

Doubs fish LCBD. %difference D

d = 50

help("LCBD comp")



Doubs fish replacement LCBD

d = 50

help("LCBD comp")



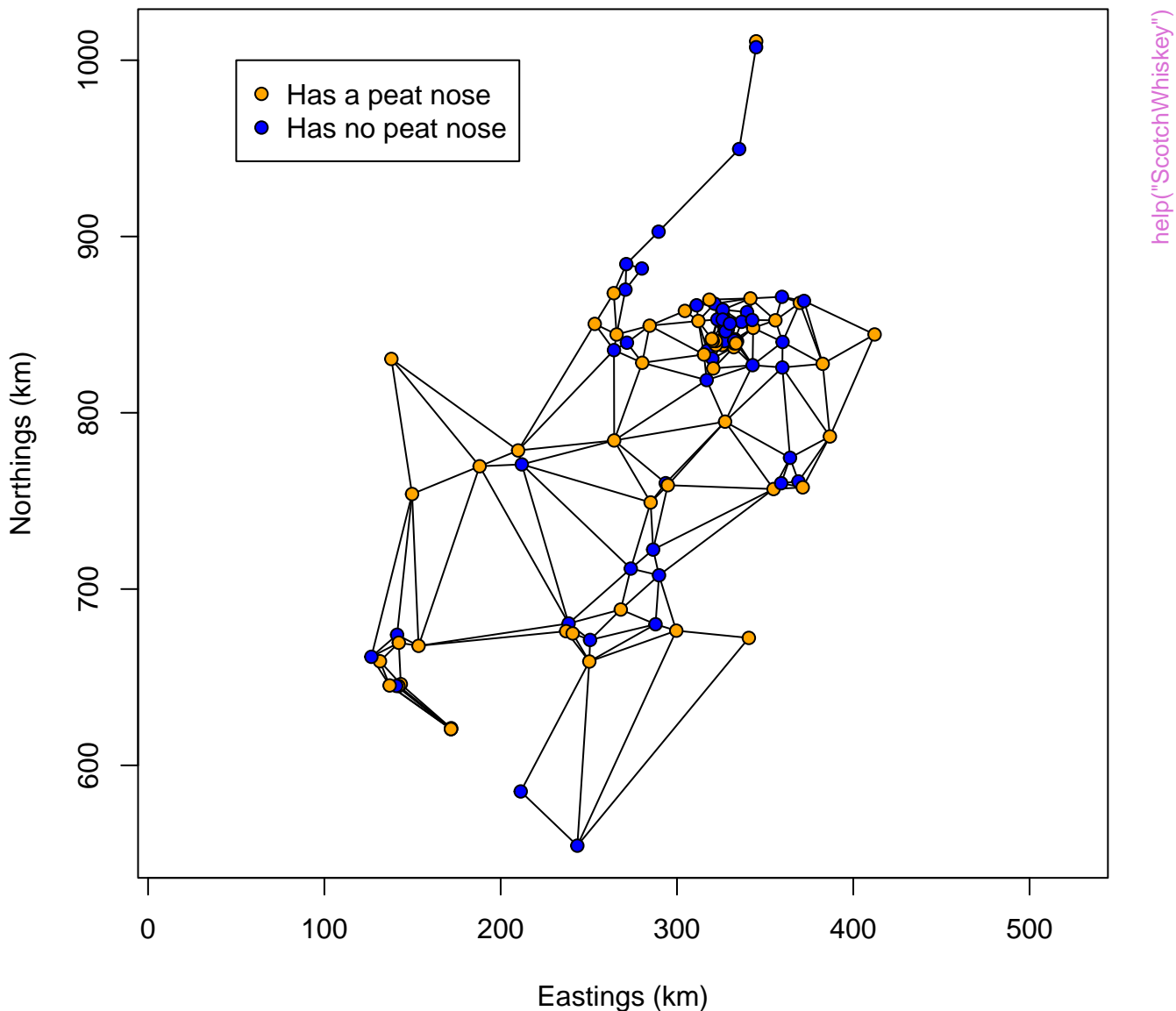
Doubs fish abundance diff. LCBD

d = 50

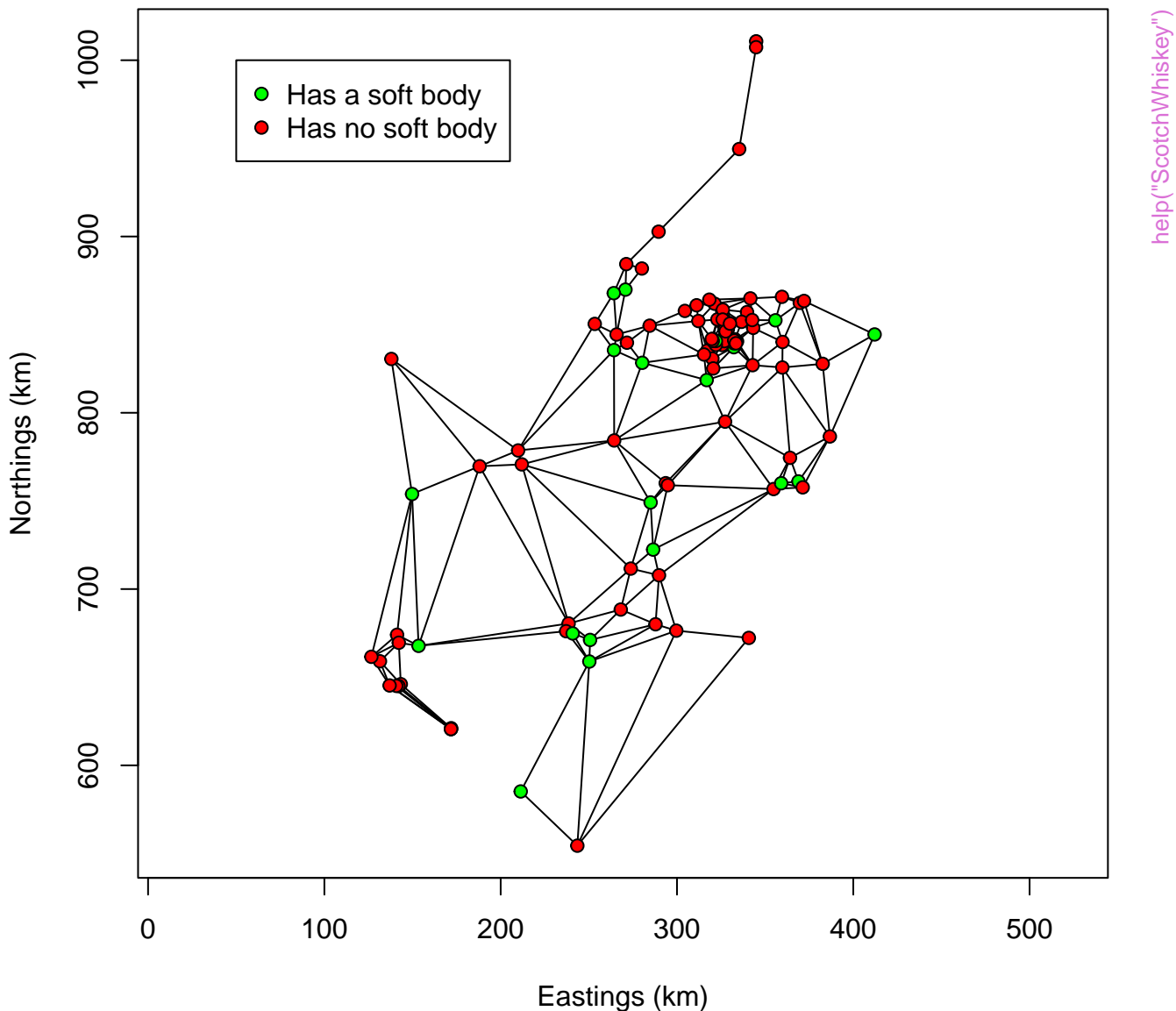
help("LCBD comp")



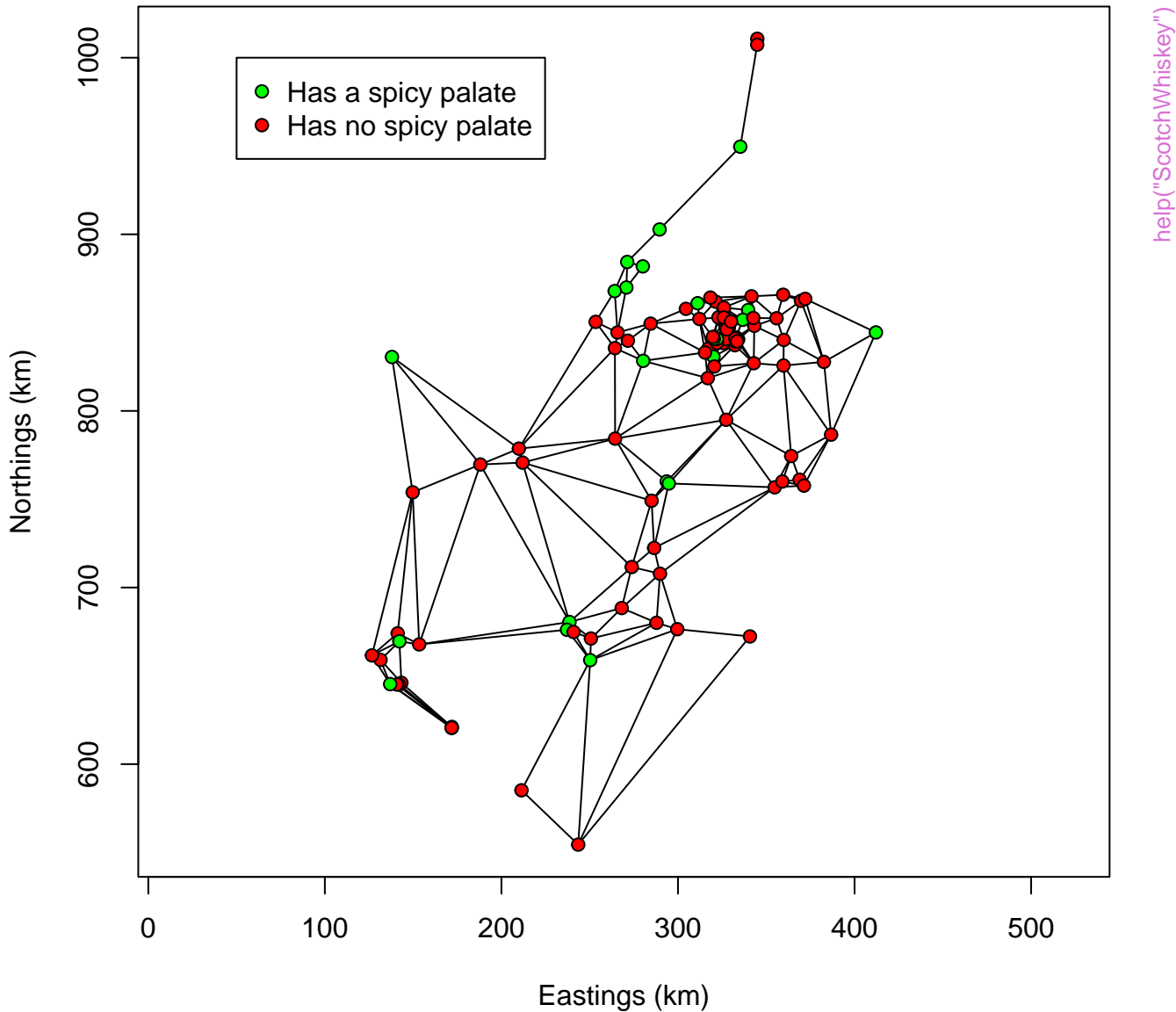
Scotch whiskey: peat nose



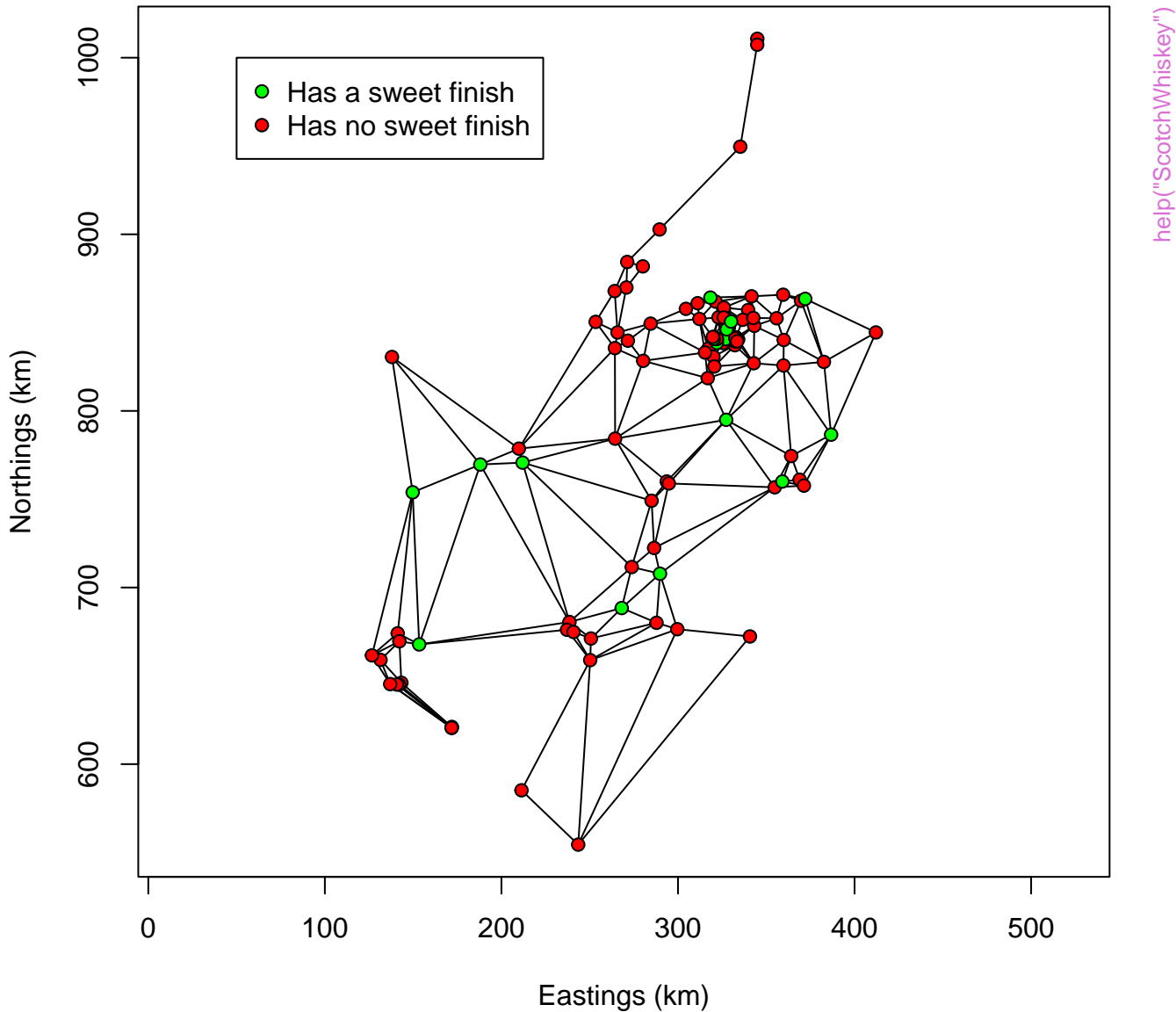
Scotch whiskey: soft body

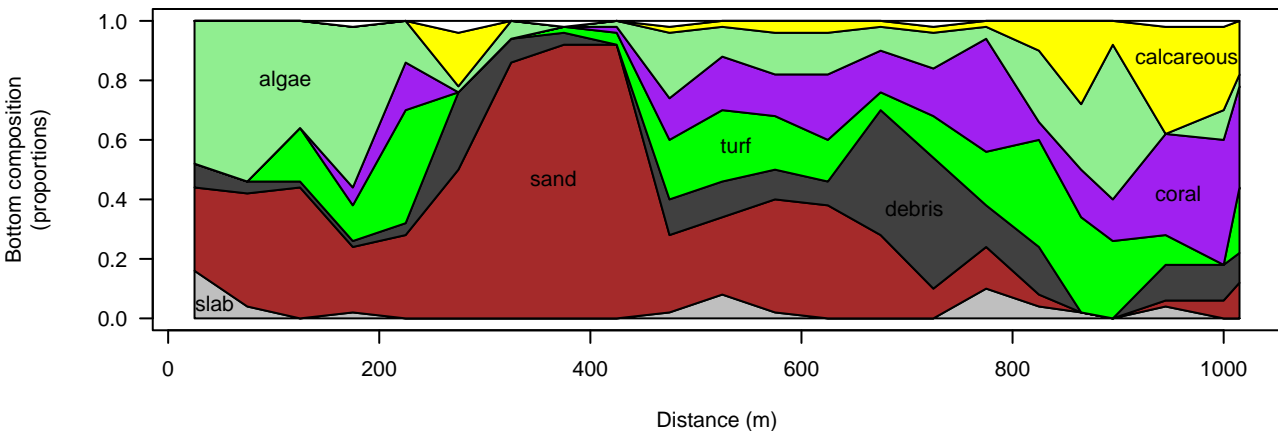
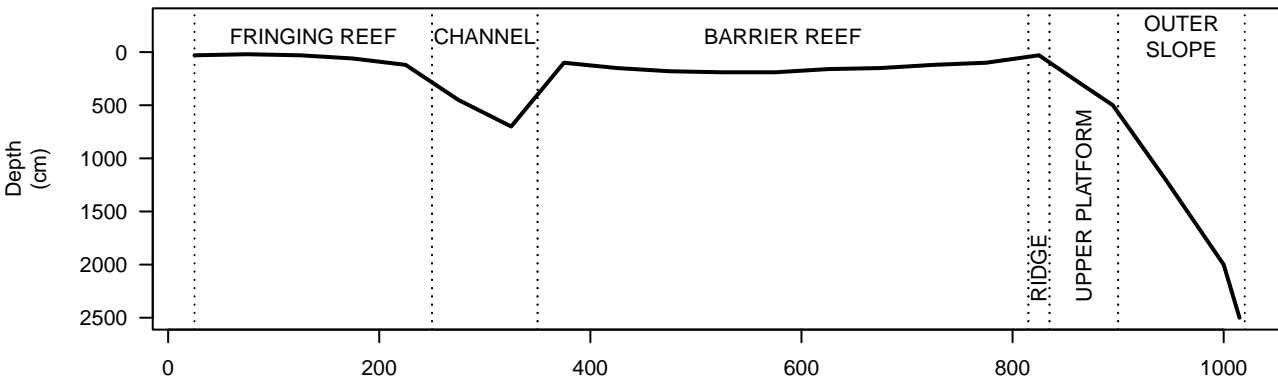
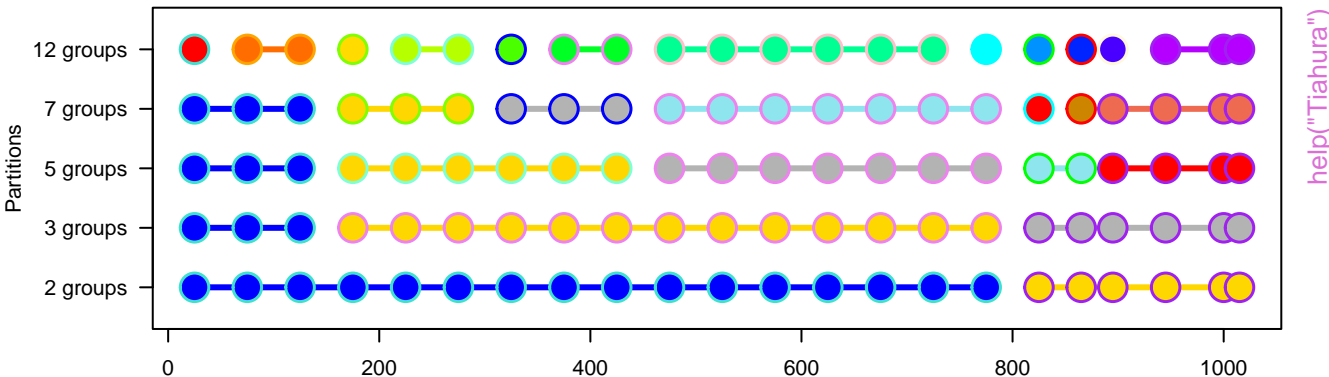


Scotch whiskey: spicy palate

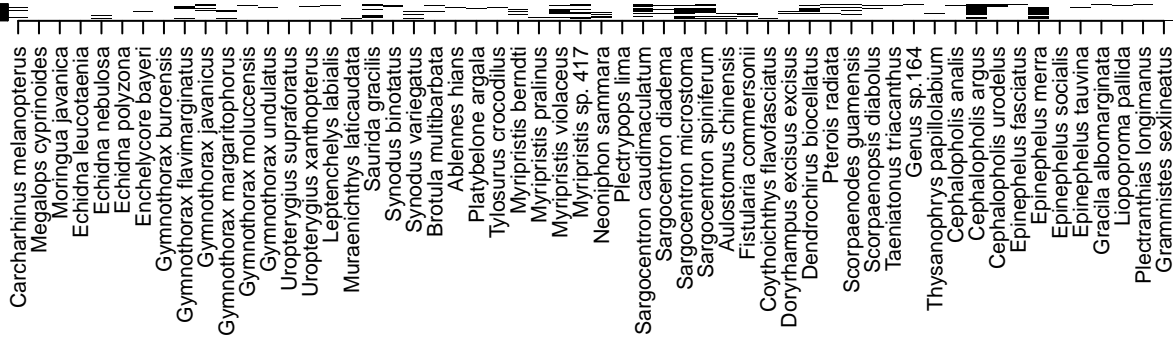


Scotch whiskey: sweet finish



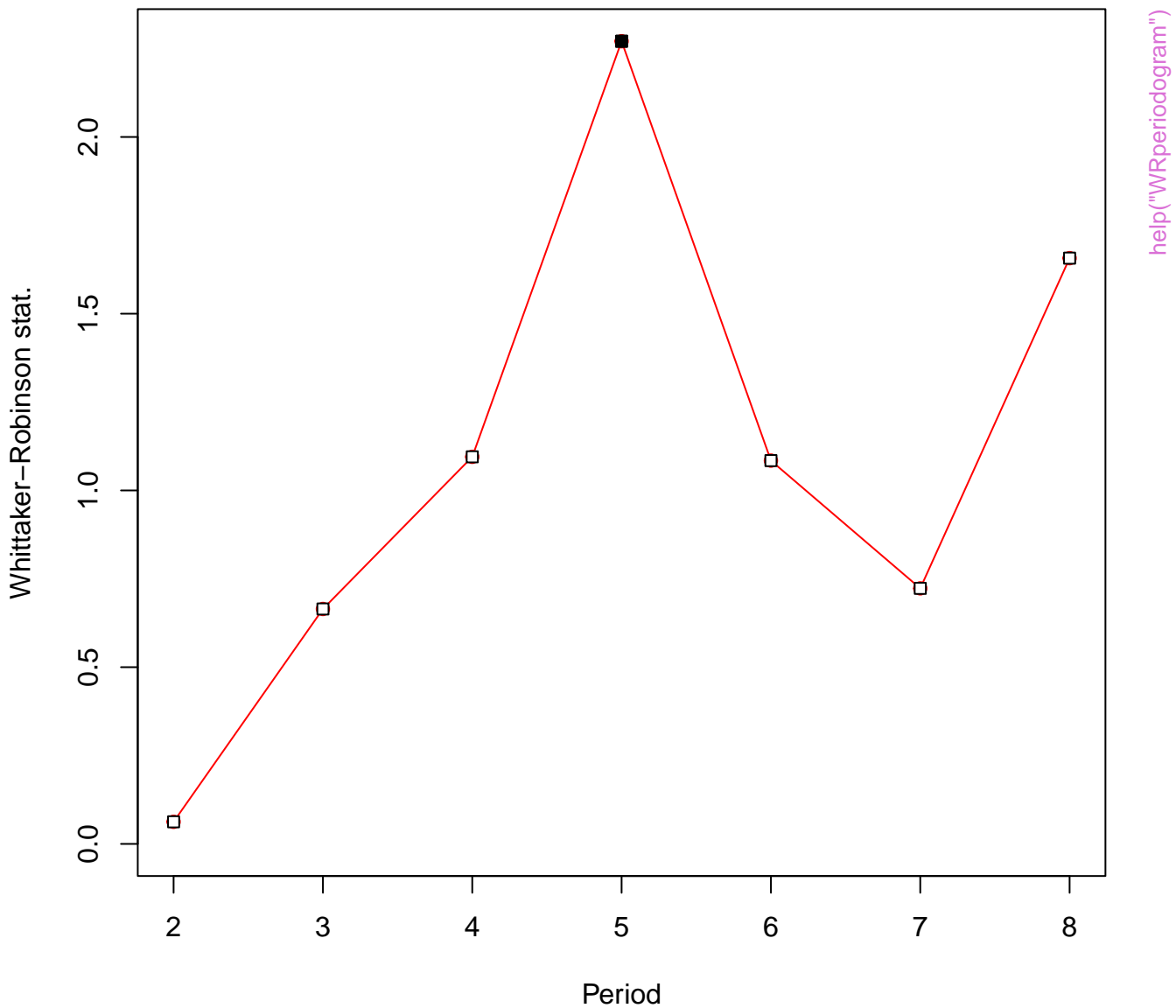


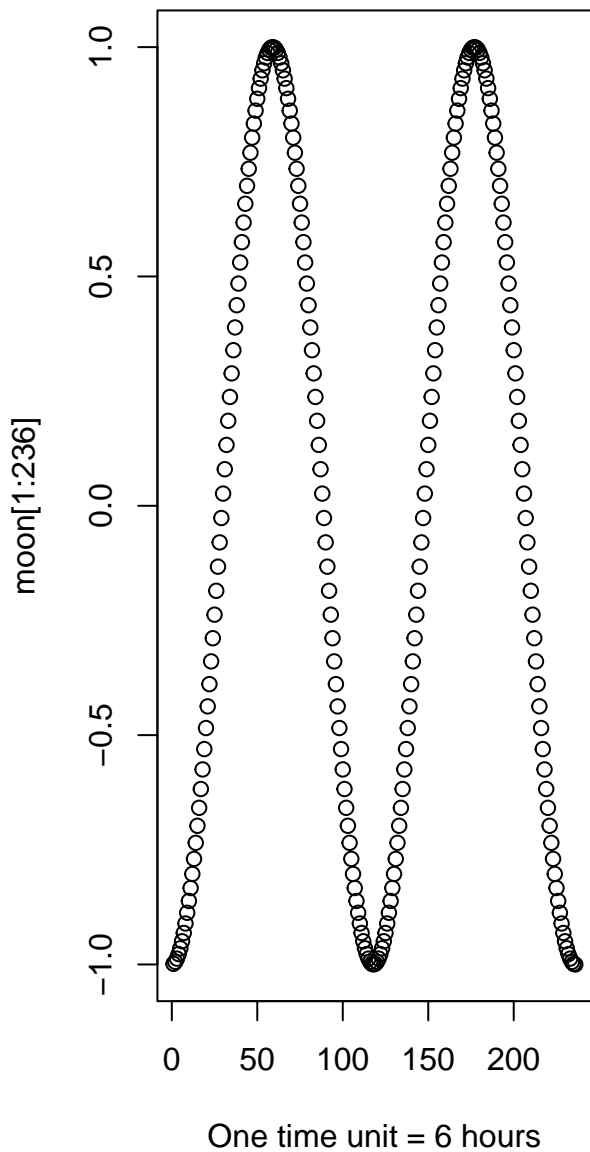
Site_1



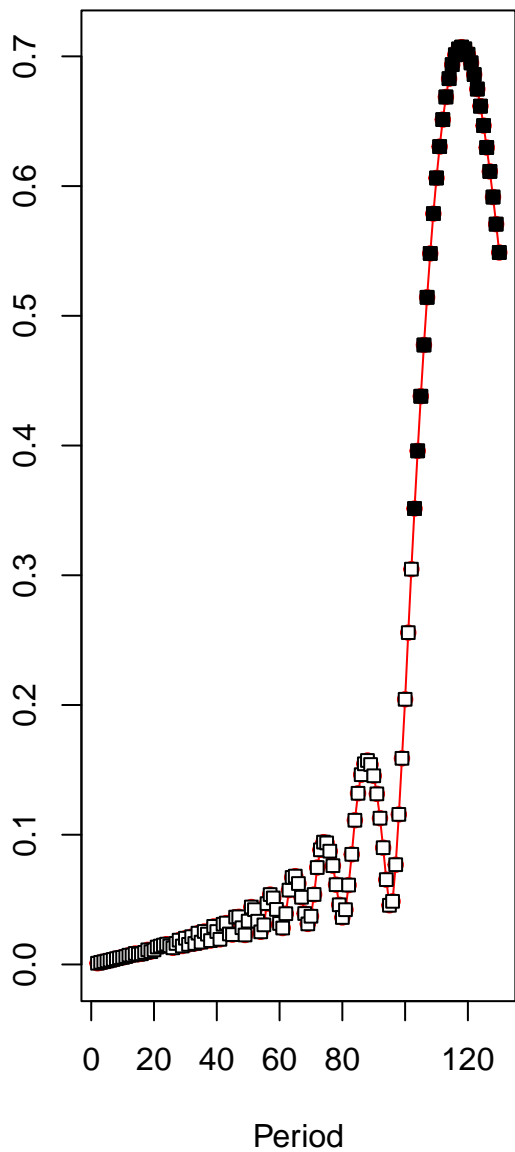
help("Tiahura")

WR Periodogram

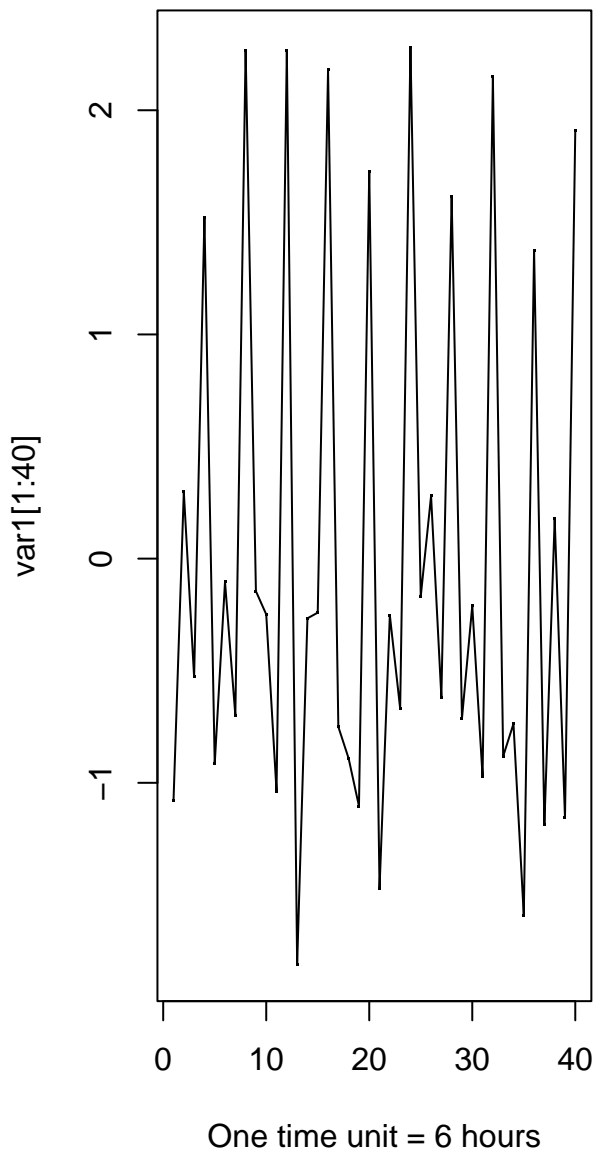




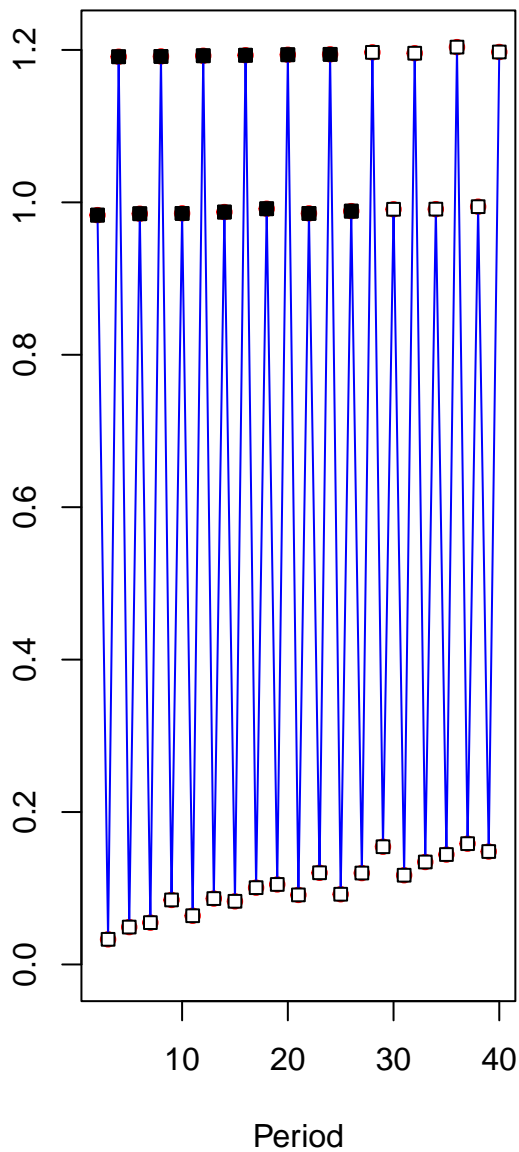
Whittaker–Robinson stat.

