

MPH Practicum

Table 1: Exclusion criteria

	n
Initial	184
Excluded	
UTUC	5
No cysto	1
No follow up	4
Insufficient RNA for biomarker analysis	7
Duplicates	9
Total	158

Table 2: Smoking count

smoking	n
never	49
former	77
current	32

Table 3: Cysto results vs risk

visual_suspicion	risk	bca	n
no	NoBC	0	81
yes	NoBC	0	11
yes	low	1	7
yes	intermediate	1	12
yes	high	1	47

Table 4: Smoking history

smoking	packyrs	yearquit	n
never	0	0	48
never	1	1	1
former	0	0	9
former	0	1	17
former	1	0	14
former	1	1	37
current	0	0	10
current	0	1	1
current	1	0	19
current	1	1	2

```
#logistic regression cancer = biomarkers
```

```
model1 <- glm(bca ~ MODEL3, family = "binomial", data = detection)
summary(model1)
```

```
##
## Call:
## glm(formula = bca ~ MODEL3, family = "binomial", data = detection)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -2.1730  -0.4505  -0.2786   0.4570   2.4043
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -3.4050     0.5000  -6.809 9.80e-12 ***
## MODEL3        5.7850     0.7659   7.553 4.26e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 214.74  on 157  degrees of freedom
## Residual deviance: 108.60  on 156  degrees of freedom
## AIC: 112.6
##
## Number of Fisher Scoring iterations: 5
```

```
#logistic regression cancer = biomarkers + smoking
```

```
model2 <- glm(bca ~ MODEL3 + smoking, family = "binomial", data = detection)
summary(model2)
```

```
##
## Call:
## glm(formula = bca ~ MODEL3 + smoking, family = "binomial", data = detection)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -2.7103  -0.3511  -0.1490   0.4085   2.4320
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -4.8601     0.8519  -5.705 1.16e-08 ***
## MODEL3        6.2710     0.9115   6.880 5.98e-12 ***
## smokingformer  1.2187     0.6523   1.868 0.06171 .
## smokingcurrent 2.3643     0.8266   2.860 0.00423 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 214.737  on 157  degrees of freedom
## Residual deviance:  99.169  on 154  degrees of freedom
## AIC: 107.17
```

```
##  
## Number of Fisher Scoring iterations: 6
```

```
#likelihood ratio test  
lrtest(model1, model2)
```

```
## Likelihood ratio test  
##  
## Model 1: bca ~ MODEL3  
## Model 2: bca ~ MODEL3 + smoking  
##   #Df  LogLik Df  Chisq Pr(>Chisq)  
## 1    2 -54.298  
## 2    4 -49.584  2  9.4263  0.008976 **  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```