# **Analysis on Dataset "teeth"**

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## 1 Introduction of Dataset

The "teeth" dataset contains 32 observations across 9 variables. It records the numbers of eight types of teeth of 32 animals. The data format is:

**teeth** animal, tincisor, bincisor, tcanine, bcanine, tprmolar, bprmolar, tmolar, bmolar ["t" = top, "b" = bottom]

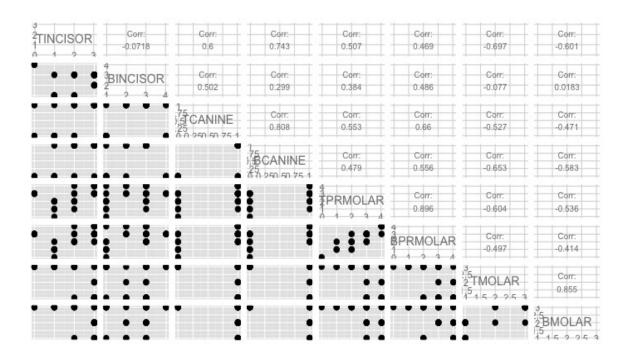
	<pre>&gt; head(teeth)</pre>								
	ANIMAL	TINCISOR	BINCISOR	TCANINE	BCANINE	TPRMOLAR	BPRMOLAR	TMOLAR	BMOLAR
1	BROWNBAT	2	3	1	1	3	3	3	3
2	MOLE	3	2	1	0	3	3	3	3
3	SILVERHAIRBAT	2	3	1	1	2	3	3	3
4	PIGMYBAT	2	3	1	1	2	2	3	3
5	HOUSEBAT	2	3	1	1	1	2	3	3
6	REDBAT	1	3	1	1	2	2	3	3

# 2 Data Analysis

## 2.1 Data Exploration

The data summary does not have an indication of extreme observations. But we do realize that there are some zero values in TCAINE, BCANINE, TPRMOLAR, BPRMOLAR, which could be our clues to further analyze the data.

```
# data exploration
>summary(teeth[,-1])
   TINCISOR
                   BINCISOR
                                   TCANINE
                                                   BCANINE
                                                                   TPRMOLAR
      :0.000
                Min. :1.000
                                Min. :0.0000
                                                Min. :0.000
Min.
                                                                Min.
                                                                       :0.000
1st Qu.:1.000
                1st Qu.:1.750
                                1st Qu.:0.0000
                                                1st Qu.:0.000
                                                                1st Qu.:2.000
Median :2.000
                Median :3.000
                                Median :1.0000
                                                Median :1.000
                                                                Median :3.000
                     :2.469
Mean :2.031
                Mean
                                Mean :0.7188
                                                Mean :0.625
                                                                Mean :2.812
3rd Qu.:3.000
                3rd Qu.:3.000
                                3rd Qu.:1.0000
                                                3rd Qu.:1.000
                                                                3rd Qu.:4.000
     :3.000
                       :4.000
                                Max. :1.0000
                                                Max. :1.000
                                                                Max. :4.000
Max.
                Max.
 BPRMOLAR
                  TMOLAR
                                  BMOLAR
Min. :0.000
                Min. :1.000
                                Min. :1.000
1st Qu.:2.000
                1st Qu.:1.000
                                1st Qu.:2.000
Median :3.000
                Median :3.000
                                Median :3.000
Mean :2.688
                Mean :2.219
                                Mean :2.438
3rd Qu.:3.250
                3rd Qu.:3.000
                                3rd Qu.:3.000
# pair plot
>library(GGally)
>ggpairs(teeth[,-1],cex=0.8)
```

