Models for Polytomous Responses

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6/5/2020

```
#install.packages("car")
#install.packages("VGAM")
```

For a target with Ordinal Values

Proportional Odds Model

Unless the response variable has numeric values, it is important to ensure that it has been defined as an ordered factor (using ordered()). In the Arthritis data, the response, Improved was setup this way, as we can check by printing some of the values

```
library(vcd)
```

```
## Loading required package: grid
```

```
library(grid)
data("Arthritis", package="vcd")
head(Arthritis$Improved, 8)
```

```
## [1] Some   None   None   Marked Marked Marked None   Marked
## Levels: None < Some < Marked
```

```
library(MASS)
arth.polr <- polr(Improved ~ Sex + Treatment + Age,data=Arthritis, Hess=TRUE)
summary(arth.polr)
```

```
## Call:
## polr(formula = Improved ~ Sex + Treatment + Age, data = Arthritis,
##     Hess = TRUE)
##
## Coefficients:
##                    Value Std. Error t value
## SexMale          -1.25168    0.54636  -2.291
## TreatmentTreated  1.74529    0.47589   3.667
## Age               0.03816    0.01842   2.072
##
## Intercepts:
##             Value   Std. Error t value
## None|Some    2.5319  1.0571     2.3952
## Some|Marked  3.4309  1.0912     3.1443
##
## Residual Deviance: 145.4579
## AIC: 155.4579
```

Summary gives us the coefficients, Intercepts labeled by the cutpoint on the ordinal response but no p-values. The car::Anova() method gives the appropriate tests

```
library(car)
```

```
## Loading required package: carData
```

```
Anova(arth.polr)
```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: Improved
##           LR Chisq Df Pr(>Chisq)
## Sex         5.6880  1  0.0170812 *
## Treatment  14.7095  1  0.0001254 ***
## Age         4.5715  1  0.0325081 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

In R, the PO and NPO models can be readily contrasted by fitting them both using vglm() in the VGAM package. This defines the cumulative family of models and allows a parallel option. With parallel=TRUE, this is equivalent to the polr() model, except that the signs of the coefficients are reversed

```
#install.packages("VGAM")
library(VGAM)
```

```
## Loading required package: stats4
```

```
## Loading required package: splines
```

```
##
## Attaching package: 'VGAM'
```

```
## The following object is masked from 'package:car':
##
##     logit
```

```
arth.po <- vglm(Improved ~ Sex + Treatment + Age, data=Arthritis,family = cumulative(
parallel=TRUE))
arth.po
```

```
##
## Call:
## vglm(formula = Improved ~ Sex + Treatment + Age, family = cumulative(parallel = TR
UE),
##     data = Arthritis)
##
##
## Coefficients:
##    (Intercept):1    (Intercept):2          SexMale TreatmentTreated
##       2.53199006       3.43098785       1.25167130      -1.74530408
##              Age
##      -0.03816279
##
## Degrees of Freedom: 168 Total; 163 Residual
## Residual deviance: 145.4579
## Log-likelihood: -72.72896
```

The more general NPO model can be fit using parallel=FALSE.

```
arth.npo <- vglm(Improved ~ Sex + Treatment + Age, data=Arthritis, family = cumulativ
e(parallel=FALSE))
arth.npo
```

```
##
## Call:
## vglm(formula = Improved ~ Sex + Treatment + Age, family = cumulative(parallel = FA
LSE),
##     data = Arthritis)
##
##
## Coefficients:
##      (Intercept):1      (Intercept):2          SexMale:1
##         2.61853875         3.43117450         1.50982704
##          SexMale:2 TreatmentTreated:1 TreatmentTreated:2
##         0.86643395        -1.83692928        -1.70401146
##              Age:1              Age:2
##        -0.04086648        -0.03729421
##
## Degrees of Freedom: 168 Total; 160 Residual
## Residual deviance: 143.5741
## Log-likelihood: -71.78703
```

The VGAM package defines a coef() method that can print the coefficients in a more readable matrix form giving the category cutpoints

```
coef(arth.po, matrix=TRUE)
```

```
##                  logitlink(P[Y<=1]) logitlink(P[Y<=2])
## (Intercept)              2.53199006         3.43098785
## SexMale                  1.25167130         1.25167130
## TreatmentTreated        -1.74530408        -1.74530408
## Age                     -0.03816279        -0.03816279
```

```
coef(arth.npo, matrix=TRUE)
```

```
##                  logitlink(P[Y<=1]) logitlink(P[Y<=2])
## (Intercept)              2.61853875         3.43117450
## SexMale                  1.50982704         0.86643395
## TreatmentTreated        -1.83692928        -1.70401146
## Age                     -0.04086648        -0.03729421
```

In most cases, nested models can be tested using an anova() method, but the VGAM pack- age has not implemented this for “vglm” objects. Instead, it provides an analogous function, lrtest()

```
VGAM::lrtest(arth.npo, arth.po)
```

```
## Likelihood ratio test
##
## Model 1: Improved ~ Sex + Treatment + Age
## Model 2: Improved ~ Sex + Treatment + Age
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1 160 -71.787
## 2 163 -72.729  3 1.8838     0.5969
```

The LR test can be also calculated as “manually” shown below using the difference in residual deviance for the two models

```
tab <- cbind(Deviance = c(deviance(arth.npo), deviance(arth.po)),df = c(df.residual(a
rth.npo), df.residual(arth.po)))
tab <- rbind(tab, diff(tab))
rownames(tab) <- c("GenLogit", "PropOdds", "LR test")
tab <- cbind(tab, pvalue=1-pchisq(tab[,1], tab[,2]))
tab
```

```
##            Deviance  df    pvalue
## GenLogit 143.574067 160 0.8196626
## PropOdds 145.457915 163 0.8343527
## LR test    1.883849   3 0.5968607
```

The vglm() can also fit partial proportional odds models, by specifying a formula giving the terms for which the PO assumption should be taken as TRUE or FALSE. Here we illustrate this using parallel=FALSE ~ Sex,tofitseparateslopesformalesandfemales,butparallellinesforthe otherpredictors.Thesamemodelwouldbefitusingparallel=TRUE ~ Treatment + Age.

```
arth.ppo <- vglm(Improved ~ Sex + Treatment + Age, data=Arthritis,family = cumulative
(parallel=FALSE ~ Sex))
coef(arth.ppo, matrix=TRUE)
```

```
##                  logitlink(P[Y<=1]) logitlink(P[Y<=2])
## (Intercept)              2.54245216         3.61556073
## SexMale                  1.48333554         0.86736192
## TreatmentTreated        -1.77574178        -1.77574178
## Age                     -0.03962233        -0.03962233
```

Graphical Assesment of Proportional Odds

```
#install.packages("polspline",dependencies = TRUE)
#install.packages("rms",dependencies = TRUE)
library("rms")
```

```
## Loading required package: Hmisc
```

```
## Loading required package: lattice
```

```
## Loading required package: survival
```

```
## Loading required package: Formula
```

```
## Loading required package: ggplot2
```

```
##
## Attaching package: 'Hmisc'
```

```
## The following objects are masked from 'package:base':
##
##     format.pval, units
```

```
## Loading required package: SparseM
```

```
##
## Attaching package: 'SparseM'
```

```
## The following object is masked from 'package:base':
##
##     backsolve
```

