Compare dxy of allopatric and sympatric species of piscivores and paedophages

Load package for plotting dots onto boxplot

```
require(beeswarm)
## Loading required package: beeswarm
```

Read in the dxy data of all pairwise comparisons of piscivores and paedophages

Note, the values of all chromosomes are listed as separate columns

```
dxy<-read.table("D:/Dropbox/victoriaGenomes/Dxy/pisci_paedo_allChr_dxy.txt",header=T)
```

Average across all sites of all chromosomes

```
## Compute the total number of pairwise differences across chromosomes
dxy$totalDiffs<-rowSums(dxy[,grepl(names(dxy),pattern="diffs")])

## Compute the total number of sites considered across chromosomes
dxy$totalCounts<-rowSums(dxy[,grepl(names(dxy),pattern="comparisons")])

## Compute dxy averaged across the entire genome
dxy$avg_dxy<-dxy$totalDiffs/dxy$totalCounts</pre>
```

Piscivores

```
grepl(dxy$pop2,pattern="pisc_Victoria")),]
## between Victoria North and Lake Kyoga
pisci_UganKyog_dxy<-dxy[(grepl(dxy$pop1,pattern="pisc_Vic_Uganda")&</pre>
                            grepl(dxy$pop2,pattern="pisc_Kyo")) |
                           (grepl(dxy$pop1,pattern="pisc_Kyo")&
                              grepl(dxy$pop2,pattern="pisc_Vic_Uganda")),]
## between Victoria North and Victoria South
pisci_Uganda_Mwanza_dxy<-dxy[(grepl(dxy$pop1,pattern="pisc_Victoria")&</pre>
                                 grepl(dxy$pop2,pattern="pisc_Vic_Uganda")) |
                                (grepl(dxy$pop1,pattern="pisc_Vic_Uganda")&
                                   grepl(dxy$pop2,pattern="pisc_Victoria")),]
## Combine sympatric and allopatric piscivore contrasts
pisci_symp_dxy<-rbind(cbind(pisci_Kyoga_dxy,site="Kyoga"),</pre>
                      cbind(pisci_Vic_dxy,site="South Victoria"),
                      cbind(pisci_Uganda_dxy,site="North Victoria"))
pisci_allo_dxy<-rbind(cbind(pisci_MwanKyog_dxy,site="South Victoria Kyoga"),</pre>
                      cbind(pisci_UganKyog_dxy,site="North Victoria Kyoga"),
                      cbind(pisci_Uganda_Mwanza_dxy,site="Victoria"))
```

Paedophages

Plot allopatric versus sympatric dxy

make boxplots with overlaid dots using different symbols for different geographic region contrasts

```
# Prepare two panels for plotting piscivores and paedophages side by side
par(mfrow=c(1,2),mar=c(5,5,1,1),cex.lab=1.3)
```

```
# Draw boxplots of sympatric and allopatric piscivore dxy comparisons
boxplot(pisci_symp_dxy$avg_dxy,pisci_allo_dxy$avg_dxy,
        vlim=c(0.0015,0.003),names=c("sympatric","allopatric"),
        vlab=expression('D'['XY']*' piscivores'),col="white",outline=F)
# Overlay dots for each dxy comparison with symbols of different geographic regions
beeswarm(list(pisci_symp_dxy$avg_dxy,pisci_allo_dxy$avg_dxy),
         col="#FF9F00",add=T,
         pwpch=c(ifelse(pisci_symp_dxy$site=="Kyoga",4,
                    ifelse(pisci_symp_dxy$site=="South Victoria",19,15)),
                      ifelse(pisci_allo_dxy$site=="Victoria",17,
                        ifelse(pisci_allo_dxy$site=="South Victoria Kyoga",6,8))))
# Add a legend
legend("top",col="#FF9F00",pch=c(19,15,4,17,6,8),
       legend=c("within South Victoria", "within North Victoria",
                "within Kyoga", "South vs North Victoria",
                "South Victoria vs Kyoga", "North Victoria vs Kyoga"),
       bty="n",ncol=2)
# Boxplot of paedophages
boxplot(paedo_symp_dxy$avg_dxy,paedo_allo_dxy$avg_dxy,
       vlim=c(0.0015,0.003),names=c("sympatric","allopatric"),
        ylab=expression('D'['XY']*' paedophages'),col="white",outline=F)
beeswarm(list(paedo_symp_dxy$avg_dxy,paedo_allo_dxy$avg_dxy),
         col="#FF9F00",add=T,
         pwpch=c(ifelse(grepl(paedo_symp_dxy$pop1,pattern="Kyoga"),4,19),
                 rep(6,times=length(paedo_allo_dxy$avg_dxy))))
```

