Project V

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Contents

1 Data Cleaning

We begin this project by bringing the data into R.

```
dat <- read.csv(file="ILPD.csv", header=FALSE, sep = ",", col.names=c("age", "gender", "
"sgpt", "sgot", "TP", "alb", "AGratio", "liver"))
dim(dat);head(dat)
```

```
## [1] 583  11
```

```
##   age gender   TB  DB alkphos sgpt sgot  TP alb AGratio liver
## 1  65 Female  0.7 0.1     187   16   18 6.8 3.3    0.90     1
## 2  62   Male 10.9 5.5     699   64  100 7.5 3.2    0.74     1
## 3  62   Male  7.3 4.1     490   60   68 7.0 3.3    0.89     1
## 4  58   Male  1.0 0.4     182   14   20 6.8 3.4    1.00     1
## 5  72   Male  3.9 2.0     195   27   59 7.3 2.4    0.40     1
## 6  46   Male  1.8 0.7     208   19   14 7.6 4.4    1.30     1
```

A quick inspection of the data shows tha our target variable `liver` is coded as either one or two, and that `gender` is coded as either male or female. In order to proceed, we recode these variables so that one means that the person has liver disease (zero means that they do not) and one means that the person is male (zero means that the person is female). We then print the mean for `dat$liver` to determine the proportion of subjects diagnosed with liver disease.

```
dat$liver <- as.integer(ifelse(dat$liver==1, 1, 0))
dat$gender <- as.integer(ifelse(dat$gender=="Male", 1, 0))
mean(dat$liver)
```

```
## [1] 0.7135506
```

From the above output we see that 71% of the subjects were diagnosed with liver disease. We do not believe that this is anywhere near the real prevalnce rate of liver disease on the general population, as it is fairly high.

Next we need to check for missing values in our data.

```
n <- nrow(dat)
out <- NULL
for (k in 1:ncol(dat)) {
  vname <- colnames(dat)[k]
  x <- as.vector(dat[,k])
  n1 <- sum(is.na(x), na.rm=TRUE)
  n2 <- sum(x=="NA", na.rm=TRUE)
  n3 <- sum(x=='', na.rm=TRUE)
  nmiss <- n1 + n2 + n3
  ncomplete <- n - nmiss
  var.type <- typeof(x)
  if (var.type == "integer") {
    if (length(unique(x)) == 2) {
      out <- rbind(out, c(col.number=k, vname=vname, mode="binary",
                          n.levels=length(unique(x)), ncomplete=ncomplete,
                          miss.prop=round(nmiss/n, digits=4)))

  } else {
      out <- rbind(out, c(col.number=k, vname=vname, mode=typeof(x),
                          n.levels=length(unique(x)), ncomplete=ncomplete,
                          miss.prop=round(nmiss/n, digits=4)))

  }
} else {
    out <- rbind(out, c(col.number=k, vname=vname, mode=typeof(x),
                        n.levels=length(unique(x)), ncomplete=ncomplete,
                        miss.prop=round(nmiss/n, digits=4)))

    }
```

```
}
out <- as.data.frame(out)
row.names(out) <- NULL
out
```

```
##    col.number   vname    mode n.levels ncomplete miss.prop
## 1           1     age integer       72       583         0
## 2           2  gender  binary        2       583         0
## 3           3      TB  double      113       583         0
## 4           4      DB  double       80       583         0
## 5           5 alkphos integer      263       583         0
## 6           6    sgpt integer      152       583         0
## 7           7    sgot integer      177       583         0
## 8           8      TP  double       58       583         0
## 9           9     alb  double       40       583         0
## 10         10 AGratio  double       70       579    0.0069
## 11         11   liver  binary        2       583         0
```

From the above output, we see that `AGratio` has some missing values. We will impute these missing values with the `mice` function in the `mice` package.

```
library(mice, quietly = TRUE)
fit.mice <- mice(dat, m=1, maxit=50, method="pmm", seed=5474, printFlag = FALSE)
dat <- complete(fit.mice, 1)
```

2 EDA and Variable Screening

From the output of the previous section, we know that `age`, `alkphos`, `sgpt`, and `sgot` are integers, `gender` is categorical, `TB`, `DB`, `TP`, `alp`, and `AGratio` are continous.

