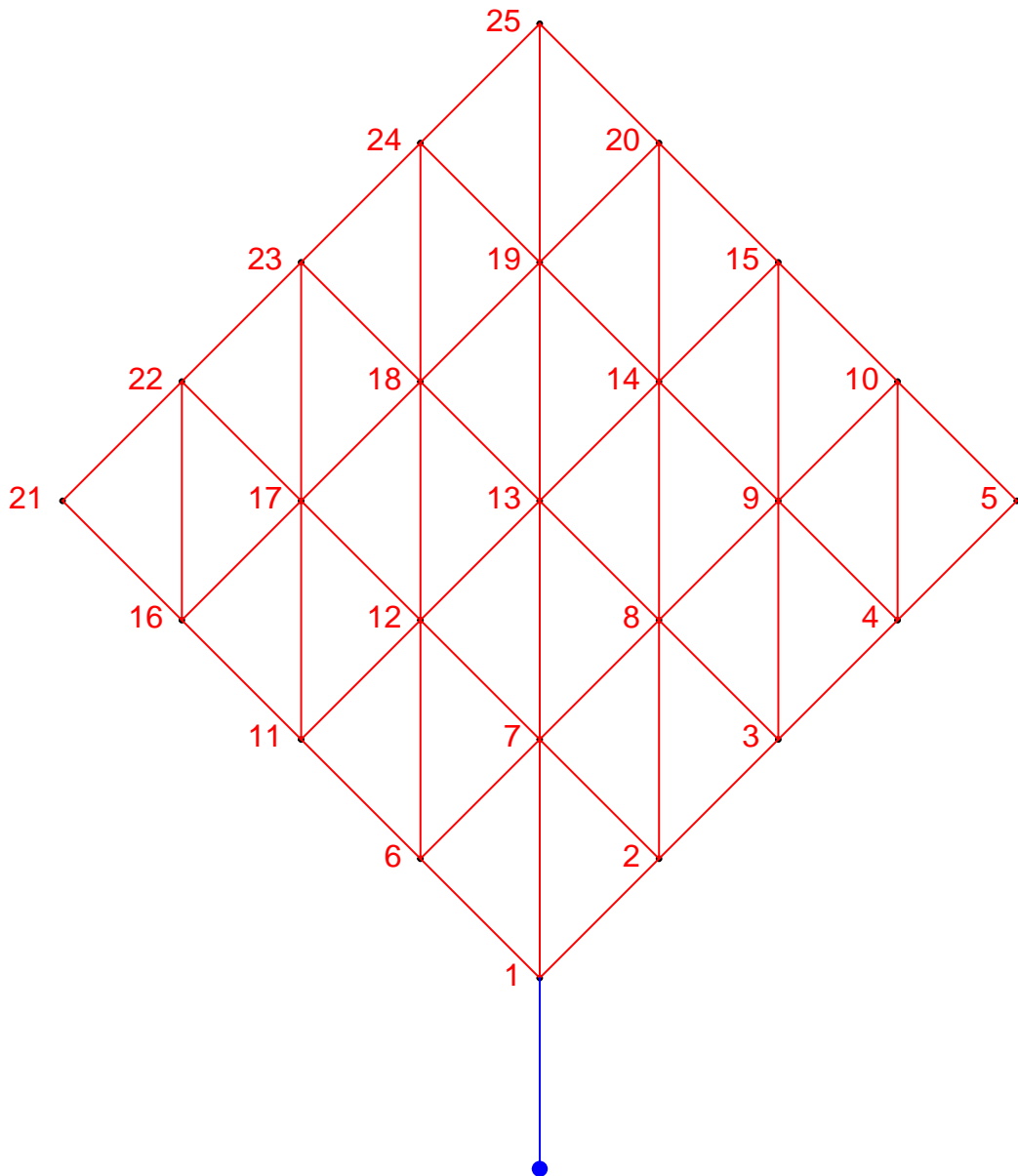
AEM 4



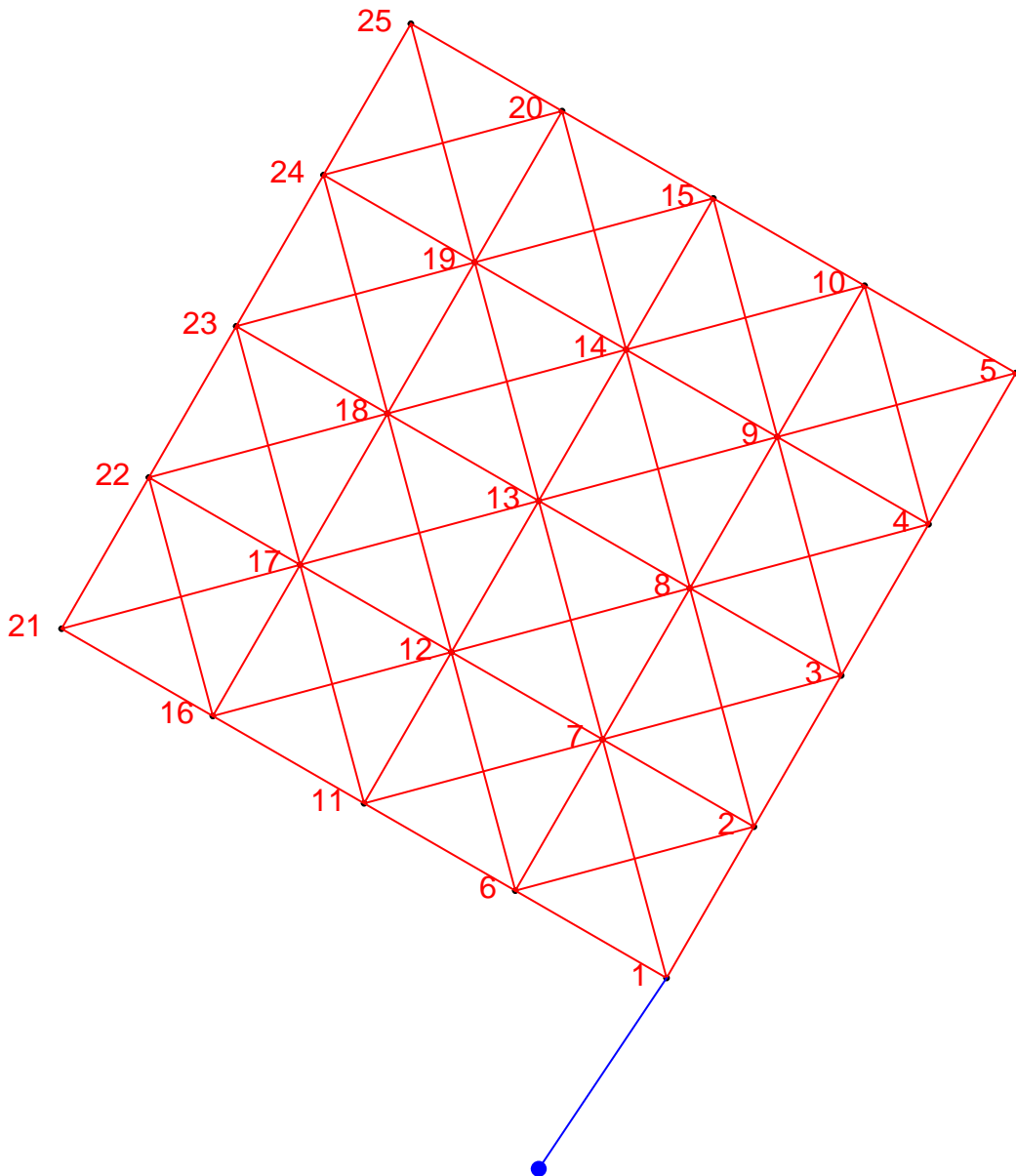








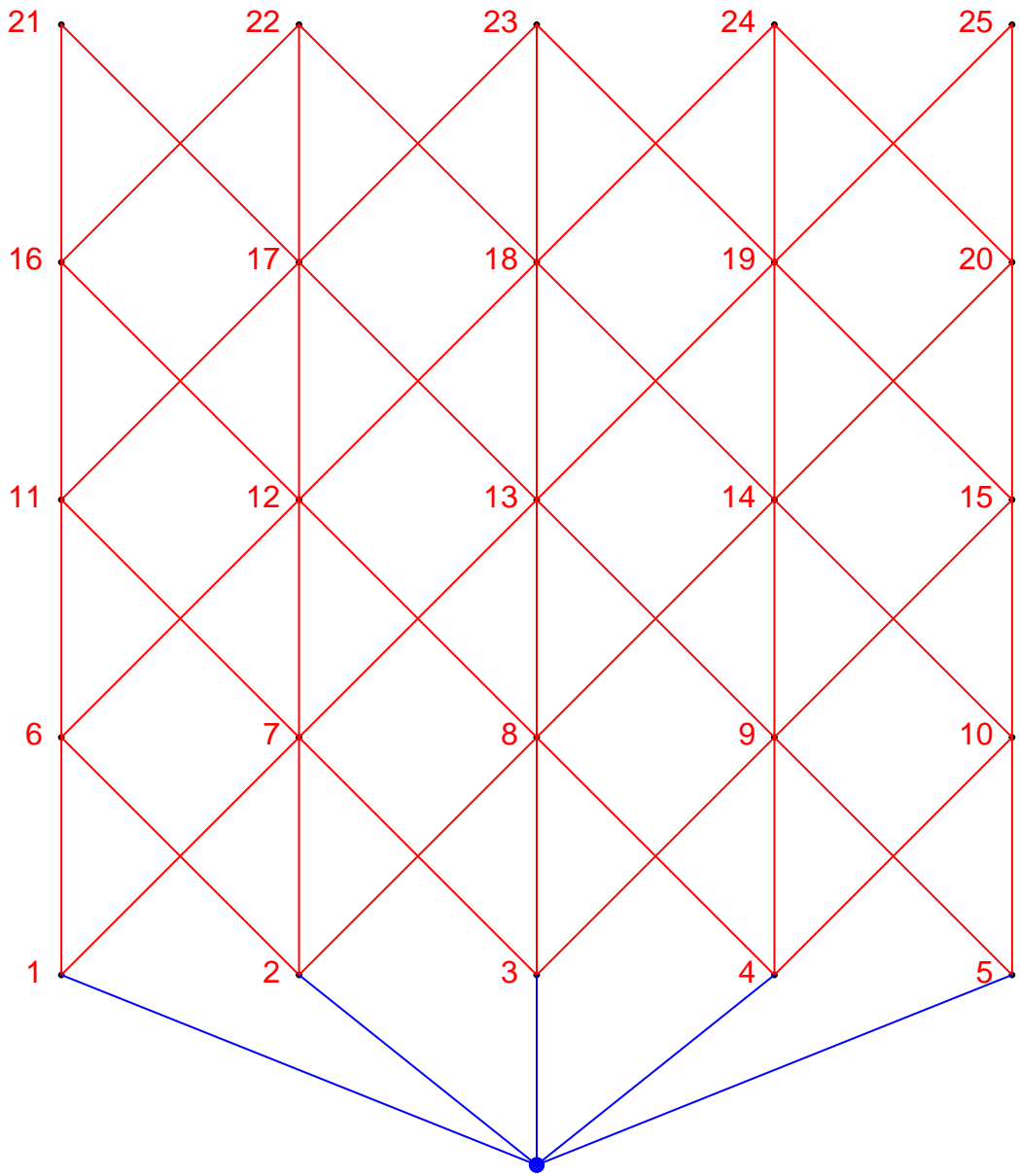
```
help("aem.build.binary")
```







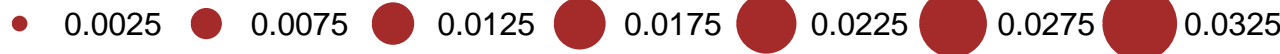
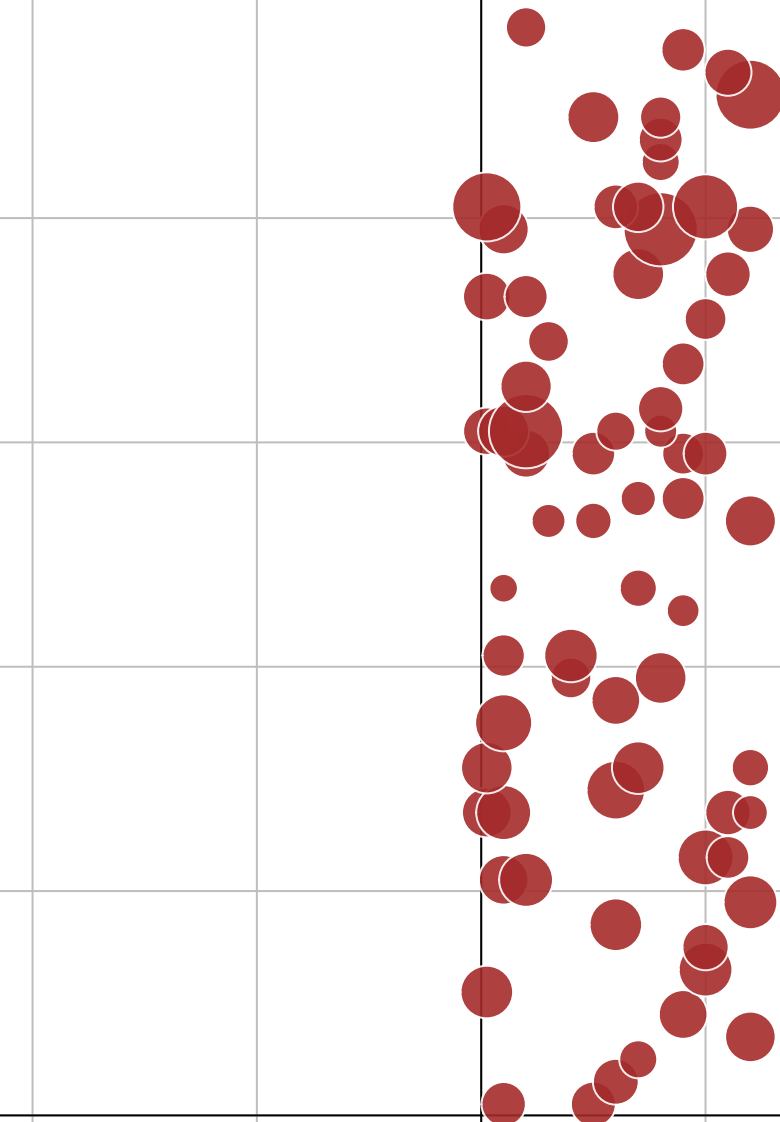


help("aem.weight.edges")

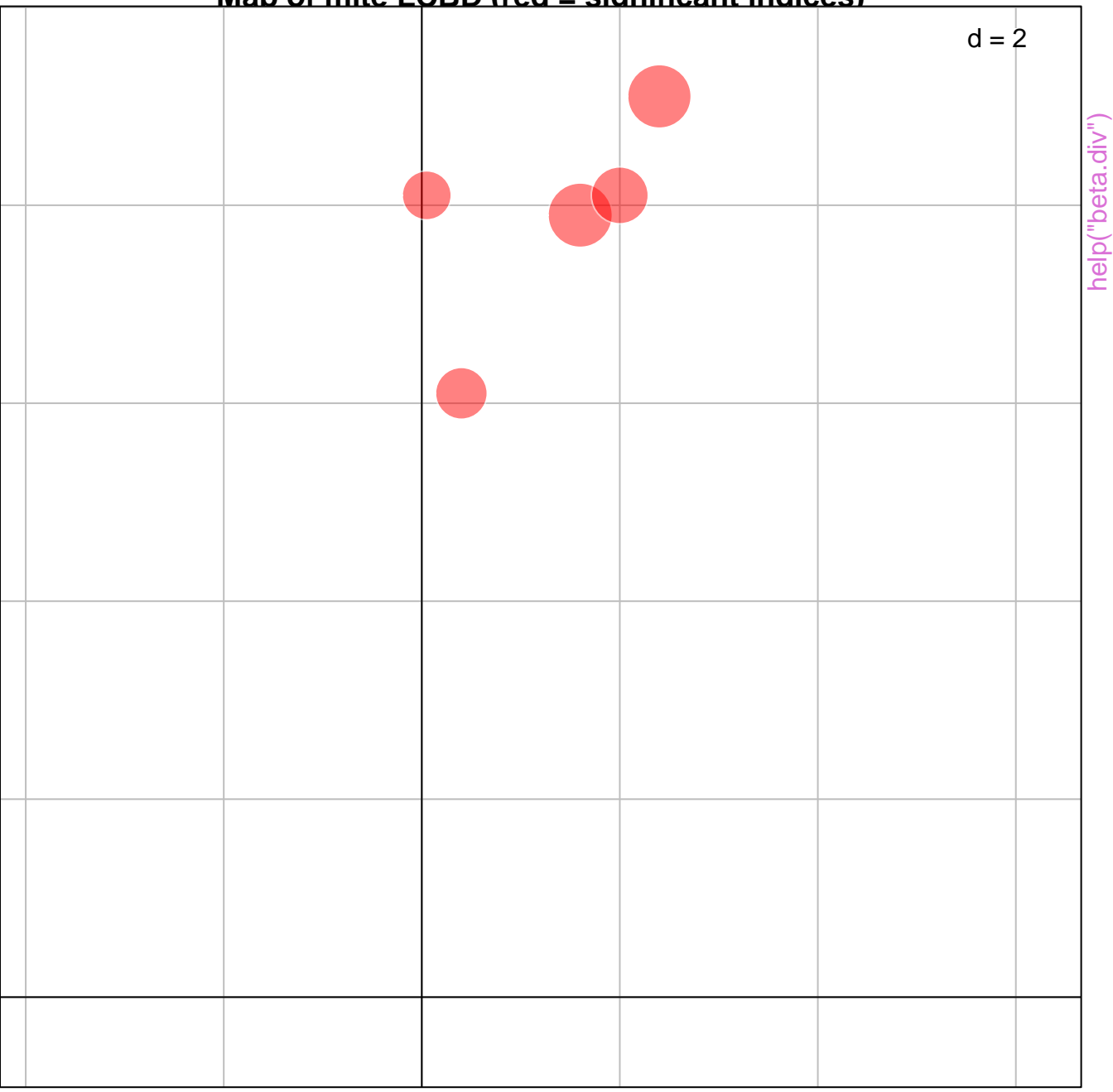
Map of mite LCBD

d = 2

help("beta div")

