HW3

Kvan Valerii

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```
library("RIdeogram")
```

```
## Warning: package 'RIdeogram' was built under R version 4.1.3
```

```
library("dplyr")
```

```
## Warning: package 'dplyr' was built under R version 4.1.3

##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

Read all data

```
gene_mapping <- read.csv('gene_mapping.tsv', sep='\t')
dongola <- read.csv("DONGOLA_genes.tsv", sep='\t')
zanu <- read.csv("ZANU_genes.tsv", sep='\t')

head(gene_mapping)
```

```
##   contig middle.position strand ord      name ref.genes
## 1      2           31135     -1   0 gene_3542         1
## 2      2           38868     -1   1 gene_3543         1
## 3      2           42746      1   2   gene_80         1
## 4      2           46243     -1   3 gene_3544         1
## 5      2           53442     -1   4 gene_3545         1
## 6      2           60574      1   5   gene_81         1
##                                                      DONG
## 1  NC_053517.1,111908344,1,6540,DONG_gene-LOC120894913
## 2  NC_053517.1,111899667,1,6539,DONG_gene-LOC120904110
## 3 NC_053517.1,111895084,-1,6538,DONG_gene-LOC120904105
## 4  NC_053517.1,111891588,1,6537,DONG_gene-LOC120904096
## 5  NC_053517.1,111884408,1,6536,DONG_gene-LOC120895288
## 6 NC_053517.1,111877309,-1,6535,DONG_gene-LOC120895290
```

Filter mapping data

Choose only 2, 3, X chr

```
gene_mapping <- gene_mapping[gene_mapping$contig %in% c('2', '3', 'X'),]
unique(gene_mapping$contig)
```

```
## [1] "2" "3" "X"
```

Split DONG column and drop it

```
gene_mapping <- cbind(gene_mapping, setNames(data.frame(x = do.call('rbind', strsplit(as.character(gene_
head(gene_mapping)
```

```
##   contig middle.position strand ord      name ref.genes    seq_id_d  middle_d
## 1      2           31135     -1   0 gene_3542         1 NC_053517.1 111908344
## 2      2           38868     -1   1 gene_3543         1 NC_053517.1 111899667
## 3      2           42746      1   2   gene_80         1 NC_053517.1 111895084
## 4      2           46243     -1   3 gene_3544         1 NC_053517.1 111891588
## 5      2           53442     -1   4 gene_3545         1 NC_053517.1 111884408
## 6      2           60574      1   5   gene_81         1 NC_053517.1 111877309
##   strand_d length_d                 name_d
## 1        1     6540 DONG_gene-LOC120894913
## 2        1     6539 DONG_gene-LOC120904110
## 3       -1     6538 DONG_gene-LOC120904105
## 4        1     6537 DONG_gene-LOC120904096
## 5        1     6536 DONG_gene-LOC120895288
## 6       -1     6535 DONG_gene-LOC120895290
```

Transform name of DONGOLA genes in gene mapping table to format that used in DONGOLA csv.

```
head(gene_mapping)
```

```
##   contig middle.position strand ord      name ref.genes    seq_id_d  middle_d
## 1      2           31135     -1   0 gene_3542         1 NC_053517.1 111908344
## 2      2           38868     -1   1 gene_3543         1 NC_053517.1 111899667
## 3      2           42746      1   2   gene_80         1 NC_053517.1 111895084
## 4      2           46243     -1   3 gene_3544         1 NC_053517.1 111891588
## 5      2           53442     -1   4 gene_3545         1 NC_053517.1 111884408
## 6      2           60574      1   5   gene_81         1 NC_053517.1 111877309
##   strand_d length_d                 name_d
## 1        1     6540 DONG_gene-LOC120894913
## 2        1     6539 DONG_gene-LOC120904110
## 3       -1     6538 DONG_gene-LOC120904105
## 4        1     6537 DONG_gene-LOC120904096
## 5        1     6536 DONG_gene-LOC120895288
## 6       -1     6535 DONG_gene-LOC120895290
```

```
head(dongola)
```

```
##                  ID start   end strand
## 1 gene-LOC120906950 59885 60345     -1
## 2 gene-LOC120906947 61728 64249      1
## 3 gene-LOC120906949 88010 88555     -1
## 4 gene-LOC120906948 90190 90789     -1
## 5 gene-LOC120906980   657  1316     -1
## 6 gene-LOC120906964 23986 24588      1
```

