

# GLM computational details

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September 26, 2018



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## Computational details of IRLS

### Coding IRLS

A family object in R is coded as a list of useful components:

```
pfamily <- poisson()
names(pfamily)

## [1] "family"      "link"        "linkfun"     "linkinv"     "variance"
## [6] "dev.resids"  "aic"         "mu.eta"      "initialize"  "validmu"
## [11] "valideta"    "simulate"

pfamily$variance

## function (mu)
## mu
## <bytecode: 0x5f96450>
## <environment: 0x5f9bc98>

pfamily$linkinv

## function (eta)
## pmax(exp(eta), .Machine$double.eps)
## <environment: namespace:stats>
```

It's not *too* hard to write your own GLM function: the hard parts are figuring out what to do about special situations (tricky starting values, poor convergence, etc..)

```
myglmfit <- function(y,X,family,tol=1e-8,maxit=50) {
  mu <- y ## set initial values
  ## set up 'oldbeta' and 'beta' so they're not identical
  oldbeta <- rep(0,ncol(X))
  beta <- rep(1,ncol(X))
  it <- 1 ## number of iterations
  while (it < maxit && max(abs((1-beta/oldbeta)))>tol) {
    oldbeta <- beta
```

```

eta <- family$linkfun(mu)    ## calc. linear predictor
mm <- family$mu.eta(eta)    ## calc. d(mu)/d(eta)
adjdev <- eta + (y-mu)/mm    ## adjusted response
W <- c(1/(mm^2*family$variance(mu))) ## weights
beta <- lm.wfit(X,adjdev,W)$coefficients ## weighted least-squares
mu <- family$linkinv(X %*% beta)    ## compute new mu
it <- it+1                      ## update
}
beta
}
X <- model.matrix(~wool*tension,data=warpbreaks)
y <- warpbreaks$breaks
myglmfit(y,X,poisson())

##      (Intercept)          woolB          tensionM          tensionH woolB:tensionM
##      3.7967368      -0.4566272      -0.6186830      -0.5957987          0.6381768
## woolB:tensionH
##      0.1883632

coef(glm(breaks~wool*tension,data=warpbreaks,family=poisson))

##      (Intercept)          woolB          tensionM          tensionH woolB:tensionM
##      3.7967368      -0.4566272      -0.6186830      -0.5957987          0.6381768
## woolB:tensionH
##      0.1883632

```

### A bad example

GLM likelihood is *log-concave* with a unique solution, so in principle we shouldn't have a problem. But the IRLS algorithm doesn't always get us there, if the data are bad enough (a more common problem is when the MLEs are infinite ... we'll discuss this situation later).

John Mount shows the results of

```

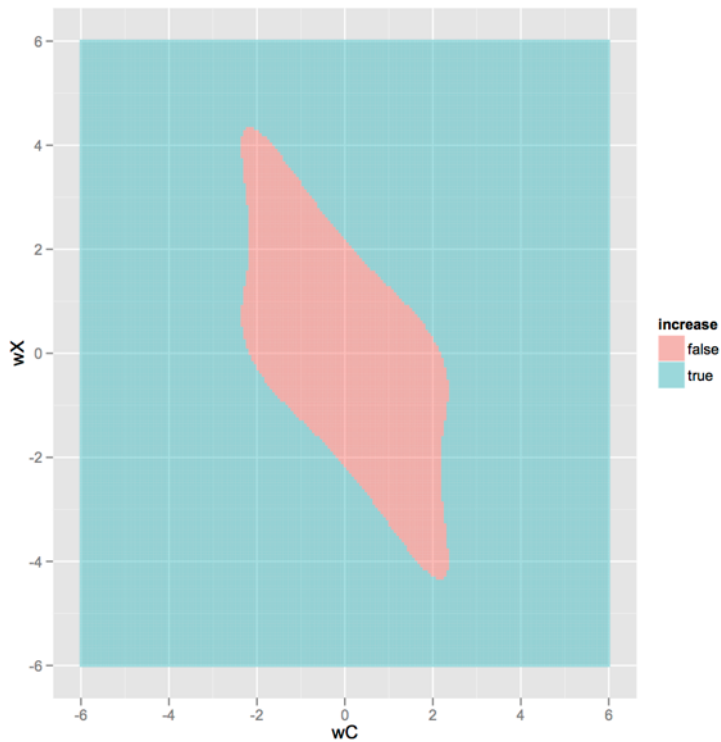
p <- data.frame(x=c(1,0,1,0),y=c(TRUE,TRUE,FALSE,FALSE))
coef(glm(y~x,data=p,family=binomial,start=c(0,0)))

## (Intercept)          x
##          0          0

badstartfun <- function(start) {
  cc <- coef(glm(y~x,data=p,family=binomial,start=start))
  sum(cc^2)>1e-12
}
badstartfun(c(0,0))

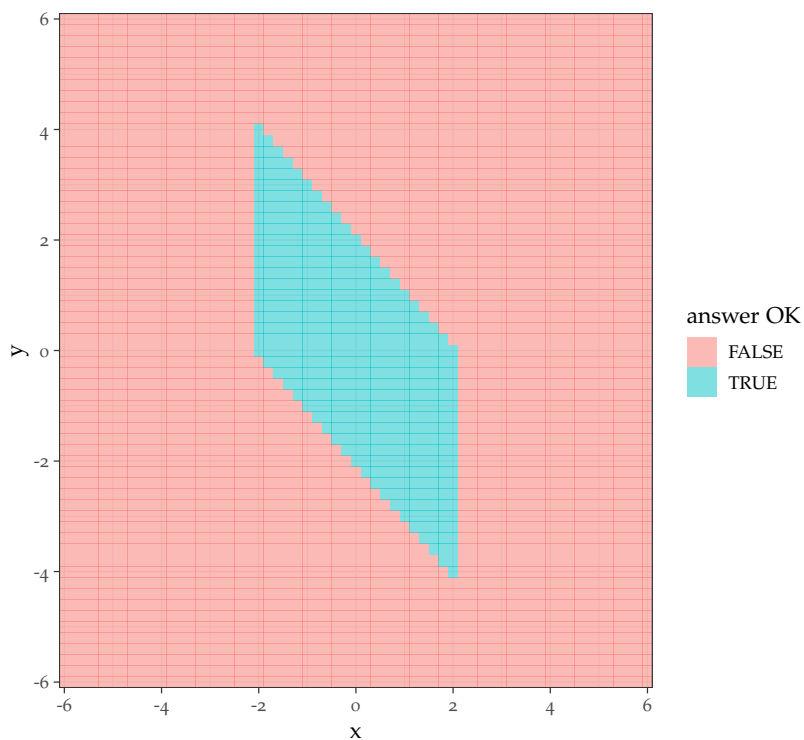
```

```
## [1] FALSE
```



