LDAvsISSR.R

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```
# Simplified/clean theme for plotting
theme_simple <- function (base_size = 12, base_family = "") {</pre>
  theme_classic(base_size = base_size, base_family = base_family) %+replace%
    theme(
      axis.text = element_text(colour = "black"),
      axis.title.x = element text(size=18),
      axis.text.x = element_text(size=12),
      axis.title.y = element text(size=18,angle=90),
      axis.text.y = element_text(size=12),
      axis.ticks = element blank(),
      panel.background = element_rect(fill="white"),
      panel.border = element_blank(),
      plot.title=element_text(face="bold", size=24),
      legend.position="none"
    )
}
# Libraries
library(ggplot2) # For plotting
library(proxy) # For similarity matrix calculations using Jaccard's coefficient
## Warning: package 'proxy' was built under R version 3.3.3
## Attaching package: 'proxy'
## The following objects are masked from 'package:stats':
##
       as.dist, dist
##
## The following object is masked from 'package:base':
##
##
       as.matrix
```

library(reshape) # For reformatting similarity matrices

```
## Import and inspect LDA coordinates and ISSR data
LDA<-read.csv("LDAData.csv",header=T,row.names="IndID")
ISSR<-read.csv("MuhaidatEtAl_ISSRData.csv",header=T,row.names="IndID")
str(LDA)</pre>
```

Warning: package 'reshape' was built under R version 3.3.3

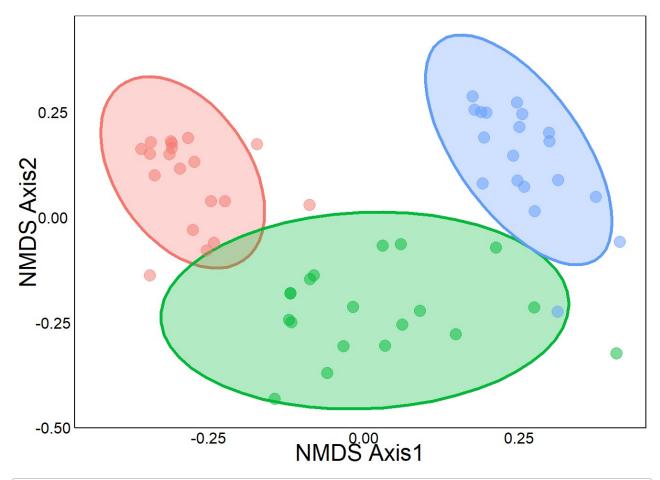
```
## 'data.frame':
                   57 obs. of 17 variables:
## $ Loc
              : Factor w/ 3 levels "AlYotm", "DeadSea", ... 3 3 3 3 3 3 3 3 3 3 ...
## $ BLen
              : num 4.8 5 5.4 5.6 5.5 5.2 5.9 5.7 4.9 5.9 ...
             : num 0.4 0.5 0.4 0.4 0.4 0.5 0.4 0.5 0.4 0.5 ...
## $ BWdth
## $ BVeins : num 3 5 3.67 3 3 ...
## $ BSpines : int 2 2 2 2 2 2 3 2 2 2 ...
## $ SpLen : num 1 1 1 1.2 1.1 0.9 0.9 1.3 1 1.5 ...
## $ NodeLen : num 1.3 1.6 1.5 1.6 1.3 1.8 1.8 1.6 1.6 2 ...
             : num 7 7 9 8.5 7.5 10 8 8 9.1 10 ...
## $ LLen
              : num 1 1 1.1 0.9 0.7 1.2 1 1.2 0.8 1.2 ...
## $ LWdth
## $ LTeeth : num 4 5 4 4 5 ...
## $ ASFillen : num 1.3 1.3 1.2 1.3 1.2 1.3 1.3 1.2 1.3 1.3 ...
## $ ASAnthLen: num 0.5 0.5 0.5 0.5 0.4 0.5 0.5 0.6 0.5 ...
## $ ASApenLen: num 0.5 0.5 0.6 0.5 0.5 0.6 0.5 0.6 0.5 ...
## $ PSFillen : num 1.2 1.19 1.1 1.2 1.1 ...
## $ PSAnthLen: num 0.5 0.5 0.5 0.5 0.5 ...
## $ LD1
             : num 2.37 2.72 4.03 4.41 3.39 ...
## $ LD2
             : num -0.21 0.514 2.335 -0.588 0.442 ...
```

