

test_highlight

```
library(DOSE)
data(geneList)
library(enrichplot)
de <- names(geneList)[1:100]
x <- enrichDO(de)
x2 <- pairwise_termsim(x)
```

cnetplot 单组数据

```
highlight_category <- x2$Description[c(1,3,4)]

p1 <- cnetplot(x2, highlight_category = highlight_category, colorEdge = FALSE)

p2 <- cnetplot(x2, highlight_category = highlight_category, colorEdge = TRUE)

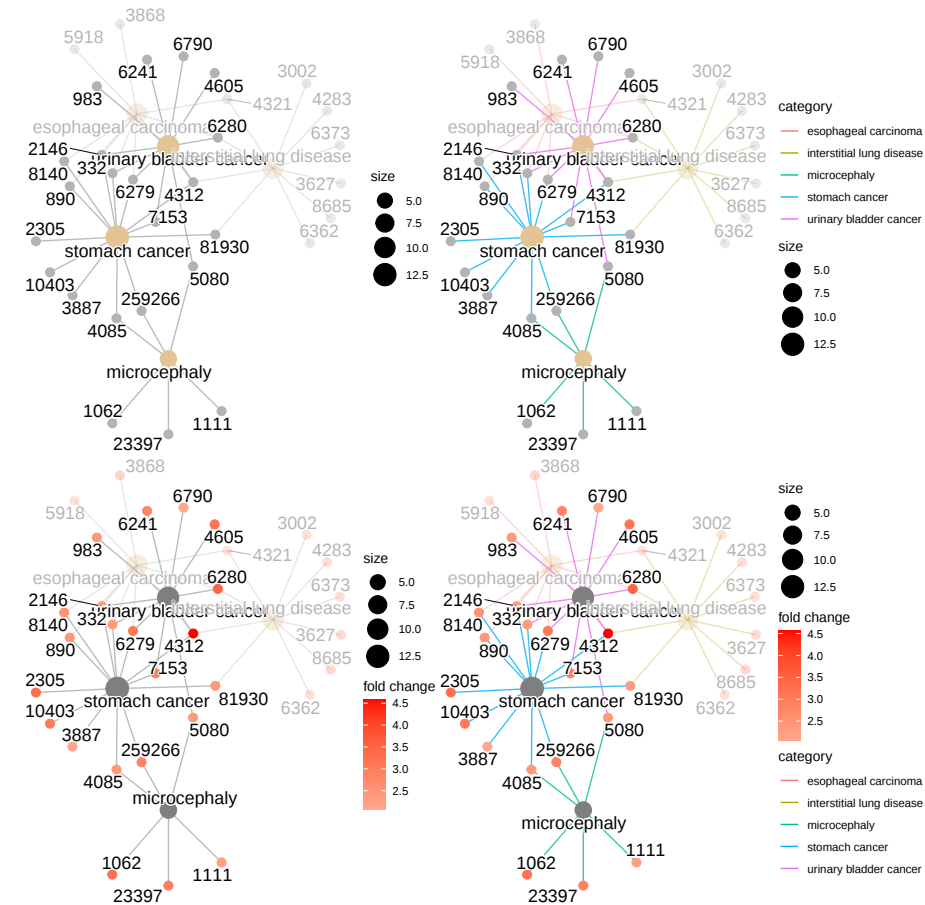
p3 <- cnetplot(x2, highlight_category = highlight_category, foldChange = geneList)

## Scale for 'size' is already present. Adding another scale for 'size', which
## will replace the existing scale.

p4 <- cnetplot(x2, highlight_category = highlight_category,
               foldChange = geneList, colorEdge = TRUE)

## Scale for 'size' is already present. Adding another scale for 'size', which
## will replace the existing scale.
```

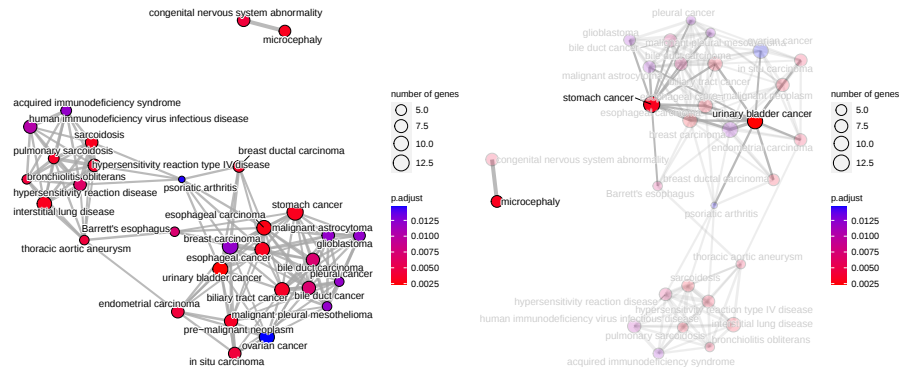
```
library(aplot)
plot_list(p1, p2, p3, p4)
```



