

Reproduction of Analyses in Lohr (1999) using the **survey** package

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1 Introduction

The Introduction chapter does not contain any numerical examples demonstrating survey methodology. Before reproducing the analyses of the following chapters, we load the SDA package

```
> library(SDaA)
```

The `survey` package is loaded as well as it was specified as a dependency of the `SDaA` package.

2 Simple Probability Samples

3 Ratio and Regression Estimation

3.1 Ratio Estimation

```
> agsrsDesign <- svydesign(ids = ~1, weights = ~1,
+   data = agsrs)
```

```
> svyratio(numerator = ~acres92, denominator = ~acres87,
+         design = agsrsDesign)
```

```
Ratio estimator: svyratio.survey.design2(numerator = ~acres92, denominator = ~acres87,
+         design = agsrsDesign)
```

```
Ratios=
```

```
          acres87
```

```
acres92 0.9865652
```

```
SEs=
```

```
          acres87
```

```
acres92 0.006053015
```

```
> seedlings <- data.frame(tree = 1:10, x = c(1, 0,
+      8, 2, 76, 60, 25, 2, 1, 31), y = c(0, 0, 1, 2,
+      10, 15, 3, 2, 1, 27))
> names(seedlings) <- c("tree", "x", "y")
```

3.2 Regression Estimation

```
> pf <- data.frame(photo = c(10, 12, 7, 13, 13, 6,
+      17, 16, 15, 10, 14, 12, 10, 5, 12, 10, 10, 9,
+      6, 11, 7, 9, 11, 10, 10), field = c(15, 14, 9,
+      14, 8, 5, 18, 15, 13, 15, 11, 15, 12, 8, 13,
+      9, 11, 12, 9, 12, 13, 11, 10, 9, 8))
```

3.3 Estimation in Domains

3.4 Models for Ratio and Regression Estimation

```
> recacr87 <- agsrs$acres87
> recacr87[recacr87 > 0] <- 1/recacr87[recacr87 > 0]
> model1 <- lm(acres92 ~ 0 + acres87, weights = recacr87,
+         data = agsrs)
> summary(model1)
```

```
Call:
```

```
lm(formula = acres92 ~ 0 + acres87, data = agsrs, weights = recacr87)
```

```
> plot(I(acres92/10^6) ~ I(acres87/10^6), xlab = "Millions of Acres Devoted to Farms (1987)",  
+      ylab = "Millions of Acres Devoted to Farms (1992)",  
+      data = agsrs)  
> abline(lm(I(acres92/10^6) ~ 0 + I(acres87/10^6),  
+      data = agsrs), col = "red", lwd = 2)
```

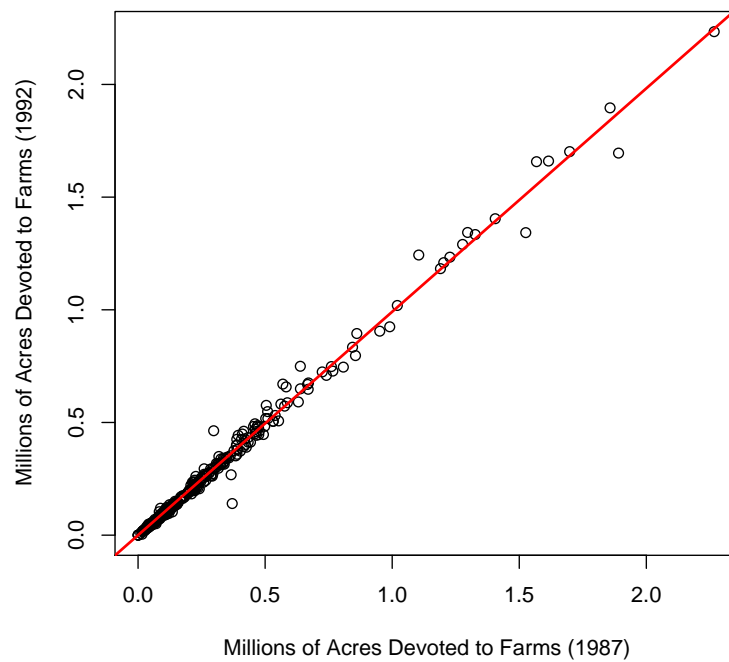


Figure 1: Figure 3.1, p. 64

```
> plot(y ~ x, data = seedlings, xlab = "Seedlings Alive (March 1992)",
+      ylab = "Seedlings That Survived (February 1994)")
```

