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library (vegan)
data (dune)

# single link
single <- hclust (vegdist (dune), method = 'single')
complete <- hclust (vegdist (dune), method = 'complete')
average <- hclust (vegdist (dune), method = 'average')

png ('classification-single-complete-average.png', width = 12, height = 4,
units = 'in', res = 300)
par (mfrow = c(1,3))
plot (as.dendrogram (single), main = 'Bray-Curtis distance\nSingle linkage',
ylim = c(0,1))
plot (as.dendrogram (complete), main = 'Bray-Curtis distance\nComplete
linkage', ylim = c(0,1))
plot (as.dendrogram (average), main = 'Bray-Curtis distance\nAverage linkage
(UPGMA)', ylim = c(0,1))
dev.off ()

png ('classification-single-complete-average_vertical.png', width = 4,
height = 12, units = 'in', res = 300, pointsize = 16)
par (mfrow = c(3,1))
plot (as.dendrogram (single), main = 'Bray-Curtis distance\nSingle linkage',
axes = F)
plot (as.dendrogram (complete), main = 'Bray-Curtis distance\nComplete
linkage', axes = F)
plot (as.dendrogram (average), main = 'Bray-Curtis distance\nAverage linkage
(UPGMA)', axes = F)
dev.off ()

ward <- hclust (sqrt (vegdist (dune)), method = 'ward')
png ('classification-ward.png', width = 4, height = 4, units = 'in', res =
300)
plot (as.dendrogram (ward), main = "sqrt (Bray-Curtis distance)\nWard's
minimum variance method")
dev.off ()

# effect of transformation
danube.spe <- read.delim
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/data/danube.
spe.txt', row.names = 1)

single.nottransf <- hclust (vegdist (danube.spe), method = 'single')
single.transf <- hclust (vegdist (log1p (danube.spe)), method = 'single')
png ('classification-effect-of-transformation.png', width = 12, height = 6,
units = 'in', res = 300)
par (mfrow = c(1,2))
plot (as.dendrogram (single.nottransf), main = 'Species data [%]\n Bray-
Curtis distance\nSingle linkage', ylim = c(0,.6))
plot (as.dendrogram (single.transf), main = 'log1p (Species data [%])\nBray-
```

```
Curtis distance\nSingle linkage', ylim = c(0,.6))  
dev.off ()
```

From:

<https://www.davidzeleny.net/anadat-r/> - **Analysis of community ecology data in R**

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https://www.davidzeleny.net/anadat-r/doku.php/en:hier-agglom_rscript?rev=1554686526

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