

Discrete Response Model

Lecture 3

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Convergence Criteria and the Case of Complete Separation

glm() Convergence Criteria

The `glm()` function uses IRLS until convergence is obtained or until the maximum number of iterations are reached. To determine convergence, `glm()` does not look at the successive estimates of the parameters directly; rather it examines the residual deviance. If we let $G^{(k)}$ denote the residual deviance at iteration k , then convergence occurs when

$$\frac{|G^{(k)} - G^{(k-1)}|}{0.1 + |G^{(k)}|} < \epsilon$$

where ϵ is some specified small number greater than 0. The numerator provides a measure to determine if the $\hat{\pi}_i$ for $i = 1, \dots, n$ are changing much from one iteration to the next. The denominator helps to take into account the relative size of the residual deviance.

glm() Convergence Criteria

The `glm()` function provides a few ways to control how convergence is decided:

- The `epsilon` argument sets ϵ above. The default is $\epsilon = 10^{-8}$.
- The `maxit` argument states the maximum number of iterations allowed for the numerical procedure. The default is `maxit = 25`.
- The `trace` argument value can be used to see the actual $G^{(k)}$ values for each iteration. The default is `trace = FALSE` (do not show these values).

glm() Convergence Criteria

Consider the model with only distance as the explanatory variable:

$$\text{logit}(\hat{\pi}) = 5.8121 - 0.1150\text{distance}$$

Below are the results from using the `glm()` to estimate the model and from including the three arguments controlling convergence. Note that these three argument values were chosen for illustrative purposes only:

```
> mod.fit<-glm(formula = good ~ distance, family =  
+ binomial(link = logit), data = placekick, trace = TRUE,  
+ epsilon = 0.0001, maxit = 50)  
Deviance = 836.7715 Iterations - 1  
Deviance = 781.1072 Iterations - 2  
Deviance = 775.8357 Iterations - 3  
Deviance = 775.7451 Iterations - 4  
Deviance = 775.745 Iterations - 5  
> mod.fit$control  
$epsilon  
[1] 1e-04  
  
$maxit  
[1] 50  
  
$trace  
[1] TRUE
```

glm() Convergence Criteria

The convergence criteria value for iteration $k = 5$ is

$$\frac{|G^{(5)} - G^{(4)}|}{0.1 + |G^{(4)}|} = \frac{|775.745 - 775.7451|}{0.1 + |775.745|} = 1.3 \times 10^{-7}$$

which is less than the stated $\epsilon = 0.0001$, so the iterative numerical procedure stopped. For iteration $k = 4$, the convergence criteria value is 0.00012, which is greater than 0.0001, so this is why the procedure continued.

If the value for maxit was changed to 3, the message

Warning message:
glm.fit: algorithm did not converge

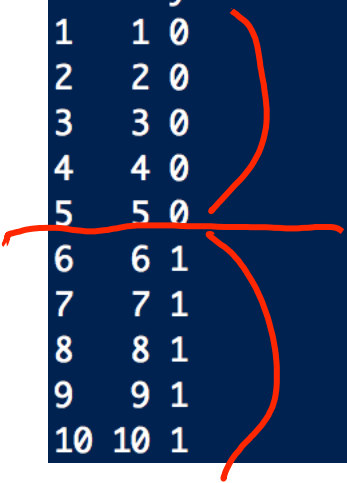
would be printed to warn you that convergence was not obtained. Of course, you would NOT use the parameter estimates in this situation!

Complete Separation

Consider a simple dataset with one explanatory variable x_1 that is less than 6 when $y = 0$ and greater than or equal to 6 when $y = 1$. Because x_1 perfectly separates out the two possible values of y , complete separation occurs. Below is the corresponding R code and output:

```
> set1<-data.frame(x1 = c(1,2,3,4,5,6,7,8,9,10), y =  
+   c(0,0,0,0,0,1,1,1,1,1))  
> set1
```

	x1	y
1	1	0
2	2	0
3	3	0
4	4	0
5	5	0
6	6	1
7	7	1
8	8	1
9	9	1
10	10	1



Complete Separation

```
> mod.fit1<-glm(formula = y ~ x1, data = set1, family = binomial(link = logit), trace = TRUE)
```

```
Deviance = 4.270292 Iterations - 1
```

```
Deviance = 2.574098 Iterations - 2
```

```
Deviance = 2.137736e-09 Iterations - 24
```

```
Deviance = 7.864775e-10 Iterations - 25
```

```
Warning messages:
```

```
1: glm.fit: algorithm did not converge
```

```
2: glm.fit: fitted probabilities numerically 0 or 1 occurred
```