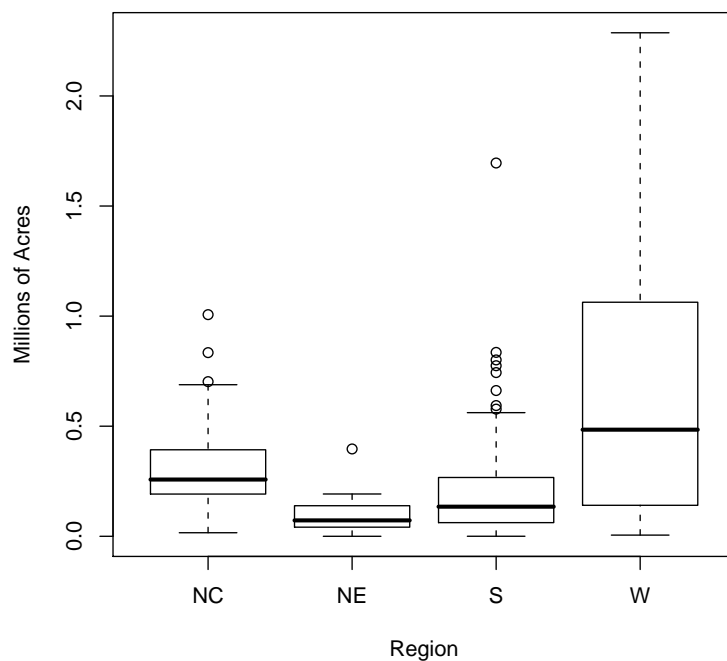


Figure 2: Figure 3.4, p. 73

Residuals:

	Min	1Q	Median	3Q	Max
	-369.878	-22.090	-5.736	10.764	311.713

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
acres87	0.986565	0.004844	203.7	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 46.1 on 298 degrees of freedom

```
> wtresid <- resid(model1)/sqrt(agsrs$acres87)
> plot(wtresid ~ I(agsrs$acres87/10^6), xlab = "Millions of Acres Devoted to Farms (1987)",
+       ylab = "Weighted Residuals")
```

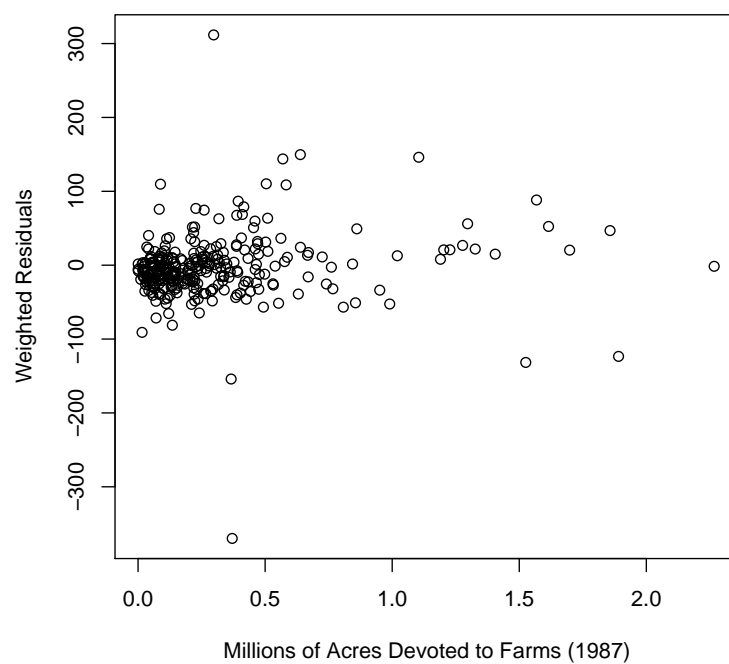


Figure 3: Figure 3.6, p. 85

Multiple R-squared: 0.9929, Adjusted R-squared: 0.9928
F-statistic: 4.149e+04 on 1 and 298 DF, p-value: < 2.2e-16

4 Stratified Sampling

```
> boxplot(acres92/10^6 ~ region, xlab = "Region", ylab = "Millions of Acres",
+         data = agstrat)
```

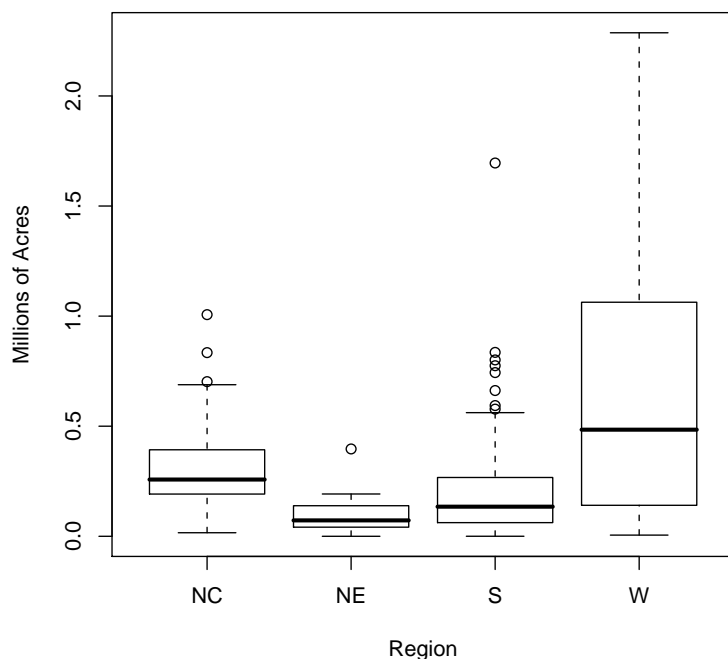


Figure 4: Figure 4.1, p. 97

5 Cluster Sampling with Equal Probabilities

5.1 Notation for Cluster Sampling

No analyses contained in this section.

