IE 5080 - EDA and Determination of Policy Form

```r
# run variable selection
source(path) # run the variable selection function
```

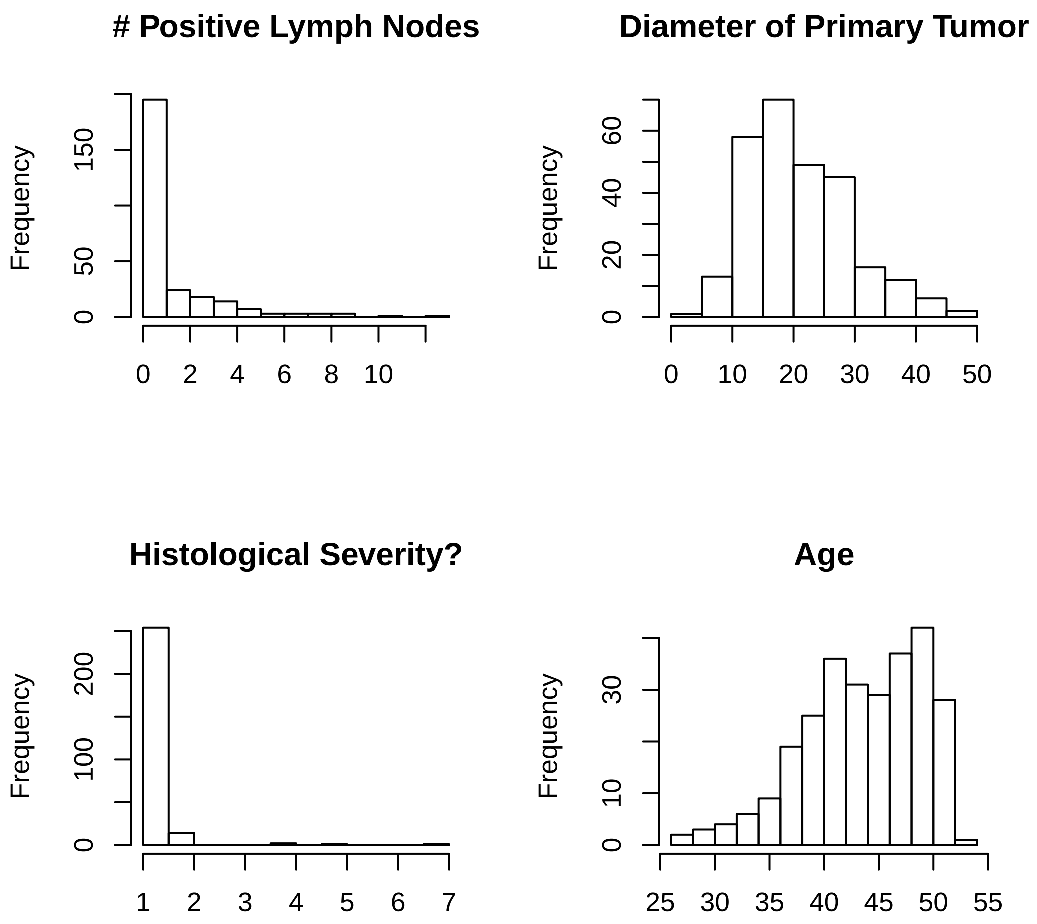
```
## Loading required package: Matrix

## Loaded glmnet 3.0-1

##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```r
set.seed(1234) # this seed results in a dataset with 28 variables
df = variable_select()$newdata
```

For practical purposes we would like to construct our policy form using only the metadata. Since the imaging data has been normalized prior to obtaining possession, a policy form using abstracted information based on characteristics of imaging is less interpretable for clinicians. So, we have five candidate variables:

- posnodes (# positive lymph nodes)
- diam (diameter of primary tumor)
- hist (a measure of the severity of the histology?)
- age
- grade (histological grade)

```r
# eda for metadata
par(mfrow=c(2,2))
hist(df$posnodes, main = "# Positive Lymph Nodes", xlab="")
hist(df$diam, main = "Diameter of Primary Tumor", xlab="")
hist(df$histtype, main = "Histological Severity?", xlab="")
hist(df$age, main = "Age", xlab="")
```



```
table(df$grade)
```

```
##
##   1   2   3
##  71  95 106
```

```
table(df$histtype)
```

```
##
##   1   2   4   5   7
## 254  14   2   1   1
```

```
table(df$posnodes)
```

```
##
##   0   1   2   3   4   5   6   7   8   9  11  13
## 137  58  24  18  14   7   3   3   3   3   1   1
```

```
table(df$angioinv)
```

```
##
##   1   2   3
## 169  30  73
```

```r
table(df$lymphinfil)
```

