# 1: Key Ideas and Issues

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### Ideas and issues illustrated by the graphs in this vignette

Ideas and issues that the graphs given here are designed to illustrate can be summarized under the headings:

- Data Issues
  - Data Exploration
  - Source/target issues
  - Data validity, accuracy and relevance
- Models and Model Assumptions
  - Model assumptions
  - Least squares, maximum likelihood and Bayesian estimation
  - Simulation from an assumed model
  - Model diagnostics
  - Weighting biases – problems for interpretation of model parameters

## 1 Code for Functions that Give the Figures

```
fig1.1 <-
function (form = depression ~ weight, data = roller, ...)
{
    yvar <- all.vars(form)[1]
    xvar <- all.vars(form)[2]
    x <- data[, xvar]
    y <- data[, yvar]
    maxx <- max(x)
    maxy <- max(y)
    plot(form, data = roller, xlim = c(0, 1.04 * maxx), ylim = c(0,
         1.04 * maxy), xaxs = "i", yaxs = "i", ...,
         main="1.1: Depression vs weight")
}
```

```
fig1.2 <-
function ()
{
print("Run the separate functions fig1.2A() and fig1.2B()")
}
```

```
fig1.2A <-
function ()
{
    require(MASS)
    plot(brain ~ body, data = mammals, pty = "s")
    mtext(side = 3, line = 0.5, adj = 0, "1.2A: Unlogged data")
}
```

```
fig1.2B <-
function ()
{
    library(MASS)
    plot(brain ~ body, data = mammals, log = "xy", pty = "s")
    mtext(side = 3, line = 0.5, adj = 0, "1.2B: Log scales on both axes")
}
```

```
fig1.3 <-
function ()
{
    opar <- par(mar=rep(0.6,4), oma=c(0,0,2,0))
    pairs(log(mammals), labels = c("log(body)", "log(brain)"))
    mtext(side=3, line=0.75, outer=TRUE, "1.3: Pairs plot")
}
```

```
fig1.4 <-
function (parset = simpleTheme(pch = 1:10, alpha = 0.6, cex = 1),
    fontsize = list(text = 14, points = 10))
{
    if (!is.null(parset))
        parset$fontsize <- fontsize
    library(MASS)
    droplevs <- fgl$type %in% c("Tabl", "Con")
    usefgl <- droplevels(subset(fgl, !droplevs))
    fgl.hat <- predict(lda(type ~ ., data = usefgl))
    gph <- xyplot(fgl.hat$x[, 2] ~ fgl.hat$x[, 1],
                  groups = usefgl$type,
                  auto.key = list(columns = 2),
                  xlab = "Axis 1", ylab = "Axis 2",
                  aspect = 1, scales = list(tck = 0.4),
                  par.settings = parset,
                  title = "1.4: Plot of first two linear discriminant scores")
    gph
}
```

```
fig1.5 <-
function ()
{
    opar <- par(mar=rep(0.5,4))
    if(!require(diagram))stop("Package 'diagram' must be installed")
    openplotmat(xlim = c(-0.1, 1.1))
    textellipse(mid=c(.5, .8), radx=0.6, rady=0.25,
                lab="Source", adj=c(.5,-2),
                box.col="gray95")
    textellipse(mid=c(.5, .7), radx=0.3, rady=0.1,
                lab="Source Sample", adj=c(.5,.5),
                box.col="gray90")
    textellipse(mid=c(.5, .2), radx=0.6, rady=0.25,
                lab="Target", adj=c(.5,-2),
                box.col="gray95")
    textellipse(mid=c(.5, .1), radx=0.3, rady=0.1,
                lab="Target Sample?", adj=c(.5,.5),
                box.col="gray90")
    par(opar)
}
```

```
fig1.6 <-
function ()
{
    library(DAAG)
    roller.obj <- lm(depression ~ weight, data = roller)
    yhat <- predict(roller.obj)
    ymax <- max(c(roller$depression, yhat))
    plot(depression ~ weight, data = roller, xlab = "Roller weight (t)",
        ylab = "Depression in lawn (mm)", pch = 4, xlim = c(0,
            max(roller$weight) * 1.01), ylim = c(0, ymax * 1.01),
        xaxs = "i", yaxs = "i", main="")
    abline(roller.obj)
    b <- summary(roller.obj)$coef
    topleft <- par()$usr[c(1, 4)]
    chw <- par()$cxy[1]
    chh <- par()$cxy[2]
    legend(topleft[1], topleft[2] + 0.25 * chh, pch = c(1, 4),
        legend = c("Fitted values", "Data values"), adj = 0,
        cex = 0.8, x.intersp = 0.8, y.intersp = 0.8, bty = "n")
    df <- cbind(roller, above = as.numeric(roller$depression >
        yhat))
    with(df, segments(weight, depression, weight, yhat, col = c("gray45",
        "black")[above + 1]))
    n <- nrow(roller)
    ns <- with(roller, min((1:n)[depression - yhat >= 0.75 *
        max(depression - yhat)]))
    ypos <- 0.5 * (roller$depression[ns] + yhat[ns])
    text(roller$weight[ns], ypos, "+ve residual", pos = 2, cex = 0.8)
    points(roller$weight, yhat, pch = 1)
    ns <- with(roller, (1:n)[depression - yhat == min(depression -
        yhat)][1])
