Complete Separation Notes

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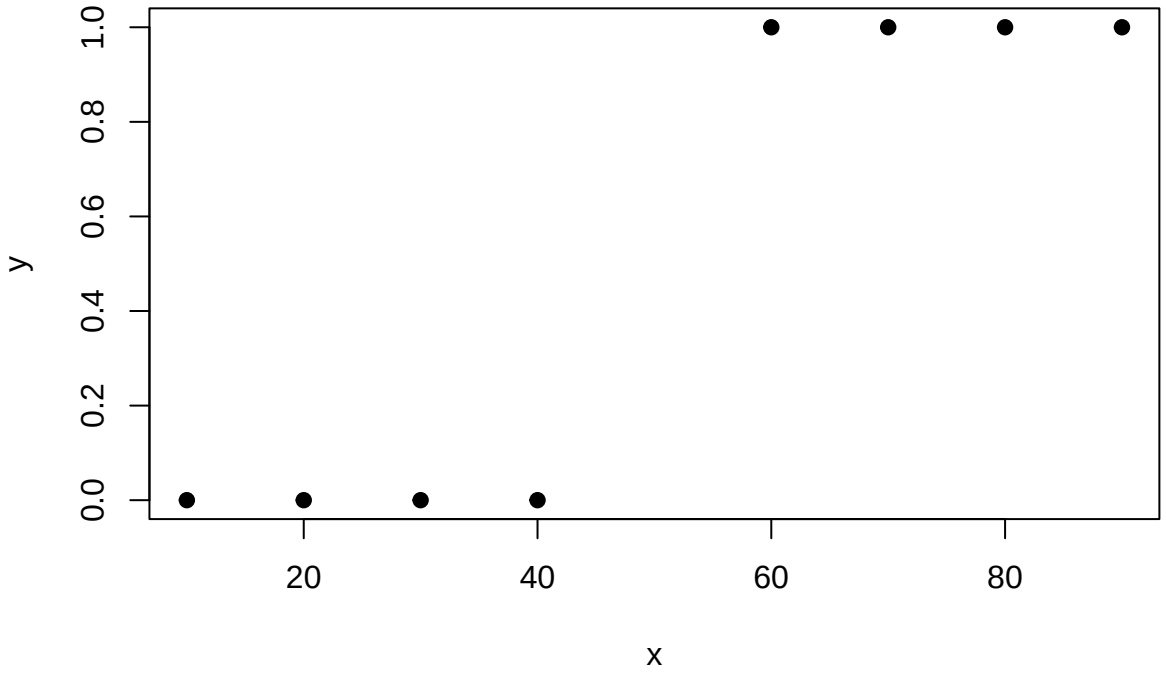
A problem with discrete exponential family models is that some data configurations can put a wrench in the gears of parameter estimation and statistical inference. In particular, when the observed value of the canonical statistic is on the boundary of its support than the exponential family is not identifiable. In logistic regression, this problem is known as complete or quasi-complete separation and it is informally described as the setting in which there exists a hyperplane which perfectly separates the successes from the failures. More formally, we say that perfect data separation (complete separation) occurs when there exists a vector b such that

$$\begin{aligned} b^T x_i &> 0 \qquad \text{whenever } y_i = 1, \\ b^T x_i &< 0 \qquad \text{whenever } y_i = 0. \end{aligned}$$

See Section 6.5.1 in Agresti for more details.

Let's look at the example in Section 6.5.1 in Agresti to describe complete separation and how to deal with it under the exponential family/maximum likelihood estimation paradigm (which isn't mentioned in Agresti). In this example, the separation is immediately evident

```
x <- (1:9 * 10)[-5]
y <- c(0,0,0,0,1,1,1,1)
plot(x, y, pch = 19)
```



If we consider a simple logisitc regression model with an intercept and predictor term, then the vector $b = (-50, 1)$ satisfies the above conditions for complete separation

```r
## separation vector
b <- c(-50, 1)

## model matrix
M <- cbind(1, x)

## check condition
cbind(M %*% b, y)
```

```
##          y
## [1,] -40 0
## [2,] -30 0
## [3,] -20 0
## [4,] -10 0
## [5,]  10 1
## [6,]  20 1
## [7,]  30 1
## [8,]  40 1
```

The data exhibits complete degeneracy, and statistical inference is essentially meaningless. Luckily the computational checks have warned the user that a potential problem has occurred. Note that these warning messages do not describe what the problem is or provide any guidance for how users should handle this problem. Morevover, these checks are purely computational and do not necessarily imply that separation has occurred.

```r
m1 <- glm(y ~ x, family = "binomial")
```

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

```r
## summary table
summary(m1)
```

```
##
## Call:
## glm(formula = y ~ x, family = "binomial")
##
## Deviance Residuals:
##        Min          1Q      Median          3Q         Max
## -1.045e-05  -2.110e-08   0.000e+00   2.110e-08   1.045e-05
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -118.158 296046.174       0        1
## x                2.363   5805.939       0        1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 1.1090e+01  on 7  degrees of freedom
## Residual deviance: 2.1827e-10  on 6  degrees of freedom
## AIC: 4
##
## Number of Fisher Scoring iterations: 25
```

```r
## LRT
anova(m1, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model: binomial, link: logit
##
## Response: y
##
## Terms added sequentially (first to last)
##
##
##      Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL                     7      11.09
## x     1    11.09         6       0.00 0.0008678 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Notice in the above that the number of Fisher scoring iterations is 25, which is the maximum allowable iterations under the default settings of the glm function. Look at what happens when change the defaults.