5.2 One-Stage Cluster Sampling

```
> GPA <- cbind(expand.grid(1:4, 1:5), gpa = c(3.08,
+       2.6, 3.44, 3.04, 2.36, 3.04, 3.28, 2.68, 2, 2.56,
+       2.52, 1.88, 3, 2.88, 3.44, 3.64, 2.68, 1.92,
```

```

+      3.28, 3.2))
> names(GPA)[1:2] <- c("person_num", "cluster")
> GPA$pwt <- 100/5
> clusterDesign <- svydesign(ids = ~cluster, weights = ~pwt,
+   data = GPA)
> svytotal(~gpa, design = clusterDesign)

```

```

      total      SE
gpa 1130.4 67.167

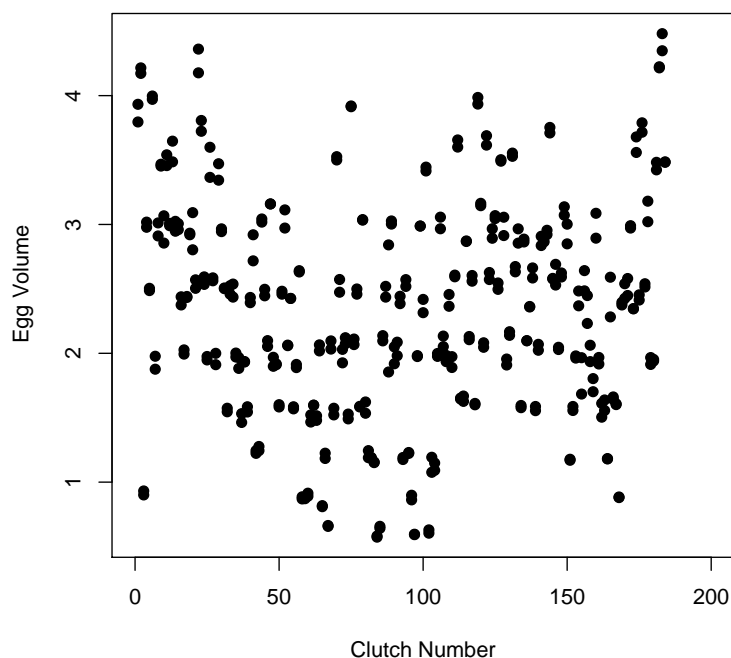
```

5.3 Two-Stage Cluster Sampling

```

> plot(volume ~ clutch, xlim = c(0, 200), pch = 19,
+   data = coots, xlab = "Clutch Number", ylab = "Egg Volume")

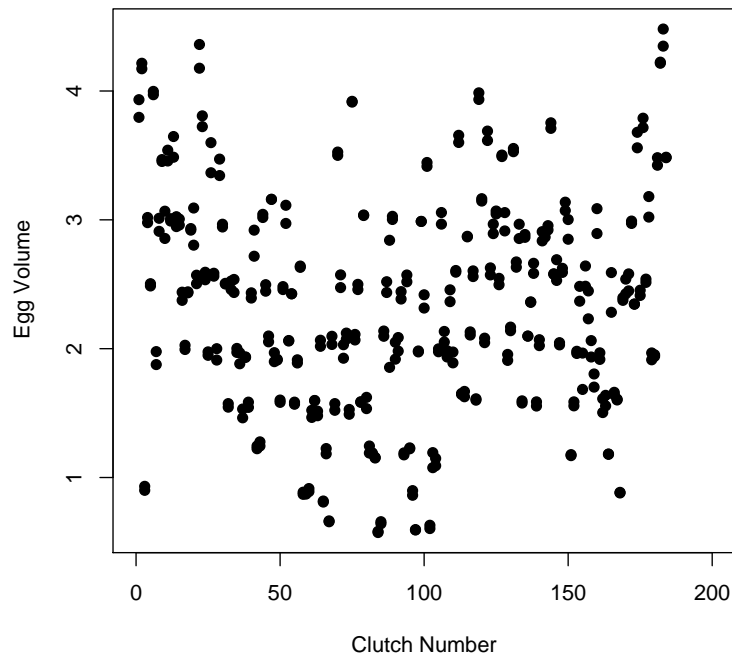
```



```

> plot(volume ~ clutch, xlim = c(0, 200), pch = 19,
+   data = coots, xlab = "Clutch Number", ylab = "Egg Volume")

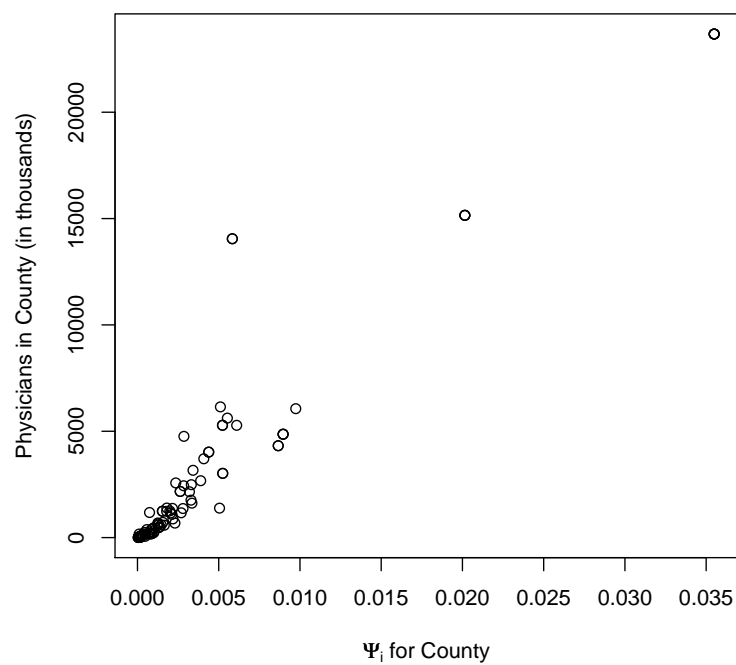
```