Now, we will perform some variable screening. For each categorical predictor we use a χ^2 test of independence to assess its association with `liver`, and for all other predictors we will use a two sample t-test. We use a threshold significance level of $\alpha = 0.20$ and remove all predictors having a p-value greater than that.

```
library(car);
```

```
## Loading required package: carData
```

```
vars.nominal <- c("gender")
cols.x <- 1:(NCOL(dat)-1)
xnames <- names(dat)[cols.x]
y <- dat$liver
OUT <- NULL
for (j in 1:length(cols.x)){
```

```
  x <- dat[, cols.x[j]]
  xname <- xnames[j]
  if (is.element(xname, vars.nominal)){
    tbl <- table(x, y)
    pvalue <- chisq.test(tbl)$p.value
} else {
    pvalue.equal.var <- (leveneTest(x~factor(y))$"Pr(>F)")[1]
    equal.var <- ifelse(pvalue.equal.var <= 0.05, FALSE, TRUE)
    pvalue <- t.test(x~y, alternative="two.sided",
            var.equal=equal.var)$p.value
  }
  OUT <- rbind(OUT, cbind(xname=xname, pvalue=pvalue))
}
OUT <- as.data.frame(OUT)
colnames(OUT) <- c("name", "pvalue")
OUT
```

```
##       name               pvalue
## 1      age 0.000884063155626139
## 2   gender   0.0596658468577747
## 3       TB 4.91200919556184e-16
## 4       DB 2.26995324945029e-19
## 5  alkphos 1.08124966726932e-08
## 6     sgpt 1.18047797924202e-09
## 7     sgot 1.40944977692876e-08
## 8       TP    0.398819127523851
## 9      alb 9.07436084295548e-05
## 10 AGratio 6.39088236401563e-05
```

From the above output we see only one predictor needs to be removed, namely, `TP`, so we remove it with the following code.

```
OUT$pvalue <- as.character(OUT$pvalue)
OUT$pvalue <- as.numeric(OUT$pvalue)
non.sig <- which(OUT$pvalue > 0.2)
dat <- dat[, -c(non.sig)]
```

3 Model Building

We will fit three different logistic regresssion models and compare their performance using the area under the curve (AUC) on a reciever operating characteristic (ROC) curve.

3.1 Full Model

The full model that we fit is nothing more than the logistic regression model containing all of the predictors

```
fit.full <- glm(liver~., family = binomial, data = dat)
```

The following output shows all the predictors in the model, and their slope parameter estimates.

```
coef(fit.full)
```

```
##  (Intercept)          age       gender           TB           DB      alkphos
## -0.861893318  0.018587980  0.038548650  0.008389071  0.506690771  0.001277385
##         sgpt         sgot          alb      AGratio
##  0.009934171  0.003333270  0.029102509 -0.537766290
```

3.2 Stepwise Variable Selection

The second model that we fit has it's predictors chocen via stepwise variable selection starting with the full model. The best model is determined based on its BIC.

```
fit.step <- step(fit.full, direction = "both",k=log(nrow(dat)), trace = FALSE)
```

The following output shows all the predictors selected from the stepwise variable selection to be used in the model, and their slope parameter estimates.

```
coef(fit.step)
```

```
## (Intercept)         age          DB        sgpt
## -1.12264221  0.01993645  0.65782404  0.01509633
```

