

# External validation - DK data

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## Start

Attach packages

```
pkgs <- c("tidyverse", "doParallel", "pROC", "rms", "givitIR")  
  
purrr::walk(pkgs, ~suppressPackageStartupMessages(library(., character.only = TRUE)))
```

Load the exported model to validate (the R object previously sent, probably with another path).

```
# Load the exported model object  
load("export_90d.RData")
```

Set random seed for reproducibility:

```
set.seed(123)
```

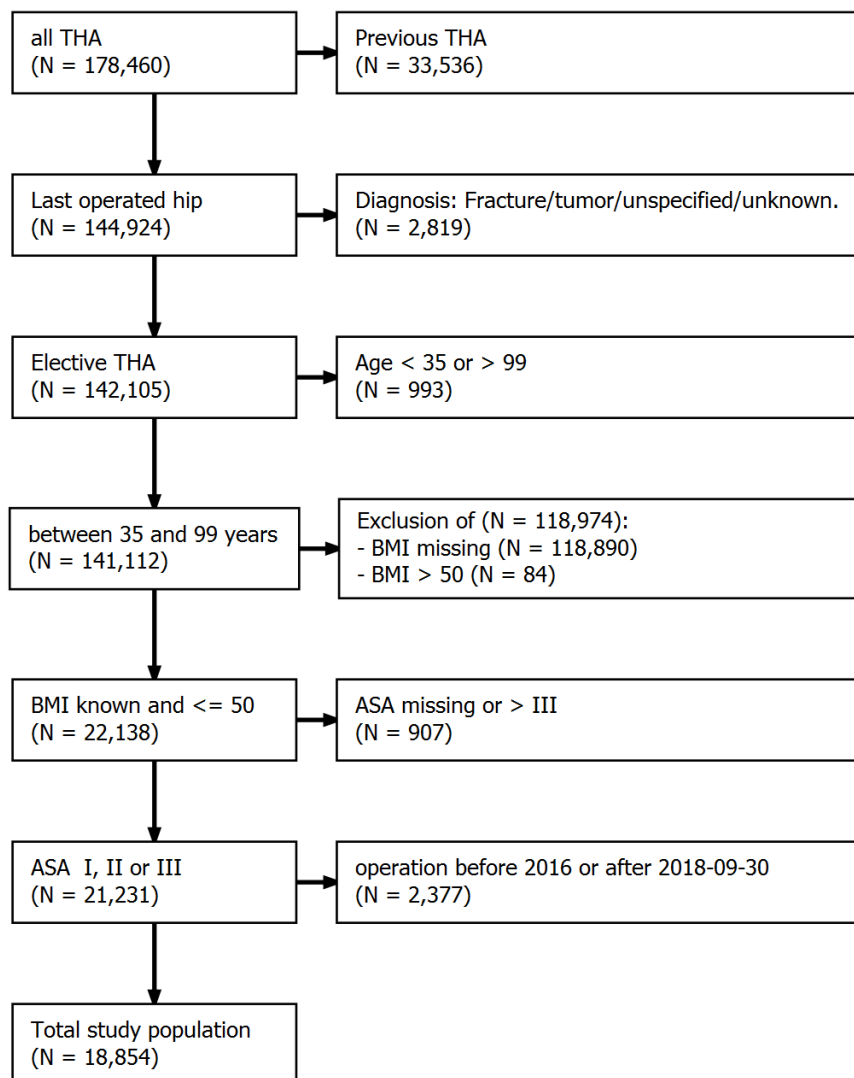
## Prepare data

### Inclusion/exclusion

Those were the inclusions/exclusions from Sweden. It might not be necessary to filter out on BMI, hospital and education however. Those variables are not used in the model.

Additional filter to ages 35-99 years to match the Swedish cohort.

```
knitr::include_graphics("../graphs/flowchartdk_detailed.png")
```



## Variables

### Outcome

The outcome variable is boolean (or numeric) indicating whether the patient died of any cause within 90 days after THA (TRUE/1) or not (FALSE/0). We did not have any censoring in Sweden. I guess we can simply drop cases where status is unknown?

The DK data set:

```
load("dkdata.RData")
```

### Predictors

The DK data look like this:

```
# head(dkdata) - data not shown here because they include age and gender
```

### Baseline variables

- **P\_Gender:** Kvinna/Man = Female/Male
- **P\_ASA:** level 1-3
- **P\_Age:** 35 - 99

### Comorbidities

Comorbidities have been handled in SAS, by Aurelie and Ina.