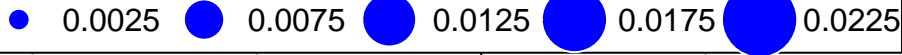


Map of mite LCBD (red = significant indices)



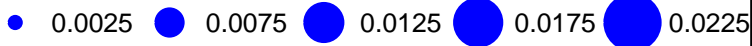
d = 2

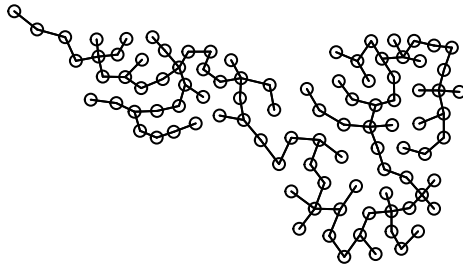
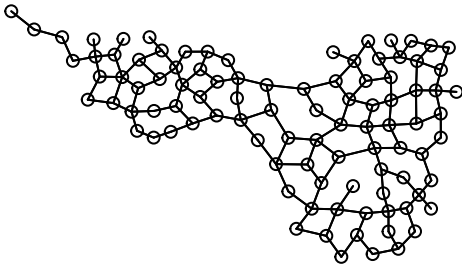
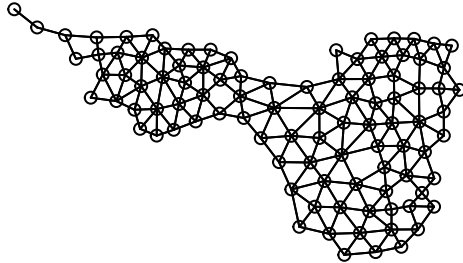
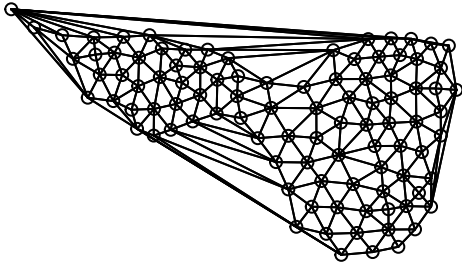
help("beta div")



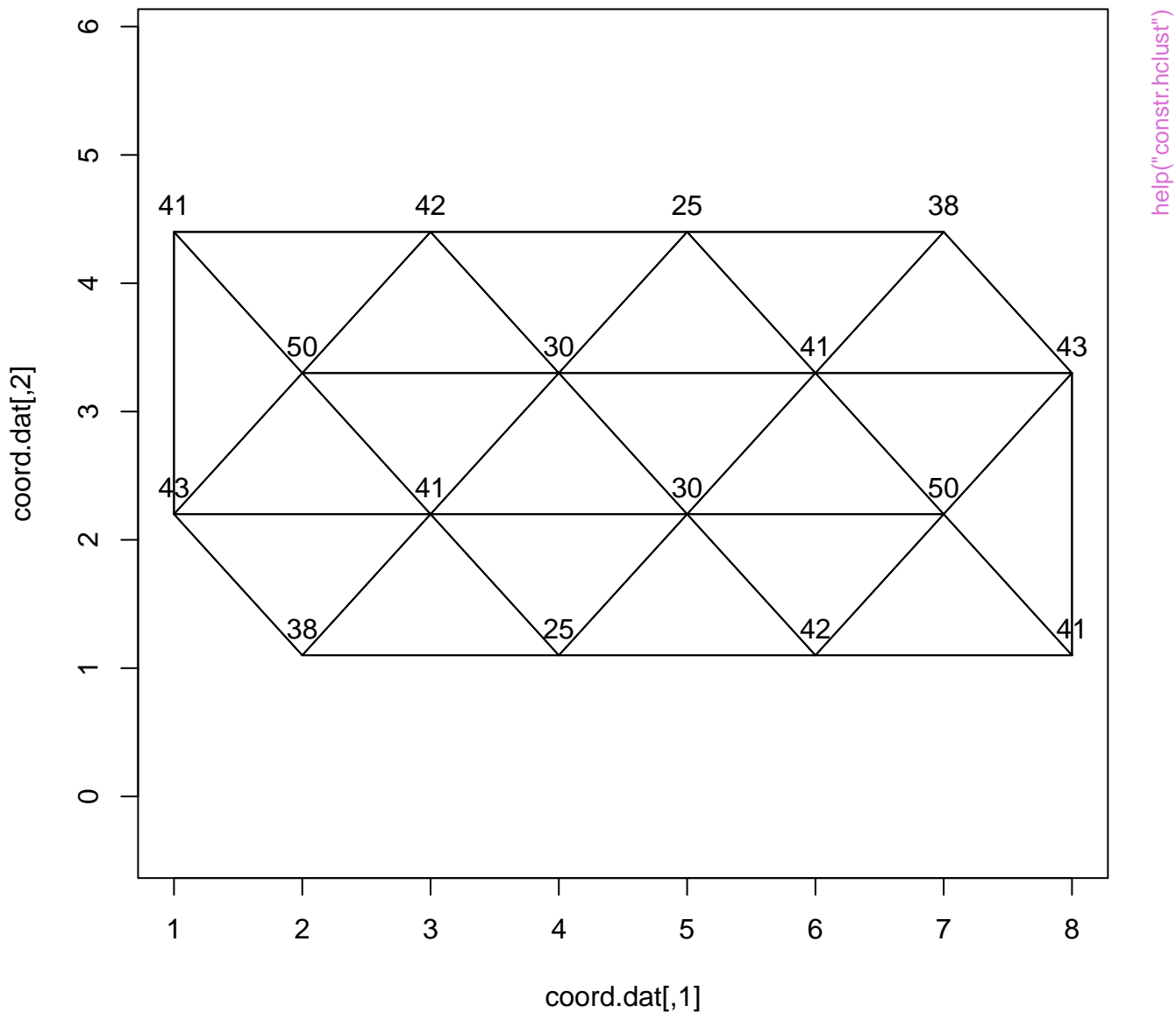
d = 2

help("beta div")

