

```

> #####
> # trout1 #
> #####
>
> library(MASS)

> trout <- read.table(file = "N:/courses/stat8230/Fall11/trout.dat", header = T)

> par(mfrow=c(2,3))

> plot(trout$age, trout$pcb, xlab = "Age (years)", ylab =
+      "PCB concentration (ppm)")

> boxcox(pcb ~ age, data = trout, lambda = seq(-0.5, 0.5, len = 110))

> plot(trout$age, log(trout$pcb), xlab = "Age (years)", ylab =
+      "log PCB concentration")

> plot((trout$age)^(1/3), log(trout$pcb), xlab = "Cube root of Age", ylab =
+      "log PCB concentration")

> m1trout.lm <- lm(l(log(pcb)) ~ l(age^(1/3)), data = trout)

> summary(m1trout.lm)

```

Call:

```
lm(formula = l(log(pcb)) ~ l(age^(1/3)), data = trout)
```

Residuals:

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      Min      1Q  Median      3Q      Max
-0.87454 -0.33400  0.07085  0.37242  1.02001

```

Coefficients:

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              Estimate Std. Error t value Pr(>|t|)
(Intercept)  -2.3907    0.3960  -6.037 2.24e-06 ***
l(age^(1/3))  2.3005    0.2295  10.023 2.02e-10 ***
---

```

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

```

Residual standard error: 0.4961 on 26 degrees of freedom
Multiple R-squared: 0.7944, Adjusted R-squared: 0.7865
F-statistic: 100.5 on 1 and 26 DF, p-value: 2.020e-10

```

```
> names(m1trout.lm)
```

```

[1] "coefficients" "residuals"   "effects"     "rank"
[5] "fitted.values" "assign"      "qr"          "df.residual"
[9] "xlevels"      "call"        "terms"       "model"

```

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> names(summary(m1trout.lm))
[1] "call"      "terms"     "residuals" "coefficients"
[5] "aliased"   "sigma"     "df"         "r.squared"
[9] "adj.r.squared" "fstatistic" "cov.unscaled"

> XXinv <- summary(m1trout.lm)$cov.unscaled

> mse <- summary(m1trout.lm)$sigma^2

> beta <- coef(m1trout.lm)

> x0 <- seq(from = min(trout$age^(1/3)), to = max(trout$age^(1/3)), by = 0.01)

> y0 <- beta[1] + beta[2] * x0

> plot((trout$age)^(1/3), log(trout$pcb), xlab = "Cube root of Age", ylab =
+      "log PCB concentration")

> lines(x0, y0, lty = 1)

> Fcrit <- qf(0.95, 2, 26)

> X0 <- cbind(rep(1, times = length(x0)), x0)

> uband <- y0 + sqrt(mse * Fcrit) * sqrt(2 * diag(X0 %*% XXinv %*% t(X0)))

> lband <- y0 - sqrt(mse * Fcrit) * sqrt(2 * diag(X0 %*% XXinv %*% t(X0)))

> lines(x0, uband, lty = 5)

> lines(x0, lband, lty = 5)
>
> tcrit <- qt(.975,26)

> beta1.low <- beta[1] - tcrit * sqrt(mse*XXinv[1,1])

> beta1.high <- beta[1] + tcrit * sqrt(mse*XXinv[1,1])

> beta2.low <- beta[2] - tcrit * sqrt(mse*XXinv[2,2])

> beta2.high <- beta[2] + tcrit * sqrt(mse*XXinv[2,2])
>
> b10 <- seq(from = -3.5, to = -1.3, by = 0.01)
>
> uellipse <- -15647/27789 * b10 + 8834241/9263000 + 1/27789000 * (
+      -14535391000000. * b10^2 - 69508239762000. * b10 - 67739046635471.)^
+      (1/2)

```

```
> lellipse <- -15647/27789 * b10 + 8834241/9263000 - 1/27789000 * (  
+   -14535391000000. * b10^2 - 69508239762000. * b10 - 67739046635471.)^  
+   (1/2)  
>  
> plot(m1trout.lm$coef[1], m1trout.lm$coef[2], xlab = "beta_1", ylab = "beta_2",  
+   xlim = c(-3.7, -1), ylim = c(1.5, 3.))  
  
> abline(v = beta1.high, lty = 5)  
> abline(v = beta1.low, lty = 5)  
> abline(h = beta2.high, lty = 5)  
> abline(h = beta2.low, lty = 5)  
> points(b10, lellipse, pch = ".")  
> points(b10, uellipse, pch = ".")  
>
```

