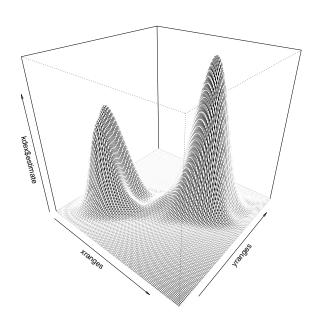
EXERCISE 10

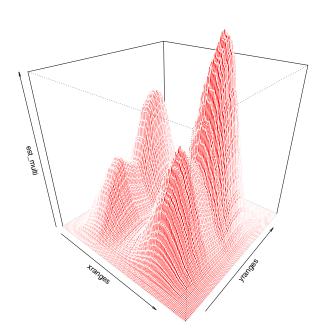
WEIYU LI

1. For the dataset faithful in R, use (i) multiplicative kernel and (ii) spherical-symmetric kernel to estimate the joint pdf of eruptions andwaiting. Consider different bandwidth selection methods.



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2 WEIYU LI

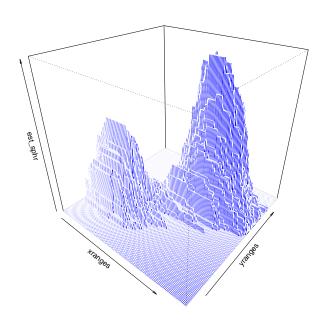


```
### (2) spherical kernel with I(|x| \le 1) / pi euclidean <- function(x){

# return the euclidean distance of each column y <- x[,1]
```

EXERCISE 10 3

```
for (i in 1:length(y)) {
    y[i] <- sqrt(sum(x[i,]^2))
  }
  return(y)
}
est_sphr <- kdex$estimate
for (i in 1:length(xranges)) {
    for (j in 1:length(yranges)) {
       tmp_pt <- cbind(rep(xranges[i], n), rep(yranges[j], n))
       est_sphr[i,j] <- sum(euclidean(x - tmp_pt) <= 1) / (pi * n)
    }
}
persp(xranges, yranges, est_sphr,
       phi = 30, theta = 40, col = 'blue', border = 0)</pre>
```



2. Suppose X_1, \ldots, X_n *i.i.d.* $\sim f(x)$, and an independent $U \sim Unif\{1, 2, \ldots, n\}$. Let $Y = X_U + hZ$, where Z has density p(x) and is independent with X_1, \ldots, X_n, U .

(1) Prove that with samples $X_1, ..., X_n$, the density of Y is exactly the KDE of f with kernel $p(\cdot)$ and bandwidth h, denoted as $\hat{f}(\cdot)$.

4 WEIYU LI

Proof. First note that the KDE

$$\hat{f}(y) = \frac{1}{nh} \sum_{i=1}^{n} p(\frac{y - X_i}{h}).$$

On the other hand, since Y given X_i is random with respect to U and Z, the pdf of Y is

$$f_Y(y) = \sum_{i=1}^n f_{Y|U}(y|U=i)P(U=i) = \sum_{i=1}^n f_{hZ}(y-X_i)\frac{1}{n} = \sum_{i=1}^n p(\frac{y-X_i}{h})\frac{1}{nh}$$

which is exactly the same as $\hat{f}(y)$.

(2) Given X_1, \ldots, X_n , solve Var(Y). Compare it with the sample variance with X_1, \ldots, X_n . Solve. From (1), we know that the pdf of Y is $\hat{f}(y) = \frac{1}{nh} \sum_{i=1}^n p(\frac{y-X_i}{h})$, then we have

$$EY = \int y \hat{f}(y) dy = \sum_{i=1}^{n} \frac{1}{n} \int y p\left(\frac{y - X_i}{h}\right) \frac{1}{h} dy$$

$$= \sum_{i=1}^{n} \frac{1}{n} \int (X_i + hz) p(z) dz$$

$$= \frac{1}{n} \sum_{i} X_i + hEZ,$$

$$EY^2 = \sum_{i=1}^{n} \frac{1}{n} \int (X_i + hz)^2 p(z) dz$$

$$= \frac{1}{n} \sum_{i} X_i^2 + \frac{1}{n} \sum_{i} 2hX_i EZ + h^2 EZ^2.$$

Therefore, we obtain

$$Var(Y) = \frac{1}{n} \sum_{i} X_i^2 - \left(\frac{1}{n} \sum_{i} X_i\right)^2 + h^2 Var Z = S_n^2 + h^2 Var Z,$$

where $S_n^2 = \frac{1}{n} \sum_i (X_i - \bar{X})^2 = \frac{n-1}{n} S^2$ and S^2 is the sample variance.