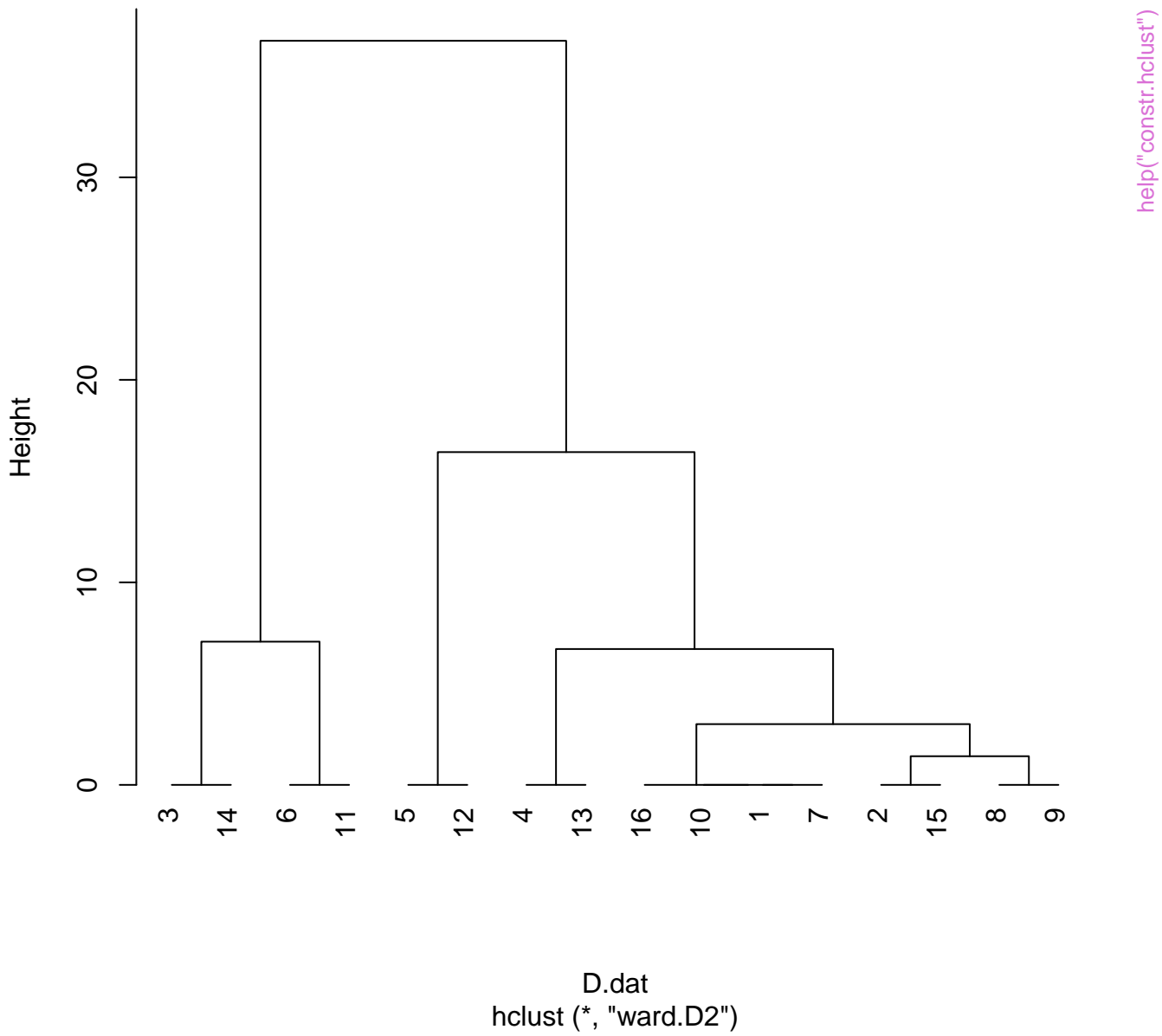




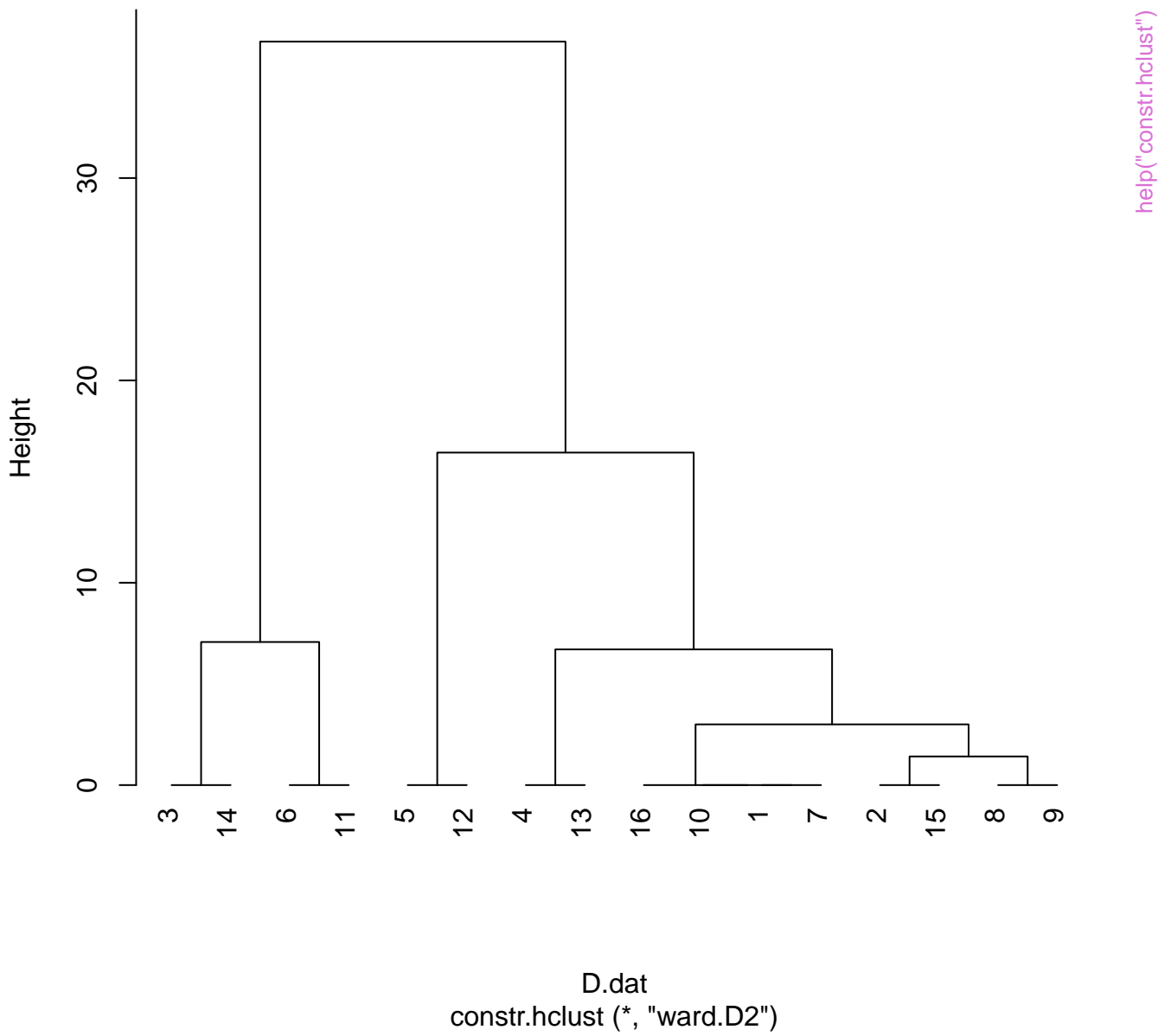
Delaunay triangulation

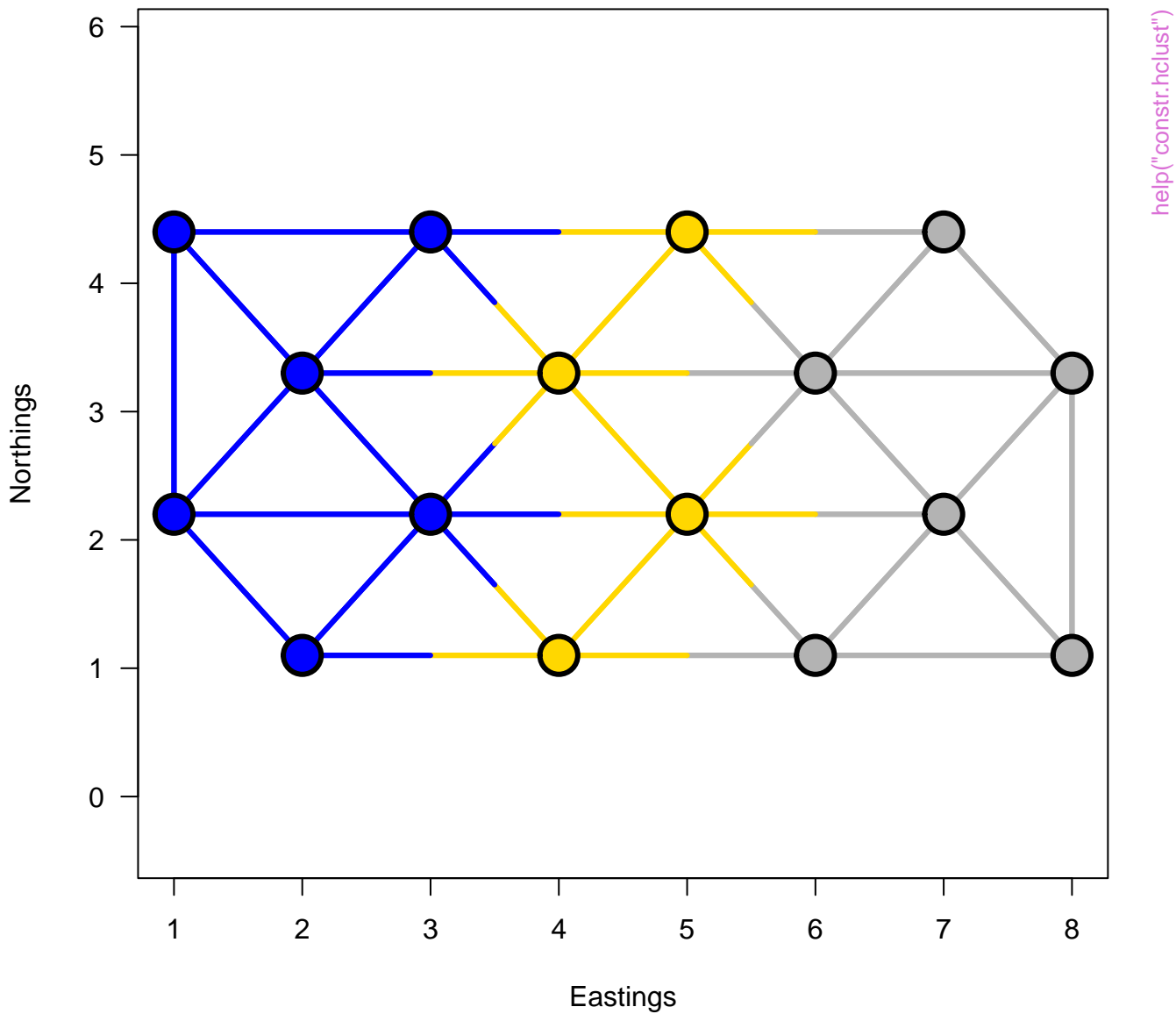


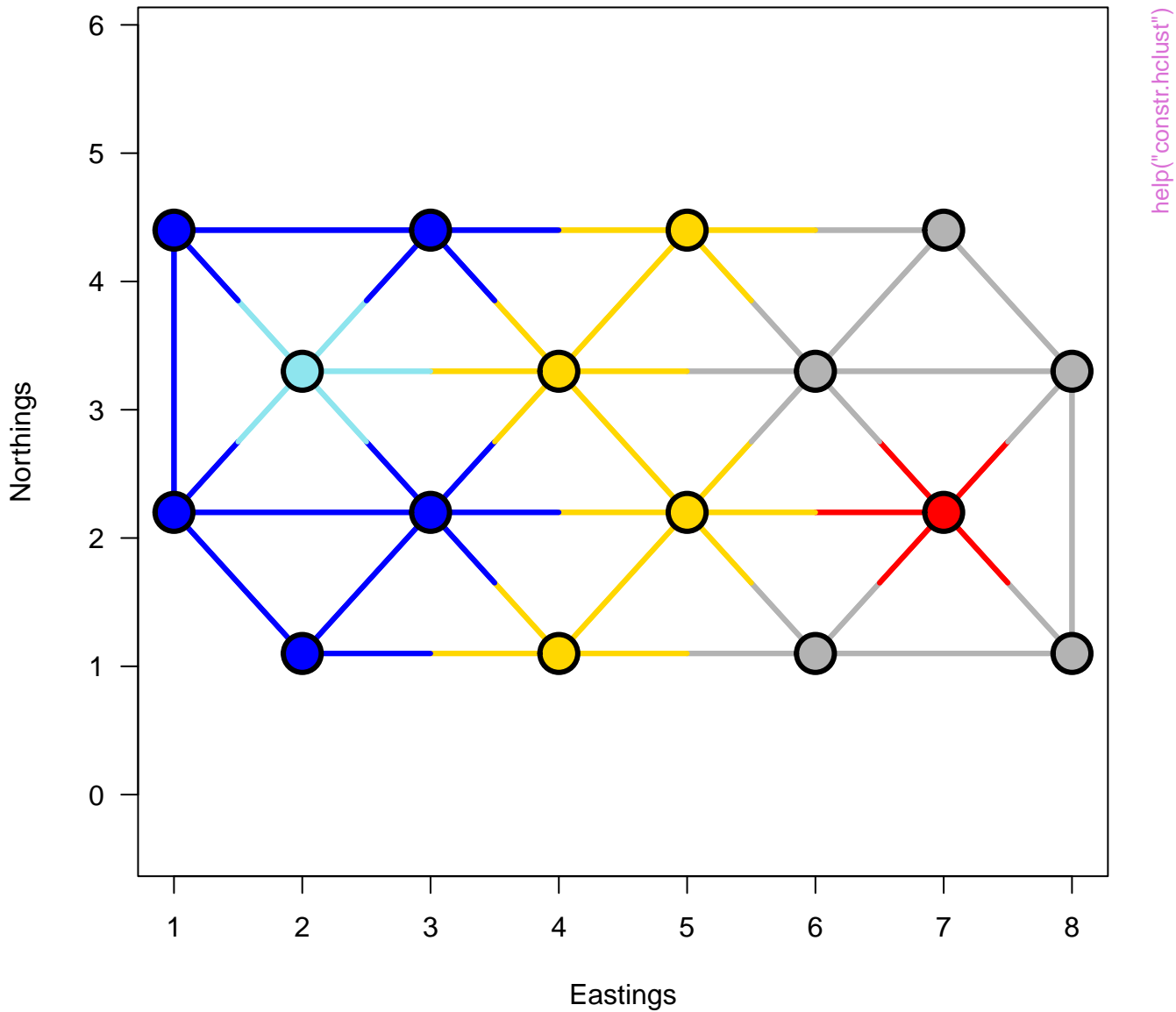
Cluster Dendrogram



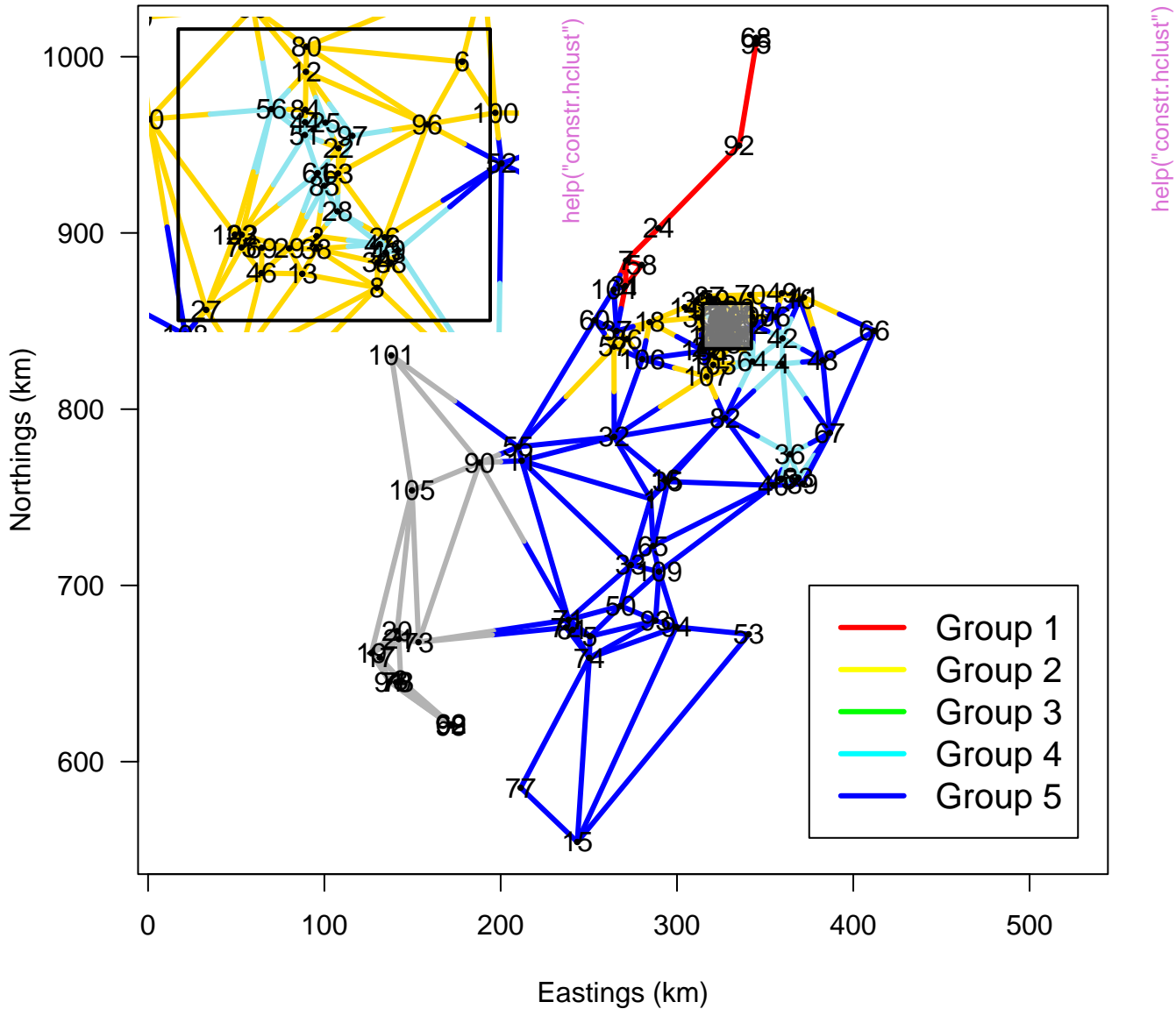
Cluster Dendrogram



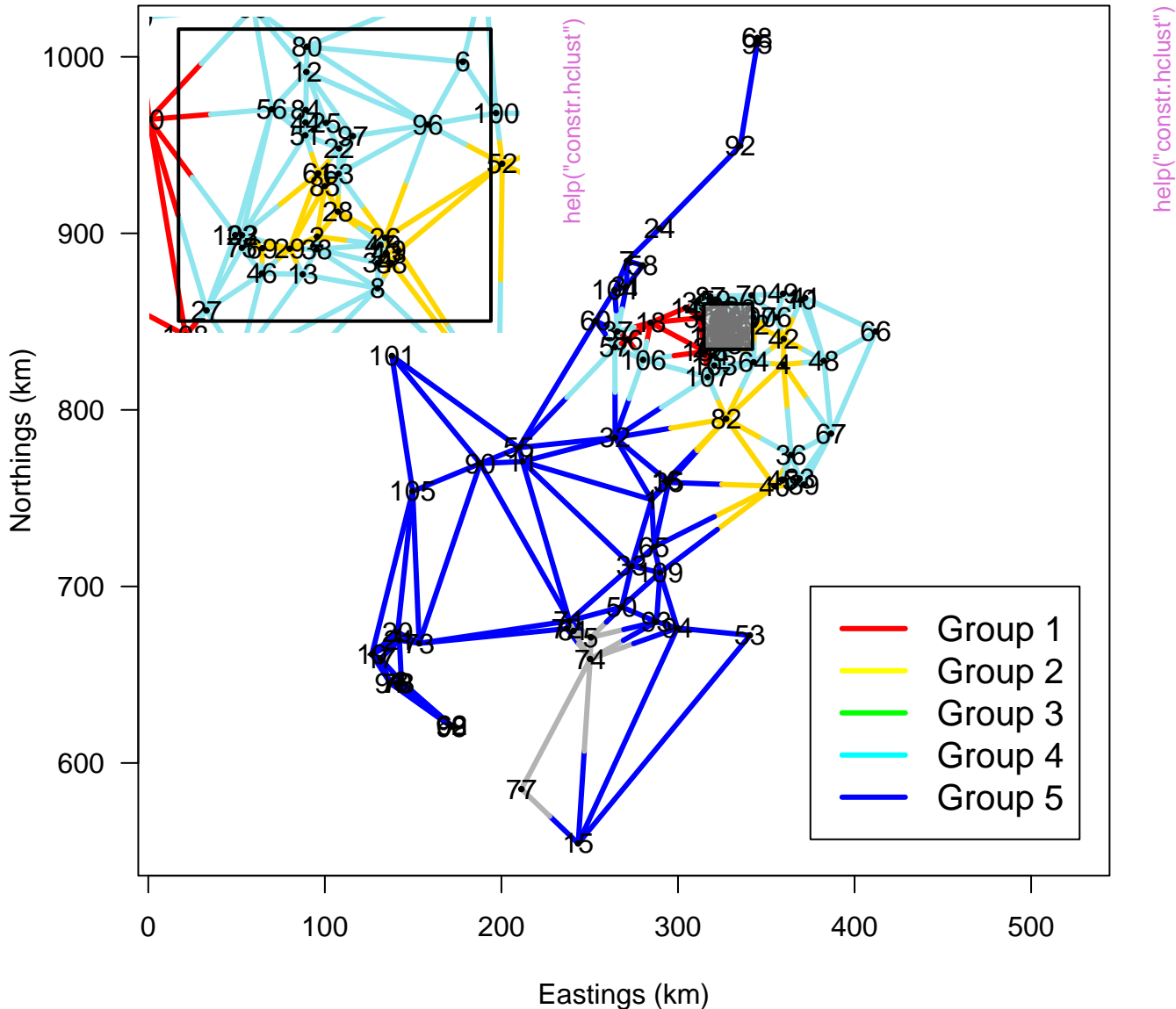




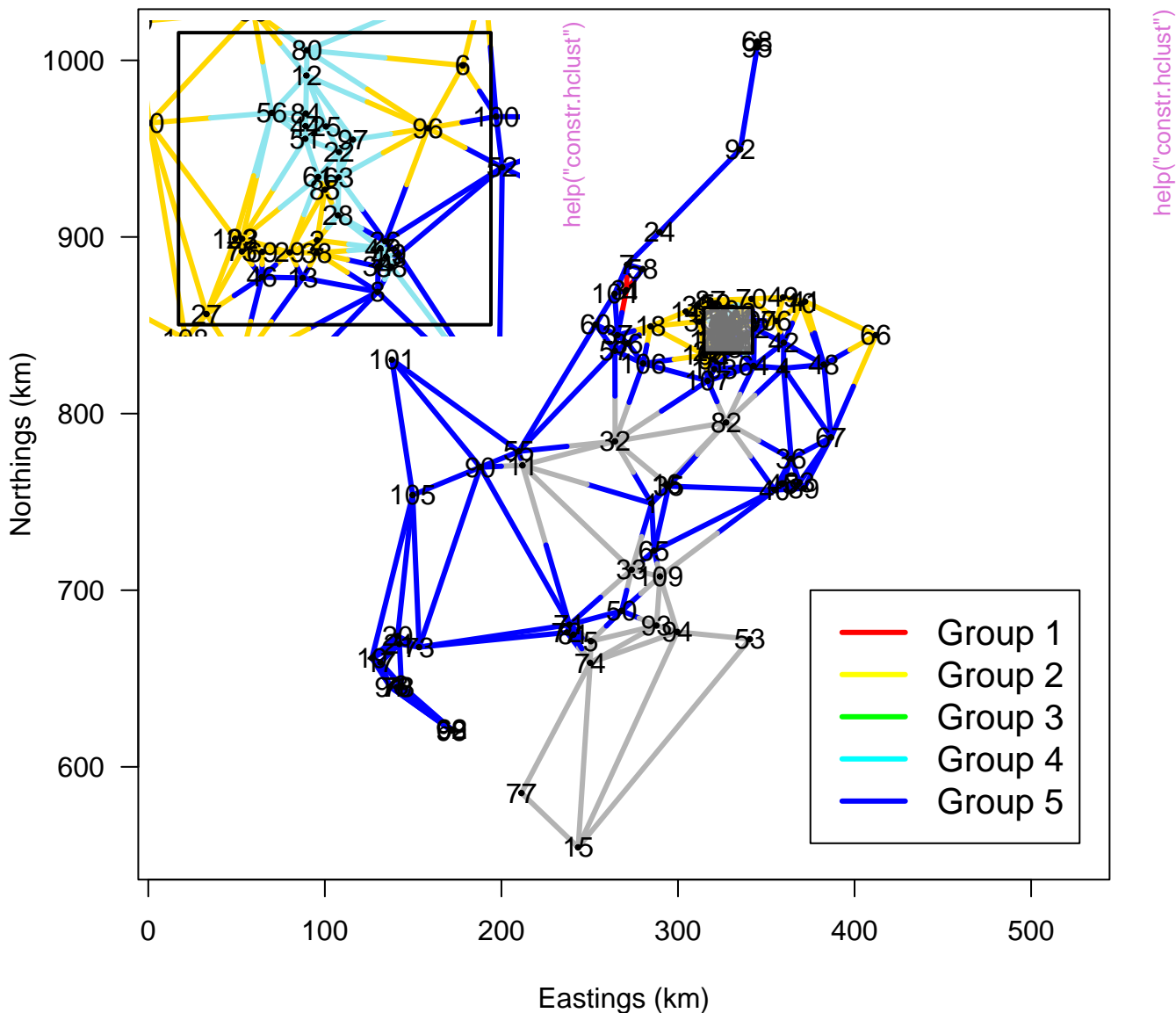
