Malaria Ebola Association Gabon Analyses

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*Be sure to first decide whether you want to run the simulations for bootstrapping the 95% Confidence Intervals for the main model! It takes a very long time to run ~20 minutes for 200 simulations. I have set a default of 5 simulations, which allows the code to run but gives obvious warnings. Otherwise, use the option "SAVED" if you have the Table1data.csv file handy.

```
run_simulations<-"SAVED"    # 3 options: "NO", "YES", or "SAVED"
if(run_simulations=="SAVED"){nsims<-5}
if(run_simulations=="NO"){nsims<-5}
if(run_simulations=="YES"){nsims<-200}
```

Required packages:

```
library(boot)
library(plotrix)
library(car)
library(lme4)
library(ggplot2)
```

Load data files: (and work directory)

```
setwd("~/Dropbox/Work_Labs/Roche/Gabon Dataset/")
Xdat <- read.csv("gabondata_master.csv", sep=",")
DeptPrevs <- read.csv("Gabon prevalence by dept.csv", sep=",")
VillPrevs <- read.csv("Gabon prevalence by vill.csv", sep=",")
setwd("~/Dropbox/Work_Labs/Roche/Gabon Dataset/Analyses/MaEb/")
```

# Correlation between EbolaAbs & Malaria Geographic Distribution

- NB: malpa = presence/absence of any of the 3 species of Plasmodium, and includes samples which were positive for Plasmodium PCR but where species was not able to be determined.

```
par(mfrow=c(1,2))
hist(asin(sqrt(DeptPrevs$malpa.prev)),main="Dept Prevs MalariaPA")
hist(asin(sqrt(DeptPrevs$ebola.prev)),main="Dept Prevs EbolaAbs")
```

Dept Prevs MalariaPA

asin(sqrt(DeptPrevs$malpa.prev))

