

Supplementary Material R code and Output

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```
{r setup, include=FALSE}
knitr::opts_chunk$set(echo = TRUE)
options(width=60)

#Supplementary Material

library(dirmult)
library(MASS)
library(AICcmodavg)
library(glmTMB)

#DALY Estimates

cases<-c(30, 35,32,26,24,12)
incidence<-rdirichlet(n=10000, alpha=cases)
pr<-rgamma(10000, 159, 5)
cases<-incidence*pr
View(cases)
quantile(cases[,1], c(0.025, 0.5, 0.975))

##      2.5%      50%      97.5%
## 4.063168 5.912168 8.313809

cases1<-cases*0.02
lexp<-c(75.09,65.14,55.235,45.385,35.715,17.705)
ylls<-lexp*cases1
ylls1<-rowSums(ylls)
quantile(ylls1, c(0.025, 0.5, 0.975))

##      2.5%      50%      97.5%
## 23.07678 30.99971 40.38210

yldliv<-0.78*2*rnorm(1,0.123,.02)*cases
yldpul<-0.13*2*rnorm(1,0.192, 0.032)*cases
yldcns<-0.07*2*rnorm(1, 0.221,0.04) *cases
ylds<-yldliv+yldpul+yldcns
DALYs<-ylds+ylls
DALYs1<-rowSums(DALYs)
quantile(DALYs1, c(0.025,0.5,0.975))

##      2.5%      50%      97.5%
## 31.86401 40.81948 51.36159

#For untreated cases
untreatedDALYs<-pr*100*rnorm( 1, 0.012, 0.001)
quantile(untreatedDALYs, c(0.026,0.5,0.975))
```

```
##      2.6%      50%      97.5%
## 29.72457 34.78164 40.63422
```

```
#Total DALYs
DALYs2<-DALYs1+untreatedDALYs
quantile(DALYs2, c(0.025,0.5,0.975))
```

```
##      2.5%      50%      97.5%
## 62.43830 75.70175 90.82092
```

```
#per 100,000
DALYs3<-DALYs2*100000/782455
quantile(DALYs3, c(0.025,0.5,0.975))
```

```
##      2.5%      50%      97.5%
## 7.979795 9.674901 11.607175
```

```
library(readxl)
# Read in data from excel file
bhu <- read_excel("bhu.xlsx", sheet = "Sheet1")
```

```
# data
bhu
```

```
## # A tibble: 6 x 9
##   district      cases  pop Cattle  Dogs  Yaks  Sheep  Goats  area
##   <chr>      <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 Bumthang      36 17820 11311 1017 3917 127    9 2717
## 2 Punakha      16 28750 11045 1394 0    146 208 1110
## 3 Trongsa       6 19960 11583 544 226 132 92 1807
## 4 Zhemgang5    1 17763 12110 581 0    0    37 2421
## 5 WangduePhodrang 32 42186 23306 1152 4115 948 88 4308
## 6 Gasa         1 3952 1163 193 6527 0    2 3118
```

```
#Forward selection Poisson regression
#data is overdispersed so generalized poisson model is used.
#Controlled for population size (offset variable)
res<-glmmTMB(cases~I(Cattle/area)+offset(log(pop)),
             family=genpois, data=bhu)
```

```
## Warning in (function (start, objective, gradient = NULL, hessian = NULL, : NA/
## NaN function evaluation
```

```
AICc(res)
```

```
## [1] 59.16588
```

```
#AICc=59.2
```

```
res<-glmmTMB(cases~I(Yaks/area)+offset(log(pop)),
             family=genpois, data=bhu)
#Yak density p=0.0519, so retained in model
AICc(res)
```

```
## [1] 56.28484
```

```
#AICc=56.3
```

```
res<-glmmTMB(cases~I(Yaks/area)+I(Dogs/area)+offset(log(pop)),
             family=genpois, data=bhu)
```

```

# Yak density and dog density retained
AICc(res)

## [1] 84.09494
# AICc = 84.1

res<-glmmTMB(cases~I(Yaks/area)+I(Dogs/area)+I(Sheep/area)+offset(log(pop)),
             family=genpois, data=bhu)
# Sheep density removed from model
AICc(res)

## [1] Inf
# overfitted; AICc inf

res<-glmmTMB(cases~I(Dogs/area)+offset(log(pop)),family=genpois, data=bhu)
AICc(res)