    ypos <- 0.5 * (roller$depression[ns] + yhat[ns])
    text(roller$weight[ns], ypos, "-ve residual", pos = 4, cex = 0.8)
    mtext(side=3, line=0.75,
          "1.6: Lawn roller plot + line & annotation")
}
```

```
fig1.7 <- function(){
    obj <- lm(depression ~ weight, data=roller)
    gph <- plotSimScat(obj, sigma=6.4, layout=c(4,1), aspect=1)
    gph <- update(gph, xlab="Roller weight (t)", ylab="Depression (mm)",
                  main="1.7: Lawn roller data")
    gph
}
```

```
fig1.8 <- function(){
    pset <- simpleTheme(col.line="gray")
    gph <- xyplot(timef~time,
                  data=nihills,
                  aspect=1,
                  type=c("p","r"),
                  par.settings=pset)
    gph <- update(gph, xlab="Male record times",
                  ylab="Female record times",
                  main="1.8: f vs m times")
    gph
}
```

```
fig1.9 <- function(obj=mftime.lm){
    gph <- plotSimScat(obj, layout=c(4,1), aspect=1)
    update(gph, xlab="Record times for males (h)",
           ylab="Record times for females (h)",
           main="1.9: f vs m times, simulation")
}
```

```
fig1.10 <- function(obj=mftime.lm){
    plot(obj, which=1, caption=NULL,
         sub.caption=NULL,
         main="1.10: Diagnostic plot 1")
}
```

```
fig1.11 <- function(obj=mftime.lm){
    gph <- plotSimScat(obj, show="residuals",
                       type=c("p","smooth"), layout=c(4,1))
    gph <- update(gph, xlab="Time (h) for males", ylab="Residuals",
                  title="1.11: Diagnostic plot 1; 4 simulations",
                  aspect=1)
    gph
}
```

```
fig1.12 <- function(obj=mftime.lm){
    plot(obj, which=2, caption=NULL,
         sub.caption=NULL,
         main="1.12: Diagnostic plot 2")
}
```

```
fig1.13 <- function(){
    gph <- plotSimDiags(obj=mftime.lm, which=2, layout=c(4,1),
                        aspect=1,
               title="1.13: Diagnostic plot 2; 4 simulations")
    gph
}
```

```
fig1.14 <- function(obj=mftime.lm){
    plot(obj, which=3, caption=NULL,
         sub.caption=NULL,
         main="1.14: Diagnostic plot 3")
}
```

```
fig1.15 <- function(obj=mftime.lm){
    gph <- plotSimDiags(obj, which=3, layout=c(4,1),
                        aspect=1,
           title="1.15: Diagnostic plot 3; 4 simulations")
    gph
}
```

```
fig1.16 <- function(){
    plot(mftime.lm, which=5, caption=NULL,
         sub.caption=NULL,
         main="1.16: Leverage plot")
}
```

```
fig1.17 <- function(){
    pset <- simpleTheme(lty=c(1,2))
    key <- list(text=c("Males", "Females"), columns=2)
    gph <- densityplot(~ time+timef, data=nihills, par.settings=pset,
                       ylab="Time (h)", auto.key=key,
           main="1.17: Overlaid F and M densities")
    gph
}
```

```
fig1.18 <- function(){
    pset <- simpleTheme(col.line="gray")
    gph <- xyplot(timef ~ time,
                  data=nihills,
                  scales=list(log=10),
                  aspect=1,
                  type=c("p","r"),
                  par.settings=pset)
    gph <- update(gph, xlab="Male record times",
                  ylab="Female record times",
           main="1.18: F vs M record times; log10 scales")
    gph
}
```

```
fig1.19 <- function(){
    obj <- lm(log(timef) ~ log(time), data=nihills)
    opar <- par(mfrow=c(1,4), mex=0.75, oma=c(0,0,2,0),
                mar=c(4.1,4.1,2.1,0.6), pty="s")
    plot(obj, cex.caption=0.75, cex.main=1.2,
         sub.caption="1.19: F vs M record times, diagnostic plots")
    par(opar)
}
```

```
fig1.20 <- function(){
    library(lattice)
    parset <- simpleTheme(cex=1.35, pch=16,
                          col=c("darkblue","turquoise"))
    gabalong <- data.frame(values=unlist(gaba["30",])[-1],
                           sex=rep(c("male", "female", "all"), rep(2,3)),
                           trt=rep(c("Baclofen","No baclofen"),3))
    gph <- stripplot(sex~values, groups=trt, data=gabalong,
                     par.settings=parset,
                     xlab=list("Average reduction: 30 min vs 0 min",
                     cex=1.0),
                     scales=list(cex=1.0),
                     panel=function(x,y,...){
                         panel.stripplot(x,y,...)
                         ltext(x,y,paste(c(3,9,15,7,22,12)), pos=1,
                               cex=0.8)
                     }, auto.key=list(columns=2, points=TRUE, cex=1.0),
                     title="1.20: Pain reduction scores")
    gph
}
```