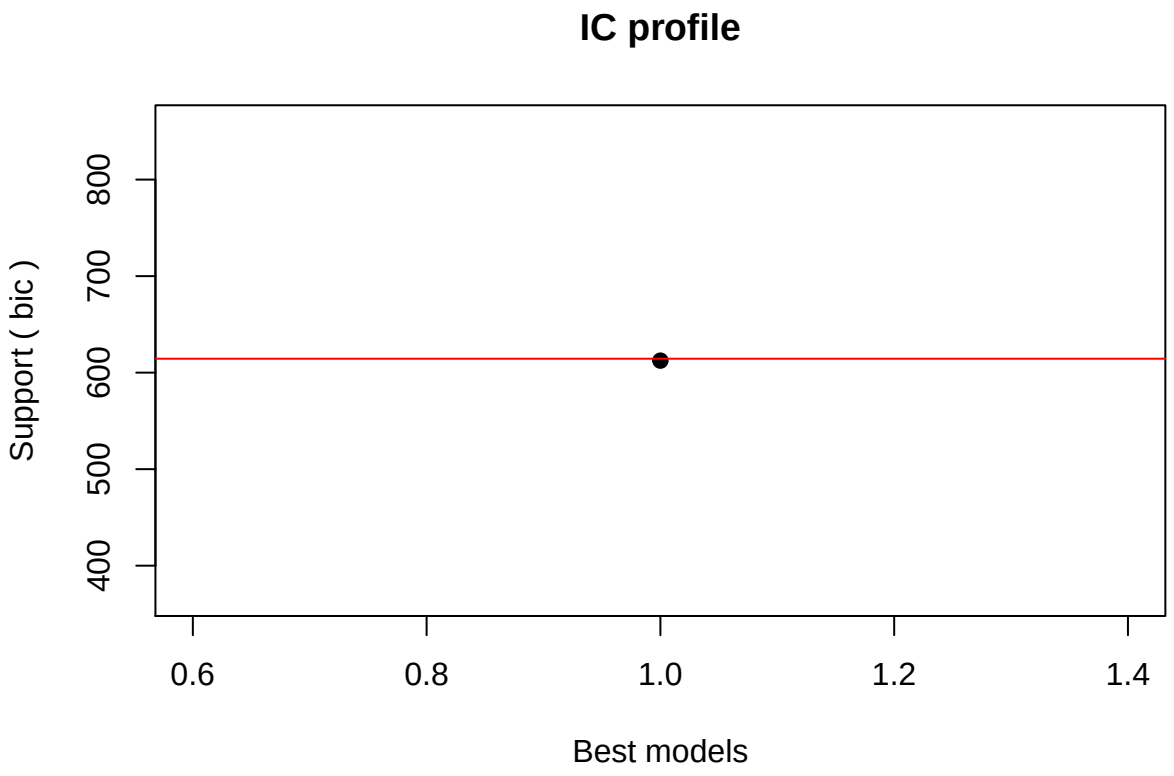
3.3 Best Subset Selection

```
library(glmulti)
fitting <- glmulti(liver~., data = dat, fitfunc = glm, family=binomial, intercept = TRUE
                   crit = bic, level = 1, method = "g", confsetsize=1)
```

```
## Initialization...
## TASK: Genetic algorithm in the candidate set.
## Initialization...
## Algorithm started...
##
## After 10 generations:
## Best model: liver~1+age+DB+sgpt
## Crit= 612.436090012312
```

```
## Mean crit= 612.436090012312
```

```
## Change in best IC: -9387.56390998769 / Change in mean IC: -9387.56390998769
##
## After 20 generations:
## Best model: liver~1+age+DB+sgpt
## Crit= 612.436090012312
## Mean crit= 612.436090012312
```




```
## Change in best IC: 0 / Change in mean IC: 0
##
## After 30 generations:
## Best model: liver~1+age+DB+sgpt
## Crit= 612.436090012312
## Mean crit= 612.436090012312
```

```
## Change in best IC: 0 / Change in mean IC: 0
##
## After 40 generations:
## Best model: liver~1+age+DB+sgpt
## Crit= 612.436090012312
## Mean crit= 612.436090012312
```

```
## Change in best IC: 0 / Change in mean IC: 0
```

```
##
## After 50 generations:
## Best model: liver~1+age+DB+sgpt
## Crit= 612.436090012312
## Mean crit= 612.436090012312

## Change in best IC: 0 / Change in mean IC: 0
##
## After 60 generations:
## Best model: liver~1+age+DB+sgpt
## Crit= 612.436090012312
## Mean crit= 612.436090012312

## Improvements in best and average IC have bebingo en below the specified goals.
## Algorithm is declared to have converged.
## Completed.
```

```
fit.bss <- attributes(fitting)$objects[[1]]
```

The following output shows all the predictors selected from best subset selection to be used in the model, and their slope parameter estimates.

```
coef(fit.bss)
```

```
## (Intercept)         age          DB        sgpt
## -1.12264221  0.01993645  0.65782404  0.01509633
```

