

```

library(ggcor)
library(devtools)
library(ggplot2)
library(dplyr)
library(scales)
library(ggpubr)
library(ggsci)
library(RColorBrewer)
spec <- read.delim('algae-abundance.txt',row.names = 1,header = T,check.names = F)
spec<-as.data.frame(t(spec))
myenv <- read.delim('environment.txt',row.names = 1,check.names = F)
env1<- fortify_cor(myenv,method = 'spearman',cor.test = TRUE, type = "upper",
+                 show.diag = TRUE,cluster.type = "all")
There were 50 or more warnings (use warnings() to see the first 50)
write.table(env1,'env_spearman.txt',row.names = F,sep = '\t',quote = F)
mylist<-as.list(colnames(spec))
names(mylist)<-colnames(spec)
mantel <- mantel_test( spec,myenv,
+                       spec.dist.method = "euclidean",#bray
+                       env.dist.method = "euclidean",
+                       spec.select = mylist,
+                       mantel.fun = "mantel.randtest") %>%
+   mutate(rd=cut(r,breaks = c(-Inf,0,0.25,0.5,Inf),
+                     labels = c('<0','<0.25','<0.5','>=0.5')),
+          rsize=cut(r,breaks = c(-Inf,0,0.25,0.5,Inf),
+                     labels = c('<0','<0.25','<0.5','>=0.5')),
+          P_value=cut(p.value,breaks = c(-Inf,0.001,0.01,0.05,Inf),
+                      labels = c('<0.001','<0.01','<0.05','>=0.05'))))
write.table(mantel,'mantle_test-algae.txt',row.names = F,sep = '\t',quote = F)
factor(mantel$rsize)
  [1] <0      <0.25 <0.25 <0.25 <0.5  <0.25 <0      <0.25 <0      <0      <0      <0
<0.25 <0      <0.25 <0      <0      <0
 [20] <0.25 <0.25 <0      <0      <0      <0      <0      <0      <0      <0      <0.25
<0.25 <0      <0      <0.25 <0      <0      <0
 [39] <0.25 <0      <0.25 <0      <0      <0.25 <0      <0.25 <0      <0      <0.25 <0.25 <0
<0      <0.25 <0.25 <0.25 <0.25 <0.25
 [58] <0.25 <0      <0      <0      <0.25 <0.5  <0.25 <0      <0.5  <0.5  >=0.5 <0
<0.25 <0      <0      <0.25 <0      <0      <0.25
 [77] <0      <0.25 <0      <0.25 <0.25 <0      <0      <0      <0.25 <0      <0      <0
<0      <0      <0.25 <0      <0      <0      <0.25
 [96] <0      <0      <0      <0.25 <0      <0      <0      <0.25 <0.25 <0      <0.25 >=0.5
<0.5  <0.25 <0      <0      <0.25 <0      <0
[115] <0      <0.25 <0.25 <0.25 <0      <0.25 <0      <0      <0.25 <0.25 <0
<0.25 >=0.5 <0.5  <0.25 <0

```

Levels: <0 <0.25 <0.5 >=0.5

```
env1$.row.names<-factor(env1$.row.names,levels = colnames(myenv))
```

```
env1$.col.names<-factor(env1$.col.names,levels = colnames(myenv))
```

```
quickcor(env1,type = "upper",legend.position="right",axis.label.drop = FALSE) +
```

```
  geom_square() +
```

```
  geom_mark(data = get_data(type = "upper"),r = NA) +
```

```
  anno_link( aes(colour=P_value,size=rd),data = mantel, curvature = 0.2) +
```

```
  scale_size_manual(values = c(0.4,0.8,1.2,1.6),name="Mantel's R") +
```

```
  scale_colour_manual(values = c('#BA3A0E','#1F7E53','#50458C','#CCCCCC'),name='p  
value')+
```

```
  scale_fill_gradientn(colours = rev(brewer.pal(n=8,name='RdBu')),name="Spearman's r")
```

```
ggsave('step49.ggcor_test.pdf',width = 10,height = 7)
```