Dept Prevs EbolaAbs
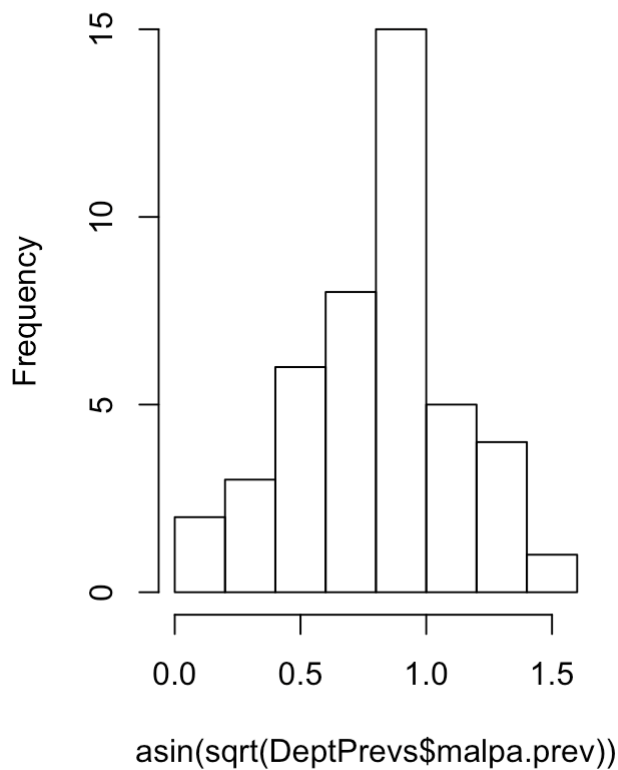
asin(sqrt(DeptPrevs$ebola.prev))
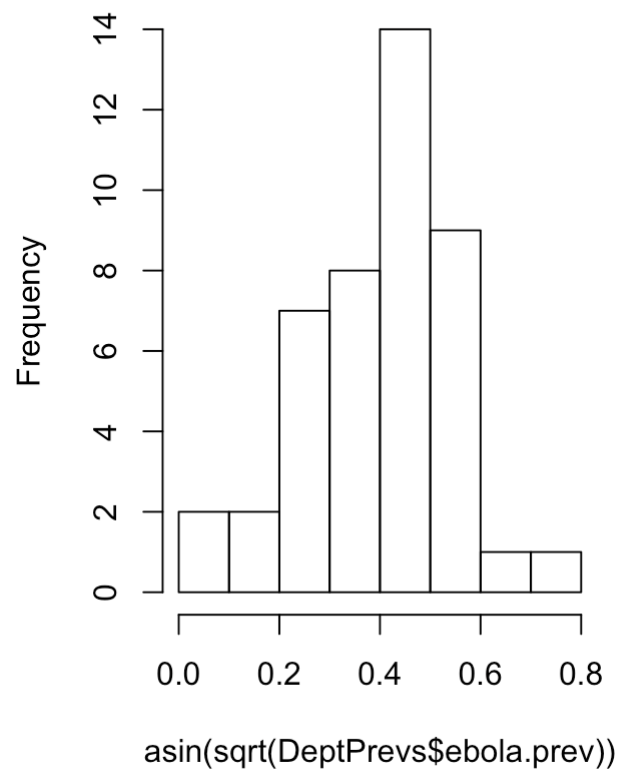
```
cor.test(DeptPrevs$malpa.prev,DeptPrevs$ebola.prev, method="spearman",exact=FALSE)
```

```
##
##   Spearman's rank correlation rho
##
## data:  DeptPrevs$malpa.prev and DeptPrevs$ebola.prev
## S = 8132.7, p-value = 0.003856
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##       rho
## 0.4268697
```

```
par(mfrow=c(1,1))
#pdf("MaEb_geog_corrASSQRT_grayCI.pdf")

df<-DeptPrevs
df$x<-asin(sqrt(df$ebola.prev))
df$y<-asin(sqrt(df$malpa.prev))
mod <- lm(y ~ x, data = df)
newx <- seq(min(df$x), max(df$x), length.out=44)
preds <- predict(mod, newdata = data.frame(x=newx), interval = 'confidence')
df$y<-sin(df$y)^2
df$x<-sin(df$x)^2
newx<-sin(newx)^2
preds<-sin(preds)^2
plot(y ~ x, data = df,pch=16, xlab="Dept Prevalence EbolaAbs", ylab="Dept Prevalence Mal
ariaPA")
color <- "gray" #also pretty if this is "mediumpurple1"
color_transparent <- adjustcolor(color, alpha.f = 0.3)
polygon(c(rev(newx), newx), c(rev(preds[ ,3]), preds[ ,2]), col=color_transparent, borde
r = NA)
#lines(newx, preds[ ,3], lty = 'dashed', col = 'red')
#lines(newx, preds[ ,2], lty = 'dashed', col = 'red')
lines(newx,preds[,1])
```
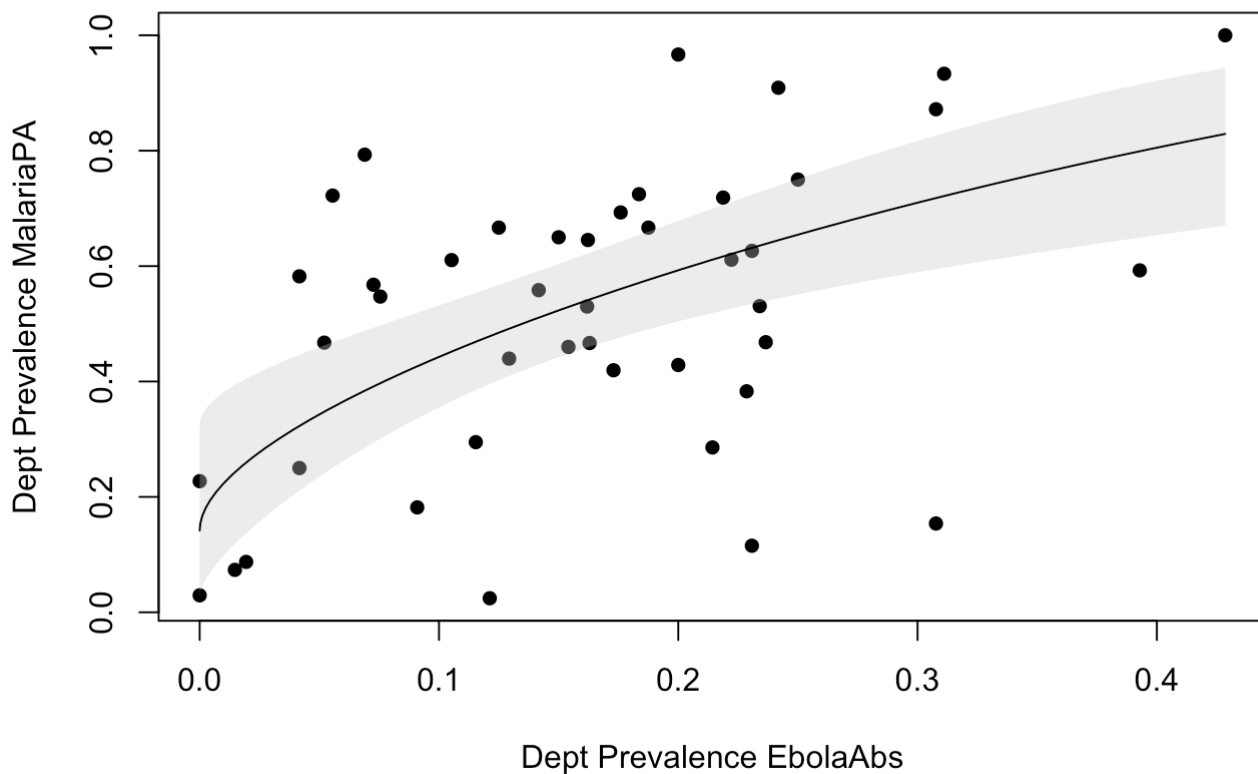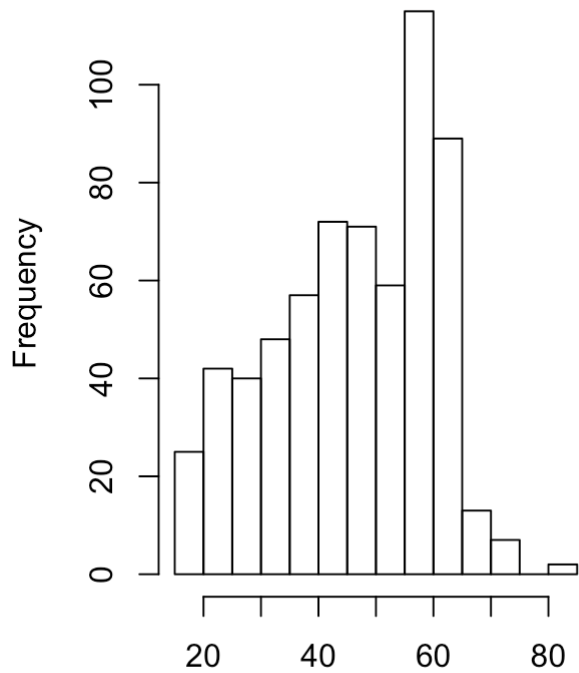


```
#dev.off()
```