- 3. For the dataset wines (https://raw.githubusercontent.com/egarpor/handy/master/datasets/wines.txt), remove variable vintage and normalize the variables, then perform PCA. Use clustering methods based on density estimation (refer to cluster.R).
- (1) With 3 PCs, how many clusters can be found? If min.clust.size is set as 5% of the data size, then what's the result? Is the result sensitive to min.clust.size?
- (2) With the same min.clust.size and 6 PCs, how many clusters can be found? Use the scatter plots to identify PCs that helps clustering or not.
- (3) With 2 PCs, how many clusters can be found? Compare the result with that of 3 PCs.
- (4) Compare the results with the true clusters.

EXERCISE 10

(5) Compare the results with the results of k-means with k = 3, 4. library('mclust') library('ks') x <- read.table('wines.txt', header = T)</pre> $n \leftarrow nrow(x)$ $p \leftarrow ncol(x) -1$ true_cl <- unclass(as.factor(x[,'vintage']))</pre> $data_cl \leftarrow as.matrix(x[, -(p + 1)])$ # data normalization: each column is with norm \$\sqrt{n}\$ # if normalizing the norm to be 1, then each entry will be too small for (i in 1:p) { data_cl[, i] <- data_cl[, i] - mean(data_cl[, i])</pre> norm <- sqrt(sum(data_cl[, i]^2))</pre> data_cl[,i] <- data_cl[,i] * sqrt(n) / norm</pre> # perform PCA pca_cl <- prcomp(data_cl, center = F, scale. = F) # PCA informations</pre> data_pca <- data_cl %*% pca_cl\$rotation # data after PCA rotation ### (1) cluster using 3 PCs kms1.1 <- kms(data_pca[, 1:3])</pre> summary(kms1.1) # 4 clusters $kms1.2 \leftarrow kms(data_pca[, 1:3], min.clust.size = 0.05 * n)$ summary(kms1.2) # 3 clusters # This is sensitive to min.clust.size ### (2) cluster using 6 PCs $kms2 \leftarrow kms(data_pca[, 1:6], min.clust.size = 0.05 * n)$ summary(kms2) # 6 clusters pairs(data_pca[, 1:6]) ### (3) cluster using 2 PCs kms3 <- kms(data_pca[, 1:2])</pre> summary(kms3) # 4 clusters ### (4) comparison with true clusters classError(kms1.1\$label, true_cl)\$errorRate # 0.05649718 classError(kms1.2\$label, true_cl)\$errorRate # 0.05084746 classError(kms2\$label, true_cl)\$errorRate # 0.2711864 classError(kms3\$label, true_cl)\$errorRate # 0.1412429 # note that all the true 1st cluster can be clustered in one cluster ### (5) comparison with kmeans # Here we only show the comparison result between (1) and k-means kmeans1.1 <- kmeans(data_pca[, 1:3], 4)

6 WEIYU LI

classError(kmeans1.1\$cluster, true_cl)\$errorRate

4-means error: 0.1016949

classError(kms1.1\$label, true_cl)\$errorRate

kms error with 4 clust: 0.05649718

all the first and last true clusters are clustered in one cluster

to see this, you can use:

cbind(kmeans1.1\$cluster, kms1.1\$label, true_cl)

kmeans1.2 <- kmeans(data_pca[, 1:3], 3)</pre>

classError(kmeans1.2\$cluster, true_cl)\$errorRate

3-means error: 0.03954802

classError(kms1.2\$label, true_cl)\$errorRate

kms error with 3 clust: 0.05084746

all the first and last true clusters are clustered in one cluster

note that with the true k, k-means performs better;

while kms is less sensitive to cluster numbers