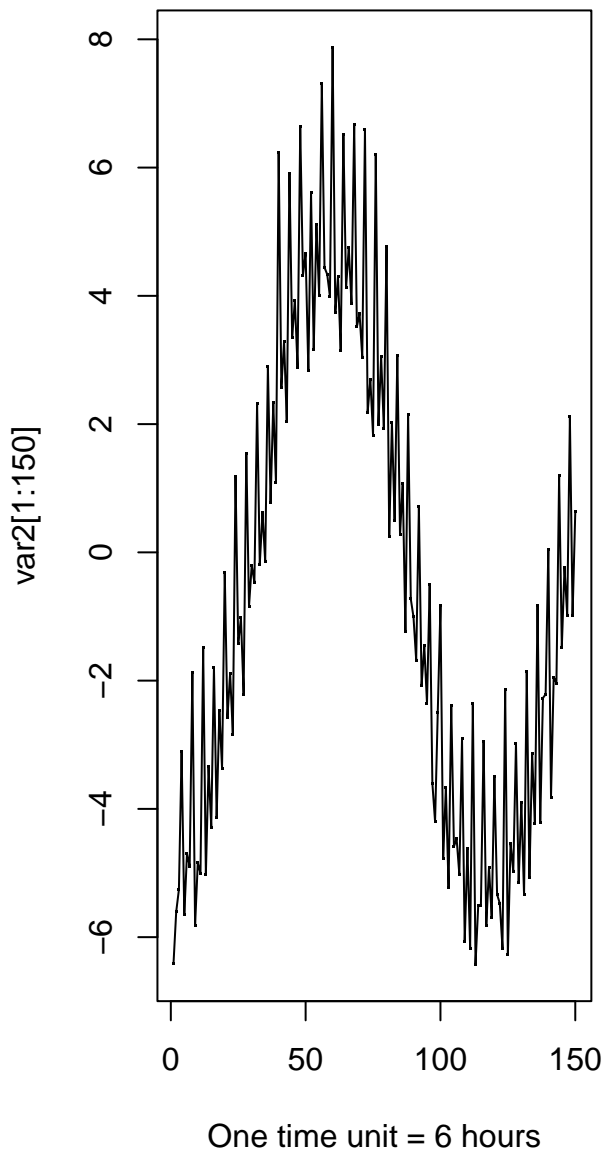


[help\("WRperiodogram"\)](#)

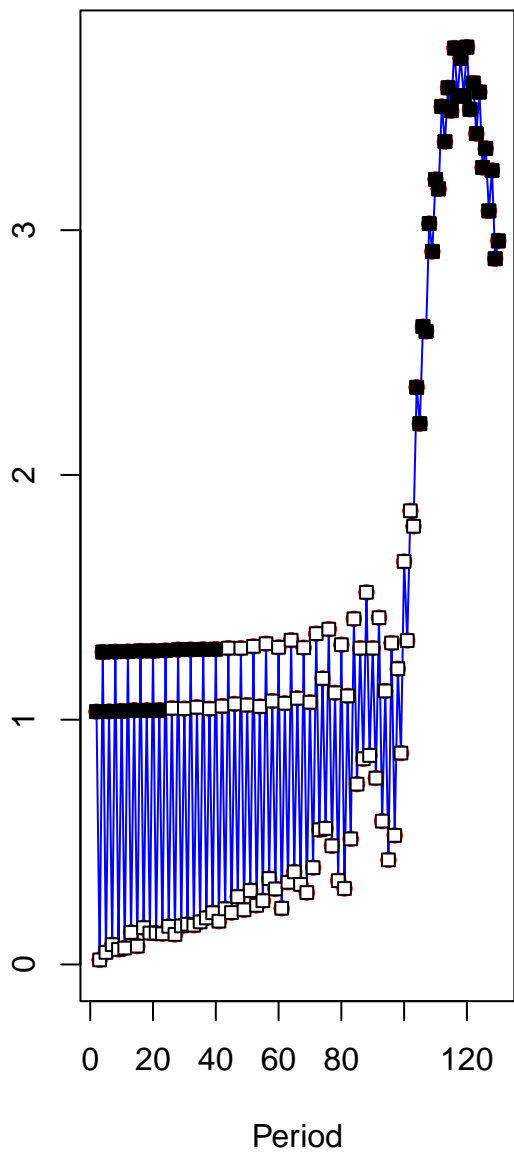


Whittaker-Robinson stat.



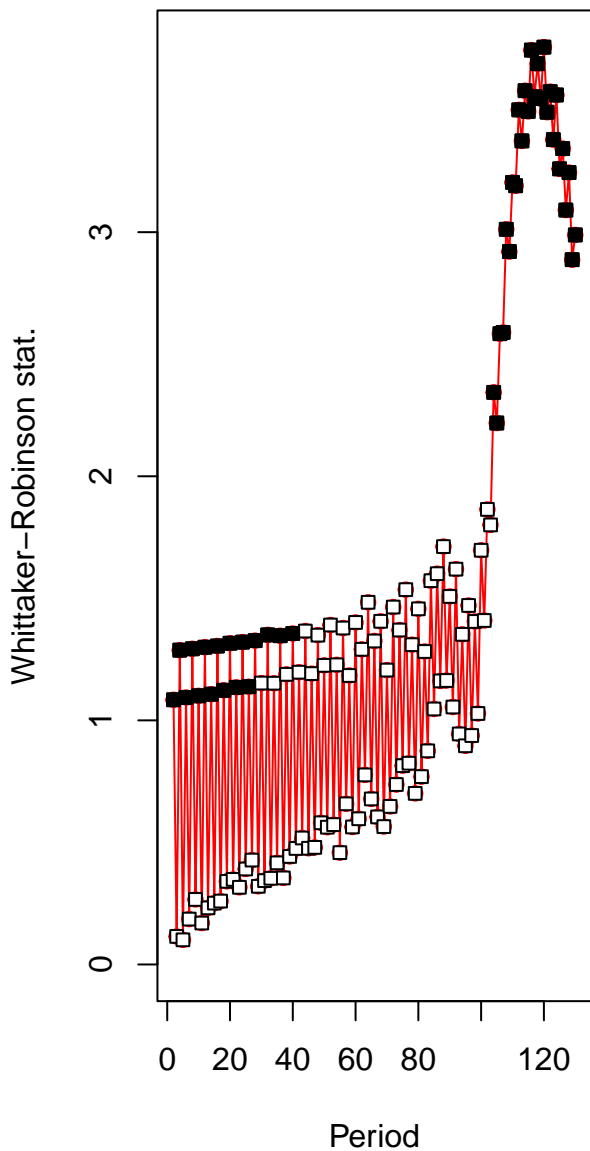


Whittaker-Robinson stat.

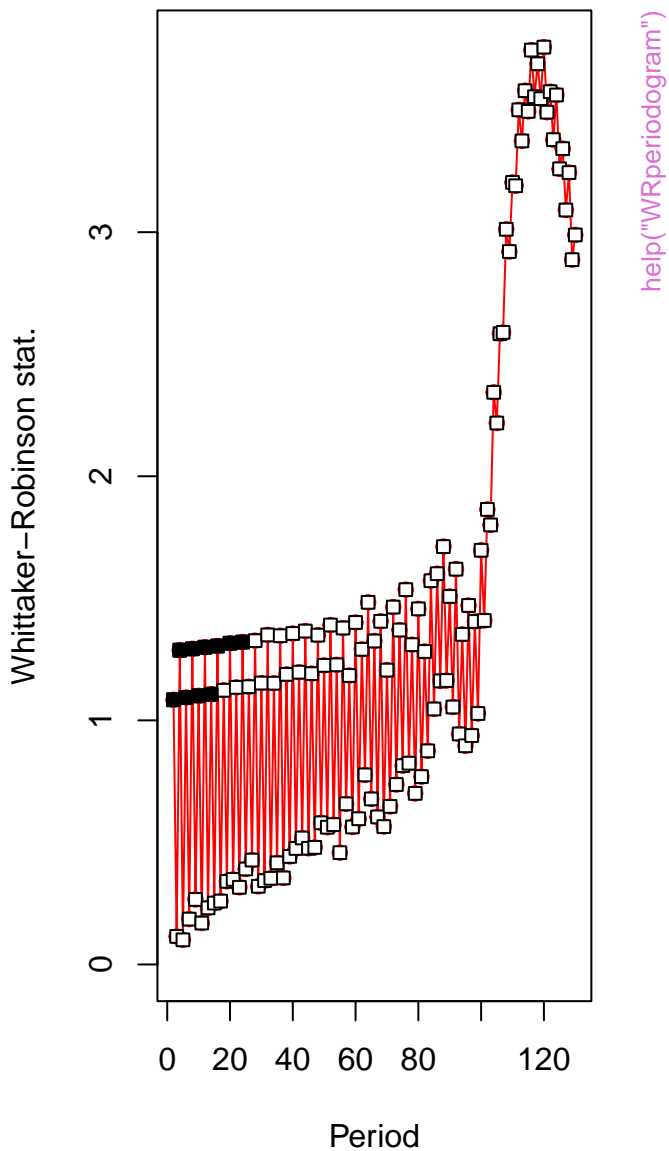


[help\("WRperiodogram"\)](#)

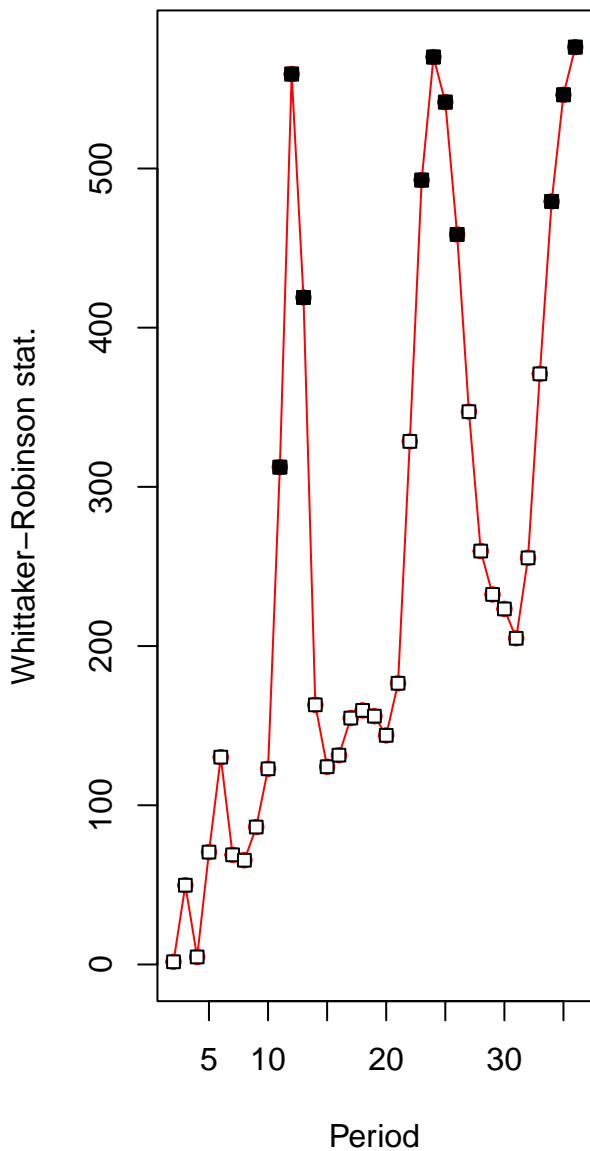
WR Periodogram



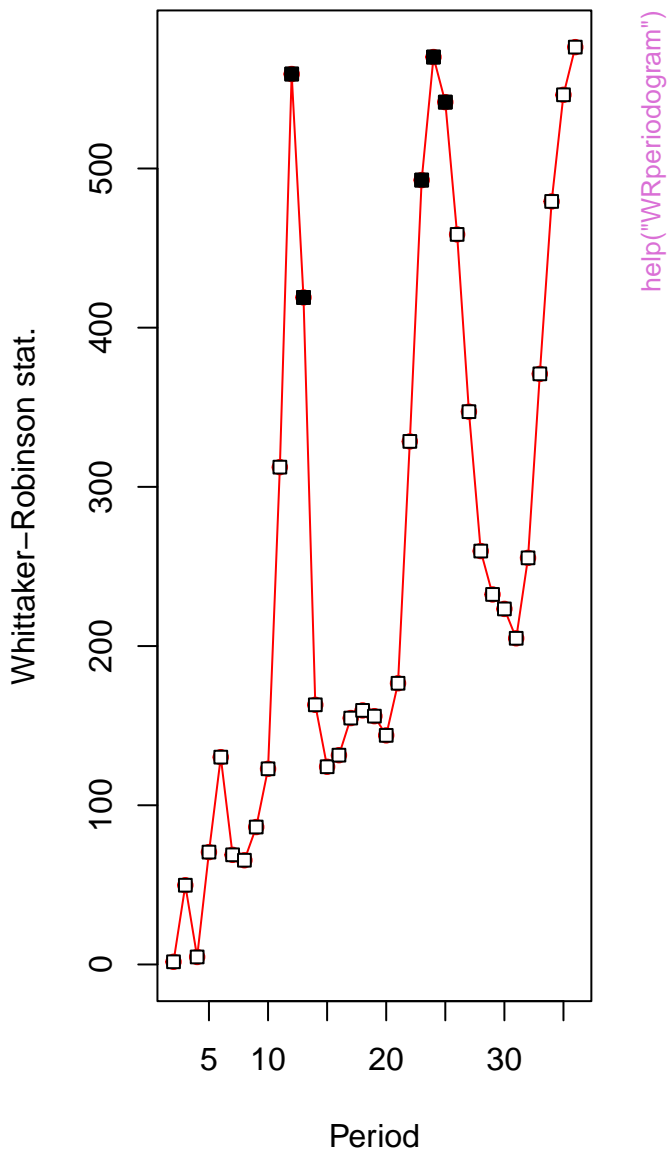
WR Periodogram



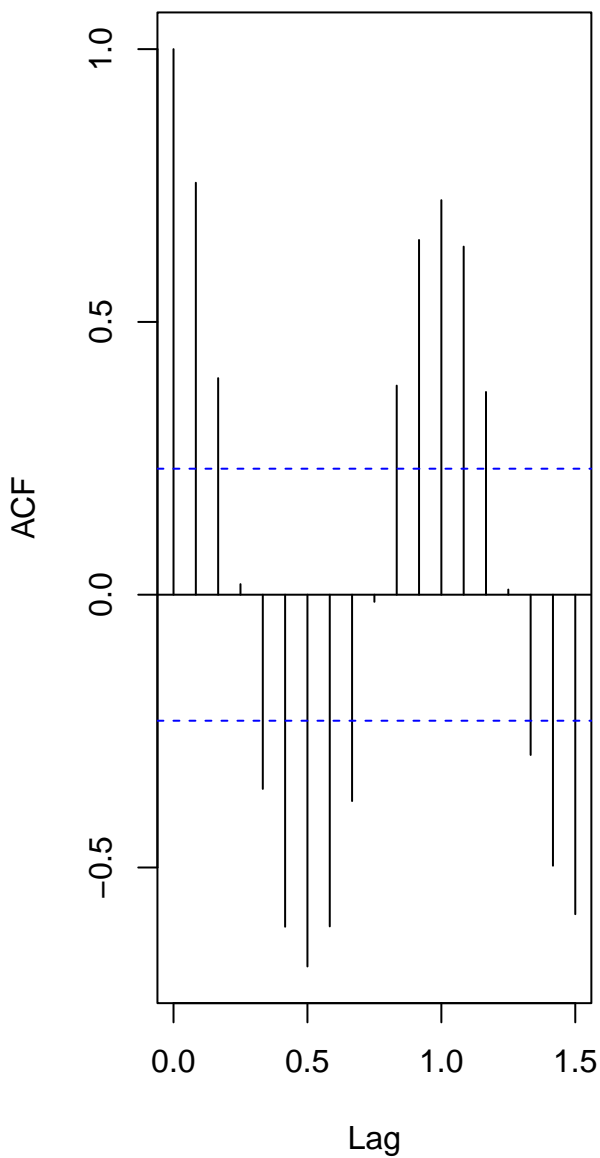
WR Periodogram

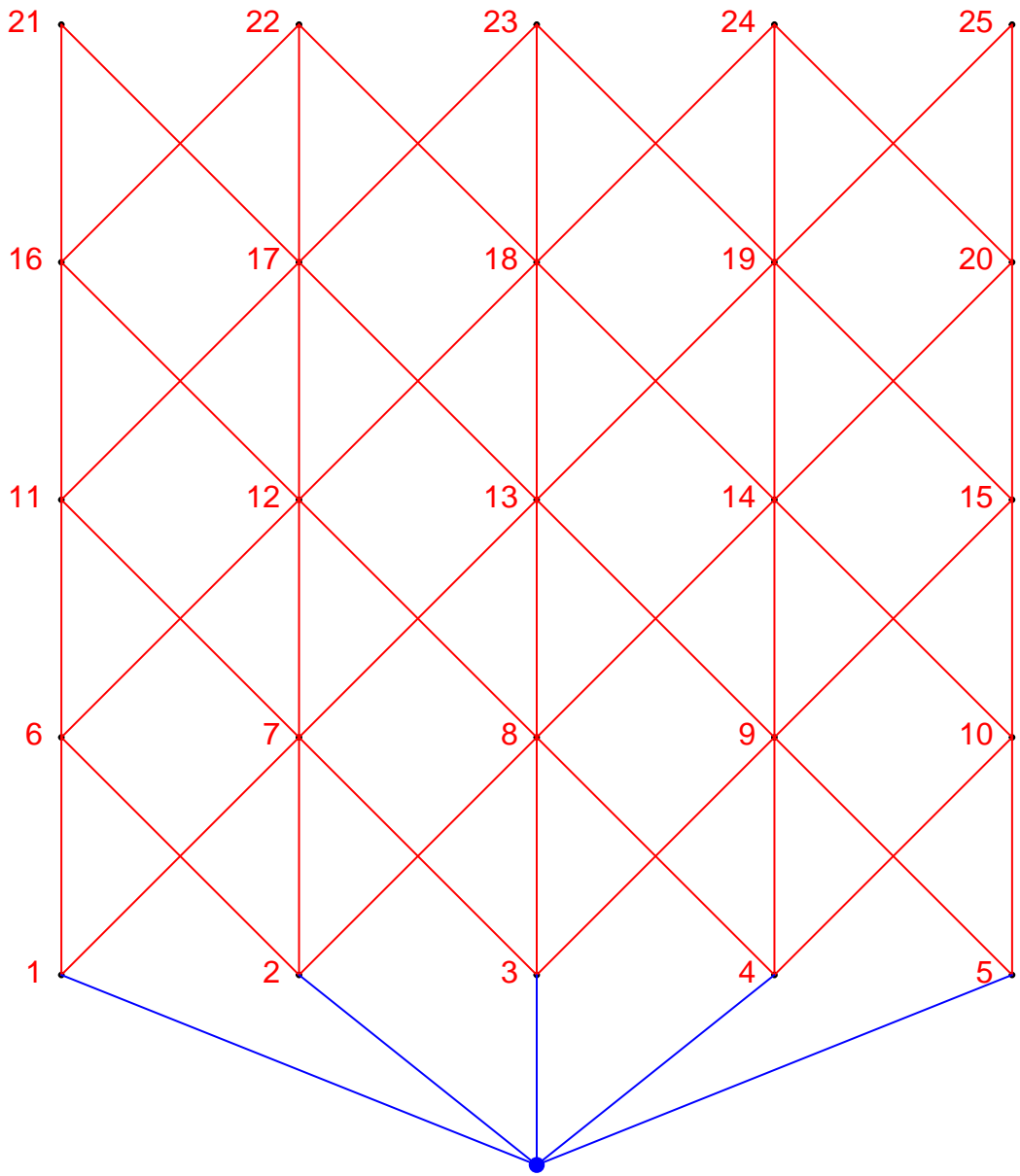


WR Periodogram



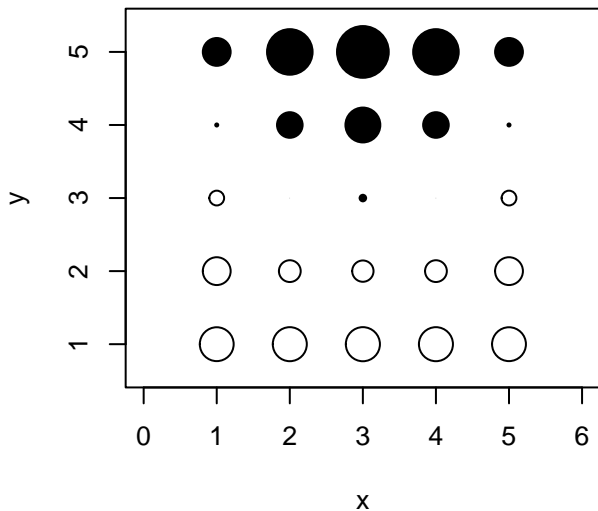
Series Ideaths



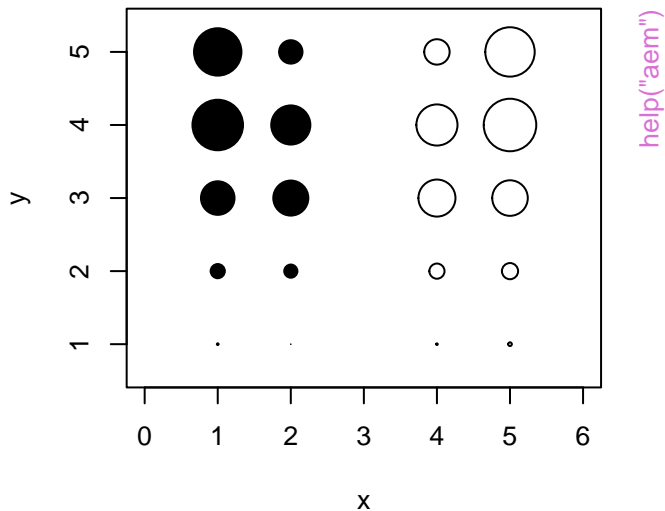


help("aem")