```
m2 <- glm(y ~ x, family = "binomial",
          control = list(maxit = 1e4, epsilon = 1e-100))
```

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

```
summary(m2)
```

```
##
## Call:
## glm(formula = y ~ x, family = "binomial", control = list(maxit = 10000,
##     epsilon = 1e-100))
##
## Deviance Residuals:
##        Min          1Q      Median          3Q         Max
## -2.107e-08  -2.107e-08   0.000e+00   2.107e-08   2.107e-08
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.546e+02  4.939e+07       0        1
## x            3.092e+00  8.664e+05       0        1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 1.1090e+01  on 7  degrees of freedom
## Residual deviance: 3.5527e-15  on 6  degrees of freedom
## AIC: 4
##
## Number of Fisher Scoring iterations: 33
```

Changing the default optimization settings changed the summary output. In particular, note that the submodel canonical parameter estimates and their corresponding standard errors are diverging when we allow for more iterations. Do not worry about this finding as a general phenomenon. We will not observe this phenomenon in well-behaved data configurations with properly conditioned model matrices, the Fisher scoring algorithm converges well before 25 iterations are observed.

Returning to the model fit with the default settings, we see large canonical parameter estimates and mean

value parameter estimates that are at the boundary of the closure of their parameter space ($0 < p < 1$). Informally, estimates are "at infinity.''

```
## submodel canonical parameter estimates
betahat <- m1$coefficients
betahat
```

```
## (Intercept)           x
##  -118.15802     2.36316
```

```
## saturated model canonical parameter estimates
thetahat <- as.numeric(M %*% betahat)
thetahat
```

```
## [1] -94.52642 -70.89481 -47.26321 -23.63160  23.63160  47.26321  70.89481
## [8]  94.52642
```

```
## saturated model mean value parameter estimates
phat <- predict(m1, type = "response")
phat
```

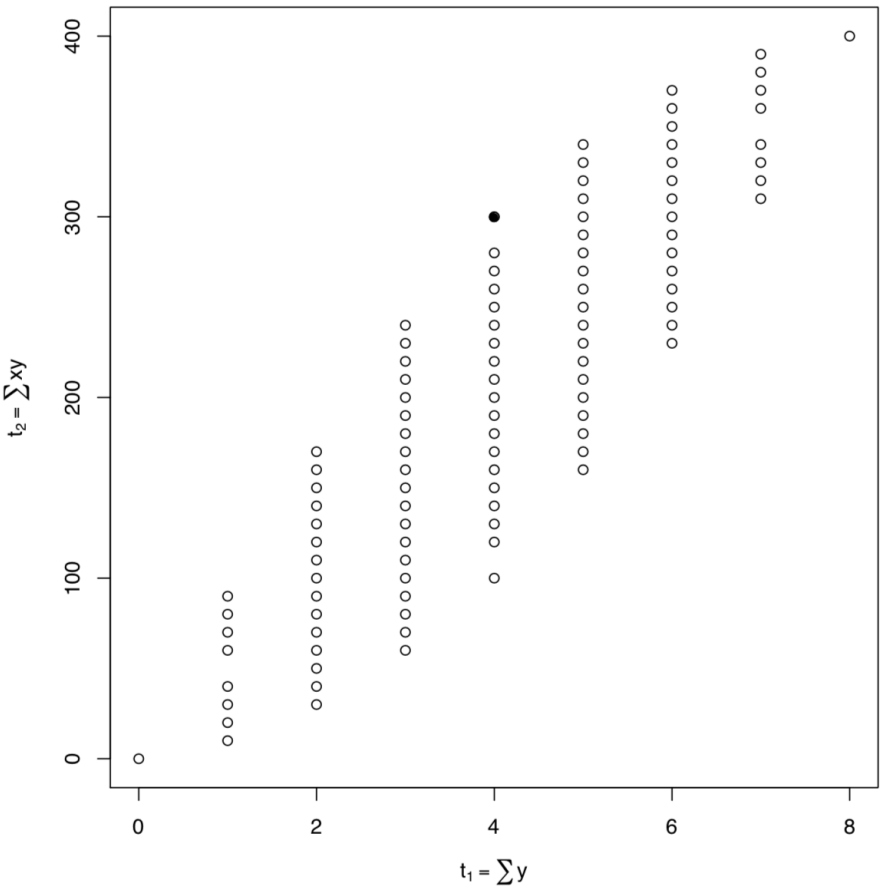
```
##            1            2            3            4            5            6
## 2.220446e-16 2.220446e-16 2.220446e-16 5.456633e-11 1.000000e+00 1.000000e+00
##            7            8
## 1.000000e+00 1.000000e+00
```

Canonical statistic on the boundary of its support

Recall that the submodel can be written as

$$\langle y, M\beta \rangle - c(M\beta) = \langle M^T y, \beta \rangle - c_\beta(\beta)$$

Also notice that the observed value of the canonical statistic $M^T y$ for the above submodel is on the boundary of the support of values for $M^T Y$ (which implies that the MLE does not exist in the traditional sense; see Geyer (2009) for technical details that are beyond the scope of this course).



Note that, by the observed equals expected property, $M^T y$ is the MLE of the submodel mean-value parameter vector. The variance of the submodel canonical statistic is the Fisher information matrix.

We now use R scripts to compute the Fisher information matrix. An eigenvector decomposition reveals that the Fisher information matrix is numerically singular.