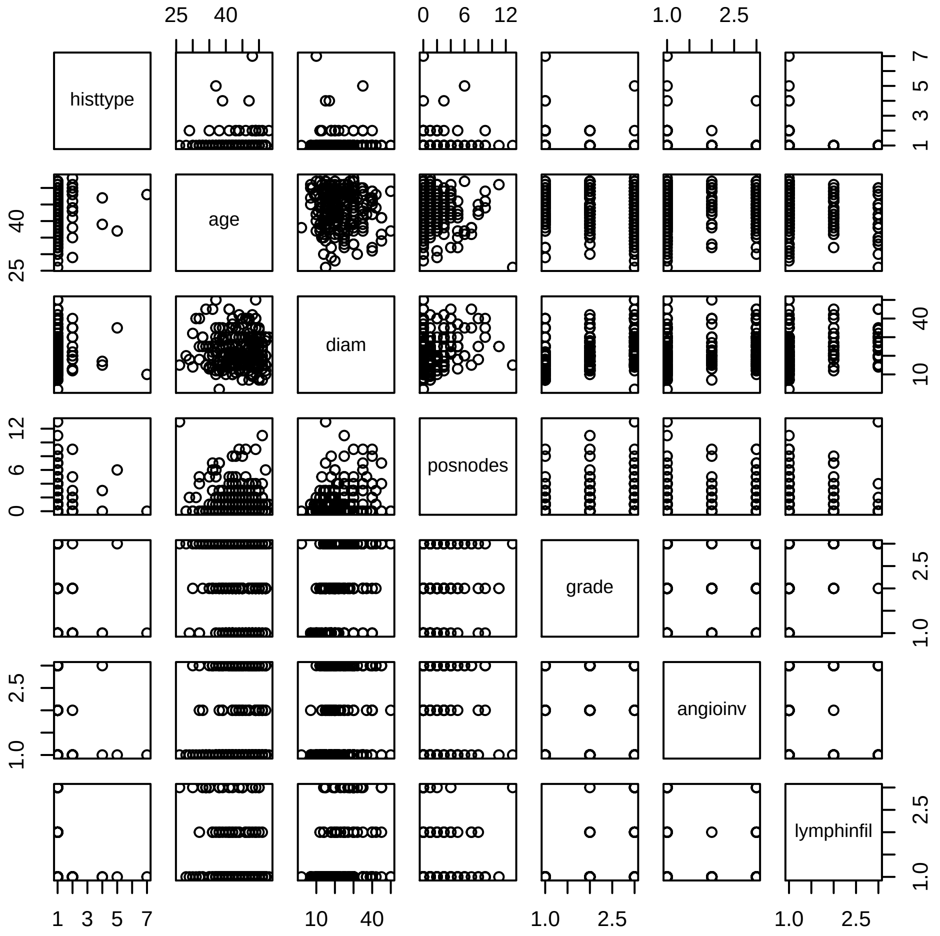
```
## 
##   1   2   3 
## 223  27  22
```

- posnodes contains a lot of zeros so any policy form with posnodes > 0 will automatically exclude 137 of the patients
- histtype contains 254 1s, so there is not enough variation to use it to determine treatment policy
- age, diameter, and grade seem like good candidates

```r
metavars = df[,8:14]
cor = cor(metavars, method="spearman")
cor
```

```
##               histtype          age        diam    posnodes       grade
## histtype    1.00000000  0.019264075 0.033572695  0.05924833 -0.22221437
## age         0.01926407  1.000000000 0.006178775 -0.03597298 -0.09107382
## diam        0.03357269  0.006178775 1.000000000  0.15083359  0.35613078
## posnodes    0.05924833 -0.035972981 0.150833586  1.00000000 -0.01546974
## grade      -0.22221437 -0.091073825 0.356130779 -0.01546974  1.00000000
## angioinv   -0.14697620  0.044579330 0.112036374  0.23911023  0.13976685
## lymphinfil -0.12412800 -0.197331436 0.228940465 -0.00553728  0.46349511
##               angioinv  lymphinfil
## histtype   -0.14697620 -0.12412800
## age         0.04457933 -0.19733144
## diam        0.11203637  0.22894047
## posnodes    0.23911023 -0.00553728
## grade       0.13976685  0.46349511
## angioinv    1.00000000 -0.07701179
## lymphinfil -0.07701179  1.00000000
```

```r
plot(metavars)
```