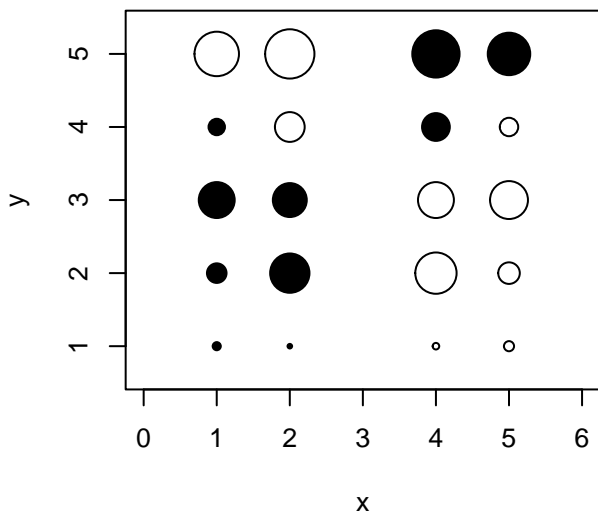
AEM 1



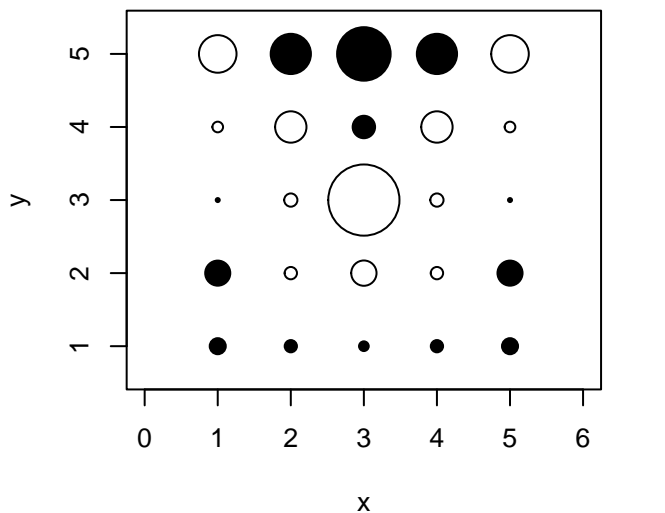
AEM 2



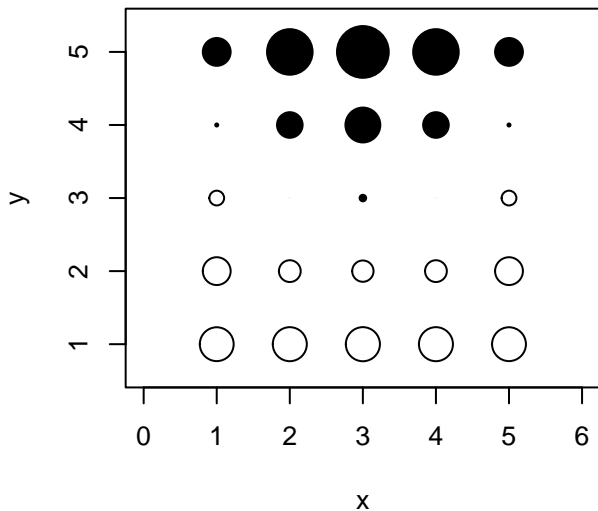
AEM 3



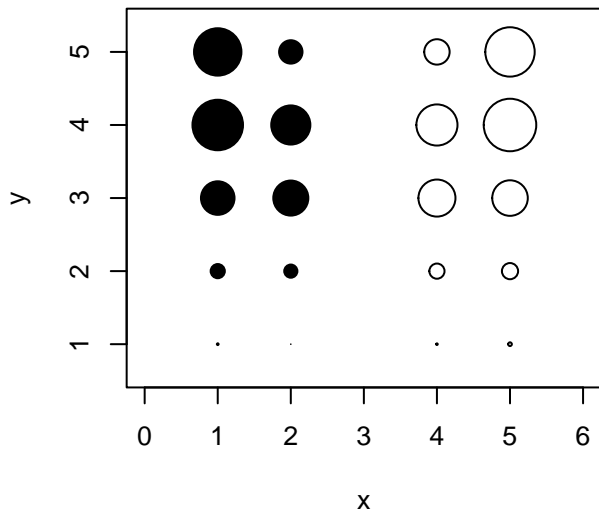
AEM 4



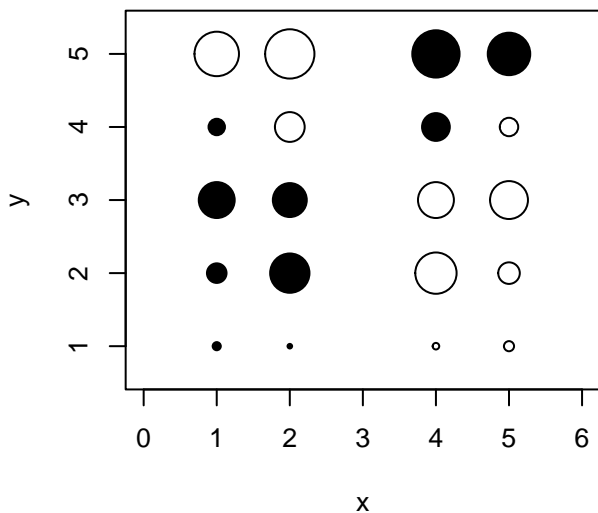
AEM 1



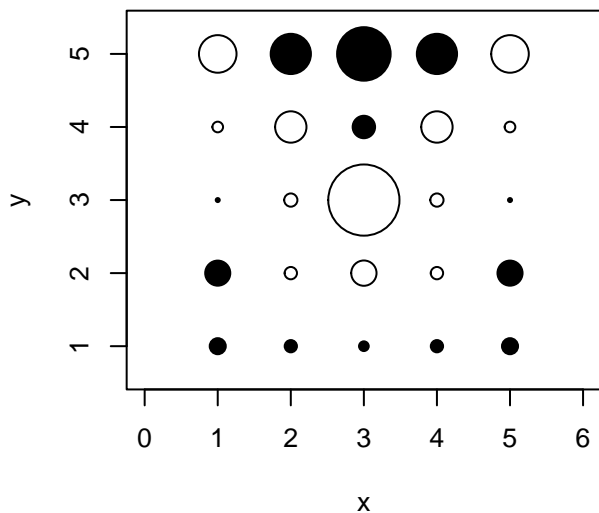
AEM 2



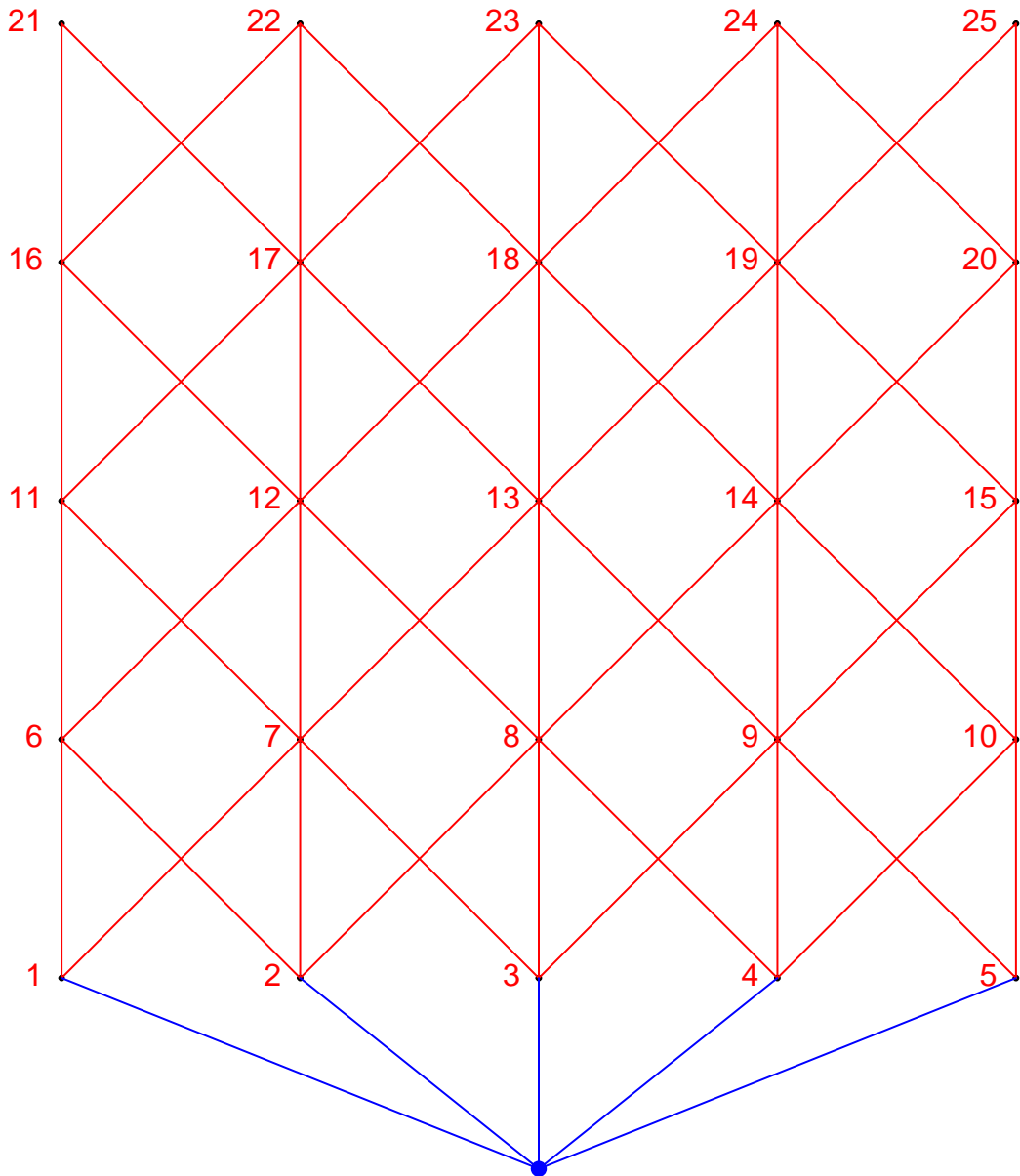
AEM 3

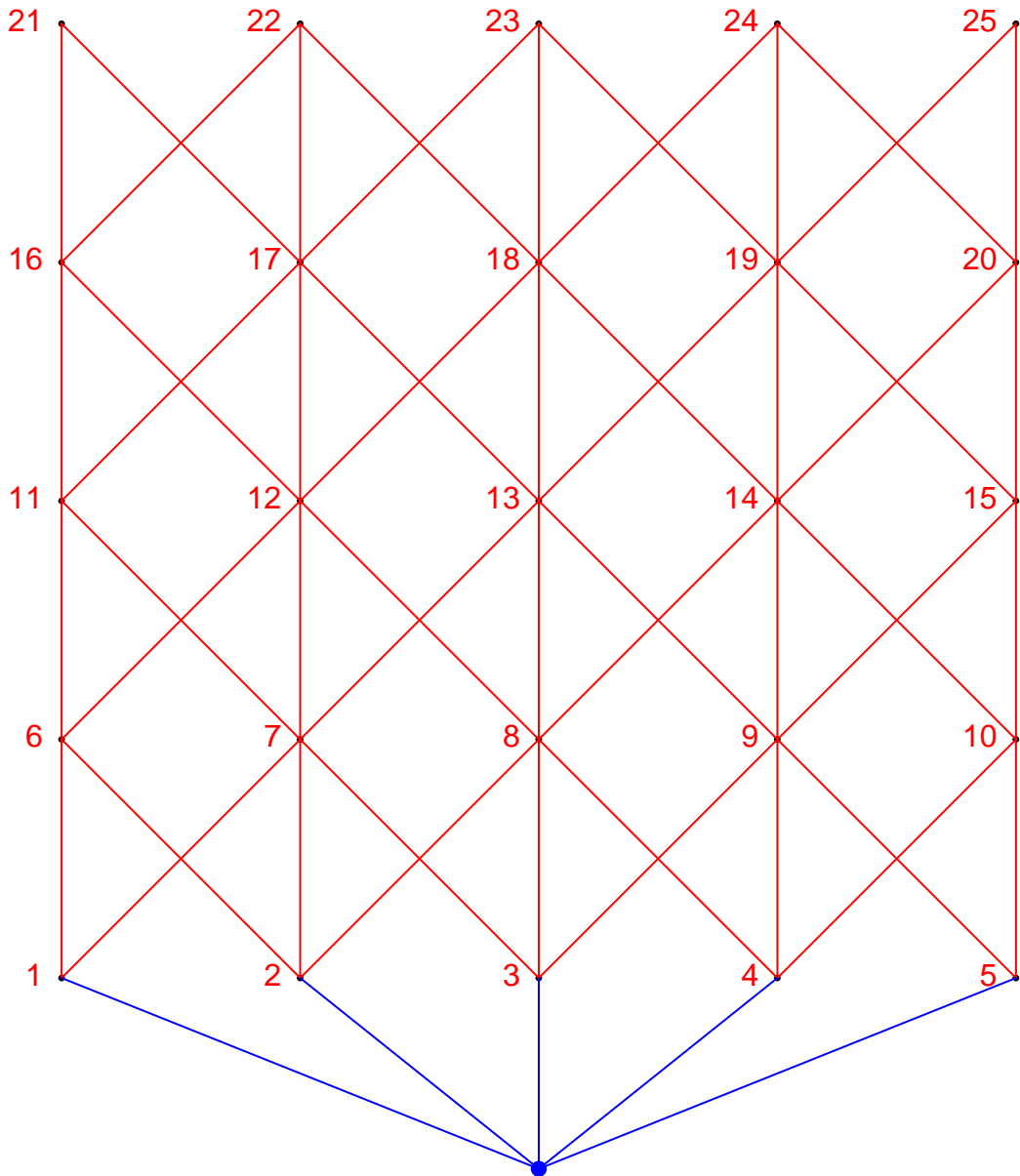


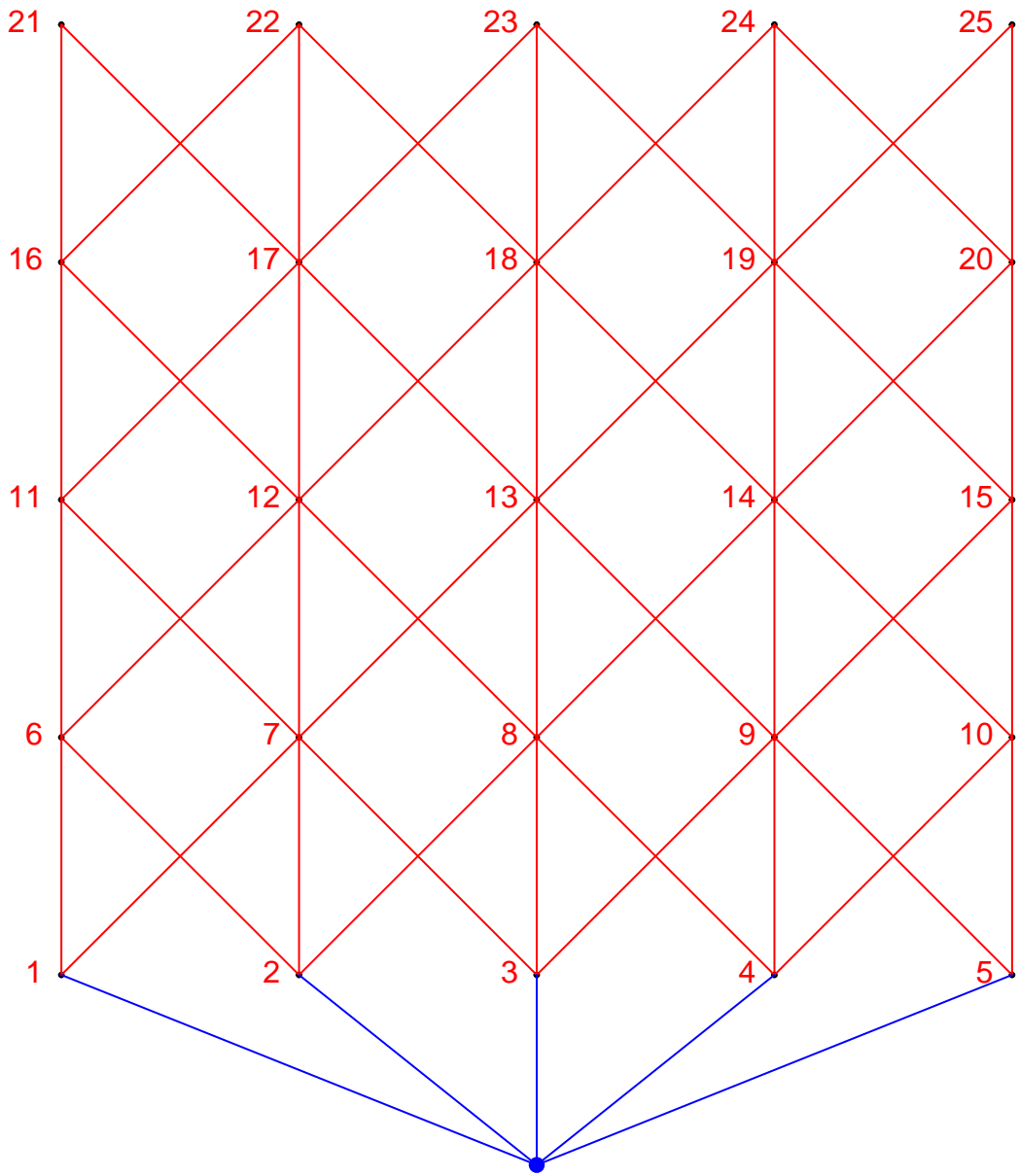
AEM 4

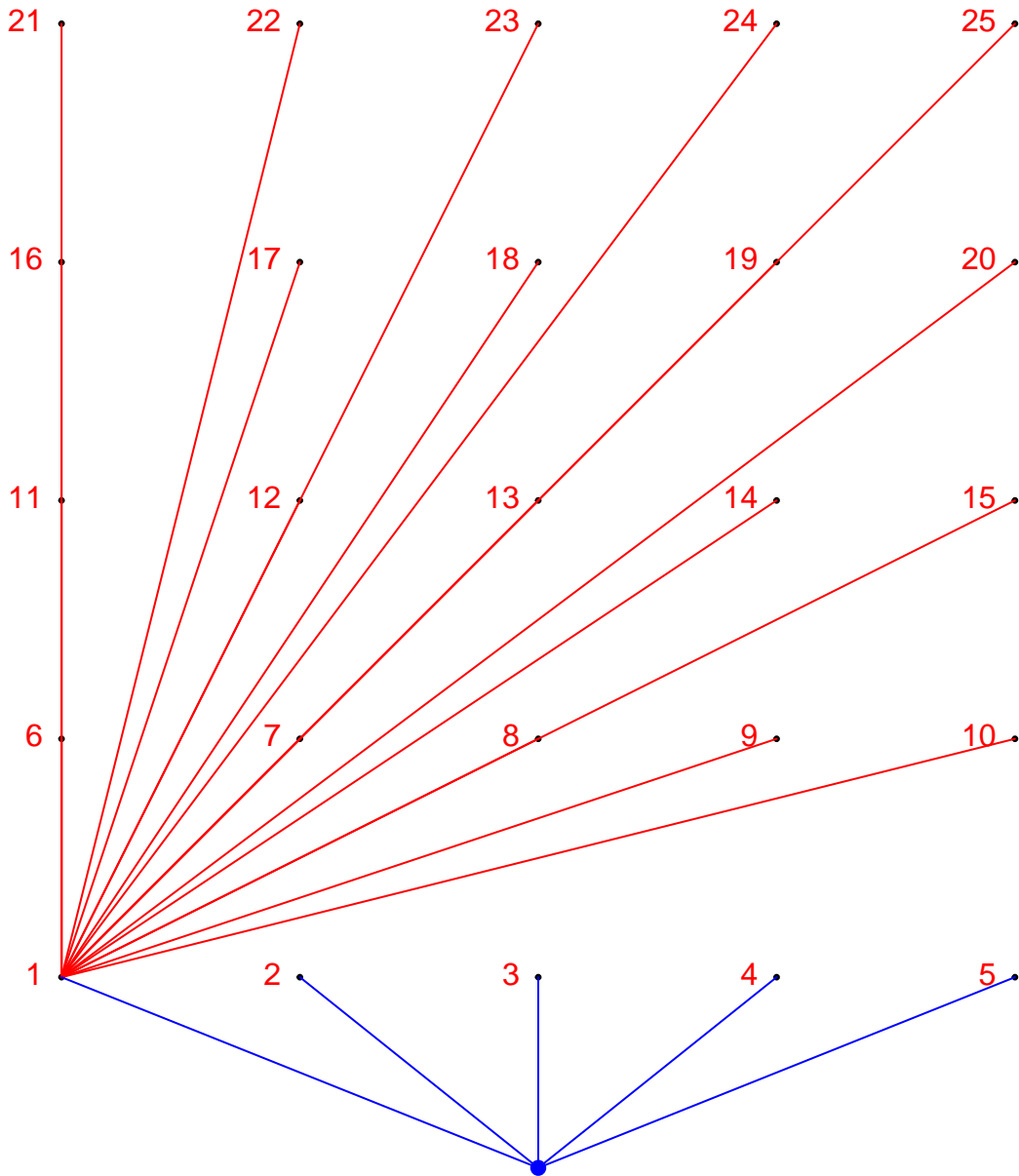


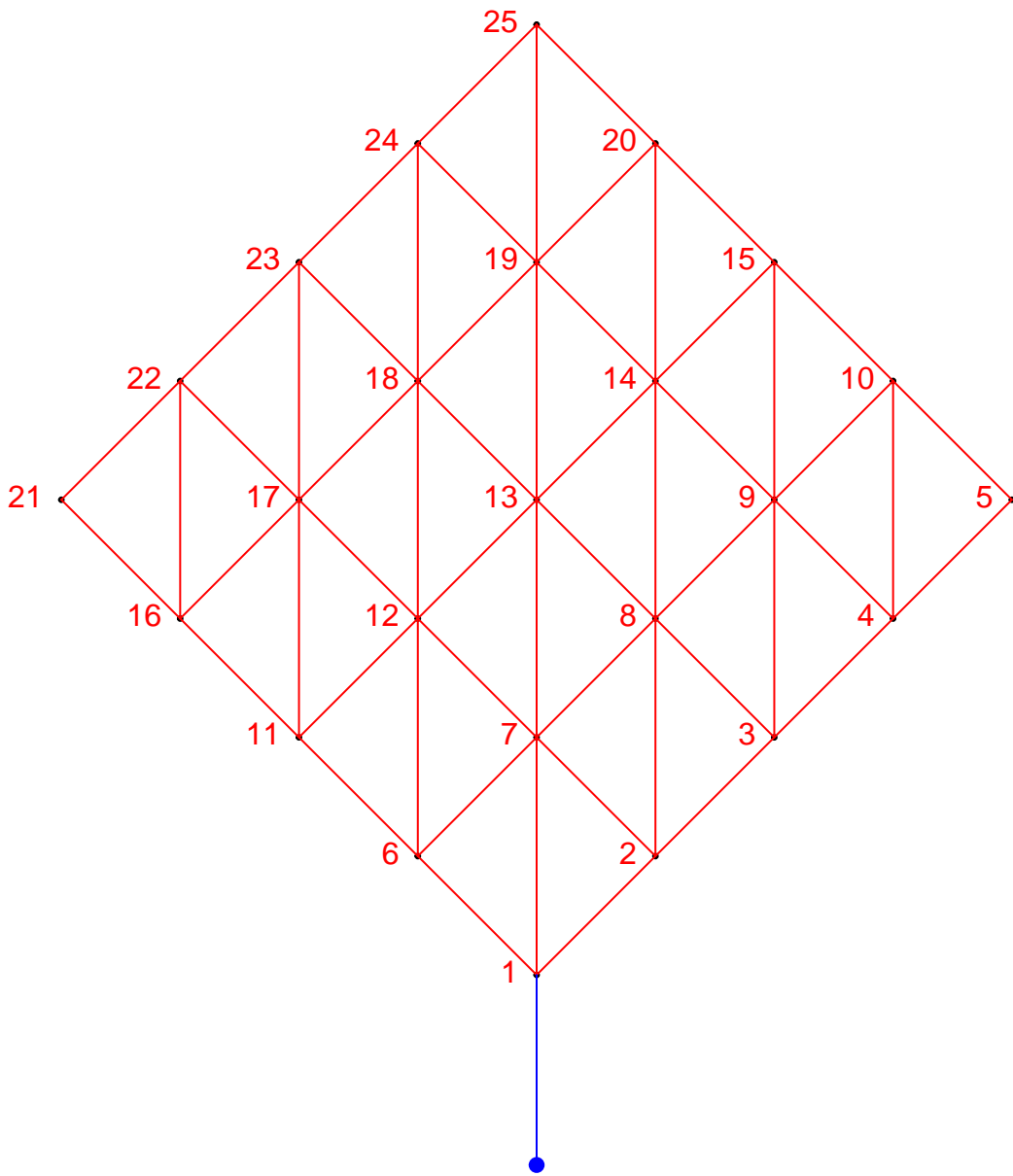
help("aem")

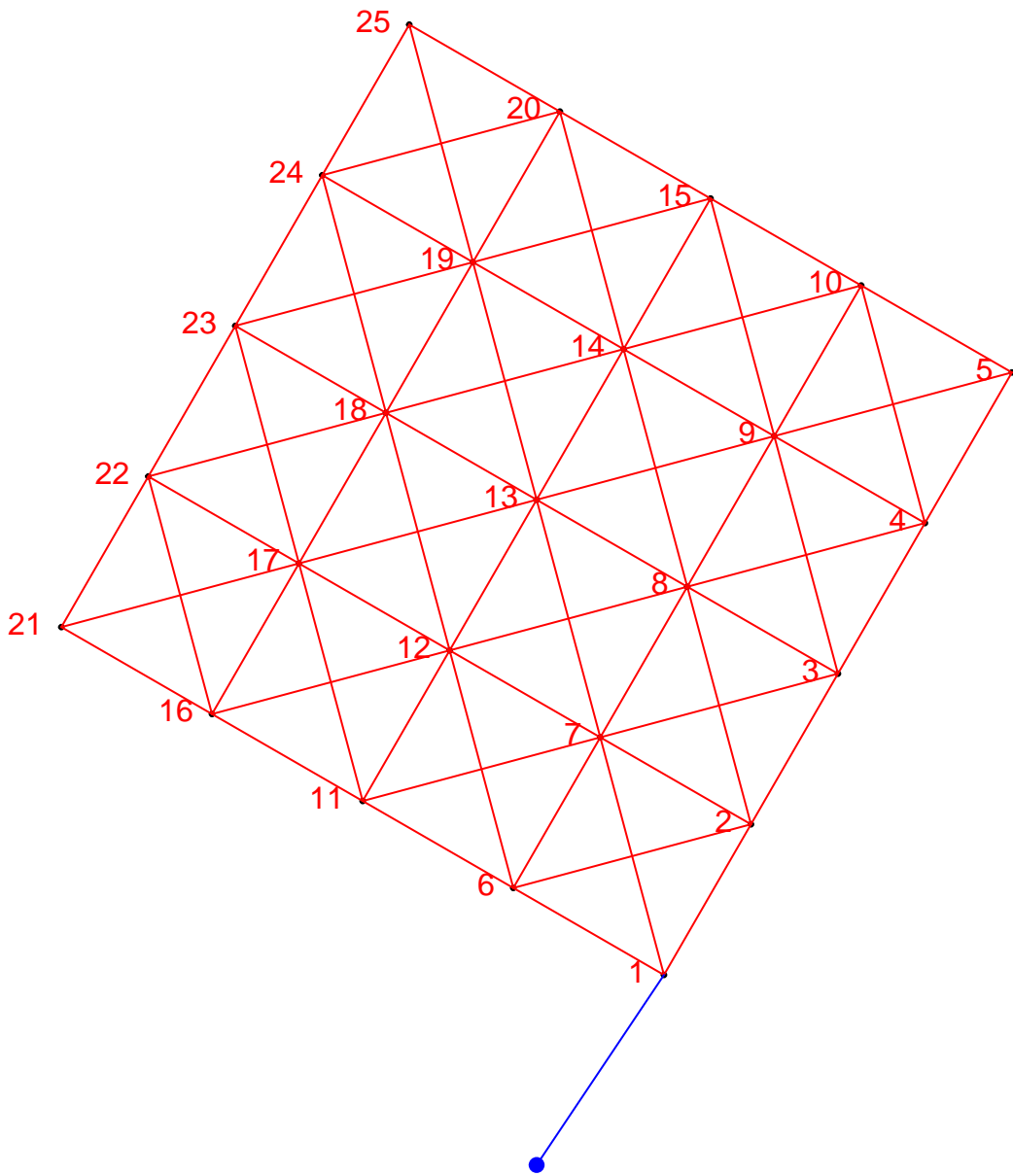










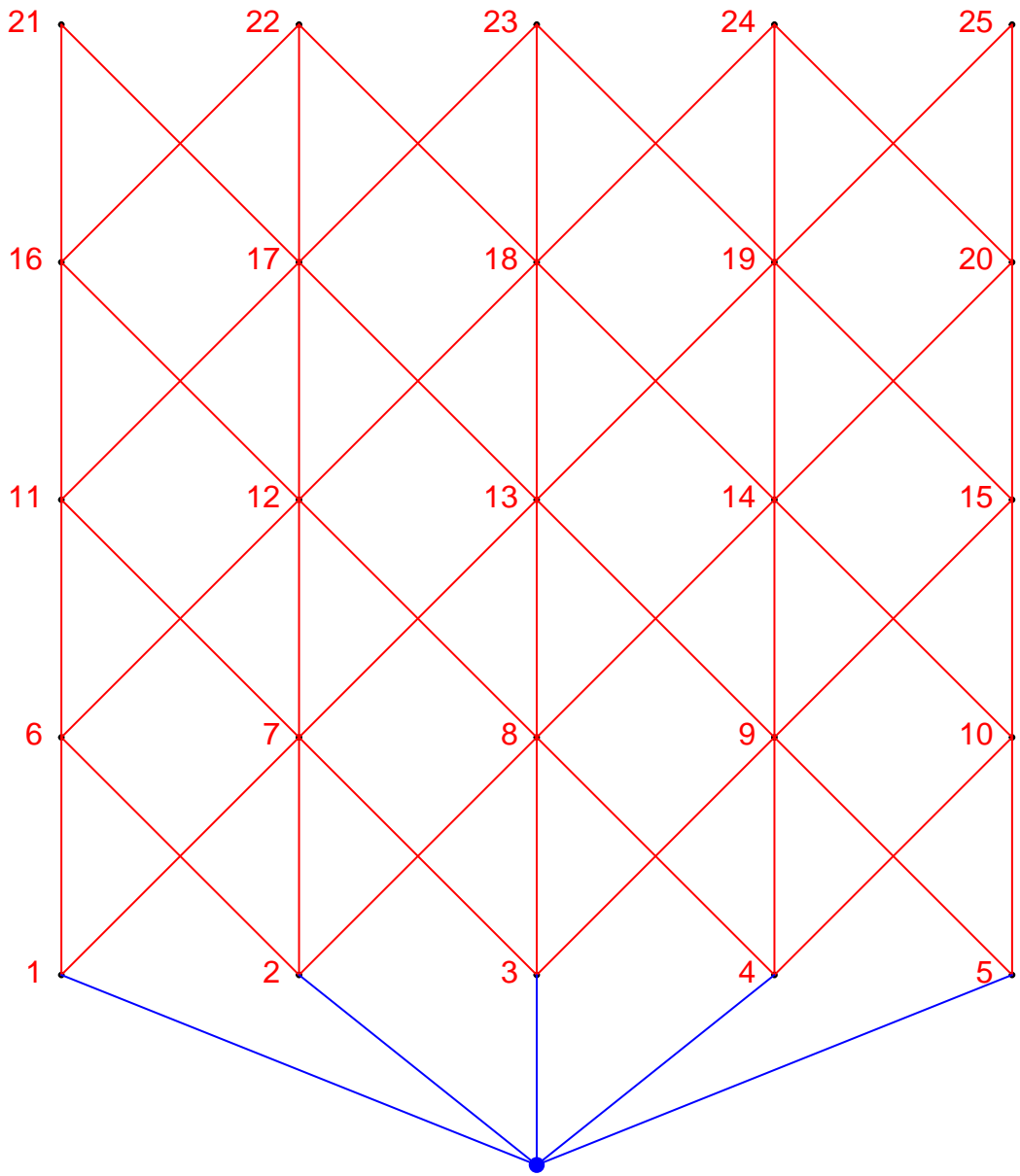


help("aem.build.binary")







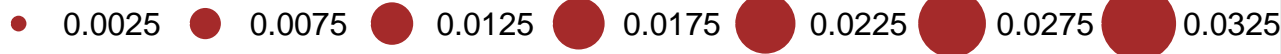


help("aem.weight.edges")

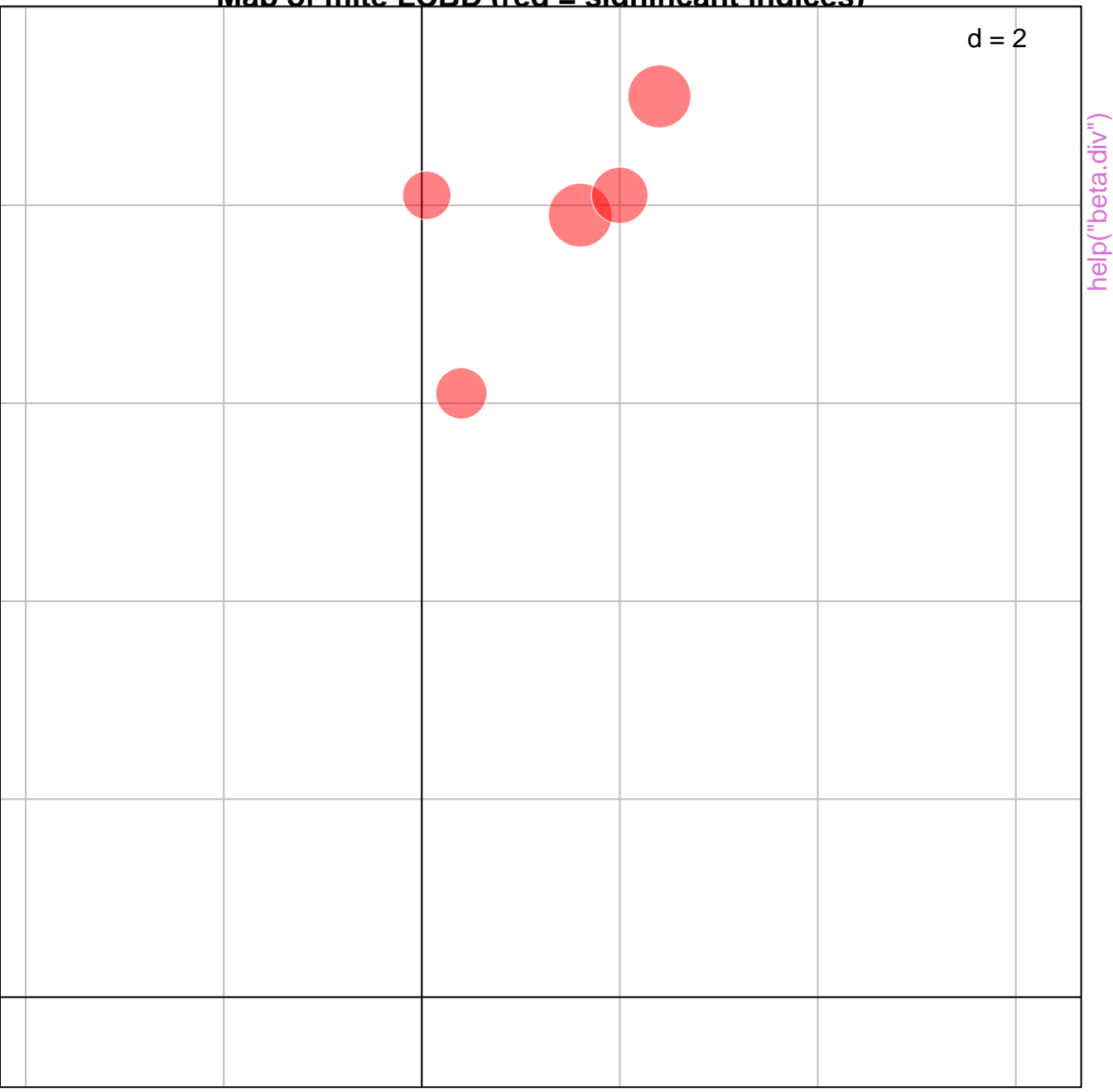
Map of mite LCBD

d = 2

help("beta div")