```
invFI <- vcov(m1)
FI <- solve(invFI)
eigen(FI)
```

```
## eigen() decomposition
## $values
## [1] 7.715655e-07 1.140566e-11
##
## $vectors
##            [,1]        [,2]
## [1,] 0.01922747 -0.99981514
## [2,] 0.99981514  0.01922747
```

This implies that $\widehat{\text{Var}}(M^T Y) = 0$. Therefore, the MLE solution to this problem is that the observed data which are on the boundary are the only possible data that could have occurred. Of course, these are estimates and not actual parameters. The problem is how to make inferential statements about model parameters given

this degeneracy.

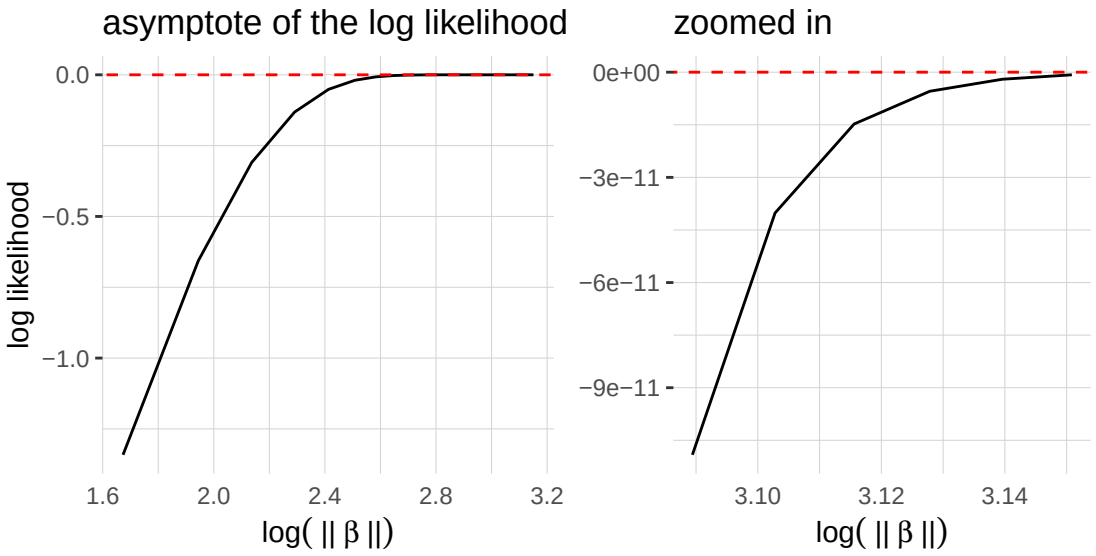
Homework: Before we discuss such an inferential approach we will give an example as motivation. The details of this example will be left for homework. Suppose that you have a coin that when flipped has a probability $0 < p < 1$ of landing heads, and that we know nothing about p. Suppose that you flip the coin four times and all four flips resulted in heads. Derive the MLE of p and the MLE of $\mathrm{Var}(Y_1)$ under the standard Bernoulli model. Now, for some error tolerance $0 < \alpha < 1$, derive a valid one-sided confidence interval for p making use of the statement $\mathbb{P}\left(\sum_{i=1}^{4} Y_i = 4\right)$.

Inference in the complete separation setting

The exponential family in this example is completely degenerate. The MLE does not exist in the traditional sense, but may (does) exist in the completion of the exponential family (the set which includes all exponential family distributions and all limits of distributions). Conventional maximum likelihood computations come close, in a sense, to finding the MLE in the completion of the exponential family. They go uphill on the likelihood function until they meet their convergence criteria and stop.

```
asymptote <- t(sapply(1:30, function(iter){
  m1 <- glm(y ~ x, family = "binomial", control = list(maxit = iter, epsilon = 1e-20))
  c(sqrt(log(crossprod(coef(m1)))), logLik(m1))
}))
asymptote <- as.data.frame(asymptote)
```