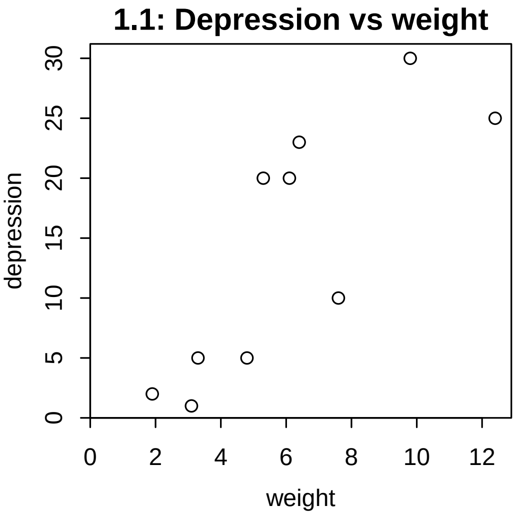
# 2 Code for the Figures

Unless `doFigs` is found in the workspace and is `FALSE`, then subject to checks that all necessary datasets and packages are available, the figures are now shown.

```
if(!exists("doFigs")) doFigs <- TRUE
```

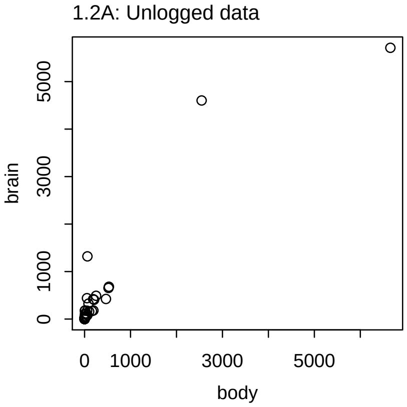
```
library(DAAG)
mftime.lm <- lm(timef ~ time, data=nihills)
```