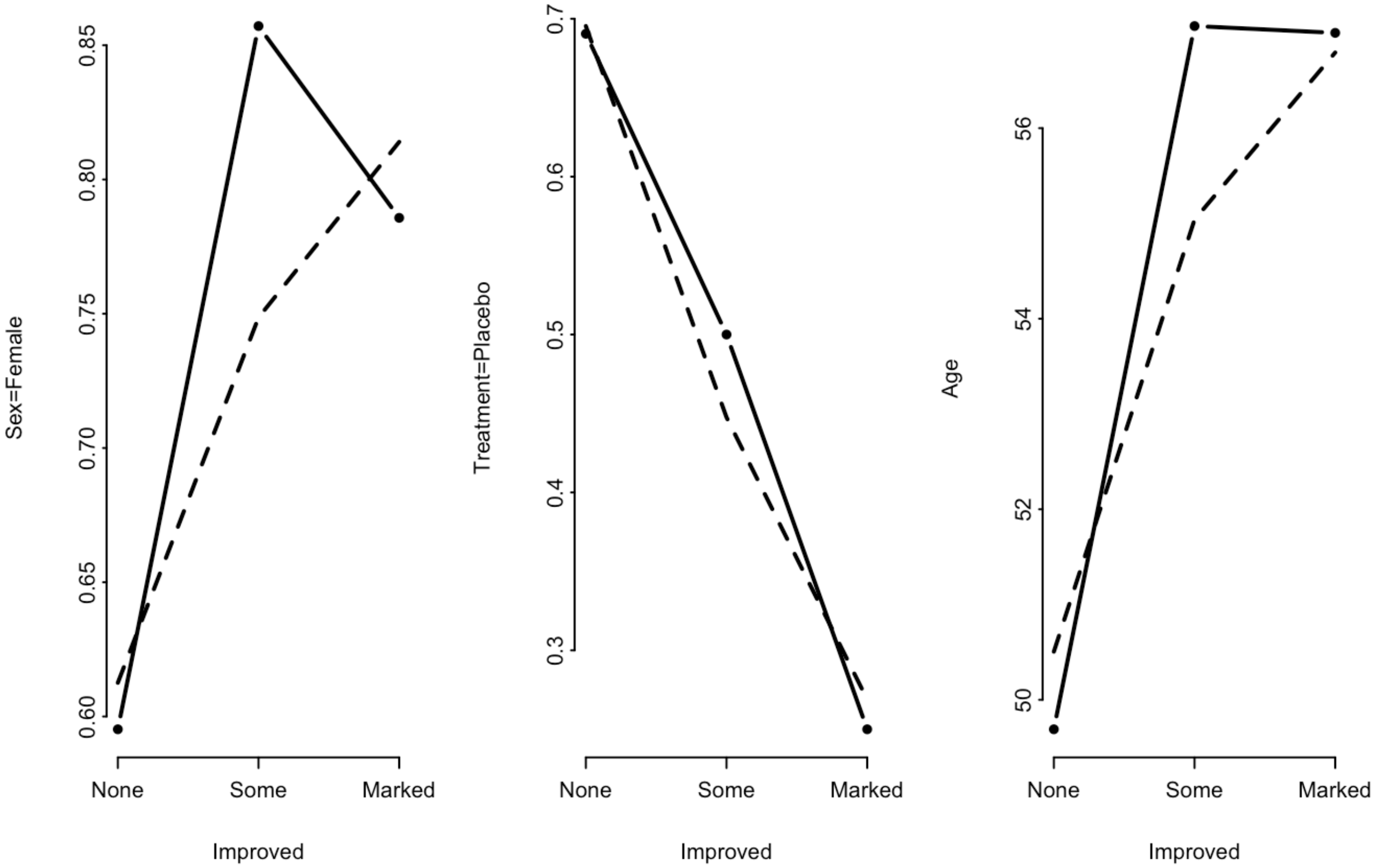
```
##
## Attaching package: 'rms'
```

```
## The following objects are masked from 'package:VGAM':
##
##     calibrate, lrtest
## The following objects are masked from 'package:car':
##
##     Predict, vif
```

```
arth.po2 <- lrm(Improved ~ Sex + Treatment + Age, data=Arthritis)
arth.po2
```

```
## Logistic Regression Model
##
##  lrm(formula = Improved ~ Sex + Treatment + Age, data = Arthritis)
##
##                        Model Likelihood     Discrimination    Rank Discrim.
##                           Ratio Test           Indexes           Indexes
##  Obs            84    LR chi2      24.46    R2       0.291    C       0.750
##   None          42    d.f.             3    g        1.335    Dxy     0.500
##   Some          14    Pr(> chi2) <0.0001    gr       3.801    gamma   0.503
##   Marked        28                          gp       0.280    tau-a   0.309
##  max |deriv| 1e-07                          Brier    0.187
##
##                     Coef    S.E.   Wald Z Pr(>|Z|)
##  y>=Some            -2.5320 1.0570 -2.40  0.0166
##  y>=Marked          -3.4310 1.0911 -3.14  0.0017
##  Sex=Male           -1.2517 0.5464 -2.29  0.0220
##  Treatment=Treated  1.7453 0.4759  3.67  0.0002
##  Age                 0.0382 0.0184  2.07  0.0382
##
```

```
op <- par(mfrow=c(1,3))
plot.xmean.ordinaly(Improved ~ Sex + Treatment + Age, data=Arthritis,lwd=2, pch=16, s
ubn=FALSE)
```



```
par(op)
```

Visualizing results for Proportional Odds Model

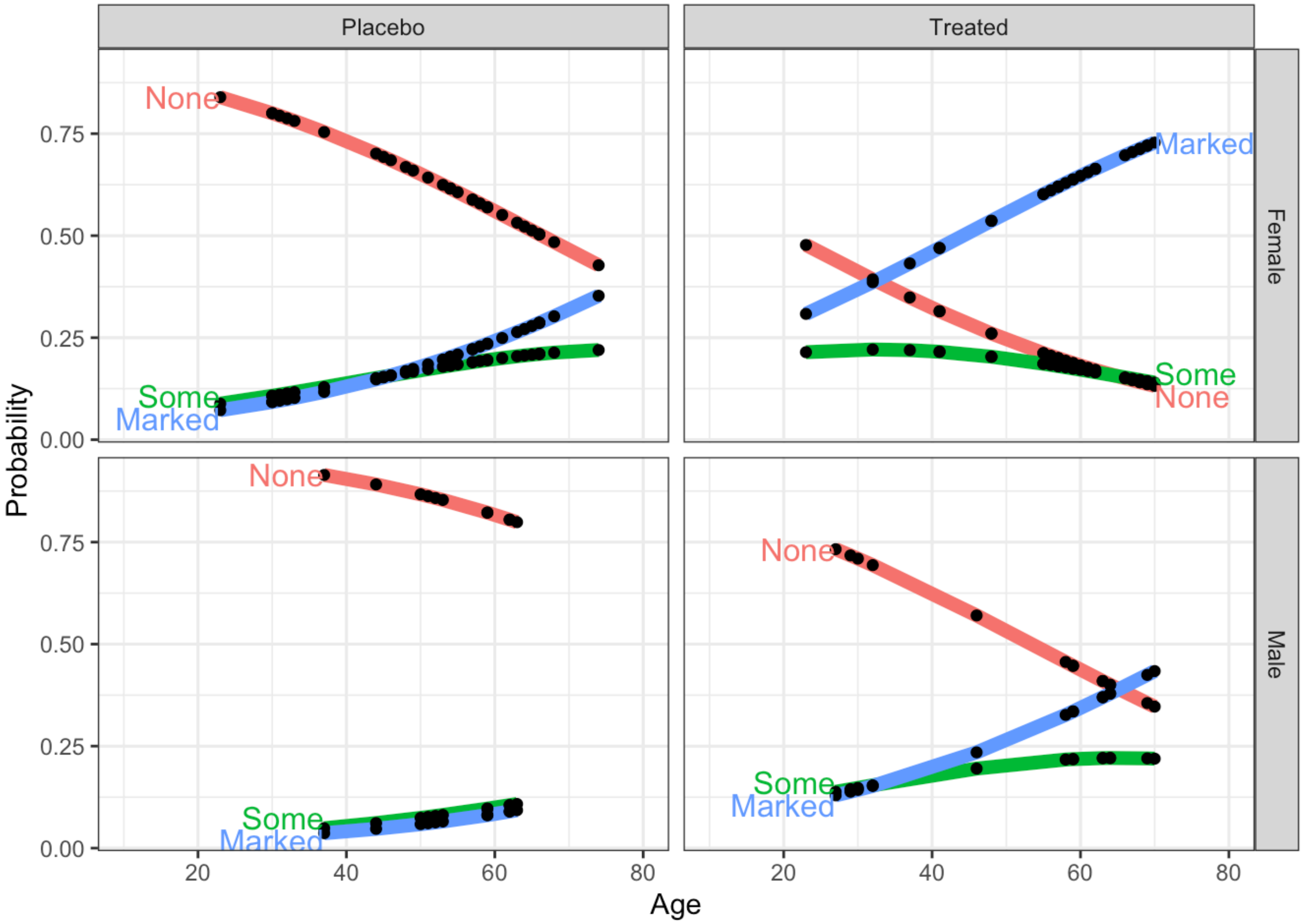
```
arth.fitp <- cbind(Arthritis,predict(arth.polr, type="probs"))
head(arth.fitp)
```

```
##   ID Treatment  Sex Age Improved      None      Some    Marked
## 1 57   Treated Male  27     Some 0.7326185 0.1380586 0.1293229
## 2 46   Treated Male  29     None 0.7174048 0.1444325 0.1381627
## 3 77   Treated Male  30     None 0.7096042 0.1476259 0.1427699
## 4 17   Treated Male  32   Marked 0.6936286 0.1540035 0.1523679
## 5 36   Treated Male  46   Marked 0.5702499 0.1950359 0.2347142
## 6 23   Treated Male  58   Marked 0.4563432 0.2171302 0.3265266
```

```
library(reshape2)
plotdat <- melt(arth.fitp,id.vars = c("Sex", "Treatment", "Age", "Improved"),measure.
vars=c("None", "Some", "Marked"),
                variable.name = "Level",
                value.name = "Probability")
head(plotdat)
```

```
##    Sex Treatment Age Improved Level Probability
## 1 Male   Treated  27     Some  None   0.7326185
## 2 Male   Treated  29     None  None   0.7174048
## 3 Male   Treated  30     None  None   0.7096042
## 4 Male   Treated  32   Marked  None   0.6936286
## 5 Male   Treated  46   Marked  None   0.5702499
## 6 Male   Treated  58   Marked  None   0.4563432
```

```
library(ggplot2)
library(directlabels)
gg <- ggplot(plotdat, aes(x = Age, y = Probability, colour = Level)) +
  geom_line(size=2.5) + theme_bw() + xlim(10,80) +
  geom_point(color="black", size=1.5) +
  facet_grid(Sex ~ Treatment) #,labeller = function(x, y) sprintf("%s = %s", x, y)
direct.label(gg)
```



