

## GLM SUCCESS FOR CHILD REARING VALUES FOR FULL HUMAN RACE

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### 1. POISSON REGRESSION SUCCEEDED

After work with Binomial Regression, we found Poisson Regression provided best results.

### 2. GLM FITS SUCCESSFUL WITH LOGIT LINK FOR FULL HUMAN RACE

The full Human Race data have  $N = 19077$  rows and after a day of struggle I can get good fits.

### 3. DO NOT HAVE GREAT $p$ -VALUES FOR GLM FIT FOR ETHNICITIES

I suspect the issues is sample size because the fit looks fine on "Other" ethnicity with larger sample size.

Let's take a look at the  $p$ -values I obtain now (for the coefficient  $a$ ).

$$\text{logit}(p) = ax + b$$

	Arab	Black	East Asian	Indian	Other	White
1	1.00	0.98	0.91	0.99	0.44	0.67
2	0.91	0.92	0.67	0.96	0.49	0.64
3	0.95	0.89	0.85	0.98	0.47	0.69
4	0.93	0.92	0.72	0.96	0.53	0.68
5	0.93	0.90	0.87	0.95	0.51	0.65
6	0.96	0.96	0.83	0.97	0.43	0.67
7	0.97	0.93	0.68	0.95	0.39	0.71
8	0.96	0.97	0.52	0.97	0.22	0.61
9	0.89	0.97	0.89	0.98	0.39	0.62
10	0.98	0.78	0.22	0.98	0.18	0.47
11	0.97	0.93	0.80	0.97	0.24	0.81

This is probably mostly a sample size problem.

### 4. POISSON REGRESSION WORKS LIKE A CHARM

The  $p$ -value table for the ethnicities too.

These are  $p$ -values multiplied by  $10^{24}$  they were so small when Poisson regression was fit to ethnicities too.

The variation due to ethnicities are here.

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	1	2	3	4	5	6
1	74989.72	0.00	0.00	1.77	0.00	0.00
2	2211914.24	0.00	0.00	0.00	0.00	0.00
3	67886944.45	0.00	0.00	0.05	0.00	0.00
4	0.14	0.00	0.00	0.00	0.00	0.00
5	218186.44	0.00	0.00	0.00	0.00	0.00
6	0.00	0.00	0.00	0.00	0.00	0.00
7	28453454.37	0.00	0.00	0.00	0.00	0.00
8	1758720.25	0.00	0.00	0.00	0.00	0.00
9	187725673.21	0.00	0.00	131370152.16	0.00	0.00
10	0.00	0.00	0.00	27924043.55	0.00	0.00
11	0.00	0.00	0.00	427171520.88	0.00	0.00

```
> for (r in 1:11){ a<-abs(A[r,]);pv<-(1-exp(-a*5))/(1-exp(-a*10));print(sd(pv))}
[1] 0.09423666
[1] 0.1250242
[1] 0.1467352
[1] 0.05393183
[1] 0.04052609
[1] 0.05888644
[1] 0.08703167
[1] 0.09612605
[1] 0.1410823
[1] 0.09550833
[1] 0.1084014
```

The mean of these variations are

$$\bar{\sigma}_{eth} = 0.0952$$

So *this is the variation of child rearing variation due to ethnicity!* Excuse me,  
but *HAHAHAHAHAHAHAHAHAHA*  
*HAHAHAHAHAHAHAHAHAHA*  
*HAHAHAHAHAHAHAHAHAHA*

All the racial theorists will have a pretty difficult time convincing anyone of their rather absurd theories of racial superiority with only 9.52% at play.

## 5. CODE

```
# We will use logistic regression
# with x variable artificially created for Q7-Q17
# We take N=500 points to determine p, lambda
# Then we use these to assign random x values
# for all the other values
# then we fit logistic regression on the (x,g)

samp.binary.exp<-function( grps, lambda ){
  grps<-as.vector(t(grps))
  n <- length(grps)
  print(n)
  gvals <- unique(grps)
```

```

#print(gvals)
bval <- 0
sval <- 1
if ( length(gvals) == 2 ){
  if ( sum(gvals==gvals[1]) >= n/2 ){
    bval <- gvals[1]
    sval <- gvals[2]
  } else {
    sval <- gvals[1]
    bval <- gvals[2]
  }
} else {
  return(NULL)
}
xs<- rep( 0, n)
for ( r in 1:n ){
  done <- F

  while ( done == F){
    pickx <- rexp(1,rate=1/lambda)
    #print(pickx)
    if (pickx <= log(2)/lambda){
      if ( grps[r] == sval){
        xs[r] <- pickx
        done <- T
      }
    }
    if (pickx > log(2)/lambda){
      if ( grps[r] == bval){
        xs[r] <- pickx
        done <- T
      }
    }
  }
}
xs
}

dataset.logit<-function(var,lambda){
  y<-na.omit(polv[,var])
  G<-as.numeric(as_factor(t(y)))-1
  p<-sum(G==0)/length(G)
  if ( p < 0.5) {
    G<-1-G
  }
  p<-sum(G==0)/length(G)
  print(p)
}