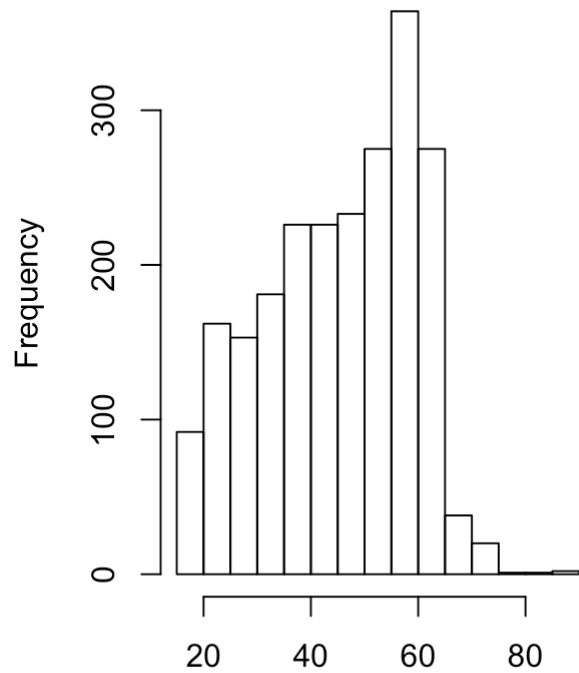# Contribution of EbolaAbs to MalariaPA

Clean dataset

```
# classify age structure
par(mfrow=c(1,2))
hist(Xdat[which(Xdat$ebola_IgG==1),]$age, main="age structure EbolaAbs")
hist(Xdat[which(Xdat$paMalaria==1),]$age, main="age structure MalariaPA")
```

age structure EbolaAbs   **age structure MalariaPA**

Xdat[which(Xdat$ebola_IgG == 1),]$age   Xdat[which(Xdat$paMalaria == 1),]$age

```
Xdat$ageclass<-NA
Xdat$ageclass[which(Xdat$age<30)]<-"0 to 29"
Xdat$ageclass[which(Xdat$age>29 & Xdat$age<45)]<-"30 to 45"
Xdat$ageclass[which(Xdat$age>44 & Xdat$age<60)]<-"45 to 60"
Xdat$ageclass[which(Xdat$age>59)]<-"60 and over"

# subset data and recode variables to (simplified) factors
maeb<-subset(Xdat,Xdat$paMalaria!="NA")
maeb<-subset(maeb,maeb$ebola_IgG!="NA")
maeb<-subset(maeb,maeb$sex!="NA")
maeb<-subset(maeb,maeb$age!="NA")
maeb<-subset(maeb,maeb$occupation!="NA")
maeb<-subset(maeb,maeb$occupation!="INCONNUE")
maeb$occup<-NA
maeb$occup[which(maeb$occupation=="CHASSEUR")]<-"YEShunter"
maeb$occup[which(maeb$occupation!="CHASSEUR")]<-"NOThunter"
maeb<-subset(maeb,maeb$ecosys2!="NA")
maeb$ecosys<-NA
maeb$ecosys[which(maeb$ecosys2=="FORET")]<-"YESforest"
maeb$ecosys[which(maeb$ecosys2!="FORET")]<-"NOTforest"

maeb$vilfac<-as.factor(as.character(maeb$VillageGPScode))
maeb$fac_eb<-as.factor(as.character(maeb$ebola_IgG))
maeb$fac_occup<-as.factor(as.character(maeb$occup))
maeb$fac_ageclass<-as.factor(as.character(maeb$ageclass))
maeb$fac_ecosys<-as.factor(as.character(maeb$ecosys))
maeb$fac_sex<-as.factor(as.character(maeb$sex))
```

Run GLMM with village as a random factor

```
mod<-glmer(maeb$paMalaria~maeb$fac_eb+maeb$fac_occup+maeb$fac_ageclass+maeb$fac_sex+maeb
$fac_ecosys+maeb$Pop_Density_Dept+(1|maeb$vilfac),family="binomial",control = glmerContr
ol(optimizer = "bobyqa"))
summary(mod)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##    Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula:
## maeb$paMalaria ~ maeb$fac_eb + maeb$fac_occup + maeb$fac_ageclass +
##     maeb$fac_sex + maeb$fac_ecosys + maeb$Pop_Density_Dept +
##     (1 | maeb$vilfac)
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC   logLik deviance df.resid
##   4775.6   4838.5  -2377.8   4755.6     3977
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.0283 -0.7607  0.3106  0.7144  3.7288
##
## Random effects:
##  Groups        Name        Variance Std.Dev.
##  maeb$vilfac (Intercept) 1.444    1.202
## Number of obs: 3987, groups:  maeb$vilfac, 210
##
## Fixed effects:
##                              Estimate Std. Error z value Pr(>|z|)
## (Intercept)                 -0.5181355  0.2391377  -2.167 0.030259 *
## maeb$fac_eb1                 0.5796762  0.1081631   5.359 8.36e-08 ***
## maeb$fac_occupYEShunter      0.1660719  0.1366967   1.215 0.224407
## maeb$fac_ageclass30 to 45   -0.2793304  0.1274283  -2.192 0.028375 *
## maeb$fac_ageclass45 to 60   -0.3603201  0.1241297  -2.903 0.003699 **
## maeb$fac_ageclass60 and over -0.4616582  0.1301896  -3.546 0.000391 ***
## maeb$fac_sexMasculin         0.2735995  0.0821663   3.330 0.000869 ***
## maeb$fac_ecosysYESforest     0.9943199  0.2271627   4.377 1.20e-05 ***
## maeb$Pop_Density_Dept        0.0008614  0.0137931   0.062 0.950205
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) mb$f_1 mb$fc_ccYES m$_3t4 m$_4t6 m$_6ao mb$f_M
## maeb$fac_b1 -0.024
## mb$fc_ccYES -0.034 -0.021
## mb$fc_30t45 -0.353 -0.016  0.018
## mb$fc_45t60 -0.369  0.001  0.025       0.699
## mb$fc_g60ao -0.351 -0.023  0.077       0.668  0.700
## mb$fc_sxMsc -0.115 -0.026 -0.368      -0.043 -0.018 -0.088
## mb$fc_csYES -0.744 -0.044  0.003      -0.004 -0.009  0.000 -0.006
## mb$Pp_Dns_D -0.334  0.011  0.037      -0.002  0.001 -0.001  0.001
##             mb$fc_csYES
## maeb$fac_b1
## mb$fc_ccYES
## mb$fc_30t45
## mb$fc_45t60
## mb$fc_g60ao
## mb$fc_sxMsc
```

```
## mb$fc_csYES
## mb$Pp_Dns_D  0.019
```

```
drop1(mod,test="Chisq")
```

```
## Single term deletions
##
## Model:
## maeb$paMalaria ~ maeb$fac_eb + maeb$fac_occup + maeb$fac_ageclass +
##      maeb$fac_sex + maeb$fac_ecosys + maeb$Pop_Density_Dept +
##      (1 | maeb$vilfac)
##                       Df   AIC     LRT   Pr(Chi)
## <none>                    4775.6
## maeb$fac_eb            1 4802.7 29.0869 6.920e-08 ***
## maeb$fac_occup         1 4775.1  1.4598 0.2269614
## maeb$fac_ageclass      3 4782.7 13.1295 0.0043648 **
## maeb$fac_sex           1 4784.6 10.9650 0.0009285 ***
## maeb$fac_ecosys        1 4792.2 18.6136 1.601e-05 ***
## maeb$Pop_Density_Dept  1 4773.6  0.0038 0.9506484
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Bootstrapping for 95% Confidence Intervals

