Figures for Chapter 9

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```
fig9.1 <- function(plotit=TRUE){
    require(DAAG)
    aupoints <- cmdscale(audists)
    plot(aupoints, bty="n", xlab="", ylab="")
    labs <- rownames(aupoints)
    labpos <- rep(1, length(labs))
    labpos[labs=="Melbourne"] <- 3
    labpos[labs=="Canberra"] <- 4
    text(aupoints, labels=labs, xpd=TRUE, pos=labpos)
}

comparePhysical <- function(lat=aulatlong$latitude,
                            long=aulatlong$longitude,
                            x1=aupoints[,1], x2 = aupoints[,2],
                            wts=NULL){
    ## Get best fit in space of (latitude, longitude)
    if(is.null(wt))wt <- rep(1,length(x1))
    fitlat <- predict(lm(lat ~ x1+x2, weights=wts))
    fitlong <- predict(lm(long ~ x1+x2, weights=wts))
    x <- as.vector(rbind(lat, fitlat, rep(NA,10)))
    y <- as.vector(rbind(long, fitlong, rep(NA,10)))
    lines(x, y, col="gray40", lwd=3)
}

fig9.2 <- function(){
    if(!require(oz))stop("Package 'oz' must be installed")
    points(aulatlong, col="red", pch=16, cex=1.5)
    comparePhysical()
}

fig9.3 <- function(){
    library(MASS)
    if(!require(oz))stop("Package 'oz' must be installed")
    aupoints.sam <- sammon(audists, trace=FALSE)
    oz()
    points(aulatlong, col="red", pch=16, cex=1.5)
```

```
    wt <- apply(as.matrix(audists), 1,function(x)sum(1/x[x>0]))
    comparePhysical(x1=aupoints.sam$points[,1],
                      x2 = aupoints.sam$points[,2], wts=wt)
}

fig9.4A <- function(seed=47){
    if(!require(DAAGbio))stop("Package 'DAAGbio' must be installed")
    if(!require(ape))stop("Package 'ape' must be installed")
    ## Calculate distances, using Kimura's K80 model
    primates.dist <- dist.dna(as.DNAbin(primateDNA), model="K80")
    primates.cmd <- cmdscale(primates.dist)
    eqscplot(primates.cmd, xlab="Axis 1", ylab="Axis 2", cex.lab=1.15)
    lefrt <- 2+2*(primates.cmd[,1] < mean(par()$usr[1:2]))
    text(primates.cmd[,1], primates.cmd[,2], row.names(primates.cmd),
        pos=lefrt)
}

fig9.4B <- function(seed=47){
    if(!require(DAAGbio))stop("Package 'DAAGbio' must be installed")
    if(!require(ape))stop("Package 'ape' must be installed")
    primates.dist <- dist.dna(as.DNAbin(primateDNA), model="K80")
    primates.cmd <- cmdscale(primates.dist)
    primates.mds <- isoMDS(primates.dist, primates.cmd, k=2, trace=FALSE)
    eqscplot(primates.mds$points, xlab="Axis 1", ylab="Axis 2",
            cex.lab=1.15)
    text(primates.mds$points[,1], primates.mds$points[,2],
        row.names(primates.mds$points), pos=lefrt)
}

fig9.5 <- function(){
    library(DAAG)
    pacific.dist <- dist(x = as.matrix(rockArt[-c(47,54,60,63,92),
                        28:641]), method = "binary")
    sum(pacific.dist==1)/length(pacific.dist)
    ## Now check that in all columns at least one distance < 1
    symmat <- as.matrix(pacific.dist)
    checksum <- sum(apply(symmat, 2, function(x) sum(x<1)))
    checksum <- sum(apply(symmat, 2, function(x) sum(x<1)==0))
    print(c("No of cols where all distances are one"=checksum))
    pacific.cmd <- cmdscale(pacific.dist)
    pacific.mds <- isoMDS(pacific.dist, pacific.cmd, trace=FALSE)
    plot(pacific.mds$points)
}

library(MASS)
library(DAAG)
library(latticeExtra)
```

fig9.1()
fig9.2()
fig9.3()
fig9.4A()
fig9.4B()
fig9.5()