

## Preamble

### Packages

```
library(arm) # standardize()
library(MuMIn) # r.squared.GLMM()
library(dplyr) # filter()
library(ggplot2) # ggplot()
library(usdm) # vif()
library(qpcR) # akaike.weights()
library(lme4) # lmer(), glmer(), glmer.nb()
```

### Loading data

```
#Set working directory
setwd("~/Dropbox/University Work/Year 4 Sem 2/Dissertation/Write Up/Data/R")
#Load raw data
RAW <- read.csv("R_seedlings.csv", header=TRUE, sep=",")
#Remove NA values from columns of interest
Seedlings <- RAW %>%
  filter(Comp.Y.N. == "Y") %>%
  filter(!is.na(LAI.4.ring)) %>%
  filter(!is.na(Comp.seed.total)) %>%
  filter(!is.na(Comp.adult.log.metric)) %>%
  filter(!is.na(Elevation)) %>%
  filter(!is.na(Species))
```

## Single fixed effect models

### Determination of random effects structure

The procedure below is conducted for all combinations of singular plant traits (response) and competition variables/elevation (fixed effect), resulting in 24 random intercept models and 24 random slope models, each with a unique response-fixed effect combination.

```
# Random intercept model
stdz.mod_fvfm_elev_ri <- standardize(lmer(D.FvFm ~ Elevation +
  (1 | Species) + (1 | Site), data = Seedlings, REML = F),
  standardize.y = T)
# Random slope model equivalent
stdz.mod_fvfm_elev_rs <- standardize(lmer(D.FvFm ~ Elevation +
  (Elevation | Species) + (1 | Site), data = Seedlings, REML = F),
  standardize.y = T)
```

For each response-fixed effect combination,  $\Delta AIC_{rsri}$  (daic\_rsri) values are assessed to determine whether a random intercept or random slope model is of better quality.

```
daic_rsri <- AIC(stdz.mod_fvfm_elev_rs) - AIC(stdz.mod_fvfm_elev_ri)
```

## Reporting the best single fixed effect models

The  $\Delta AIC_r$  (daic1),  $R_M^2$  (rm1),  $R_C^2$  (rc1), slope (slope1) and standard error of the slope estimate (se1) was calculated for the best models (random slope or random intercept) to assess model quality.  $\Delta AIC_r$  is calculated as the AIC difference between a random effects model and the model in question

```
# Random effects model
stdz.mod_fvfm_null <- standardize(lmer(D.FvFm ~ (1 | Species) +
  (1 | Site), data = Seedlings), standardize.y = T)
# Delta AIC
daic1 <- AIC(stdz.mod_fvfm_null) - AIC(stdz.mod_fvfm_elev_ri)
# pseudo-r-squared
r1 <- unname(r.squaredGLMM(stdz.mod_fvfm_elev_ri))
# Variance explained by fixed effects
rm1 <- r1[1]
# Variance explained by whole model
rc1 <- r1[2]
# Slope estimate
slope1 <- unname(coef(summary(stdz.mod_fvfm_elev_ri))[, "Estimate"])
# Slope estimate standard error
se1 <- sqrt(diag(vcov(stdz.mod_fvfm_elev_ri)))
```

## Multiple fixed effect models

### Variance inflation factors

```
VIF <- data.frame(vif(dplyr::select(Seedlings, LAI.4.ring, Comp.seed.total,
  Comp.adult.log.metric, Elevation)))
```