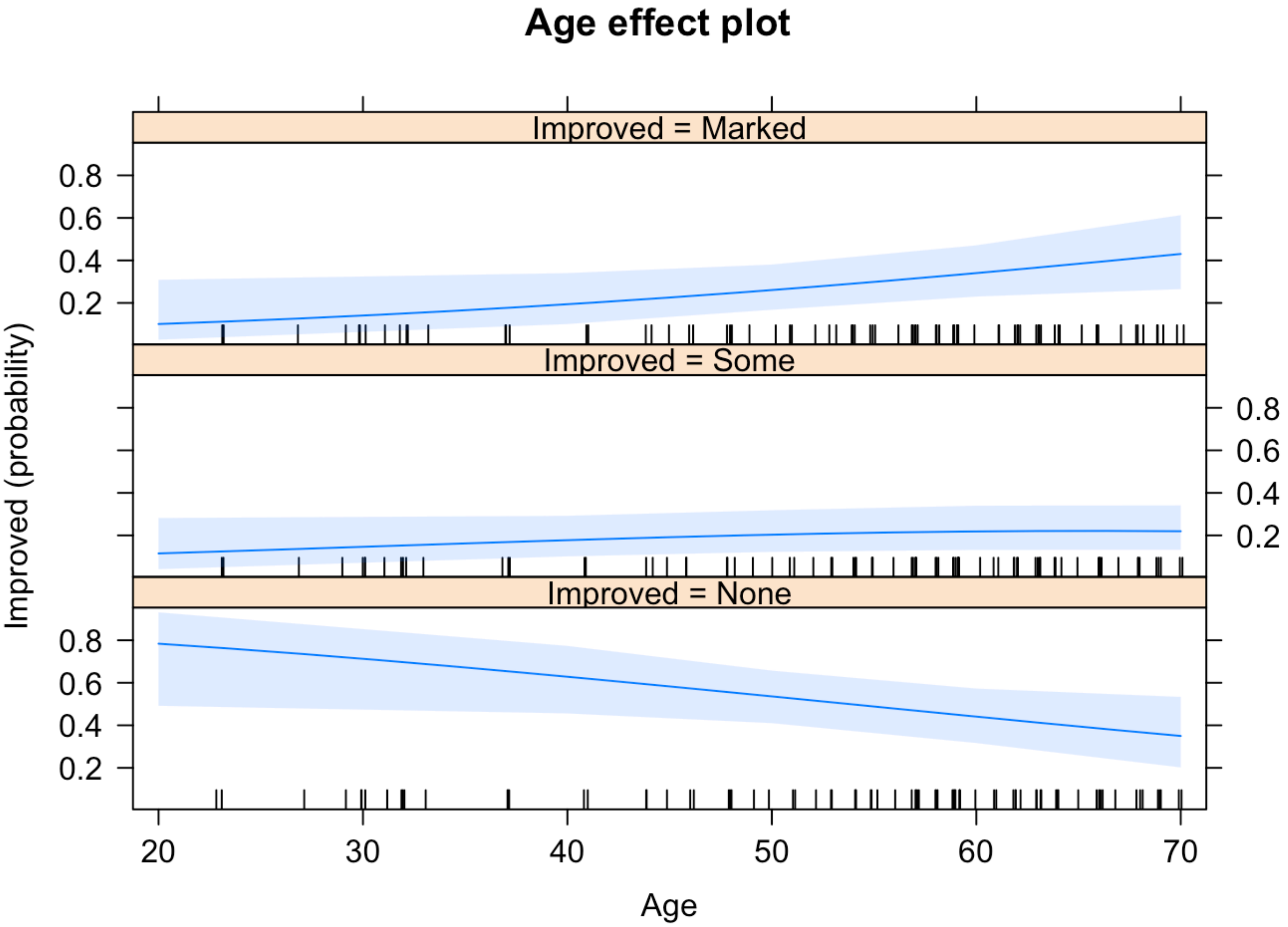
Although we now have three response curves in each panel, this plot is relatively easy to un- derstand: (a) In each panel, the probability of no improvement decreases with age, while that for marked improvement increases. (b) It is easy to compare the placebo and treated groups in each row, showing that no improvement decreases, while marked improvement increases with the active treatment. (On the other hand, this layout makes it harder to compare panels vertically for males and females in each condition.) (c) The points show where the observations are located in each panel; so, we can see that the data is quite thin for males given the placebo