### Danish data into variables

The outcome needs to be a numeric variable, not logical. Otherwise we get an error `Fejl i givitiCheckArgs(o, e, devel, thres, maxDeg) : The vector 'o' must be a numeric vectors with 0/1 values..`

```
y <- as.numeric(dkdata$outcome)
```

```
X <- dkdata
```

### Eriks fitted model

```
load("../cache/model_reduced_lean.RData")
```

### Validation of model as is

```
obspred <-  
  tibble(  
    obs = y,
```

```

    pred = predict(model_reduced_lean, X, type = "response")
  )

# Tibble with observed and predicted outcome
obspred <-
  tibble(
    obs = y,
    pred = predict(model_reduced_lean, X, type = "response")
  )

# ROC curve
ROC <- pROC::roc(obspred, "obs", "pred", direction = "<")

# Estimate CI for AUC based on bootstrapping
# Use parallel processing to speed up the process
doParallel::registerDoParallel()
AUCci <-
  pROC::ci.auc(
    ROC,
    method = "bootstrap",
    #boot.n = 100,
    boot.stratified = FALSE,
    parallel = TRUE
  )

# Check calibration. Note that devel should actually be "internal" for this example but I use
# "external", since that's what you will use for the DK data.
calibration <-
  givitiR::givitiCalibrationBelt(
    obspred$obs,
    obspred$pred,
    devel = "external"
  )

```

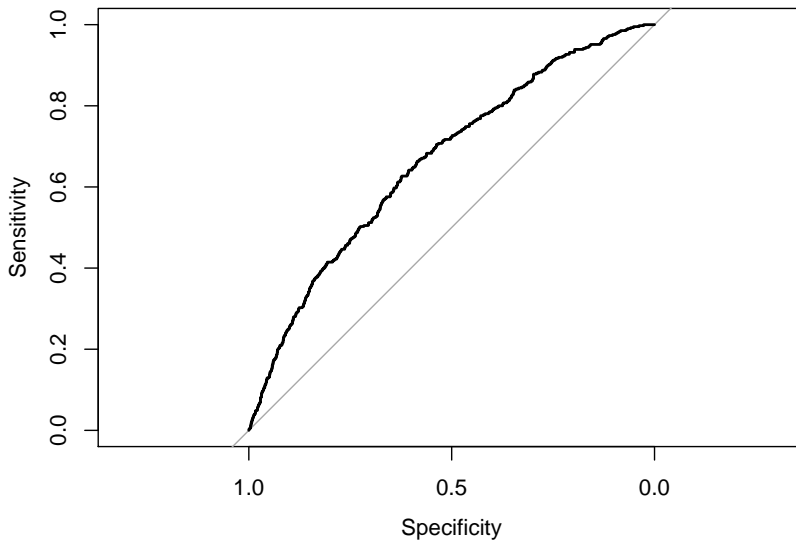
## Results

For this example we had AUC:

```
AUCci
```

```
## 95% CI: 0.6373-0.6906 (2000 non-stratified bootstrap replicates)
```

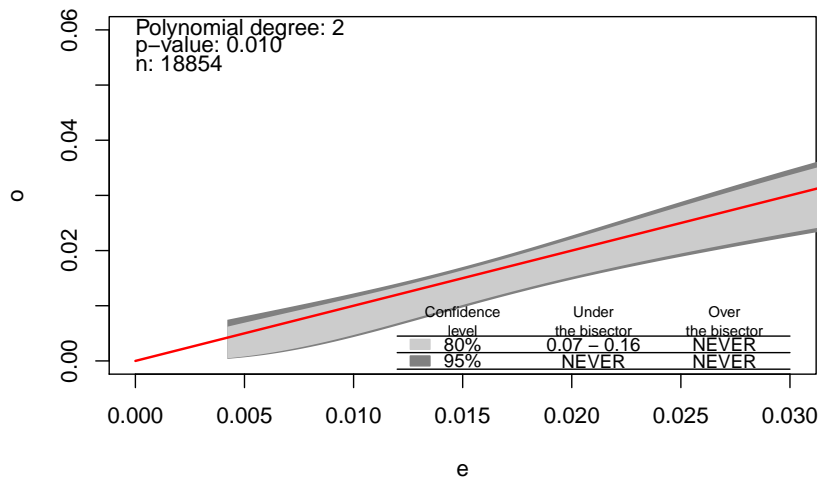
```
plot(ROC)
```



A calibration belt plot might be illustrated as:

```
plot(calibration, xlim = c(0, 0.03), ylim = c(0, 0.06))
```

