

# **STK2100**

## **Oblig 1**

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## Oppgave 1

a)

i)

The only model that can be written as a linear model as is, is model 2.

$$2. \quad Y = \beta_0 + \frac{\beta_1}{x} + \beta_2 x^2 + \epsilon$$

ii)

For model 4 we can fix  $\beta_2$  to a constant, say  $c$  and get

$$4. \quad \beta_0 + \beta_1 x^c + \epsilon$$

iii)

For model 5 we can log-transform such as this:

$$Y = \beta_0 x^{\beta_1} \epsilon$$

$$\log(Y) = \log(\beta_0 x^{\beta_1} \epsilon)$$

$$\log(Y) = \log(\beta_0) + \log(x^{\beta_1}) + \log(\epsilon)$$

$$\log(Y) = \log(\beta_0) + \beta_1 \log(x) + \log(\epsilon)$$

**b)**

1.	$X = \begin{bmatrix} \frac{1}{1+x_i} & x_i^{1/2} \end{bmatrix},$	$\beta = \begin{bmatrix} \beta_0 \\ \beta_2 \end{bmatrix}$
2.	$X = \begin{bmatrix} 1 & \frac{1}{x_i} & x_i^2 \end{bmatrix},$	$\beta = \begin{bmatrix} \beta_0 \\ \beta_1 \\ \beta_2 \end{bmatrix}$
3.	$X = \begin{bmatrix} 1 & x_i & x_i^2 \end{bmatrix},$	$\beta = \begin{bmatrix} \beta_0 \\ \beta_1 \\ \beta_2 \end{bmatrix}$
4.	$X = \begin{bmatrix} 1 & x_i \end{bmatrix},$	$\beta = \begin{bmatrix} \beta_0 \\ \beta_1' \end{bmatrix}$
5.	$X = \begin{bmatrix} 1 & \log(x_i) \end{bmatrix},$	$\beta = \begin{bmatrix} \beta_0' \\ \beta_1 \end{bmatrix}$

## Oppgave 2

a)

```
1 # set seed for replication!
2 set.seed(1814)
3
4 # loading packages
5 library(tidyverse)
6
7 # reading data
8 nuclear <- read_delim("nuclear.dat")
9
10 # a)
11
12 # fitting the data using linear regression
13 lm1 <- lm(log(cost)~., nuclear)
14 lm1 %>% summary()
15
16 # creating a 95 percent confidence interval
17 confint(lm1, level = 0.95)[c("t1", "t2", "bw"),]
```

A 95% confidence interval is then found to be the following.

	2.5 %	97.5 %
t1	-0.041123331	0.05162679
t2	-0.003949911	0.01516185
bw	-0.184211843	0.25780411

b)

```
1 # b)
2
3 # creating a new dataframe
4 df <- tibble(
5   date = 70.0,
6   t1 = 13,
7   t2 = 50,
8   cap = 800,
9   pr = 1,
10  ne = 0,
11  ct = 0,
12  bw = 1,
13  cum.n = 8,
14  pt = 1
15 )
16
```

```

17 # predicting on data using linear regression
18 pred1 <- predict(lm1, newdata = df, interval = "prediction", level =
    0.95)
19
20 # retrieving the coefficients
21 yhat <- pred1[1,"fit"]
22 lwry <- pred1[1,"lwr"]
23 upry <- pred1[1,"upr"]
24
25 # transforming y to find z
26 zfit <- exp(yhat)
27 zlwr <- exp(lwry)
28 zupr <- exp(upry)
29
30 # saving coefficients for z
31 predz <- data.frame(
32   fit = zfit,
33   lwr = zlwr,
34   upr = zupr
35 )
36
37 # presenting my findings
38 print(pred1)
39 print(predz)

```

The 95% prediction interval with the cost  $Z$  is then found to be the following.

```

> print(pred1)
      fit      lwr      upr
1 5.964135 5.394248 6.534022
> print(predz)
      fit      lwr      upr
1 389.2163 220.1366 688.1607

