8.1 Introduction

8.2 Density Estimation

The three kernel functions are implemented in R as shown in lines 1–3 of Figure 8.1. For some grid x, the kernel functions are plotted using the R statements in lines 5–11 (Figure 8.1).

The kernel estimator $\hat{f}$ is a sum of ‘bumps’ placed at the observations. The kernel function determines the shape of the bumps while the window width $h$ determines their width. Figure 8.2 (redrawn from a similar plot in Silverman, 1986) shows the individual bumps $n^{-1}h^{-1}K((x-x_i)/h)$, as well as the estimate $\hat{f}$ obtained by adding them up for an artificial set of data points.

R> x <- c(0, 1, 1.1, 1.5, 1.9, 2.8, 2.9, 3.5)
R> n <- length(x)

For a grid
R> xgrid <- seq(from = min(x) - 1, to = max(x) + 1, by = 0.01)

on the real line, we can compute the contribution of each measurement in x, with $h = 0.4$, by the Gaussian kernel (defined in Figure 8.1 line 3) as follows;

R> h <- 0.4
R> bumps <- sapply(x, function(a) gauss((xgrid - a)/h)/(n * h))

A plot of the individual bumps and their sum, the kernel density estimate $\hat{f}$, is shown in Figure 8.2.

8.3 Analysis Using R

8.3.1 A Parametric Density Estimate for the Old Faithful Data

R> logL <- function(param, x) {
+   d1 <- dnorm(x, mean = param[2], sd = param[3])
+   d2 <- dnorm(x, mean = param[4], sd = param[5])
+   -sum(log(param[1] * d1 + (1 - param[1]) * d2))
+ }
R> startparam <- c(p = 0.5, mu1 = 50, sd1 = 3, mu2 = 80, sd2 = 3)
R> opp <- optim(startparam, logL, x = faithful$waiting,
4 DENSITY ESTIMATION

\begin{verbatim}
R> rec <- function(x) (abs(x) < 1) * 0.5
R> tri <- function(x) (abs(x) < 1) * (1 - abs(x))
R> gauss <- function(x) 1/sqrt(2*pi) * exp(-x^2/2)
R> x <- seq(from = -3, to = 3, by = 0.001)
R> plot(x, rec(x), type = "l", ylim = c(0,1), lty = 1,
R> + ylab = expression(K(x)))
R> lines(x, tri(x), lty = 2)
R> lines(x, gauss(x), lty = 3)
R> legend(-3, 0.8, legend = c("Rectangular", "Triangular",
R> + "Gaussian"), lty = 1:3, title = "kernel functions",
R> + bty = "n")
\end{verbatim}

\begin{figure}[h]
\centering
\includegraphics[width=\textwidth]{kernelfunctions.png}
\caption{Three commonly used kernel functions.}
\end{figure}
ANALYSIS USING R

```r
R> plot(xgrid, rowSums(bumps), ylab = expression(hat(f)(x)),
+       type = "l", xlab = "x", lwd = 2)
R> rug(x, lwd = 2)
R> out <- apply(bumps, 2, function(b) lines(xgrid, b))
```

**Figure 8.2** Kernel estimate showing the contributions of Gaussian kernels evaluated for the individual observations with bandwidth $h = 0.4$.

```r
R> opp

$par
  p   mu1   sd1  mu2   sd2
0.361 54.612  5.872 80.093  5.867

$value
[1] 1034

$counts
```
R> epa <- function(x, y)
+   ((x^2 + y^2) < 1) * 2/pi * (1 - x^2 - y^2)
R> x <- seq(from = -1.1, to = 1.1, by = 0.05)
R> epavals <- sapply(x, function(a) epa(a, x))
R> persp(x = x, y = x, z = epavals, xlab = "x", ylab = "y",
+       zlab = expression(K(x, y)), theta = -35, axes = TRUE,
+       box = TRUE)