```
mySumm2 <- function(.) {
          c(beta=fixef(.),sigma=sigma(.), sig01=sqrt(unlist(VarCorr(.))))}


set.seed(101)
system.time( boo01 <- bootMer(mod, mySumm2, nsim = nsims) )


boo01
boo01$t0<-boo01$t0[1:9]
boo01$t<-boo01$t[,1:9]
head(as.data.frame(boo01))


## ------ Bootstrap-based confidence intervals ------------
## warnings about "Some ... intervals may be unstable" go away
##    for larger bootstrap samples, e.g. nsim=500


## intercept
(bCI.1 <- boot.ci(boo01, index=1, type=c("norm", "basic", "perc")))# beta


## Copy of unexported stats:::format.perc helper function
format.perc <- function(probs, digits) {
              paste(format(100 * probs, trim = TRUE,
              scientific = FALSE, digits = digits),"%")}


## Extract all CIs
bCI.tab <- function(b,ind=length(b$t0), type="perc", conf=0.95) {
  btab0 <- t(sapply(as.list(seq(ind)),
                  function(i)
                    boot.ci(b,index=i,conf=conf, type=type)$percent))
  btab <- btab0[,4:5]
  rownames(btab) <- names(b$t0)
  a <- (1 - conf)/2
  a <- c(a, 1 - a)
  pct <- format.perc(a, 3)
  colnames(btab) <- pct
  return(btab)
}
bCI.tab(boo01)


#   #Graphical examination:
#   plot(boo01,index=3)
```

Odds Ratios and 95% confidence intervals:

```
Table1<-summary(boo01)
Table1<-cbind(Table1,bCI.tab(boo01))
Table1<-cbind(Table1,exp(Table1[,2]))
Table1<-cbind(Table1,exp(Table1[,6]))
Table1<-cbind(Table1,exp(Table1[,7]))
#Table1<-cbind(Table1,rownames(Table1))
Table1<-cbind(Table1,c("Intercept","EbolaIgG:Positive","Occupation:Hunter","Age:30-45",
"Age:45-60","Age:Over60","Sex:Male","Ecosystem:Forest","Dept Population Density"))
colnames(Table1)[8:11]<-c("OR","LCL","UCL","group")
Table1[,c("OR","LCL","UCL")]
```

```
##                                       OR       LCL       UCL
## beta.(Intercept)                 0.5956301 0.5458411 0.8189985
## beta.maeb$fac_eb1                1.7854601 1.6767692 2.0343695
## beta.maeb$fac_occupYEShunter     1.1806580 1.0820910 1.5504246
## beta.maeb$fac_ageclass30 to 45   0.7562900 0.6405679 0.9084567
## beta.maeb$fac_ageclass45 to 60   0.6974530 0.5909859 0.7796521
## beta.maeb$fac_ageclass60 and over 0.6302377 0.5672587 0.6834656
## beta.maeb$fac_sexMasculin        1.3146882 1.1929597 1.2526011
## beta.maeb$fac_ecosysYESforest    2.7028854 1.9351210 2.6494167
## beta.maeb$Pop_Density_Dept       1.0008617 0.9882729 1.0246223
```