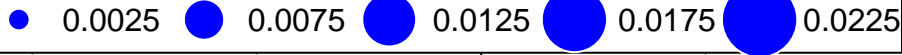


Map of mite LCBD (red = significant indices)



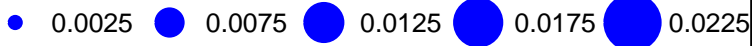
d = 2

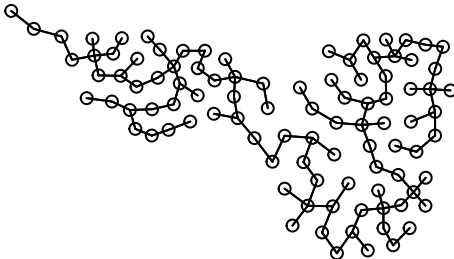
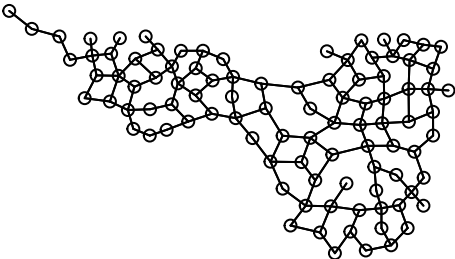
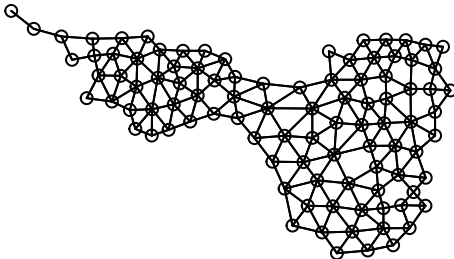
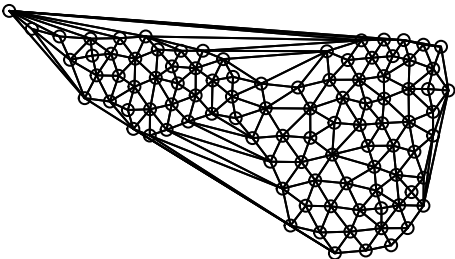
help("beta div")



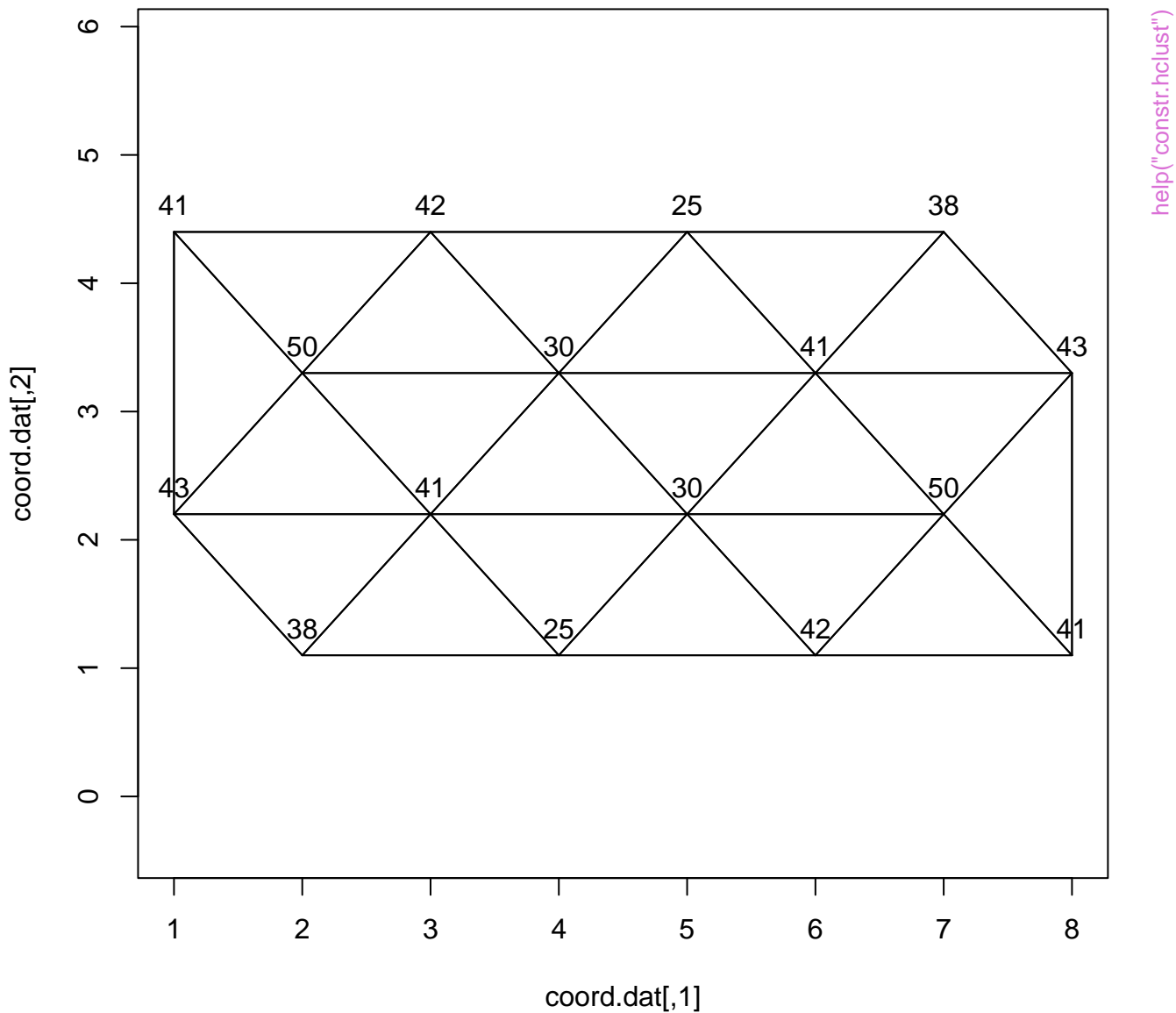
d = 2

help("beta div")