Feature: nose



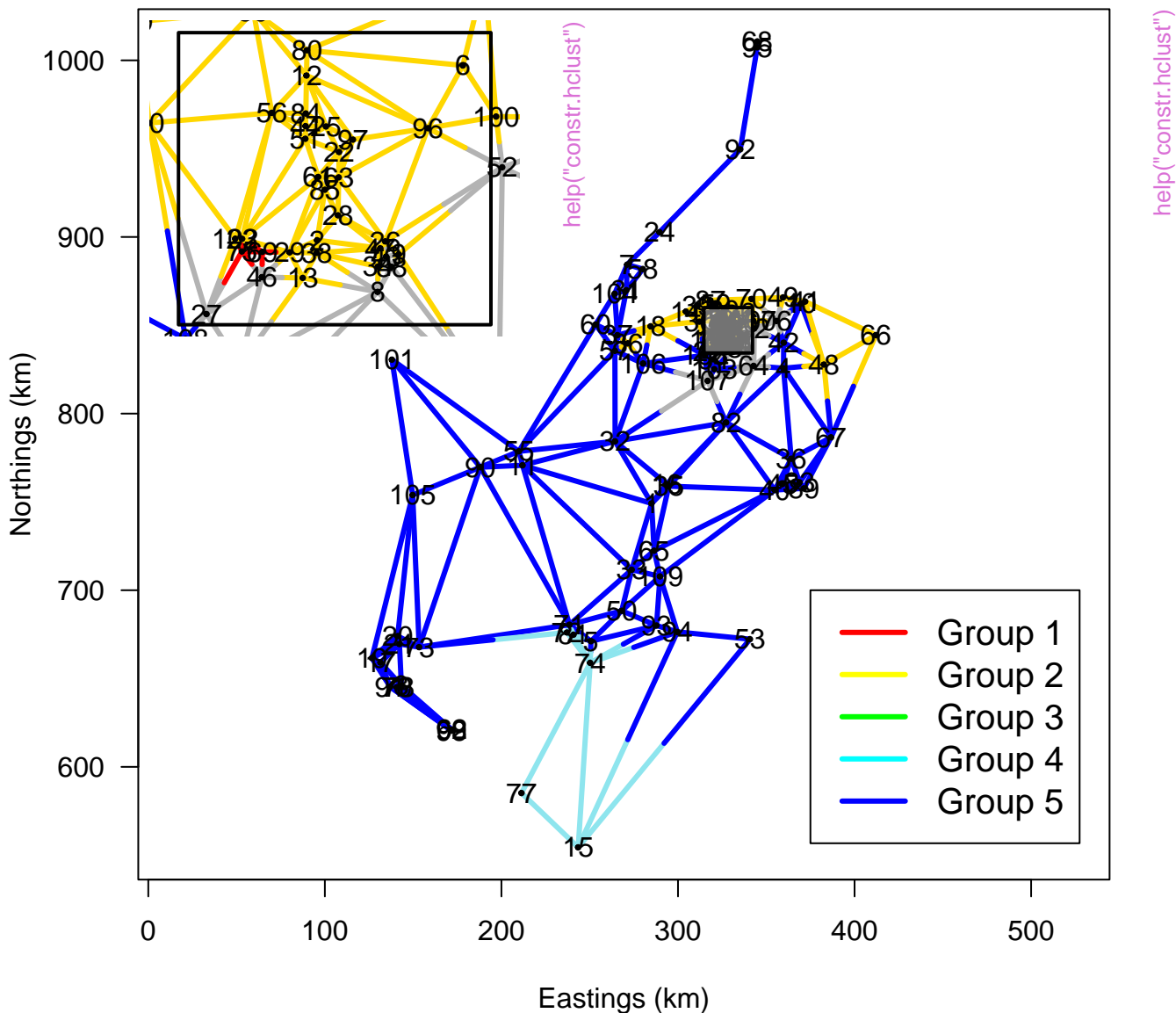
Feature: body



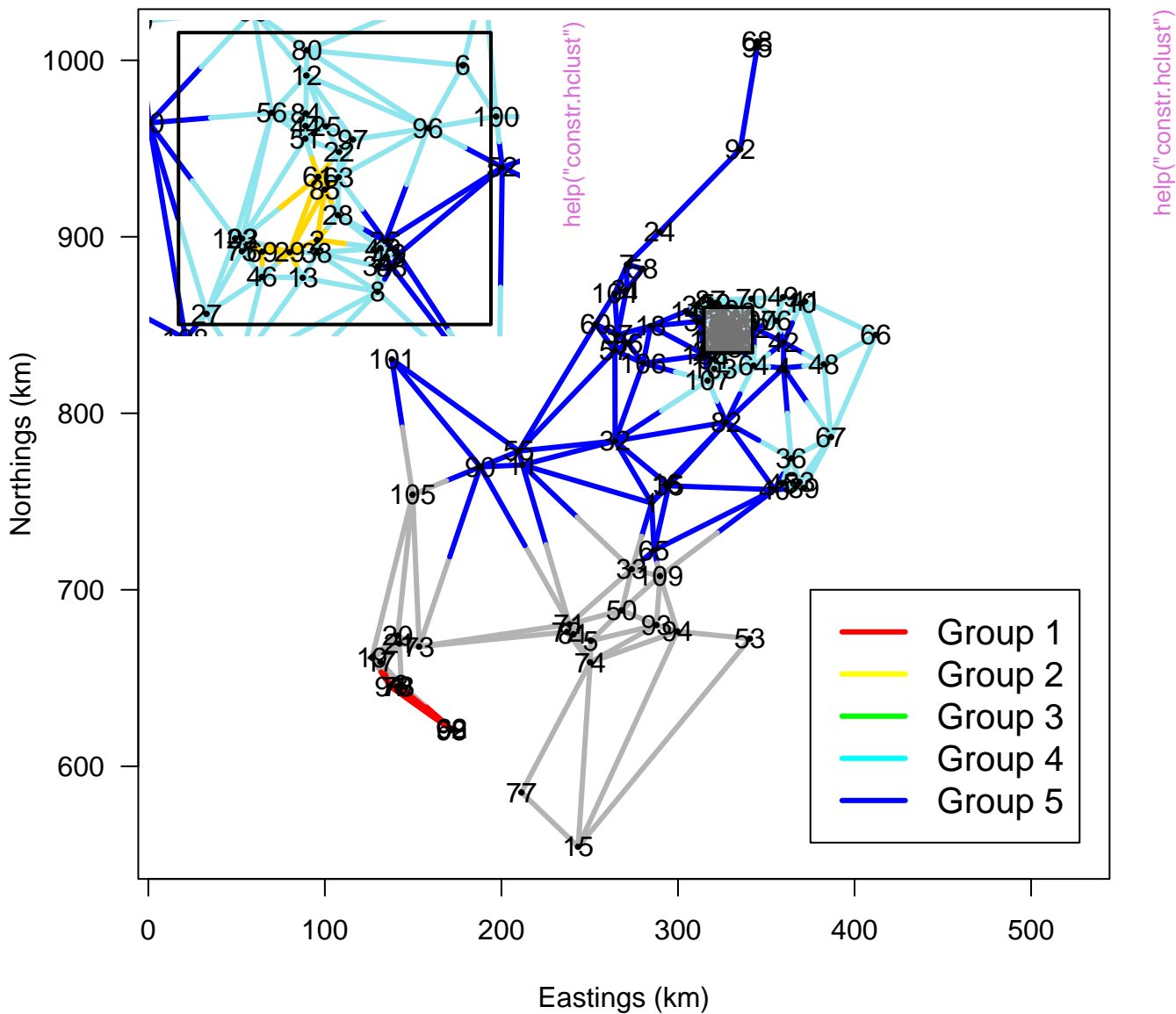
Feature: palate



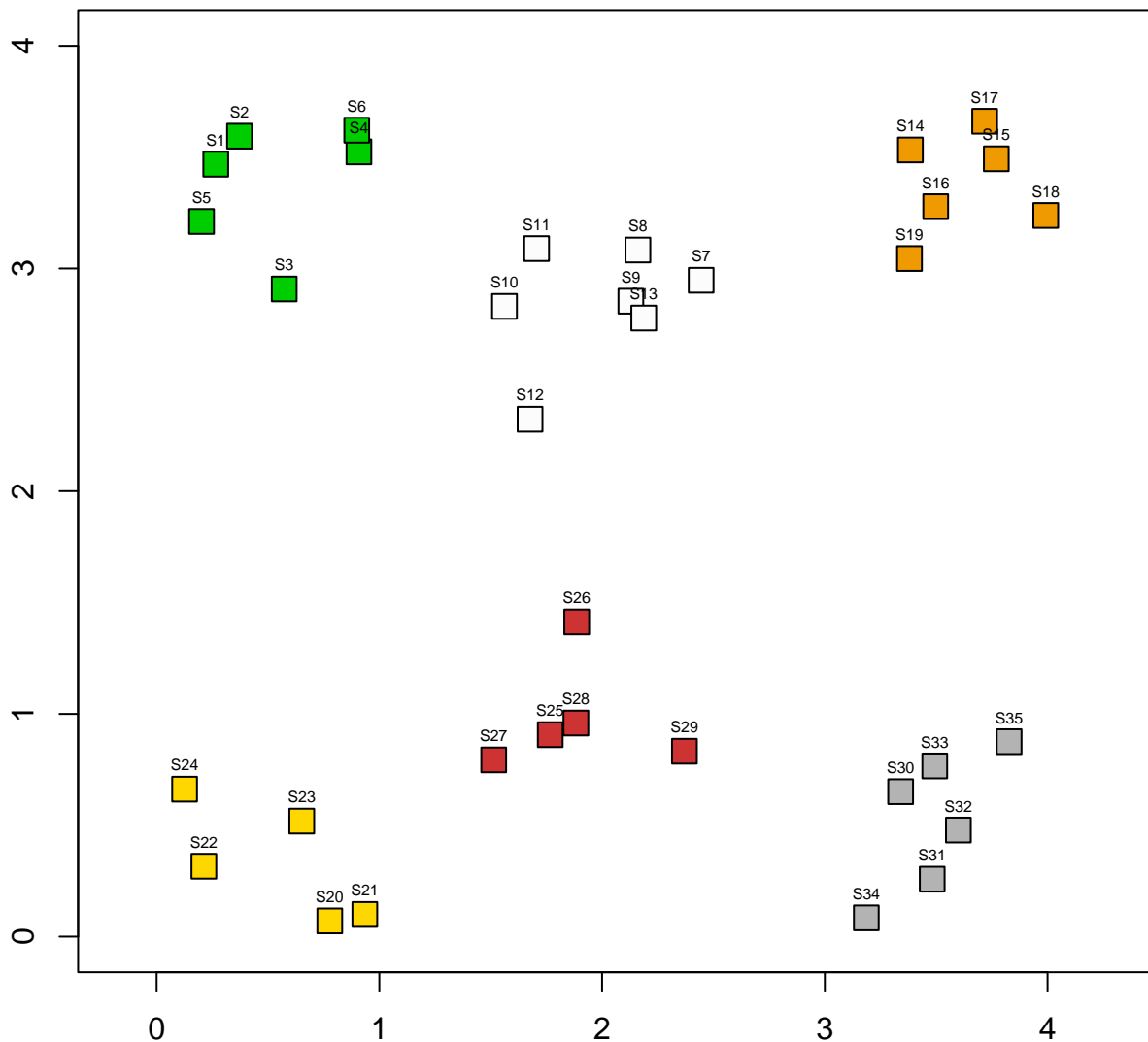
Feature: finish



Feature: norm

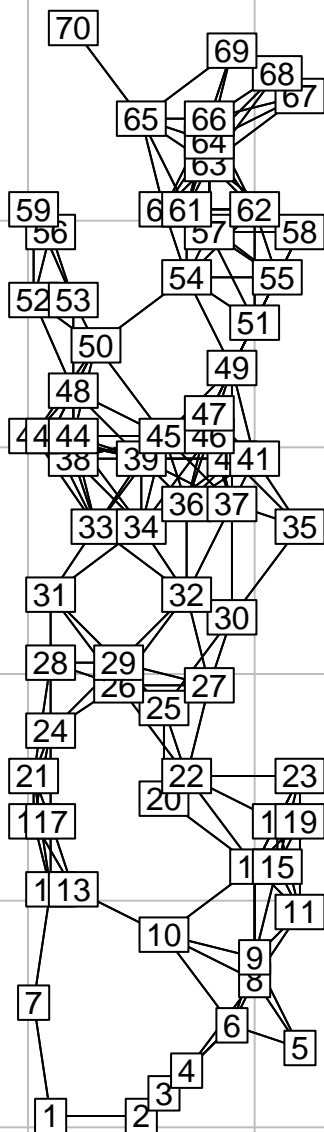


Northing

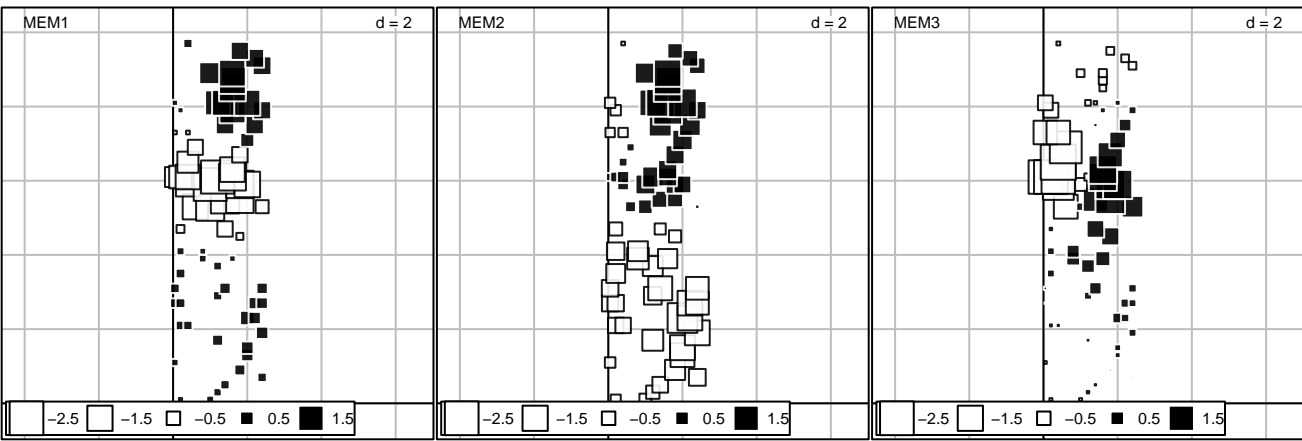


help("create.dbMEM.model")