We need to remove "DONG" at the beginning of the name.

```
gene_mapping$name_d <- gsub("^DONG_(\\w+)", "\\1", gene_mapping$name_d)
```

Calculate distance between genes

```
gene_mapping$middle_d <- as.numeric(gene_mapping$middle_d)
gene_mapping$distance <- abs(gene_mapping$middle.position - gene_mapping$middle_d)
```

Mapping 1:1 ZANU to DONGOLA genes

Function to choose closest not reserved dongola gene for mapping

```
choose_closest_not_used_gene <- function(final_mapping) {

  #first we will map the genes with less distance.
  #For this we will sort all possible maps by distance in ascending order
  #p.s. That is not best options, because it can be more suitable variations
  #of closest genes
  gene_mapping <<- gene_mapping[order(gene_mapping$distance),]

  #here will be present the name of Dongola genes that were already mapped with
  #some ZANU gene.
  #It is need, because we have duplicated DONGOLA genes that shared between
  #multiple ZANU genes
  dongola_name_buffer <- c()

  for (zname in unique(gene_mapping$name)){
    #choose rows with this name
    tmp_rows = gene_mapping[gene_mapping$name == zname,]

    #sort by distance to iterate from min to max
    tmp_rows <- tmp_rows[order(tmp_rows$distance),]
    for (i in 1:nrow(tmp_rows)) {
      dname <- tmp_rows[i, ]$name_d
      contig <- tmp_rows[i, ]$contig

      if (!(dname %in% dongola_name_buffer)) {
        #add to buffer
        append(dongola_name_buffer, dname)

        #add to final mapping table
        final_mapping <- rbind(final_mapping, data.frame(chr=contig, zname=zname,
                                                          dname=dname))
        break
      }
    }
  }
  return(final_mapping)
}
```

make table with the most closest genes

```
final_mapping <- setNames(data.frame(matrix(ncol = 3, nrow = 0)), c("chr", "zname", "dname"))

final_mapping <- choose_closest_not_used_gene(final_mapping)
head(final_mapping)
```

```
##   chr      zname             dname
## 1   2  gene_1586 gene-LOC120904129
## 2   X gene_13388 gene-LOC120905991
## 3   X gene_13057 gene-LOC120906736
## 4   X gene_13164 gene-LOC120905715
## 5   X gene_13015 gene-LOC120905674
## 6   X gene_13389 gene-LOC120905990
```

Make tables for plots

```
create_karyotype_table <- function(final_mapping, specie1, specie2) {

  synteny_table_dual <- setNames(data.frame(matrix(ncol = 7, nrow = 0)),
                                   c("Species_1", "Start_1", "End_1", "Species_2",
                                     "Start_2", "End_2", "fill"))

  final_mapping <- final_mapping[order(final_mapping$chr),]

  j = 1

  for(i in 1:nrow(final_mapping)) {
    tmp_row <- final_mapping[i, ]


    zname = tmp_row$zname[1]
    dname = tmp_row$dname[1]
    chr = tmp_row$chr[1]

    specie1_row <- specie1[specie1$ID == zname,]
    specie2_row <- specie2[specie2$ID == dname,]

    specie_num <- switch(chr, "X" = 1, "2" = 2, "3" = 3)

    #5891bf - blue
    #db4527 - red
    color_to_fill <- if (specie1_row$strand[1] == specie2_row$strand[1]) '5891bf' else 'db4527'

    synteny_table_dual <- rbind(synteny_table_dual,
                                data.frame(Species_1=specie_num, Start_1=specie1_row$start,
                                           End_1=specie1_row$end,
               Species_2=specie_num, Start_2=specie2_row$start, End_2=specie2_row$end,
               fill=color_to_fill))
```

```r
    j <- j + 2
  }

  return (synteny_table_dual)
}
```