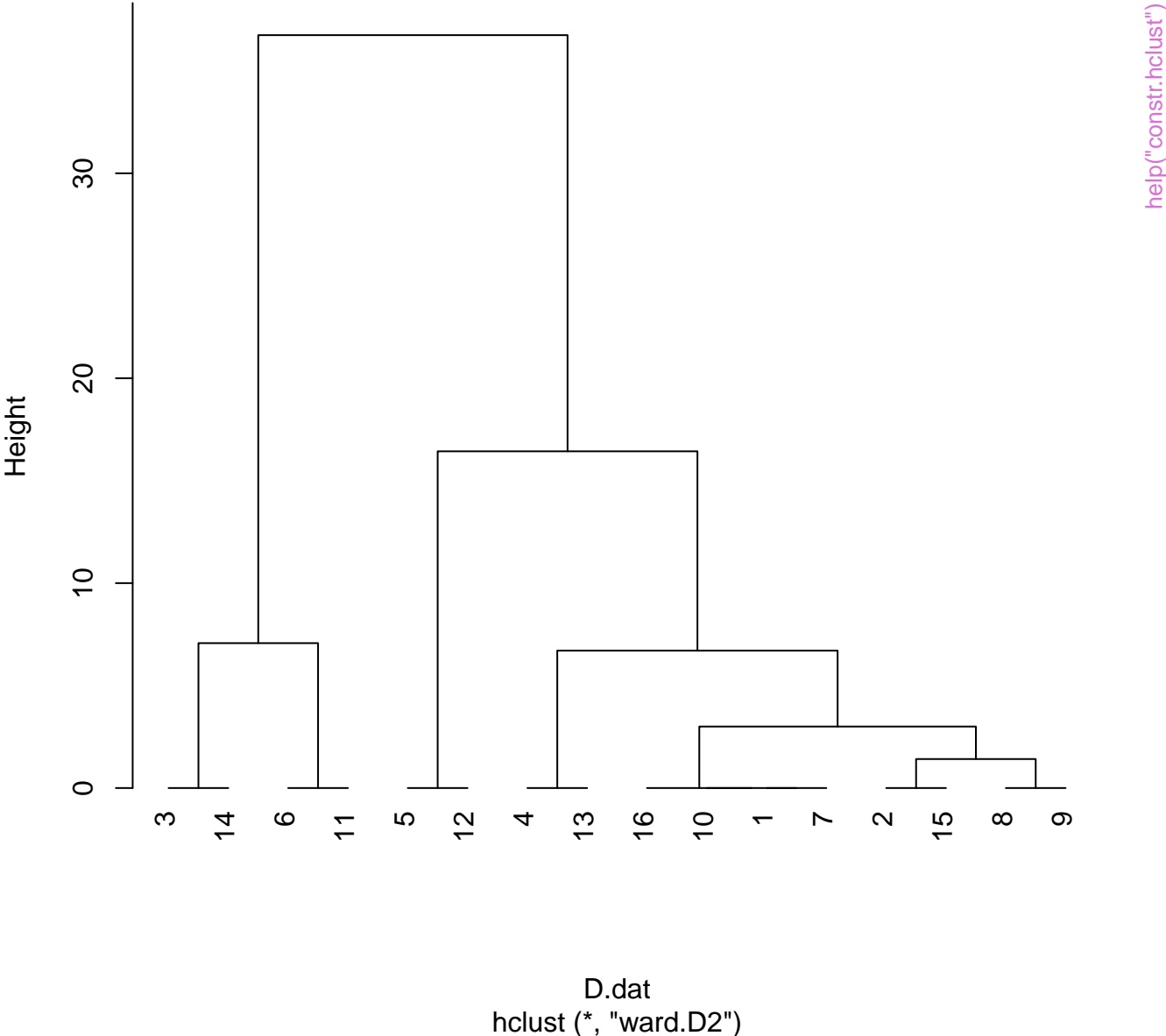




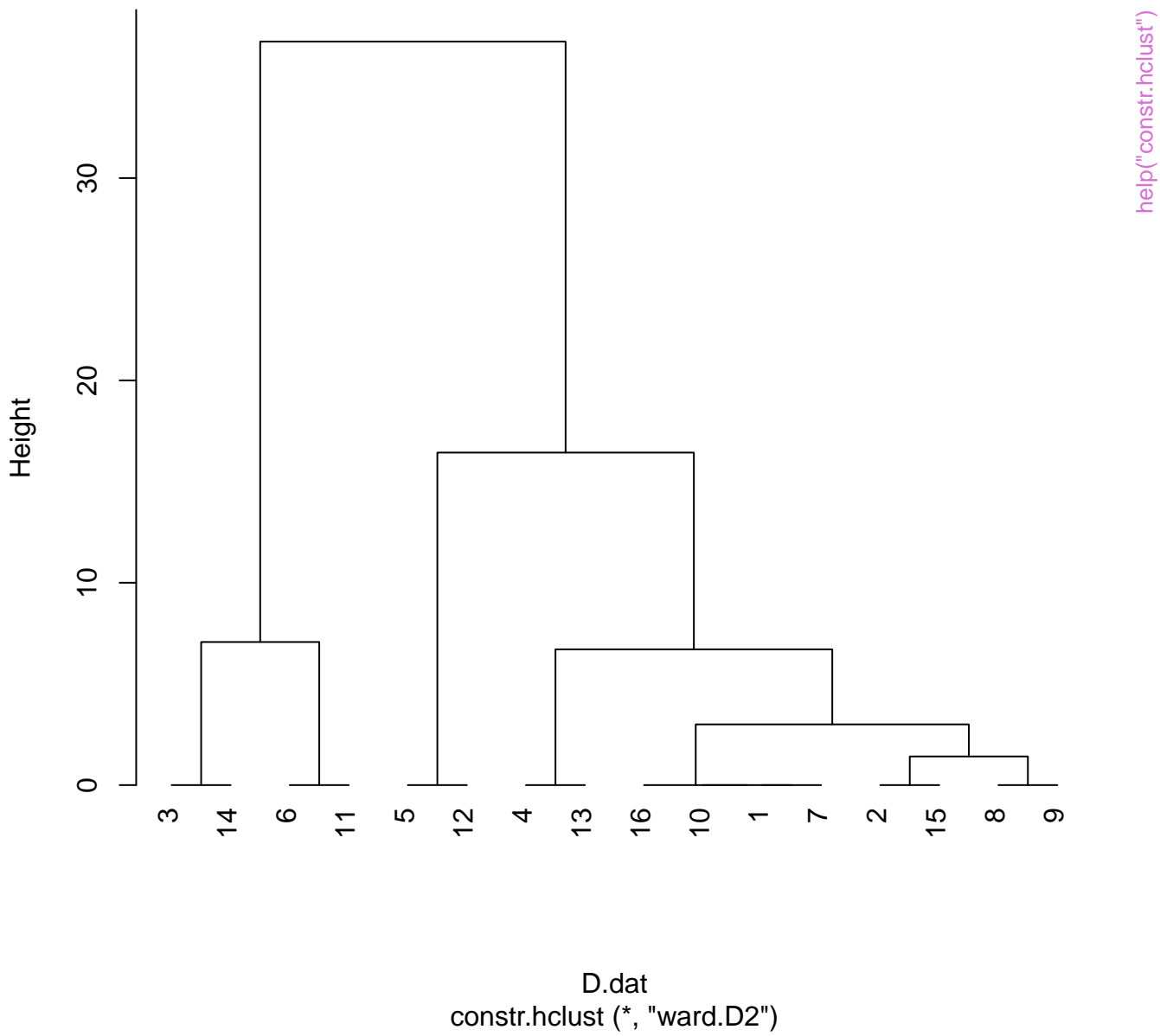
Delaunay triangulation

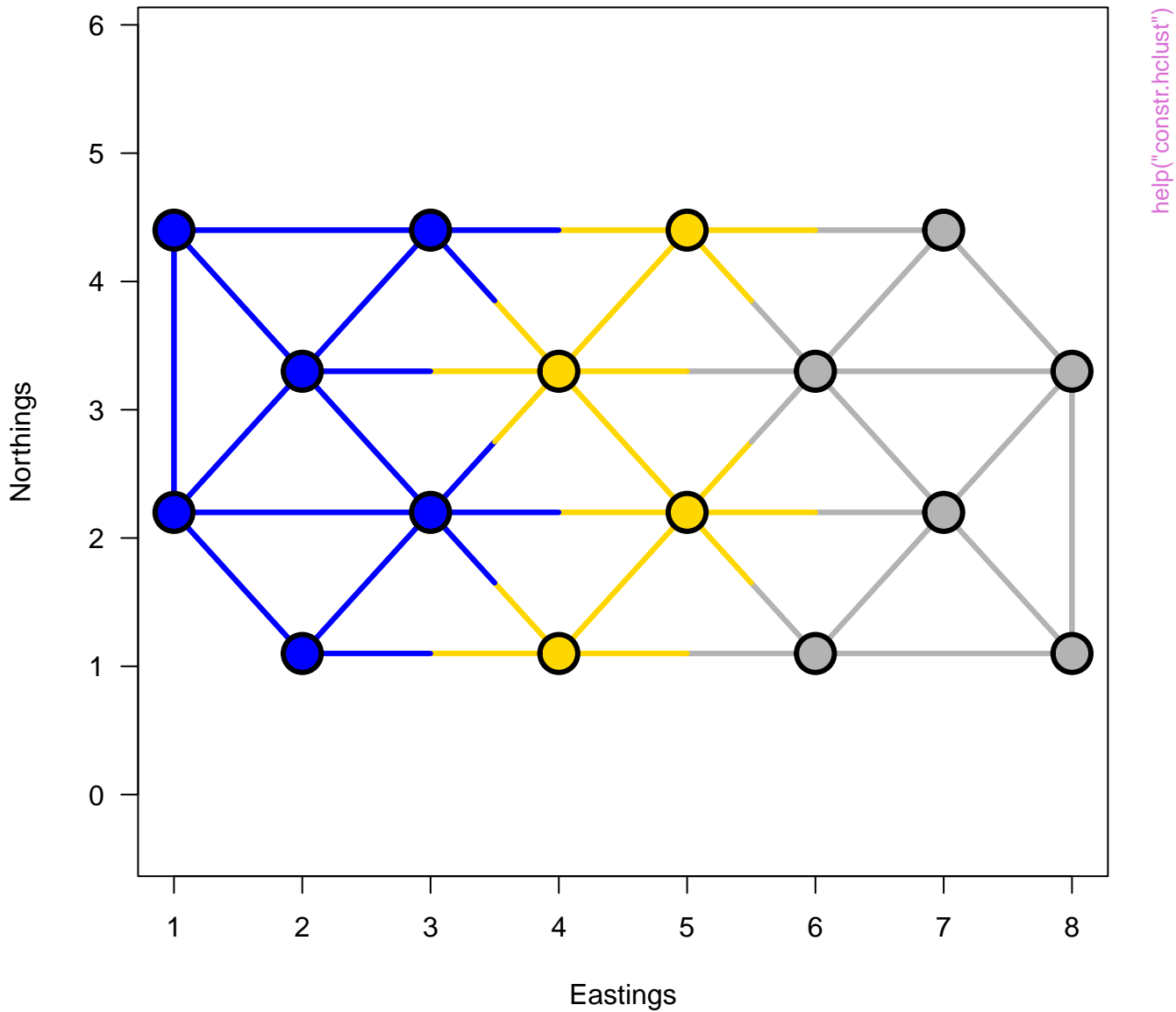


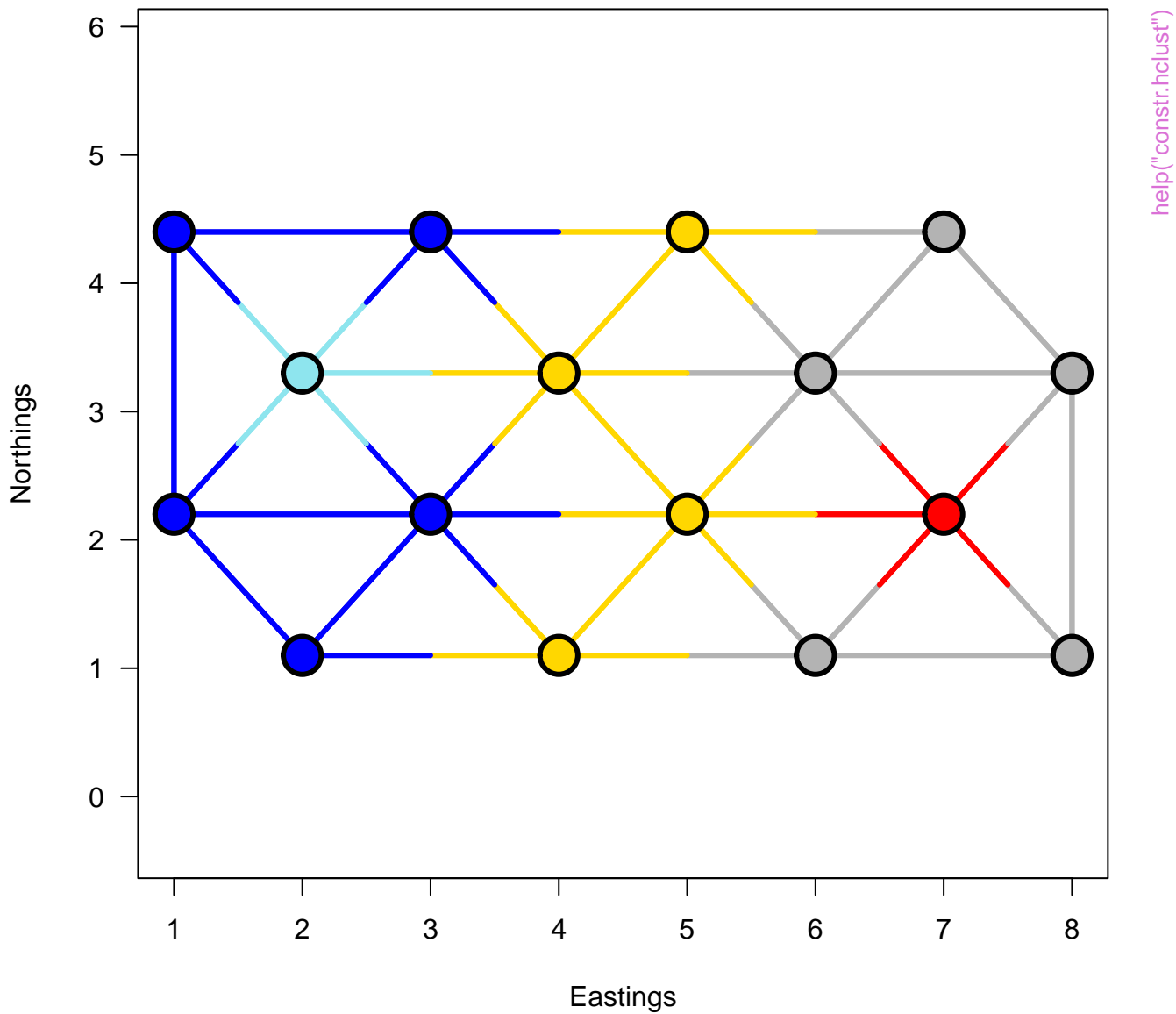
Cluster Dendrogram



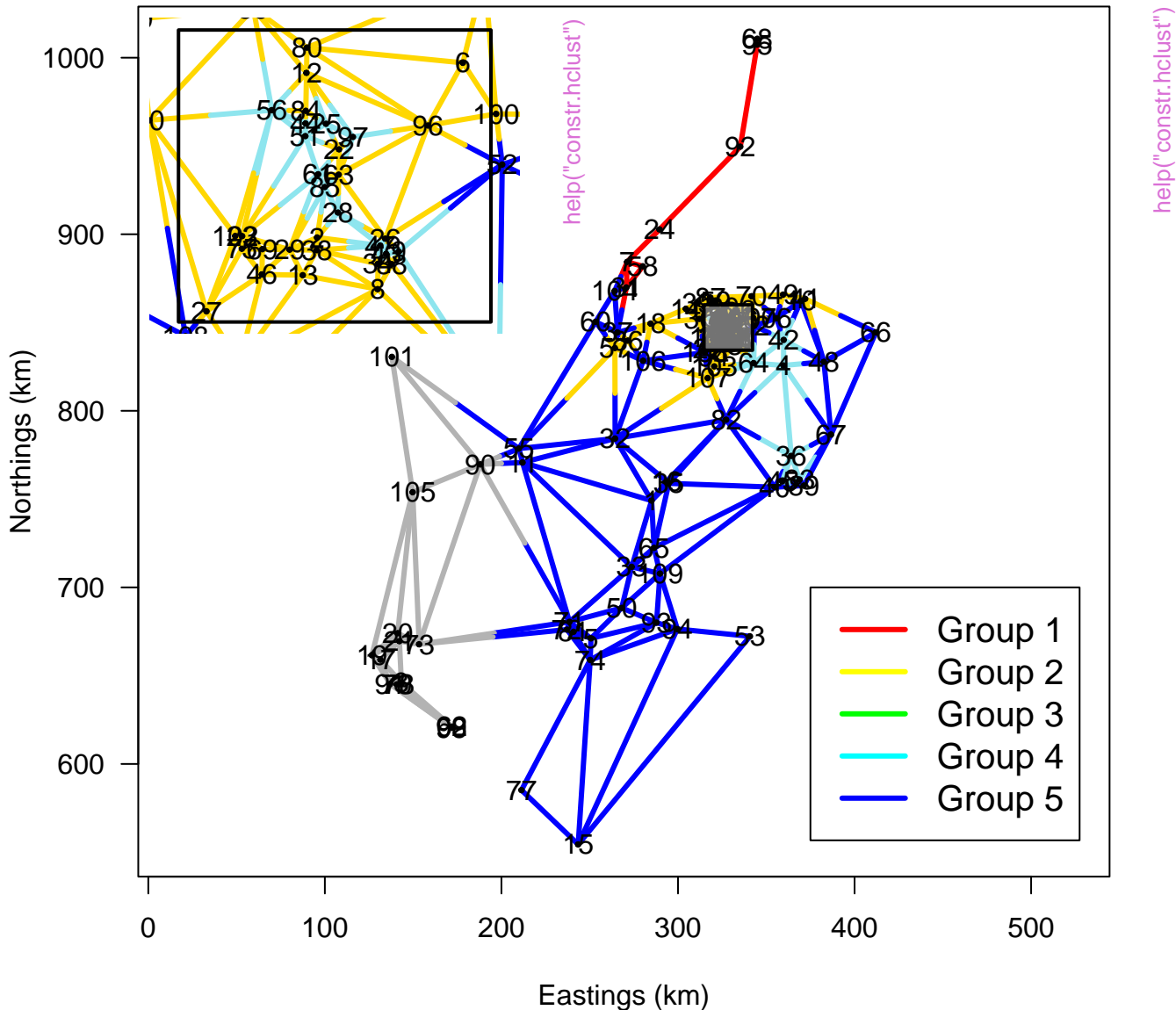
Cluster Dendrogram



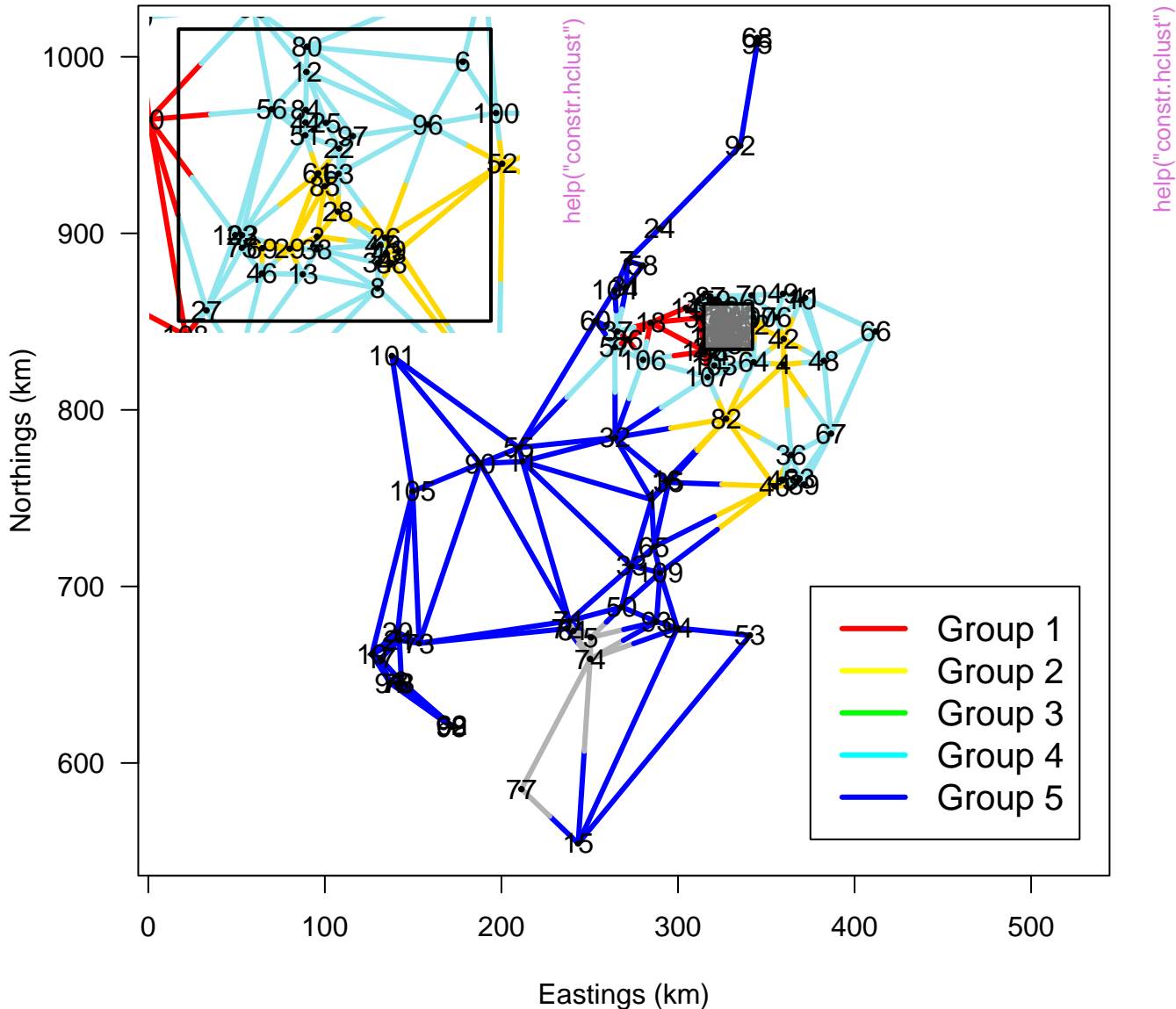




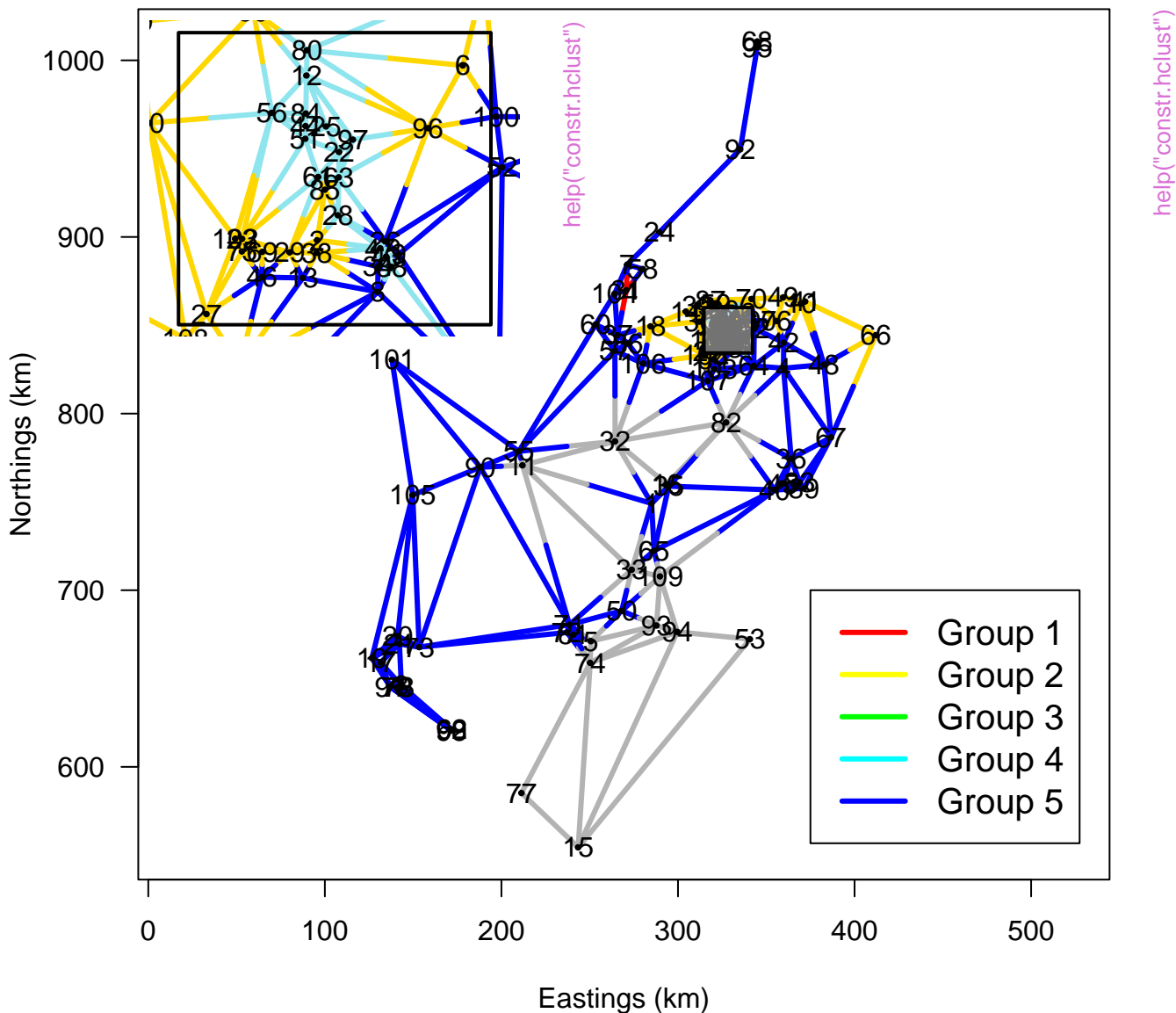
Feature: nose



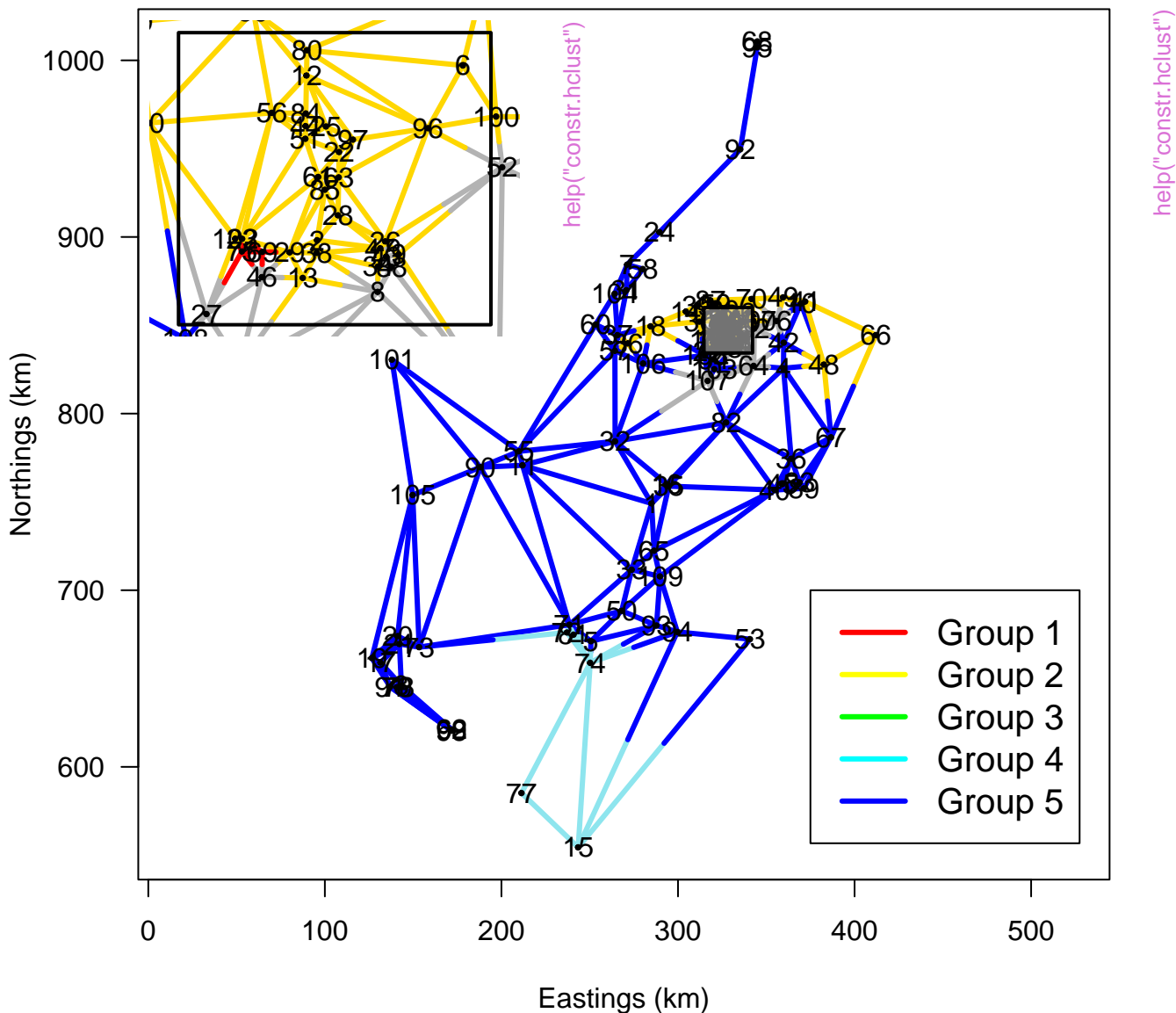
Feature: body



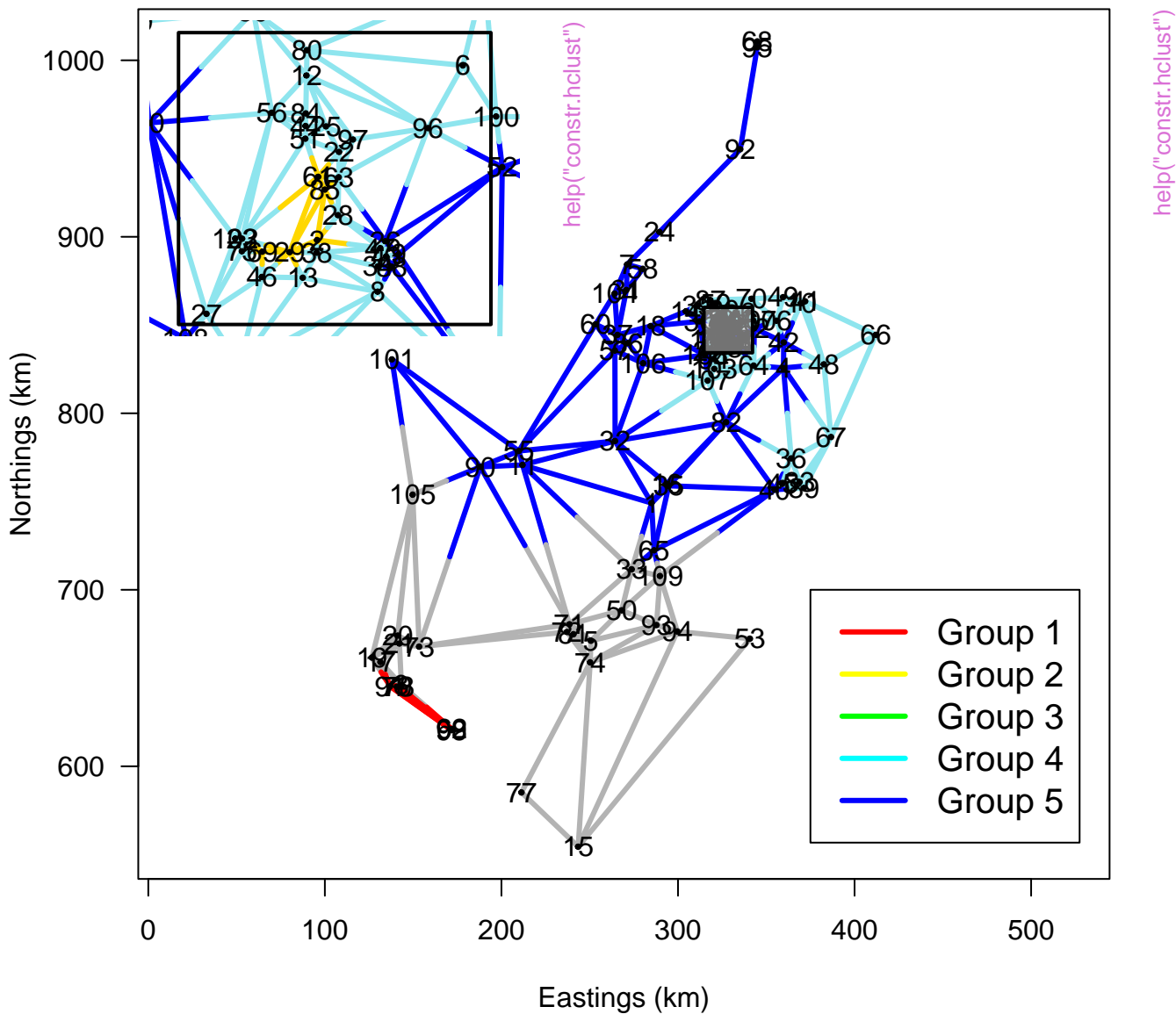
Feature: palate



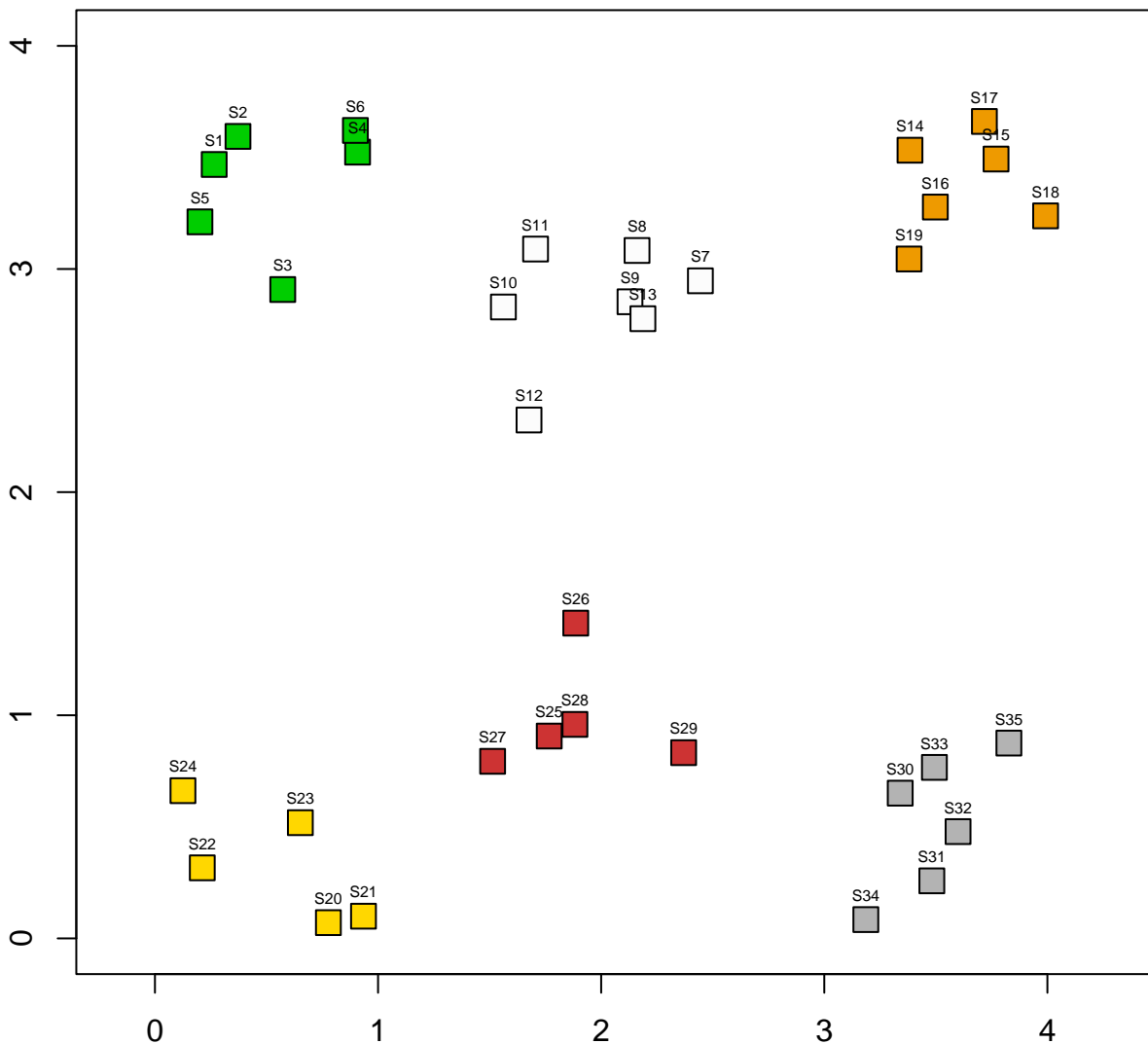
Feature: finish



Feature: norm

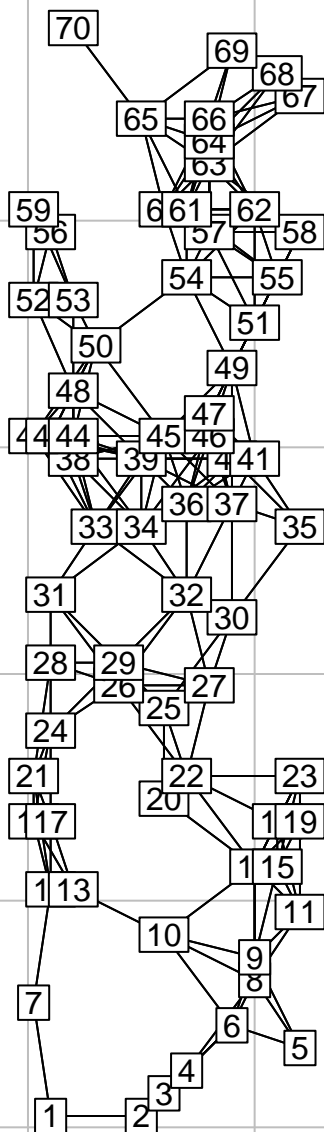


Northing

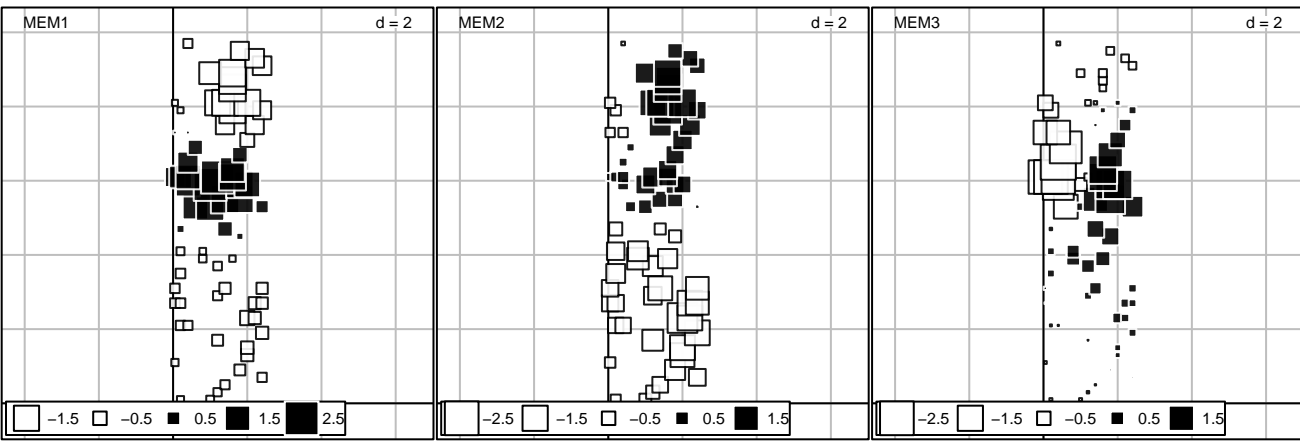


help("create.dbMEM.model")

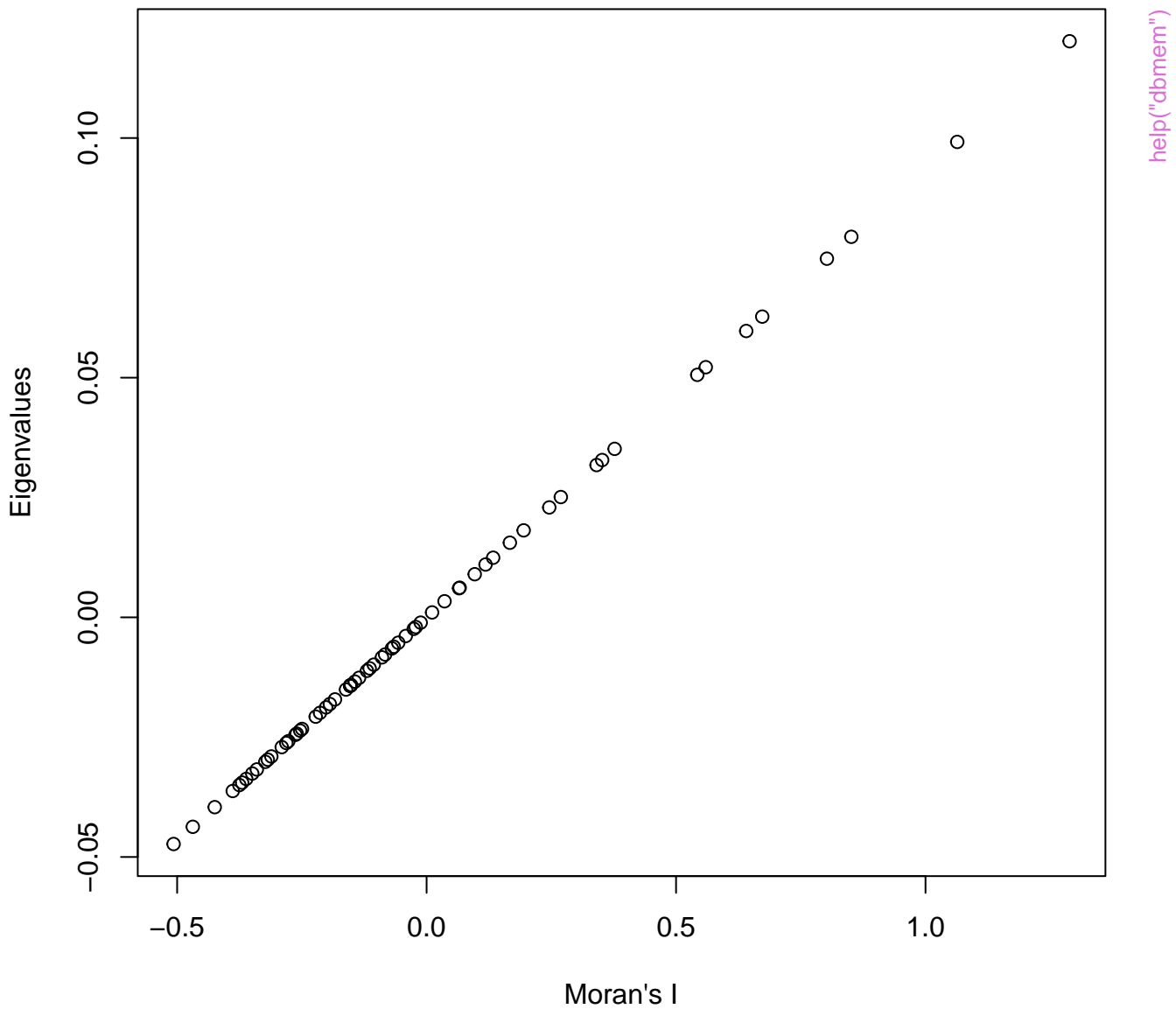
d = 2

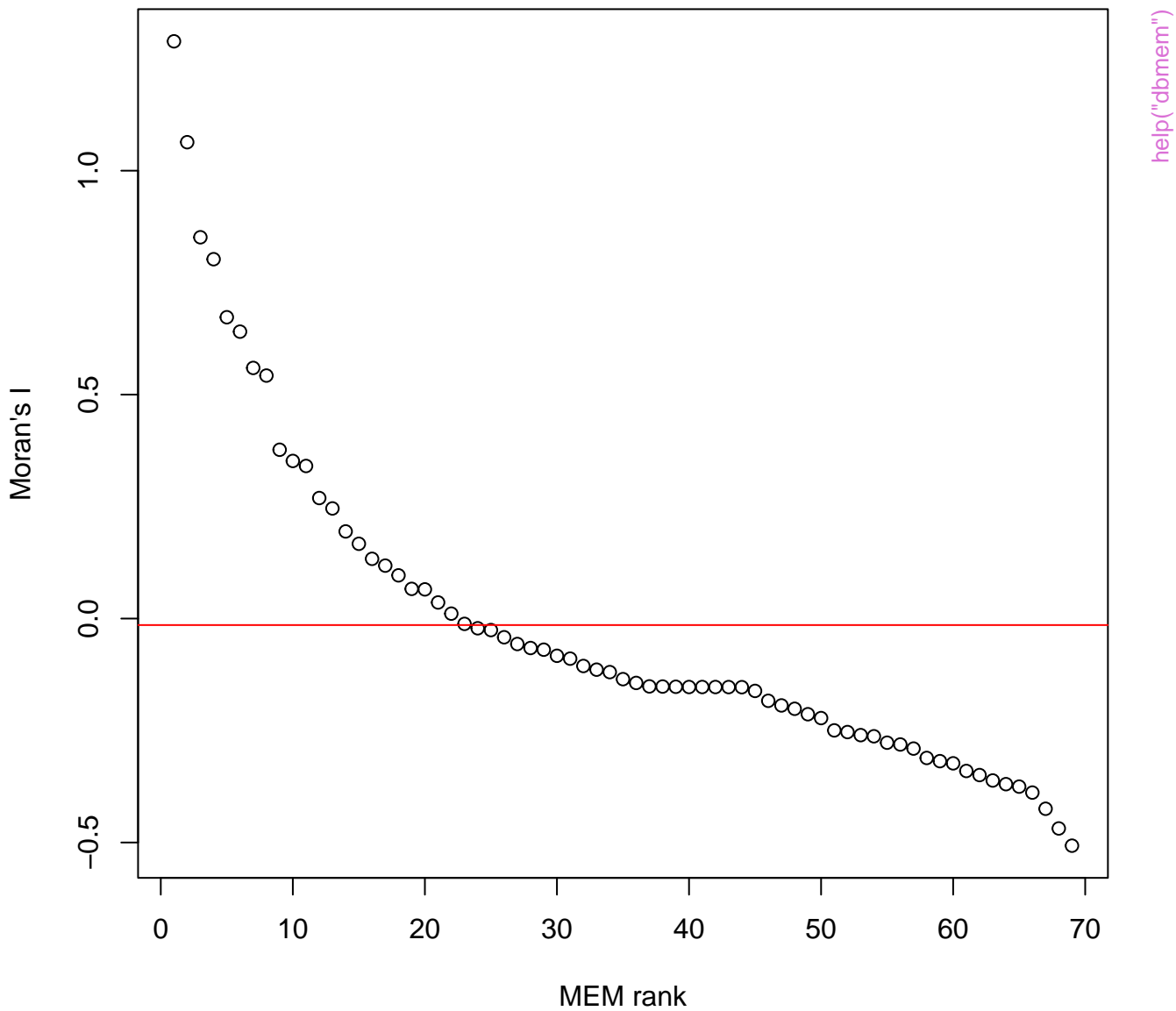


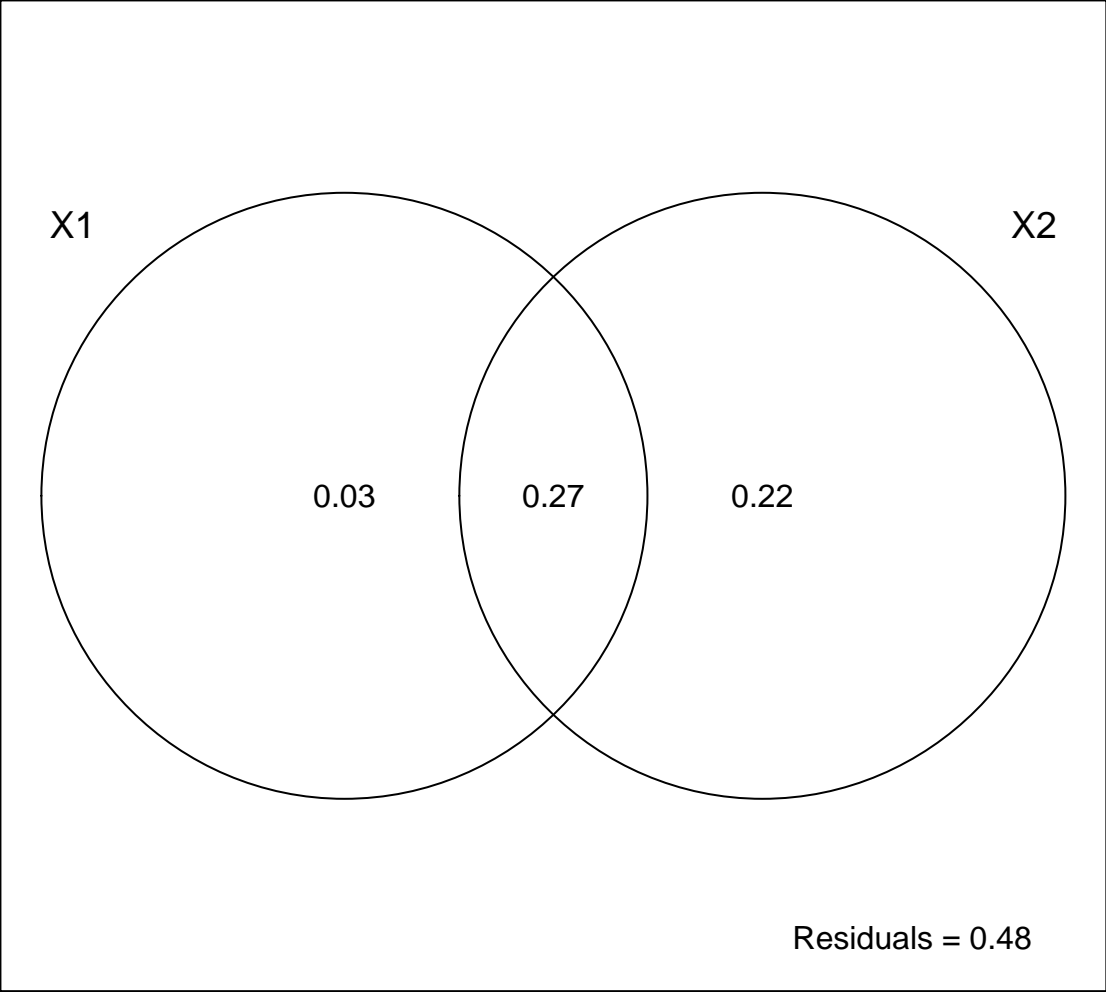
help("dbmem")