6 Sampling with Unequal Probabilities

```
> data(statepop)
> statepop$psi <- statepop$popn/255077536

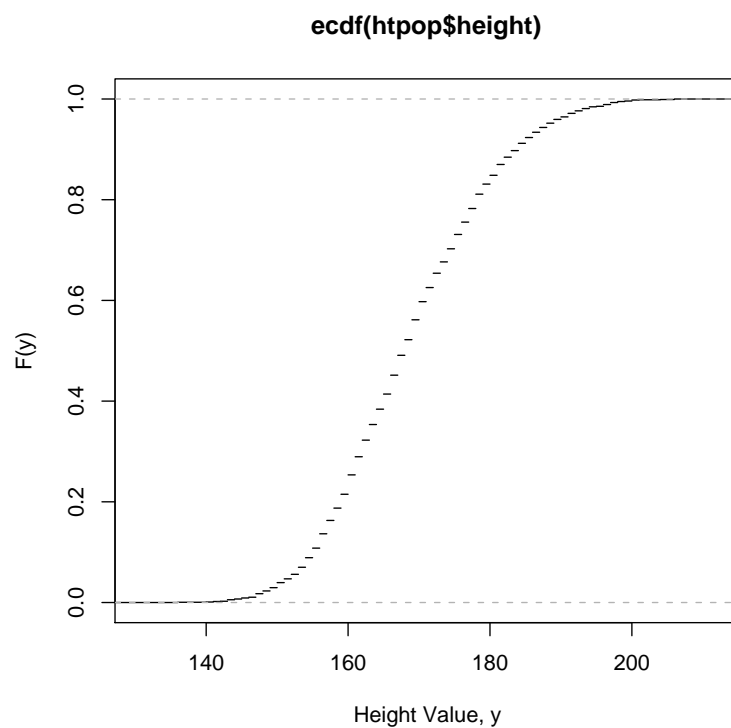
> plot(phys ~ psi, data = statepop, xlab = expression(paste(Psi[i],
+ " for County")), ylab = "Physicians in County (in thousands)")
```