### Model comparison

Model comparison was conducted for each plant trait. Models with different fixed effect combinations were compared using AIC and  $R_C^2$  (Appendix IV).

```
# All fixed effects
stdz.mod_fvfm_full <- standardize(lmer(D.FvFm ~ LAI.4.ring +
  Comp.seed.total + Comp.adult.log.metric + Elevation + (1 |
  Species) + (1 | Site), data = Seedlings, REML = F), standardize.y = T)
# -Elevation
stdz.mod_fvfm_lai_seed_isi <- standardize(lmer(D.FvFm ~ LAI.4.ring +
  Comp.seed.total + Comp.adult.log.metric + (1 | Species) +
  (1 | Site), data = Seedlings, REML = F), standardize.y = T)
# -ISI
stdz.mod_fvfm_lai_seed_elev <- standardize(lmer(D.FvFm ~ LAI.4.ring +
  Comp.seed.total + Elevation + (1 | Species) + (1 | Site),
  data = Seedlings, REML = F), standardize.y = T)
# -Herbaceous plant abundance
stdz.mod_fvfm_lai_isi_elev <- standardize(lmer(D.FvFm ~ LAI.4.ring +
  Comp.adult.log.metric + Elevation + (1 | Species) + (1 |
  Site), data = Seedlings, REML = F), standardize.y = T)
# -LAI
stdz.mod_fvfm_seed_isi_elev <- standardize(lmer(D.FvFm ~ Comp.seed.total +
  Comp.adult.log.metric + Elevation + (1 | Species) + (1 |
  Site), data = Seedlings, REML = F), standardize.y = T)
```

```

# Elevation + random effects
stdz.mod_fvfm_elev_ri <- standardize(lmer(D.FvFm ~ Elevation +
  (1 | Species) + (1 | Site), data = Seedlings, REML = F),
  standardize.y = T)
# LAI + random effects
stdz.mod_fvfm_lai_ri <- standardize(lmer(D.FvFm ~ LAI.4.ring +
  (1 | Species) + (1 | Site), data = Seedlings, REML = F),
  standardize.y = T)
# ISI + random effects
stdz.mod_fvfm_isi_ri <- standardize(lmer(D.FvFm ~ Comp.adult.log.metric +
  (1 | Species) + (1 | Site), data = Seedlings, REML = F),
  standardize.y = T)
# Herbaceous plant abundance + random effects
stdz.mod_fvfm_seed_ri <- standardize(lmer(D.FvFm ~ Comp.seed.total +
  (1 | Species) + (1 | Site), data = Seedlings, REML = F),
  standardize.y = T)
# Random effects + random effects
stdz.mod_fvfm_rand <- standardize(lmer(D.FvFm ~ (1 | Species) +
  (1 | Site), data = Seedlings, REML = F), standardize.y = T)

# Example of model using random slope terms for some fixed
# effects
stdz.mod_area_int <- standardize(lmer(Leaf.area ~ LAI.4.ring +
  Comp.seed.total + Comp.adult.log.metric + Elevation + (1 +
  LAI.4.ring + Comp.seed.total + Elevation | Species) + (1 |
  Site), data = R_seedlings_D.FvFm, REML = F), standardize.y = T)

```

## Reporting the best multiple fixed effect models

The  $\Delta AIC_r$  (daic2), Akaike weight ( $W_i$ ),  $R_C^2$  (rc2),  $R_M^2$  (rm2), slope of each fixed effect (slope2) and standard error (se2) of each slope estimate was calculated to assess model quality.

```

# Random effects model
stdz.mod_fvfm_null <- standardize(lmer(D.FvFm ~ (1 | Species) +
  (1 | Site), data = Seedlings), standardize.y = T)
# Delta AIC
daic2 <- AIC(stdz.mod_fvfm_null) - AIC(stdz.mod_fvfm_lai_isi_elev)
# Dataframe of model iterations with AIC values for Akaike
# weights
stdz.mod_fvfm_aic <- c(AIC(stdz.mod_fvfm_full), AIC(stdz.mod_fvfm_lai_seed_isi),
  AIC(stdz.mod_fvfm_lai_seed_elev), AIC(stdz.mod_fvfm_lai_isi_elev),
  AIC(stdz.mod_fvfm_seed_isi_elev), AIC(stdz.mod_fvfm_rand),
  AIC(stdz.mod_fvfm_elev_ri), AIC(stdz.mod_fvfm_lai_ri), AIC(stdz.mod_fvfm_isi_ri),
  AIC(stdz.mod_fvfm_seed_ri))
stdz.mod_fvfm_model_name <- c("stdz.mod_fvfm_full", "stdz.mod_fvfm_lai_seed_isi",
  "stdz.mod_fvfm_lai_seed_elev", "stdz.mod_fvfm_lai_isi_elev",
  "stdz.mod_fvfm_seed_isi_elev", "stdz.mod_fvfm_rand", "stdz.mod_fvfm_elev_ri",
  "stdz.mod_fvfm_lai_ri", "stdz.mod_fvfm_isi_ri", "stdz.mod_fvfm_seed_ri")
stdz.mod_fvfm_aic <- data.frame(stdz.mod_fvfm_model_name, stdz.mod_fvfm_aic)
# Akaike weights
stdz.mod_fvfm_wi <- akaike.weights(stdz.mod_fvfm_aic$stdz.mod_fvfm_aic)
# pseudo-r-squared
r2 <- unname(r.squaredGLMM(stdz.mod_fvfm_lai_isi_elev))
# Variance explained by fixed effects
rm2 <- r2[1]
# Variance explained by whole model

```

```
rc2 <- r2[2]
# Slope estimate
slope2 <- unname(coef(summary(stdz.mod_fvfm_lai_isi_elev))[,
  "Estimate"])
# Slope estimate standard error
se2 <- sqrt(diag(vcov(stdz.mod_fvfm_lai_isi_elev)))
```