Effect Plots

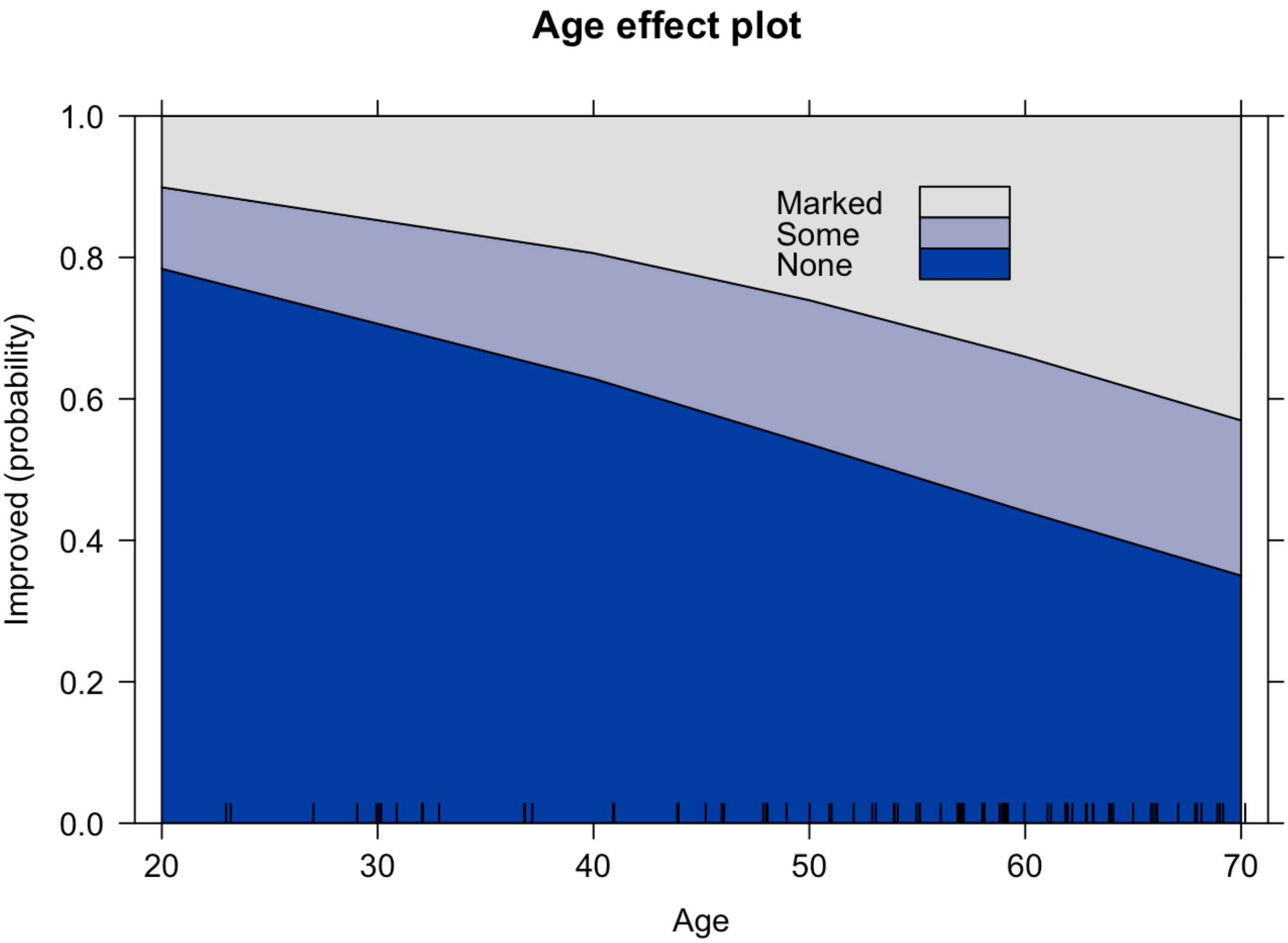
```
#install.packages("effects")
library(effects)
```

```
## Use the command
##     lattice::trellis.par.set(effectsTheme())
##   to customize lattice options for effects plots.
## See ?effectsTheme for details.
```

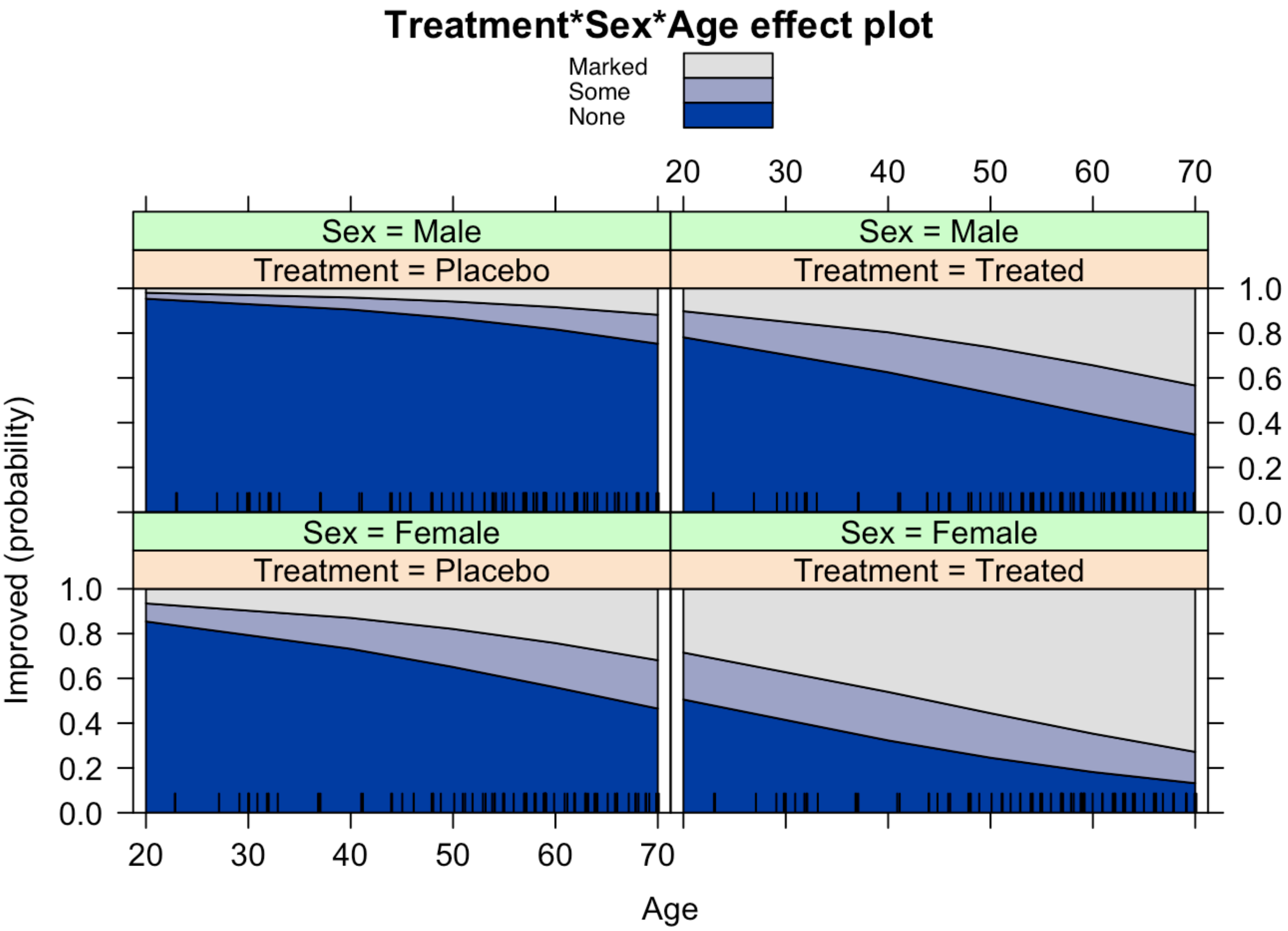
```
plot(Effect("Age", arth.polr))
```



```
plot(Effect("Age", arth.polr), style='stacked',key.args=list(x=.55, y=.9))
```