### GiViTI Calibration Belt



```
## $m
## [1] 2
##
## $p.value
## [1] 0.01013039
```

## Re-calibrated intercept

Method 2 from table 1 in Steyerberg 2004.

```

Z <- predict(model_reduced_lean, X, type = "response")

# Refit the intercept using  $Z = a + Xb$  from above as offset
fit2 <- glm(y ~ 1, offset = Z)

# Same calibration and validation as above
obspred2 <- tibble(obs = y, pred = predict(fit2, type = "response"))
ROC2 <- pROC::roc(obspred2, "obs", "pred", direction = "<")
AUCci2 <- pROC::ci.auc(ROC2, method = "bootstrap",
                      # boot.n = 100,
                      boot.stratified = FALSE, parallel = TRUE)
calibration2 <- givitiR::givitiCalibrationBelt(obspred2$obs, obspred2$pred, devel = "external")

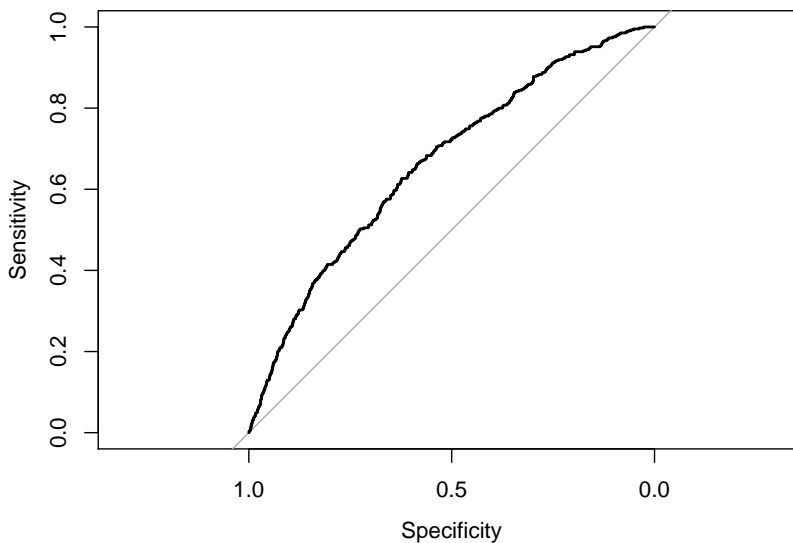
```

## Results

```
AUCci2
```

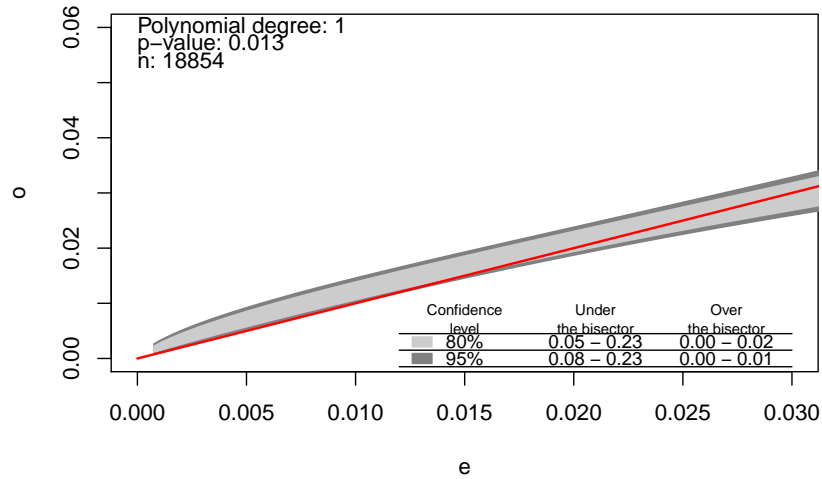
```
## 95% CI: 0.6387-0.6912 (2000 non-stratified bootstrap replicates)
```

```
plot(ROC2)
```



```
plot(calibration2, xlim = c(0, 0.03), ylim = c(0, 0.06))
```

### GiVITI Calibration Belt



```
## $m  
## [1] 1  
##  
## $p.value  
## [1] 0.01328765
```

## Re-calibration of intercept and calibration slope

Method 3 from table 1 in Steyerberg 2004.