```
str(ISSR)
```

```
## 'data.frame':
                57 obs. of 52 variables:
##
   $ X16.280 : int 1 1 0 1 1 1 1 1 1 1 ...
   $ X16.480 : int 1 1 0 1 1 1 1 1 1 1 ...
   $ X16.400 : int 00000000000...
##
##
   $ X16.700 : int 0000010000...
   $ X16.1000: int 0 0 0 0 0 0 0 0 0 0 ...
##
##
   $ X16.1200: int 00000000000...
##
   $ X14.400 : int 1 1 0 1 1 1 1 1 1 1 ...
##
   $ X14.500 : int 0000000001 ...
   $ X14.800 : int 1 0 0 1 1 0 0 0 0 1 ...
##
   $ X14.1000: int 1 0 0 1 1 0 1 0 1 1 ...
##
   $ X14.1500: int 1 0 0 0 0 0 0 0 0 1 ...
   $ X14.600 : int 00000000001 ...
##
##
   $ X11.280 : int 1001100001 ...
   $ X11.320 : int 1 1 0 1 1 1 1 1 1 1 ...
##
   $ X11.370 : int 1001100001 ...
##
   $ X11.550 : int 1000110001 ...
##
   $ X11.700 : int 1 1 0 1 1 1 0 1 0 1 ...
##
   $ X11.1000: int 1 1 0 1 1 1 0 0 0 1 ...
##
   $ X11.1200: int 1 0 0 0 0 0 0 0 0 0 ...
##
   $ X3.200 : int 0 0 0 1 1 1 1 1 0 0 ...
   $ X3.300
           : int
                1111111001...
##
   $ X3.400
           : int
                1111111111...
##
   $ X3.500
           : int 0001111000...
##
   $ X3.600
           : int
                1110011101...
##
   $ X3.900
           : int
                1010011101...
   $ X3.950 : int 0001100000...
##
   $ X3.1050 : int 1 0 1 1 1 1 1 1 0 1 ...
##
##
   $ X9.270
           : int
                1111111111...
##
   $ X9.310
           : int 0011011010...
##
   $ X9.400
           : int 0010000000...
           : int 0010000000...
##
   $ X9.700
   $ X9.1100 : int 0 0 1 0 0 0 0 1 0 0 ...
##
   $ X4.600
           : int 0000000000...
##
##
   $ X4.500
           : int 0000000000...
##
   $ X4.400
           : int 0000000000...
##
   $ X4.350
           : int 0000000000...
##
   $ X4.300
           : int 0000000000...
   $ X4.250
           : int 0000000000...
##
   $ X4.200
           : int
                00000000000...
##
##
   $ X5.200
           : int 111111111...
##
   $ X5.300
           : int
                1111111111...
##
   $ X5.350
           : int
                 1 1 1 1 1 1 1 1 1 1 ...
##
   $ X5.550
           : int 0000011001...
##
   $ X5.730
           : int 1101111111...
##
   $ X5.900
           : int 0000011101...
##
   $ X7.300
           : int 0000000000...
   $ X7.350
           : int 1010100111...
```

```
## $ X7.370 : int 0001000000...
## $ X7.400 : int 0 1 0 0 1 0 0 1 0 0 ...
## $ X7.450 : int 1000100000...
  $ X7.500 : int 0 1 1 1 1 0 1 1 1 0 ...
## $ X7.600 : int 1 0 0 0 0 0 0 0 0 ...
## Nonmetric Multidimensional Scaling (NMDS) of ISSR Data
NMDS<-cmdscale(dist(ISSR, method = "Jaccard",upper=F),k=2)
str(NMDS)
## num [1:57, 1:2] -0.1179 0.0617 -0.1436 -0.1183 -0.0809 ...
## - attr(*, "dimnames")=List of 2
    ..$ : chr [1:57] "D1" "D2" "D3" "D4" ...
##
    ..$ : NULL
##
#### Merge LDA & NMDS
Coords<-merge(LDA[,c("Loc","LD1","LD2")],NMDS,by="row.names",all=T)</pre>
names(Coords)[grep("V[0-9]$",names(Coords))]<-c("NMDS1","NMDS2")</pre>
head(Coords)
##
     Row.names
                 Loc
                           LD1
                                       LD2
                                                NMDS1
                                                            NMDS2
## 1
           A1 AlYotm -4.527856 1.24321681 -0.3444122 -0.13830252
          A10 AlYotm -6.014491 0.58384566 -0.2961578 0.11496876
## 2
          A11 AlYotm -4.709414 -0.02153503 -0.3092342 0.16413962
## 3
          A12 AlYotm -6.373753 1.09055544 -0.2750844 -0.03046156
## 4
          A13 AlYotm -7.201540 -0.14078594 -0.2730852 0.13114528
## 5
## 6
          A14 AlYotm -6.403451 -0.49441686 -0.2413878 -0.06031499
## Plot NMDS
p<-ggplot(data=Coords,aes(x=NMDS1,y=NMDS2)) +</pre>
```

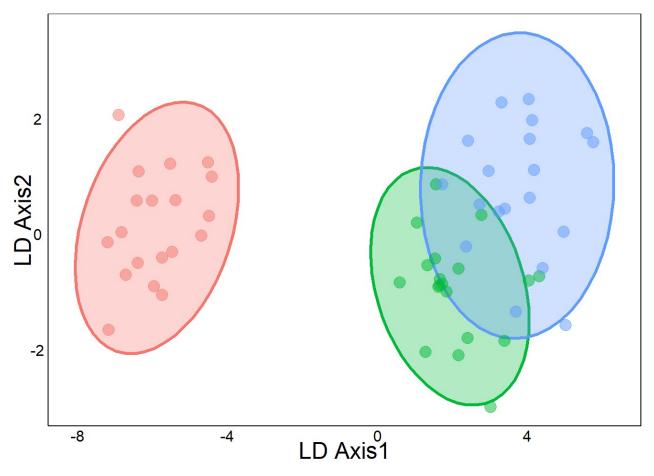
```
## Plot NMDS
p<-ggplot(data=Coords,aes(x=NMDS1,y=NMDS2)) +
   stat_ellipse(geom="polygon",aes(colour=Loc),fill=NA,size=1.2,alpha=0.3)+
   stat_ellipse(geom="polygon",aes(fill=Loc,colour=Loc),size=1.2,alpha=0.3)+
   geom_point(aes(colour=Loc),alpha=0.5,size=I(4)) +
   xlab("NMDS Axis1")+ylab("NMDS Axis2")+theme_simple()
print(p)</pre>
```



