

Ace2 PCR results, Culex pipiens complex

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R build: Geospatial 4.4.0

Import species/hybrid counts per site

```
counts <- read.csv("../data/ThisStudy.txt", sep = "\t")
countsSp <- SpatialPoints(coords = cbind(counts$long, counts$lat))
```

Genotypes in p/q notation: Cx. pipiens = pp Cx. quinquefasciatus = qq

Create a dataframe of counts

```
# start data frame and name fields
countsDf <- as.data.frame(counts[,c(2,1,4,5,6,9,10,7,8)])
names(countsDf) <- c("locality", "site", "pp", "pq", "qq", "latitude", "longitude", "year", "h_index")

# name rows
rownames(countsDf) <- countsDf$site
```

Pie charts on a map

Convert counts to proportions (frequency):

```
freqsDf <- as.data.frame(countsDf[,c("pp", "pq", "qq")])
freqsDf <- as.matrix.data.frame(t(apply(freqsDf, 1, function(row) row / sum(row))))
```

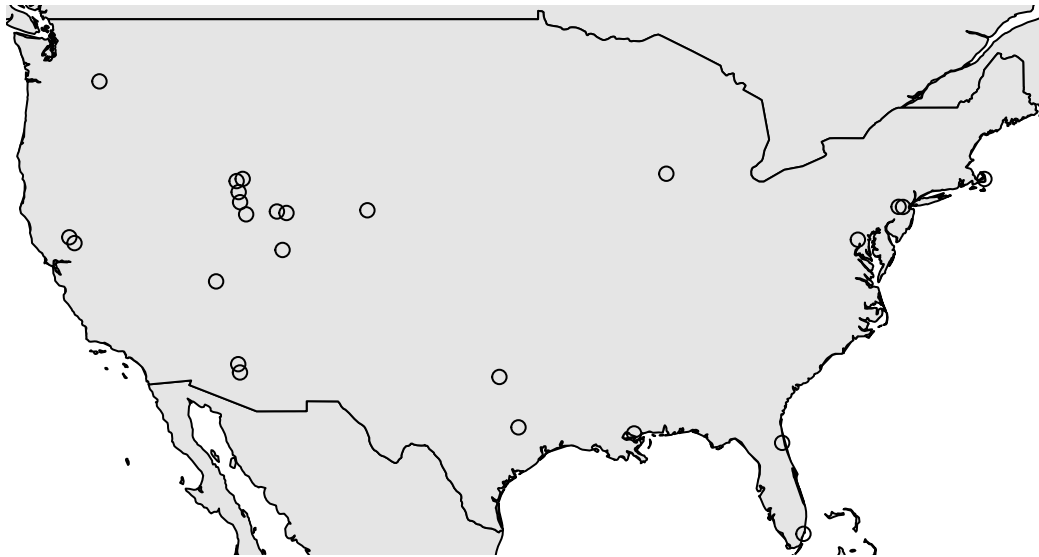
One pie chart at a time, to check code

Plot points on map to check data:

```
# Set xpd to NA to allow for plotting in the margins
#par(xpd = NA)

#create and plot coord = long, lat
coord <- as.data.frame(countsDf[,c("longitude", "latitude")])

#plot coordinates onto map
map("usa") # world, usa, state, county, etc.
map(add = T, col = "grey90", fill = TRUE)
points(coord, col="black", cex=1)
```