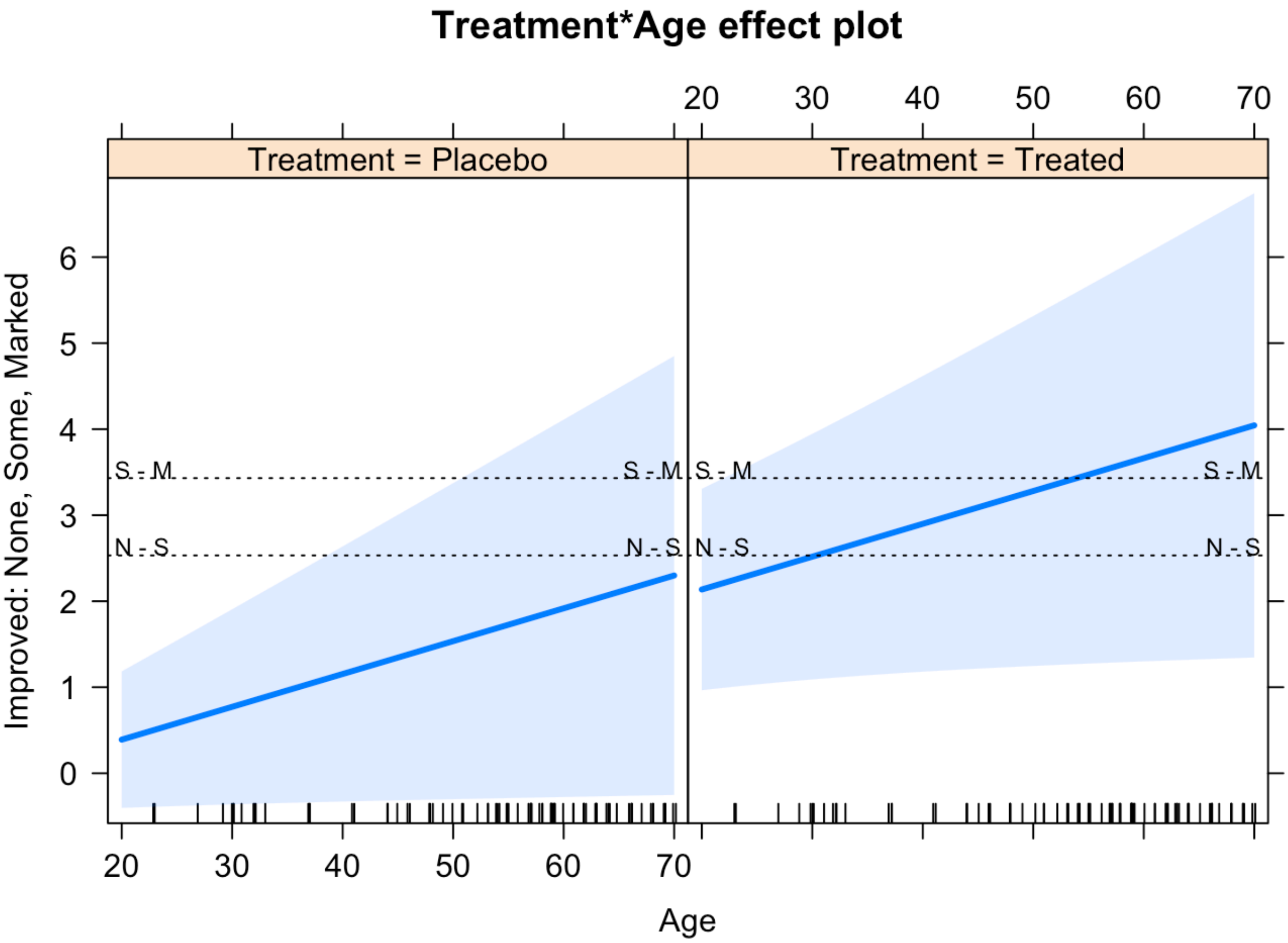


```
plot(Effect(c("Treatment", "Sex", "Age"), arth.polr),style="stacked", key.arg=list(x=
.8, y=.9))
```



Latent variable effect plot for the effects of Treatment and Age in the Arthritis data

```
plot(Effect(c("Treatment", "Age"), arth.polr, latent=TRUE), lwd=3)
```



EXAMPLE 8.1: Women’s labor force participation

```
library(car)
rm(Womenlf)
data("Womenlf", package="car")
#head(Womenlf)
```

```
Womenlf <- Womenlf
```

In this example, it makes sense to consider a first dichotomy (working) between women who are not working, vs. those who are (full time or part time). A second dichotomy (fulltime) contrasts full time work vs. part time work, among those women who are working at least part time. These two binary variables are created in the data frame using the recode() function from the car package

```
#Create dichotomies// using ifelse. Recode is another option which was not working in
this case
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:Hmisc':
##
##     src, summarize
```

```
## The following object is masked from 'package:car':
##
##     recode
```

```
## The following object is masked from 'package:MASS':
##
##     select
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
working = ifelse(Womenlf$partic=='not.work',"no","yes")
fulltime = ifelse(Womenlf$partic=='fulltime',"yes",
                  ifelse(Womenlf$partic=='parttime',"no",NA)
                  )
Womenlf = cbind(Womenlf,working,fulltime)
#Womenlf = cbind(Womenlf,fulltime)
head(Womenlf)
```

```
##     partic hincome children  region working fulltime
## 1 not.work      15  present Ontario      no     <NA>
## 2 not.work      13  present Ontario      no     <NA>
## 3 not.work      45  present Ontario      no     <NA>
## 4 not.work      23  present Ontario      no     <NA>
## 5 not.work      19  present Ontario      no     <NA>
## 6 not.work       7  present Ontario      no     <NA>
```

```
with(Womenlf, table(partic, working))
```

```
##           working
## partic      no yes
##   fulltime   0  66
##   not.work 155   0
##   parttime   0  42
```

```
with(Womenlf, table(partic, fulltime, useNA="ifany"))
```

```
##           fulltime
## partic      no yes <NA>
##   fulltime   0  66    0
##   not.work   0   0  155
##   parttime  42   0    0
```

We proceed to fit two separate binary logistic regression models for the derived dichotomous variables. For the working dichotomy, we get the following results:

```
mod.working <- glm(working ~ hincome + children, family=binomial,data=Womenlf)
summary(mod.working)
```

```
##
## Call:
## glm(formula = working ~ hincome + children, family = binomial,
##     data = Womenlf)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.6767  -0.8652  -0.7768   0.9292   1.9970
##
## Coefficients:
##                 Estimate Std. Error z value Pr(>|z|)
## (Intercept)      1.33583    0.38376   3.481   0.0005 ***
## hincome         -0.04231    0.01978  -2.139   0.0324 *
## childrenpresent -1.57565    0.29226  -5.391    7e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 356.15  on 262  degrees of freedom
## Residual deviance: 319.73  on 260  degrees of freedom
## AIC: 325.73
##
## Number of Fisher Scoring iterations: 4
```

```
mod.fulltime <- glm(fulltime ~ hincome + children, family=binomial,data=Womenlf)
summary(mod.fulltime)
```

```
##
## Call:
## glm(formula = fulltime ~ hincome + children, family = binomial,
##     data = Womenlf)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.4047  -0.8678   0.3949   0.6213   1.7641
##
## Coefficients:
##                 Estimate Std. Error z value Pr(>|z|)
## (Intercept)      3.47777    0.76711   4.534 5.80e-06 ***
## hincome         -0.10727    0.03915  -2.740  0.00615 **
## childrenpresent -2.65146    0.54108  -4.900 9.57e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 144.34  on 107  degrees of freedom
## Residual deviance: 104.49  on 105  degrees of freedom
##   (155 observations deleted due to missingness)
## AIC: 110.49
##
## Number of Fisher Scoring iterations: 5
```

Although these were fit separately, we can view this as a combined model for the three-level response, with the following coefficients

```
cbind(working=coef(mod.working), fulltime=coef(mod.fulltime))
```

```
##                     working   fulltime
## (Intercept)      1.33582979  3.4777735
## hincome         -0.04230843 -0.1072679
## childrenpresent -1.57564843 -2.6514557
```

For both dichotomies, increasing income of the husband and the presence of young children decrease the log odds of a greater level of work. However, for those women who are working the effects of husband’s income and and children are greater on the choice between full time and part time work than they are for all women on the choice between working and not workin

```
LRtest <- function(model) c(LRchisq=(model$null.deviance - model$deviance),df=(model$
df.null - model$df.residual))
tab <- rbind(working=LRtest(mod.working),fulltime=LRtest(mod.fulltime))
tab <- rbind(tab, All = colSums(tab))
tab <- cbind(tab, pvalue = 1- pchisq(tab[,1], tab[,2]))
tab
```

```
##           LRchisq df       pvalue
## working  36.41835  2 1.235536e-08
## fulltime 39.84682  2 2.225215e-09
## All      76.26518  4 1.110223e-15
```

```
Anova(mod.working)
```

```
## Analysis of Deviance Table (Type II tests)
## 
## Response: working
##          LR Chisq Df Pr(>Chisq)    
## hincome    4.8264  1    0.02803 *  
## children  31.3229  1  2.185e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Anova(mod.fulltime)
```