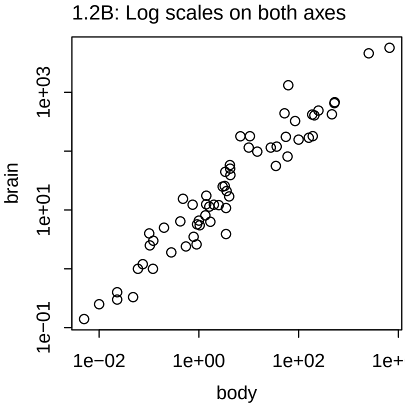
```
fig1.1()
```



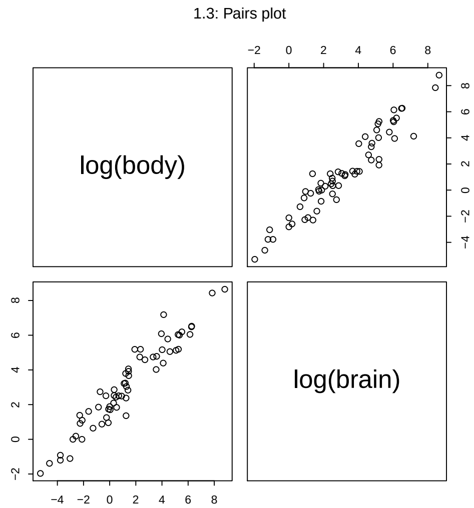
```
fig1.2()

[1] "Run the separate functions fig1.2A() and fig1.2B()"
```

```
fig1.2A()
fig1.2B()
```