```
### Output as pdf
pdf("NMDSplot.pdf",width=6,height=6)
  print(p)
dev.off()
```

```
## png
## 2
```

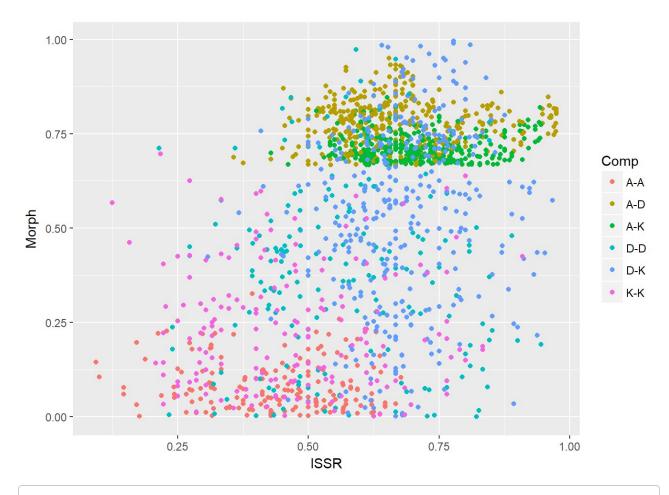
```
## Plot LDA
p2<-ggplot(data=Coords,aes(x=LD1,y=LD2)) +
   stat_ellipse(geom="polygon",aes(colour=Loc),fill=NA,size=1.2,alpha=0.3)+
   stat_ellipse(geom="polygon",aes(fill=Loc,colour=Loc),size=1.2,alpha=0.3)+
   geom_point(aes(colour=Loc),alpha=0.5,size=I(4)) +
   xlab("LD Axis1")+ylab("LD Axis2")+theme_simple()
print(p2)</pre>
```



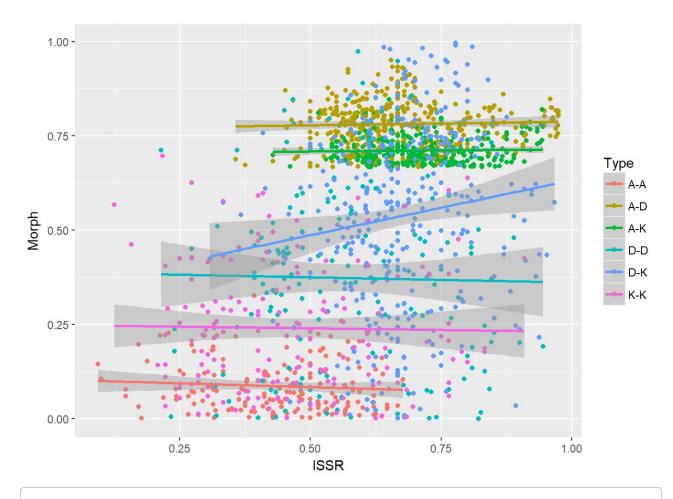
```
pdf("NMDSvsLDAplot.pdf",width=6,height=6)
  print(p2)
dev.off()
```