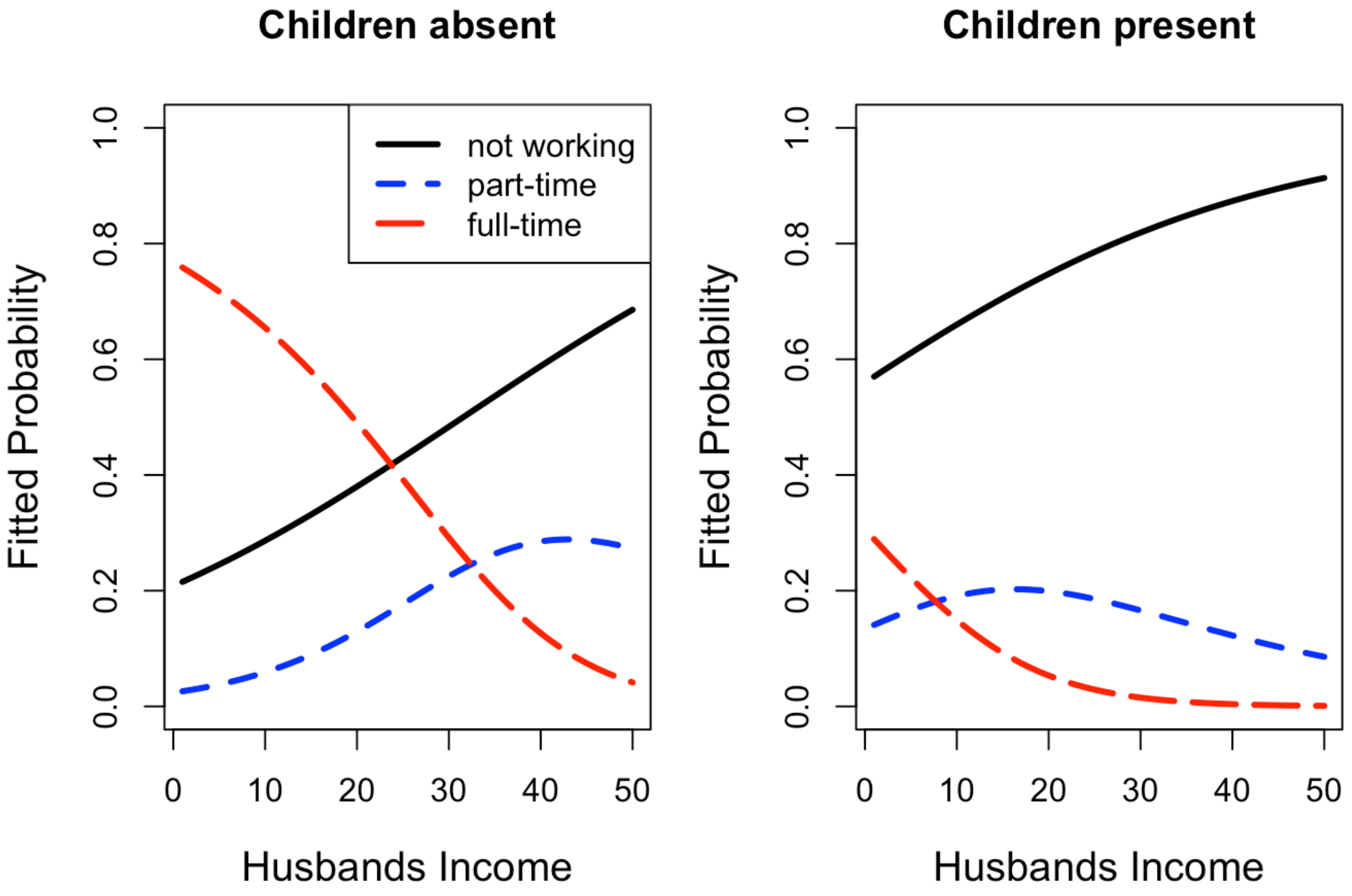
```
## Analysis of Deviance Table (Type II tests)
## 
## Response: fulltime
##          LR Chisq Df Pr(>Chisq)    
## hincome     8.981  1   0.002728 ** 
## children   32.136  1  1.437e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
predictors <- expand.grid(hincome=1:50,children=c('absent', 'present'))
fit <- data.frame(predictors,
                  p.working = predict(mod.working, predictors, type='response'),
                  p.fulltime = predict(mod.fulltime, predictors, type='response'),
                  l.working = predict(mod.working, predictors, type='link'),
                  l.fulltime = predict(mod.fulltime, predictors, type='link')
)
print(some(fit, 5), digits=3)
```

```
##    hincome children p.working p.fulltime l.working l.fulltime
## 18      18   absent     0.640     0.8245     0.574      1.547
## 29      29   absent     0.527     0.5907     0.109      0.367
## 34      34   absent     0.474     0.4578    -0.103     -0.169
## 37      37   absent     0.443     0.3796    -0.230     -0.491
## 96      46  present     0.101     0.0162    -2.186     -4.108
```

```
fit <- within(fit, { full <- p.working * p.fulltime
part <- p.working * (1 - p.fulltime)
not  <- 1 - p.working
})
```

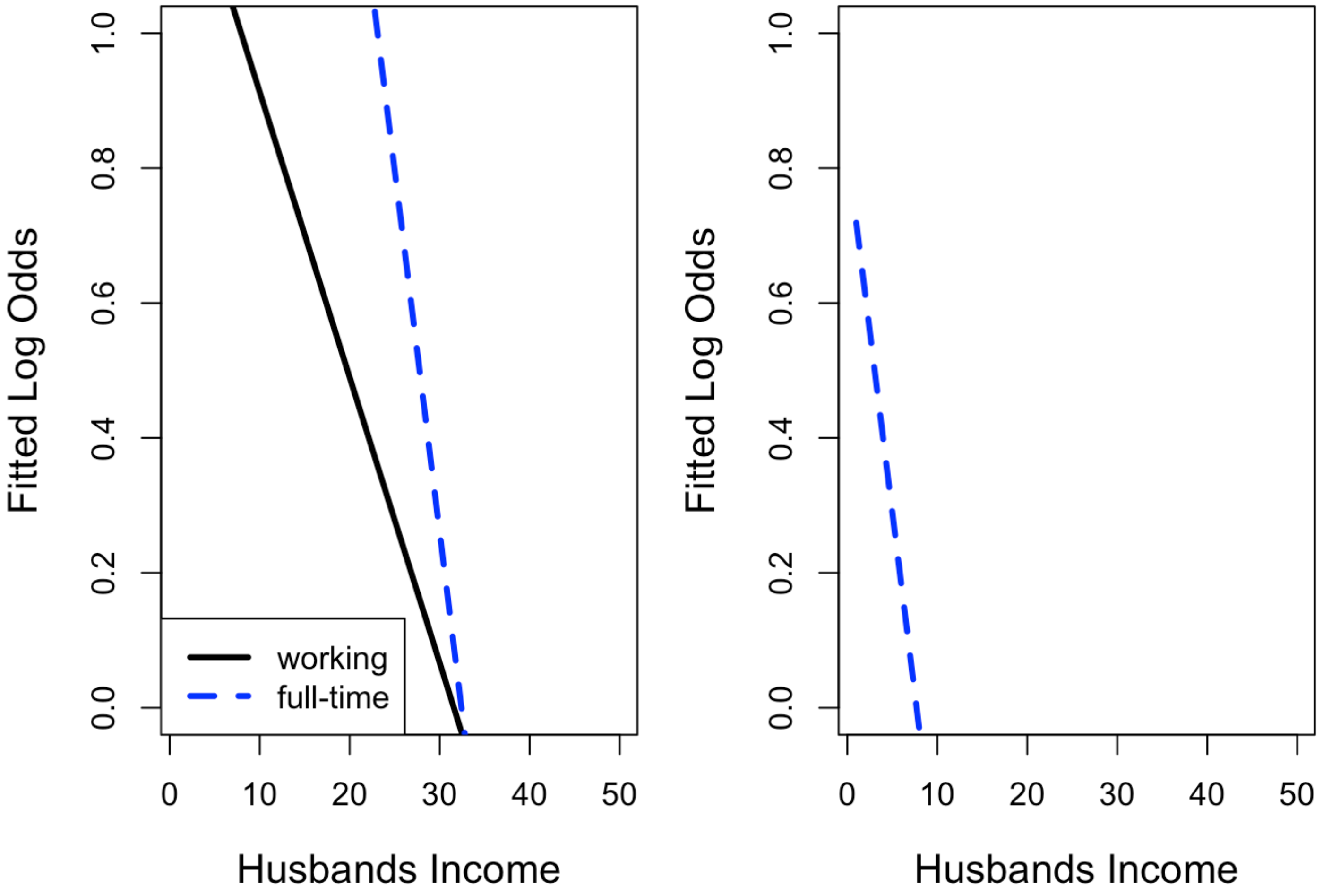
```
op <- par(mfrow=c(1,2), mar=c(5,4,4,1)+.1)
Hinc <- 1:max(fit$hincome)
for ( kids in c("absent", "present") )
{
  dat <- subset(fit,children==kids)
  plot(range(Hinc),c(0,1),type="n",cex.lab=1.25,
       xlab="Husbands Income",ylab="Fitted Probability",
       main=paste("Children",kids))
  lines(Hinc, dat$not, lwd=3, col="black", lty=1)
  lines(Hinc, dat$part, lwd=3, col="blue", lty=2)
  lines(Hinc, dat$full, lwd=3, col="red", lty=5)
  if(kids=="absent")
    {
    legend("topright", lty=c(1,2,5), lwd=3, col=c("black", "blue", "red"),
           legend=c('not working', 'part-time', 'full-time'))
  }
}
```



```
par(op)
```