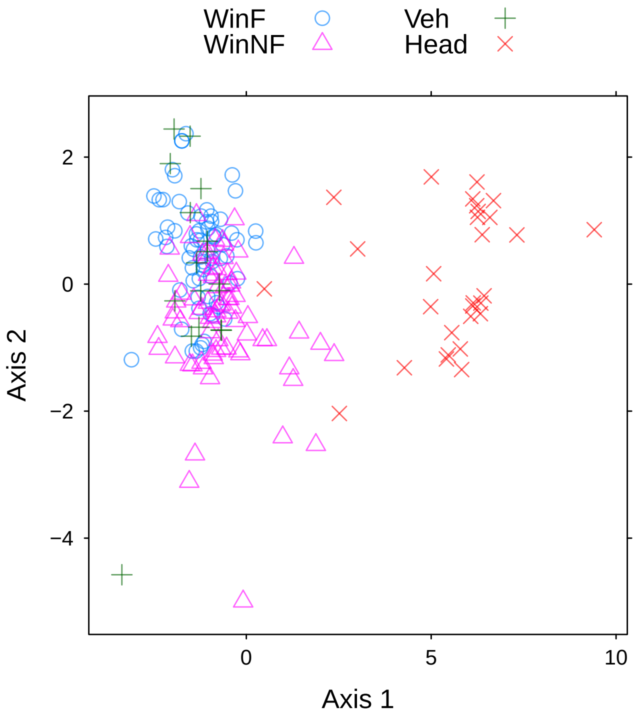




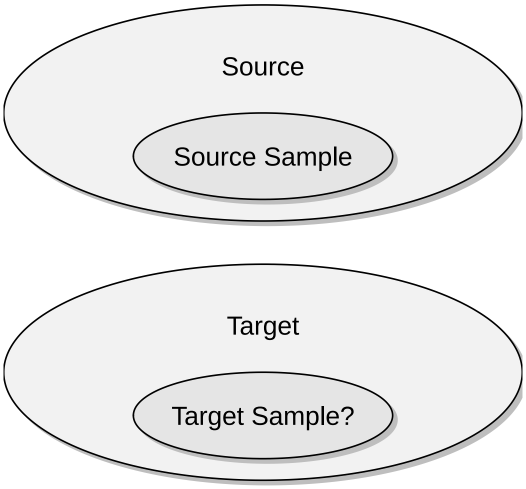
```
fig1.3()
```


1.3: Pairs plot
log(body)
log(brain)
−2
0
2
4
6
8
−4
−2
0
2
4
6
8

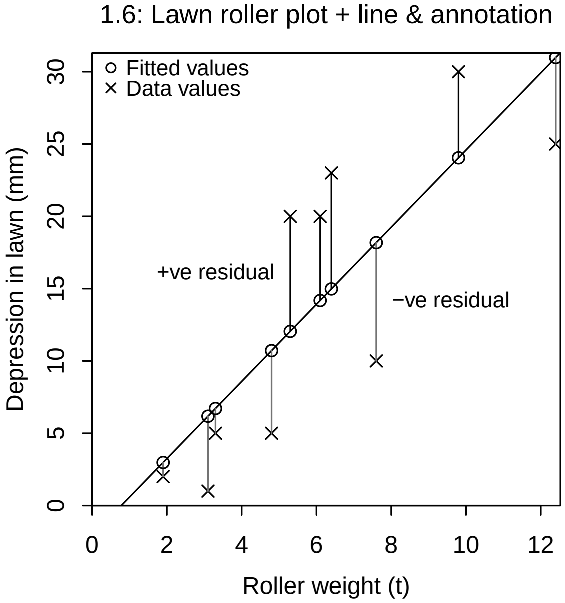
```
fig1.4()
```


WinF ○
WinNF △
Veh +
Head ×
Axis 2
Axis 1
2
0
−2
−4
0
5
10

```r
fig1.5()
```

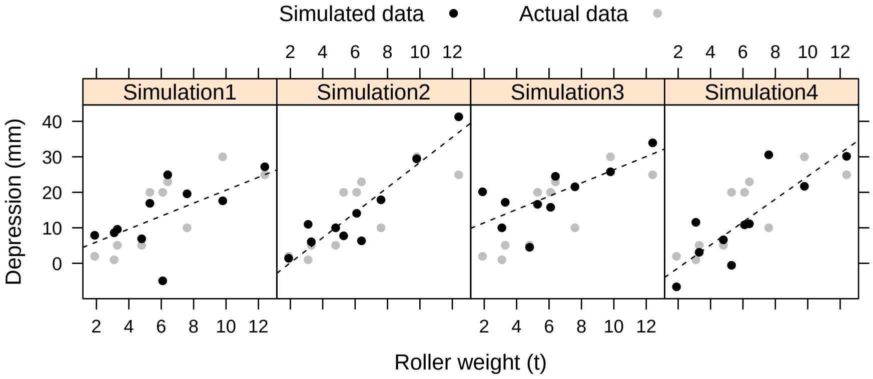


```r