Figure 8.3  Epanechnikov kernel for a grid between \((-1.1, -1.1)\) and \((1.1, 1.1)\).
ANALYSIS USING R

```r
R> data("faithful", package = "datasets")
R> x <- faithful$waiting
R> layout(matrix(1:3, ncol = 3))
R> hist(x, xlab = "Waiting times (in min.)", ylab = "Frequency",
+       probability = TRUE, main = "Gaussian kernel",
+       border = "gray")
R> lines(density(x, width = 12), lwd = 2)
R> rug(x)
R> hist(x, xlab = "Waiting times (in min.)", ylab = "Frequency",
+       probability = TRUE, main = "Rectangular kernel",
+       border = "gray")
R> lines(density(x, width = 12, window = "rectangular"), lwd = 2)
R> rug(x)
R> hist(x, xlab = "Waiting times (in min.)", ylab = "Frequency",
+       probability = TRUE, main = "Triangular kernel",
+       border = "gray")
R> lines(density(x, width = 12, window = "triangular"), lwd = 2)
R> rug(x)
```

**Figure 8.4** Density estimates of the geyser eruption data imposed on a histogram of the data.
R> library("KernSmooth")
R> data("CYGOB1", package = "HSAUR2")
R> CYGOB1d <- bkde2D(CYGOB1, bandwidth = sapply(CYGOB1, dpik))
R> contour(x = CYGOB1d$x1, y = CYGOB1d$x2, z = CYGOB1d$fhat,
+ xlab = "log surface temperature",
+ ylab = "log light intensity")

Figure 8.5 A contour plot of the bivariate density estimate of the CYGOB1 data, i.e., a two-dimensional graphical display for a three-dimensional problem.

Of course, optimising the appropriate likelihood ‘by hand’ is not very convenient. In fact, (at least) two packages offer high-level functionality for estimating mixture models. The first one is package mclust (Fraley et al., 2012).
implementing the methodology described in [Fraley and Raftery (2002)]. Here, a Bayesian information criterion (BIC) is applied to choose the form of the mixture model:

```r
R> library("mclust")
R> mc <- Mclust(faithful$waiting)
R> mc

'Mclust' model object: (E,2)

Available components:

Figure 8.6  The bivariate density estimate of the CYGOB1 data, here shown in a three-dimensional fashion using the persp function.

and the estimated means are
R> mc$parameters$mean
   1 2
54.6 80.1

with estimated standard deviation (found to be equal within both groups)
R> sqrt(mc$parameters$variance$sigmasq)
   [1] 5.87

The proportion is $\hat{p} = 0.36$. The second package is called \texttt{flexmix} whose functionality is described by Leisch (2004). A mixture of two normals can be fitted using
R> library("flexmix")
R> fl <- flexmix(waiting ~ 1, data = faithful, k = 2)

with $\hat{p} = 0.52$ and estimated parameters
R> parameters(fl, component = 1)
Comp.1
coef. (Intercept) 70.8
sigma 13.6

R> parameters(fl, component = 2)
Comp.2
coef. (Intercept) 71.0
sigma 13.6

We can get standard errors for the five parameter estimates by using a bootstrap approach (see Efron and Tibshirani [1993]). The original data are slightly perturbed by drawing $n$ out of $n$ observations \textit{with replacement} and those artificial replications of the original data are called \textit{bootstrap samples}. Now, we can fit the mixture for each bootstrap sample and assess the variability of the estimates, for example using confidence intervals. Some suitable R code based on the \texttt{Mclust} function follows. First, we define a function that, for a bootstrap sample $\text{indx}$, fits a two-component mixture model and returns $\hat{p}$ and the estimated means (note that we need to make sure that we always get an estimate of $p$, not $1 - p$):
R> library("boot")
R> fit <- function(x, indx) {
+    a <- Mclust(x[indx], minG = 2, maxG = 2,
+        modelNames="E")$parameters
+    if (a$pro[1] < 0.5)
+        return(c(p = a$pro[1], mu1 = a$mean[1],
+                mu2 = a$mean[2]))
+    return(c(p = 1 - a$pro[1], mu1 = a$mean[2],
+              mu2 = a$mean[1]))
+  }
ANALYSIS USING R

R> opar <- as.list(opp$par)
R> rx <- seq(from = 40, to = 110, by = 0.1)
R> d1 <- dnorm(rx, mean = opar$mu1, sd = opar$sd1)
R> d2 <- dnorm(rx, mean = opar$mu2, sd = opar$sd2)
R> f <- opar$p * d1 + (1 - opar$p) * d2
R> hist(x, probability = TRUE, xlab = "Waiting times (in min.)",
+ border = "gray", xlim = range(rx), ylim = c(0, 0.06),
+ main = "")
R> lines(rx, f, lwd = 2)
R> lines(rx, dnorm(rx, mean = mean(x), sd = sd(x)), lty = 2,
+ lwd = 2)
R> legend(50, 0.06, lty = 1:2, bty = "n",
+ legend = c("Fitted two-component mixture density",
+ "Fitted single normal density"))

![Graph](image)

**Figure 8.7** Fitted normal density and two-component normal mixture for geyser eruption data.
The function `fit` can now be fed into the `boot` function (Canty and Ripley, 2012) for bootstrapping (here 1000 bootstrap samples are drawn)