```
## Warning: The `size` argument of `element_line()` is deprecated as of ggplot2 3.4.0.
## i Please use the `linewidth` argument instead.
```



At this point, canonical parameter estimates $\hat{\theta}$ and $\hat{\beta}$ are still infinitely far away from the MLE in the completion, but mean value parameter estimates $\hat{\mu}$ are close to the MLE in the completion, and the corresponding probability distributions are close in total variation norm to the MLE probability distribution in the completion.

Some theoretical details Consider an exponential family with log likelihood

$$l(\theta) = \langle y, \theta \rangle - c(\theta)$$

with submodel $\theta = M\beta$ that has corresponding log likelihood

$$l(\beta) = \langle M^T y, \beta \rangle - c_\beta(\beta)$$

We first define the completion of the exponential family.

Definition 1. *Let θ_n, $n = 1, \ldots,$ be a sequence of canonical parameter vectors for an exponential family having above log likelihood. Let $h_n(y) = l(\theta_n)$, and suppose that $h_n(y) \to h(y)$ pointwise as $n \to \infty$ where limits $-\infty$ and $+\infty$ are allowed. The limiting functions h form the closure of the exponential family.*

In the above definition h_n is a sequence of affine functions and the limiting function h is a generalized affine function. Generalized affine functions and their properties are defined and discussed in Section 6.1 of Eck and Geyer (2021).

We let θ_n be a likelihood maximizing sequence of canonical parameter vectors, that is,

$$l(\theta_n) \to \sup_{\theta \in \Theta} l(\theta), \qquad \text{as } n \to \infty,$$

where $\sup_{\theta \in \Theta} l(\theta) < \infty$. Define $h_n(y) = l(\theta_n)$ as in the definition about the closure of exponential families. The limiting density e^h corresponds to the MLE distribution in the completion. Again, mathematical properties of these objects are discussed in Section 6 of Eck and Geyer (2021).

Suppose that the MLE does not exist in the traditional exist and it exists in the completion of the exponential family, and suppose that we know the convex support set of the MLE distribution in the completion. This support is the smallest affine set (translate of a vector subspace) that contains the canonical statistic with probability one. Denote the affine support by A. Since the observed value of the canonical statistic is contained in A with probability one, and the canonical statistic for a GLM is $M^T Y$, then we have $A = M^T y + V$ where Y is the response vector, and y its observed value, and V is a vector space [Geyer, 2009, Section 3.9].

Then the limiting exponential family model (refered to as a limiting conditional model, or LCM for short) in which the MLE in the completion is found is the original model (OM) conditioned on the event

$$M^T(Y - y) \in V, \qquad \text{almost surely.}$$

Suppose we characterize V as the subspace where a finite set of linear equalities are satisfied

$$V = \{w \in \mathbb{R}^p : \langle w, \eta_i \rangle = 0, i = 1, \ldots, j\}.$$

Then the LCM is the OM conditioned on the event

$$\langle M^T(Y - y), \eta_i \rangle = \langle Y - y_i, M\eta_i \rangle = 0, \qquad i = 1, \ldots, j.$$

Recall that Fisher information is the variance for $M^T Y$. From this we see that the vectors $\eta_1, \ldots, \eta_j$ span the null space of the Fisher information matrix for the LCM.

The null space of the Fisher information matrix for the LCM is well approximated by the Fisher information matrix for the OM at parameter values that are close to maximizing the likelihood. The LCM is the OM conditioned on the event

$$\langle Y, M\eta_i \rangle = \langle y, M\eta_i \rangle, \qquad \text{almost surely for } i \in 1, \ldots, j. \tag{1}$$

The event (1) fixes some components of the response vector at their observed values and leaves the rest entirely unconstrained. Those components that are entirely unconstrained are those for which the corresponding component of $M\eta_i$ is zero (or, taking account of the inexactness of computer arithmetic, nearly zero) for all $i = 1, \ldots, j$. We see no such points in our example, therefore all components of the response are fixed at their observed value in this example.

```
M %*% eigen(FI)$vec
```

```
##          [,1]       [,2]
## [1,] 10.01738 -0.8075404
## [2,] 20.01553 -0.6152657
## [3,] 30.01368 -0.4229910
## [4,] 40.01183 -0.2307163
## [5,] 60.00814  0.1538330
## [6,] 70.00629  0.3461077
## [7,] 80.00444  0.5383824
## [8,] 90.00259  0.7306571
```

We now provide a method for calculating these one-sided confidence intervals. Let I denote the index set of the components of the response vector on which we condition the OM to get the LCM, and let Y_I and y_I denote these components considered as a random vector and as an observed value, respectively. Then endpoints for a $100(1 - \alpha)\%$ confidence interval for a scalar parameter $g(\beta)$ are

$$\min_{\substack{\gamma \in \Gamma_{\lim} \\ \mathbb{P}_{\hat{\beta}+\gamma}(Y_I = y_I) \geq \alpha}} g(\hat{\beta} + \gamma) \qquad \text{and} \qquad \max_{\substack{\gamma \in \Gamma_{\lim} \\ \mathbb{P}_{\hat{\beta}+\gamma}(Y_I = y_I) \geq \alpha}} g(\hat{\beta} + \gamma) \tag{2}$$

where $\hat{\beta}$ is the estimated MLE of β in the LCM, $\Gamma_{\lim}$ is the null space of the Fisher information matrix. In our Agresti example, $\hat{\beta}$ is 0 and $\Gamma_{\lim} = \mathbb{R}^2$. Note that at least one of (2) is at the end of the range of this parameter (otherwise we can use conventional two-sided intervals).

Logistic and binomial regression

For logistic and binomial regression, let $p = \text{logit}^{-1}(\theta)$ denote the mean value parameter vector (here logit^{-1} operates componentwise). Then,

$$\mathbb{P}_\beta(Y_I = y_I) = \prod_{i \in I} p_i^{y_i} (1 - p_i)^{n_i - y_i}$$

where the n_i are the binomial sample sizes. In logistic regression we have $n_i = 1$ for all i, but in binomial regression we have $n_i \geq 1$ for all i. We could take the confidence interval problem to be

$$\begin{aligned} &\text{maximize} \quad p_k, \qquad \text{subject to} \quad \prod_{i \in I} p_i^{y_i} (1 - p_i)^{n_i - y_i} \geq \alpha, \text{ or} \\ &\text{minimize} \quad p_k, \qquad \text{subject to} \quad \prod_{i \in I} p_i^{y_i} (1 - p_i)^{n_i - y_i} \geq \alpha \end{aligned} \tag{3}$$

where p is taken to be the function of γ described above. And this can be done for any $k \in I$. However, the problem will be more computationally stable if we state it as

$$\begin{aligned} &\text{maximize} \quad \theta_k \\ &\text{subject to} \quad \sum_{i \in I} \bigl[y_i \log(p_i) + (n_i - y_i) \log(1 - p_i) \bigr] \geq \log(\alpha); \\ &\text{minimize} \quad \theta_k \\ &\text{subject to} \quad \sum_{i \in I} \bigl[y_i \log(p_i) + (n_i - y_i) \log(1 - p_i) \bigr] \geq \log(\alpha) \end{aligned} \tag{4}$$

Since $\theta_k = \text{logit}(p_k)$ is a monotone transformation and log is a monotone transformation, the two problems (3) and (4) are equivalent. We maximize canonical rather than mean value parameters to avoid extreme inexactness of computer arithmetic in calculating mean value parameters near zero and one. We take logs in the constraint for the same reasons we take logs of likelihoods.

Poisson regression

For Poisson sampling, let $\mu = \exp(\theta)$ denote the mean value parameter (here exp operates componentwise like the R function of the same name does), then

$$\mathbb{P}_\beta(Y_I = y_I) = \exp\left(-\sum_{i \in I} \mu_i\right).$$

We take the confidence interval problem to be

$$\text{maximize} \quad \mu_k, \qquad \text{subject to} \quad -\sum_{i \in I} \mu_i \geq \log(\alpha) \tag{5}$$

where μ is taken to be the function of γ described in (2). The optimization in (5) can be done for any $k \in I$.

Software and return to Agresti example

The `inference` function in the R package `glmdr` (see the `glmdr` directory in the stat528resources repo; you will have to install the package locally) determines one-sided confidence intervals for mean value parameters corresponding to response values y_I for logistic and binomial regression as in (4) and Poisson regression as in (5).