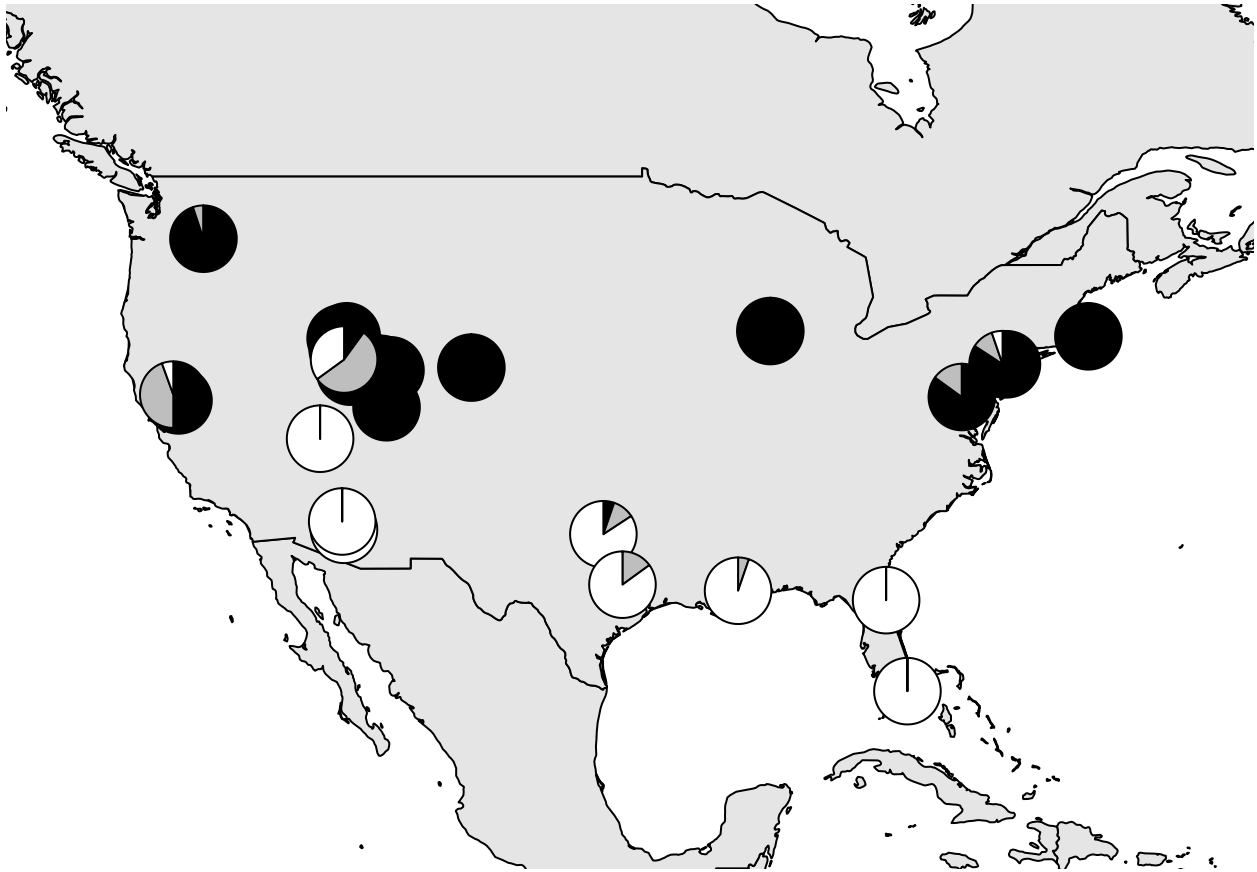


Add pies to map following: “<http://membres-timc.imag.fr/Olivier.Francois/Conversion.R>”

```
# Set xpd to NA to allow for plotting in the margins
par(xpd = NA)

# Determine plot order by descending h_index
plot_order <- rev(order(countsDf$h_index))

# plot pies onto map
map("usa")
map(add = T, col = "grey90", fill = TRUE)
for (i in plot_order){
  add.pie(z = freqsDf[i,],
    x = coord[i,1],
    y = coord[i,2],
    clockwise=TRUE,
    labels = "",
    col = c("black","grey","white"),
    cex = 1.5, radius = 1.5 )
}
```



Create a jitter data frame by hand:

```
# Create a jitter df
jitterDf <- data.frame(x_jitter = rep(0,25), y_jitter = rep(0,25))
rownames(jitterDf) <- rownames(countsDf)
jitterDf[3,] <- c(0,1)
jitterDf[4,] <- c(5,-1)
jitterDf[5,] <- c(1,-1)
jitterDf[6,] <- c(-2,0)
jitterDf[8,] <- c(2,-3)
jitterDf[9,] <- c(5,-1)
jitterDf[14,] <- c(-7,3.5)
jitterDf[16,] <- c(-6,-1.5)
jitterDf[19,] <- c(1,1)
jitterDf[20,] <- c(1,-1)
```

Calculate bounds of map based on coordinates + jitter:

```
# Expand x/y limits by a small margin (e.g., 2 degrees)
x_range <- range(coord[, 1] + jitterDf[, 1], na.rm = TRUE)
y_range <- range(coord[, 2] + jitterDf[, 2], na.rm = TRUE)

x_margin <- 2
y_margin <- 2

x_lim <- c(x_range[1] - x_margin, x_range[2] + x_margin)
y_lim <- c(y_range[1] - y_margin, y_range[2] + y_margin)
```