```
if(run_simulations=="YES"){write.csv(Table1,"Table1data.csv")} # to store
```
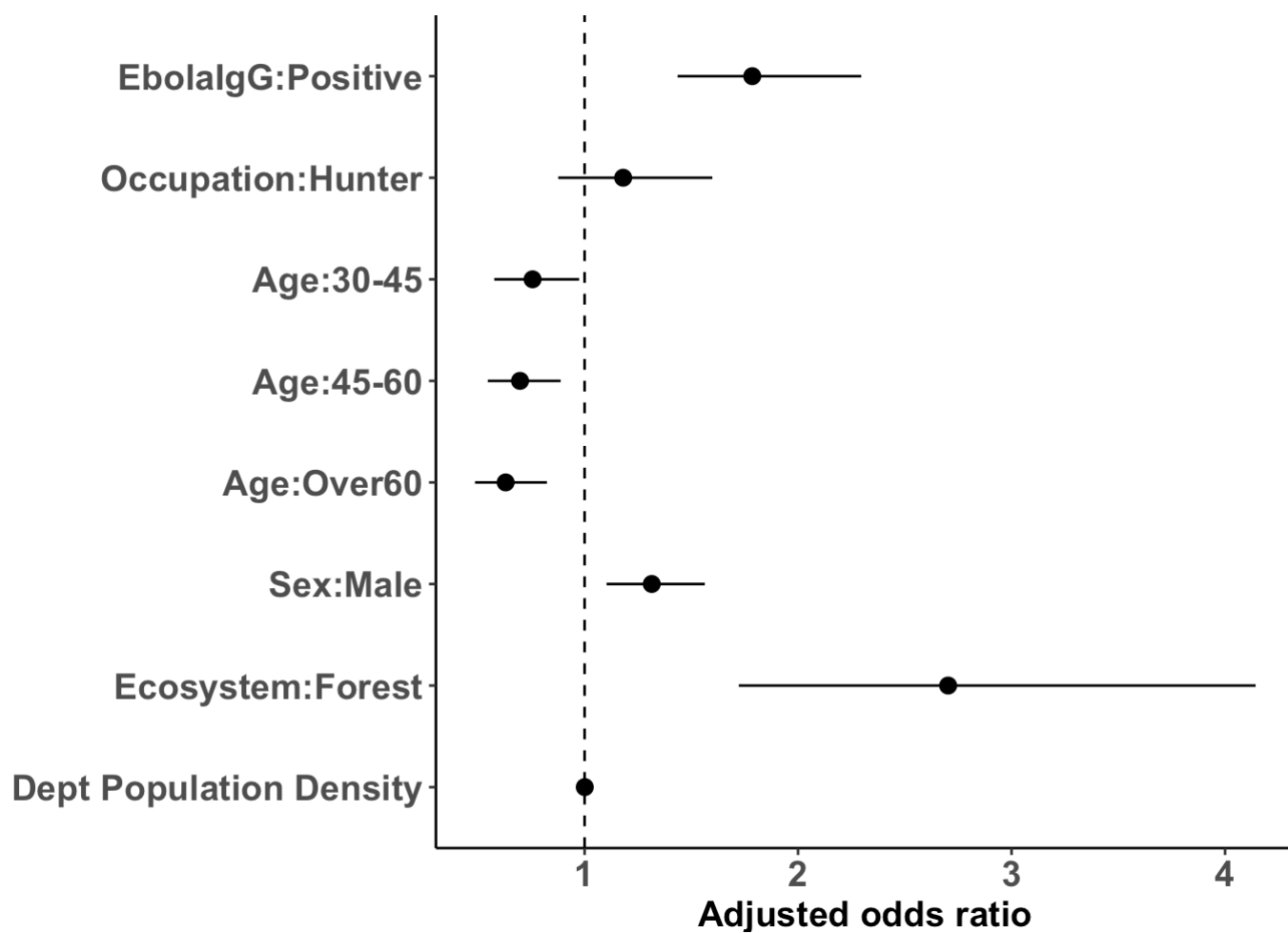
Forest Plot for Figure 2:

```r
if(run_simulations=="SAVED"){Table1<-read.table("Table1data.csv",as.is=T, header=T, sep=
",")}

library(ggplot2)
theme_set(theme_bw())
theme_update(
    axis.line = element_line(colour = "black"),
    panel.grid.major = element_blank(),
    panel.grid.minor = element_blank(),
    panel.border = element_blank(),
    panel.background = element_blank(),
    axis.text=element_text(size=14,face="bold"),
    axis.title=element_text(size=14,face="bold"),
    plot.margin = unit(c(0,0,0,0), "lines")
)

credplot.gg <- function(d){
 p <- ggplot(d, aes(x=x, y=y, ymin=ylo, ymax=yhi))+
 geom_pointrange()+
 geom_hline(yintercept = 1, linetype=2)+
 coord_flip()+
 xlab(NULL)+
 ylab('Adjusted odds ratio')
 return(p)
}

d<-data.frame(x=Table1[2:9,"group"],y=Table1[2:9,"OR"],ylo=Table1[2:9,"LCL"],yhi=Table1[
2:9,"UCL"])
d$x = factor(d$x, levels=rev(c("Intercept","EbolaIgG:Positive","Occupation:Hunter","Age:
30-45","Age:45-60","Age:Over60","Sex:Male","Ecosystem:Forest","Dept Population Density")
))
credplot.gg(d)
```

Alternatively, we could report the effect sizes directly, as those are easier to interpret relative to one-another in a figure:

```r
if(run_simulations=="SAVED"){Table1<-read.table("Table1data.csv",as.is=T, header=T, sep=
",")}

library(ggplot2)
theme_set(theme_bw())
theme_update(
    axis.line = element_line(colour = "black"),
    panel.grid.major = element_blank(),
    panel.grid.minor = element_blank(),
    panel.border = element_blank(),
    panel.background = element_blank(),
    axis.text=element_text(size=14,face="bold"),
    axis.title=element_text(size=14,face="bold"),
    plot.margin = unit(c(0,0,0,0), "lines")
)

credplot.gg2 <- function(d2){
 p2 <- ggplot(d2, aes(x=x2, y=y2, ymin=ylo2, ymax=yhi2))+
 geom_pointrange()+
 geom_hline(yintercept = 0, linetype=2)+
 coord_flip()+
 xlab(NULL)+
 ylab('Bootstrapped median effect size')
 return(p2)
}