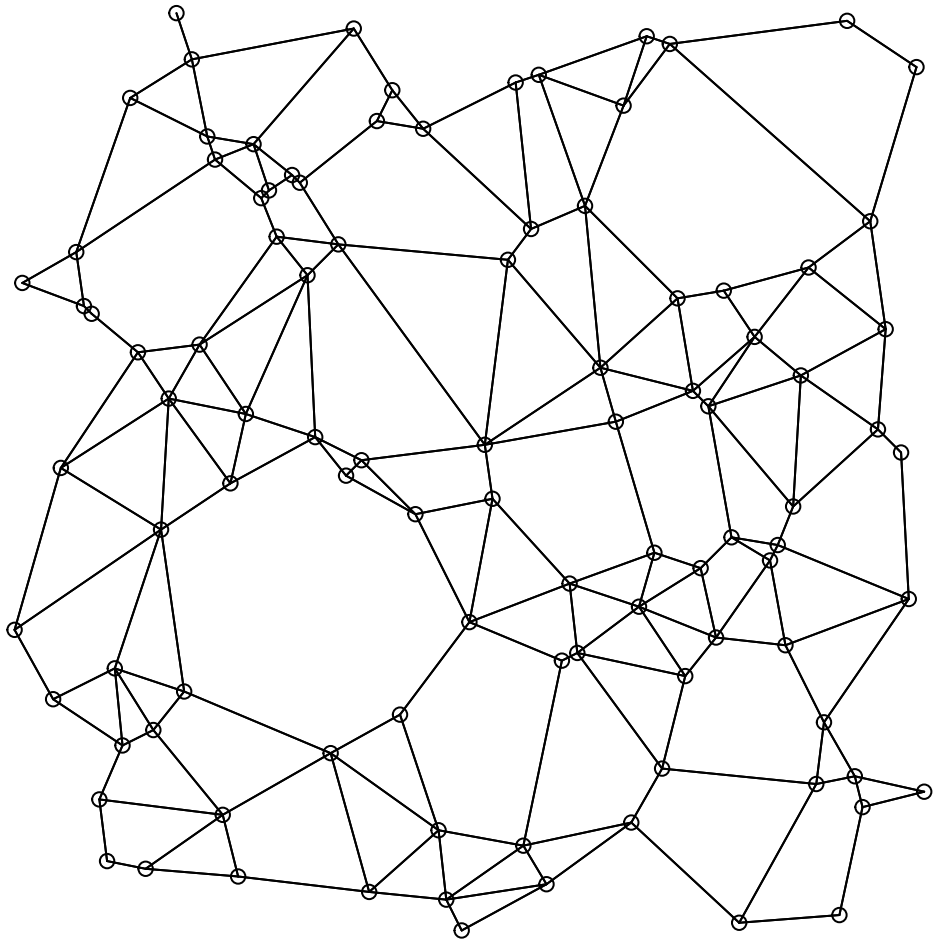


`help("dbmem")`

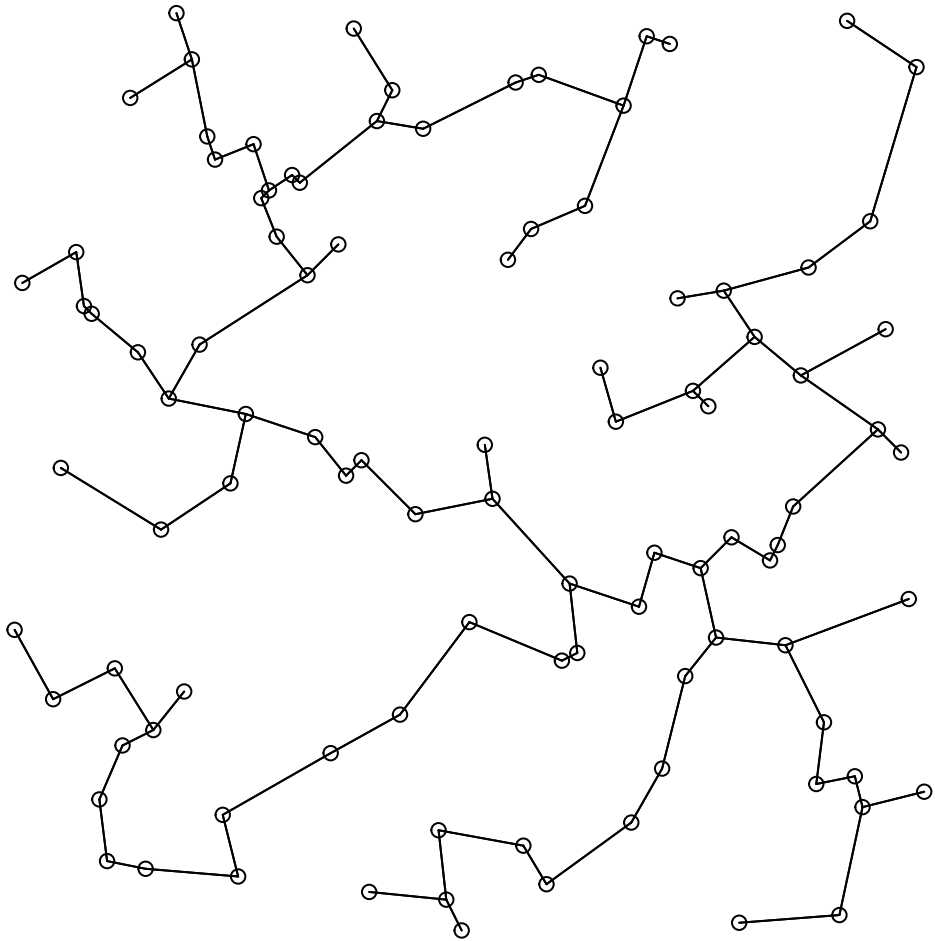




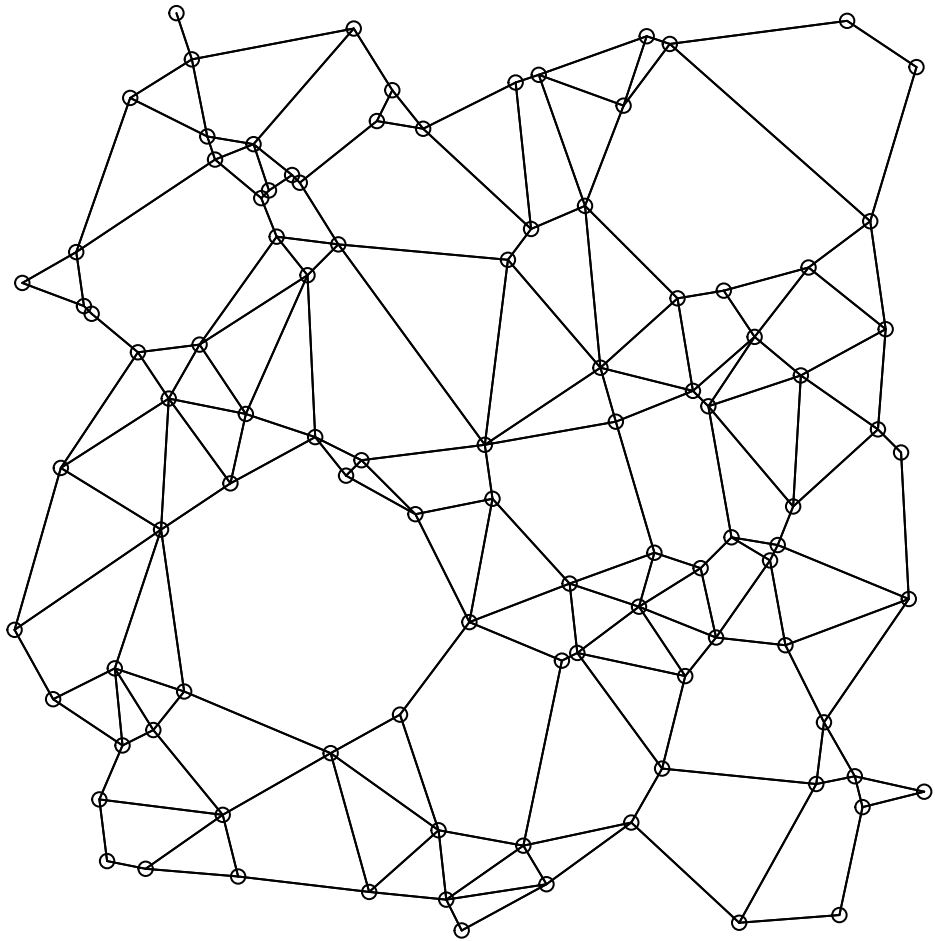




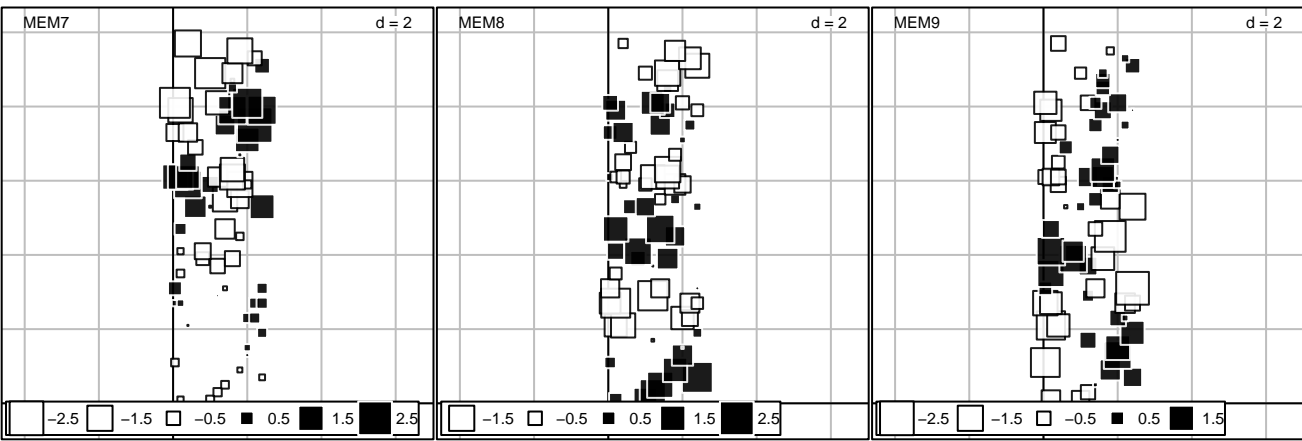
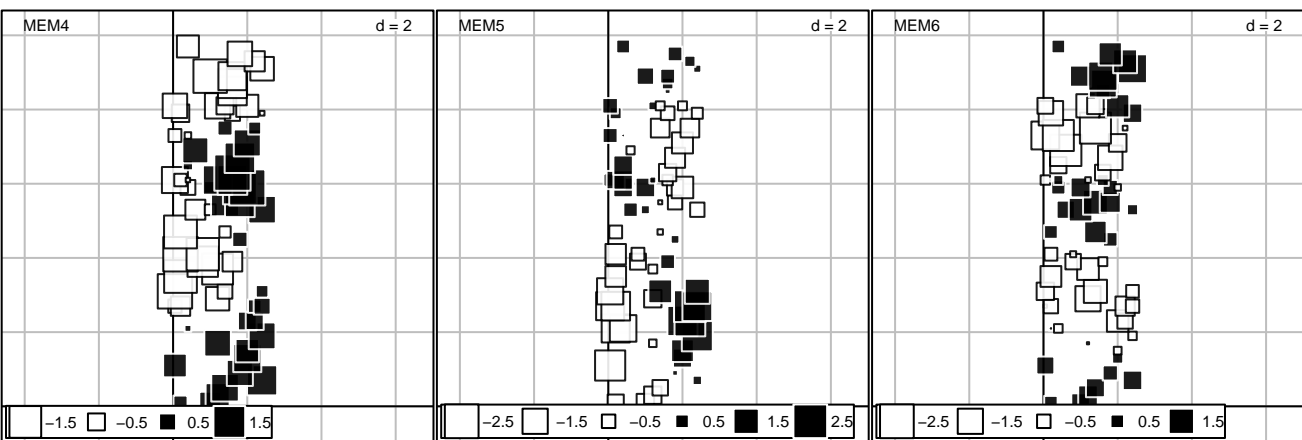
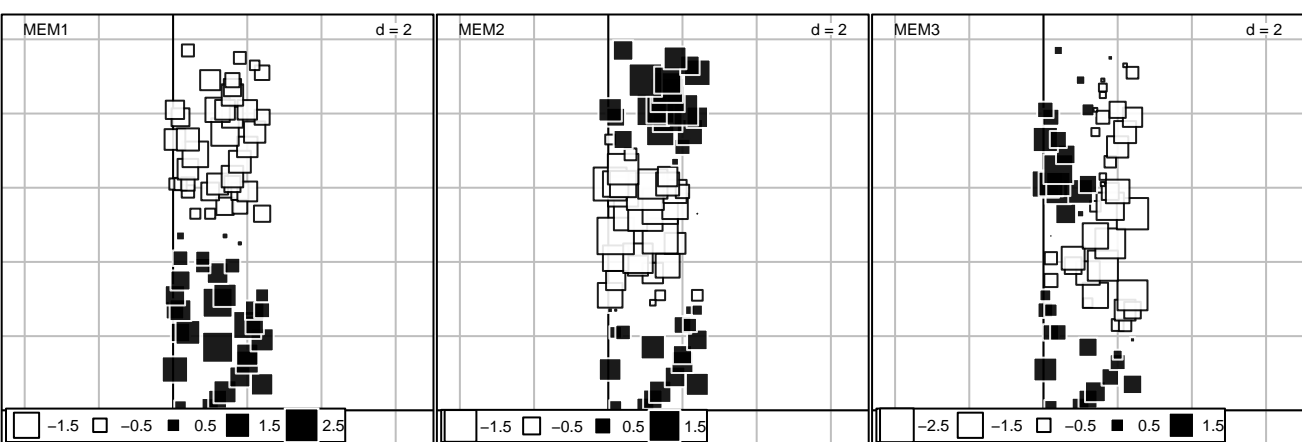
help("listw.candidates")



`help("listw.candidates")`



help("listw.candidates")



```
help("mem")
```

MEM1



MEM2



MEM3



MEM4

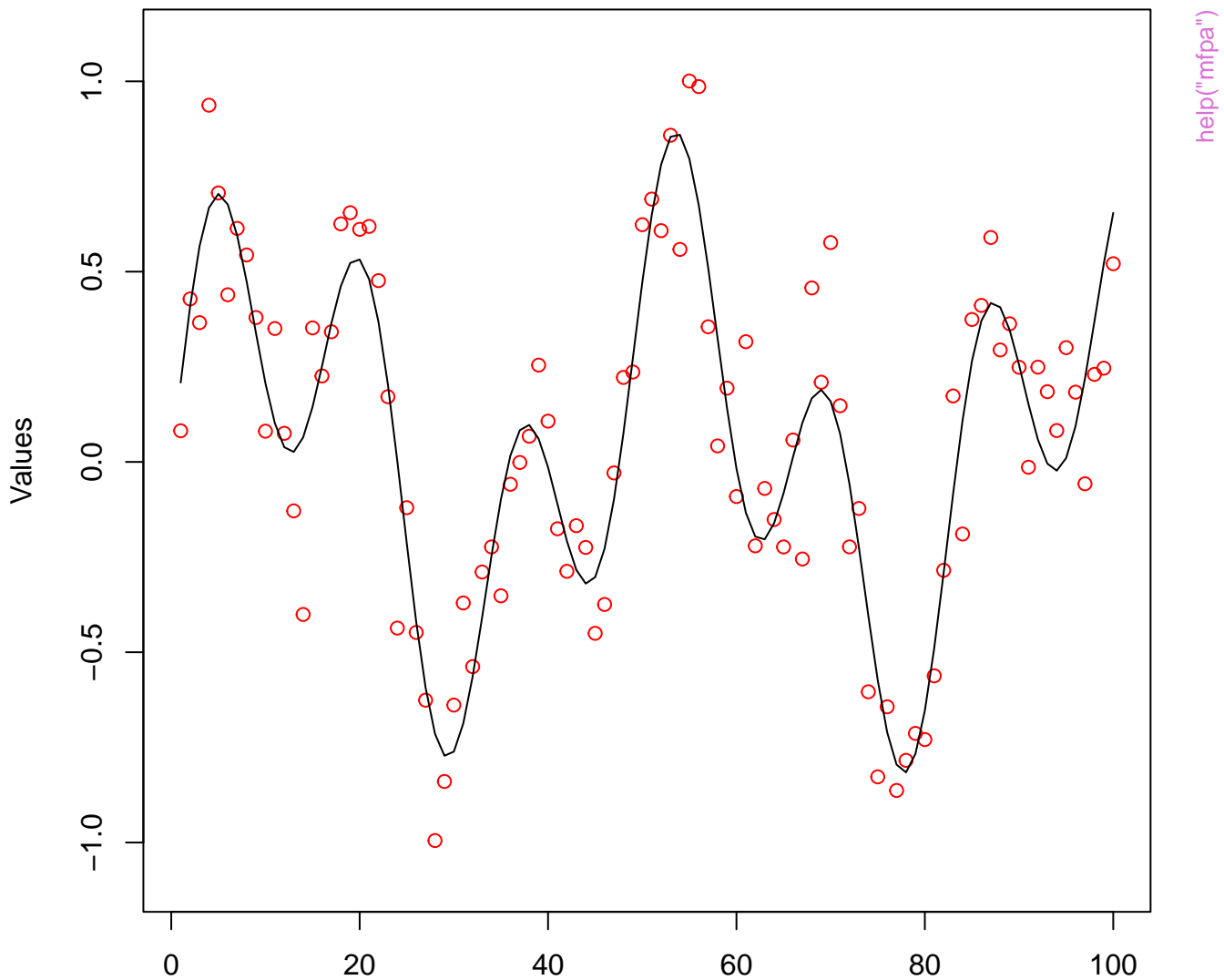


MEM5



MEM6





Values

-1.0
-0.5
0.0
0.5
1.0

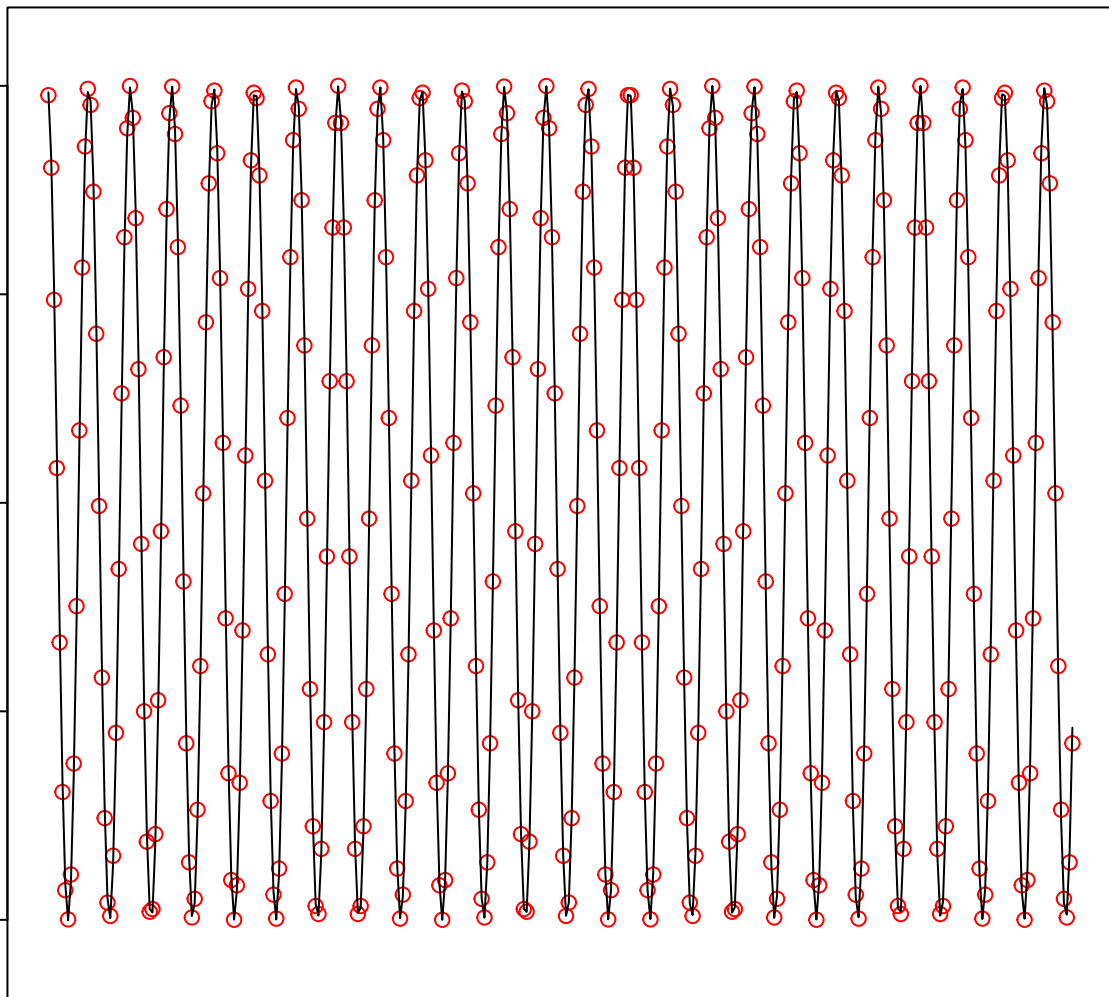
0

100

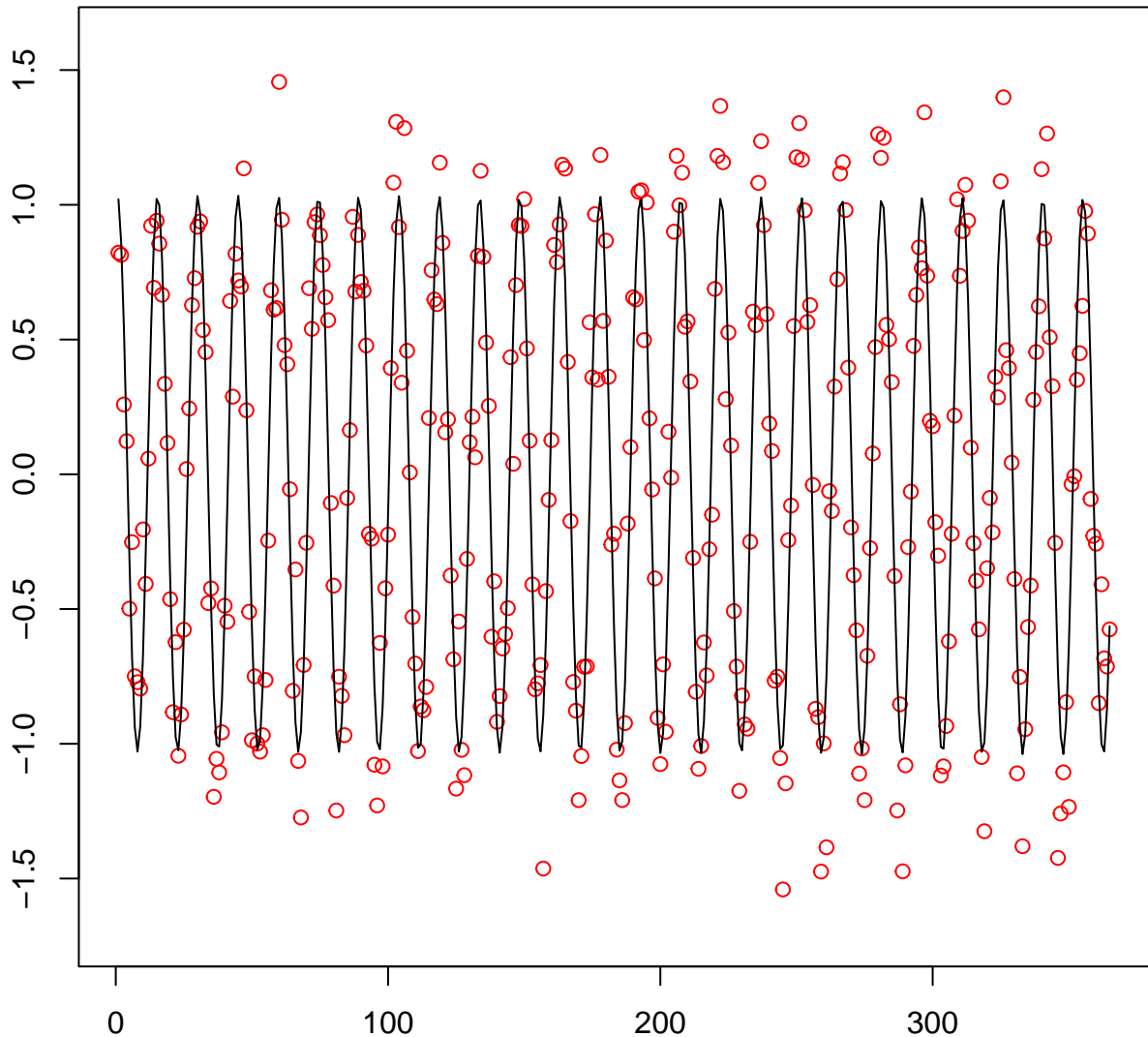
200

300

help("mfpa")



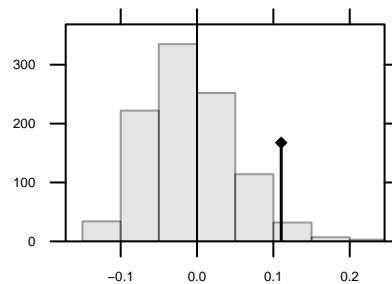
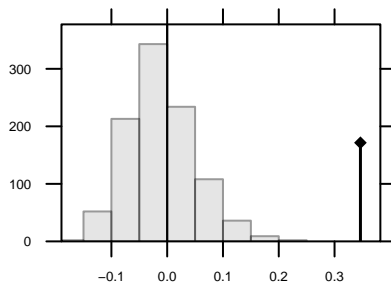
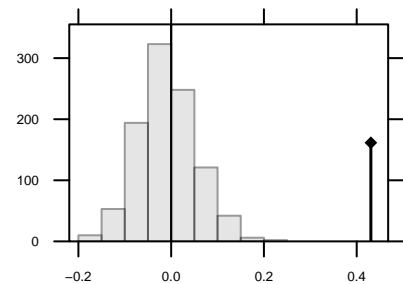
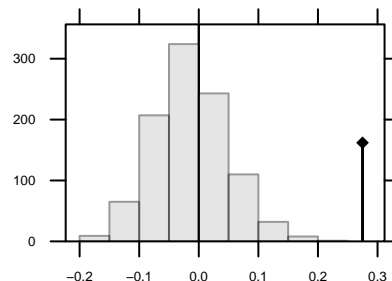
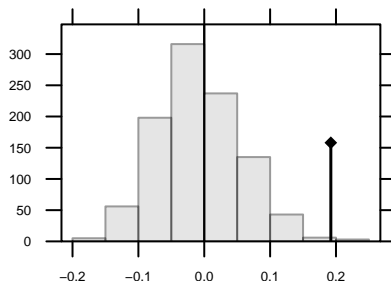
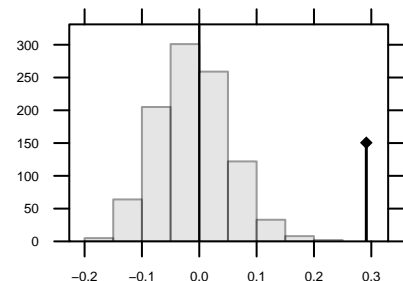
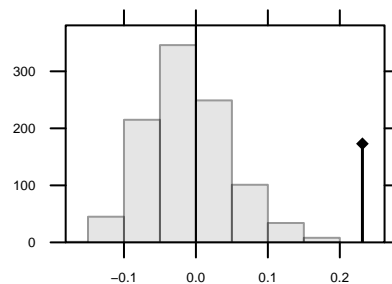
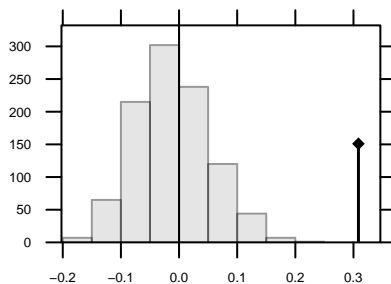
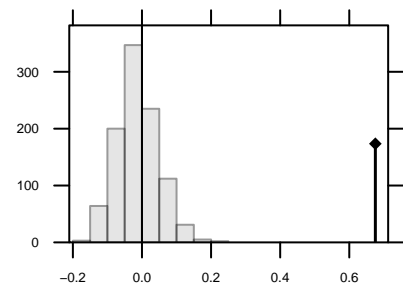
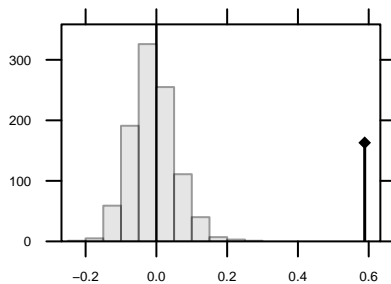
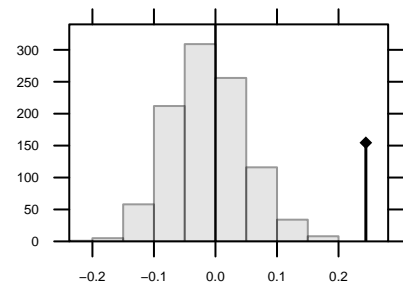
Values