3.4 LASSO

Finally, the fourth model that we fit is a LASSO model. Since LASSO requires us to find a λ, we accomplish this task via cross-validation. We select the smallest λ and use this for our model.

```
library(glmnet, quietly = TRUE)
```

```
## Loaded glmnet 3.0-2
```

```
X <- model.matrix(~., data = dat)
X <- X[,-c(1,11)]
y <- dat$liver
CV <- cv.glmnet(x=X, y=y, family="binomial", alpha=1,
                lambda.min = 1e-4, nlambda = 200, standardize = T, thresh = 1e-07,
                maxit=1000)
b.lambda <- CV$lambda.min
fit.pen <- glmnet(x=X, y=y, family="binomial", alpha = 1,
                  lambda = b.lambda, standardize = T, thresh = 1e-07,
                  matit = 1000)
```

The following output shows all the predictors selected from the regularzation to be used in the model, and their slope parameter estimates.

```
t(as.matrix(coef(fit.pen)))
```

```
##    (Intercept)        age     gender          TB        DB     alkphos
## s0  -0.5748613 0.01671355 0.04885677 0.001972972 0.4357566 0.001309377
##           sgpt        sgot alb    AGratio
## s0 0.007322405 0.001894452   0 -0.4565881
```

4 Model Comparison

Next, we compute the jackknife residuals for each of the models from the previous section

```
suppressMessages(library(pROC, quietly = TRUE))
# Compute jackknife values for the full model
n <- NROW(dat)
p.jk <- rep(0, n)
for (i in 1:n){
  fit.i <- glm(formula(fit.full), data = dat[-i,],
                                  family = "binomial")
  p.jk[i] <- predict(fit.i, newdata = dat[i,], type="response")
}
y <- dat$liver
yhat.full <- p.jk

# Compute jackknife values for step model
n <- NROW(dat)
p.jk <- rep(0, n)
for (i in 1:n){
  fit.i <- glm(formula(fit.step), data = dat[-i,], family = "binomial")
  p.jk[i] <- predict(fit.i, newdata = dat[i,], type="response")
}
y <- dat$liver
yhat.step <- p.jk

# Compute jackknife values for best subset model
n <- NROW(dat)
p.jk <- rep(0, n)
for (i in 1:n){
  fit.i <- glm(formula(fit.bss), data = dat[-i,], family = "binomial")
  p.jk[i] <- predict(fit.i, newdata = dat[i,], type="response")
}
y <- dat$liver
```

```
yhat.bss <- p.jk

# Compute jackknife values for LASSO
terms <- colnames(X)[as.vector(coef(fit.pen)) != "."]
formula.pen <- as.formula(paste(c("liver ~ 1", terms[1:length(terms)-1]),
                                collapse = " + "))
n <- nrow(dat)
p.jk <- rep(0, n)
for (i in 1:n){
  fit.i <- glm(formula.pen, data = dat[-i,], family="binomial")
  p.jk[i] <- predict(fit.i, newdata = dat[i,], type = "response")
}
y <- dat$liver
yhat.pen <- p.jk
```

We next plot the ROC curves for each of the models.

```
par(mfrow=c(2, 2), mar = rep(4,4), pty = "s")
plot.roc(y, yhat.full, main="(a) ROC for fit.full", percent = TRUE,
          print.auc = TRUE, print.auc.cex = 1.0, col = "blue", xlim = c(100, 0))
plot.roc(y, yhat.step, main="(b) ROC for fit.step", percent = TRUE,
          print.auc = TRUE, print.auc.cex = 1.0, col = "blue", xlim = c(100, 0))
plot.roc(y, yhat.bss, main="(c) ROC for fit.bss", percent = TRUE,
          print.auc = TRUE, print.auc.cex = 1.0, col = "blue", xlim = c(100, 0))
plot.roc(y, yhat.pen, main="(d) ROC for fit.pen", percent = TRUE,
          print.auc = TRUE, print.auc.cex = 1.0, col = "blue", xlim = c(100, 0))
```

In Figure 1, we that model fitted using stepwise selection (b) and best subset selection (c) have the highest AUC compared to the other methods with its AUC begin 74.4%, compared to the AUC of 73% obtained with both the full model and LASSO. We Will go with the stepwise selection since it is faster to compute.