d2<-data.frame(x2=Table1[2:9,"group"],y2=Table1[2:9,"bootMed"],ylo2=Table1[2:9,7],yhi2=T
able1[2:9,8])
d2$x2 = factor(d2$x, levels=rev(c("Intercept","EbolaIgG:Positive","Occupation:Hunter","A
ge:30-45","Age:45-60","Age:Over60","Sex:Male","Ecosystem:Forest","Dept Population Densit
y")))
credplot.gg2(d2)
```
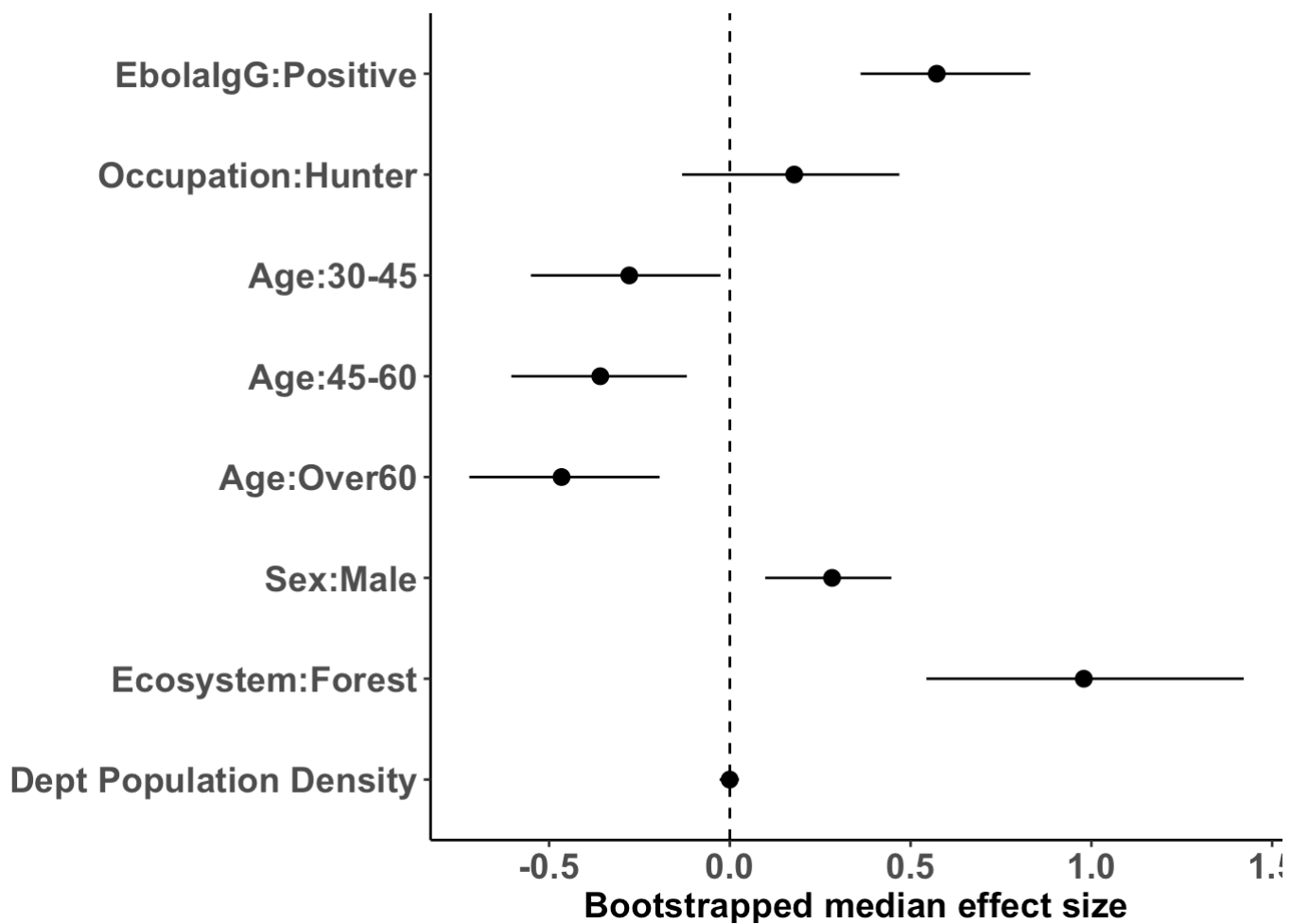
For the two Plasmodium species with adequate numbers (P. falciparum and P. malariae), the results are qualitatively identical.

```
maebSPP<-subset(maeb,maeb$Pfalci!="NA")
modPf<-glmer(maebSPP$Pfalci~maebSPP$fac_eb+maebSPP$fac_occup+maebSPP$fac_age+maebSPP$fac
_sex+maebSPP$fac_ecosys+maebSPP$Pop_Density_Dept+(1|maebSPP$vilfac),family="binomial",co
ntrol = glmerControl(optimizer = "bobyqa"))
summary(modPf)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula:
## maebSPP$Pfalci ~ maebSPP$fac_eb + maebSPP$fac_occup + maebSPP$fac_age +
##      maebSPP$fac_sex + maebSPP$fac_ecosys + maebSPP$Pop_Density_Dept +
##      (1 | maebSPP$vilfac)
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC   logLik deviance df.resid
##   3966.8   4028.2  -1973.4   3946.8     3403
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.6907 -0.6693 -0.3069  0.7228  3.6890
##
## Random effects:
##  Groups         Name        Variance Std.Dev.
##  maebSPP$vilfac (Intercept) 1.562    1.25
## Number of obs: 3413, groups:  maebSPP$vilfac, 210
##
## Fixed effects:
##                              Estimate Std. Error z value Pr(>|z|)
## (Intercept)                 -1.184648   0.258502  -4.583 4.59e-06 ***
## maebSPP$fac_eb1              0.445883   0.115941   3.846 0.000120 ***
## maebSPP$fac_occupYEShunter   0.275499   0.151067   1.824 0.068200 .
## maebSPP$fac_age30 to 45     -0.273700   0.138682  -1.974 0.048430 *
## maebSPP$fac_age45 to 60     -0.494586   0.135920  -3.639 0.000274 ***
## maebSPP$fac_age60 and over  -0.474139   0.142744  -3.322 0.000895 ***
## maebSPP$fac_sexMasculin      0.227580   0.090984   2.501 0.012373 *
## maebSPP$fac_ecosysYESforest  1.091511   0.244032   4.473 7.72e-06 ***
## maebSPP$Pop_Density_Dept     0.009126   0.014586   0.626 0.531518
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##               (Intr) mSPP$_1 mbSPP$fc_ccYES mSPPt4 mSPPt6 mSPPao mSPP$_M
## mbSPP$fc_b1    -0.027
## mbSPP$fc_ccYES -0.043 -0.006
## mSPP$_30t45    -0.353 -0.015  0.023
## mSPP$_45t60    -0.361  0.001  0.030          0.689
## mbSPP$_60ao    -0.347 -0.021  0.089          0.658  0.686
## mbSPP$fc_sM    -0.122 -0.034 -0.370         -0.039 -0.018 -0.090
## mbSPP$fc_csYES -0.748 -0.050  0.001         -0.002 -0.016 -0.002 -0.003
## mbSPP$P_D_D    -0.330  0.018  0.043         -0.001  0.001 -0.003  0.003
##               mbSPP$fc_csYES
## mbSPP$fc_b1
## mbSPP$fc_ccYES
## mSPP$_30t45
## mSPP$_45t60
## mbSPP$_60ao
## mbSPP$fc_sM
```