Add jitter with a line from true origin:

```
# Open PDF device
#pdf("../figs/ace2_pies_ThisStudy.pdf", width = 8, height = 6)

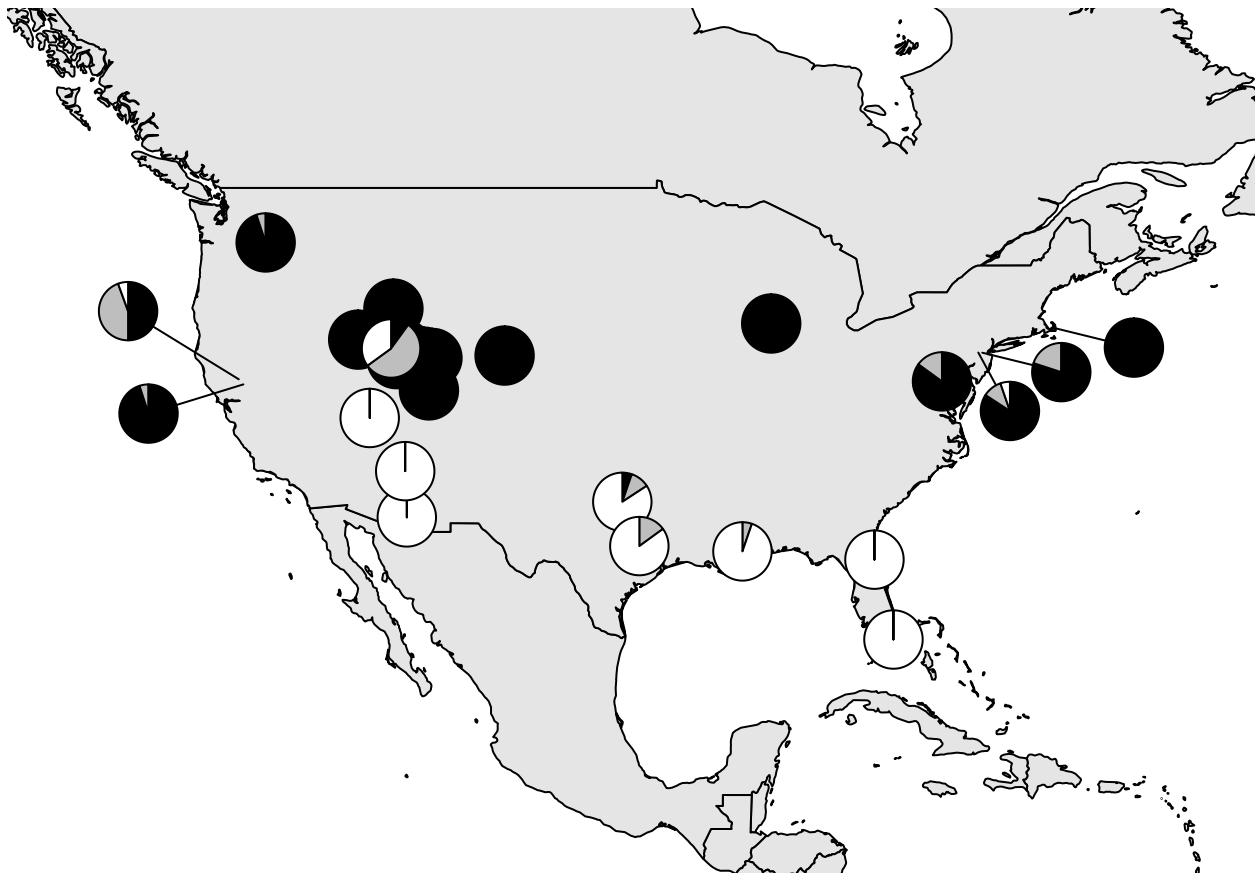
# Set xpd to NA to allow for plotting in the margins
par(xpd = NA)

# Plot map with expanded margins
map("usa", xlim = x_lim, ylim = y_lim)
map(add = TRUE, col = "grey90", fill = TRUE)

for (i in plot_order) {
  # Jittered coordinates
  jittered_x <- coord[i, 1] + (jitterDf[i, 1])
  jittered_y <- coord[i, 2] + (jitterDf[i, 2])

  # Draw line from true location to jittered pie
  segments(x0 = coord[i, 1],
           y0 = coord[i, 2],
           x1 = jittered_x,
           y1 = jittered_y,
           col = "black", lty = 1, lwd = 1)

  # Plot pie chart at jittered location
  add.pie(z = freqsDf[i,],
          x = jittered_x,
          y = jittered_y,
          clockwise = TRUE,
          labels = "",
          col = c("black", "grey", "white"),
          cex = 1.5, radius = 1.5)
}
```



`#dev.off()`