Rock Crabs 1

Radial axes

This is the **first** in a series of questions on the exploration of some data on rock crabs.

The context for the data as well as the data itself is explained in more detail in the **background** document accompanying the assignment.

Since you will be using loon's interactive graphics to explore the data, you might also want to occasionally save some plots from your interactive analysis to include in your solution(s). Information on how to do this appears in the document **SavingLoonPlots**. Be sure to read that document (and even its "Rmd" version) before attempting to save loon plots.

```
library("loon")
library(loon.data); data("lepto")
```

16 marks

a. (4 marks) Construct a radial axis plot in loon showing all 200 crabs in the data set. In constructing this plot, the axes are to be arranged so that every variate axis appears next to every other variate axis. The radial axis plot must also be constructed so as to be part of the linkingGroup "lepto". Assign the radial axis plot to the symbol sa1 when you first construct it.

Show the code you use to construct the plot.

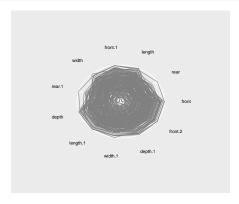
Show the plot.

ar = eulerian (5)

```
summary(lepto)
##
        front
                        rear
                                       length
                                                        width
##
   Min. : 7.20
                   Min. : 6.50
                                   Min.
                                         :14.70
                                                          :17.10
                                                   Min.
##
   1st Qu.:12.90
                   1st Qu.:11.00
                                   1st Qu.:27.27
                                                   1st Qu.:31.50
   Median :15.55
##
                   Median :12.80
                                   Median :32.10
                                                   Median :36.80
##
   Mean
         :15.58
                   Mean
                         :12.74
                                   Mean :32.11
                                                   Mean
                                                          :36.41
##
   3rd Qu.:18.05
                    3rd Qu.:14.30
                                   3rd Qu.:37.23
                                                   3rd Qu.:42.00
##
   Max.
          :23.10
                   Max.
                         :20.20
                                   Max. :47.60
                                                   Max.
                                                           :54.60
##
        depth
##
  Min. : 6.10
   1st Qu.:11.40
##
##
   Median :13.90
##
   Mean
          :14.03
   3rd Qu.:16.60
           :21.60
##
   Max.
front = l_hist(lepto$front, color="grey", xlabel = "front")
rear = l_hist(lepto$rear, color="grey", xlabel = "rear")
length = l_hist(lepto$length, color="grey", xlabel = "length")
width = l_hist(lepto$width, color="grey", xlabel = "width")
depth = 1_hist(lepto$depth, color="grey", xlabel = "depth")
library(PairViz)
```

sa1 <- l_serialaxes(lepto[,ar],color = "grey", linkingGroup = "lepto")</pre>

plot(sa1)



b. Each crab in the radial axis display sa1 appears as a star shaped glyph. These are individually selectable and any number can be selected at once by clicking on the display and extending the line from the mouse over any of the lines in the star displays.

Click outside all of the glyphs, between any two of the radial axes, and drag the line segment towards the centre of the display so that more and more glyphs are being included in the selection as you move toward the centre.

i. (1 mark) Describe how the glyph patterns change (if at all) as you move the mouse selection toward the centre.

most features goes to zero with same rate as our selected feature. There is no significant change in shape.

ii. (1 mark) Choose another pair of axes and repeat the selection process. Is the order in which the glyphs are selected substantively different from your first pair of axes? Why? Or why not?

it doesn't. because the features are positively correlated

iii. (1 mark) Again choose another pair of axes **but this time** begin your selection at the centre of the display and move out towards the edge. Describe how the glyphs change as you add more to the selected group in this way.

the polygen's shape changes by a lot at first, then it stays roughly the same

- iv. (1 mark) Given your observations (i iii above) about the selection of the glyphs in the order from centre to the maximum radius (or vice versa), what geometric structure might summarize the positions of the 200 points in the five-dimensional space of the measurements?
- v. (1 mark) What characteristics of purple rock crabs would naturally explain your observations (i iii above) about the selection of the glyphs in the order from centre to the maximum radius (or vice versa)?

there are many different subcatogries (of species) when the overall size is small, but fewer subcatogries with large overall size

c. Construct a second radial axis display sa2 identical to sa1 and have them both appear side by side on your screen.