```
## mbSPP$fc_csYES
## mbSPP$P_D_D      0.020
```

```
drop1(modPf,test="Chisq")
```

```
## Single term deletions
##
## Model:
## maebSPP$Pfalci ~ maebSPP$fac_eb + maebSPP$fac_occup + maebSPP$fac_age +
##     maebSPP$fac_sex + maebSPP$fac_ecosys + maebSPP$Pop_Density_Dept +
##     (1 | maebSPP$vilfac)
##                          Df    AIC     LRT   Pr(Chi)
## <none>                      3966.8
## maebSPP$fac_eb            1 3979.5 14.6222 0.0001314 ***
## maebSPP$fac_occup         1 3968.1  3.2689 0.0706030 .
## maebSPP$fac_age           3 3976.6 15.7432 0.0012801 **
## maebSPP$fac_sex           1 3971.0  6.1472 0.0131624 *
## maebSPP$fac_ecosys        1 3984.2 19.3823  1.07e-05 ***
## maebSPP$Pop_Density_Dept  1 3965.2  0.3883 0.5332136
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
maebSPP<-subset(maeb,maeb$Pmalariae!="NA")
modPm<-glmer(maebSPP$Pmalariae~maebSPP$fac_eb+maebSPP$fac_occup+maebSPP$fac_ageclass+mae
bSPP$fac_sex+maebSPP$fac_ecosys+maebSPP$Pop_Density_Dept+(1|maebSPP$vilfac),family="bino
mial",control = glmerControl(optimizer = "bobyqa"))
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control
## $checkConv, : Model failed to converge with max|grad| = 0.10312 (tol =
## 0.001, component 1)
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, : Model
is nearly unidentifiable: very large eigenvalue
##  - Rescale variables?
```

```
summary(modPm)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula:
## maebSPP$Pmalariae ~ maebSPP$fac_eb + maebSPP$fac_occup + maebSPP$fac_ageclass +
##     maebSPP$fac_sex + maebSPP$fac_ecosys + maebSPP$Pop_Density_Dept +
##     (1 | maebSPP$vilfac)
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC   logLik deviance df.resid
##   2114.6   2175.9  -1047.3   2094.6     3403
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -0.9376 -0.3476 -0.2547 -0.1855  5.2660
##
## Random effects:
##  Groups          Name          Variance Std.Dev.
##  maebSPP$vilfac (Intercept) 0.768    0.8764
## Number of obs: 3413, groups:  maebSPP$vilfac, 210
##
## Fixed effects:
##                                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)                     -3.1123867  0.0007402   -4205   <2e-16 ***
## maebSPP$fac_eb1                  0.5786648  0.0007797     742   <2e-16 ***
## maebSPP$fac_occupYEShunter      -0.1842872  0.0007797    -236   <2e-16 ***
## maebSPP$fac_ageclass30 to 45    -0.3195321  0.0007398    -432   <2e-16 ***
## maebSPP$fac_ageclass45 to 60    -0.1999152  0.0007642    -262   <2e-16 ***
## maebSPP$fac_ageclass60 and over -0.5253952  0.0007797    -674   <2e-16 ***
## maebSPP$fac_sexMasculin          0.3733555  0.0007642     489   <2e-16 ***
## maebSPP$fac_ecosysYESforest      0.7559786  0.0007401    1021   <2e-16 ***
## maebSPP$Pop_Density_Dept         0.0072963  0.0007421      10   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) mSPP$_1 mbSPP$fc_ccYES mSPPt4 mSPPt6 mSPPao mSPP$_M
## mbSPP$fc_b1     0.000
## mbSPP$fc_ccYES  0.000 -0.200
## mSPP$_30t45     0.000  0.000   0.000
## mSPP$_45t60     0.000  0.000   0.000           0.000
## mbSPP$_60ao     0.000 -0.200  -0.200           0.000  0.000
## mbSPP$fc_sM     0.000  0.000   0.000           0.000 -0.250  0.000
## mbSPP$fc_csYES  0.001  0.000   0.000           0.000  0.000  0.000  0.000
## mbSPP$P_D_D     0.000  0.000   0.000           0.000  0.000  0.000  0.000
##              mbSPP$fc_csYES
## mbSPP$fc_b1
## mbSPP$fc_ccYES
## mSPP$_30t45
## mSPP$_45t60
## mbSPP$_60ao
## mbSPP$fc_sM
## mbSPP$fc_csYES
```

```
## mbSPP$P_D_D      0.000
## convergence code: 0
## Model failed to converge with max|grad| = 0.10312 (tol = 0.001, component 1)
## Model is nearly unidentifiable: very large eigenvalue
##  - Rescale variables?
```