I did it by brute force, using 'emdbook::curve3d()' and the 'glm()' function:

```
library(ggplot2)
theme_set(theme_bw())
brkvec <- seq(-6,6,by=2) ## for compatibility with previous plot
ggplot(ccm,aes(x,y,fill=!value))+geom_tile(alpha=0.5)+
  scale_fill_discrete(name="answer OK")+
  scale_x_continuous(expand=c(0,0),breaks=brkvec)+
  scale_y_continuous(expand=c(0,0),breaks=brkvec)
```



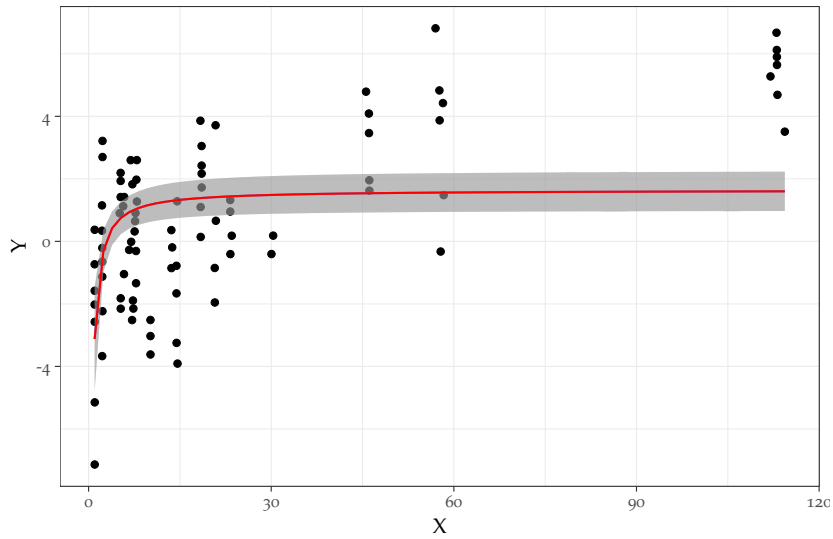
### Another bad example

Fitting a *Beverton-Holt* model (*Michaelis-Menten*, *Monod*, ...):  $y = ax/(b+x)$

Inverse-link trick:  $1/y = (b+x)/ax = (b/a)(1/x) + (1/a)$ :  
`glm(y ~ I(1/x), family=gaussian(link="inverse"))`

```
L <- load("../data/bevholt_ex.RData")
g1 <- ggplot(dat, aes(X, Y)) + geom_point()
g1 + geom_smooth(method = "glm", family = gaussian(link = "inverse"),
                 formula = y ~ I(1/x), start = c(0.01, 1)) +
  geom_smooth(method = "glm", family = gaussian(link = "inverse"),
              formula = y ~ I(1/x), colour="red")

## Warning: Ignoring unknown parameters: family, start
## Warning: Ignoring unknown parameters: family
```



```
## Warning in readChar(con, 5L, useBytes = TRUE): cannot  
open compressed file 'bevholt_ex.RData', probable reason 'No  
such file or directory'  
## Error in readChar(con, 5L, useBytes = TRUE): cannot open  
the connection  
## Error in ff(x, y): object 'dat' not found
```