```
library(glmdr)
```

We return to the motivating Agresti example. Here we see that the Fisher information matrix has only null eigenvectors.

```
eigen(FI)
```

```
## eigen() decomposition
## $values
## [1] 7.715655e-07 1.140566e-11
##
## $vectors
##            [,1]        [,2]
## [1,] 0.01922747 -0.99981514
## [2,] 0.99981514  0.01922747
```

In this case the MLE of the saturated model mean value parameters agree with the observed data; they are on the boundary of the set of possible values, either zero or one. Thus the LCM is completely degenerate at the one point set containing only the observed value of the canonical statistic of this exponential family. One-sided confidence intervals for mean value parameters (success probability considered as a function of the predictor x) are now computed. We first the logistic regression model using the `glmdr` fitting function instead of `glm`.

```
m_glmdr <- glmdr(y ~ x)

## summary information
summary(m_glmdr)
```

```
## MLE exists in Barndorff-Nielsen completion
## it is completely degenerate
## the MLE says the response actually observed is the only
## possible value that could ever be observed
```

```
## $overview
## NULL
```

```
##
## $type
## [1] "degenerate"
##
## $linearity
## [1] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
##
## attr(,"class")
## [1] "summary.glmdr"
```

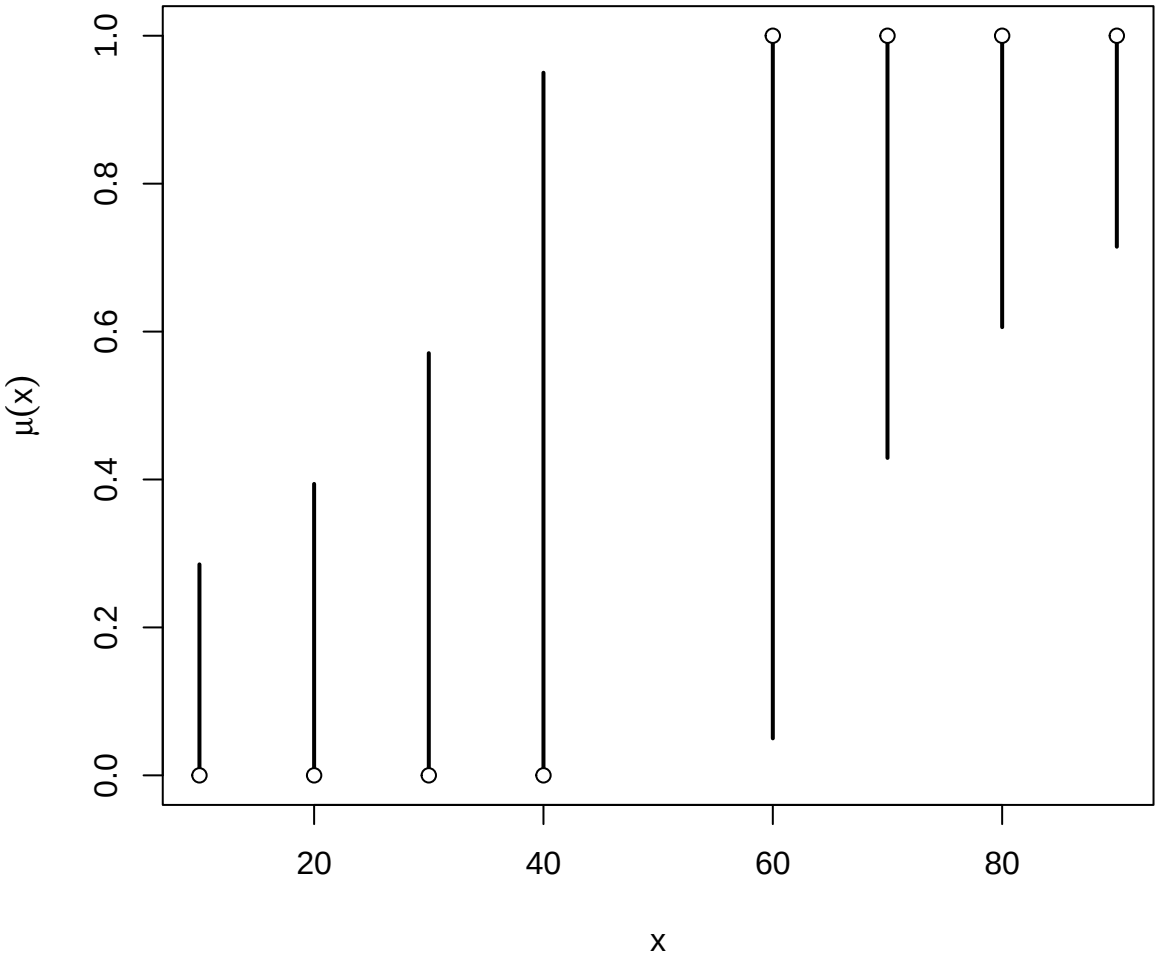
We then use the `inference` function to obtain one sided confidence intervals for mean-value parameters corresponding to components Y_I that are constrained to be their observed values. This function performs the optimization in (2) where the function g in (2) is taken to be the map from submodel canonical parameter to saturated model mean-value parameters (ie the conditional success probabilities).