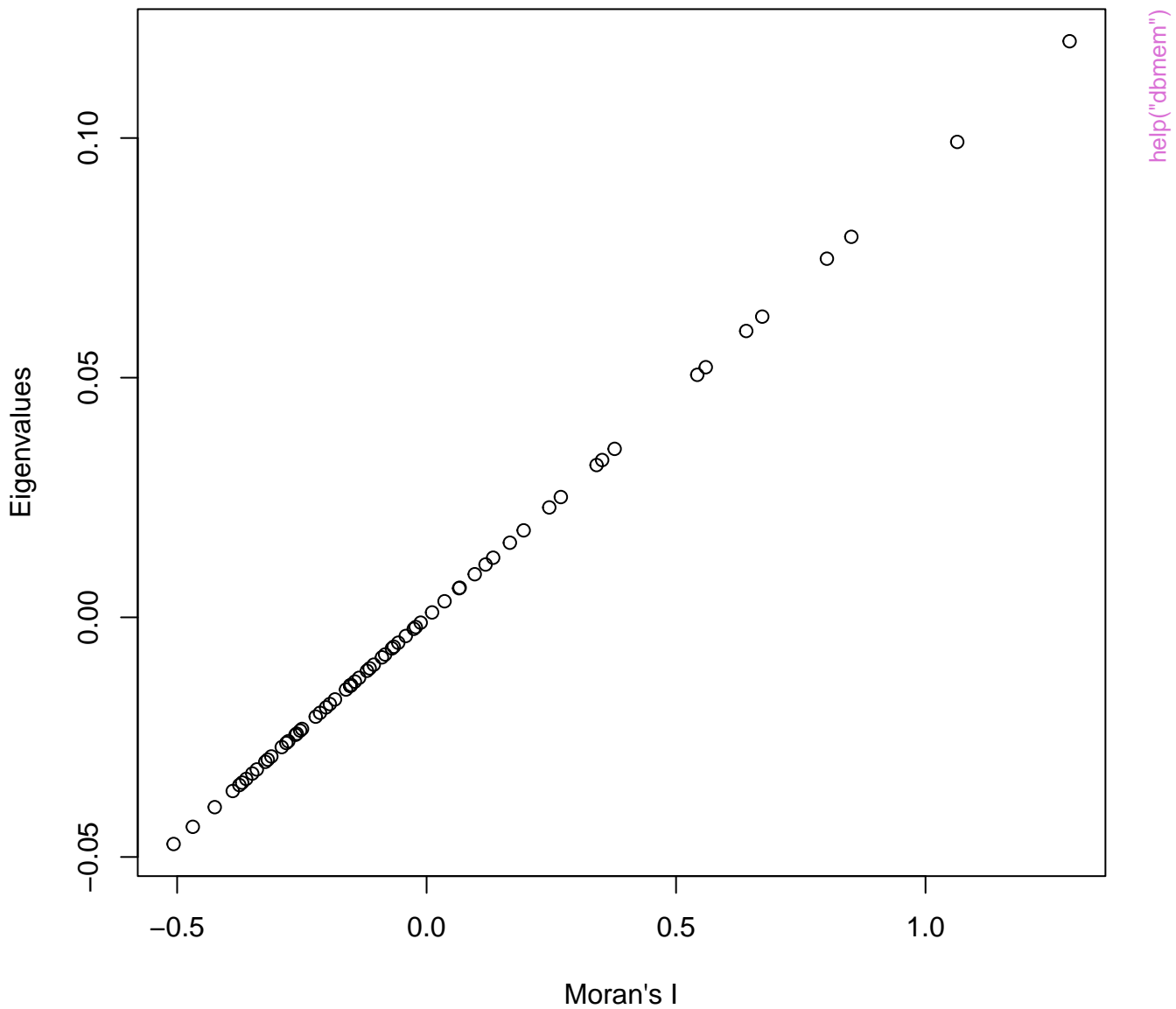
d = 2

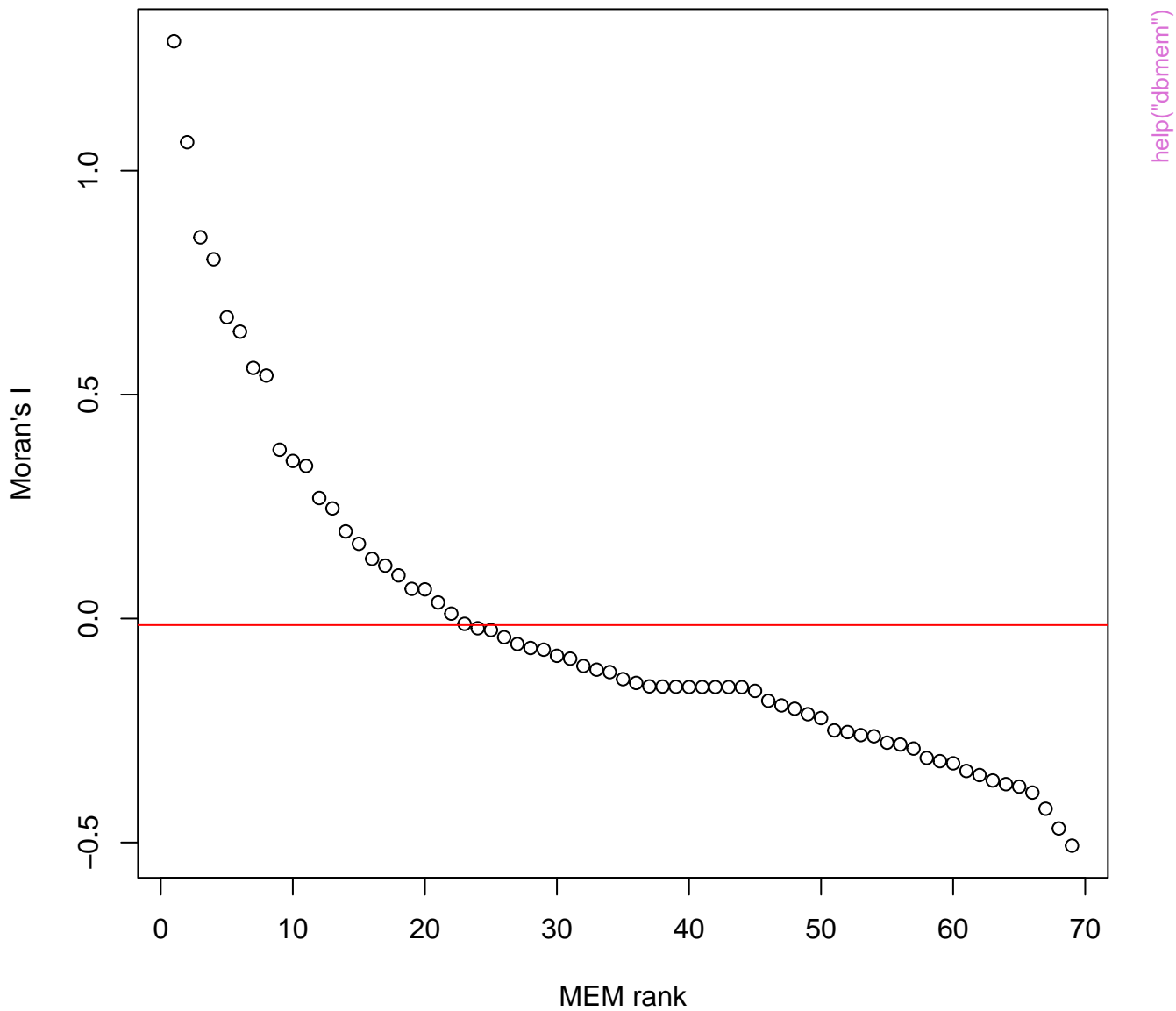


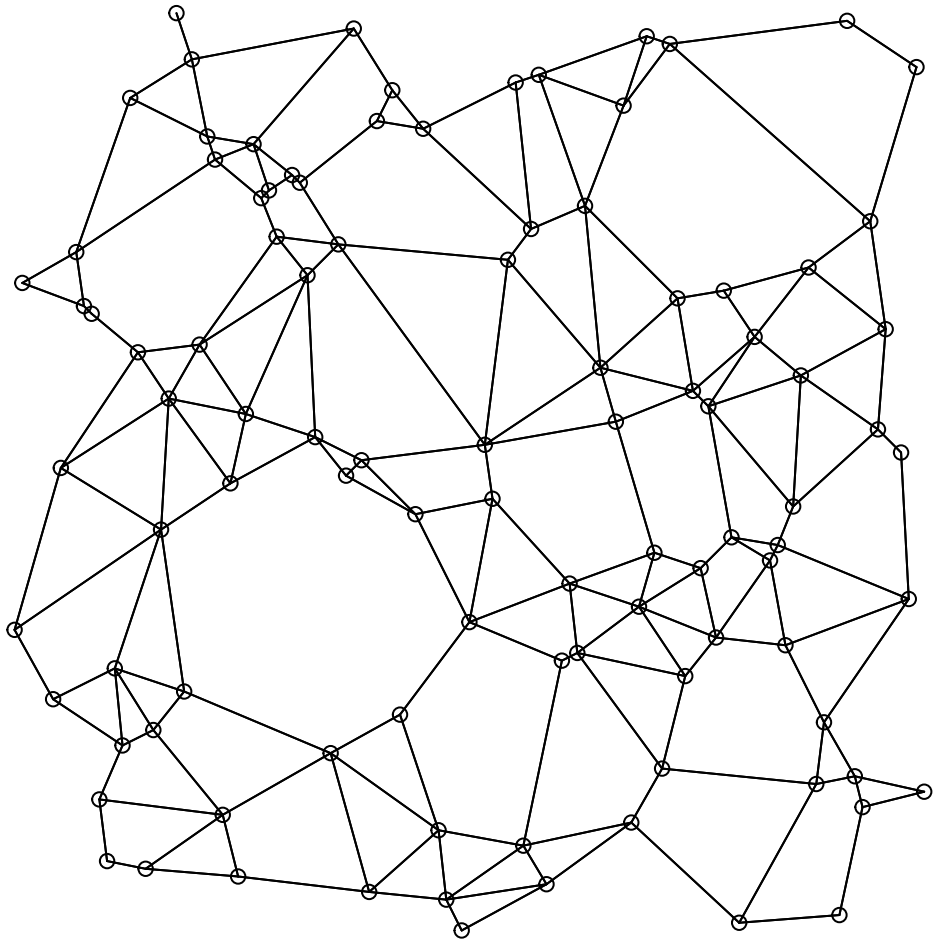
help("dbmem")



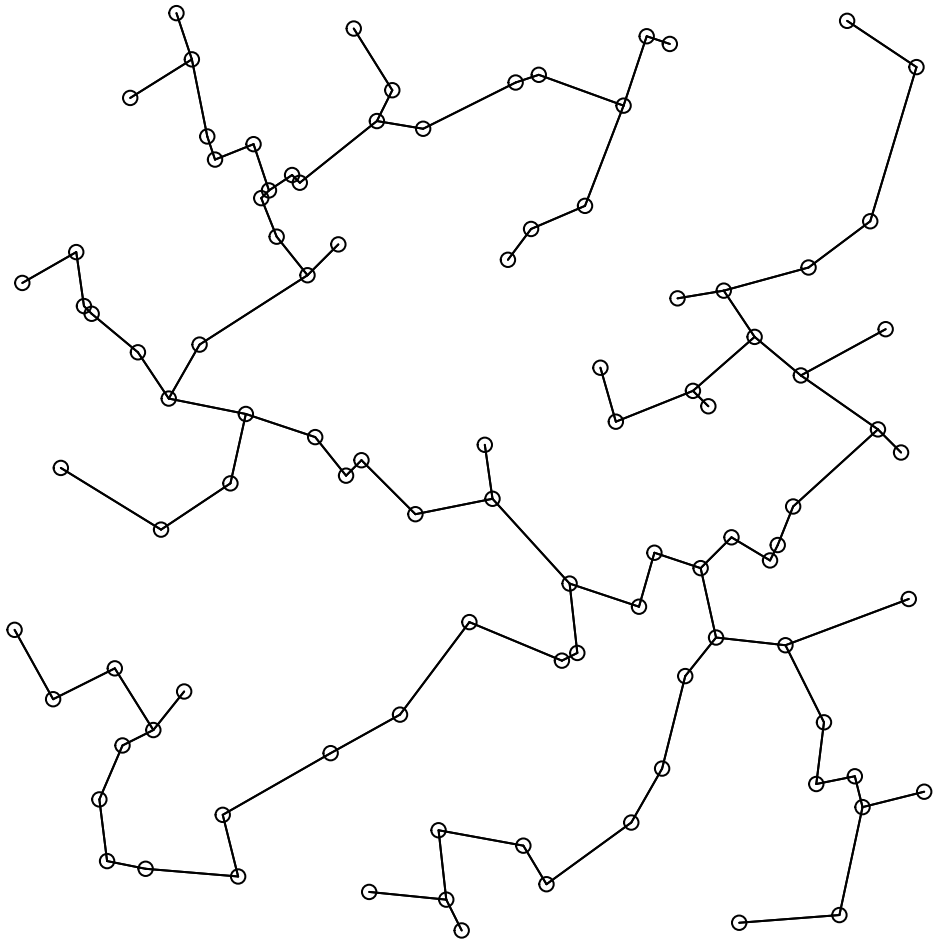
`help("dbmem")`



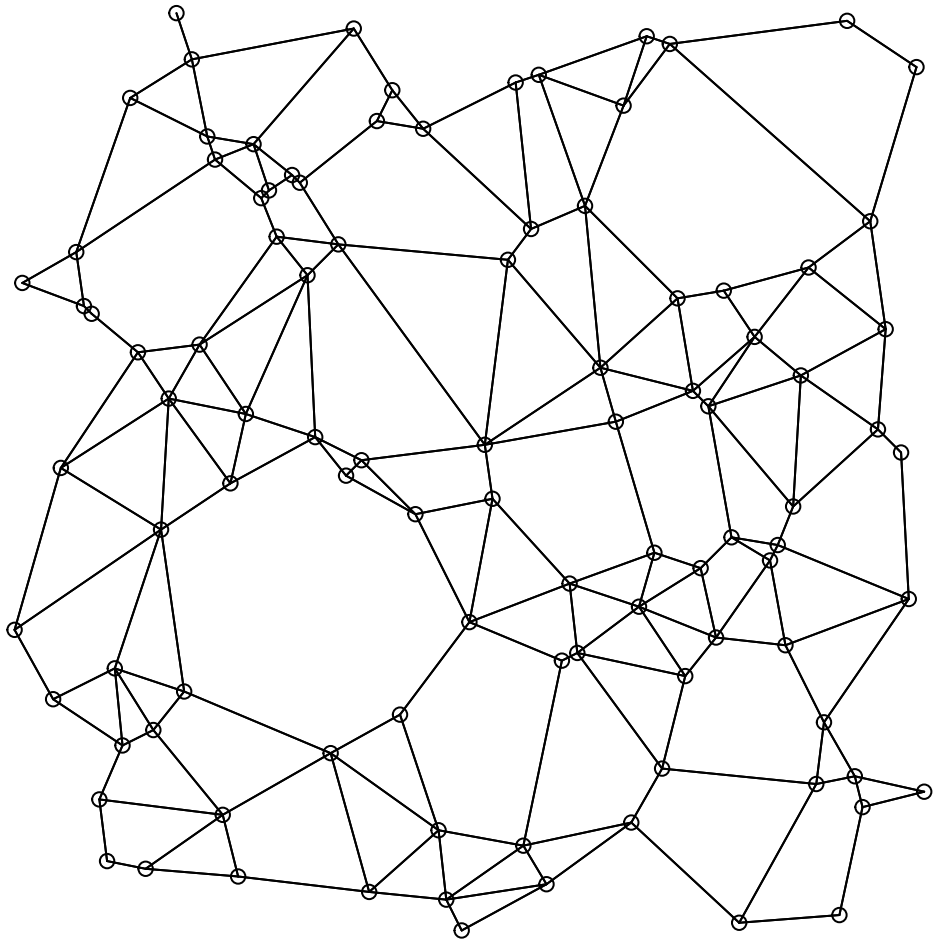




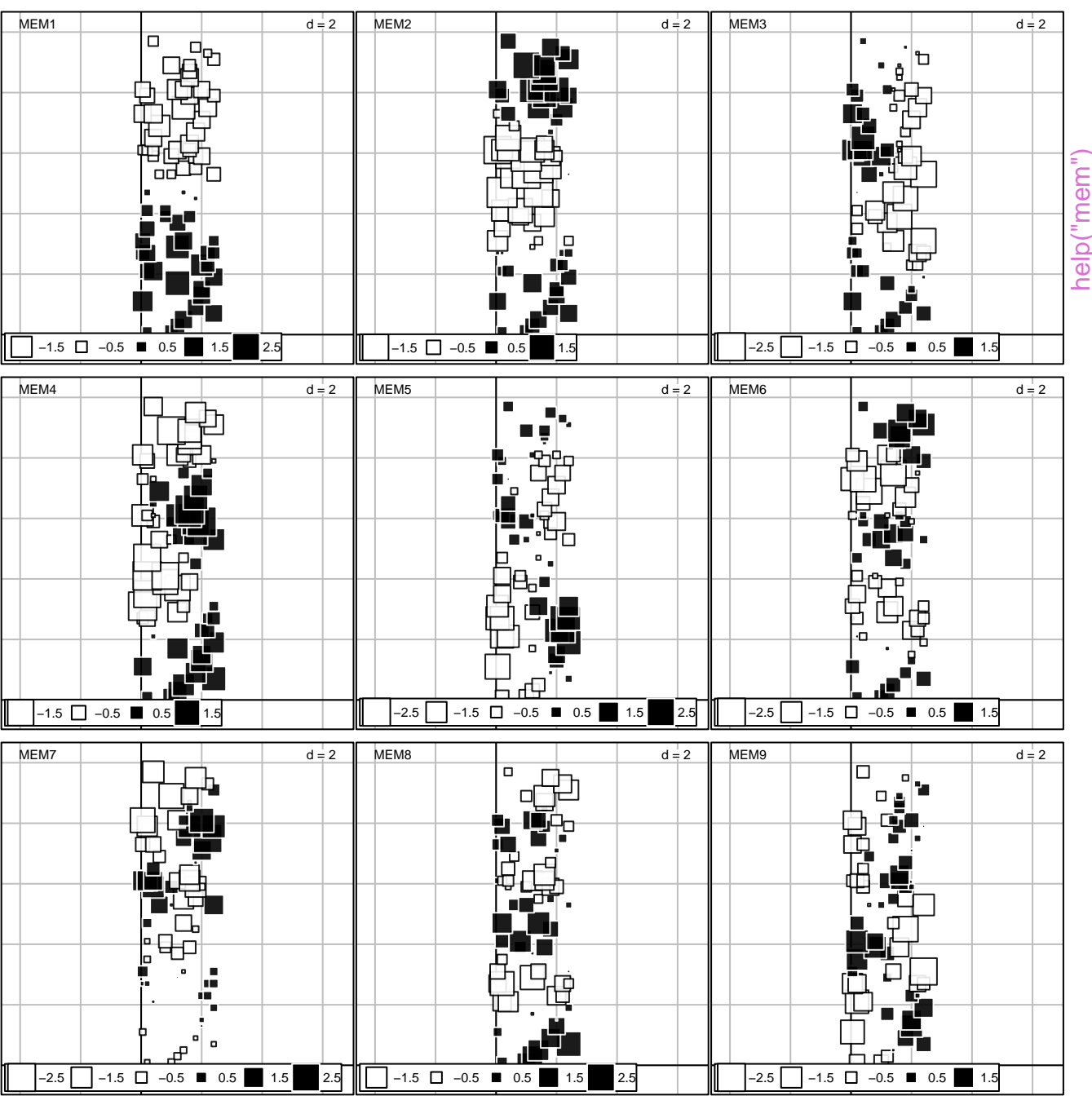
help("listw.candidates")



help("listw.candidates")



help("listw.candidates")