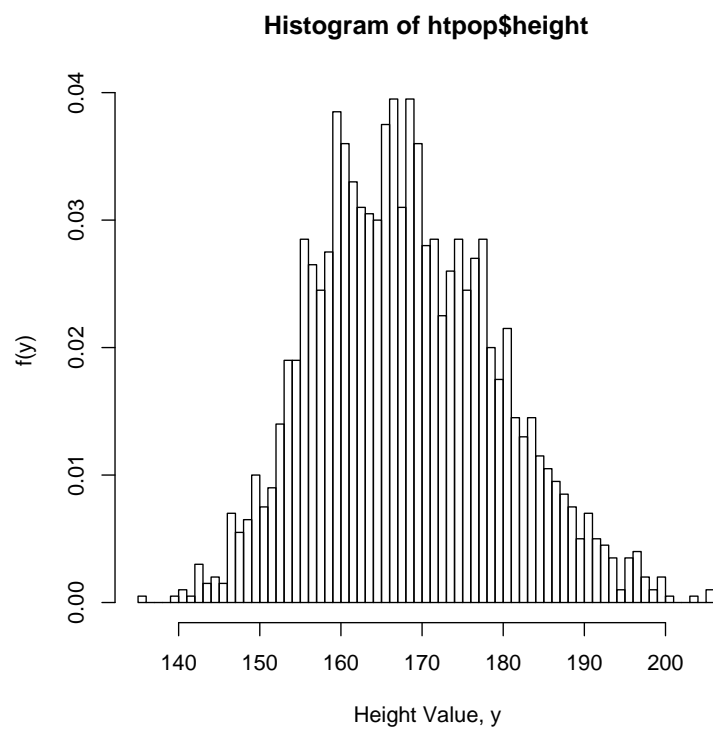
7 Complex Surveys

7.1 Estimating a Distribution Function

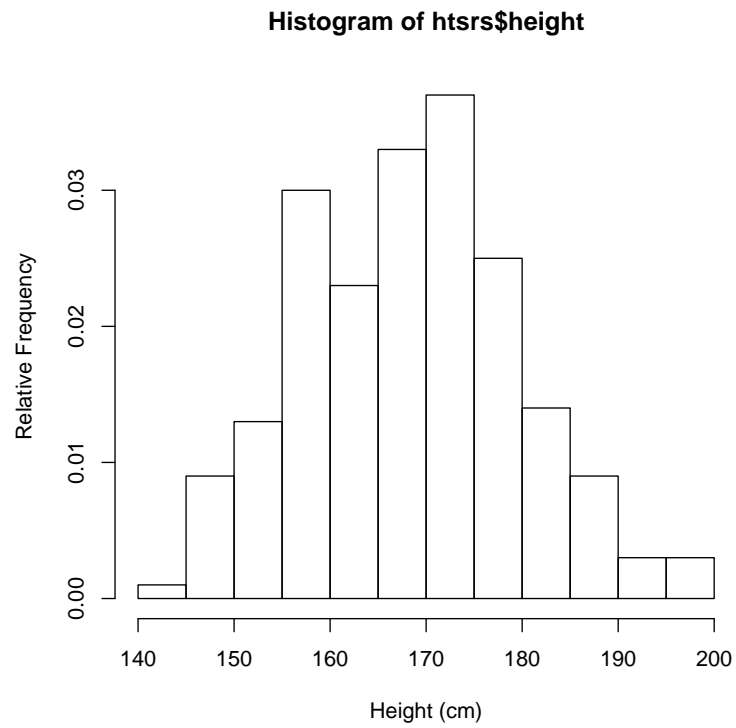
```
> data(htpop)
> popecdf <- ecdf(htpop$height)
> plot(popecdf, do.points = FALSE, ylab = "F(y)", xlab = "Height Value, y")
```



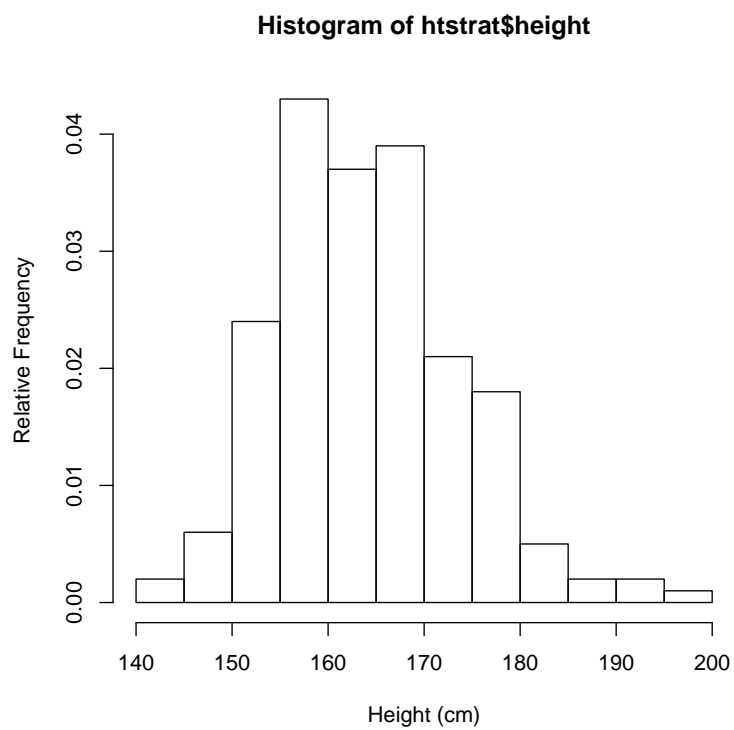
```
> minht <- min(htpop$height)
> breaks <- c(minht - 1, seq(from = minht, to = max(htpop$height),
+   by = 1))
> hist(htpop$height, ylab = "f(y)", breaks = breaks,
+   xlab = "Height Value, y", freq = FALSE)
```



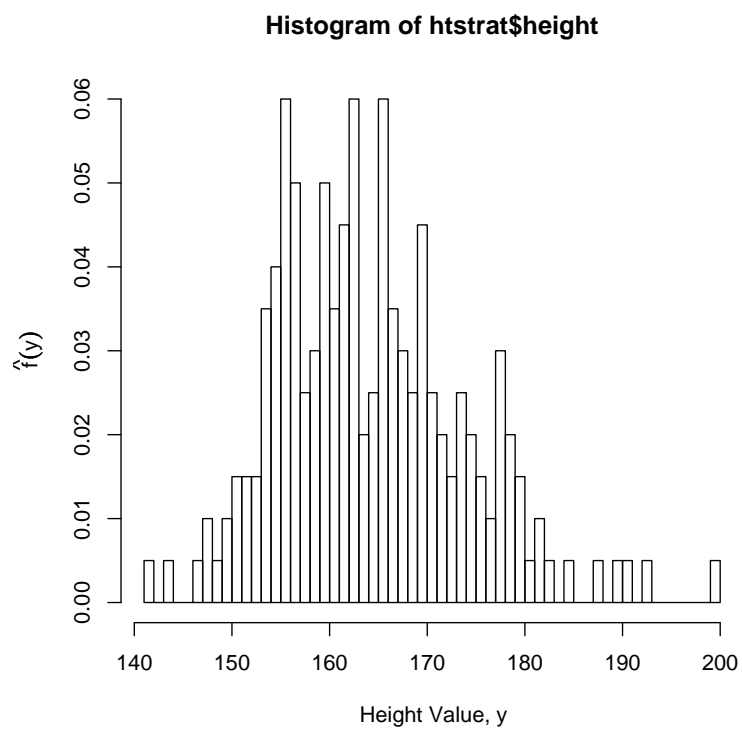
```
> data(htsrs)
> hist(htsrs$height, ylab = "Relative Frequency", xlab = "Height (cm)",
+      freq = FALSE)
```