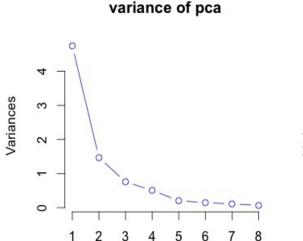


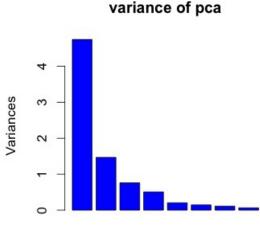
According to the pair correlations, we found strong some positive correlations: TCANINE vs BCANINE (corr=0.808), TPRMOLAR vs BPRMOLAR (corr=0.896), TMOLAR vs BMOLAR(corr=0.855) and TINCISOR vs BCANINE(corr=0.743). The result indicates the number of top and bottom teeth is highly related, the more top teeth, the more bottom teeth, except the incisor teeth.

#### 2.2 Principal Component Analysis

Since there are as many as eight variables recording the numbers of different types of teeth, and strong correlations exist among them. Naturally, we should consider to reduce the data dimension to simplify the further analysis.

Based on the output of principal component analysis, the first component(PC1) alone explains 59% of the variance, the second component(PC2) explains 7.7%, and the first four components (PC1+PC2+PC3+PC4) together account for 93.4% of the variance. Therefore, we may consider apply these four components in further data analysis instead.





```
>round(teeth.pca$rotation,3)
                                         PC5
                                                PC6
            PC1
                   PC2
                          PC3
                                  PC4
                                                        PC7
                                                               PC8
TINCISOR
         0.360
                 0.330 -0.214
                                0.473 - 0.485
                                              0.316 -0.341
                                                             0.201
         0.168 -0.691 -0.153
BINCISOR
                              -0.446 -0.436
                                              0.081
                                                     -0.253
          0.383 -0.198 -0.437
                                0.036
                                       0.507
                                              0.539
                                                      0.237
BCANINE
          0.391
                0.049 -0.498
                                0.040
                                       0.025
                                             -0.735
                                                    -0.025
TPRMOLAR
         0.373 -0.193
                        0.553
                                0.214 -0.044
                                              0.037
                                                     -0.142
         0.371 -0.323
                        0.348
                                       0.211 -0.239
                                                     0.169
BPRMOLAR
                                0.333
TMOLAR
         -0.382 -0.307 -0.156
                                       0.374 -0.057 -0.667 -0.017
                               0.383
                               0.522 -0.360 -0.019 0.519 -0.175
         -0.348 -0.369 -0.202
BMOLAR
```

The rotation table above shows how the PCs are consist of the original eight variables. Clearly, the weights of PC1 are quite similar(around 0.35), except BINCISOR. On the contrary, the PC2 and PC4 mainly explain BINCISOR (-0.691, 0.473 and -0.446). PC3 primarily relates to CANINE and PRMOLAR teeth.

### 2.3 Cluster Analysis

The dataset covers 32 animals, checking the records of their teeth, we found some of them actually have quite similar values. Then, it is reasonable that we may divide these animals into a few groups based on their teeth numbers. Therefore, we are going to apply cluster analysis to further explore this dataset.

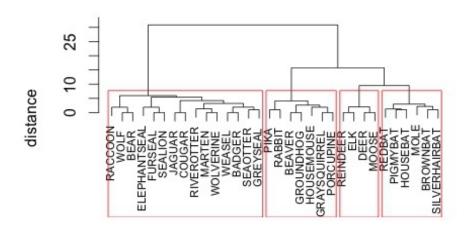
## 2.3.1 Hierarchical and K-means Cluster Analysis

First, we try hierarchical cluster analysis.

```
# hierarchical cluster analysis
> teeth2<-teeth[-1]
> dis<-dist(teeth2,method='euclidean')
> dis.matrix=as.matrix(dis)
> teeth ward<-hclust(dis, method="ward")</pre>
```

```
#plot the dendrogram cluster with city names at the bottom
> plot(teeth_ward, labels=teeth$ANIMAL, ylab='distance',cex=0.7)
> #cut the tree into 4 clusters and draw dendrogram with red borders around the clusters
> groups<-cutree(teeth_ward,k=4)
> rect.hclust(teeth_ward, k=4, border="red")
```