We can see how that the decision not to work outside the home increases strongly with husband’s income, and is higher when there are children present. As well, among working women, the decision to work full time as opposed to part time decreases strongly with husband’s income, and is less likely with young children. Similarly, we plot the fitted logits for the two dichotomies in l.working and l.fulltime as shown below:

```
op <- par(mfrow=c(1,2), mar=c(5,4,1,1)+.1)
for ( kids in c("absent", "present") )
  {
  dat <- subset(fit,children==kids)
  plot(range(Hinc),c(0,1),type="n",cex.lab=1.25,
       xlab="Husbands Income",ylab="Fitted Log Odds")
  lines(Hinc, dat$l.working, lwd=3, col="black", lty=1)
  lines(Hinc, dat$l.fulltime, lwd=3, col="blue", lty=2)
  text(25, 4.5, paste("Children", kids), cex=1.4)
  if (kids=="absent")
    {
    legend("bottomleft", lty=1:2, lwd=3, col=c("black", "blue"),
           legend=c('working', 'full-time'))
    }
}
```



These Graphs didn’t come out as expected

Generalized Logit Model

Response : Women working full time, part time or not working Variables: Husbands Income (Continuous), Children Present vs. Absent (Categorical)

```
levels(Womenlf$partic)
```

```
## [1] "fulltime" "not.work" "parttime"
```

```
# choose not working as baseline category
Womenlf$partic <- relevel(Womenlf$partic, ref="not.work")
```

We fit the main effects model for husband’s income and children as follows. As we did with polr() (Section 8.1), specifying Hess=TRUE saves the Hessian and facilitates calculation of standard errors and hypothesis tests

```
library(nnet)
wlf.multinom <- multinom(partic ~ hincome + children,data=Womenlf, Hess=TRUE)
```

```
## # weights:  12 (6 variable)
## initial  value 288.935032
## iter  10 value 211.454772
## final  value 211.440963
## converged
```

The summary() method for “multinom” objects doesn’t calculate test statistics for the esti- mated coefficients by default. The option Wald=TRUE produces Wald z-test statistics, calculated as z = β/SE(β)

```
summary(wlf.multinom, Wald=TRUE)
```

```
## Call:
## multinom(formula = partic ~ hincome + children, data = Womenlf,
##     Hess = TRUE)
##
## Coefficients:
##          (Intercept)      hincome childrenpresent
## fulltime    1.982842 -0.097232073     -2.55860537
## parttime   -1.432321  0.006893838      0.02145558
##
## Std. Errors:
##          (Intercept)    hincome childrenpresent
## fulltime   0.4841789 0.02809599       0.3621999
## parttime   0.5924627 0.02345484       0.4690352
##
## Value/SE (Wald statistics):
##          (Intercept)    hincome childrenpresent
## fulltime    4.095266 -3.4607098     -7.06407045
## parttime   -2.417573  0.2939197      0.04574407
##
## Residual Deviance: 422.8819
## AIC: 434.8819
```

Notice that the coefficients, their standard errors and the Wald test z values are printed in separate tables. The first line in each table pertains to the logit comparing full time work with the not working reference level; the second line compares part time work against not working

For those who like p-values for significance tests, you can calculate these from the results re- turned by the summary() method in the Wald.ratios component, using the standard normal asymptotic approximation

```
stats <- summary(wlf.multinom, Wald=TRUE)
z <- stats$Wald.ratios
p <- 2 * (1 - pnorm(abs(z)))
zapsmall(p)
```

```
##          (Intercept)   hincome childrenpresent
## fulltime   0.0000422 0.0005388       0.0000000
## parttime   0.0156244 0.7688193       0.9635142
```

```
wlf.multinom2 <- multinom(partic ~ hincome * children, data=Womenlf, Hess=TRUE)
```

```
## # weights:  15 (8 variable)
## initial  value 288.935032
## iter  10 value 210.797079
## final  value 210.714841
## converged
```

```
Anova(wlf.multinom2)
```

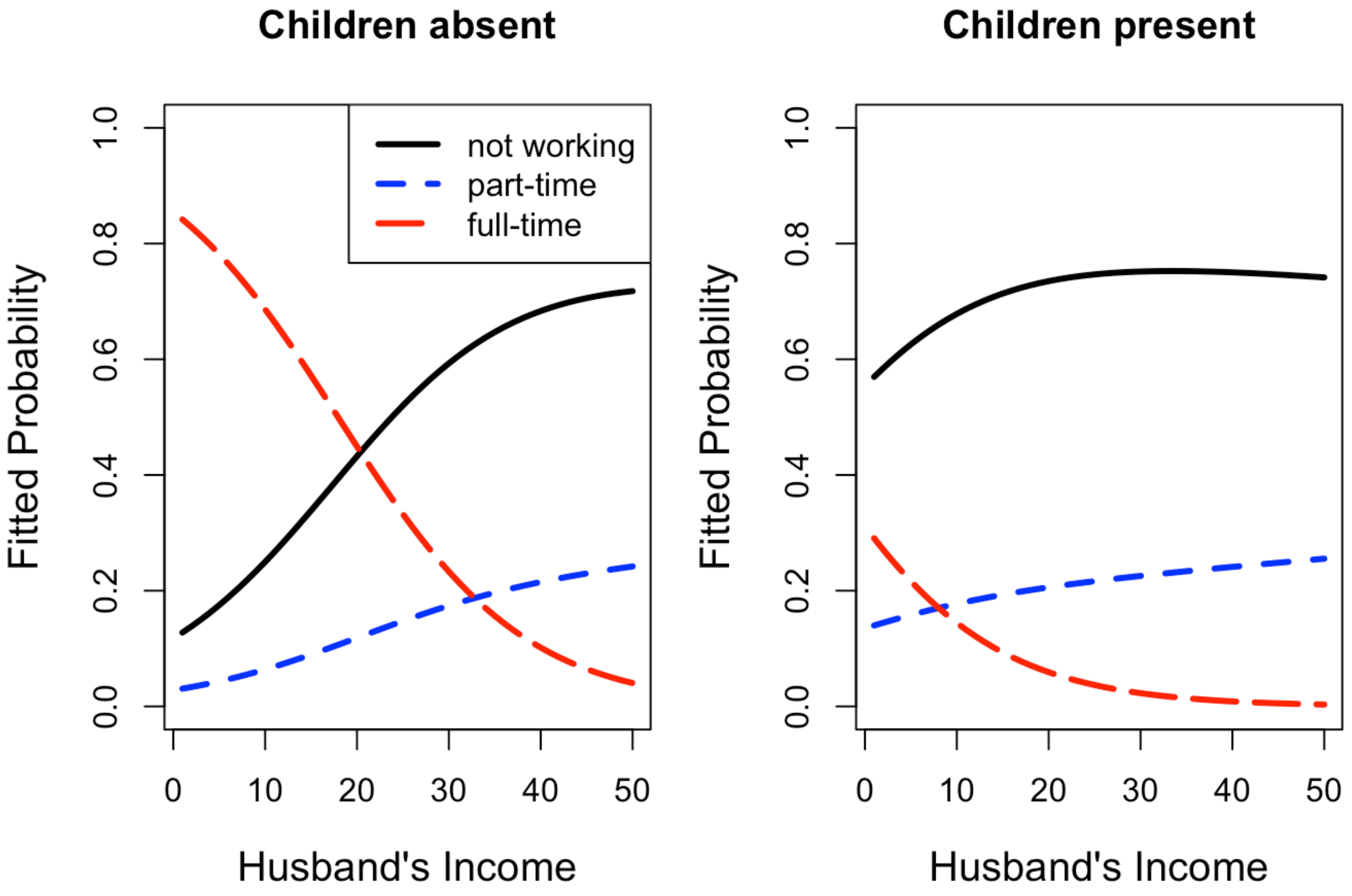
```
## Analysis of Deviance Table (Type II tests)
## 
## Response: partic
##                  LR Chisq Df Pr(>Chisq)    
## hincome            15.153  2  0.0005123 ***
## children           63.559  2  1.579e-14 ***
## hincome:children    1.452  2  0.4837815    
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Full model plots of the fitted values can be plotted as shown earlier in Example 8.1: obtain the fitted values over a grid of the predictors and plot these