fig1.6()
```



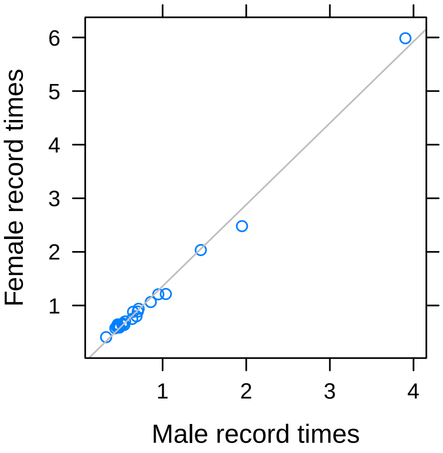
```r
fig1.7()
```

**1.7: Lawn roller data**

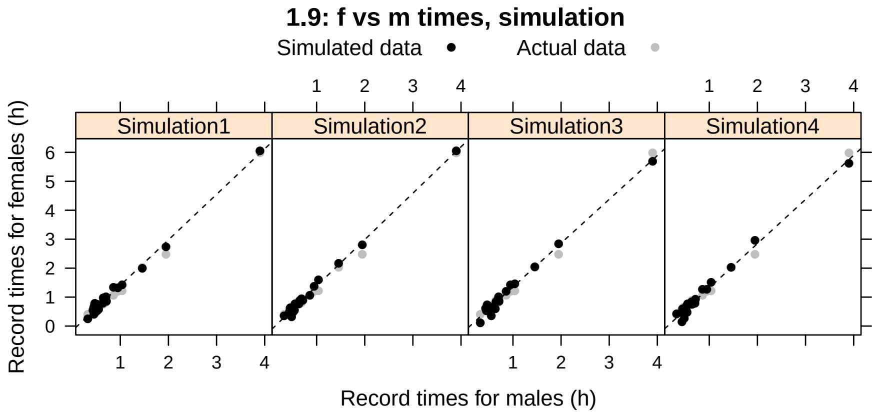


```
fig1.8()
```

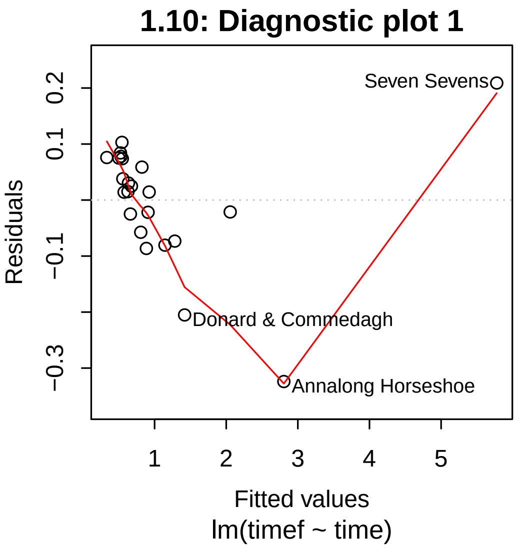
**1.8: f vs m times**



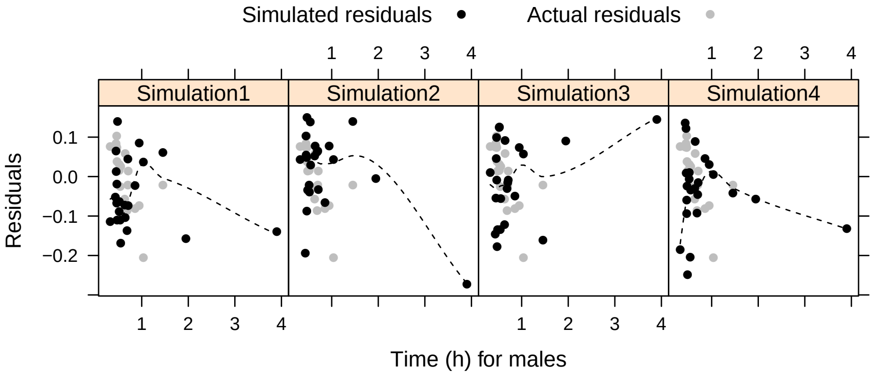
```
fig1.9()
```



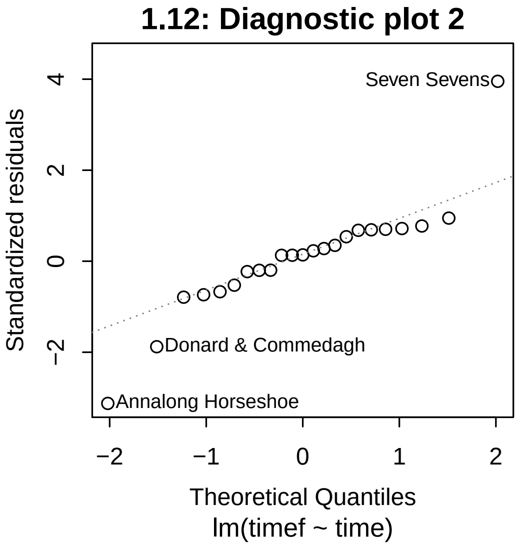
```
fig1.10()
```