MEM1



MEM2



MEM3



MEM4

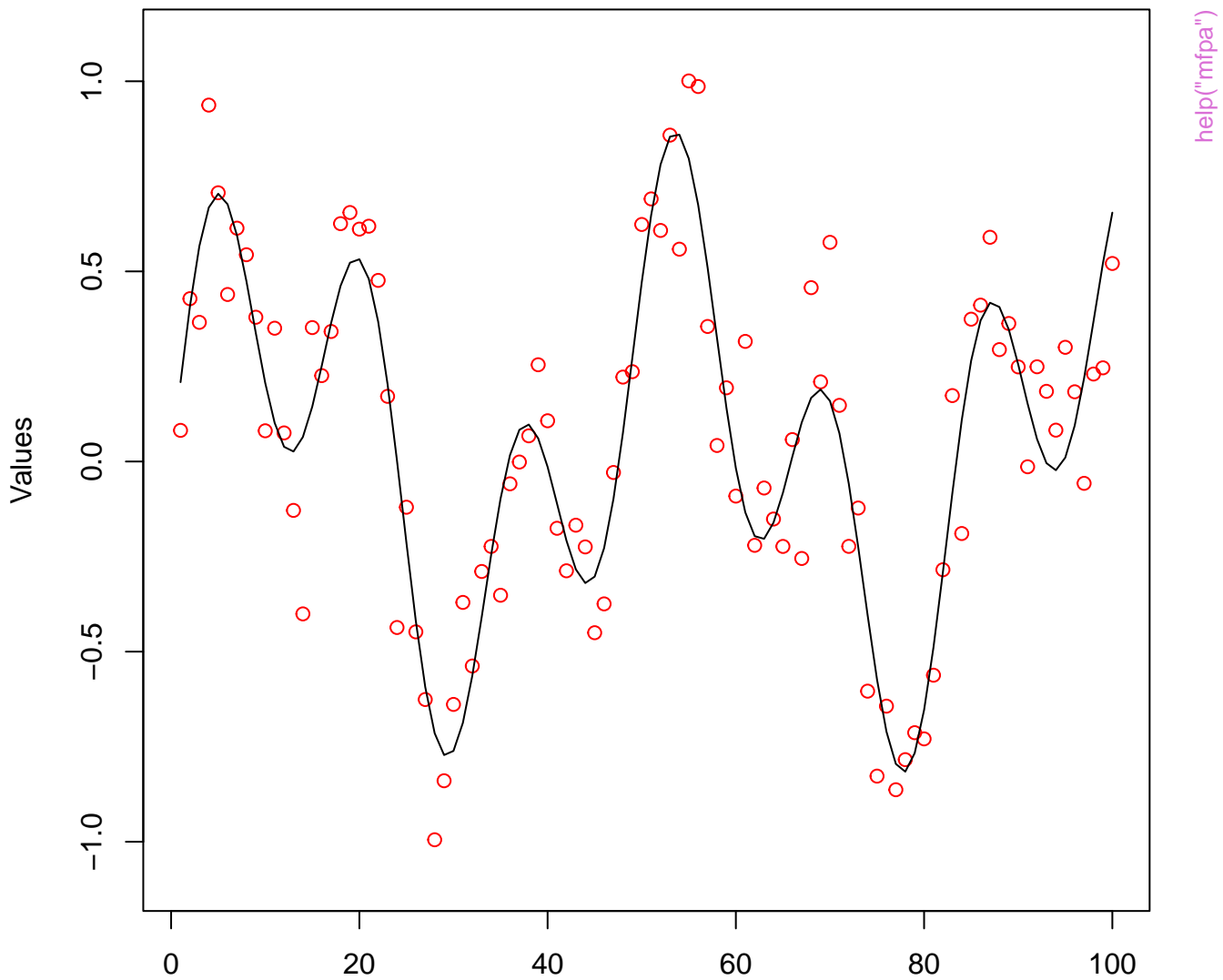


MEM5



MEM6





Values

-1.0
-0.5
0.0
0.5
1.0

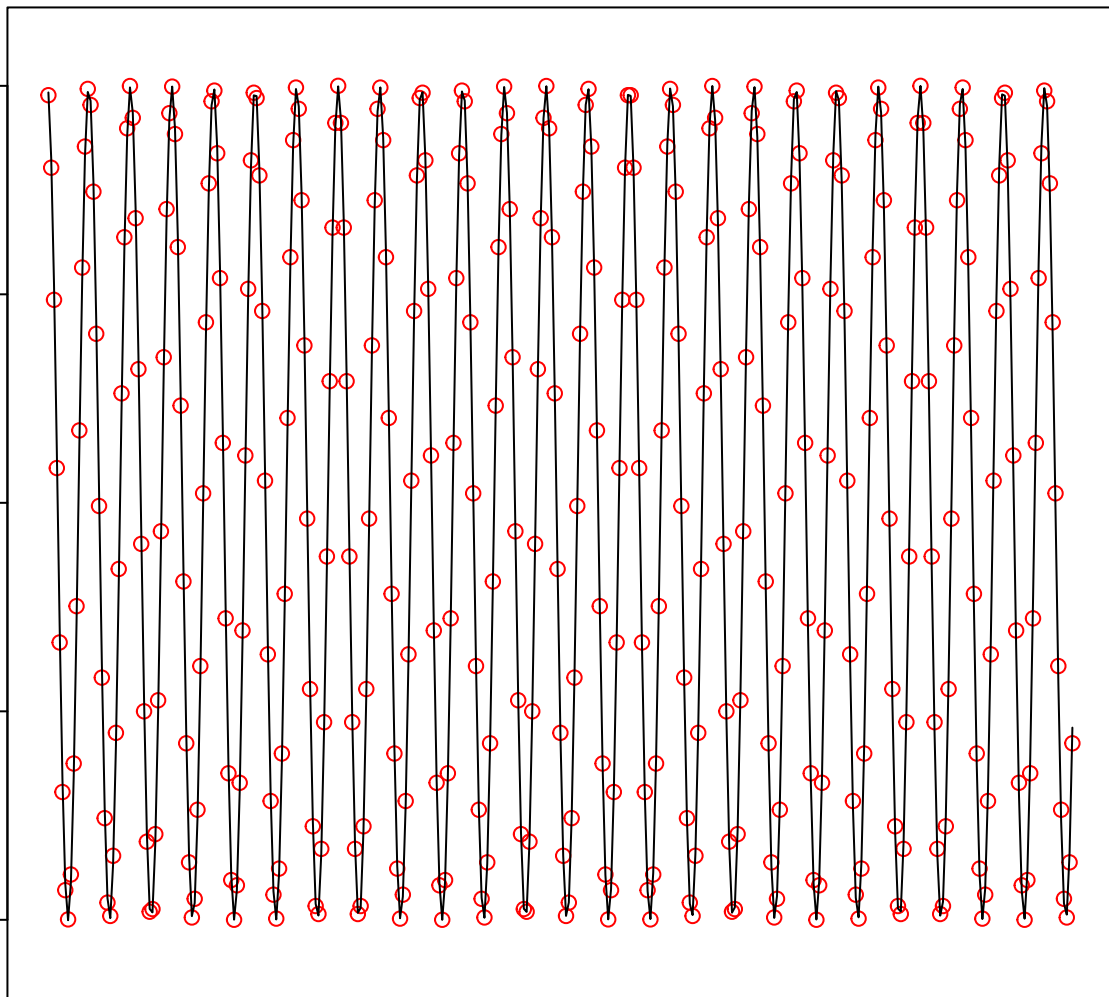
0

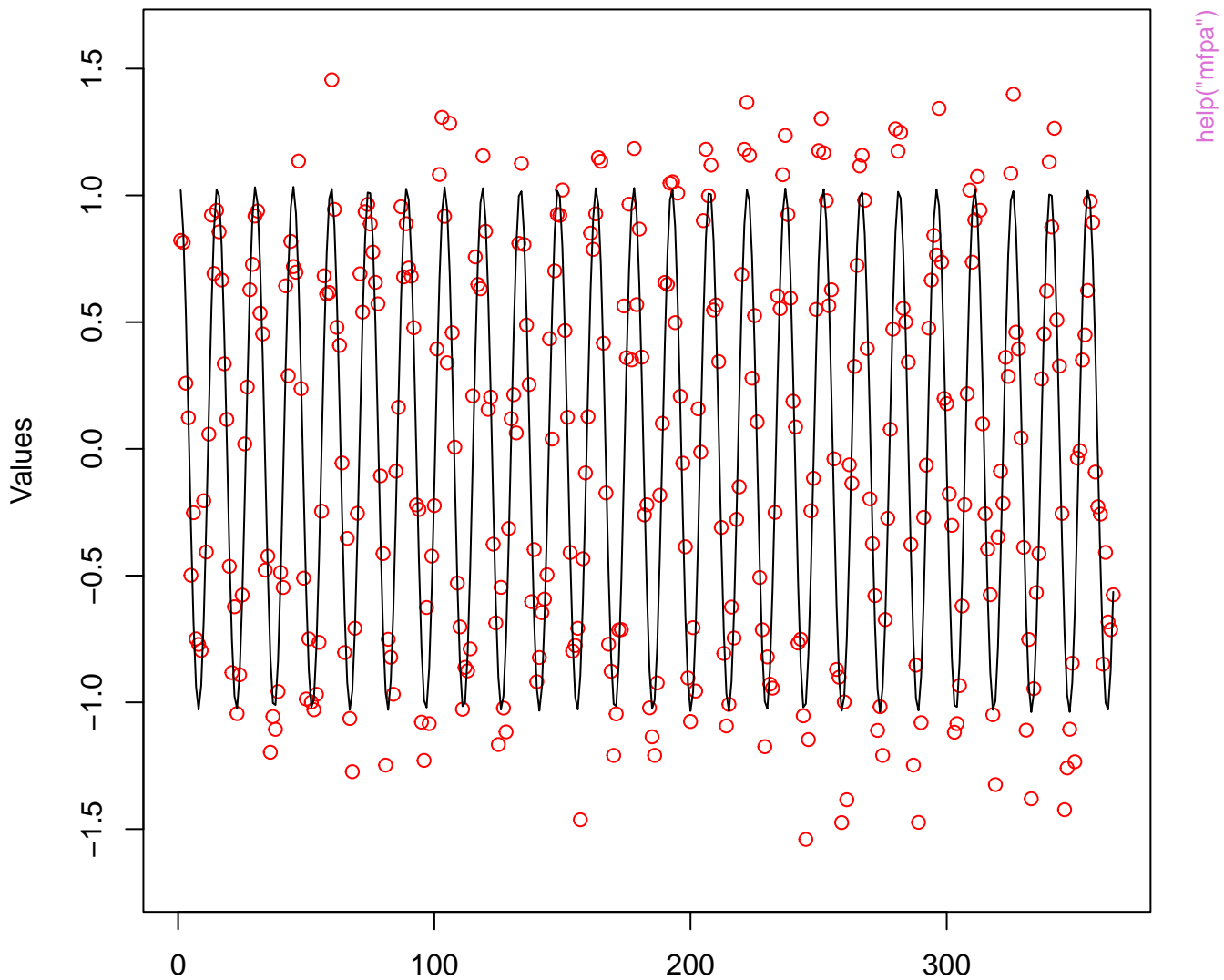
100

200

300

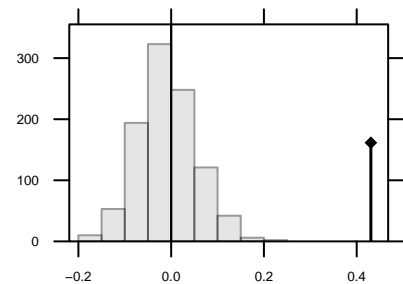
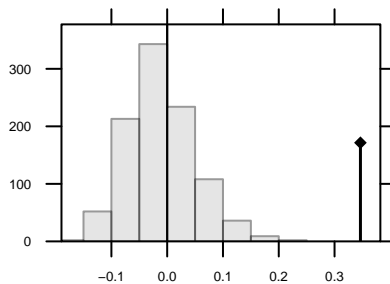
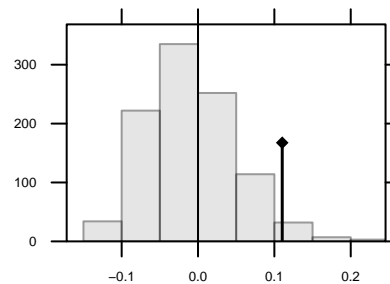
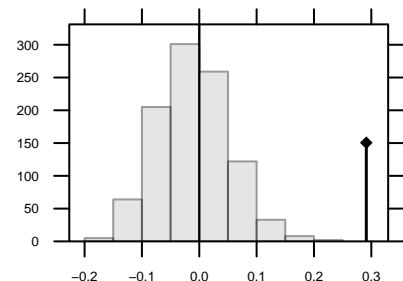
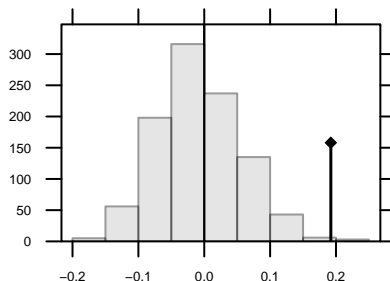
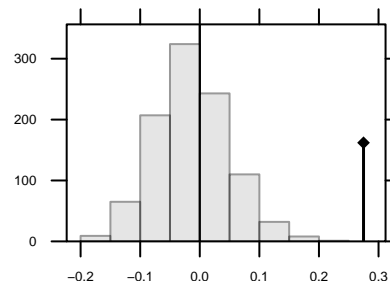
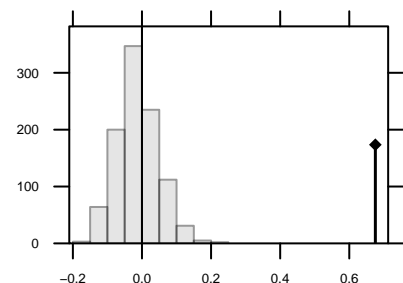
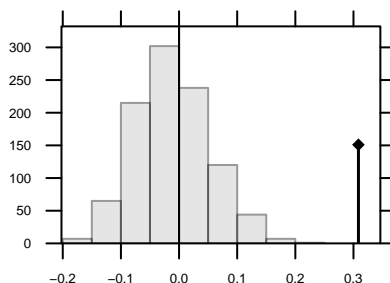
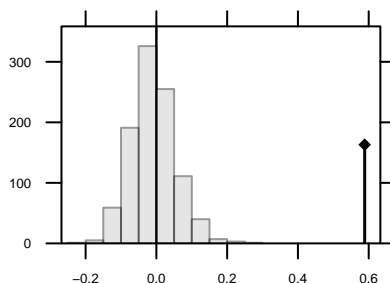
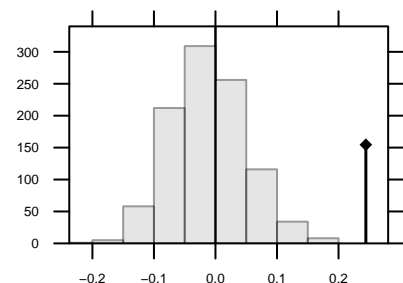
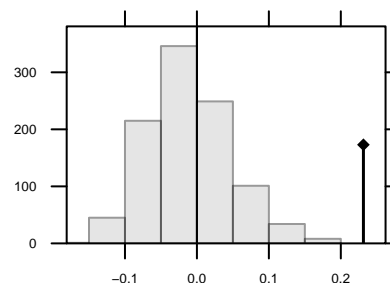
help("mfpa")

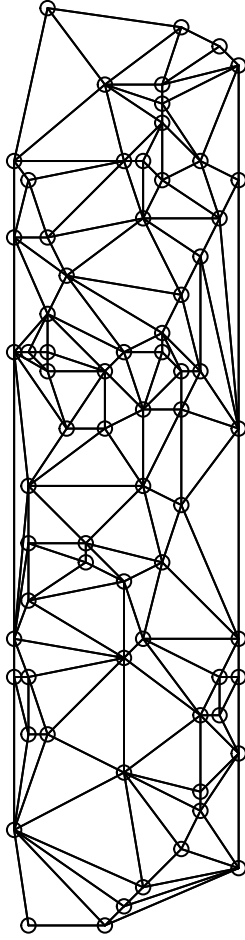


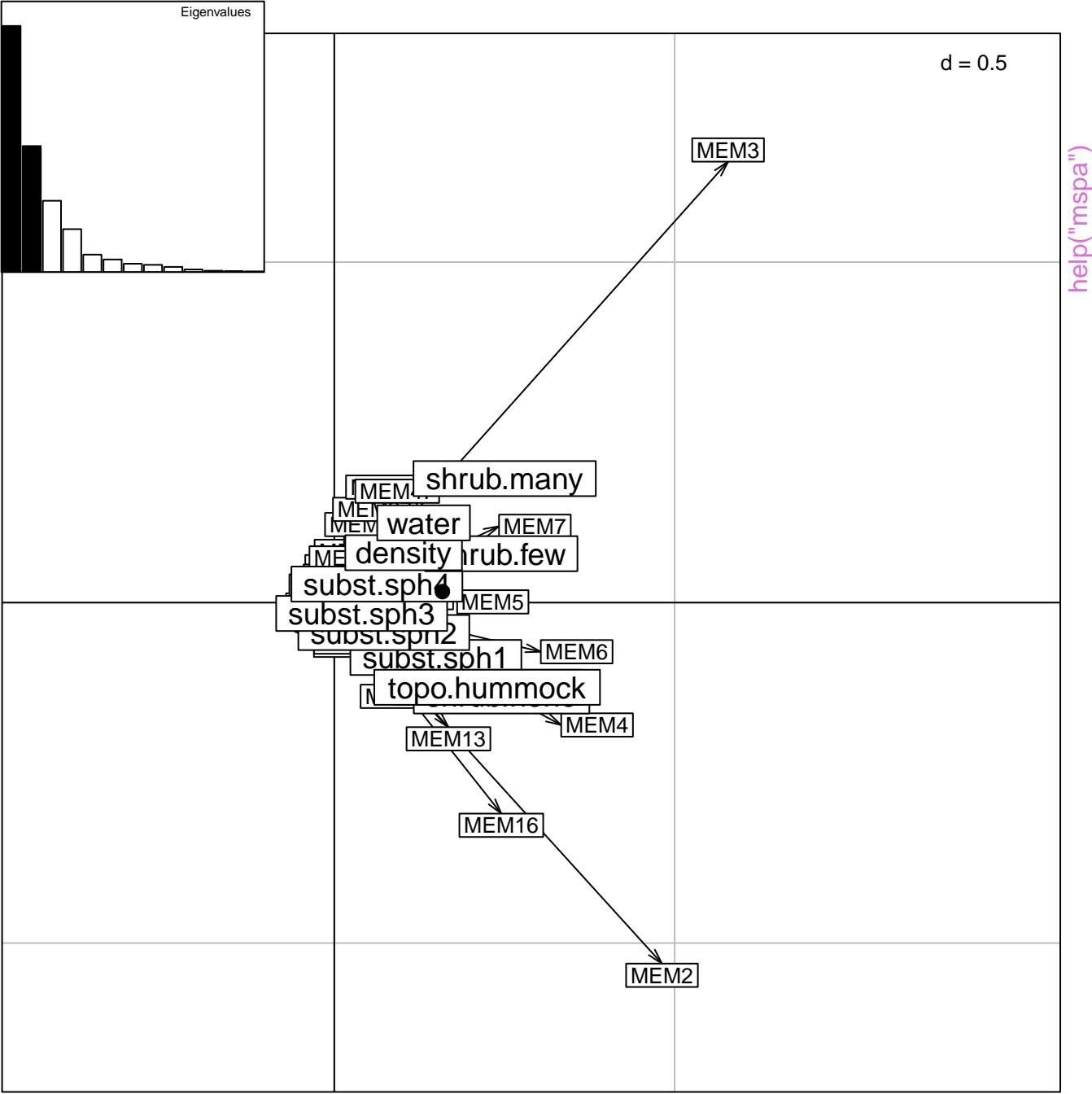


Clay**Silt****Sand**

help("morand.randtest")