```

c)

```

1 # c)
2
3 # individual t-tests
4 sum_lm1 <- summary(lm1)
5 print(sum_lm1$coefficients[c("t1", "t2", "bw"),
6                             c("Estimate", "Pr(>|t|)"),
7                             drop = FALSE])
8
9 # joint F-tests
10 lm1red <- lm(log(cost)~date+cap+pr+ne+ct+cum.n+pt, data = nuclear)
11 anova(lm1red, lm1)

```

Find the output for the individual t-test, where we find that the p-value is larger than 0.5 for all predictors t1, t2, and bw, such that we fail to reject the null-hypothesis  $H_0 : \beta_j = 0$  that the predictors are significant.

	Estimate	Pr(> t )
t1	0.005251730	0.8160981
t2	0.005605968	0.2359862
bw	0.036796131	0.7326075

For the joint F-test, we find a p-value of  $0.5173 > 0.5$  where we fail to reject the  $H_0$  at a 5% confidence level.

### Analysis of Variance Table

Model 1:  $\log(\text{cost}) \sim \text{date} + \text{cap} + \text{pr} + \text{ne} + \text{ct} + \text{cum.n} + \text{pt}$

Model 2:  $\log(\text{cost}) \sim \text{date} + \text{t1} + \text{t2} + \text{cap} + \text{pr} + \text{ne} + \text{ct} + \text{bw} + \text{cum.n} + \text{pt}$

	Res.Df	RSS	Df	Sum of Sq	F	Pr(>F)
1	24	0.67195				
2	21	0.60443	3	0.06752	0.782	0.5173

**d)**

```

1 # d)
2
3 library(leaps)
4
5 fwd1 <- regsubsets(log(cost) ~ ., data = nuclear, method = "forward",
6                   , nvmax = 10)
7 sum1 <- summary(fwd1)
8 sum1$outmat %>% as_tibble()
9
10 bic1 <- sum1$bic
11 bicb <- names(which(sum1$which[which.min(bic1), ]))[-1]
12
13 all1 <- names(nuclear)[-1]
14 aic1 <- which.max(sum1$adjr2) # Fixed: max adj R²
15 aicb <- names(which(sum1$which[aic1, ]))[-1]
16
17 bicb
18 aicb
19
20 fitaic <- lm(log(cost) ~ ., data = nuclear[, c("cost", aicb)])
21 fitbic <- lm(log(cost) ~ ., data = nuclear[, c("cost", bicb)])
22
23 aic2 <- AIC(fitaic)
24 bic2 <- BIC(fitbic)

```

```

24
25 aic2
26 bic2

```

The output of the order matrix is below, which gives the following order of variables included: cap → date → ne → ct → bw → pr → t2 → t1.

```

# A tibble: 10 × 10
  date t1 t2 cap pr ne ct bw
  <chr> <chr> <chr> <chr> <chr> <chr> <chr> <chr>
1 " " " " " " " " " " " "
2 " " " " " " "*" " " " " " "
3 "*" " " " " "*" " " " " " "
4 "*" " " " " "*" " " "*" " " " "
5 "*" " " " " "*" " " "*" "*" " "
6 "*" " " " " "*" " " "*" "*" " "
7 "*" " " " " "*" " " "*" "*" "*"
8 "*" " " " " "*" "*" "*" "*" "*"
9 "*" " " "*" "*" "*" "*" "*" "*"
10 "*" "*" "*" "*" "*" "*" "*" "*"
# 2 more variables: cum.n <chr>, pt <chr>

```

Using forward selection I end up with variables [1] "date" "cap" "ne" "ct" "pt" selected on *BIC*, and with "date" "t2" "cap" "pr" "ne" "ct" "bw" "cum.n" "pt" selected on *AIC*. This yields respectively *AIC* and *BIC*:

```

> aic2
[1] -14.11792
> bic2
[1] -5.034235