# Cluster Dendrogram



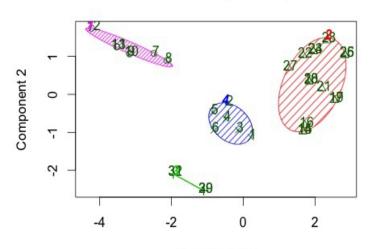
# dis hclust (\*, "ward")

```
##analyze the result
> round(aggregate(teeth[,2:9], by=list(groups),FUN=mean),3)
  Group.1 TINCISOR BINCISOR TCANINE BCANINE TPRMOLAR BPRMOLAR TMOLAR BMOLAR
             2.000
                       2.833
                                 1.0
                                        0.833
                                                 2.167
                                                           2.500
2
                       1.000
                                 0.0
                                        0.000
                                                                 3.000
                                                                            3.0
             1.286
                                                 1.571
                                                           1.143
3
        3
             2.933
                       2.600
                                 1.0
                                        1.000
                                                 3.600
                                                           3.400
                                                                  1.333
                                                                            1.8
             0.000
                       4.000
                                 0.5
                                        0.000
                                                 3.000
                                                           3.000
                                                                  3.000
> GROUP<-as.factor(groups)</pre>
 clusters<-cbind(teeth, GROUP)
 table(clusters$GROUP)
1
    2 3
    7 15
```

Through Ward method, the 32 animals are nicely divided into 4 clusters with size 6, 7, 15, 4. To confirm our analysis, we continue to apply k-means cluster analysis. And it turns out we got the same clusters with exactly size.

```
# K-means
>teeth.k<-kmeans(teeth2,centers=4)</pre>
> teeth.k$size
    7 15 4 6
> round(aggregate(teeth2,by=list(teeth.k$cluster),FUN=mean),3)
  Group.1 TINCISOR BINCISOR TCANINE BCANINE TPRMOLAR BPRMOLAR TMOLAR BMOLAR
             1.286
                       1.000
                                 0.0
                                       0.000
                                                 1.571
                                                           1.143
                                                                 3.000
        2
             2.933
                       2.600
                                 1.0
                                       1.000
                                                 3.600
                                                           3.400
                                                                  1.333
                                                                           1.8
3
        3
             0.000
                       4.000
                                 0.5
                                       0.000
                                                 3.000
                                                           3.000
                                                                  3.000
                                                                           3.0
                                                                 3.000
             2.000
                       2.833
                                 1.0
                                       0.833
                                                 2.167
                                                           2.500
> clusplot(teeth2, teeth.k$cluster, color=TRUE, shade=TRUE,labels=2, lines=0)
```

# CLUSPLOT( teeth2 )



Component 1
These two components explain 77.61 % of the point va

## 2.3.2 Summary and Conclusion

Since both hierarchical and k-means analysis yield the same result, in the summary, we just quote the result form k-means.

Group	Size	TINCISOR	BINCISOR	TCANINE	BCANINE	<b>TPRMOLAR</b>	<b>BPRMOLAR</b>	TMOLAR	BMOLAR
1	7	1.29	1.00	0.0	0.00	1.57	1.14	3.00	3.0
2	15	2.93	2.60	1.0	1.00	3.60	3.40	1.33	1.8
3	4	0.00	4.00	0.5	0.00	3.00	3.00	3.00	3.0
4	6	2.00	2.83	1.0	0.83	2.17	2.50	3.00	3.0

According to the summary table, we come up with the following conclusions:

- These 32 animals can be divided into four groups with size 7,15,4,and 6, and each group has similar teeth record.
- The seven animals in group 1 all have no CANINE teeth(top and bottom), three MOLAR teeth(top and bottom), one bottom INCISOR tooth. Furthermore, they also have 1.29 top INCISOR, 1.57 top PRMOLAR and 1.14 bottom PRMOLAR teeth on average.