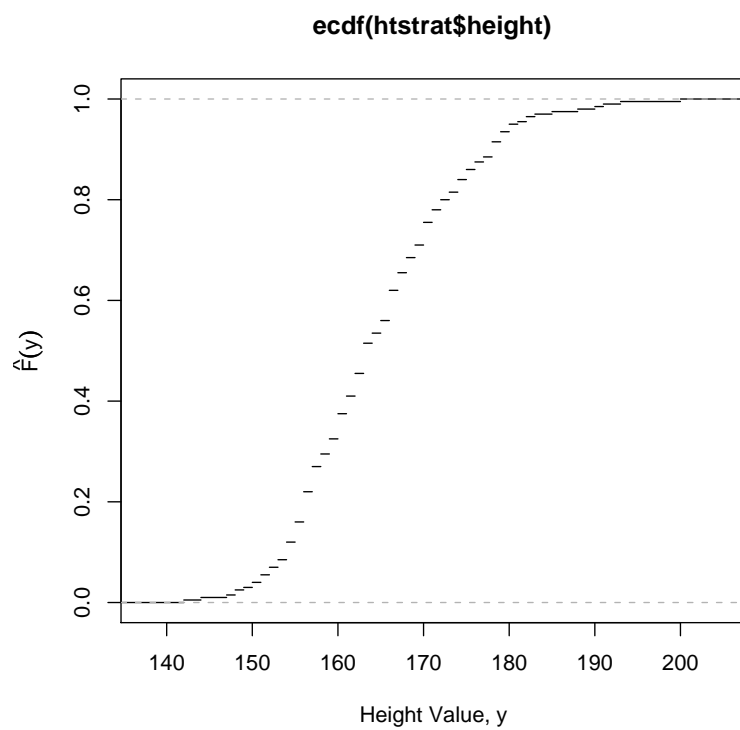
```
> data(htstrat)
> hist(htstrat$height, ylab = "Relative Frequency",
+       xlab = "Height (cm)", freq = FALSE)
```



```
> minht <- min(htstrat$height)
> breaks <- c(minht - 1, seq(from = minht, to = max(htstrat$height),
+   by = 1))
> hist(htstrat$height, ylab = expression(hat(f)(y)),
+   breaks = breaks, xlab = "Height Value, y", freq = FALSE)
```

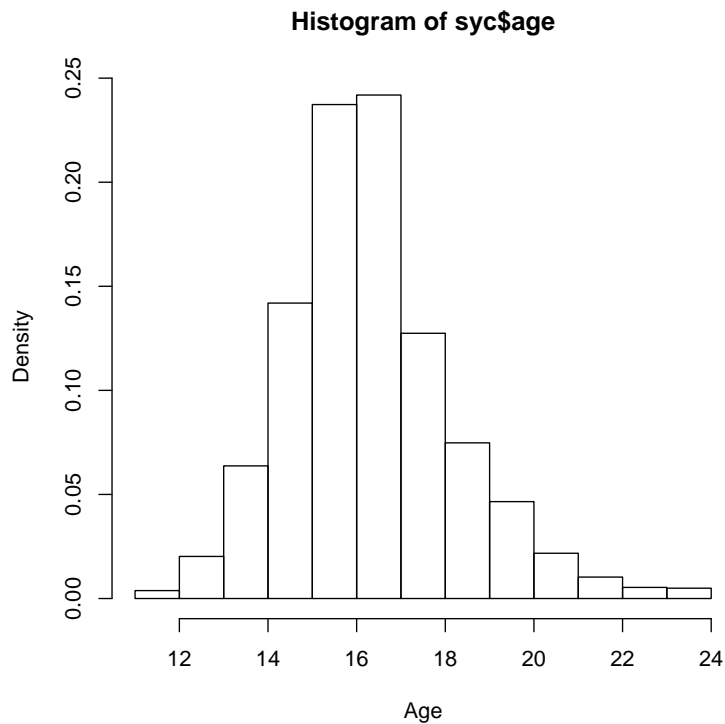


```
> stratecdf <- ecdf(htstrat$height)
> plot(stratecdf, do.points = FALSE, ylab = expression(hat(F)(y)),
+       xlab = "Height Value, y")
```