5 Final Model

Since the model using stepwise selection has the highest AUC, we will use this as our final model. We next compute, and output, the 95% confidence intervals for the odds ratios from the final model.

```
ci <- suppressWarnings(suppressMessages(confint(fit.step, level = 0.95)))
exp(ci)
```

```
##                 2.5 %    97.5 %
## (Intercept) 0.1698137 0.6127237
## age         1.0080930 1.0326225
```

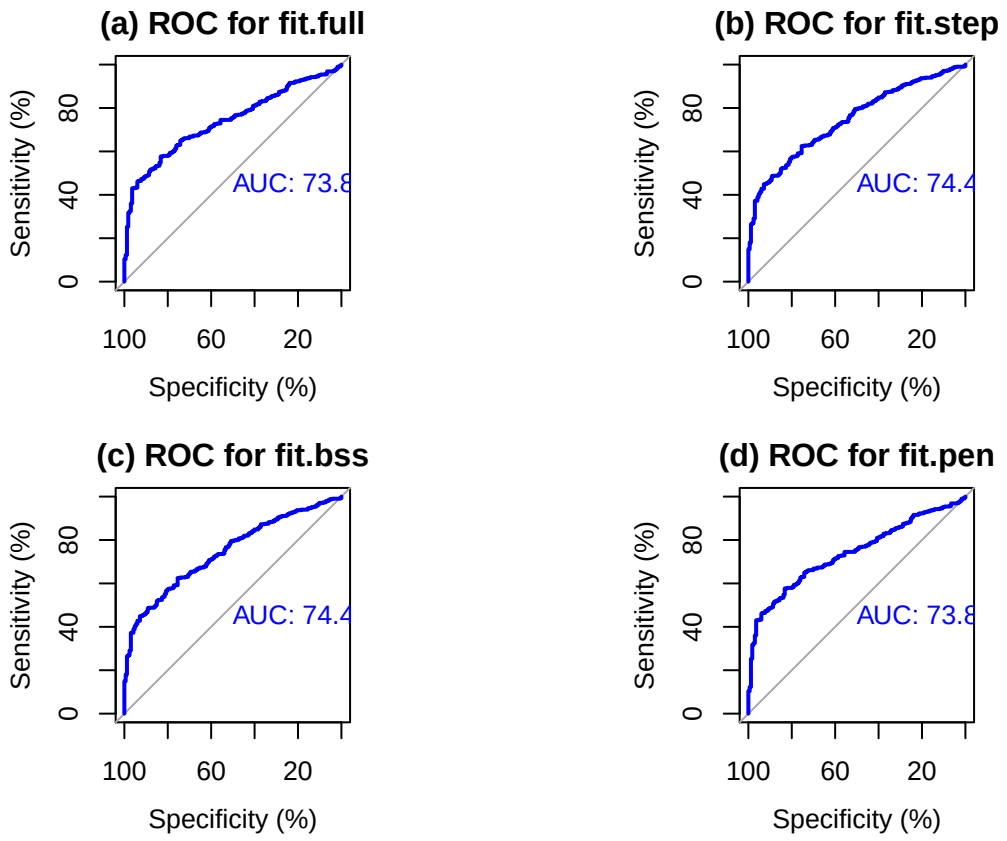


Figure 1: ROC curves for each of the logistic regression models fit.

```
## DB          1.4296011 2.8357334
## sgpt        1.0082985 1.0234853
```

The first thing that we notice is that none of these intervals contain any values less than one. This is important in this context because odds ratios less than one would imply that the predictor is a protective factor, but since we do not see this with our predictors—they all contain values greater than one—we conclude that they are all risk factors.

Looking specifically at `DB` (direct bilirubin), we see that it appears to be a significant risk factor relative to `age` and `sgp` because it's odds ratio is somewhere in the interval (1.43, 2.84), as oppossed to being relatively close to one. On the lower end of the interval there is a 1.43 relative increase in the odds of disease, and on the upper end there is 2.84 relative increase in the odds of disease. Checking the measurements of `DB` in data set the confirms that there are some individuals that have high `DB` levels, and many have measurements that are well above normal.