emapplot 单组数据

```
p1 <- emapplot(x2, cex_label_category = 0.8)
p2 <- emapplot(x2, cex_label_category = 0.8,
               highlight_category = highlight_category,
               alpha_nohilight = 0.2)

library(aplot)
plot_list(p1, p2)
```



cnetplot 多组数据

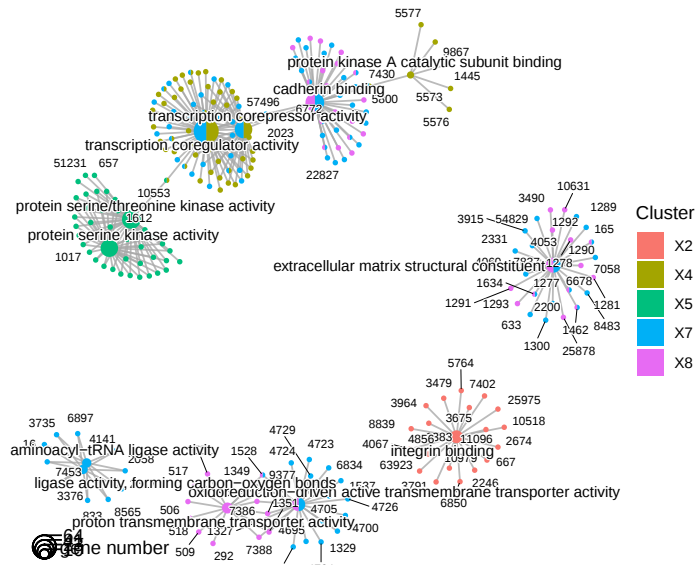
```
library(clusterProfiler)
library(DOSE)
library(org.Hs.eg.db)
data(gcSample)
xx <- compareCluster(gcSample, fun="enrichGO", OrgDb="org.Hs.eg.db")
xx2 <- pairwise_termsim(xx)
highlight_category <- xx2@compareClusterResult$Description[c(1,2)]

p1 <- cnetplot(xx2, showCategory = 3, cex_category = 1.3,
               cex_label_category = 1.3, cex_gene = 3)
p2 <- cnetplot(xx2, showCategory = 3, cex_category = 1.3,
               highlight_category = highlight_category,
               cex_label_category = 1.3, cex_gene = 3)

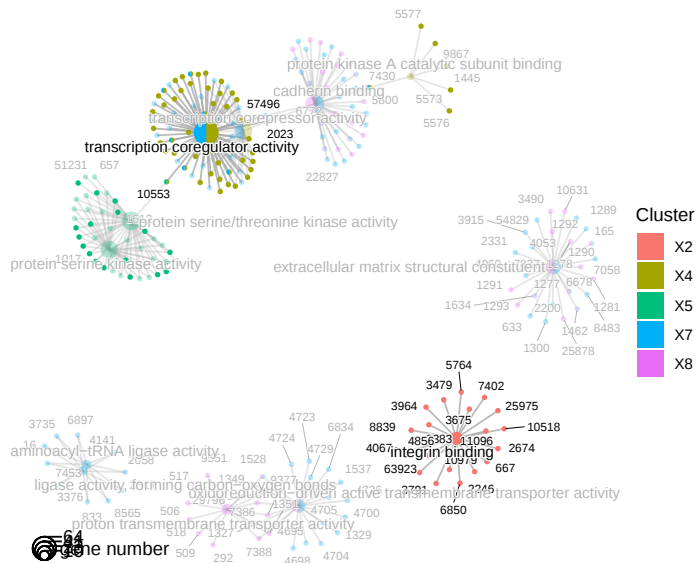
library(aplot)
plot_list(p1, p2, ncol = 1, labels = c("without highlight", "highlight"))
```

```
## Warning: ggrepel: 141 unlabeled data points (too many overlaps). Consider increasing
## ggrepel: 141 unlabeled data points (too many overlaps). Consider increasing max.over
```

without hilight



hilight



emapplot 多组数据

```
p1 <- emapplot(xx2, showCategory = 3)
p2 <- emapplot(xx2, showCategory = 3, highlight_category = highlight_category)
library(aplot)
plot_list(p1, p2)
```