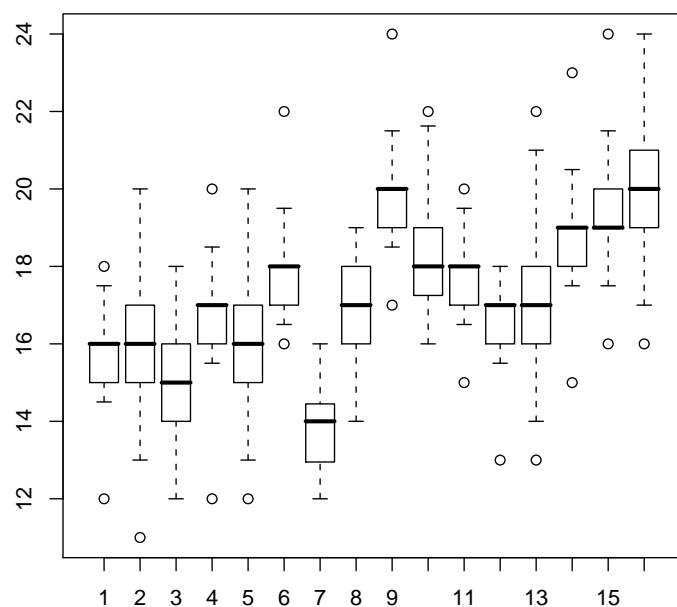
7.2 Plotting Data from a Complex Survey

```
> data(syc)
> hist(syc$age, freq = FALSE, xlab = "Age")
```

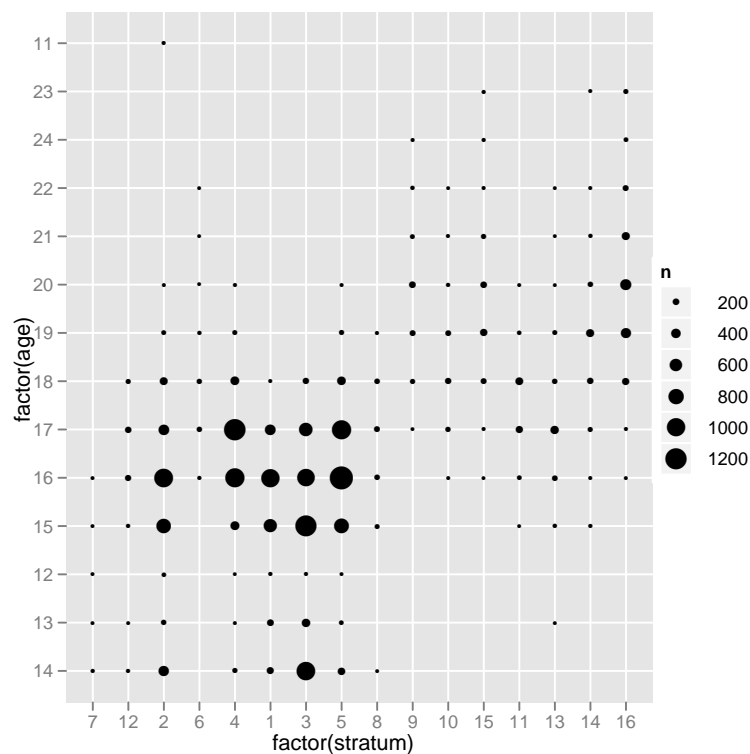
Note that in its current implementation, `svyboxplot` will only plot minimum and maximum as outliers if they are situated outside the whiskers. Other outliers are not plotted (see `?svyboxplot`). This explains the minor difference with Figure 7.8 on p. 237 of Lohr (1999).

```
> sycdesign <- svydesign(ids = ~psu, strata = ~stratum,  
+   data = syc, weights = ~finalwt)  
> oo <- options(survey.lonely.psu = "certainty")  
> svyboxplot(age ~ factor(stratum), design = sycdesign)  
> options(oo)
```



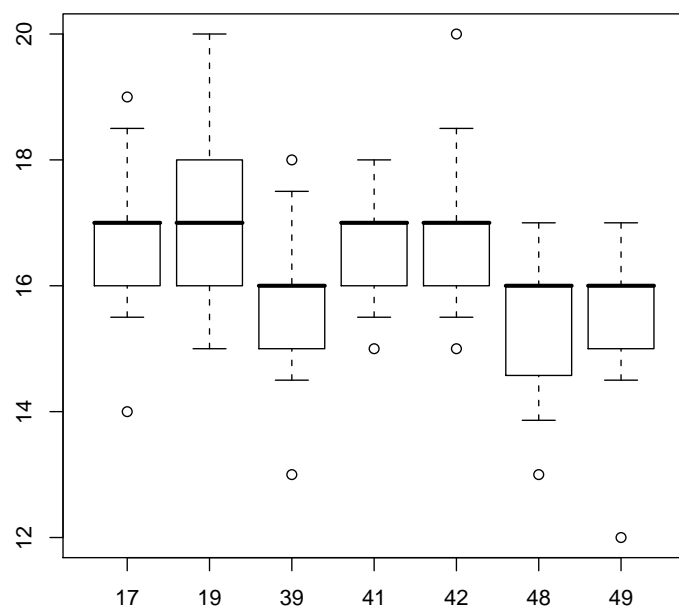
This kind of plot is particularly easy to formulate in the grammar of graphics, i.e. using the `ggplot2` package :

```
> p <- ggplot(syc, aes(x = factor(stratum), y = factor(age)))
> g <- p + stat_sum(aes(group = 1, weight = finalwt,
+   size = ..n..))
> print(g)
```

