Spatial turnover in host-plant availability drives host-associated divergence in a South African leafhopper (*Cephalelus uncinatus*)

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Background
Aim

Geographic mosaic of plant distributions leads to host shifts in herbivorous insects

- Host preference experiments
- Colour matching
- Body morphology
Getting Data

- Reflectance measurements
  - Leafhoppers
  - Host plants
### Processing

**Pavo** (Rafael Maia, Chad Eliason, Pierre-Paul Bitton, Thomas White)

```r
##check that specs are in correct format
specsplants <- lapply(specsplants, function(x){x <- as.rspec(x)}

##fix negatives to zero
specsplants <- lapply(specsplants, function(x){x <- is.rspec(x)})

namesconde <- gsub( "[^conw1[:digit:]]" , "", names(specsplants[[1]]))
condeagged <- aggspec(specsplants[[1]], by = namesconde, FUN = mean)
```

```
wl  con1  con2  con3  con4  con5  con6
1  300 1.3380000 1.3266667 1.1580000 0.7186667 0.3943333 0.4526667
2  301 1.4452105 1.3388596 1.0987719 0.6472281 0.2686667 0.3069123
3  302 1.2330175 1.2049474 1.1475439 0.5428070 0.2968333 0.2120351
4  303 0.7778559 0.9668919 0.9587928 0.5197568 0.3238108 0.2091171
5  304 0.3008246 0.9952281 0.9033333 0.4607544 0.5603158 0.4177719
6  305 0.2586140 0.9631754 0.7955088 0.4213158 0.6085088 0.7596491
```
#model

colspacemod <- vismodel(specsvismod[,c(1,105:115)], visual = "avg.v", illum = "D65", bkg = 'green', relative = F)
colspacemod2 <- vismodel(specsvismod[,c(1,16:26)], visual = "avg.v", illum = "D65", bkg = 'green', relative = F)

plot(colspace(colspacemod, space = c("tcs")))
points(colspace(colspacemod2, space = c("tcs")), col = "blue")
Distances

```r
#model
vismodel1 <- vismodel(specsvismod, visual = "avg.v", illum = "D65", bkg = 'green', relative = F)

coldist1 <- coldist(vismodel1, noise = 'neural', subset = c("X","^mas.*|^con.|^wil.*|^hyp.*"))

##short test distances
coldist1 <- as.data.frame(coldist1)
coldist1[,3] <- as.numeric(coldist1[,3])

plantcol <- function(x){
  splitcol <- vector(length = (nrow(x)))
  for(i in seq(nrow(x))){
    if(grepl("^con.", x[i,2], fixed = F) == T){splitcol[i] <- "con"}
    if(grepl("^mas.", x[i,2], fixed = F) == T){splitcol[i] <- "mas"}
    if(grepl("^masp.", x[i,2], fixed = F) == T){splitcol[i] <- "masp"}
    if(grepl("^hyp.", x[i,2], fixed = F) == T){splitcol[i] <- "hyp"}
    if(grepl("^wil.", x[i,2], fixed = F) == T){splitcol[i] <- "wil"}
  }
  data <- cbind(x, splitcol)
  data
}

usedata <- plantcol(coldist1)
usedata <- split(usedata, interaction(usedata$patch1, usedata$splitcol))
```
names <- names(usedata)
matches <- #Add regex matches
delete.ele <- grep(matches, names)

usedata2 <- usedata[delete.ele]
names(usedata2)

usedata2 <- lapply(usedata2, function(x){x[order(x$dS),]})
shortest.list <- lapply(usedata2, function(x){y <- x[1,]})
shortest.dist <- do.call("rbind", shortest.list)
data.final <- shortest.dist[,c(1,5,3)]
colnames(data.final) <- c("Indiv", "Plant", "Shortest")
addsex <- function(x){
  sex <- vector(length = nrow(x))
  for(i in seq(nrow(x))){
    if(grepl("[F]", x[i,1]) == T){
      sex[i] <- "Female"
    } else{
      sex[i] <- "Male"
    }
  }
  data <- cbind(x,sex)
  data
}

data.final <- addsex(data.final)

addorigin <- function(x){
  Origin <- vector(length = nrow(x))
  for(i in seq(nrow(x))){
    if(grepl("^X\d*\_C[FM]\d$", x[i,1], fixed = F) == T){
      Origin[i] <- "con"}
    if(grepl("^X\d*\_M[FM]\d$", x[i,1], fixed = F) == T){
      Origin[i] <- "mas"}
    if(grepl("^X\d*\_M[FM]p\d$", x[i,1], fixed = F) == T){
      Origin[i] <- "masp"}
    if(grepl("^X\d*\_H[FM]\d$", x[i,1], fixed = F) == T){
      Origin[i] <- "hyp"}
    if(grepl("^X\d*\_W[FM]\d$", x[i,1], fixed = F) == T){
      Origin[i] <- "wil"}
  }
  data <- cbind(x,Origin)
  data
}

data.final <- addorigin(data.final)

write.csv(data.final, "Distances/shortest_distances.csv")
Data and Test

> head(data.final)

| Indiv   | Plant | Shortest | sex  | Origin |
|---------|-------|----------|------|--------|
| X1_CF_2.con | X1_CF_2 | con 6.043993 | Female | con   |
| X10_CM_2.con | X10_CM_2 | con 5.459684 | Male  | con   |
| X11_CM_2.con | X11_CM_2 | con 5.218688 | Male  | con   |
| X12_CF_2.con | X12_CF_2 | con 2.416695 | Female | con   |
| X13_CM_2.con | X13_CM_2 | con 6.017687 | Male  | con   |
| X14_CM_2.con | X14_CM_2 | con 5.470643 | Male  | con   |

two-way repeated measures ANOVAs

aov(Shortest ~ Origin * Plant + Error(Indiv), data=FemaleShortestAllo)
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