```

e)

```

1 # e)
2
3 bwd2 <- regsubsets(log(cost) ~ ., data = nuclear, method = "backward
4      ", nvmax = 10)
5 sum2 <- summary(bwd2)
6 sum2$outmat %>% as_tibble()
7
8 bic2 <- sum2$bic
9 bicc <- names(which(sum2$which[which.min(bic2), ]))[-1]
10
11 all2 <- names(nuclear)[-1]
12 aic2 <- which.max(sum2$adjr2) # Fixed: max adj R²
13 aicc <- names(which(sum2$which[aic2, ]))[-1]

```

```

13
14 bicc
15 aicc
16
17 fitaic3 <- lm(log(cost) ~ ., data = nuclear[, c("cost", aicc)])
18 fitbic3 <- lm(log(cost) ~ ., data = nuclear[, c("cost", bicc)])
19
20 aic3 <- AIC(fitaic3)
21 bic3 <- BIC(fitbic3)
22
23 aic3
24 bic3

```

For backward selection we find the order `cap → date → ct → t2 → pr → bw → t1`.

```

# A tibble: 10 × 10
  date t1 t2 cap pr ne ct bw
  <chr> <chr> <chr> <chr> <chr> <chr> <chr> <chr>
1 " " " " " " " " " " " "
2 " " " " " " "*" " " " " " "
3 "*" " " " " "*" " " " " " "
4 "*" " " " " "*" " " "*" " " " "
5 "*" " " " " "*" " " "*" "*" " "
6 "*" " " " " "*" " " "*" "*" " "
7 "*" " " "*" "*" " " "*" "*" " "
8 "*" " " "*" "*" "*" "*" "*" " "
9 "*" " " "*" "*" "*" "*" "*" "*"
10 "*" "*" "*" "*" "*" "*" "*" "*"
# 2 more variables: cum.n <chr>, pt <chr>

```

Using *BIC* we find the selected variables "date" "cap" "ne" "ct" "pt" and for *AIC* we find "date" "t2" "cap" "pr" "ne" "ct" "cum.n" "pt" , and their respective *AIC* and *BIC*:

```

> aic3
[1] -16.00549
> bic3
[1] -5.034235

```

**f)**

```

1 # f)
2
3 faic <- aicb
4 fbic <- bicb
5 baic <- aicc
6 bbic <- bicc

```



```

7
8 cv <- function(vars, data, k=10){
9   n = nrow(data)
10  folds = sample(rep(1:k, length.out = n))
11  errors = numeric(k)
12  for (i in 1:k){
13    train = data[folds != i, ]
14    test = data[folds == i, ]
15    fit = lm(log(cost)~., data = train[, c("cost", vars)])
16    pred = predict(fit, newdata = test)
17    errors[i] = mean((log(test$cost) - pred)^2)
18  }
19  mean(errors)
20 }
21
22 cv_faic <- cv(faic, nuclear)
23 cv_fbic <- cv(fbic, nuclear)
24 cv_baic <- cv(baic, nuclear)
25 cv_bbic <- cv(bbic, nuclear)
26 cvs <- c(cv_faic, cv_fbic, cv_baic, cv_bbic)
27 names(cvs) <- c("fwd-aic", "fwd-bic", "bwd-aic", "bwd-bic")
28 bestcv <- names(cvs)[which.min(cvs)]
29 bestcv
30 min(cvs)

```

Using K-folds cross validation with  $K = 10$  I find that the backward selection using *BIC* gives the best model, and now prefer the model using date, cap, ne, ct, pt.

```

> bestcv <- names(cvs)[which.min(cvs)]
> bestcv
[1] "bwd-bic"
> min(cvs)
[1] 0.03565251

```

g)

```

1 # g)
2
3 library(boot)
4
5 boot632 <- function(vars, data, B = 1000) {
6   set.seed(1814)
7   fit <- lm(log(cost) ~ ., data = data[, c("cost", vars)])
8   err_app <- mean(resid(fit)^2)
9   boot_fn <- function(data, indices) {
10    d <- data[indices, ]
11    fit_boot <- lm(log(cost) ~ ., data = d[, c("cost", vars)])
12    pred <- predict(fit_boot, newdata = data)