```R
R> bootpara <- boot(faithful$waiting, fit, R = 1000)
```

We assess the variability of our estimates $\hat{p}$ by means of adjusted bootstrap percentile (BCa) confidence intervals, which for $\hat{p}$ can be obtained from

```R
R> boot.ci(bootpara, type = "bca", index = 1)
```

<table>
<thead>
<tr>
<th>Level</th>
<th>BCa</th>
</tr>
</thead>
<tbody>
<tr>
<td>95%</td>
<td>(0.304, 0.423)</td>
</tr>
</tbody>
</table>

Calculations and Intervals on Original Scale

We see that there is a reasonable variability in the mixture model; however, the means in the two components are rather stable, as can be seen from

```R
R> boot.ci(bootpara, type = "bca", index = 2)
```

<table>
<thead>
<tr>
<th>Level</th>
<th>BCa</th>
</tr>
</thead>
<tbody>
<tr>
<td>95%</td>
<td>(53.4, 56.1)</td>
</tr>
</tbody>
</table>

Calculations and Intervals on Original Scale

for $\hat{\mu}_1$ and for $\hat{\mu}_2$ from

```R
R> boot.ci(bootpara, type = "bca", index = 3)
```

<table>
<thead>
<tr>
<th>Level</th>
<th>BCa</th>
</tr>
</thead>
<tbody>
<tr>
<td>95%</td>
<td>(79, 81)</td>
</tr>
</tbody>
</table>

Calculations and Intervals on Original Scale

Finally, we show a graphical representation of both the bootstrap distribution of the mean estimates and the corresponding confidence intervals. For convenience, we define a function for plotting, namely

```R
R> bootplot <- function(b, index, main = "") {
+   dens <- density(b$t[,index])
+   ci <- boot.ci(b, type = "bca", index = index)$bca[4:5]
+   est <- b$t0[index]
+   plot(dens, main = main)
+   y <- max(dens$y) / 10
+   segments(ci[1], y, ci[2], y, lty = 2)
+   points(ci[1], y, pch = "(")
```
R> layout(matrix(1:2, ncol = 2))
R> bootplot(bootpara, 2, main = expression(mu[1]))
R> bootplot(bootpara, 3, main = expression(mu[2]))

Figure 8.8  Bootstrap distribution and confidence intervals for the mean estimates of a two-component mixture for the geyser data.

+   points(ci[2], y, pch = "*")
+   points(est, y, pch = 19)
+ }

The element t of an object created by boot contains the bootstrap replications of our estimates, i.e., the values computed by fit for each of the 1000 bootstrap samples of the geyser data. First, we plot a simple density estimate and then construct a line representing the confidence interval. We apply this function to the bootstrap distributions of our estimates $\hat{\mu}_1$ and $\hat{\mu}_2$ in Figure 8.8.
Bibliography


