

This document shows how to use R to replicate Display 20.7 to compute the drop-in-deviance test for the lung cancer example.

```
> case2002 <- read.table("sleuth/case2002.csv", header = T, sep = ",")
> attach(case2002)
> full <- glm(LC ~ SEX + SS + BK + AG + YR, family = "binomial")
> reduced <- glm(LC ~ SEX + SS + AG + YR, family = "binomial")
> summary(full)
```

Call:

```
glm(formula = LC ~ SEX + SS + BK + AG + YR, family = "binomial")
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-2.2207	-0.9938	0.4522	0.8722	1.5193

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-0.58210	1.68168	-0.346	0.729236
SEXMALE	0.52134	0.52936	0.985	0.324698
SSLOW	0.13209	0.46398	0.285	0.775886
BKNOBIRD	1.33487	0.40900	3.264	0.001099 **
AG	0.04634	0.03489	1.328	0.184068
YR	-0.08288	0.02480	-3.342	0.000831 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 187.14 on 146 degrees of freedom
 Residual deviance: 155.24 on 141 degrees of freedom
 AIC: 167.24

Number of Fisher Scoring iterations: 4

```
> summary(reduced)
```

Call:

```
glm(formula = LC ~ SEX + SS + AG + YR, family = "binomial")
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-2.4812	-1.1680	0.5443	0.9846	1.2655

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-0.76810	1.59707	-0.481	0.630558
SEXMALE	0.72137	0.50258	1.435	0.151193
SSLOW	-0.05645	0.43658	-0.129	0.897121

```
AG          0.06320    0.03370    1.875 0.060739 .
YR          -0.08726    0.02476   -3.524 0.000425 ***
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

(Dispersion parameter for binomial family taken to be 1)

```
Null deviance: 187.14 on 146 degrees of freedom
Residual deviance: 166.53 on 142 degrees of freedom
AIC: 176.53
```

Number of Fisher Scoring iterations: 4

Here is code to pick out the deviance from the output and to compute the p-value.

```
> deviance(reduced)

[1] 166.5320

> deviance(full)

[1] 155.2404

> df.residual(reduced)

[1] 142

> df.residual(full)

[1] 141

> 1 - pchisq(deviance(reduced) - deviance(full), df.residual(reduced) -
+           df.residual(full))

[1] 0.0007785639
```