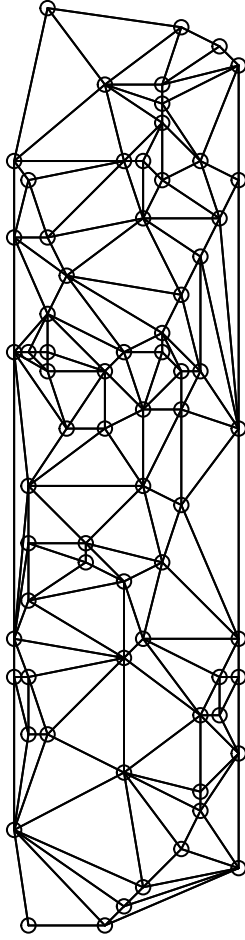


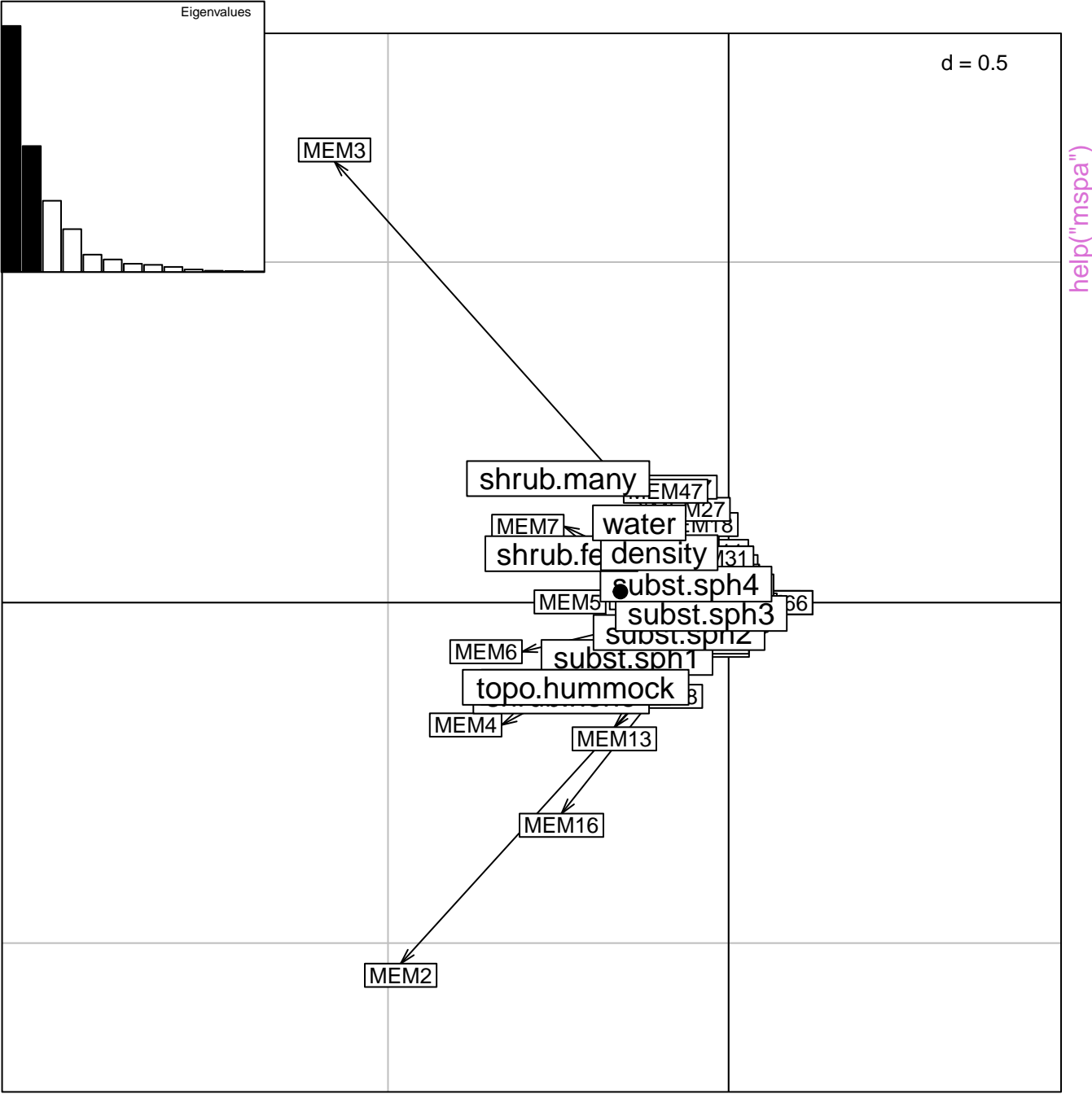
help("mfpa")

Clay**Silt****Sand**

help("morand.randtest")

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





Eigenvalues

d = 0.2

help("mspa")

Trimalaco2

Oppia.minus

Stegana

Ceratoz3

MEM1

LRUG

Epidozetes

Minigalumna

MEM5

SUCT

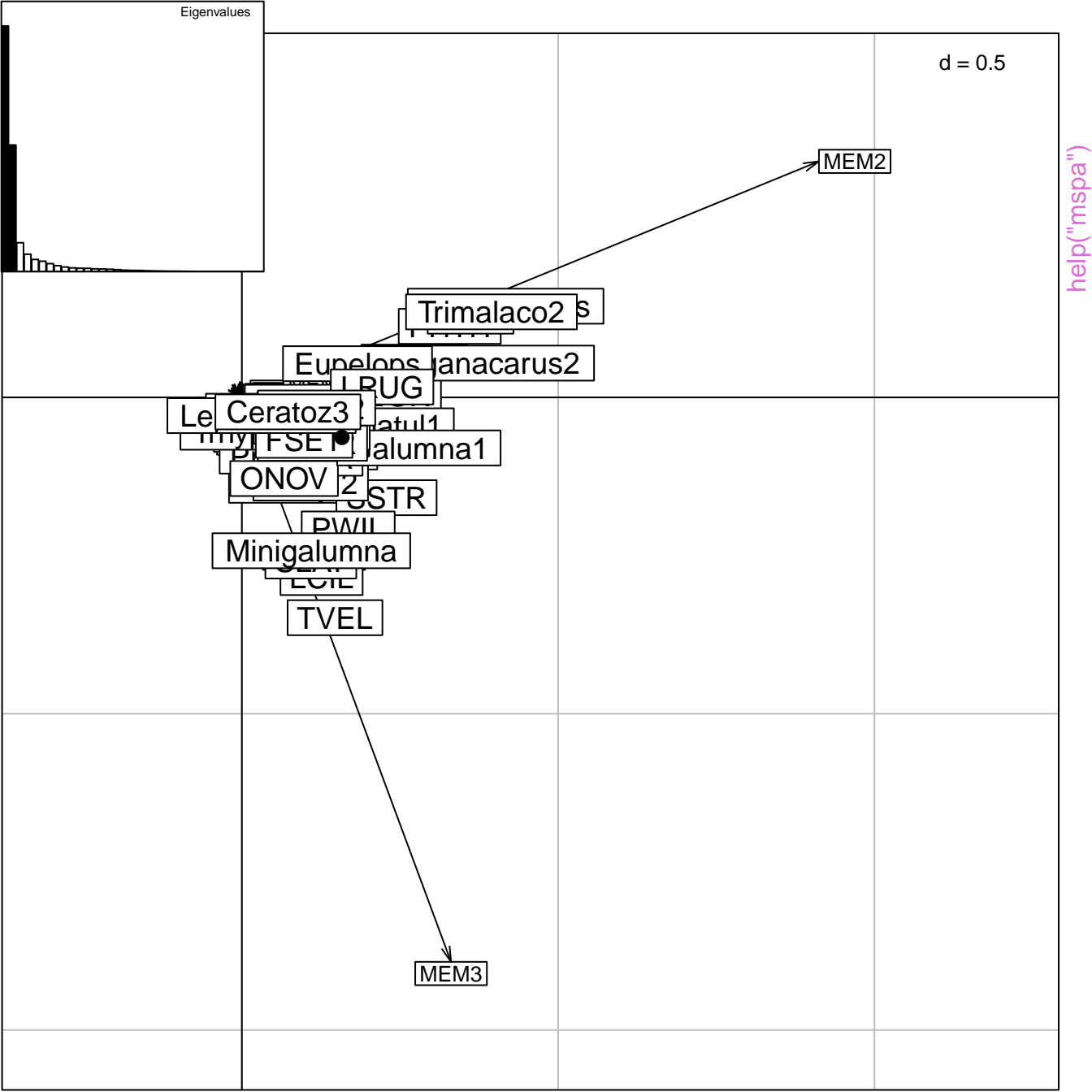
MEM2

LCIL

TVEL

MEM4

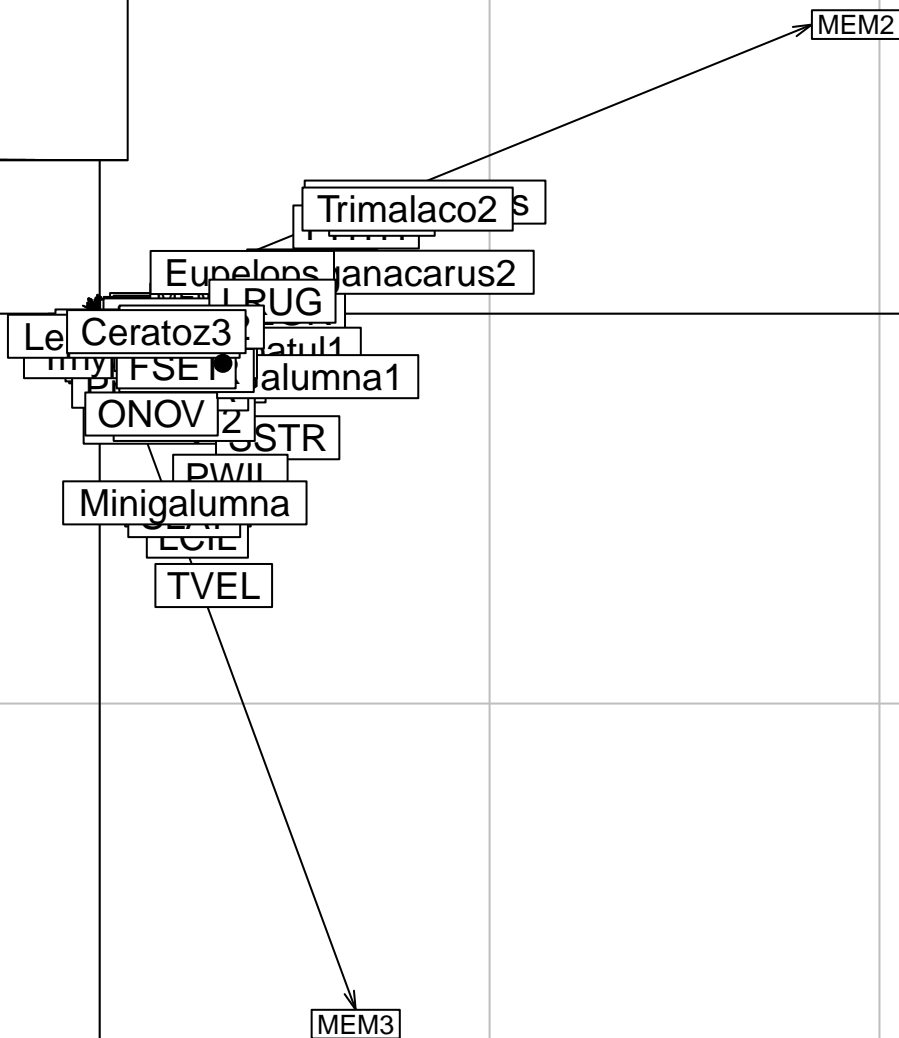
MEM3



Eigenvalues

d = 0.5

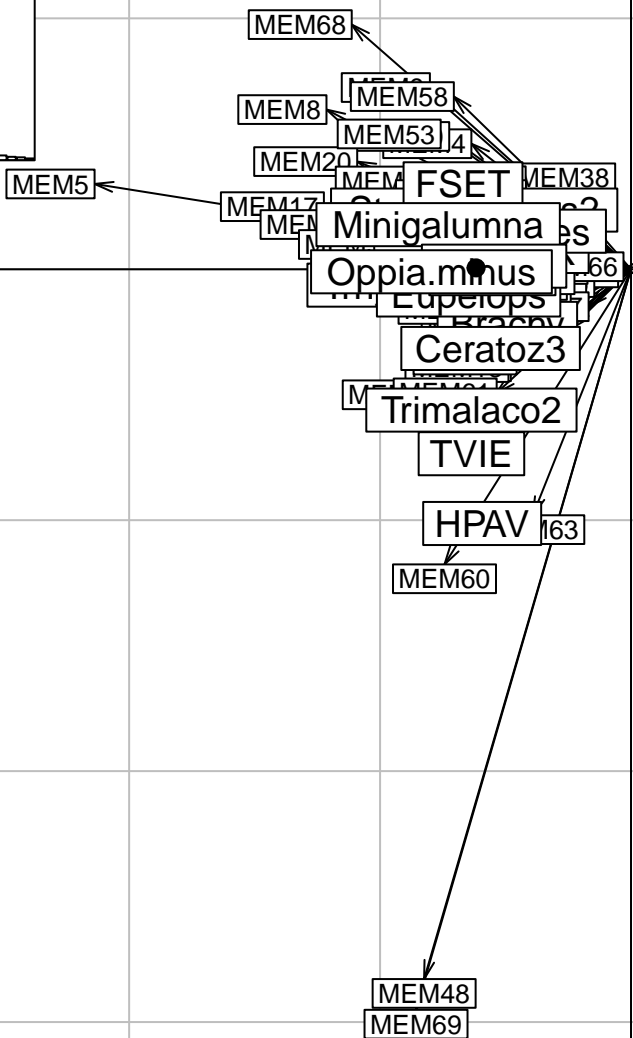
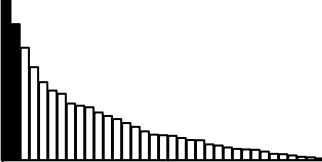
help("mspa")



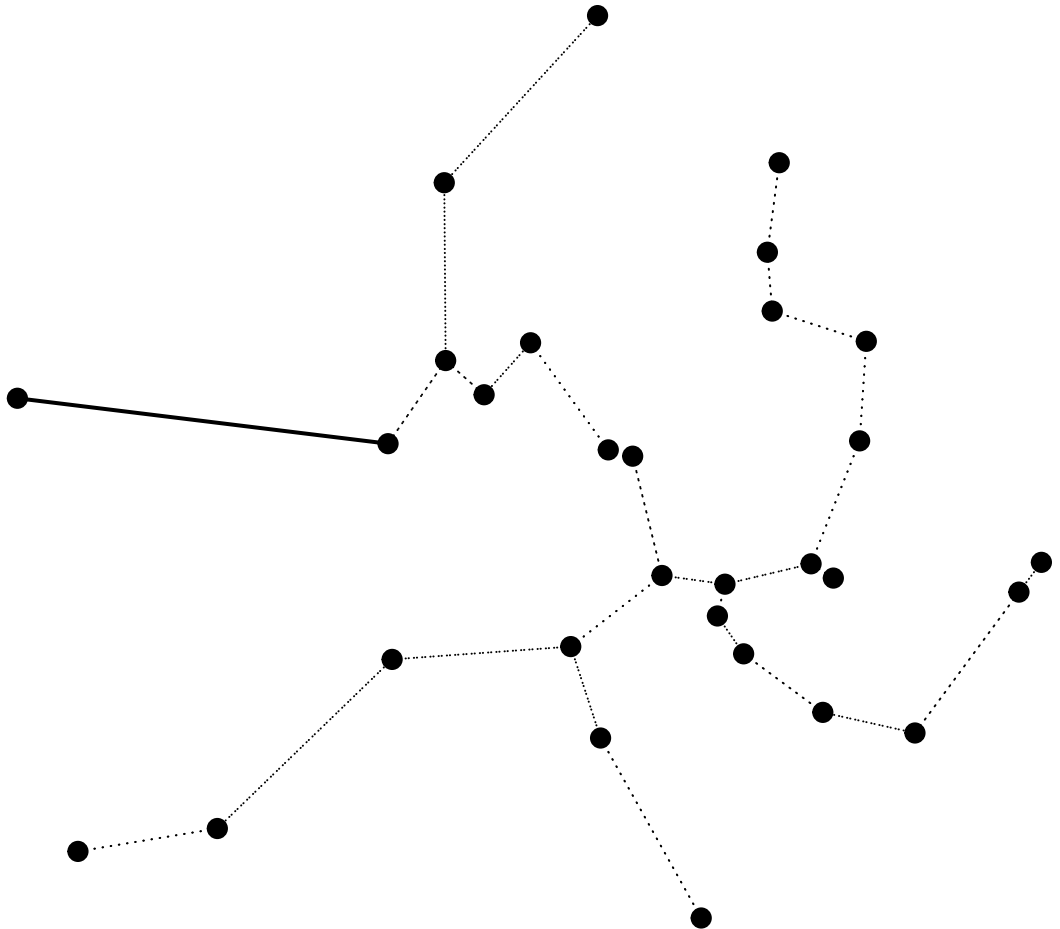
Eigenvalues

d = 0.2

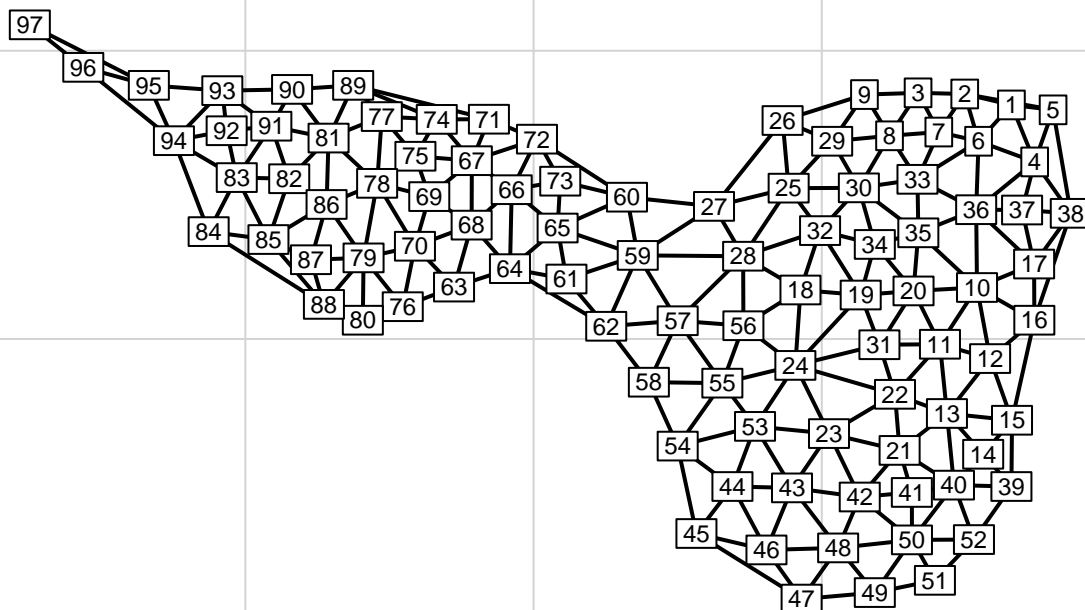
help("mspa")



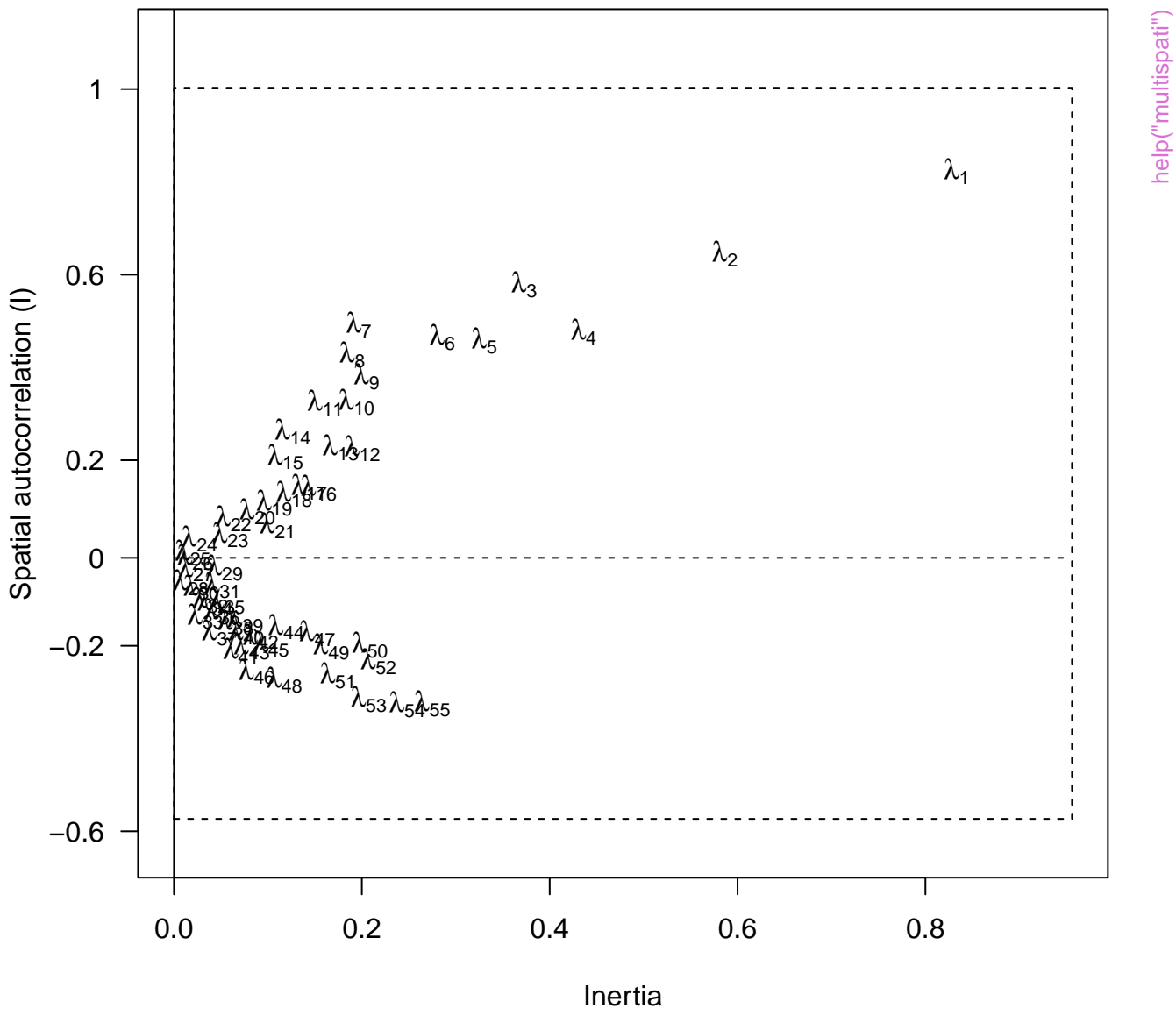
Maximum distance of the minimum spanning tree in bold

