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Visual modelling with *Pavo*



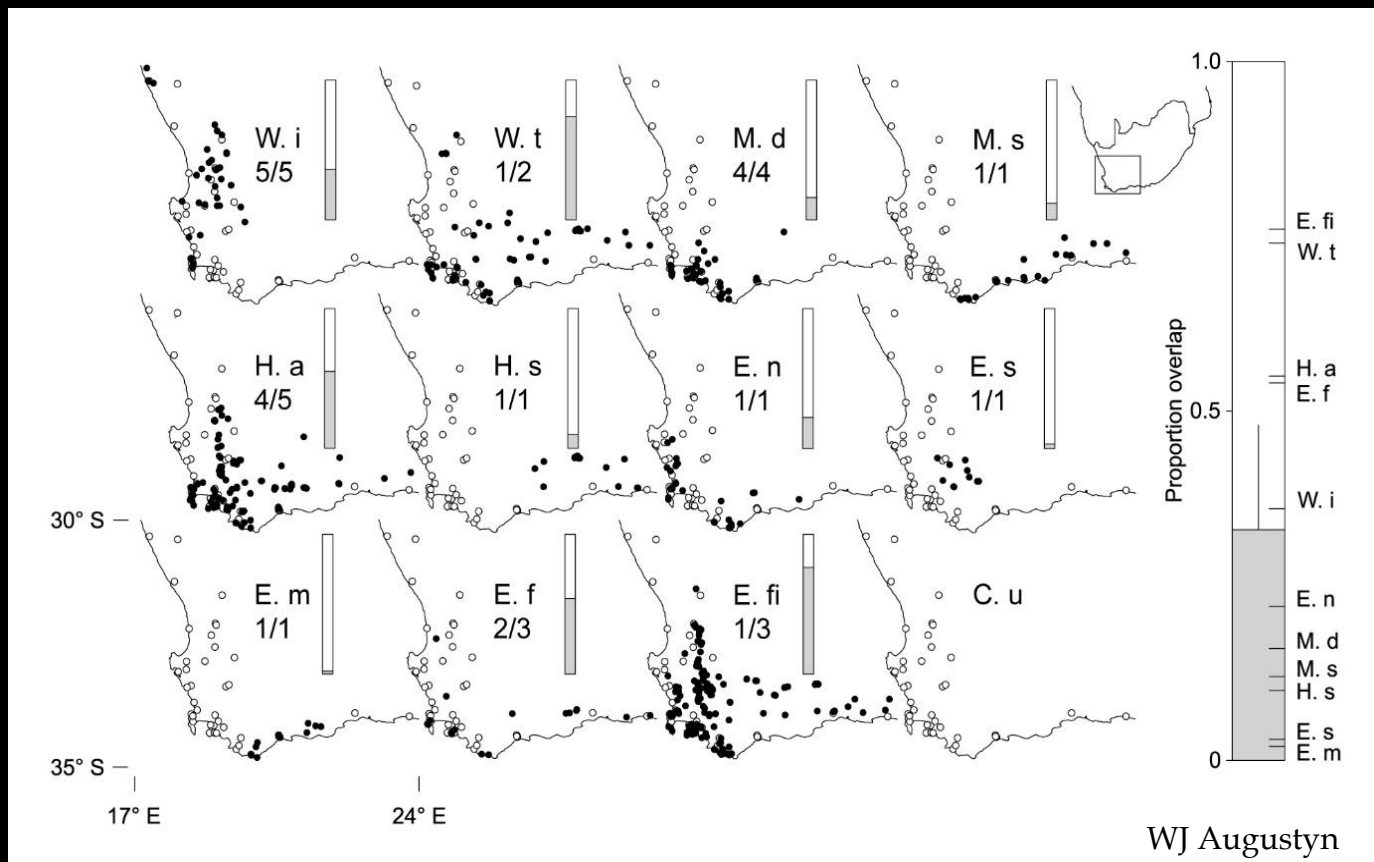
Jeroen van der Merwe

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

WJ Augustyn, B Anderson, J van der Merwe, Allan Ellis

BMC Evolutionary Ecology In press

Background



Aim



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

Host preference experiments

Colour matching

Body morphology



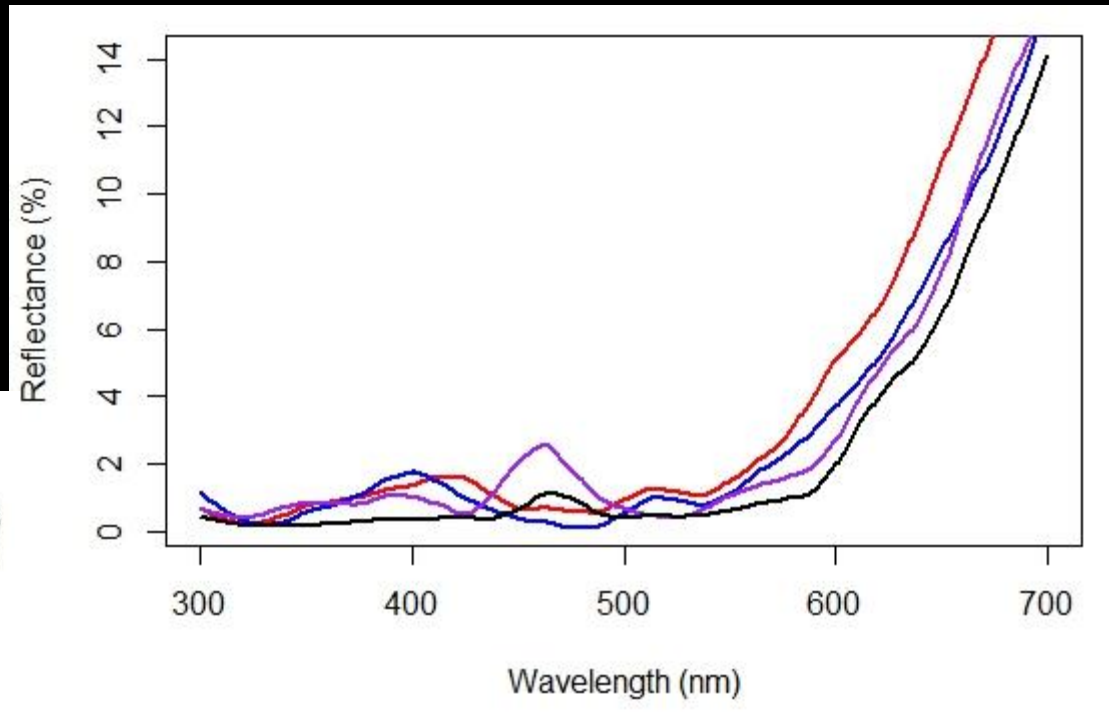
Getting Data



Reflectance measurements

