

***This coding requires the "car" package in order to use the recode function
library(car)

***This assumes that the dataframe containing the GSS is called "GSS"
attach(GSS)

**If you are updating datasets that already contain reltrad variables, please scroll down for the corrected coding **

***Coding begins here

```
xaffil <- relig  
xaffil <- recode(xaffil, "1=1; 2=4; 3=5; 4=9; 5:10=6; 11=1; 12=6; 13=1")
```

```
xbp <- other  
xbp <- recode(xbp, "7=1; 14:15=1; 21=1; 37:38=1; 56=1; 78:79=1; 85:88=1; 98=1; 103:104=1; 128=1;  
133=1; else=0")  
xbp[denom==12] <- 1  
xbp[denom==13] <- 1  
xbp[denom==20] <- 1  
xbp[denom==21] <- 1  
xbp[is.na(xbp)] <- 0
```

```
bl <- race  
bl <- recode(bl, "2=1; else=0")  
bldenom <- denom * bl  
bldenom[is.na(bldenom)] <- 0
```

```
xbp[bldenom==23] <- 1  
xbp[bldenom==28] <- 1  
xbp[bldenom==18] <- 1  
xbp[bldenom==15] <- 1  
xbp[bldenom==10] <- 1  
xbp[bldenom==11] <- 1  
xbp[bldenom==14] <- 1  
xbp[is.na(xbp)] <- 0
```

```
blother <- other * bl  
xbp[blother==93] <- 1
```

```
xev <- other  
xev <- recode(xev, "2=1; 3=1; 5:6=1; 9:10=1; 12:13=1; 16=1; 18=1; 20=1; 22=1; 24=1; 26:28=1; 31:32=1;  
34:36=1; 39=1; 41:43=1; 45=1; 47=1; 51:53=1; 55=1; 57=1; 63=1; 65:69=1; 76:77=1; 83:84=1; 90:92=1;  
94=1; 97=1; 100:102=1; 106:112=1; 115:118=1; 120:122=1; 124:125=1; 127=1; 129=1; 131:132=1;  
134:135=1; 138:140=1; 146=1; else=0")  
xev[denom ==32] <- 1  
xev[denom ==33] <- 1  
xev[denom ==34] <- 1
```

```
xev[denom ==42] <- 1
```

```
wh <- race
```

```
wh <- recode(wh, "1=1; 2=0; 3=1")
```

```
whdenom <- denom*wh
```

```
xev[whdenom ==23] <- 1
```

```
xev[whdenom ==18] <- 1
```

```
xev[whdenom ==15] <- 1
```

```
xev[whdenom ==10] <- 1
```

```
xev[whdenom ==14] <- 1
```

```
whother <- other*wh
```

```
xev[whother ==93] <- 1
```

```
xev[xbp ==1] <- 0
```

```
dev <- other
```

```
dev <- recode(dev, "2=1; 3=1; 5=1; 6=1; 9=1; 10=1; 12=1; 13=1; 16=1; 18=1; 20=1; 22=1; 24=1; 26=1;  
27=1; 28=1; 31=1; 32=1; 34=1; 35=1; 36=1; 39=1; 41=1; 42=1; 43=1; 45=1; 47=1; 51=1; 52=1; 53=1; 55=1;  
57=1; 63=1; 65=1; 66=1; 67=1; 68=1; 69=1; 76=1; 77=1; 83=1; 84=1; 90=1; 91=1; 92=1; 94=1; 97=1;  
100=1; 101=1; 102=1; 106=1; 107=1; 108=1; 109=1; 110=1; 111=1; 112=1; 115=1; 116=1; 117=1; 118=1;  
120=1; 121=1; 122=1; 124=1; 125=1; 127=1; 129=1; 131=1; 132=1; 134=1; 135=1; 138=1; 139=1; 140=1;  
146=1; else=0")
```

```
dev[denom ==32] <- 1
```

```
dev[denom ==33] <- 1
```

```
dev[denom ==34] <- 1
```

```
dev[denom ==42] <- 1
```

```
dev[denom ==32] <- 1
```

```
dev[whdenom ==23] <- 1
```

```
dev[whdenom ==18] <- 1
```

```
dev[whdenom ==15] <- 1
```

```
dev[whdenom ==10] <- 1
```

```
dev[whdenom ==14] <- 1
```

```
dev[whother ==93] <- 1
```

```
dev[xbp ==1] <- 0
```

```
xml <- other
```

```
xml <- recode(xml, "1=1; 8=1; 19=1; 23=1; 25=1; 40=1; 44=1; 46=1; 48:50=1; 54=1; 70:73=1; 81=1; 89=1;  
96=1; 99=1; 105=1; 119=1; 148=1; else=0")
```

```
xml[denom ==22] <- 1
```

```
xml[denom ==30] <- 1
```

```
xml[denom ==31] <- 1
```

```
xml[denom ==35] <- 1
```

```
xml[denom ==38] <- 1
```

```
xml[denom ==40] <- 1
```

```
xml[denom ==41] <- 1
```

```
xml[denom ==43] <- 1
```

```

xml[denom ==48] <- 1
xml[denom ==50] <- 1
xml[whdenom ==11] <- 1
xml[whdenom ==28] <- 1
xml[xbp ==1] <- 0

xcath <- other
xcath <- recode(xcath, "123=1; else=0")
xcath[xaffil ==4] <- 1

xjew <- xaffil
xjew <- recode(xjew, "5=1; else=0")

xother <- other
xother <- recode(xother, "11=1; 17=1; 29=1; 30=1; 33=1; 58=1; 59=1; 60=1; 61=1; 62=1; 64=1; 74=1;
75=1; 80=1; 82=1; 95=1; 113=1; 114=1; 130=1; 136=1; 141=1; 145=1; else=0")
noxev <- 1-xev
noxevxaf <- noxev*xaffil

xother[noxevxaf ==6] <-1
xother[is.na(xother)] <- 0