Grade and age are moderately correlated (r = 0.36).

```r
# run glm to determine which vars most influence death
# don't want to control for treatment
df_for_fit = df[, c(2, 8:14, 16:ncol(df))]
m1 = glm(eventdeath ~ ., data=df_for_fit, family=binomial)
summary(m1) # none of the metadata significant
```

```
##
## Call:
## glm(formula = eventdeath ~ ., family = binomial, data = df_for_fit)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.8668  -0.5517  -0.1994   0.2208   2.9002
##
## Coefficients:
##                 Estimate Std. Error z value Pr(>|z|)
## (Intercept)    2.3339205  2.2753820   1.026 0.305020
## histtype      -0.1630684  0.5897857  -0.276 0.782174
## age           -0.0898589  0.0375750  -2.391 0.016782 *
## diam             0.0393134  0.0230403   1.706 0.087955 .
## posnodes        -0.0114412  0.0865753  -0.132 0.894863
## grade            0.5992251  0.3382211   1.772 0.076445 .
## angioinv         0.1717580  0.2224016   0.772 0.439944
## lymphinfil      -1.6684194  0.4352339  -3.833 0.000126 ***
## NM_003258       -0.1379107  0.9337216  -0.148 0.882580
## NM_012067       -1.1060752  0.5642943  -1.960 0.049984 *
## NM_003430       -2.5261652  1.1783658  -2.144 0.032050 *
## AL117418        -0.5839900  0.9198213  -0.635 0.525497
## NM_006096        1.1455149  0.8556600   1.339 0.180652
## Contig23211_RC  3.3647197  1.5761202   2.135 0.032776 *
## NM_016109        1.2508821  0.7830600   1.597 0.110170
## AL049265        -0.0006939  0.7799368  -0.001 0.999290
## Contig55725_RC -0.0023075  0.7232520  -0.003 0.997454
## NM_016359        4.4894323  1.2946990   3.468 0.000525 ***
## Contig48913_RC  0.5169789  1.2654989   0.409 0.682893
## NM_001109        1.5655974  0.9619570   1.628 0.103628
## NM_001124       -0.6178550  0.7638710  -0.809 0.418603
## NM_001333        0.2912375  0.8078340   0.361 0.718461
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 324.14  on 271  degrees of freedom
## Residual deviance: 187.92  on 250  degrees of freedom
## AIC: 231.92
##
## Number of Fisher Scoring iterations: 6
```

Indeed, histtype and posnodes have the largest pvalues of the 5 metadata variables.

Next try a model with only the metadata:

```
m2 = glm(eventdeath ~ histtype + age + diam + posnodes + grade + angioinv + lymphinfil, data=df, family=
summary(m2)
```

```
##
## Call:
## glm(formula = eventdeath ~ histtype + age + diam + posnodes +
##     grade + angioinv + lymphinfil, family = binomial, data = df)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.6664  -0.7813  -0.4585   0.8599   2.5268
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.98579    1.48510  -1.337   0.1812
## histtype     0.28904    0.30870   0.936   0.3491
## age         -0.05926    0.02762  -2.146   0.0319 *
## diam         0.02834    0.01815   1.562   0.1184
## posnodes     0.02123    0.06821   0.311   0.7556
## grade        1.22355    0.24899   4.914 8.92e-07 ***
## angioinv     0.24476    0.17002   1.440   0.1500
## lymphinfil  -0.45202    0.26267  -1.721   0.0853 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 324.14  on 271  degrees of freedom
## Residual deviance: 272.40  on 264  degrees of freedom
## AIC: 288.4
##
## Number of Fisher Scoring iterations: 4
```

Once again, age, diam, and grade have the smallest p-values. Surprisingly, older ages correspond to higher death rates.

```
car::vif(m2)
```

```
##   histtype        age       diam   posnodes      grade   angioinv
##   1.068335   1.100621   1.125099   1.080445   1.293845   1.094403
## lymphinfil
##   1.335235
```

```
m3 = glm(eventdeath ~ age + diam + grade + lymphinfil, data=df, family=binomial)
summary(m3)
```

```
##
## Call:
## glm(formula = eventdeath ~ age + diam + grade + lymphinfil, family = binomial,
##     data = df)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.6123  -0.7712  -0.4590   0.9195   2.5206
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.17937    1.36504  -0.864   0.3876
## age         -0.06045    0.02720  -2.223   0.0262 *
## diam         0.03319    0.01779   1.866   0.0620 .
## grade        1.22738    0.24032   5.107 3.27e-07 ***
## lymphinfil  -0.53640    0.25671  -2.089   0.0367 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 324.14  on 271  degrees of freedom
## Residual deviance: 275.39  on 267  degrees of freedom
## AIC: 285.39
##
## Number of Fisher Scoring iterations: 4
```

```
car::vif(m3)
```

```
##        age       diam      grade lymphinfil
##   1.079144   1.080935   1.224555   1.292567
```

Based on these results, I think we should define the policy form based on three different sets of variables:

- age, diam, grade, lymphinfil
- age, diam, grade, lymphinfil, NM_003430, Contig23211_RC, NM_016359
- NM_003430, Contig23211_RC, NM_016359

The coefficient values for the variables were:

- positive for diam, grade, Contig23211_RC, and NM_016359
- negative for age (surprisingly), lymphinfil, and NM_003430