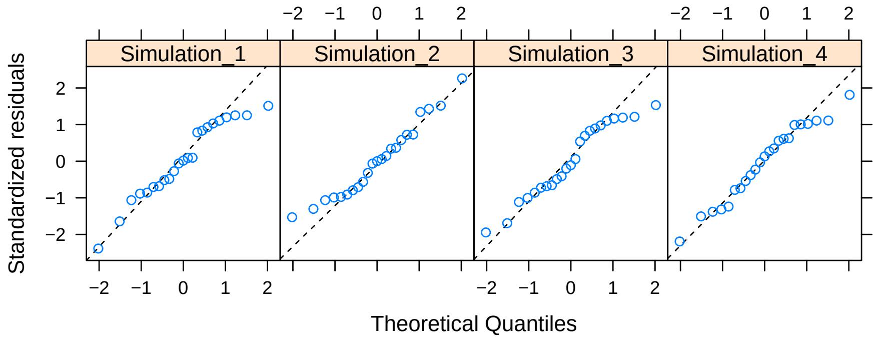
```
fig1.11()
```



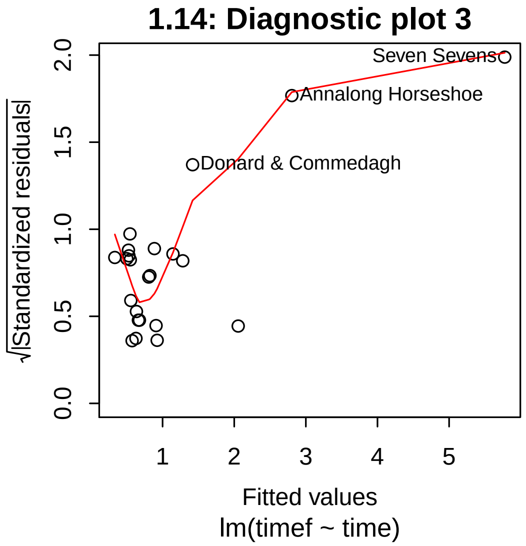
```
fig1.12()
```



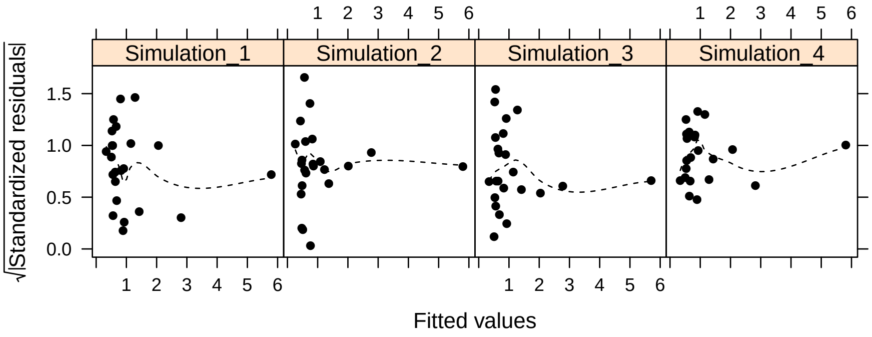
```
fig1.13()
```



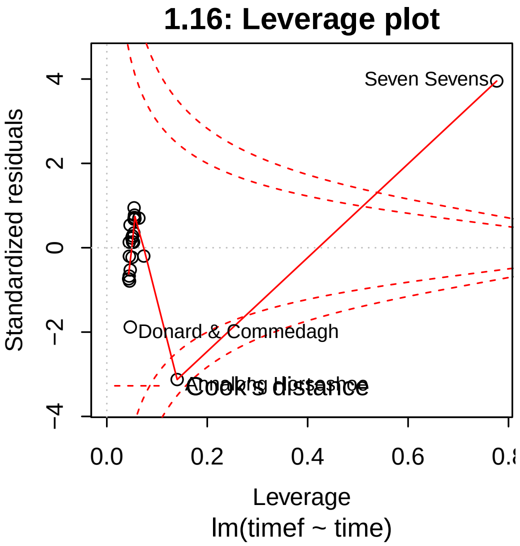
```
fig1.14()
```



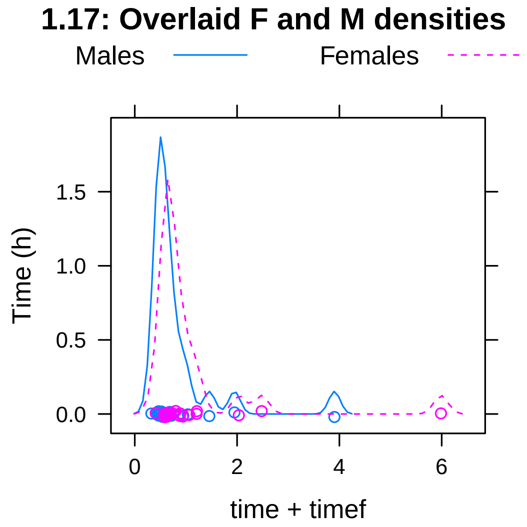
```
fig1.15()
```



```
fig1.16()
```

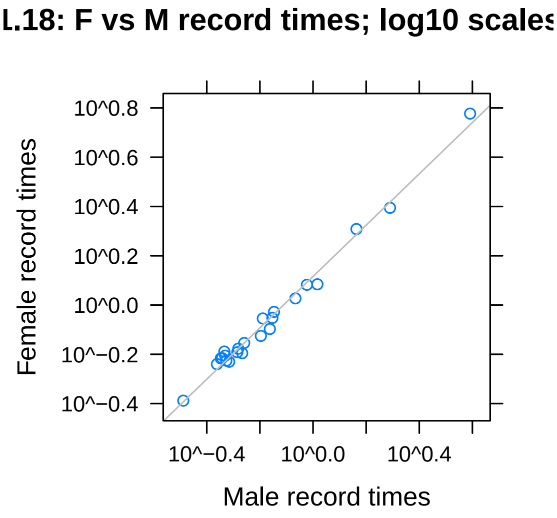