Function for map initial specie table with info about chr

```r
add_chr_info <- function(s1, gene_mapping) {
  s1 <- cbind(s1, setNames(data.frame(matrix(ncol = 1, nrow = nrow(s1))),
                                   c("Chr")))

  for (name in unique(gene_mapping$name_d)) {

    chr <- gene_mapping[gene_mapping$name_d == name,]$contig[1]

    s1$Chr[s1$ID == name] <- chr[1]
  }

  return (s1)
}
```

calculate approx. length of DONGOLA chr

```r
#calculate approx. length of DONGOLA chr
dongola <- add_chr_info(dongola, gene_mapping)
maxX <- max(dongola[dongola$Chr == 'X',]$end[!is.na(dongola[dongola$Chr == 'X',]$end)])
max2 <- max(dongola[dongola$Chr == '2',]$end[!is.na(dongola[dongola$Chr == '2',]$end)])
max3 <- max(dongola[dongola$Chr == '3',]$end[!is.na(dongola[dongola$Chr == '3',]$end)])
```

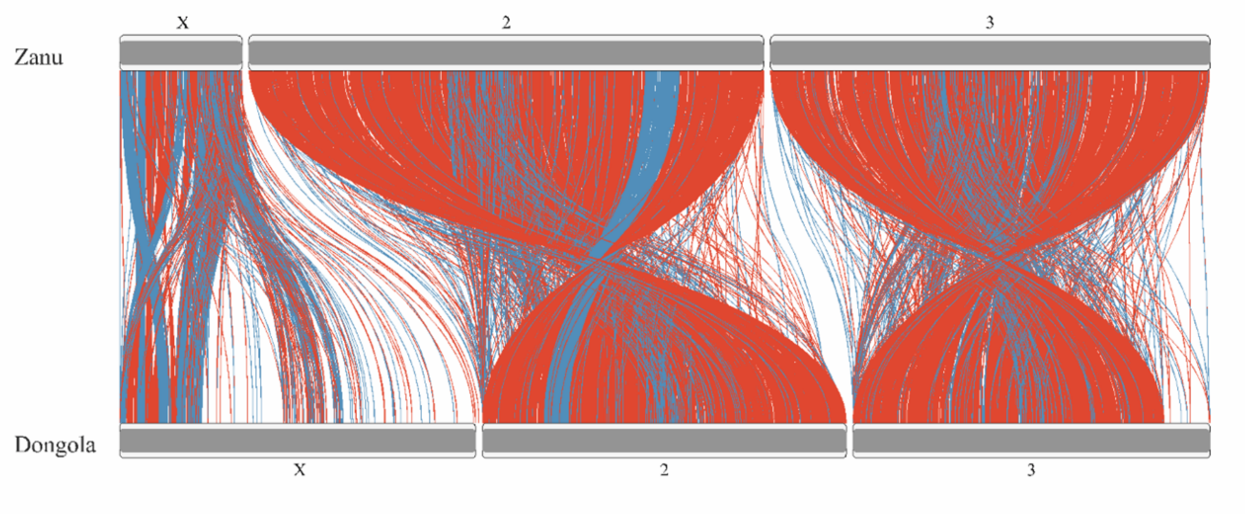
Final

```r
synteny_table_dual <- create_karyotype_table(final_mapping, zanu, dongola)

#karyotype table contains info about chromosomes
karyotype_table_dual <- setNames(data.frame(matrix(ncol = 7, nrow = 0)),
                                   c("Chr", "Start", "End", "fill",
                                     "species", "size", "color"))
#the length of ZENU chr was taken from HW3 description
karyotype_table_dual <- rbind(karyotype_table_dual,
                              data.frame(Chr=c('X','2','3'), Start=c(1, 1, 1),
                                             End=c(27238055, 114783175, 97973315),
                                         fill='969696',
                                             species='Zanu', size=12, color='252525'))
karyotype_table_dual <- rbind(karyotype_table_dual,
                              data.frame(Chr=c('X','2','3'), Start=c(1, 1, 1),
                                             End=c(maxX, max2, max3),
                                         fill='969696',
                                             species='Dongola', size=12, color='252525'))
```

Plot with Rideogram

```
ideogram(karyotype = karyotype_table_dual, synteny = synteny_table_dual)
convertSVG("chromosome.svg", device = "png")
```


X
Zanu
Dongola
X