```
## one-sided CIs
CIs <- inference(m_glmdr)
CIs
```

```
##       lower     upper
## 1 0.0000000 0.2852500
## 2 0.0000000 0.3940359
## 3 0.0000000 0.5708292
## 4 0.0000000 0.9500000
## 5 0.0500000 1.0000000
## 6 0.4291708 1.0000000
## 7 0.6059641 1.0000000
## 8 0.7147500 1.0000000
```

We now plot these one-sided confidence intervals.

```
bounds.lower.p <- CIs$lower
bounds.upper.p <- CIs$upper
par(mar = c(4, 4, 0, 0) + 0.1)
plot(x, y, axes = FALSE, type = "n",
    xlab = expression(x), ylab = expression(mu(x)))
segments(x, bounds.lower.p, x, bounds.upper.p, lwd = 2)
box()
axis(side = 1)
axis(side = 2)
points(x, y, pch = 21, bg = "white")
```



These confidence intervals are quite wide. This is due to the relatively lack of data.

Commentary on Agresti

The $n = 8$ data point example that we analyzed comes from Section 6.5.1 in Agresti. However, this textbook provides no model based inferential solution to this problem. In the above, we provided such a solution that exists within the exponential family modeling and maximum likelihood estimation paradigms. To be fair to Agresti, "solutions" to complete separation are discussed in Sections 7.4.8. This approach circumvents the model-based approach. **Summarise the approach mentioned in Section 7.4.8 and compare/contrast it with the approach outlined in these notes. What are the strengths and weaknesses of each?**

Not completely degenerate

In the Agresti example we noticed that the estimated Fisher information matrix was completely degenerate. This need not be so in generality, the Fisher information matrix can exhibit partial degeneracy. When this is so the LCM is not trivially degenerate like in the Agresti example. Data pairs (y_i, x_i) corresponding to response vectors which are left unconstrained form the LCM and parameter estimation can be conducted in a traditional manner. We will explore an example where with partial degeneracy.

We will condsider the endometrial example in which the a histology grade and risk factors for 79 cases of endometrial cancer are analyzed.

```
library(enrichwith)
data(endometrial)
```

```
head(endometrial)
```

```
##   NV PI   EH HG
## 1  0 13 1.64  0
## 2  0 16 2.26  0
## 3  0  8 3.14  0
## 4  0 34 2.68  0
## 5  0 20 1.28  0
## 6  0  5 2.31  0
```

We begin with a standard logistic regression fit.

```
m <- glm(HG ~ ., data = endometrial, family = "binomial",
         x = TRUE, y = TRUE)
summary(m)
```

```
##
## Call:
## glm(formula = HG ~ ., family = "binomial", data = endometrial,
##     x = TRUE, y = TRUE)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.50137  -0.64108  -0.29432   0.00016   2.72777
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   4.30452    1.63730   2.629 0.008563 **
## NV           18.18556 1715.75089   0.011 0.991543
## PI           -0.04218    0.04433  -0.952 0.341333
## EH           -2.90261    0.84555  -3.433 0.000597 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 104.903  on 78  degrees of freedom
## Residual deviance:  55.393  on 75  degrees of freedom
## AIC: 63.393
##
## Number of Fisher Scoring iterations: 17
```

We observe **quasi-complete separation** in NV (a categorical variable with two levels), where we note that a 2×2 contingency table with an empty (zero) cell is an example of quasi-complete separation.

```
b <- c(0,1,0,0)
library(data.table)
foo <- setDT(as.data.frame(cbind(m$y, m$x %*% b)))
colnames(foo) <- c("y", "sep")
foo[, .(.N), by = c("y", "sep")]
```

```
##    y sep  N
## 1: 0   0 49
## 2: 1   0 17
## 3: 1   1 13
```

We now use `glmdr` to do our fitting.