Leafhoppers

Host plants



Processing



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

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

##fix negatives to zero
specsplants <- lapply(specsplants, function(x){procspec(x, fixneg = 'zero')})

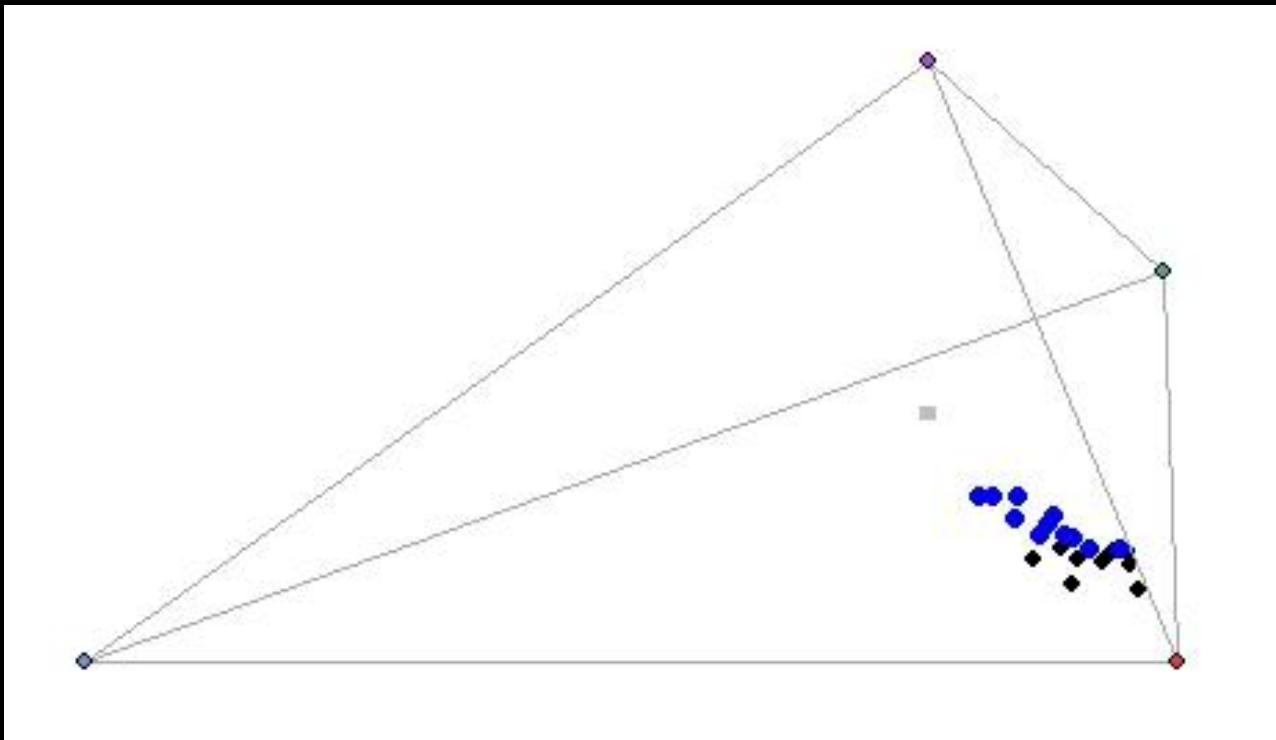
namesconde <- gsub( "[^conwl[:digit:]]" , "", names(specsplants[[1]]))
condeagged <- aggspec(specsplants[[1]], by = namesconde, FUN = mean)
```

	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