**K2O****Mg++****Na+/100g****K+****Conductivity****Retention****Na+/l****Elevation**

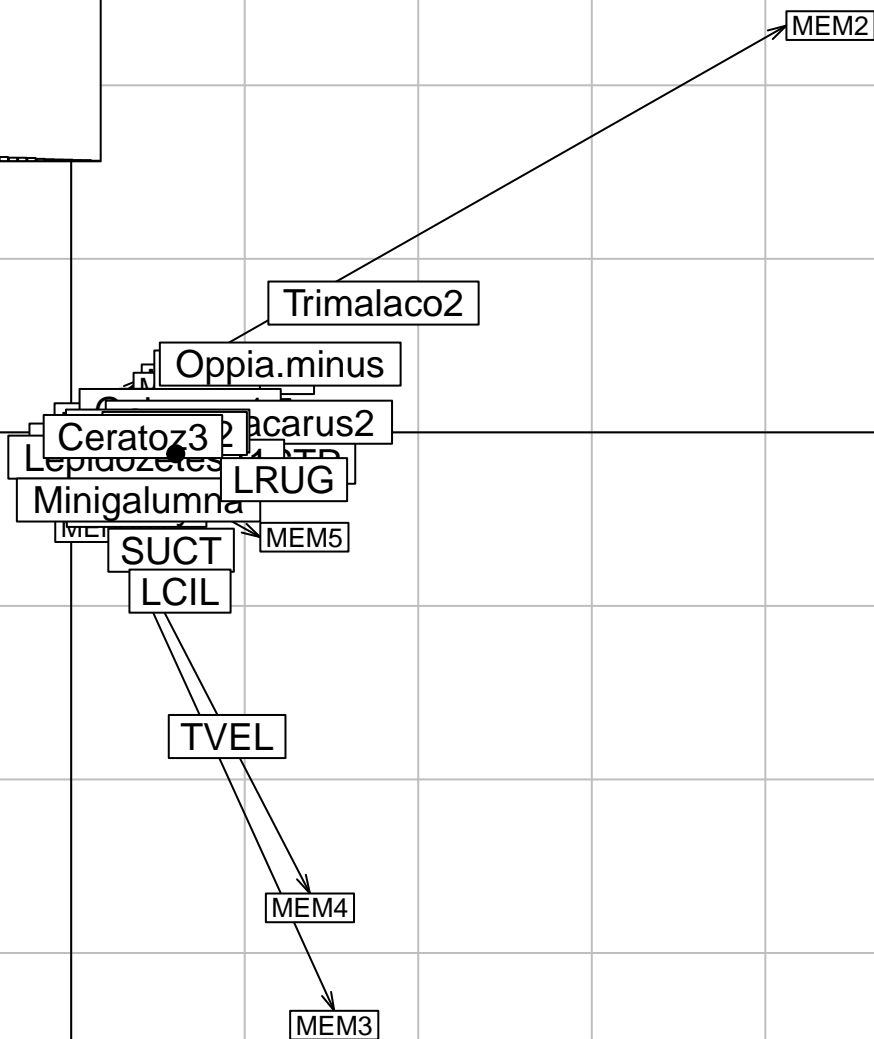




Eigenvalues

d = 0.2

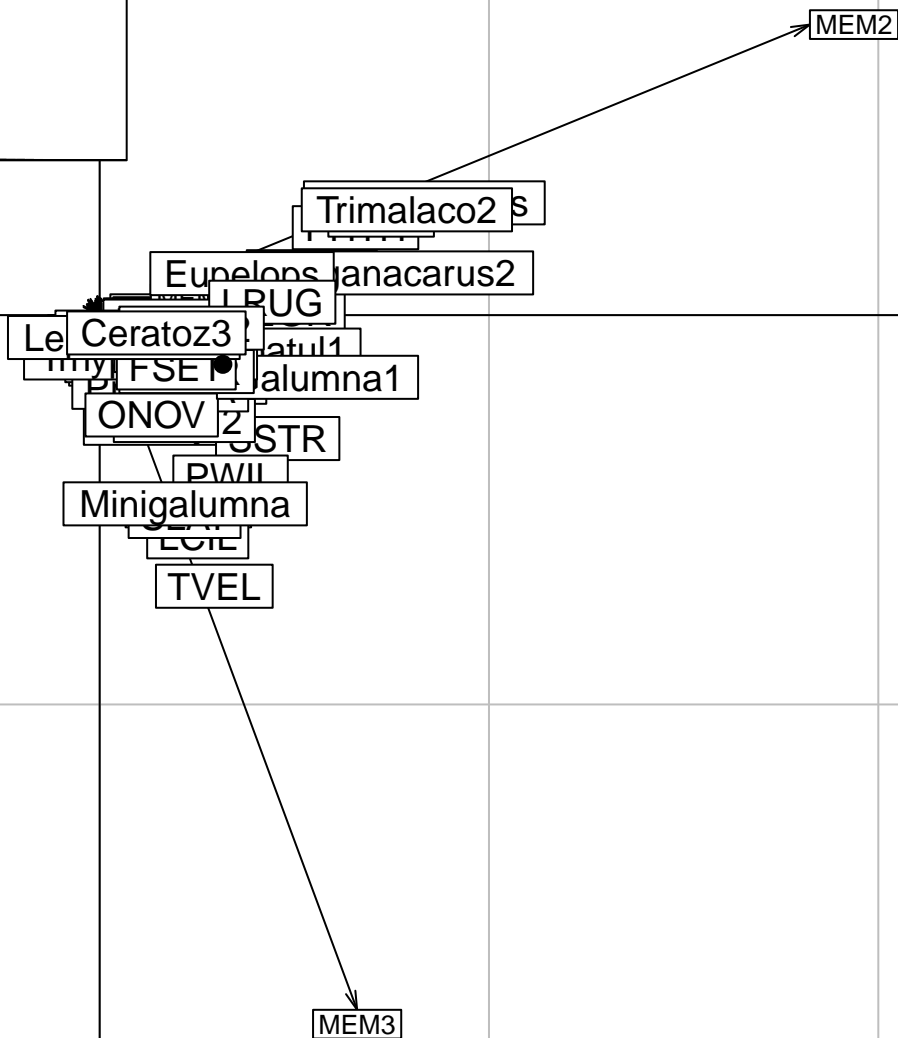
help("mspa")



Eigenvalues

d = 0.5

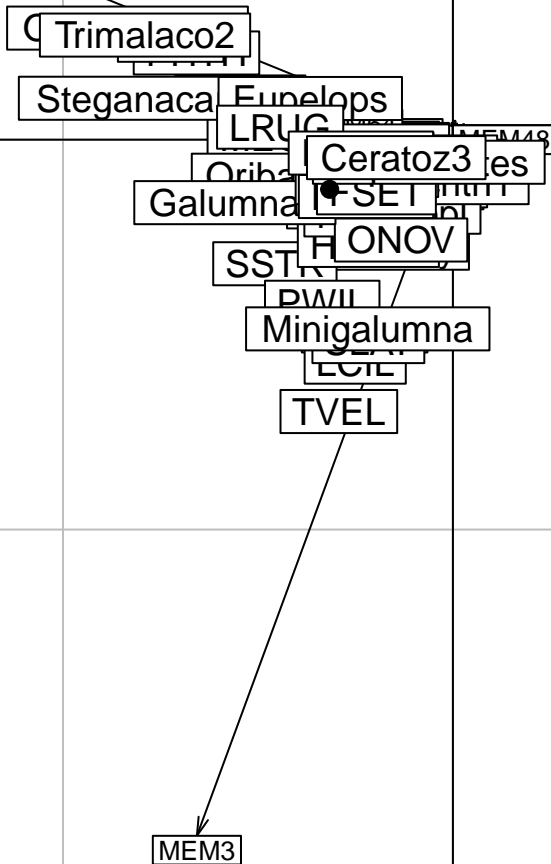
help("mspa")



Eigenvalues

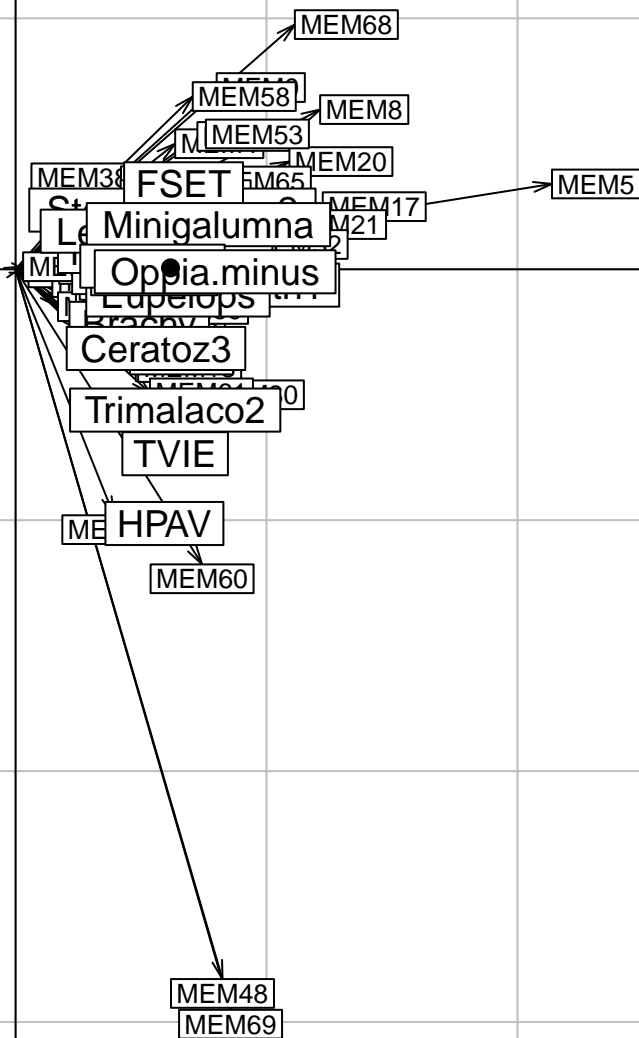
d = 0.5

help("mspa")



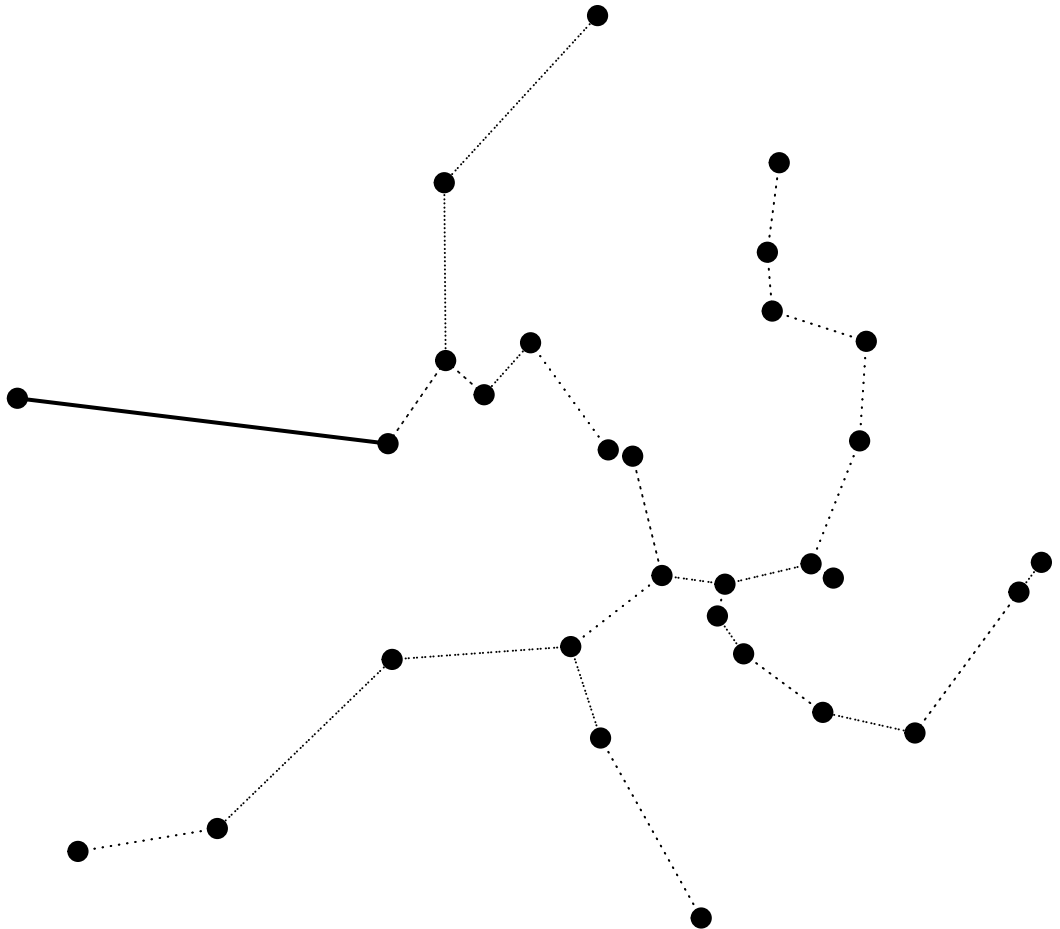
Eigenvalues

d = 0.2

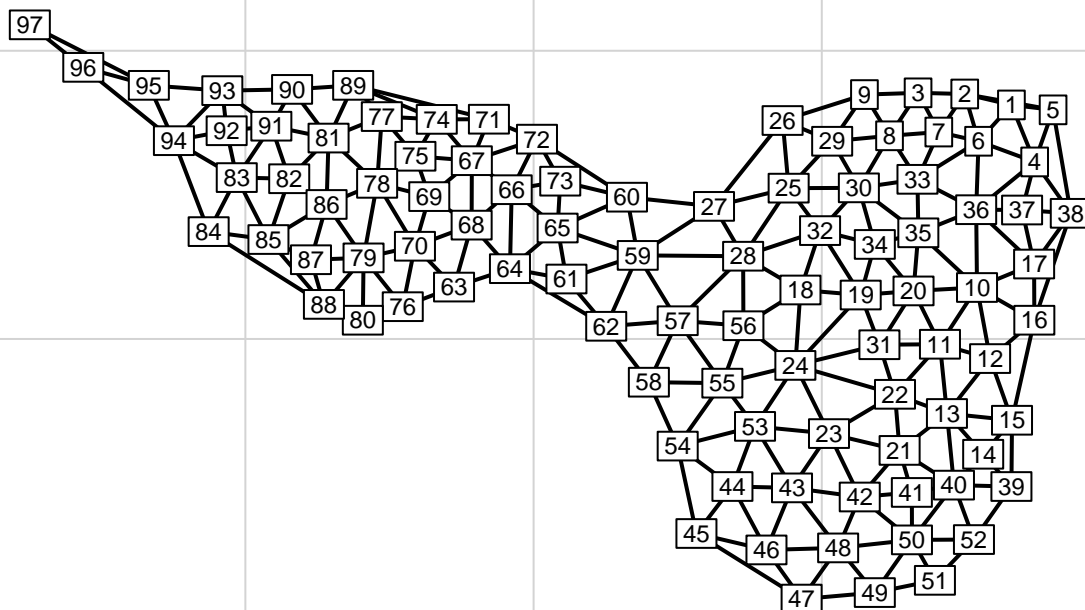


help("mspa")

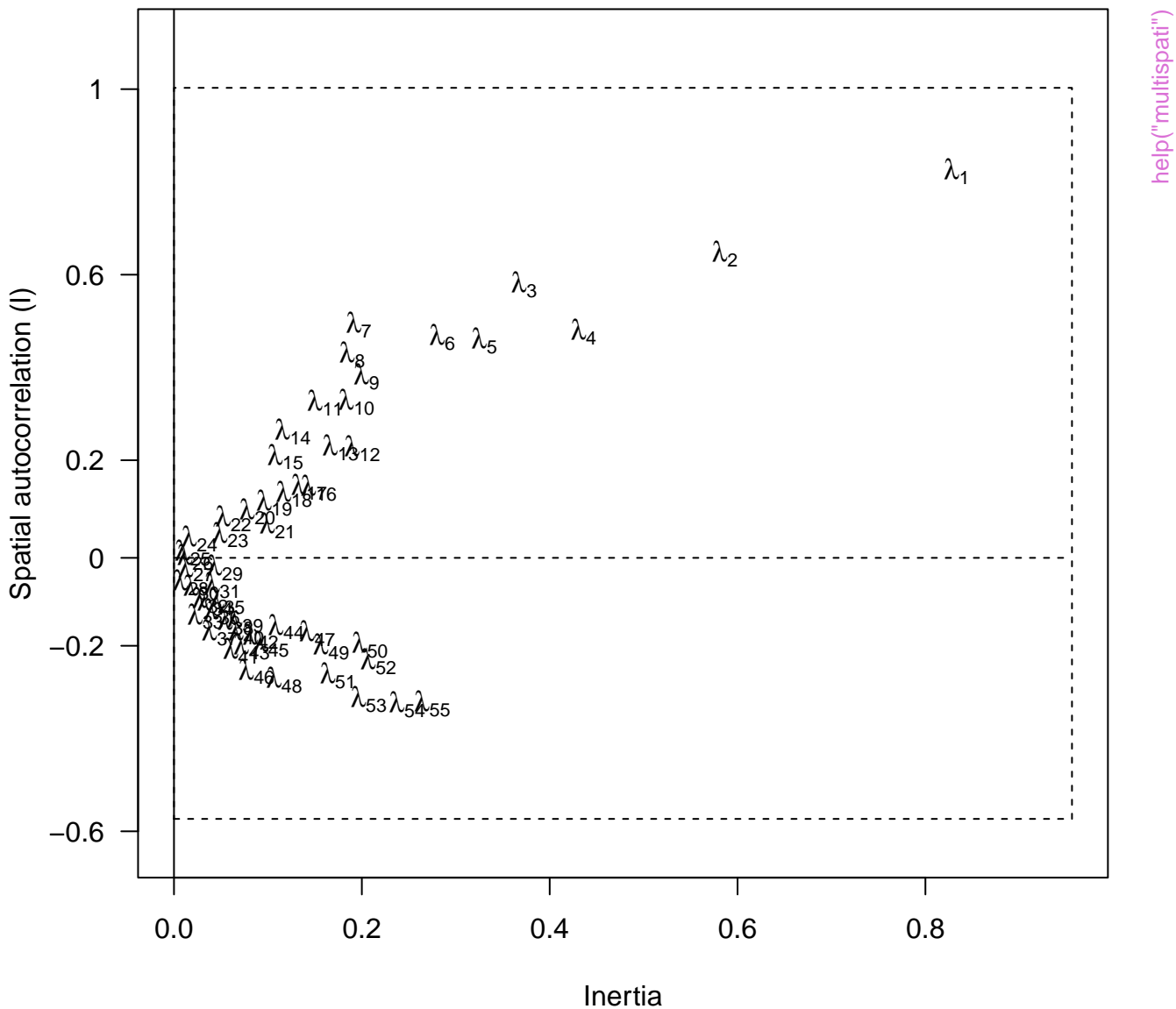
Maximum distance of the minimum spanning tree in bold