```r
m_glmdr <- glmdr(HG ~ ., data = endometrial, family = "binomial")
summary(m_glmdr)
```

```
## MLE exists in Barndorff-Nielsen completion
## it is conditional on components of the response
## corresponding to object$linearity == FALSE being
## conditioned on their observed values
```

```
## $overview
## NULL
##
## $type
## [1] "lcm"
##
## $summary
##
## Call:
## stats::glm(formula = HG ~ ., family = "binomial", data = endometrial,
##     subset = c("1", "2", "3", "4", "5", "6", "7", "8", "9", "10",
##     "11", "12", "13", "14", "15", "16", "17", "18", "19", "20",
##     "21", "27", "28", "29", "30", "31", "32", "33", "34", "35",
##     "36", "37", "38", "39", "40", "41", "42", "43", "44", "45",
##     "46", "47", "52", "53", "54", "55", "56", "57", "58", "59",
##     "60", "61", "62", "63", "64", "65", "66", "67", "68", "69",
##     "70", "72", "73", "74", "77", "79"), x = TRUE, y = TRUE)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.5014  -0.6634  -0.3856   0.2126   2.7278
##
## Coefficients: (1 not defined because of singularities)
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  4.30452    1.63720   2.629 0.008559 **
## NV                NA         NA      NA       NA
## PI          -0.04218    0.04433  -0.952 0.341310
## EH          -2.90261    0.84549  -3.433 0.000597 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 75.307  on 65  degrees of freedom
## Residual deviance: 55.393  on 63  degrees of freedom
## AIC: 61.393
##
## Number of Fisher Scoring iterations: 5
##
##
## $linearity
##     1     2     3     4     5     6     7     8     9    10    11    12    13
##  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
##    14    15    16    17    18    19    20    21    22    23    24    25    26
##  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE FALSE FALSE FALSE FALSE FALSE
##    27    28    29    30    31    32    33    34    35    36    37    38    39
```

```
##  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
##    40    41    42    43    44    45    46    47    48    49    50    51    52
##  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE FALSE FALSE FALSE FALSE  TRUE
##    53    54    55    56    57    58    59    60    61    62    63    64    65
##  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
##    66    67    68    69    70    71    72    73    74    75    76    77    78
##  TRUE  TRUE  TRUE  TRUE  TRUE FALSE  TRUE  TRUE  TRUE FALSE FALSE  TRUE FALSE
##    79
##  TRUE
##
## attr(,"class")
## [1] "summary.glmdr"
```

We now obtain inference for all mean-value parameters in two steps. We first use traditional methods to obtain inferences for mean-value parameters that are unconstrained. Then we can use the `inference` function to obtain one-sided confidence intervals for components of the response vector that are constrained at their observed values.

```
m2 <- update(m, subset = m_glmdr$linearity)
summary(m2)
```

```
##
## Call:
## glm(formula = HG ~ ., family = "binomial", data = endometrial,
##     subset = m_glmdr$linearity, x = TRUE, y = TRUE)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.5014  -0.6634  -0.3856   0.2126   2.7278
##
## Coefficients: (1 not defined because of singularities)
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  4.30452    1.63720   2.629 0.008559 **
## NV                NA         NA      NA       NA
## PI          -0.04218    0.04433  -0.952 0.341310
## EH          -2.90261    0.84549  -3.433 0.000597 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 75.307  on 65  degrees of freedom
## Residual deviance: 55.393  on 63  degrees of freedom
## AIC: 61.393
##
## Number of Fisher Scoring iterations: 5
```

```
## get estimates of mean-value parameters in the LCM
preds <- predict(m2, se.fit = TRUE, type = "response")
head(cbind(preds$fit, preds$se.fit))
```

```
##          [,1]        [,2]
## 1 0.268128294 0.074778103
## 2 0.050675634 0.034991612
## 3 0.005782436 0.008046224
## 4 0.007327976 0.010484202
```

```
## 5 0.436719783 0.095750088
## 6 0.068407171 0.053127413
```

```
## get one-sided CIs for constrained responses
preds_constrained <- inference(m_glmdr)
cbind(endometrial[!m_glmdr$linearity, ], preds_constrained)
```

```
##    NV PI   EH HG     lower upper
## 22  1 38 0.97  1 0.7071451     1
## 23  1 22 1.14  1 0.7432730     1
## 24  1  7 0.88  1 0.9205964     1
## 25  1 25 0.91  1 0.8325905     1
## 26  1 15 0.58  1 0.9518366     1
## 48  1 22 1.44  1 0.5479196     1
## 49  1 40 1.18  1 0.5467740     1
## 50  1  5 0.93  1 0.9160397     1
## 51  1  0 1.17  1 0.8703443     1
## 71  1 49 0.27  1 0.9205150     1
## 75  1 11 1.01  1 0.8703894     1
## 76  1 21 0.98  1 0.8277338     1
## 78  1 19 1.02  1 0.8231611     1
```

We can test for the significance of the `NV` variable in the presence of quasi-complete separation using traditional means. Methods get harder when the degeneracy exists in the null model as explained in Section 3.15 of Geyer (2009).

```
m_small <- glm(HG ~ PI + EH, data = endometrial, family = "binomial",
         x = TRUE, y = TRUE)
anova(m_small, m, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: HG ~ PI + EH
## Model 2: HG ~ NV + PI + EH
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1        76     64.751
## 2        75     55.393  1   9.3576 0.002221 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
AIC(m); AIC(m_small)
```

```
## [1] 63.39326
```

```
## [1] 70.7509
```

Other approaches: the problem with priors

We now demonstrate inferential inconsistencies between the Bayesian methods, namely the inconsistencies with the weakly informative prior advocated here and implemented in the `bayesglm` package and Jeffrey's prior based approaches advocated for by Ioannis Kosmidis and David Firth in several papers and implemented in the `brglm2` package.

We first show that the `bayesglm` defaults produce p-values for the `NV` variable that are close to 0.05. Modest changes to these defaults can change decisions about this variable's significance when testing at the 0.05 level.