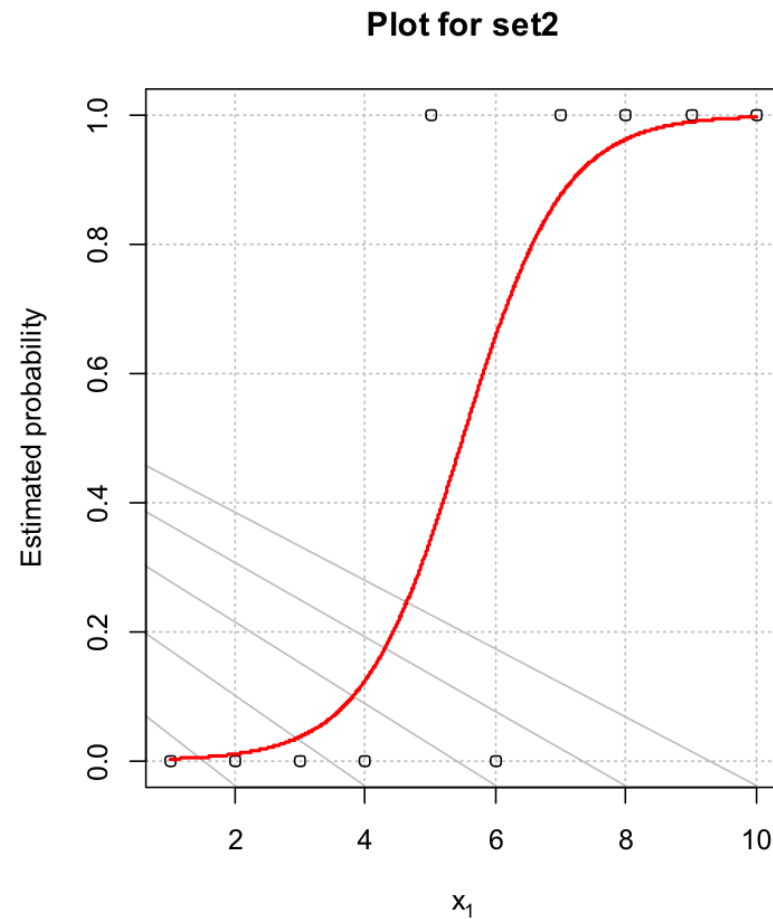
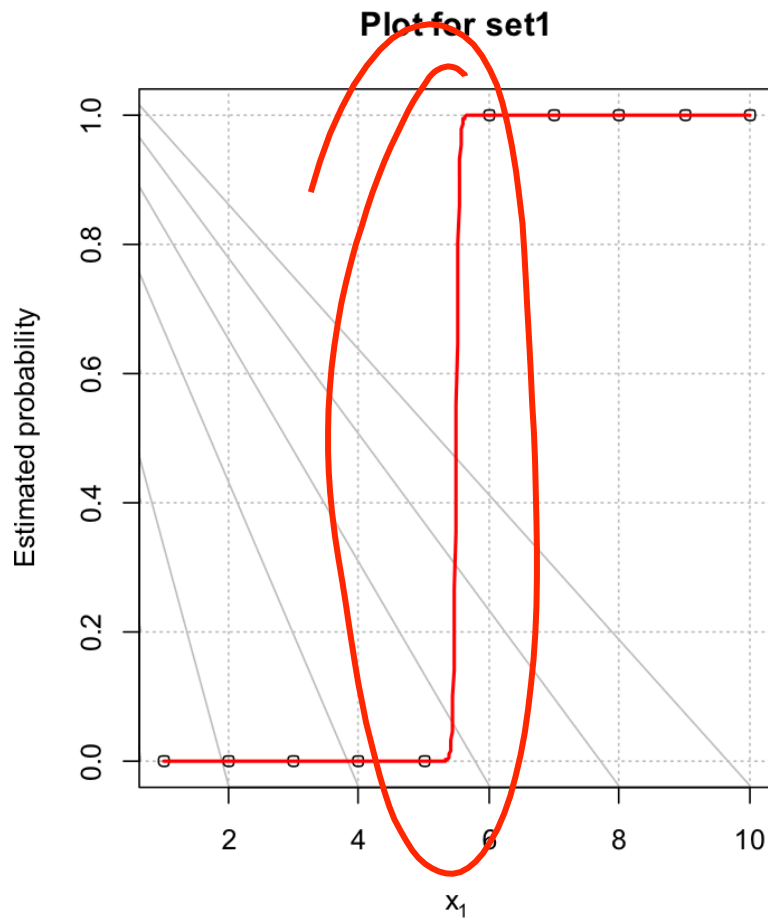
```
> mod.fit1$coefficients
```

```
(Intercept)      x1
```

```
-245.84732    44.69951
```

R indicates that both convergence did not occur and at least some estimates of π are 0 or 1. Next is a plot (left side) of the data and the model at iteration #25:

Complete Separation



Complete Separation

Because there is a separation between the $y = 0$ and 1 values, the slope of the line between $x = 5$ and 6 will continue to get larger as the iterations continue. Essentially, the β_1 estimate is going to infinity with continued iterations. Notice this means the estimate is VERY biased.

Interestingly, R indicates “convergence” after 26 iterations if you increase maxit! However, the same

`glm.fit: fitted probabilities numerically 0 or 1 occurred`

message will occur. You should not use logistic regression here because the parameter estimates will continue to change for a larger number of iterations. Try this yourself with a larger maxit and smaller epsilon.

By reversing the y values at $x_1 = 5$ and 6, we obtain model convergence in 6 iterations (not shown here). The right plot above shows the data and the final model. The slope of the model is now not as great as was before.

Complete Separation: Remarks

- Complete separation is not necessarily bad if you want to distinguish between the response levels of y . The problem is that the model estimated by maximum likelihood does not provide a good way to interpret the relationship between y and the explanatory variables.
- It can be difficult to see complete separation graphically if there is more than one explanatory variable. There may be times even when the `glm()` function does not provide a warning. When parameter estimates are very large or very small with large estimated standard deviations, this is a sign that complete separation may exist. These types of parameter estimates can then lead to many observations with estimated probabilities of success close to 0 or 1.

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