```
fig1.17()
```



1.17: Overlaid F and M densities

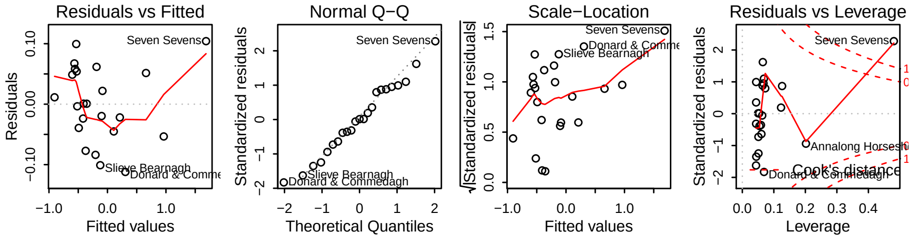
```r
fig1.18()
```



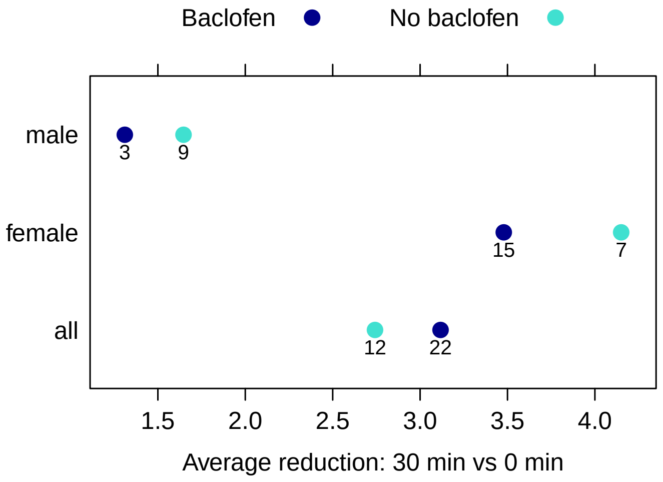
l.18: F vs M record times; log10 scales

```r
fig1.19()
```

1.19: F vs M record times, diagnostic plots



```
fig1.20()
```


Baclofen ●
No baclofen ●
male
female
all
Average reduction: 30 min vs 0 min