```
library(arm) # for bayesglm
library(brglm2) # for brglm2
```

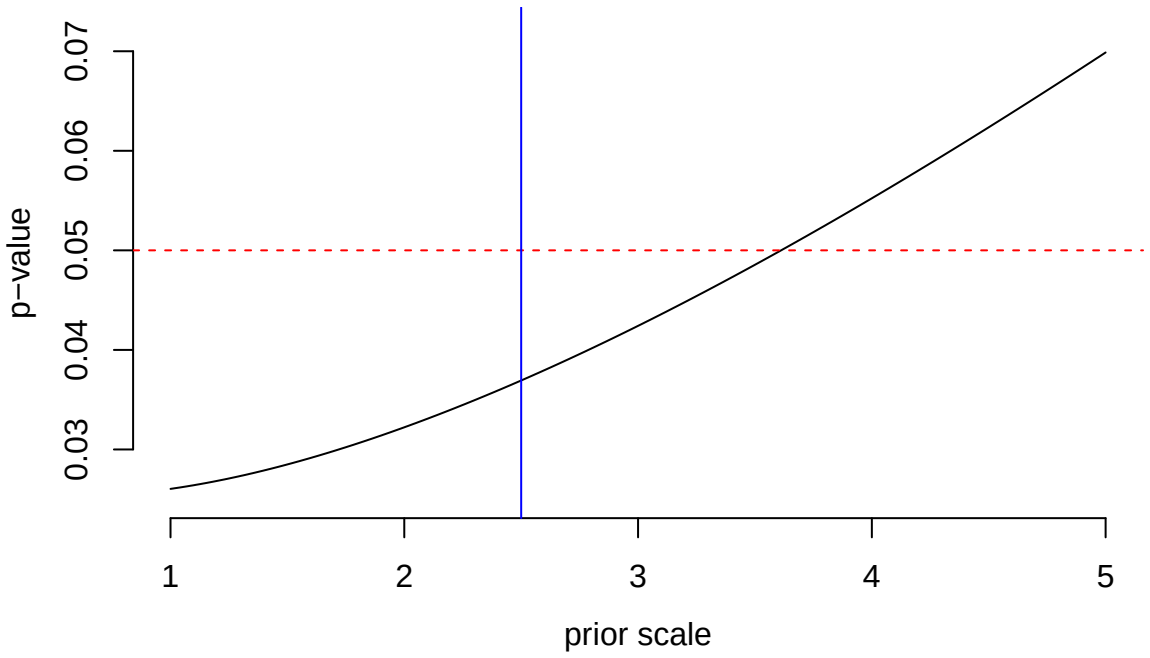
```
#bayesglm
bayes_mod1 <- bayesglm(HG~.,data=endometrial,family="binomial",
                       prior.scale = 1)
bayes_mod <- bayesglm(HG~.,data=endometrial,family="binomial")
bayes_mod5 <- bayesglm(HG~.,data=endometrial,family="binomial",
                       prior.scale = 5)
bayes_mod10 <- bayesglm(HG~.,data=endometrial,family="binomial",
                       prior.scale = 10)

c(summary(bayes_mod1)$coef[2,4],
  summary(bayes_mod)$coef[2,4],
  summary(bayes_mod5)$coef[2,4],
  summary(bayes_mod10)$coef[2,4])
```

```
## [1] 0.02604166 0.03692929 0.06987578 0.15445148
```

```
xx <- seq(from = 1, to = 5, length = 1e3)
foo <- unlist(lapply(xx, function(j){
  summary(bayesglm(HG~.,data=endometrial,family="binomial",
                   prior.scale = j))$coef[2,4]
}))

plot.new()
plot.window(xlim = c(1,5), ylim = c(0.025, 0.0725))
title("Neovasculization p-value vs prior scale")
lines(xx, foo)
axis(1)
axis(2)
abline(h = 0.05, col = "red", lty = 2)
abline(v = 2.5, col = "blue", lty = 1)
mtext("prior scale", side = 1, line = 2.5)
mtext("p-value", side = 2, line = 2.5)
```



Different `brglm` fitting options yield different results, although these differences do not materialize in different conclusions for the `NV` variable when testing at the 0.05 significance level. However, these results conflict those produced by the `bayesglm` package.

```
#brglm2
brglm_mod <- glm(HG~.,data=endometrial,family = "binomial",
                 method = "brglm_fit", type = "MPL_Jeffreys")
brglm_mod_AS_mean <- glm(HG~.,data=endometrial,family = "binomial",
                 method = "brglm_fit", type = "AS_mean")
brglm_mod_AS_median <- glm(HG~.,data=endometrial,family = "binomial",
                         method = "brglm_fit", type = "AS_median")
brglm_mod_AS_mixed <- glm(HG~.,data=endometrial,family = "binomial",
                        method = "brglm_fit", type = "AS_mixed")
#brglm_mod_AS_correction <- glm(HG~.,data=endometrial,family = "binomial",
#                          method = "brglm_fit", type = "correction")
summary(brglm_mod)$coef[2,4]
```

```
## [1] 0.05890214
```

```
summary(brglm_mod_AS_mean)$coef[2,4]
```

```
## [1] 0.05890214
```

```
summary(brglm_mod_AS_median)$coef[2,4]
```

```
## [1] 0.09226858
```

```
summary(brglm_mod_AS_mixed)$coef[2,4]
```

```
## [1] 0.05890214
```

So which prior do we use?

Acknowledgments

These notes borrow materials from Charles Geyer's notes on exponential families. We also borrow materials from **?**, **?**, and **?**. Special thanks to Suyoung Park for his work on the `glmdr` package.