```
predictors <- expand.grid(hincome=1:50,
                          children=c('absent', 'present'))
fit <- data.frame(predictors,predict(wlf.multinom, predictors, type='probs'))
```

Plotting these fitted values gives the plot shown in Figure 8.12.

```
op <- par(mfrow=c(1,2), mar=c(5,4,4,1)+.1)
Hinc <- 1:max(fit$hincome)
for ( kids in c("absent", "present") ) {
  dat <- subset(fit, children==kids)
  plot( range(Hinc), c(0,1), type="n", cex.lab=1.25,
        xlab="Husband's Income", ylab='Fitted Probability',
        main = paste("Children", kids))
  lines(Hinc, dat$not.work, lwd=3, col="black", lty=1)
  lines(Hinc, dat$parttime, lwd=3, col="blue", lty=2)
  lines(Hinc, dat$fulltime, lwd=3, col="red", lty=5)
  if (kids=="absent") {
    legend("topright", lty=c(1,2,5), lwd=3, col=c("black", "blue", "red"),legend=c('n
ot working', 'part-time','full-time'))
  }
}
```



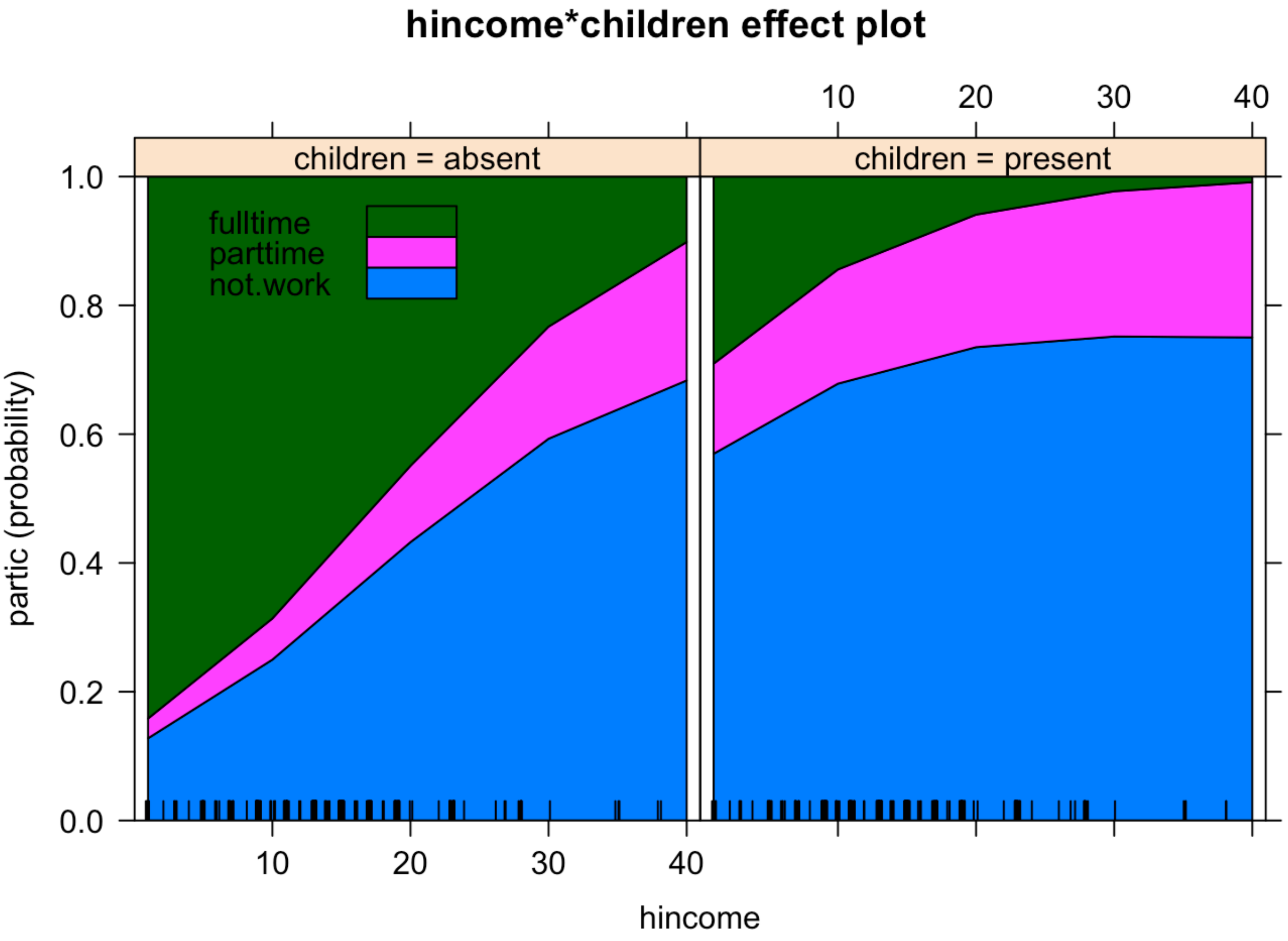
The effects package has special methods for “multinom” models. It treats the response levels in the order given by levels(), so before plotting we use ordered() to arrange levels in their nat- ural order. The update() method provides a simple way to get a new fitted model; in the call, the modelformula. ~ .meanstofitthesamemodelasbefore,i.e.,partic ~ hincome + children

```
Womenlf$partic <- ordered(Womenlf$partic,
                          levels=c('not.work', 'parttime', 'fulltime'))
wlf.multinom <- update(wlf.multinom, . ~ .)
```

```
## # weights:  12 (6 variable)
## initial  value 288.935032
## iter  10 value 211.454772
## final  value 211.440963
## converged
```

Asillustratedearlier,youcanuseplot(allEffects(model), …)toplotallthehigh- order terms in the model, either with separate curves for each response level (style=“lines”) or as cumulative filled polygons (style=“stacked”). Here, we simply plot the effects for the combinations of husband’s income and children in stacked style, giving a plot (Figure 8.13) that is analogous to the full-model plot shown in Figure 8.12.

```
plot(Effect(c("hincome", "children"), wlf.multinom),
     style="stacked", key.args=list(x=.05, y=.9))
```


hincome*children effect plot
children = absent
children = present
fulltime
parttime
not.work
partic (probability)
hincome