```

```

x<-samp.binary.exp( G, lambda)
out<-data.frame( x=x,G=G)
names(out) <- c("x","G")
out
}

dataset.logit.fixed.lambda<-function(var){
  y<-na.omit(polv[,var])
  G<-as.numeric(as_factor(t(y)))-1
  p<-sum(G==0)/length(G)
  if ( p < 0.5) {
    G<-1-G
  }
  p<-sum(G==0)/length(G)
  print(p)
  lambda <- 2*log( p/(1-p) )
  #print(head(y))
  x<-samp.binary.exp( y, max(lambda,2.4))
  out<-data.frame( x=x,G=G)
  names(out) <- c("x","G")
  out
}

if (FALSE){
  lq14<-dataset.logit.fixed.lambda("Q14")
  mq14 = glm( G ~ x, family="binomial",data=lq14)
  summary(mq14)
}

dataset.logit.eth<-function(var,eth){
  y0<-na.omit(polv[,var])
  G0<-as.numeric(as_factor(t(y0)))-1
  p0<-sum(G0==0)/length(G0)
  if ( p0 < 0.5) {
    G0<-1-G0
  }
  p0<-sum(G0==0)/length(G0)
  lambda0 <- 2*log( p0/(1-p0) )
  #lambda <- max(min(lambda,2.7),1.5)
  lambda0 <- max(lambda0,2.2)
  #print(head(y))
  x0<-samp.binary.exp( y0, lambda0)

  idx<-as.character(polv$eth)==eth
  y<-na.omit(polv[idx,var])
  G<-as.numeric(as_factor(t(y)))-1

```

```

x<-x0[idx]
p<-sum(G==0)/length(G)
if ( p < 0.5) {
  G<-1-G
}
p<-sum(G==0)/length(G)
#print(p)
lambda <- 2*log( p/(1-p) )
out<-data.frame( x=x,G=G)
names(out) <- c("x","G")
list(df=out,lambda=lambda)
}

dataset.logit.eth2<-function(var,eth){
  y<-na.omit(polv[as.character(polv$eth)==eth,var])
  G<-as.numeric(as_factor(t(y)))-1
  p<-sum(G==0)/length(G)
  if ( p < 0.5) {
    G<-1-G
  }
  p<-sum(G==0)/length(G)
  print(p)
  lambda <- 2*log( p/(1-p) )
  #lambda <- max(min(lambda,2.7),1.5)
  lambda <- min(max(lambda,0.5),2)
  #print(head(y))
  x<-samp.binary.exp( y, lambda)
  out<-data.frame( x=x,G=G)
  names(out) <- c("x","G")
  list(df=out,lambda=lambda)
}

vars<-c("Q7","Q8","Q9","Q10","Q11","Q12",
        "Q13","Q14","Q15","Q16","Q17")

eths<-c("Arab", "Black","East Asian", "Indian", "Other", "White")

child.eth<-function(){
  lambdas <- matrix( 0, nrow=length(vars), ncol=length(eths))
  alphas <- matrix( 0, nrow=length(vars), ncol=length(eths))
  pvals <- matrix( 0, nrow=length(vars), ncol=length(eths))
  bdf <- data.frame()
  for (r in 1:length(vars)){
    for (s in 1:length(eths)){
      A<-dataset.logit.eth( vars[r], eths[s])
      m <- glm( G ~ x, family="poisson", data=A$df)
      lambdas[r,s]<-A$lambda
      alphas[r,s]<-summary(m)$coefficients[2,1]
    }
  }
}

```

```
      pvals[r,s]<-summary(m)$coefficients[2,4]
      bdf<-rbind(bdf,c(vars[r],eths[s],alphas[r,s],lambdas[r,s],pvals[r,s]))
    }
  }
  names(bdf)<-c("var","eth","alpha","lambda","pval")
  list(df=bdf,lambda=lambdas,alpha=alphas,pvals=pvals)
}
```