## [1] 59.09987
# Dog densisty
# AICc = 59.1

res<-glmmTMB(cases~I(Yaks/area)+I(Dogs/area)+I(Goats/area)+offset(log(pop)),
             family=genpois, data=bhu)
AICc(res)

## [1] Inf
#over fitted, AICc inf

res<-glmmTMB(cases~offset(log(pop)),family=genpois, data=bhu)

## Warning in (function (start, objective, gradient = NULL, hessian = NULL, : NA/
## NaN function evaluation

## Warning in (function (start, objective, gradient = NULL, hessian = NULL, : NA/
## NaN function evaluation

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## NaN function evaluation

## Warning in (function (start, objective, gradient = NULL, hessian = NULL, : NA/
## NaN function evaluation

AICc(res)

## [1] 49.19919
# null model
# AICc=49.2

```

```

res<-glmmTMB(cases~I(Sheep/area)+offset(log(pop)),
             family=genpois, data=bhu)

## Warning in (function (start, objective, gradient = NULL, hessian = NULL, : NA/
## NaN function evaluation
AICc(res)

## [1] 58.24506
# model sheep only
#AICc = 58.24506

# All models with covariates had a higher AICc than null model,
#which suggests that there is insufficient evidence to conclude
#that density of livestock or dogs is associated with the incidence of echinococcosis.

#Likewise using the negative binomial model as alternative overdispersed model

# null model
res<-glm.nb(cases~offset(log(pop)), data=bhu)
AICc(res)

## [1] 50.08705
summary(res)

##
## Call:
## glm.nb(formula = cases ~ offset(log(pop)), data = bhu, init.theta = 1.269242805,
## link = log)
##
## Coefficients:
## Estimate Std. Error z value Pr(>|z|)
## (Intercept) -7.3013 0.3857 -18.93 <2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(1.2692) family taken to be 1)
##
## Null deviance: 6.3245 on 5 degrees of freedom
## Residual deviance: 6.3245 on 5 degrees of freedom
## AIC: 46.087
##
## Number of Fisher Scoring iterations: 1
##
##
## Theta: 1.269
## Std. Err.: 0.799
##
## 2 x log-likelihood: -42.087
#lowest AICc
#Conclude no significant explanatory variables

# dogs
res<-glm.nb(cases~I(Dogs/area)+(offset(log(pop))), data=bhu)

```

```
AICc(res)
```

```
## [1] 60.05561
```

```
summary(res)
```

```
##
## Call:
## glm.nb(formula = cases ~ I(Dogs/area) + (offset(log(pop))), data = bhu,
##       init.theta = 1.270574786, link = log)
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -7.3913      0.5794 -12.756  <2e-16 ***
## I(Dogs/area)   0.2050      0.9851   0.208   0.835
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(1.2706) family taken to be 1)
##
## Null deviance: 6.3300 on 5 degrees of freedom
## Residual deviance: 6.2986 on 4 degrees of freedom
## AIC: 48.056
##
## Number of Fisher Scoring iterations: 1
##
##              Theta:  1.271
##             Std. Err.: 0.798
##
## 2 x log-likelihood:  -42.056
```

```
#etc with other animal species.
```

```
#Alternatively random effects model with district as the random effect.
```

```
#Models overdispersion by the random effect
```

```
res<-glmmTMB(cases~I(Dogs/area)+(offset(log(pop))+(1|district)),
             poisson, data=bhu)
```

```
summary(res)
```

```
## Family: poisson ( log )
## Formula:      cases ~ I(Dogs/area) + (offset(log(pop)) + (1 | district))
## Data: bhu
##
##      AIC      BIC  logLik deviance df.resid
##    47.9    47.3   -20.9    41.9        3
##
## Random effects:
##
## Conditional model:
##   Groups   Name      Variance Std.Dev.
## district (Intercept) 0.8742   0.935
## Number of obs: 6, groups: district, 6
##
## Conditional model:
```

```
##           Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -7.9601    0.6695 -11.890  <2e-16 ***
## I(Dogs/area)  0.5553    1.0786   0.515   0.607
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
AICc(res)
```

```
## [1] 59.89844
```

```
res<-glmmTMB(cases~I(Yaks/area)+(offset(log(pop))+(1|district)),
             poisson, data=bhu)
```