```
drop1(modPm,test="Chisq")
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, : Model
failed to converge with max|grad| = 0.0980374 (tol = 0.001, component 1)

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, : Model
is nearly unidentifiable: very large eigenvalue
##  - Rescale variables?
```

```
## Single term deletions
##
## Model:
## maebSPP$Pmalariae ~ maebSPP$fac_eb + maebSPP$fac_occup + maebSPP$fac_ageclass +
##     maebSPP$fac_sex + maebSPP$fac_ecosys + maebSPP$Pop_Density_Dept +
##     (1 | maebSPP$vilfac)
##                         Df    AIC     LRT    Pr(Chi)
## <none>                      2114.6
## maebSPP$fac_eb           1 2128.4 15.8425 6.884e-05 ***
## maebSPP$fac_occup        1 2112.5 -0.0209  1.000000
## maebSPP$fac_ageclass     3 2116.1  7.4875  0.057881 .
## maebSPP$fac_sex          1 2120.8  8.1961  0.004198 **
## maebSPP$fac_ecosys       1 2123.2 10.6485  0.001102 **
## maebSPP$Pop_Density_Dept 1 2112.6  0.0475  0.827392
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
maebSPP<-subset(maeb,maeb$Povale!="NA")
modPo<-glmer(maebSPP$Povale~maebSPP$fac_eb+maebSPP$fac_occup+maebSPP$fac_age+maebSPP$fac
_sex+maebSPP$fac_ecosys+maebSPP$Pop_Density_Dept+(1|maebSPP$vilfac),family="binomial",co
ntrol = glmerControl(optimizer = "bobyqa"))
summary(modPo)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##    Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula:
## maebSPP$Povale ~ maebSPP$fac_eb + maebSPP$fac_occup + maebSPP$fac_age +
##      maebSPP$fac_sex + maebSPP$fac_ecosys + maebSPP$Pop_Density_Dept +
##      (1 | maebSPP$vilfac)
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC   logLik deviance df.resid
##    390.4    451.8   -185.2    370.4     3403
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -0.4536 -0.0774 -0.0605 -0.0465 16.9265
##
## Random effects:
##  Groups          Name        Variance Std.Dev.
##  maebSPP$vilfac (Intercept) 2.046    1.43
## Number of obs: 3413, groups:  maebSPP$vilfac, 210
##
## Fixed effects:
##                             Estimate Std. Error z value Pr(>|z|)
## (Intercept)                 -6.17338    0.88927  -6.942 3.86e-12 ***
## maebSPP$fac_eb1             -0.03625    0.46888  -0.077    0.938
## maebSPP$fac_occupYEShunter  -0.93635    0.78425  -1.194    0.233
## maebSPP$fac_age30 to 45     -0.93246    0.58053  -1.606    0.108
## maebSPP$fac_age45 to 60     -0.40875    0.49579  -0.824    0.410
## maebSPP$fac_age60 and over  -0.52850    0.53694  -0.984    0.325
## maebSPP$fac_sexMasculin      0.43000    0.36542   1.177    0.239
## maebSPP$fac_ecosysYESforest  1.03068    0.70187   1.468    0.142
## maebSPP$Pop_Density_Dept     0.03081    0.03016   1.021    0.307
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##               (Intr) mSPP$_1 mbSPP$fc_ccYES mSPPt4 mSPPt6 mSPPao mSPP$_M
## mbSPP$fc_b1     0.008
## mbSPP$fc_ccYES -0.027 -0.038
## mSPP$_30t45    -0.296 -0.012   0.039
## mSPP$_45t60    -0.333  0.003   0.061          0.570
## mbSPP$_60ao    -0.337 -0.027   0.095          0.529  0.618
## mbSPP$fc_sM    -0.151 -0.055  -0.239         -0.049 -0.034 -0.120
## mbSPP$fc_csYES -0.703 -0.071  -0.003          0.000 -0.024 -0.004 -0.004
## mbSPP$P_D_D    -0.287  0.020   0.072          0.002  0.010  0.007 -0.010
##               mbSPP$fc_csYES
## mbSPP$fc_b1
## mbSPP$fc_ccYES
## mSPP$_30t45
## mSPP$_45t60
## mbSPP$_60ao
## mbSPP$fc_sM
```

```
## mbSPP$fc_csYES
## mbSPP$P_D_D      0.060
```

```
drop1(modPo,test="Chisq")
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control
## $checkConv, : unable to evaluate scaled gradient
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control
## $checkConv, : Model failed to converge: degenerate Hessian with 1 negative
## eigenvalues
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control
## $checkConv, : Model failed to converge with max|grad| = 0.0599014 (tol =
## 0.001, component 1)
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, : Model
## is nearly unidentifiable: very large eigenvalue
##  - Rescale variables?
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control
## $checkConv, : Model failed to converge with max|grad| = 0.054477 (tol =
## 0.001, component 1)
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, : Model
## is nearly unidentifiable: very large eigenvalue
##  - Rescale variables?
```

```
## Single term deletions
##
## Model:
## maebSPP$Povale ~ maebSPP$fac_eb + maebSPP$fac_occup + maebSPP$fac_age +
##     maebSPP$fac_sex + maebSPP$fac_ecosys + maebSPP$Pop_Density_Dept +
##     (1 | maebSPP$vilfac)
##                            Df    AIC     LRT  Pr(Chi)
## <none>                        390.41
## maebSPP$fac_eb             1 388.42 0.00600  0.9383
## maebSPP$fac_occup          1 390.20 1.78746  0.1812
## maebSPP$fac_age            3 387.09 2.67305  0.4448
## maebSPP$fac_sex            1 389.78 1.36565  0.2426
## maebSPP$fac_ecosys         1 390.89 2.48200  0.1152
## maebSPP$Pop_Density_Dept  1 389.40 0.98422  0.3212
```