	ANIMAL	TINCISOR	BINCISOR	TCANINE	BCANINE	TPRMOLAR	BPRMOLAR	TMOLAR	BMOLAR	GROUP
7	PIKA	2	1	0	0	2	2	3	3	1
8	RABBIT	2	1	Θ	Θ	3	2	3	3	1
9	BEAVER	1	1	Θ	Θ	2	1	3	3	1
10	GROUNDHOG	1	1	Θ	Θ	2	1	3	3	1
11	GRAYSQUIRREL	1	1	Θ	Θ	1	1	3	3	1
12	HOUSEMOUSE	1	1	Θ	Θ	0	0	3	3	1
13	PORCUPINE	1	1	0	0	1	1	3	3	1

• For group 2, the fifteen animals do not miss any of the eight kinds of teeth. They all have one top and bottom CANINE tooth. Furthermore, they tend to have around 3 INCISOR teeth(top and bottom respectively), around 3.5 PRMOLAR teeth, 1.33 top MOLAR tooth and 1.8 on

average, and bottom MOLAR tooth on average.

	ANIMAL	TINCISOR	BINCISOR	TCANINE	BCANINE	TPRMOLAR	BPRMOLAR	TMOLAR	BMOLAR	GROUP
14	WOLF	3	3	1	1	4	4	2	3	2
15	BEAR	3	3	1	1	4	4	2	3	2
16	RACCOON	3	3	1	1	4	4	3	2	2
17	MARTEN	3	3	1	1	4	4	1	2	2
18	WEASEL	3	3	1	1	3	3	1	2	2
19	WOLVERINE	3	3	1	1	4	4	1	2	2
20	BADGER	3	3	1	1	3	3	1	2	2
21	RIVEROTTER	3	3	1	1	4	3	1	2	2
22	SEAOTTER	3	2	1	1	3	3	1	2	2
23	JAGUAR	3	3	1	1	3	2	1	1	2
24	COUGAR	3	3	1	1	3	2	1	1	2
25	FURSEAL	3	2	1	1	4	4	1	1	2
26	SEALION	3	2	1	1	4	4	1	1	2
27	GREYSEAL	3	2	1	1	3	3	2	2	2
28	ELEPHANTSEAL	2	1	1	1	4	4	1	1	2

• Group 3 covers four animals, they are quite close to each other: no top INCISOR and bottom CANINE teeth, 4 bottom INCISOR teeth, 3 PRMOLAR teeth(top and bottom) and MOLAR teeth(top and bottom), either one or zero top CANINE tooth.

	ANIMAL	TINCISOR	BINCISOR	TCANINE	BCANINE	TPRMOLAR	BPRMOLAR	TMOLAR	BMOLAR	GROUP
2	REINDEER	0	4	1	0	3	3	3	3	3
3 (	Ð ELK	0	4	1	0	3	3	3	3	3
3	L DEER	0	4	0	0	3	3	3	3	3
3	2 MOOSE	0	4	0	0	3	3	3	3	3

• Group 4 consists of six animals, as for INCISOR and CANINE teeth, this group is pretty similar with group 2. The most difference relies on top MOLAR teeth, group 4 have 3 top MOLAR teeth while group 2 posses 1.33 on average.

	ANIMAL	TINCISOR	BINCISOR	TCANINE	BCANINE	TPRMOLAR	BPRMOLAR	TMOLAR	BMOLAR	GROUP
1	BROWNBAT	2	3	1	1	3	3	3	3	4
2	MOLE	3	2	1	0	3	3	3	3	4
3	SILVERHAIRBAT	2	3	1	1	2	3	3	3	4
4	PIGMYBAT	2	3	1	1	2	2	3	3	4
5	HOUSEBAT	2	3	1	1	1	2	3	3	4
6	REDBAT	1	3	1	1	2	2	3	3	4