```
summary(res)
```

```
## Family: poisson ( log )
## Formula:          cases ~ I(Yaks/area) + (offset(log(pop)) + (1 | district))
## Data: bhu
##
##           AIC          BIC    logLik deviance df.resid
##          46.7          46.1    -20.4    40.7         3
##
## Random effects:
##
## Conditional model:
## Groups   Name          Variance Std.Dev.
## district (Intercept) 0.5251   0.7246
## Number of obs: 6, groups: district, 6
##
## Conditional model:
##           Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -8.1010    0.4866 -16.649  <2e-16 ***
## I(Yaks/area)  0.6379    0.4553   1.401   0.161
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
AICc(res)
```

```
## [1] 58.71032
```

```
res<-glmmTMB(cases~I(Cattle/area)+(offset(log(pop))+(1|district)),
             poisson, data=bhu)
```

```
summary(res)
```

```
## Family: poisson ( log )
## Formula:          cases ~ I(Cattle/area) + (offset(log(pop)) + (1 | district))
## Data: bhu
##
##           AIC          BIC    logLik deviance df.resid
##          48.1          47.5    -21.1    42.1         3
##
## Random effects:
##
## Conditional model:
## Groups   Name          Variance Std.Dev.
## district (Intercept) 0.8975   0.9473
## Number of obs: 6, groups: district, 6
##
```

```
## Conditional model:
##           Estimate Std. Error z value Pr(>|z|)
## (Intercept) -7.89546    1.02968  -7.668 1.75e-14 ***
## I(Cattle/area) 0.03311    0.16295   0.203  0.839
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
AICc(res)
```

```
## [1] 60.12713
```

```
res<-glmmTMB(cases~I(Sheep/area)+(offset(log(pop))+(1|district)),
             poisson, data=bhu)
summary(res)
```

```
## Family: poisson ( log )
## Formula:          cases ~ I(Sheep/area) + (offset(log(pop)) + (1 | district))
## Data: bhu
##
##           AIC          BIC    logLik deviance df.resid
##          47.1          46.4    -20.5     41.1         3
##
## Random effects:
##
## Conditional model:
## Groups Name          Variance Std.Dev.
## district (Intercept) 0.8004   0.8946
## Number of obs: 6, groups: district, 6
##
## Conditional model:
##           Estimate Std. Error z value Pr(>|z|)
## (Intercept) -8.2061    0.6654 -12.333 <2e-16 ***
## I(Sheep/area)  5.6092    5.4152   1.036   0.3
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
AICc(res)
```

```
## [1] 59.0517
```

```
res<-glmmTMB(cases~I(Goats/area)+(offset(log(pop))+(1|district)),
             poisson, data=bhu)
summary(res)
```

```
## Family: poisson ( log )
## Formula:          cases ~ I(Goats/area) + (offset(log(pop)) + (1 | district))
## Data: bhu
##
##           AIC          BIC    logLik deviance df.resid
##          48.2          47.5    -21.1     42.2         3
##
## Random effects:
##
## Conditional model:
## Groups Name          Variance Std.Dev.
## district (Intercept) 0.8875   0.9421
## Number of obs: 6, groups: district, 6
```

```

##
## Conditional model:
##           Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -7.7237    0.5540 -13.942  <2e-16 ***
## I(Goats/area)  0.2979    6.3244  0.047   0.962
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

AICc(res)

## [1] 60.16706

res<-glmmTMB(cases~I(Goats/area)+(offset(log(pop))+(1|district)),
             poisson, data=bhu)
summary(res)

## Family: poisson ( log )
## Formula:         cases ~ I(Goats/area) + (offset(log(pop)) + (1 | district))
## Data: bhu
##
##           AIC      BIC   logLik deviance df.resid
##          48.2    47.5   -21.1    42.2        3
##
## Random effects:
##
## Conditional model:
## Groups Name      Variance Std.Dev.
## district (Intercept) 0.8875  0.9421
## Number of obs: 6, groups: district, 6
##
## Conditional model:
##           Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -7.7237    0.5540 -13.942  <2e-16 ***
## I(Goats/area)  0.2979    6.3244  0.047   0.962
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

AICc(res)

## [1] 60.16706

# Null random effects model with intercept only
res<-glmmTMB(cases~(offset(log(pop))+(1|district)),
             poisson, data=bhu)
AICc(res)

## [1] 50.16929

#lowest AICc
#Conclude no significant explanatory variables

```