```

```

13   mean((log(data$cost) - pred)^2)
14 }
15 boot_res <- boot(data, boot_fn, R = B)
16 err_boot <- mean(boot_res$t)
17 0.368 * err_app + 0.632 * err_boot
18 }
19
20 boot_faic <- boot632(faic, nuclear)
21 boot_fbic <- boot632(fbic, nuclear)
22 boot_baic <- boot632(baic, nuclear)
23 boot_bbic <- boot632(bbic, nuclear)
24
25 boot_faic
26 boot_fbic
27 boot_baic
28 boot_bbic

```

Find the following *AIC* and *BIC*, with the best being the backward model selected based on *AIC*.

```

> boot_faic
[1] 0.02699085
> boot_fbic
[1] 0.02738823
> boot_baic
[1] 0.02579897
> boot_bbic
[1] 0.02738823

```

**h)**

```

1 # h)
2 library(glmnet) # For ridge regression
3
4 x <- as.matrix(nuclear[, -1]) # All predictors, no cost
5 y <- log(nuclear$cost)       # Response
6
7 ridge_cv <- cv.glmnet(x, y, alpha = 0, nfolds = 10)
8 best_lambda <- ridge_cv$lambda.min
9
10 ridge_fit <- glmnet(x, y, alpha = 0, lambda = best_lambda)
11
12 cv <- function(vars, data, k = 10) {
13   set.seed(1814)
14   n <- nrow(data)
15   folds <- sample(rep(1:k, length.out = n))
16   errors <- numeric(k)
17   for (i in 1:k) {
18     train <- data[folds != i, ]

```

```

19   test <- data[folds == i, ]
20   fit <- lm(log(cost) ~ ., data = train[, c("cost", vars)])
21   pred <- predict(fit, newdata = test)
22   errors[i] <- mean((log(test$cost) - pred)^2)
23 }
24 mean(errors)
25 }
26
27 cv_ridge <- cv(all1, nuclear) # all1 from d) is all predictors
28
29 best_lambda
30 cv_ridge
31
32 cv_faic
33 cv_fbic
34 cv_baic
35 cv_bbic

```

We can now assess how the ridge regression compares to the cross-validated subset models. The best lambda  $\lambda$  we found was  $\lambda \approx 0.0697$  which gave a cross-validated ridge-regression of 0.0513, this is though higher than all of the subset models shown below, having values lower than 0.05.

```

> best_lambda
[1] 0.06978489
> cv_ridge
[1] 0.05138956

```

```

> cv_faic
[1] 0.04475947
> cv_fbic
[1] 0.03703112
> cv_baic
[1] 0.04238047
> cv_bbic
[1] 0.03565251

```

**i)**

```

1 # i)
2
3 library(glmnet)
4
5 x <- as.matrix(nuclear[, -1])
6 y <- log(nuclear$cost)
7
8 lasso_cv <- cv.glmnet(x, y, alpha = 1, nfolds = 10)
9 best_lambda_lasso <- lasso_cv$lambda.min

```

```
10 lasso_fit <- glmnet(x, y, alpha = 1, lambda = best_lambda_lasso)
11
12 # True Lasso CV error
13 cv_lasso <- lasso_cv$cvm[which(lasso_cv$lambda == best_lambda_lasso)
14 ]
15
16 best_lambda_lasso
17 cv_lasso
18 cv_faic
19 cv_fbic
20 cv_baic
21 cv_bbic
cv_ridge
```

Here again we find a best lambda of  $\lambda \approx 0.0245$ , which gives a prediction error of 0.0387, which in this case is better than that of ridge regression. This is also better than the subset models selected on *AIC*.

```
> best_lambda_lasso
[1] 0.02450281
> cv_lasso
[1] 0.03874789
```

```
> cv_faic
[1] 0.04837609
> cv_fbic
[1] 0.03693269
> cv_baic
[1] 0.04351076
> cv_bbic
[1] 0.03808641
> cv_ridge
[1] 0.05138956
```