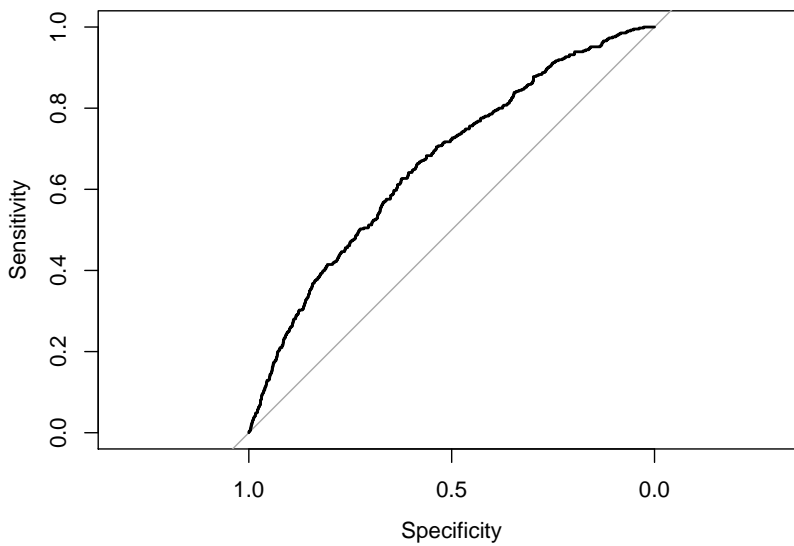
```
fit3 <- glm(y ~ 1 + Z)  
obspred3 <- tibble(obs = y, pred = predict(fit3, type = "response"))  
ROC3 <- pROC::roc(obspred3, "obs", "pred", direction = "<")  
AUCci3 <- pROC::ci.auc(ROC3, method = "bootstrap",  
                      #boot.n = 100,  
                      boot.stratified = FALSE, parallel = TRUE)  
calibration3 <- givitiR::givitiCalibrationBelt(obspred3$obs, obspred3$pred, delev = "external")
```

## Results

```
AUCci3
```

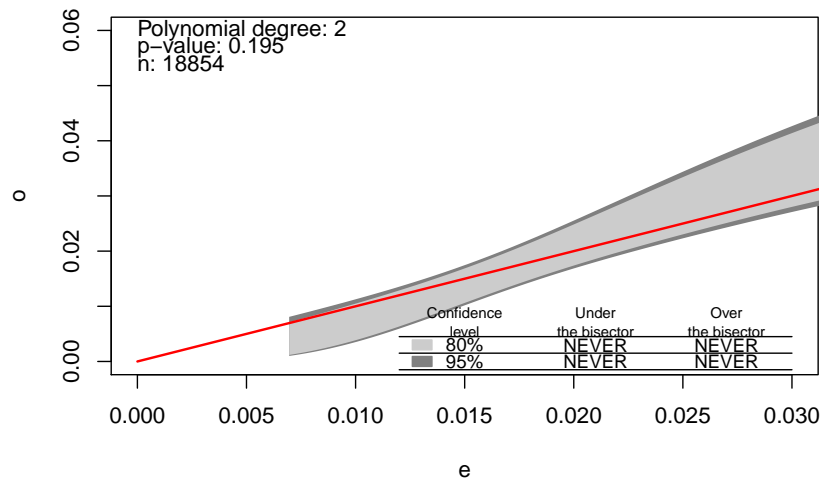
```
## 95% CI: 0.6389-0.6907 (2000 non-stratified bootstrap replicates)
```

```
plot(ROC3)
```



```
plot(calibration3, xlim = c(0, 0.03), ylim = c(0, 0.06))
```

### GiViTI Calibration Belt



```
## $m
## [1] 2
##
## $p.value
## [1] 0.1953893
```

## Export data to Sweden

Store data here:



```
exportdir <- "../output_R/"
```

## ROC

If it would be OK to export coordinates for ROC-plots I would recommend this code to extract only the minimal data needed:

```
roc_plot_coords <-  
  data.frame(  
    specificities = ROC$specificities,  
    sensitivities = ROC$sensitivities  
  )  
  
roc3_plot_coords <-  
  data.frame(  
    specificities = ROC3$specificities,  
    sensitivities = ROC3$sensitivities  
  )
```

