GLM computational details

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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()</pre>
names(pfamily)
## [1] "family"
                     "link"
                                   "linkfun"
                                                "linkinv"
                                                              "variance"
  [6] "dev.resids" "aic"
                                   "mu.eta"
                                                "initialize" "validmu"
                     "simulate"
## [11] "valideta"
pfamily$variance
## function (mu)
## mu
## <bytecode: 0x5242148>
## <environment: 0x5243b60>
pfamily$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</pre>
```

```
eta <- family$linkfun(mu) ## calc. linear predictor
        mm <- family$mu.eta(eta)</pre>
                                      ## 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$linkinv(X %*% beta)</pre>
                                                    ## compute new mu
        it <- it+1
                                                    ## update
    }
    beta
X <- model.matrix(~wool*tension,data=warpbreaks)</pre>
y <- warpbreaks$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
##
```

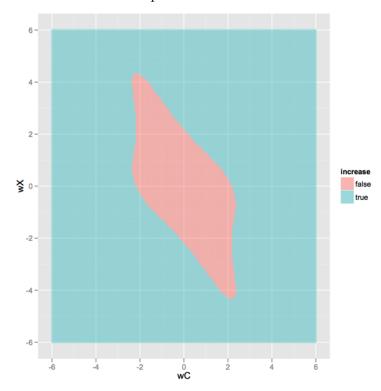
A bad example

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

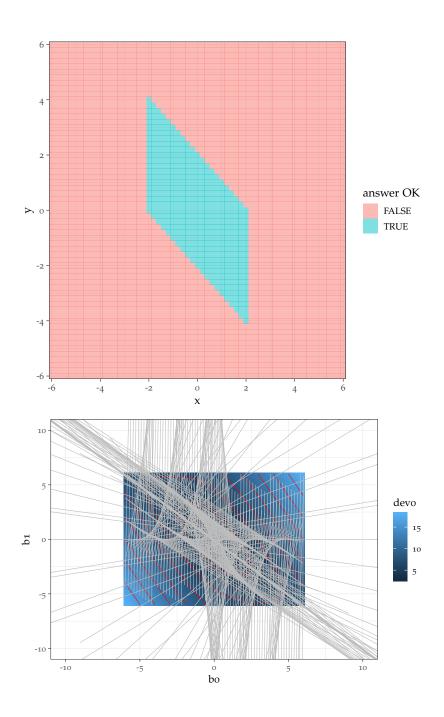
```
p <- data.frame(x=c(1,0,1,0),y=c(TRUE,TRUE,FALSE,FALSE))</pre>
coef(glm(y\sim x, data=p, family=binomial, start=c(0,0)))
coef(glm(y~x,data=p,family=binomial,start=c(5,5)))
## Warning: glm.fit: fitted probabilities numerically 0 or
1 occurred
badstartfun <- function(start) {</pre>
    cc <- coef(glm(y~x,data=p,family=binomial,start=start))</pre>
    sum(cc^2)>1e-12
badstartfun(c(0,0))
```

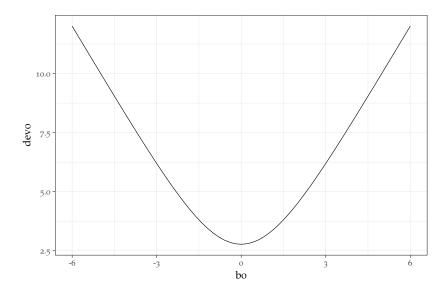
Picture from Mount's blog on starting conditions for which the fit gets worse on the initial step:



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 pllot
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 \sim I(1/x), family=gaussian(link="inverse"))
```

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