Using the loon inspector for sa2, change its scaling from variable to observation.

In a radial axis display in **loon** there are circular rings marking distance from the centre of the display. These mark the distance along each axis and are helpful in locating positions along any axis.

In the first display, sa1, go between any pair of axes and select the single star shape nearest the centre. Colour it a different colour from the rest.

Now select the single star that is farthest from the centre and colour it another colour different from the rest.

Consider the distance between the innermost and outermost stars you have selected and coloured. Move in from the outermost star about a third of the way towards the centre, select a star there and colour it a third colour different from the rest.

Finally, about half way between the innermost star and the one just coloured in the previous stem, select a fourth star and give it a fourth different colour.

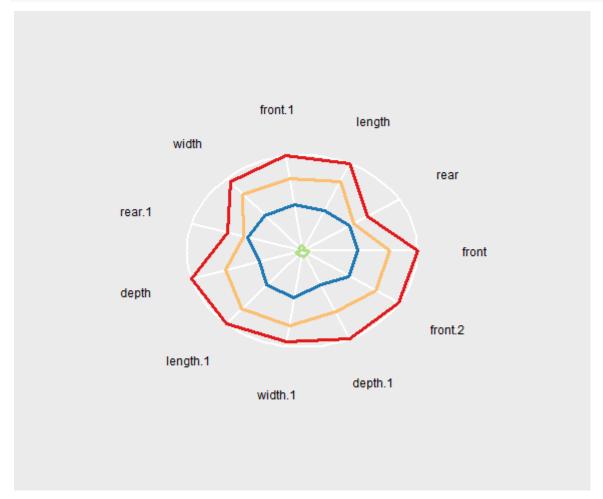
Using their common colour in the inspector, select the remaining stars (excluding those you coloured in the previouse steps) and deactivate them from the display.

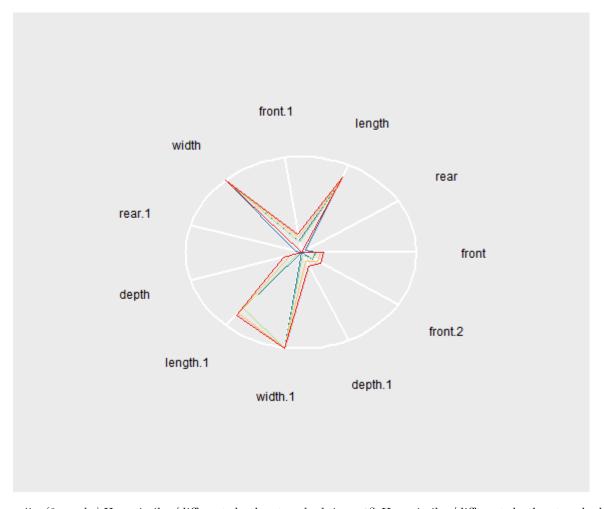
The following questions pertain to the four remaining stars.

```
sa2 <- l_serialaxes(lepto[,ar],color = "grey", linkingGroup = "lepto")</pre>
```

i. (3 marks) Show a picture of the four remaining stars as they appear in sa1 and in sa2.

```
workdir = "C:\\Users\\VIVRE\\Desktop\\Dulcinea\\stat442R\\a6"
p1 = "ci1.png"
p2 = "ci2.png"
#knitr::include_graphics(path_concat(workdir, p1))
#nitr::include_graphics(path_concat(workdir, p2))
```





- ii. (2 marks) How similar/different do the stars look in sa1? How similar/different do the stars look in sa2? in sa1, the largest seems similar to 2nd largest star. The other stars have different shapes in sa2, the shapes looks the same
- iii. (1 mark) What feature of the crabs is dominating the display in sa2? length and width
- iv. (1 mark) Why would you be interested in using observation scaling for this data? we could see the absolute value of some features compared with others.

Reactivate all stars in the radial axes plots and colour them all the same before proceeding to the next questions.