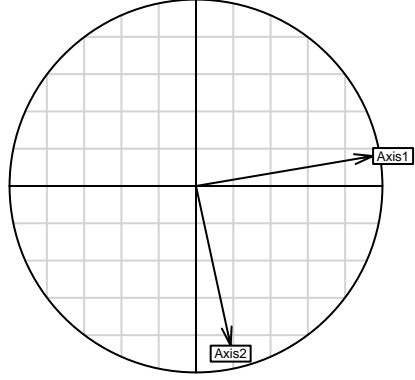
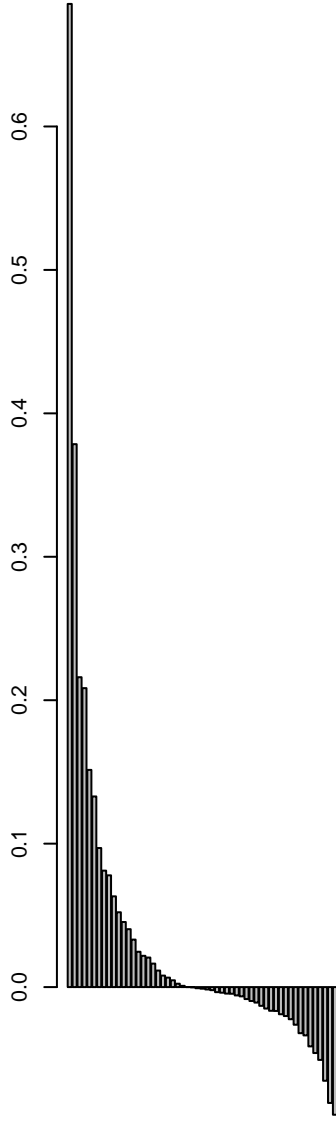
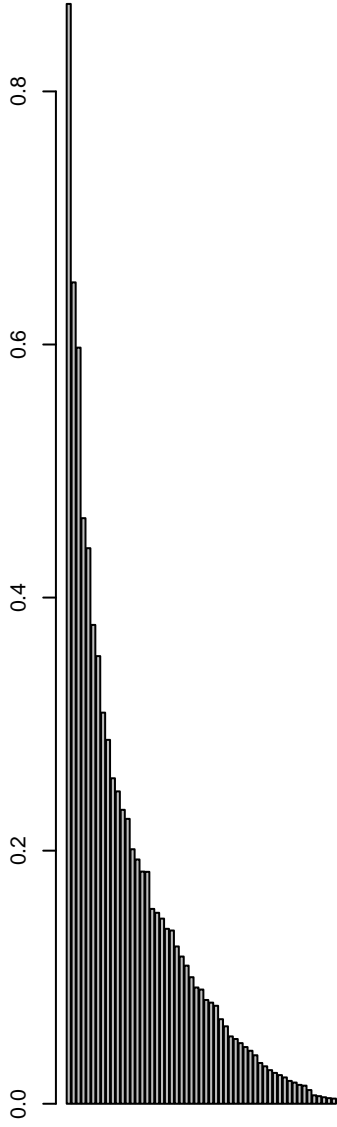


```
help("mst.nb")
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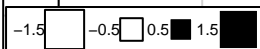
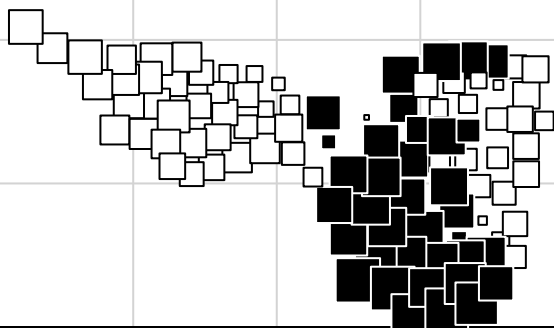


Spatial and inertia components of the eigenvalues

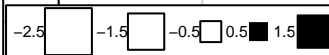
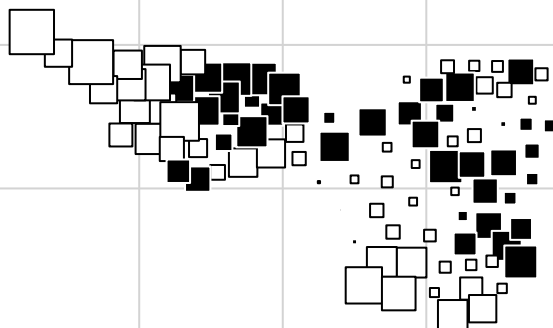




d = 100

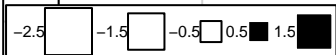
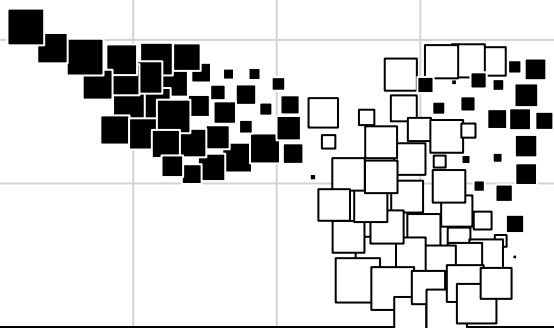


d = 100

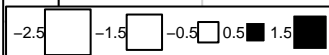
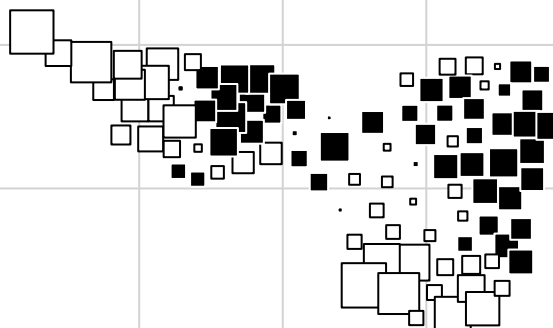


help("multispati

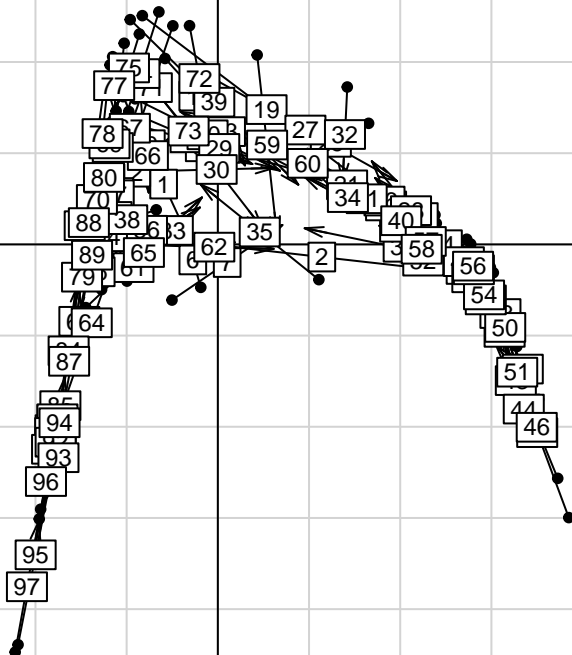
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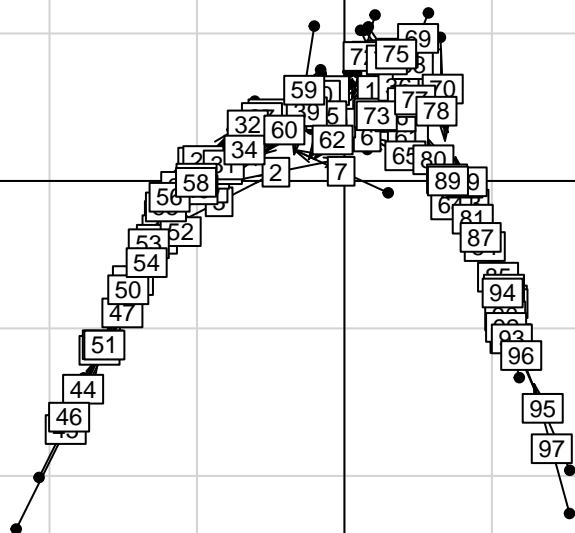
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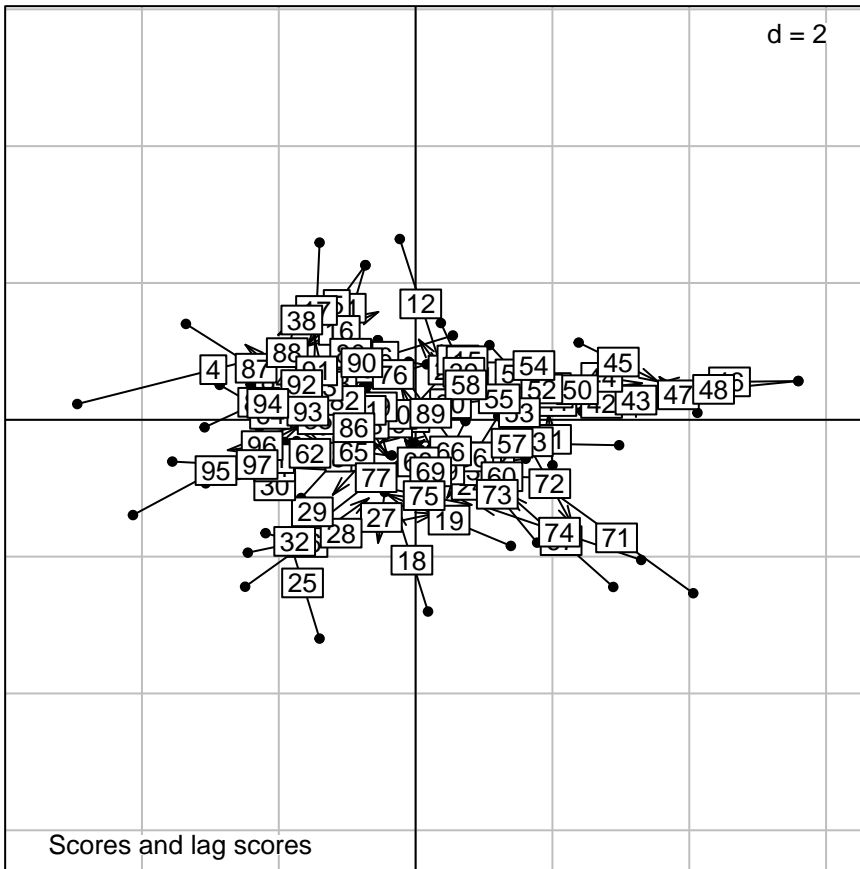
d = 0.5



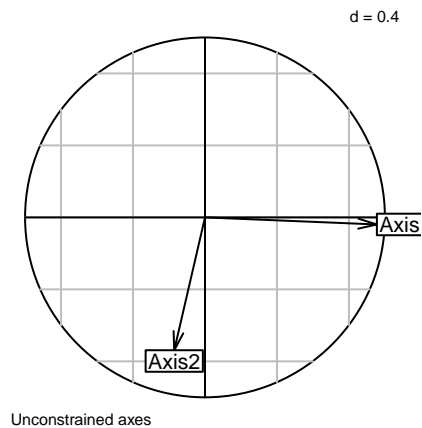
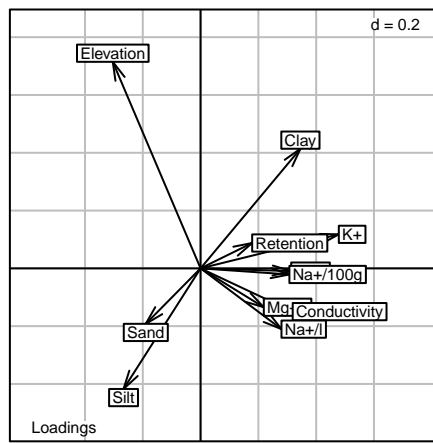
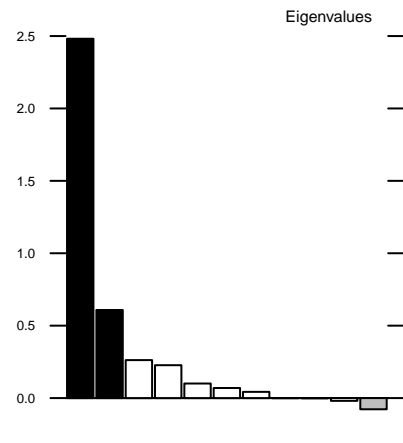
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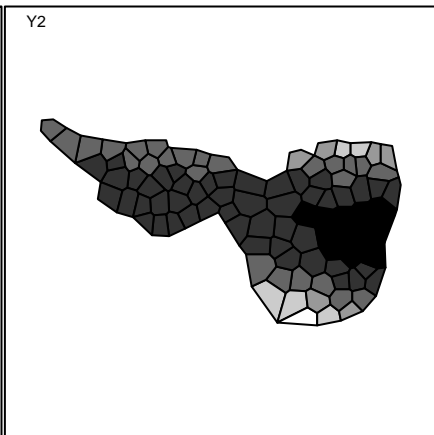
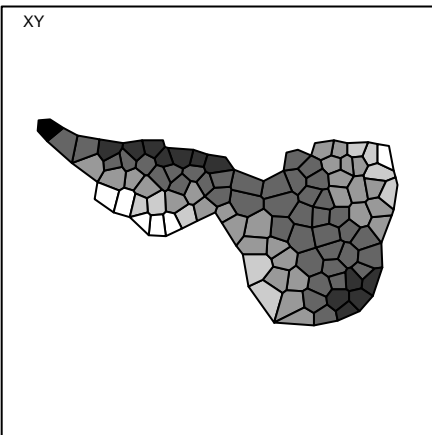
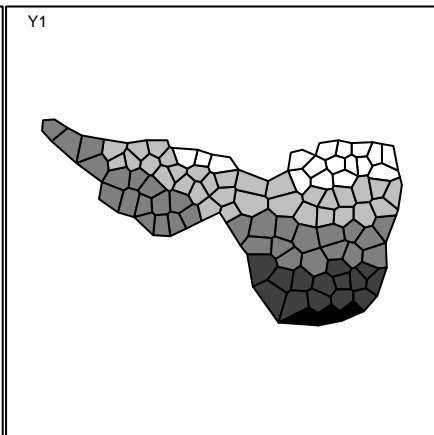
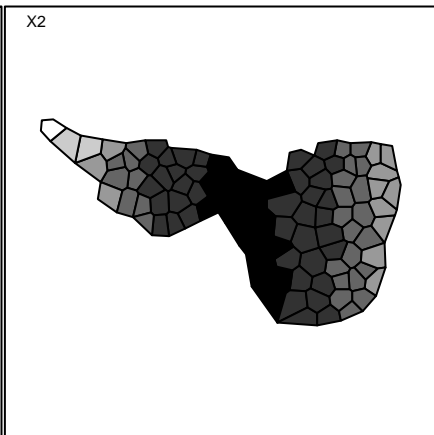
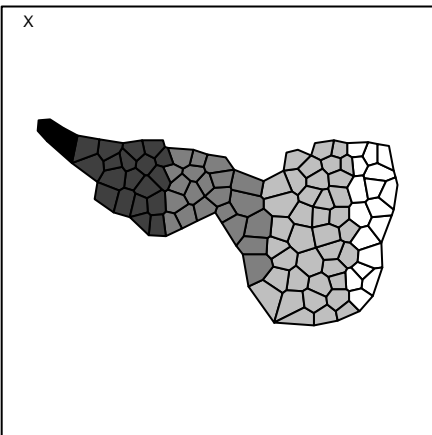


[help\("multispc"\)](#)

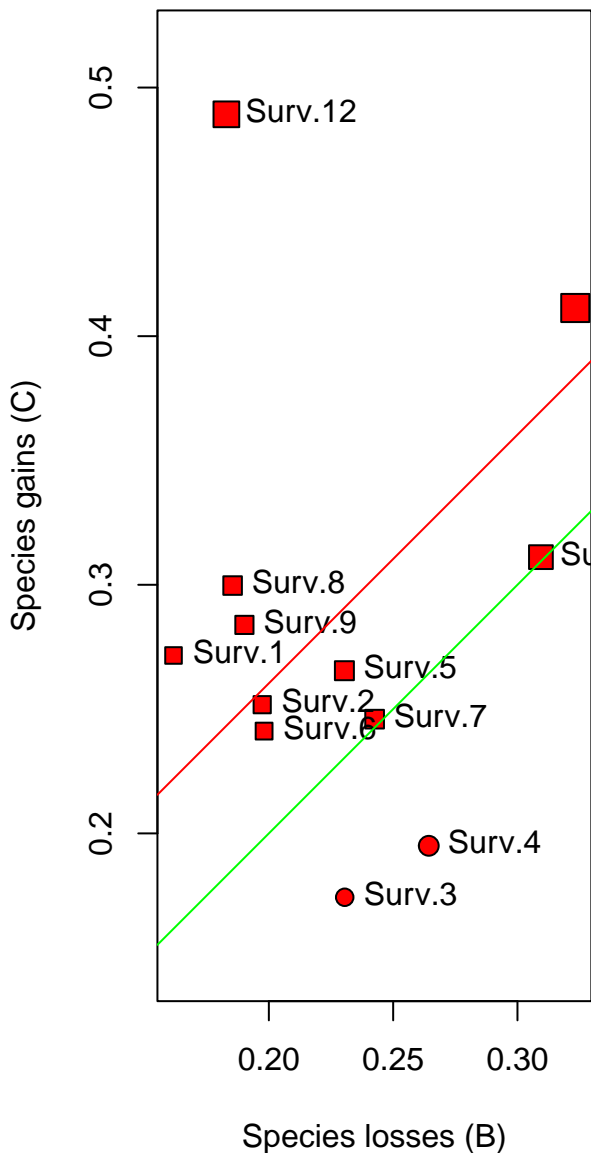


help("multispati")

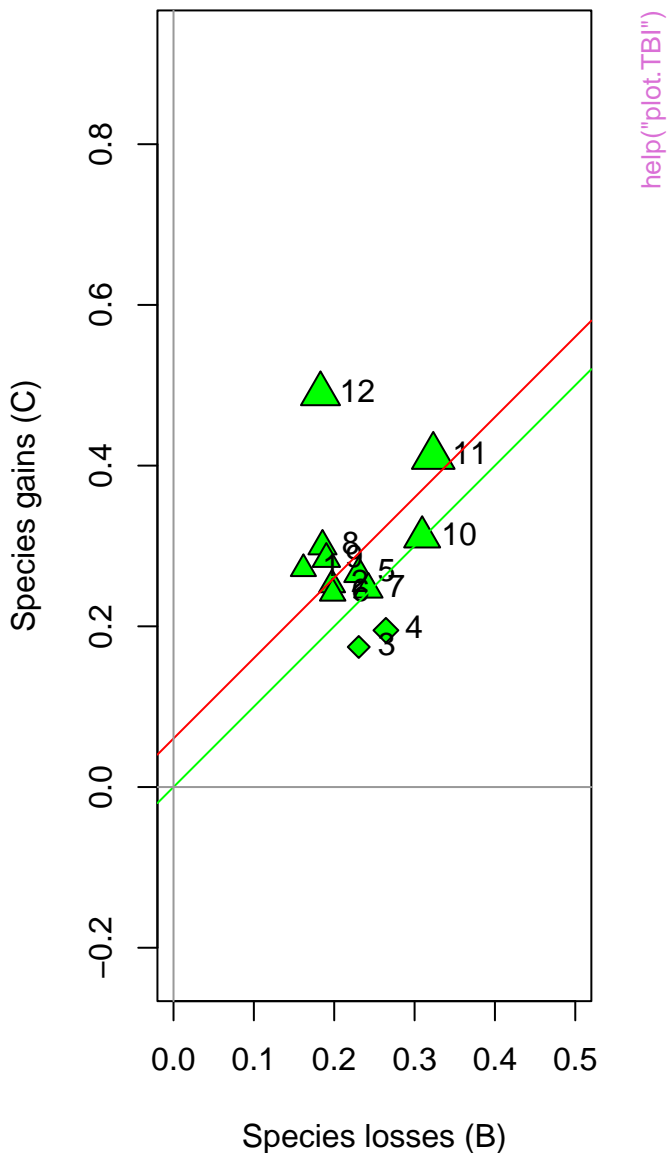




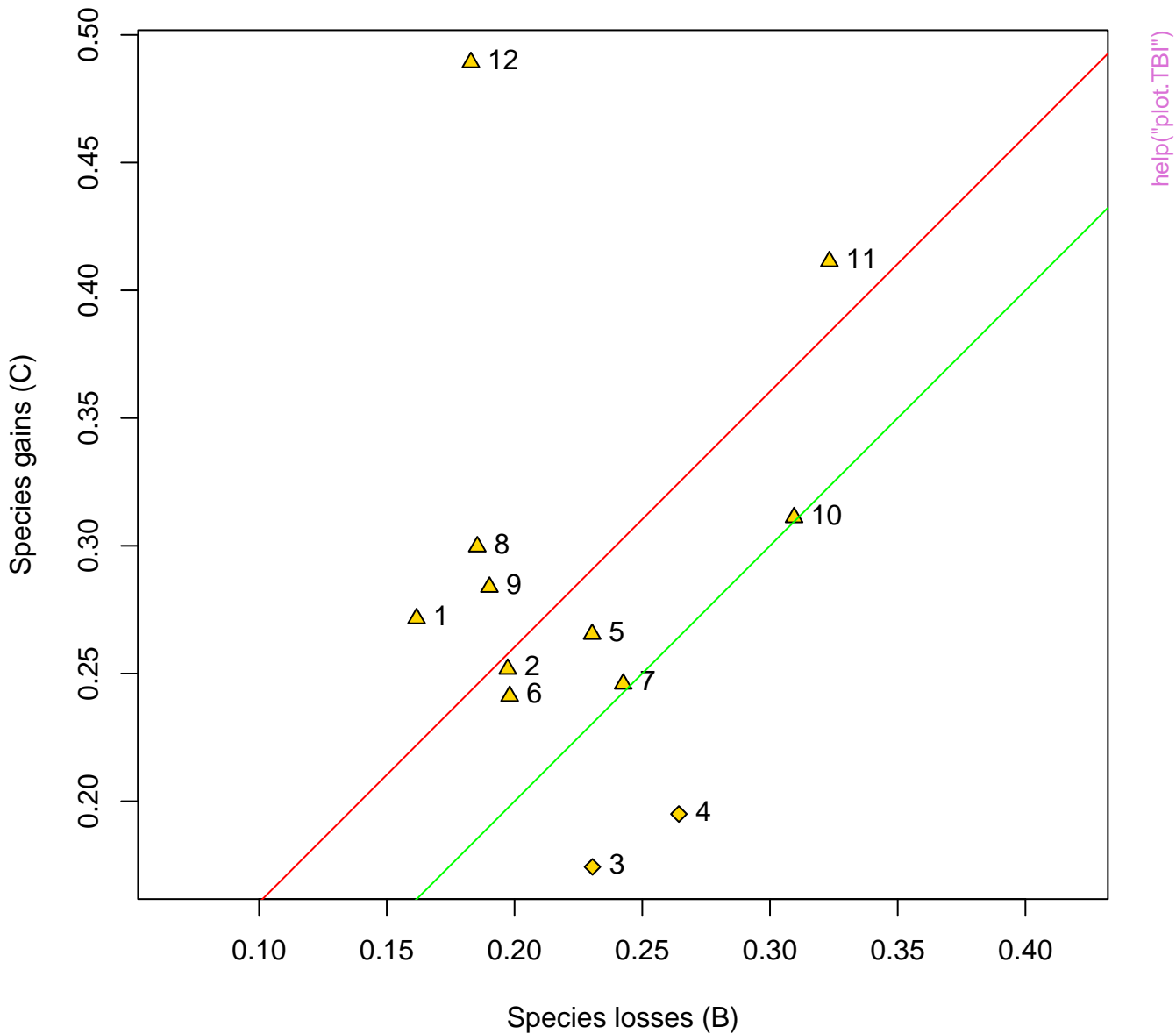
B-C plot, Pyrifos, surveys 4 & 11



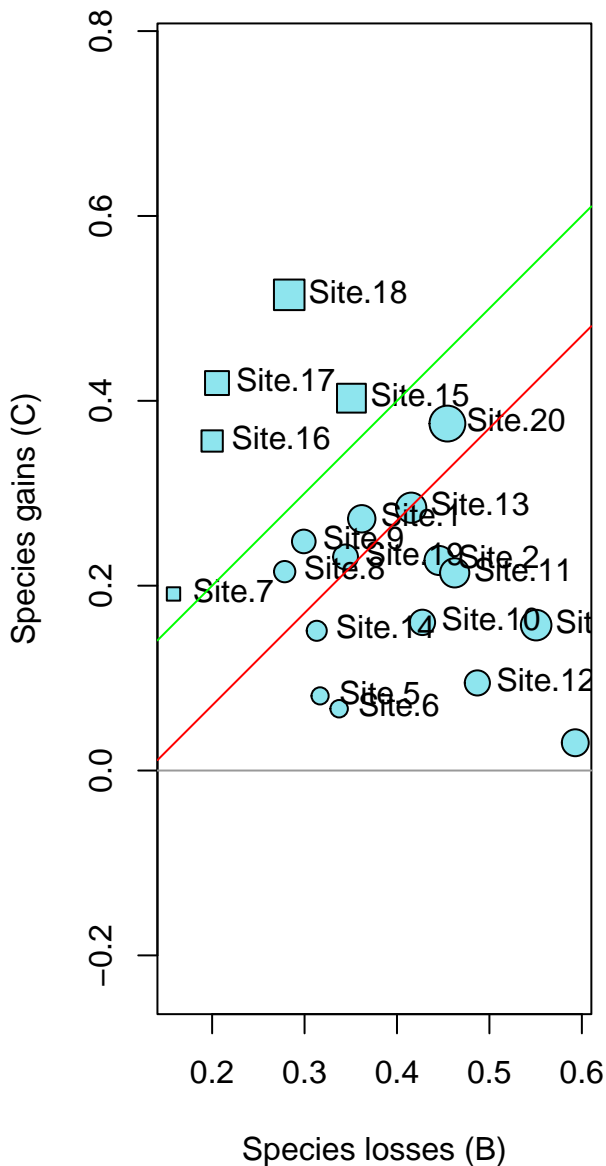
B-C plot, Pyrifos, surveys 4 & 11



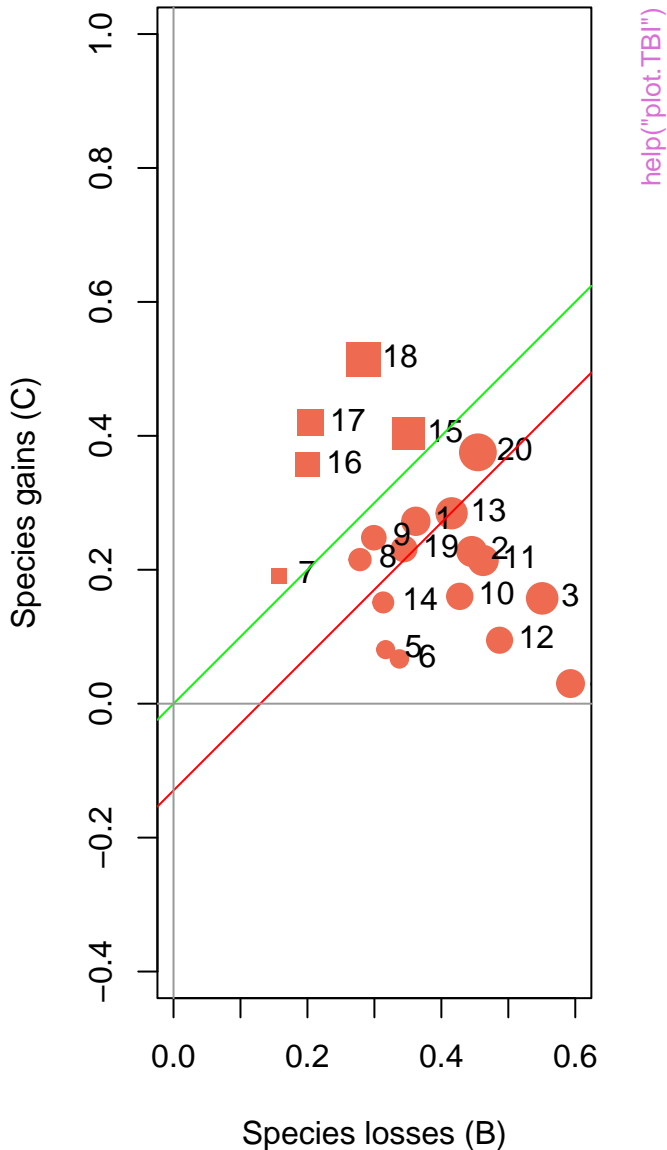
B-C plot, Pyrifos, surveys 4 & 11



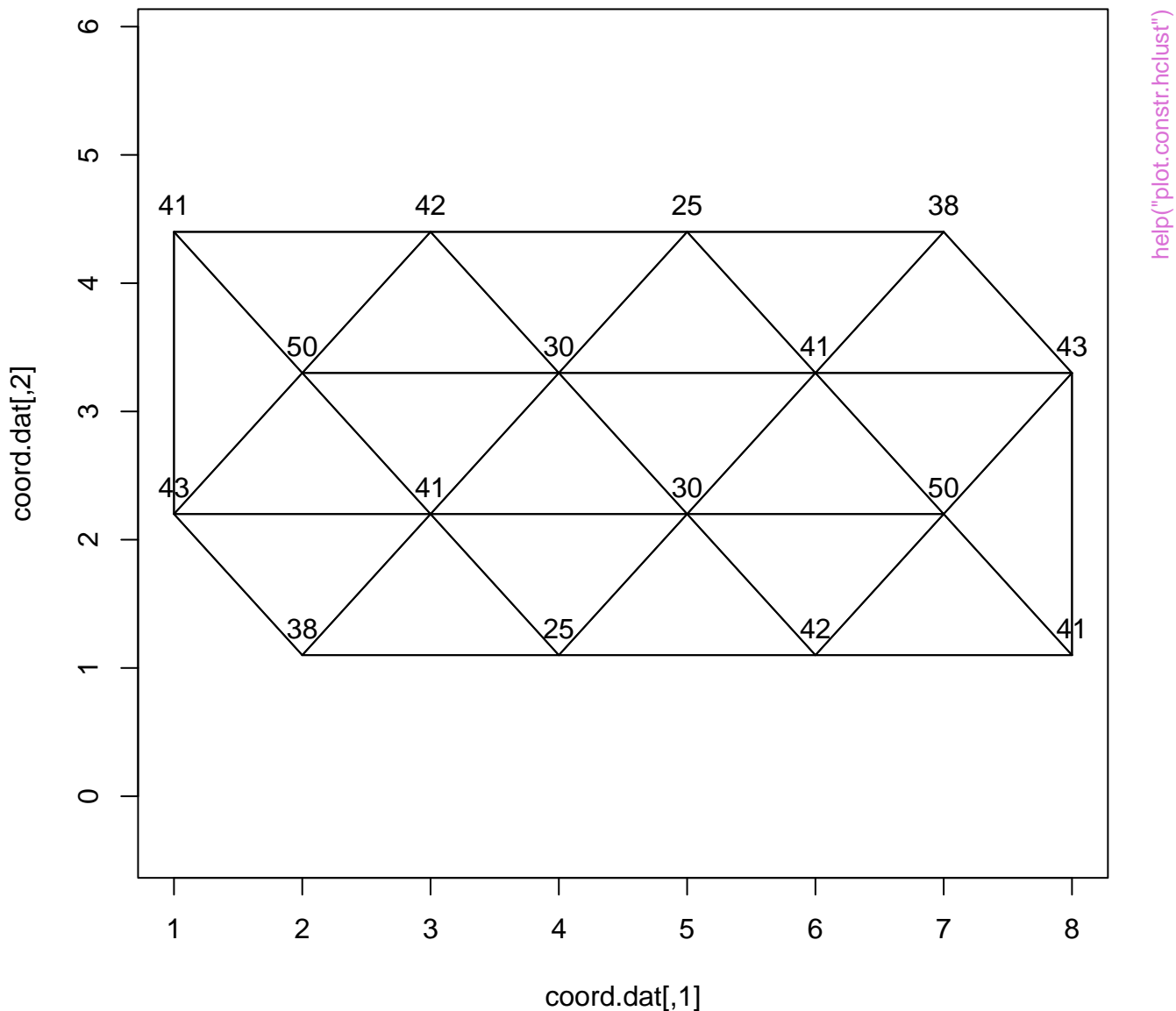
B-C plot, Mite data

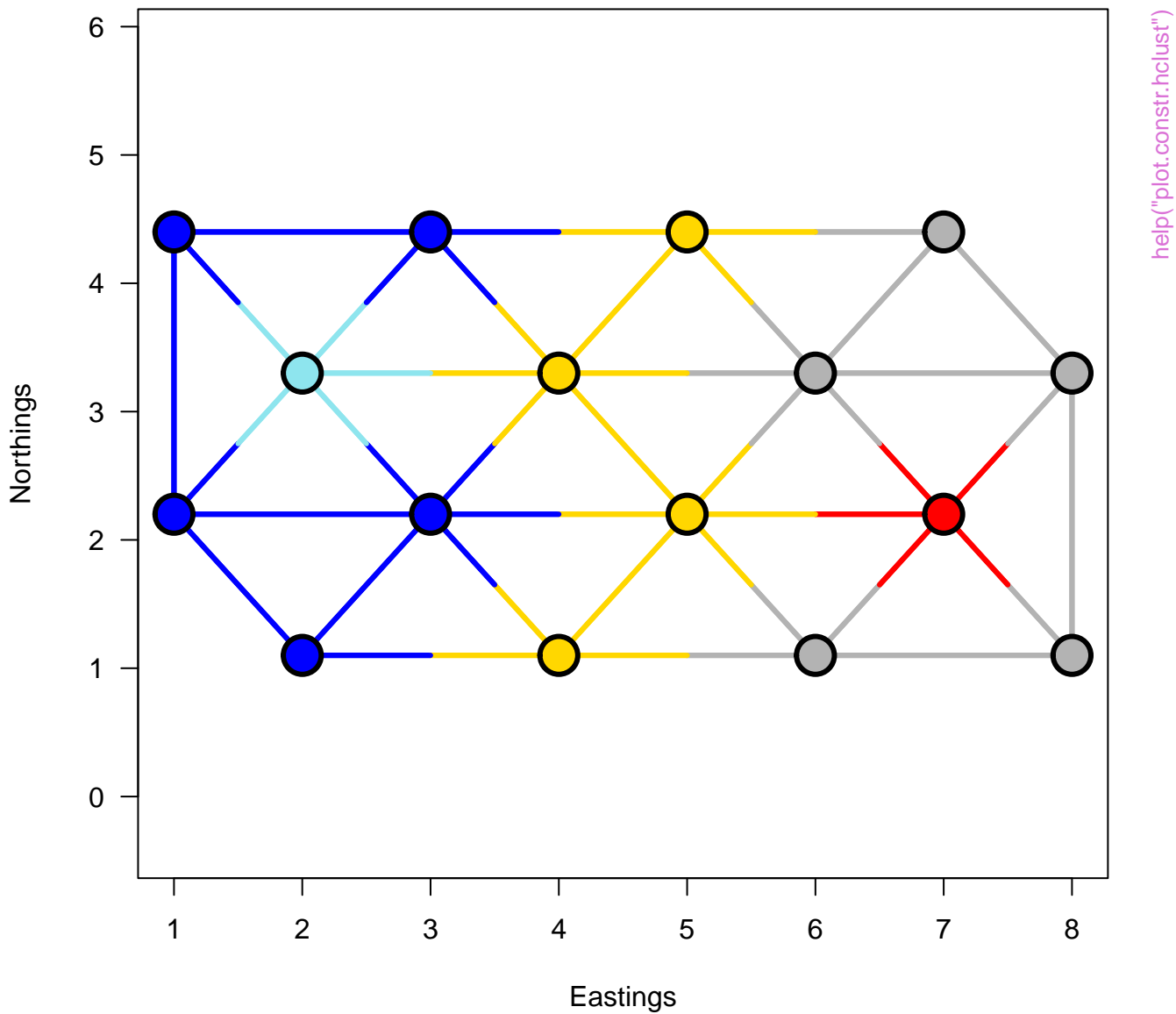


B-C plot, Mite data

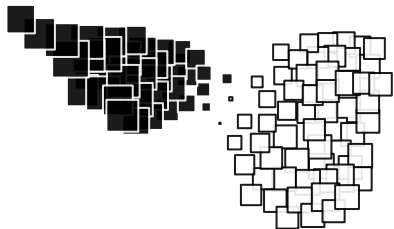


Delaunay triangulation

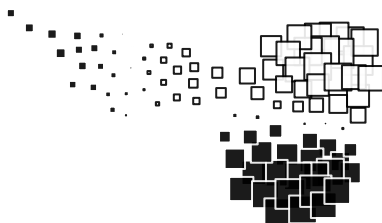




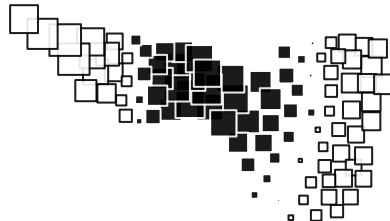
MEM1



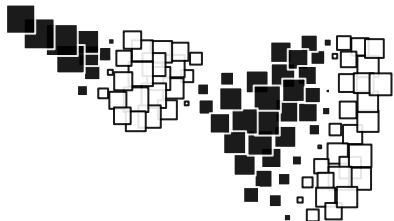
MEM2



MEM3



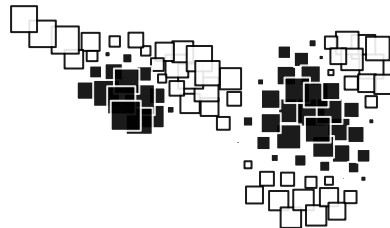
MEM4



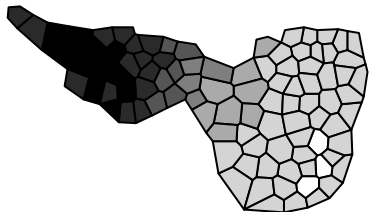
MEM5



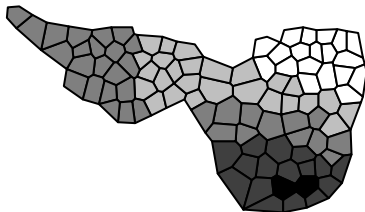
MEM6



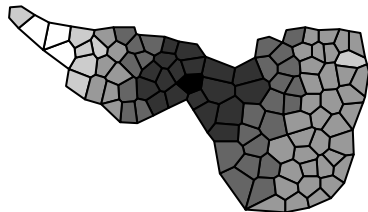
MEM1



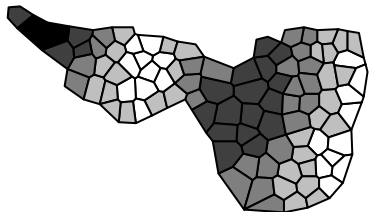
MEM2



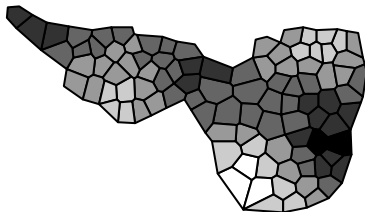
MEM3



MEM4



MEM5



MEM6