## AUC with CI

The text output from AUCci and AUCci3 should be enough. Hence, the same character string that gets printed above (but now stored in an object).

```
AUCci_print <- capture.output(AUCci)  
AUCci3_print <- capture.output(AUCci3)
```

## Export objects

Save objects above to file `export.RData` (in the current working directory).

```
save(  
  roc_plot_coords,  
  roc3_plot_coords,  
  AUCci_print,  
  AUCci3_print,  
  file = paste0(exportdir, "export.RData")  
)
```

## Calibration plots

### Help function

This is a simple help function to make a clean calibration belt plot and save it as TIFF (in the current working directory):

```
makeplot <- function(x, file_name = deparse(substitute(x))) {  
  tiff(  
    paste0(exportdir, file_name, ".tiff"),  
    1024, 1024, pointsize = 36,  
    compression = "lzw"  
  )  
}
```

```

)

tcks <- seq(.0, .1, .01)

plot(
  x,
  xlim           = c(0, .06),
  ylim           = c(0, .08),
  xlab           = "Predicted probabilities [%]",
  ylab           = "Observed probabilities [%]",
  main           = NULL,
  table         = FALSE,
  polynomialString = FALSE,
  pvalueString  = FALSE,
  nString       = FALSE,
  mar           = c(5, 4, 0, 0) + 0.1,
  xaxt          = "n",
  yaxt          = "n"
)
abline(v = .03, lty = "dashed", col = "darkgreen", lwd = 3)
axis(1, at = tcks, lab = sprintf("%.0f", tcks * 100), las = TRUE)
axis(2, at = tcks, lab = sprintf("%.0f", tcks * 100), las = TRUE)

dev.off()
}

```

## Make and save figures

```
makeplot(calibration)
```

```
## pdf
## 2
```

```
makeplot(calibration3)
```

```
## pdf
## 2
```

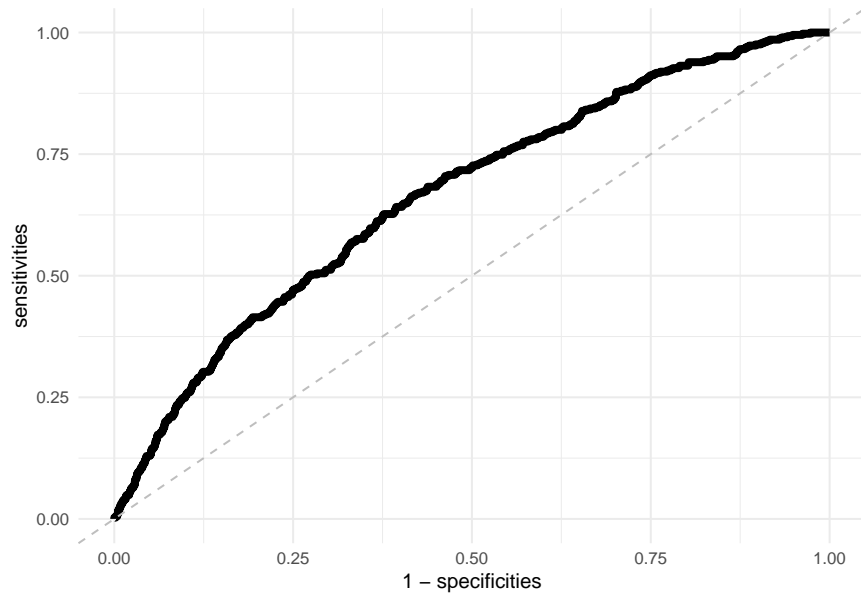
## ROC plots

If it not possible to export data for ROC-plot, here is some code to make a figure and save it as TIFF (in the current working directory) instead:

```

roc_plot_coords %>%
  ggplot(aes(1 - specificities, sensitivities)) +
  geom_path(size = 2) +
  geom_abline(intercept = 0, slope = 1, color = "grey", linetype = 2) +
  theme_minimal() +
  theme(
    legend.position = c(1, 0),
    legend.justification = c(1, 0),
    legend.title = element_blank()
  )
)

```



```
ggsave(  
  paste0(exportdir, "roc.tiff"),  
  height = 10,  
  width = 10,  
  unit = "cm",  
  dpi = 900,  
  compression = "lzw"  
)
```