```
#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.*"))

##shrotest 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\\d*_C[FM]_\\d$",x[i,1], fixed = F)
      == T){Origin[i] <- "con"}
    if(grepl("^X\\d\\d*_M[FM]_\\d$",x[i,1], fixed = F)
      == T){Origin[i] <- "mas"}
    if(grepl("^X\\d\\d*_M[FM]p_\\d$",x[i,1], fixed = F)
      == T){Origin[i] <- "masp"}
    if(grepl("^X\\d\\d*_H[FM]_\\d$",x[i,1], fixed = F)
      == T){Origin[i] <- "hyp"}
    if(grepl("^X\\d\\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

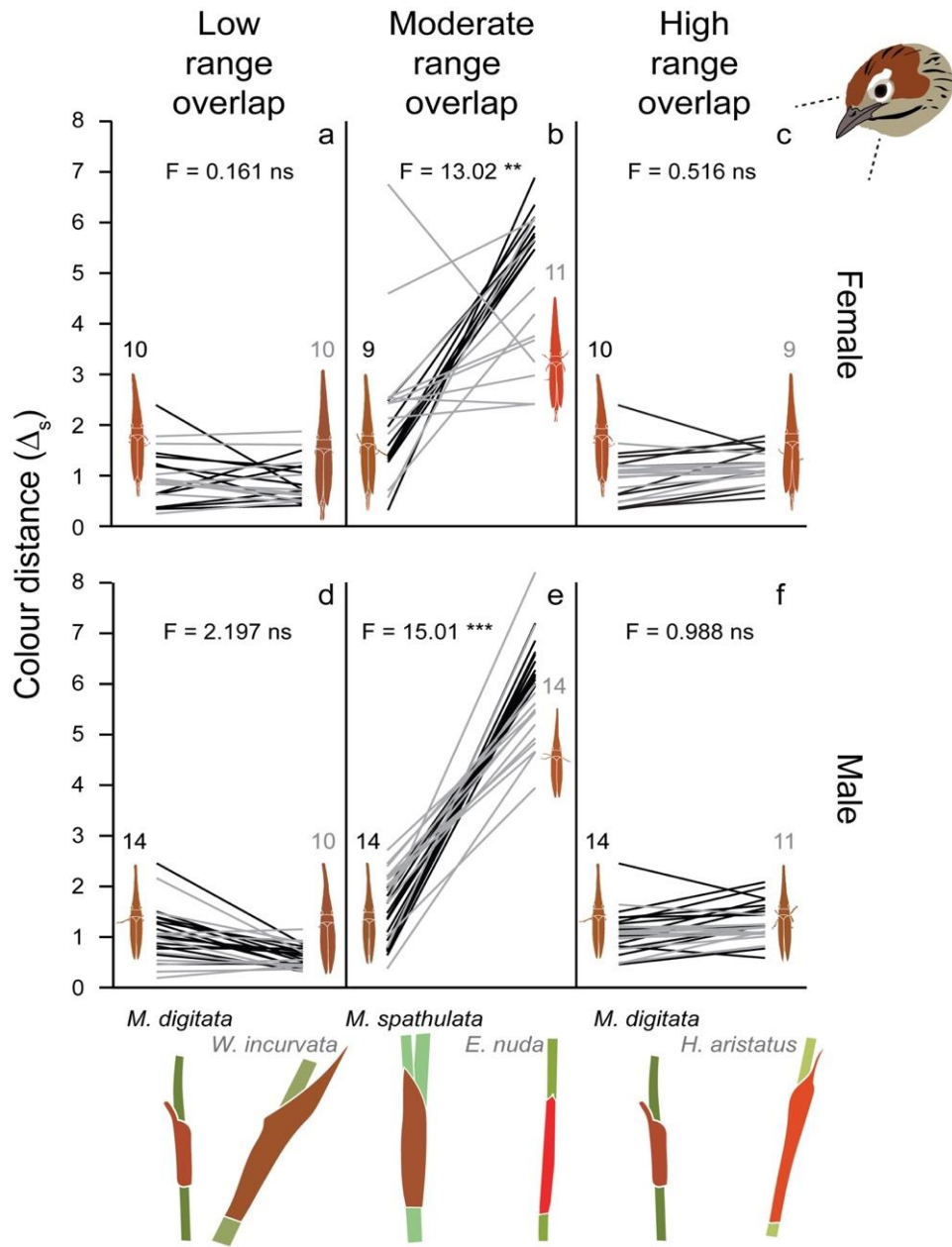


```
> head(data.final)
```

	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)
```



Acknowledgements



- ∞ Dr WJ Augustyn (lead author)
- ∞ Prof B Anderson
- ∞ Prof Allan Ellis
- ∞ NRF South African Biosystematics Initiative
- ∞ Stellenbosch University for funding



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NRF