## Variation among species in plant trait-elevation relationship

The procedure below was conducted for each plant trait.

```
# linear mixed model
All_fvfm_lmer_rs <- lmer(D.FvFm ~ Elevation + (Elevation | Species) +
  (1 | Site), data = Seedlings, REML = F)

# Scatter plot of trait-elevation relationship with linear
# regressions for each species
ALL_fvfm_scatter <- ggplot(Seedlings, aes(x = Elevation, y = D.FvFm)) +
  geom_smooth(aes(fill = Species, colour = Species), method = lm,
    se = T) + geom_point(aes(colour = Species), alpha = 0.5)

# Interval plot of slope estimates for trait-elevation
# relationship Slope estimate for each species
fvfm1 <- unname(coef(lm(D.FvFm ~ Elevation, data = subset(Seedlings,
  Species == "AV"))))
# Combining slope estimates into a list
fvfm_slope <- c(fvfm1[2], fvfm2[2], fvfm3[2], fvfm4[2], fvfm5[2],
  fvfm6[2], fvfm7[2], fvfm8[2], fvfm9[2])
# Slope standard error estimates for each species
fvfme1 <- unname(sqrt(diag(vcov(lm(D.FvFm ~ Elevation, data = subset(Seedlings,
  Species == "AV"))))))
# Combining slope estimates into a list
fvfm_se <- c(fvfme1[2], fvfme2[2], fvfme3[2], fvfme4[2], fvfme5[2],
  fvfme6[2], fvfme7[2], fvfme8[2], fvfme9[2])
# Creating a dataframe of slope estimates of standard errors
# for all species
species <- c("AV", "CR", "CT", "DL", "HG", "ID", "MS", "SP",
  "TG")
fvfm_slope <- data.frame(species, fvfm_slope, fvfm_se)

# Interval plot of slope estimates
fvfm <- ggplot(fvfm_slope, aes(x = species)) + geom_point(aes(y = fvfm_slope,
  colour = species), size = 2) + geom_errorbar(aes(ymin = fvfm_slope -
  fvfm_se, ymax = fvfm_slope + fvfm_se, colour = species),
  width = 1) + geom_hline(aes(yintercept = 0), linetype = 5)
```

## Relationship between competition/abiotic environmental variables and elevation

The procedure below was conducted for each competition/abiotic environmental variable.

```
# Linear mixed model
LAI4ring_vs_elev_lmer <- lmer(LAI.4.ring ~ Elevation + (1 | Site),
  data = Seedlings, REML = F)
```

Generalised linear mixed model forms assuming different distributions of herbaceous plant abundance data are compared.

```
# Poisson distribution
comp_seed_elev_glmr_pois <- glmer(Comp.seed.total ~ Elevation +
  (1 | Site), data = Seedlings, family = poisson, REML = F)

# Negative binomial distribution
comp_seed_elev_glmr_negbi <- glmer.nb(Comp.seed.total ~ Elevation +
  (1 | Site), data = Seedlings, REML = F)

# Comparison
summary(comp_seed_elev_glmr_negbi)
AIC(comp_seed_elev_glmr_negbi)
summary(comp_seed_elev_glmr_pois)
AIC(comp_seed_elev_glmr_pois)
```

Scatter plot of competition-elevation relationship with fixed effect regression line.

```
# Prediction grid for every combination of parameter values
LAI4ring_pred <- expand.grid(Elevation = c(seq(from = 378, to = 3224,
  by = 1)), Site = c("PA400", "PA800", "VC", "SP1500", "SP1750",
  "TRU08", "TRU07", "TRU06", "TRU04", "TRU02"), LAI.4.ring = 0)

# Model matrix
matrix_LAI4ring = model.matrix(terms(LAI4ring_vs_elev_lmer),
  data = LAI4ring_pred)
head(matrix_LAI4ring)

# Calculate predictions
LAI4ring_pred$LAI.4.ring = matrix_LAI4ring %*% fixef(LAI4ring_vs_elev_lmer)
head(LAI4ring_pred)

# Add variance term for each prediction
LAI4ring_var <- diag(matrix_LAI4ring %*% tcrossprod(vcov(LAI4ring_vs_elev_lmer),
  matrix_LAI4ring))

# Create combined data frame for scatter plot
LAI4ring_pred <- data.frame(LAI4ring_pred, plo = LAI4ring_pred$LAI.4.ring -
  2 * sqrt(LAI4ring_var), phi = LAI4ring_pred$LAI.4.ring +
  2 * sqrt(LAI4ring_var))

# Scatterplot
LAI4ring_elev <- ggplot(Seedlings, aes(x = Elevation, y = LAI.4.ring)) +
  geom_point(aes(colour = Site), alpha = 0.8) + layer(data = LAI4ring_pred,
  geom = "line", mapping = aes(x = Elevation, y = LAI.4.ring),
  stat = "identity", position = "identity", params = list(na.rm = F,
  alpha = 1, size = 1)) + layer(data = LAI4ring_pred, geom = "ribbon",
  mapping = aes(x = Elevation, ymin = plo, ymax = phi), stat = "identity",
  position = "identity", params = list(na.rm = F, alpha = 0.6))
```