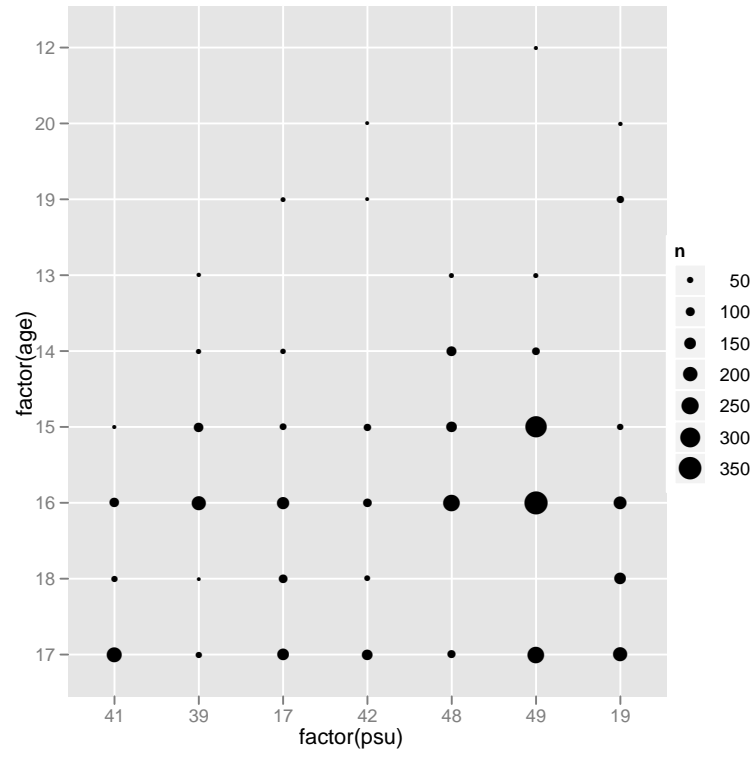


Note that in its current implementation, `svyboxplot` will only plot minimum and maximum as outliers if they are situated outside the whiskers. Other outliers are not plotted (see `?svyboxplot`). This explains the minor difference with Figure 7.10 on p. 238 of Lohr (1999).

```
> oo <- options(survey.lonely.psu = "certainty")
> sycstrat5 <- subset(sycdesign, stratum == 5)
> svyboxplot(age ~ factor(psu), design = sycstrat5)
> options(oo)
```



```
> sycstrat5df <- subset(syc, stratum == 5)
> p <- ggplot(sycstrat5df, aes(x = factor(psu), y = factor(age)))
> g <- p + stat_sum(aes(group = 1, weight = finalwt,
+   size = ..n..))
> print(g)
```



8 Nonresponse

9 Variance Estimation in Complex Surveys

9.1 Linearization (Taylor Series) Methods

9.2 Random Group Methods

9.3 Resampling and Replication Methods

9.4 Generalized Variance Functions

9.5 Confidence Intervals

10 Categorical Data Analysis in Complex Surveys

10.1 Chi-Square Tests with Multinomial Sampling

```
> hh <- rbind(c(119, 188), c(88, 105))
> rownames(hh) <- c("cableYes", "cableNo")
> colnames(hh) <- c("computerYes", "computerNo")
> addmargins(hh)
```

	computerYes	computerNo	Sum
cableYes	119	188	307
cableNo	88	105	193
Sum	207	293	500

```
> chisq.test(hh, correct = FALSE)
```

Pearson's Chi-squared test

data: hh

X-squared = 2.281, df = 1, p-value = 0.1310

```
> nst <- rbind(c(46, 222), c(41, 109), c(17, 40), c(8,
+      26))
```

```
> colnames(nst) <- c("NR", "R")
> rownames(nst) <- c("generalStudent", "generalTutor",
+   "psychiatricStudent", "psychiatricTutor")
> addmargins(nst)
```

	NR	R	Sum
generalStudent	46	222	268
generalTutor	41	109	150
psychiatricStudent	17	40	57
psychiatricTutor	8	26	34
Sum	112	397	509

```
> chisq.test(nst, correct = FALSE)
```

Pearson's Chi-squared test

data: nst

X-squared = 8.2176, df = 3, p-value = 0.04172

```
> afp <- data.frame(nAccidents = 0:7, nPilots = c(12475,
+   4117, 1016, 269, 53, 14, 6, 2))
> lambdahat <- sum(afp$nAccidents * afp$nPilots/sum(afp$nPilots))
> observed <- afp$nPilots
> expected <- dpois(0:7, lambda = lambdahat) * sum(afp$nPilots)
> sum((observed - expected)^2/expected)
```

```
[1] 1935.127
```

10.2 Effects of Survey Design on Chi-Square Tests

```
> hh2 <- rbind(c(238, 376), c(176, 210))
> rownames(hh2) <- c("cableYes", "cableNo")
> colnames(hh2) <- c("computerYes", "computerNo")
> addmargins(hh2)
```

	computerYes	computerNo	Sum
cableYes	238	376	614
cableNo	176	210	386
Sum	414	586	1000

```
> chisq.test(hh2, correct = FALSE)
```

Pearson's Chi-squared test

data: hh2

X-squared = 4.5621, df = 1, p-value = 0.03269

10.3 Corrections to Chi-Square Tests

11 Regression with Complex Survey Data

11.1 Model-Based Regression in Simple Random Samples

11.2 Regression in Complex Surveys

12 Other Topics in Sampling