```

```

xnonaff <- relig
xnonaff <- recode(xnonaff, "4=1; else=0")

```

```

xprot dk <- denom
xprot dk <- recode(xprot dk, "70=1; else=0")
xprot dk[attend ==0] <- 0
xprot dk[attend ==1] <- 0
xprot dk[attend ==2] <- 0
xprot dk[attend ==3] <- 0
xprot dk[attend ==9] <- 0
xprot dk[attend ==NA] <- 0
xev[xprot dk ==1] <- 1

```

THIS IS THE CORRECTED CODING

If you are trying to update datasets that have already have reitard coding in them, use the syntax from this point forward

This takes people who responded that they were Christian in the relig variable but didn't get asked the followup and puts them into reltrad

```

xtn <- relig
denom2 <- denom
denom2 <- recode(denom2, "70=1; else=0")
xtn <- recode(xtn, "11=1; else=0")
xtn[denom2 ==1] <- 2
xtn <- recode(xtn, "1=1; 2=0")

```

```
xtn[attend ==0] <- 0
xtn[attend ==1] <- 0
xtn[attend ==2] <- 0
xtn[attend ==3] <- 0
xtn[attend ==9] <- 0
xtn[attend ==NA] <- 0
xev[xtn ==1] <- 1
```

```
inter <- relig
inter <- recode(inter, "13=1; else=0")
inter[attend ==0] <- 0
inter[attend ==1] <- 0
inter[attend ==2] <- 0
inter[attend ==3] <- 0
inter[attend ==9] <- 0
inter[attend ==NA] <- 0
xev[inter ==1] <- 1
```

****CORRECTED CODING OVER****

The following section will create two things: a reltrad variable coded from 1-7 for each of the seven categories of reltrad and seven dummy variables for each of the seven categories

```
evangelical <- xev
mainline <- xml
blackprot <- xbp
catholic <- xcath
jewish <- xjew
other <- xother
none <- xnonaff
```

```
detach(GSS)
```

```
evan <- evangelical
ml <- recode(mainline, "1=2; else=0")
bprot <- recode(blackprot, "1=3; else=0")
cath <- recode(catholic, "1=4; else=0")
jew <- recode(jewish, "1=5; else=0")
oth <- recode(other, "1=6; else=0")
nne <- recode(none, "1=7; else=0")
```

```
reltrad <- evan + ml + bprot + cath + jew + oth + nne
```

If using the GSS cumulative file from 1972-2014 there should be a total of 14,579 evangelicals in the sample

These are unweighted frequencies, generated by using the formula -- tab evangelical if year == 2012, for example

*Evangelicals in 2014 = 585
*Evangelicals in 2012 = 503
*Evangelicals in 2010 = 484

*Evangelicals in 2008 = 481
*Evangelicals in 2006 = 1088
*Evangelicals in 2004 = 746
*Evangelicals in 2002 = 644
*Evangelicals in 2000 = 679
*Evangelicals in 1998 = 713
*Evangelicals in 1996 = 733
*Evangelicals in 1994 = 797