S2 Appendix

R code for meta-analysis

# Packages

library(meta)

# Set the working directory

setwd("C://R//meta\_analysis//")

# Import data from .csv

meta\_data<-read.csv("GLM\_data\_for\_meta-analysis\_04Aug2016.csv")

# Subset data table to run a single subset of the studies to be used

sub <- meta\_data[meta\_data$Main\_category == "AbioticCascadingEcological\_process",]

# Runs a meta-analysis using the metacont function with pooled variance and Cohen's d

meta <- metacont(sub$Exp\_n, # Number of observations in experimental group.

sub$Exp\_mean, # Estimated mean in experimental group.

sub$Exp\_SD, # Standard deviation in experimental group.

sub$Control\_n, # Number of observations in control group.

sub$Control\_mean, # Estimated mean in control group.

sub$Control\_SD, # Standard deviation in control group.

studlab = sub$Study\_name , # An optional vector with study labels.

data=sub,

comb.fixed = T , # A logical indicating whether a random effects meta-analysis

sm="SMD", # Which summary measure is to be used for pooling of studies

pooledvar=TRUE , # Pooled variance should be used for the mean difference?

method.smd="Cohen") # Which method is used to estimate the standardised

mean difference

R code for the generalised linear mixed effects models

# Packages

library(MuMIn)

library(lme4)

# Directories for input and output

setwd("C:/R/meta\_analysis/glm/")

# Read in the data

dat <- read.csv(file = "GLM\_data\_for\_meta-analysis\_04Aug2016.csv", header=T)

# Subset the data to select “Direct”

subset\_dat<-dat[dat$Direct\_or\_cascading == "Direct",]

# Attach data

attach(subset\_dat)

# GLMM

glmmFULL<-glmer(Elephant\_effect~ Elephant\_density +

Tree\_cover + MAP + Exclosure\_duration + Management\_intervention + EVI +

(1|Study\_ID)

, family=gaussian, data=subset\_dat, na.action = na.fail)

# Model Summary

summary(glmmFULL)

# Model selection

model\_selection\_table <- dredge(glmmFULL,rank="AIC")