```
## png
## 2
```

```
## Calculate Jaccard's distance for molecular and morphological traits
ISSRdist<-melt(as.matrix(dist(ISSR, method = "Jaccard",upper=F)))</pre>
Morphdist<-melt(as.matrix(dist(LDA[,grep("LD",names(LDA))],method = "eJaccard",upper=
F)))
### Merge distance matrices
Dist<-merge(ISSRdist,Morphdist,by=c("X1","X2"))</pre>
names(Dist)<-c("ID1","ID2","ISSR","Morph")</pre>
#### Remove duplicates
for (row in 1:nrow(Dist)){
  Dist[row,grep("ID",names(Dist))]<-sort(Dist[row,grep("ID",names(Dist))])</pre>
}
Dist<-Dist[!duplicated(Dist),]</pre>
Dist<-Dist[Dist$ID1!=Dist$ID2,]</pre>
### Categorize comparisons for colour coding
Dist$Comp<-paste0(gsub("[0-9]*","",Dist$ID1),"-",gsub("[0-9]*","",Dist$ID2))</pre>
Dist$Type<-Dist$Comp</pre>
#Dist$Type[Dist$Comp %in% c("A-A", "D-D", "K-K")]<-"Within"</pre>
#Dist$Type[Dist$Comp %in% c("A-D","A-K","D-K")]<-"A-D"
## Plot similarity
qplot(ISSR,Morph,colour=Comp,data=Dist)
```

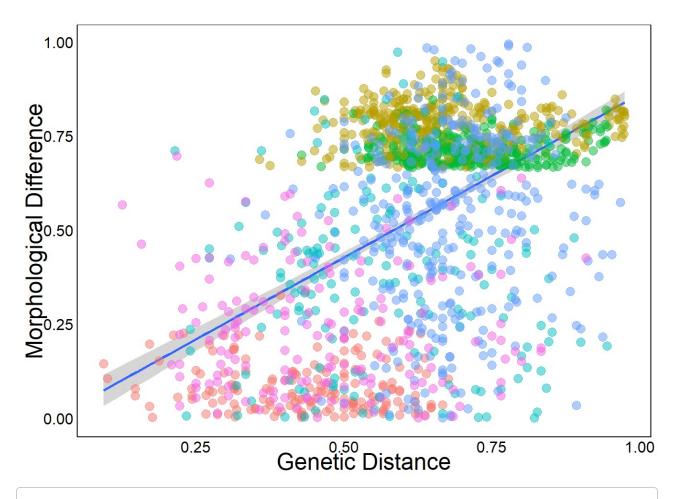


qplot(ISSR,Morph,colour=Type,data=Dist) + geom_smooth(method="lm")



anova(lm(Morph~ISSR+I(ISSR^2),data=Dist))

```
p<-ggplot(data=Dist,aes(x=ISSR,y=Morph)) + geom_smooth(method="lm") +
  geom_point(aes(colour=Type),alpha=0.5,size=3) +
  xlab("Genetic Distance")+ylab("Morphological Difference")+theme_simple()
p</pre>
```



Software version info
sessionInfo()

```
## R version 3.3.2 (2016-10-31)
## Platform: x86_64-w64-mingw32/x64 (64-bit)
## Running under: Windows 10 x64 (build 15063)
##
## locale:
## [1] LC_COLLATE=English_Canada.1252 LC_CTYPE=English_Canada.1252
## [3] LC_MONETARY=English_Canada.1252 LC_NUMERIC=C
## [5] LC_TIME=English_Canada.1252
##
## attached base packages:
## [1] stats
                graphics grDevices utils
                                              datasets methods
                                                                 base
##
## other attached packages:
## [1] reshape_0.8.6 proxy_0.4-17 ggplot2_2.2.1
## loaded via a namespace (and not attached):
## [1] Rcpp_0.12.9
                        assertthat_0.1
                                         digest_0.6.12
                                                          rprojroot_1.2
## [5] MASS_7.3-45
                        plyr_1.8.4
                                         grid_3.3.2
                                                          gtable_0.2.0
## [9] backports_1.0.5 magrittr_1.5
                                         evaluate_0.10
                                                         scales_0.4.1
## [13] stringi_1.1.2
                        lazyeval_0.2.0
                                         rmarkdown_1.3
                                                         labeling_0.3
                        stringr_1.1.0
## [17] tools 3.3.2
                                         munsell 0.4.3
                                                          colorspace_1.3-2
## [21] htmltools_0.3.5 knitr_1.15.1
                                         tibble_1.2
```