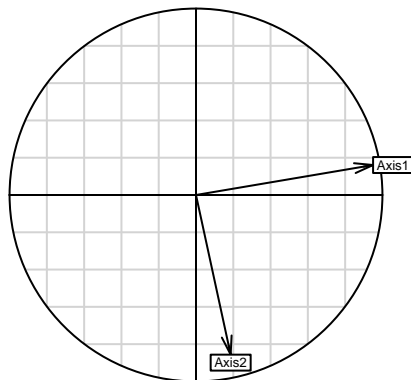
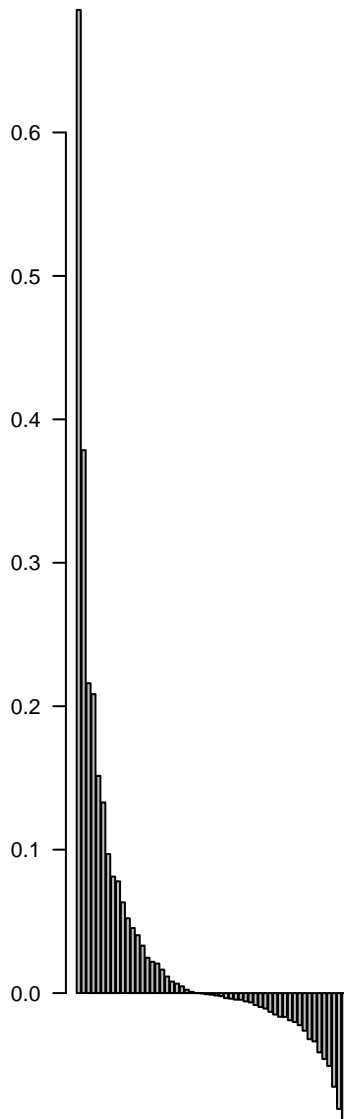
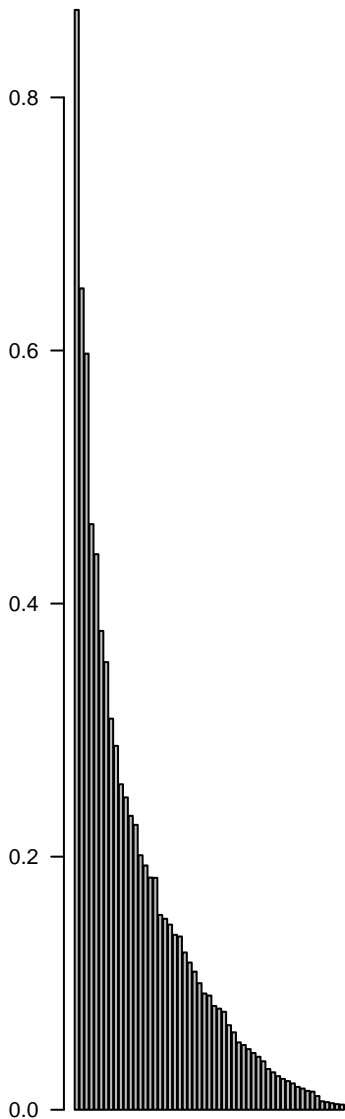


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help("mst.nb")
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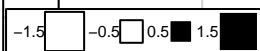
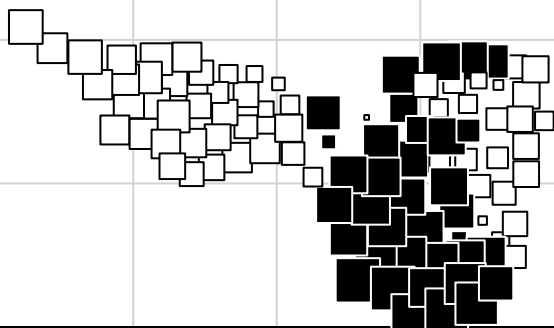


Spatial and inertia components of the eigenvalues

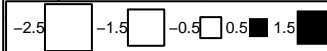
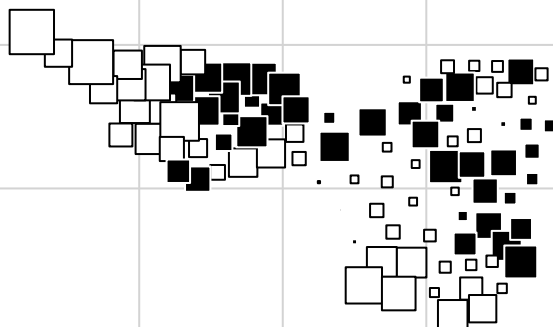




d = 100

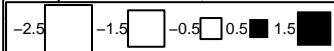
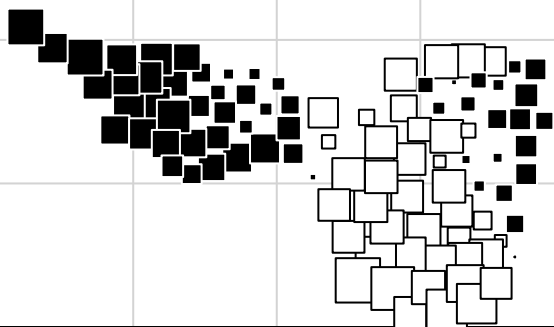


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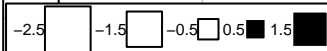
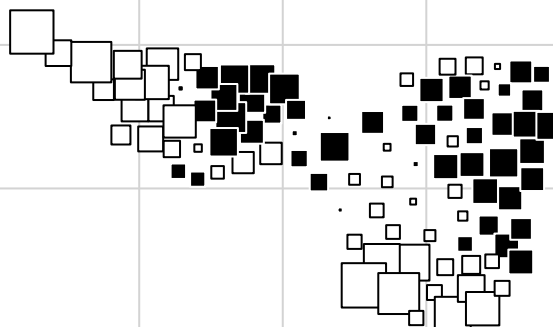


help("multispati

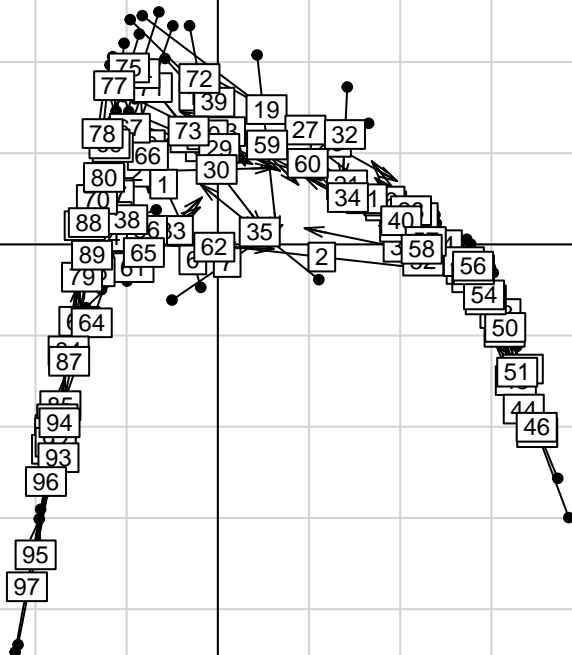
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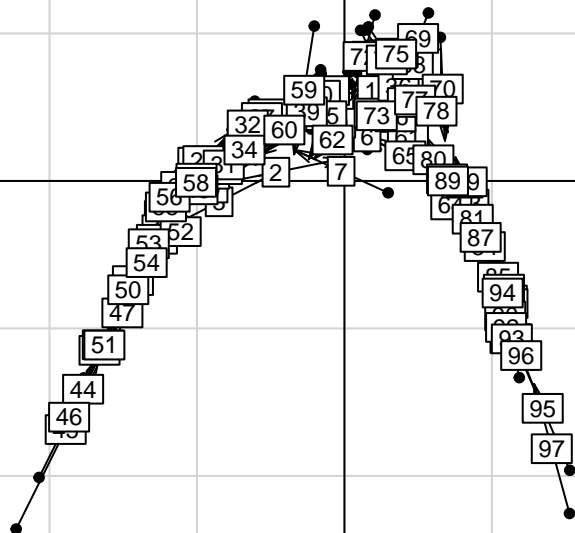
d = 100



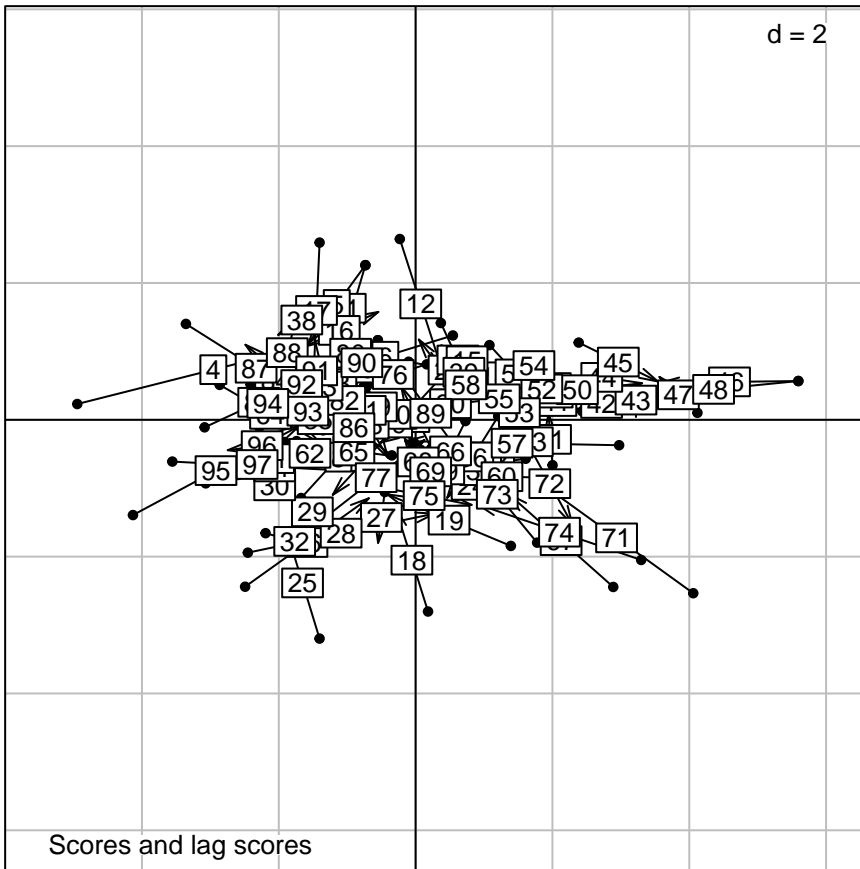
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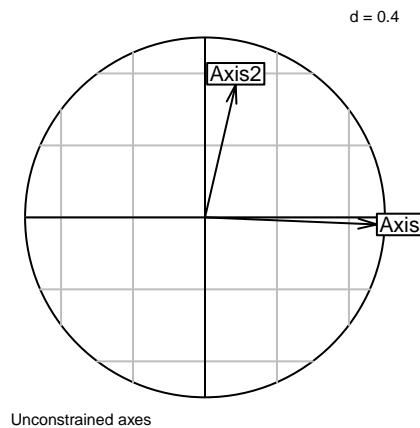
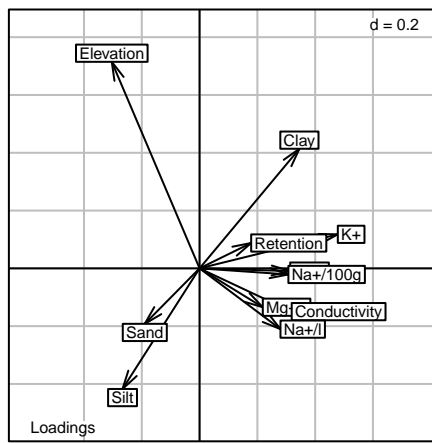
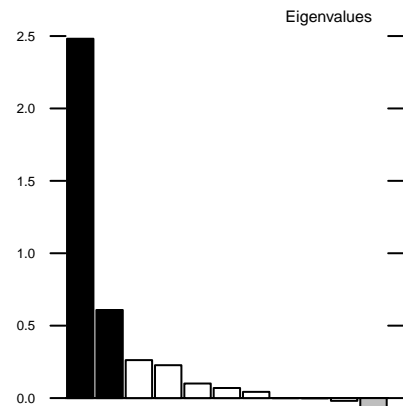
d = 1

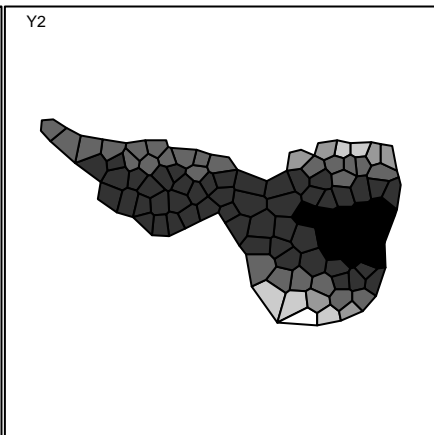
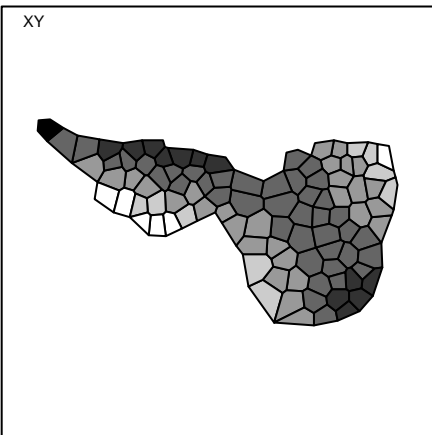
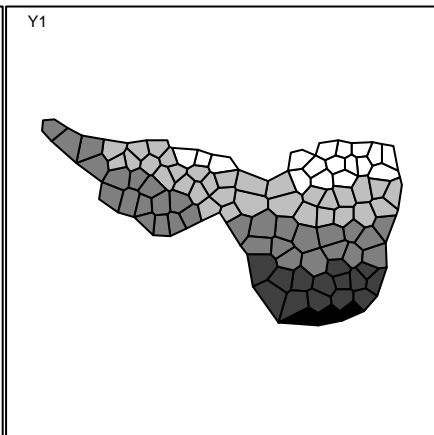
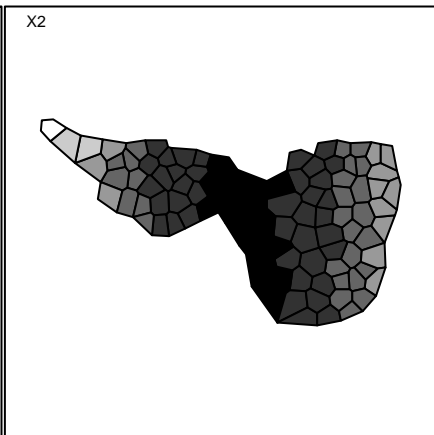
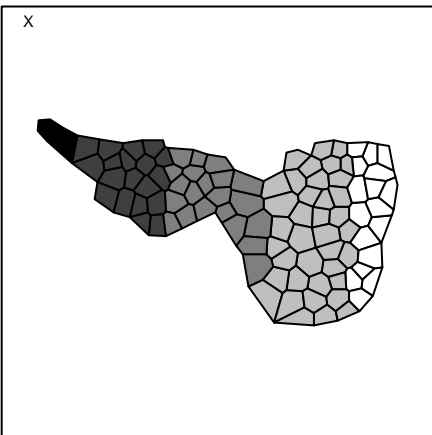


[help\("multispc"\)](#)

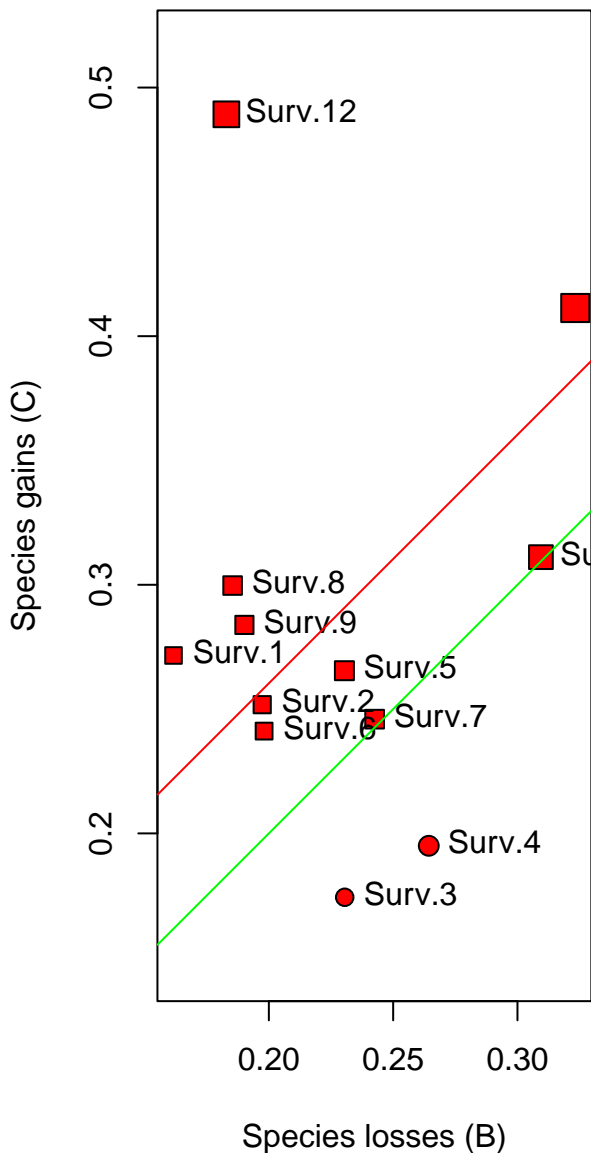


help("multispati")





B-C plot, Pyrifos, surveys 4 & 11



B-C plot, Pyrifos, surveys 4 & 11

