

Verweis von Bosker & Snijder 2012

2. Analysis of colour morphs (Binomial mixed models)

```
# Clear memory
rm(list = ls())
# Read colour morph data (Binary, available for males only)

library(AzureML)
ws <- workspace()

Data <- download.datasets(
  dataset = ws,
  name     = "BeetlesMale.csv")



---


# Fit null model without fixed effects (but including all random effects)
m0 <- glmer(Colour ~ 1 + (1 | Population) + (1 | Container),
            family = "binomial", data = Data)
summary(m0)

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula: Colour ~ 1 + (1 | Population) + (1 | Container)
## Data: Data
##
##      AIC      BIC    logLik deviance df.resid
##    602.4    614.9   -298.2    596.4      477
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.5040 -0.7071 -0.3306  0.8486  3.0248
##
## Random effects:
## Groups      Name      Variance Std.Dev.
## Container (Intercept) 0.0000   0.0000
## Population (Intercept) 0.9458   0.9725
## Number of obs: 480, groups: Container, 60; Population, 12
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -0.3779     0.2997  -1.261   0.207



---


# Fit alternative model including fixed and all random effects
mF <- glmer(Colour ~ Treatment + Habitat + (1 | Population) + (1 | Container),
            family = "binomial", data = Data)
summary(mF)

## Generalized linear mixed model fit by maximum likelihood (Laplace
```

```

## Approximation) [glmerMod]
## Family: binomial (logit)
## Formula: Colour ~ Treatment + Habitat + (1 | Population) + (1 | Container)
## Data: Data
##
##      AIC      BIC    logLik deviance df.resid
##    573.1    594.0   -281.6    563.1     475
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.3762 -0.7204 -0.3274  0.7662  3.2282
##
## Random effects:
## Groups      Name      Variance Std.Dev.
## Container (Intercept) 0.005793 0.07611
## Population (Intercept) 1.110213 1.05367
## Number of obs: 480, groups: Container, 60; Population, 12
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -1.2511     0.3641  -3.436  0.00059 ***
## TreatmentExp    1.0118     0.2147   4.712 2.45e-06 ***
## HabitatB        0.6760     0.2118   3.192  0.00141 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) TrtmnE
## TreatmentExp -0.343
## HabitatB      -0.332  0.079

```

```

# Extraction of fitted value for the alternative model
# fixef() extracts coefficients for fixed effects
# mF@X returns fixed effect design matrix
Fixed <- fixef(mF)[2] * getME(mF,"X")[, 2] + fixef(mF)[3] * getME(mF,"X")[, 3]

fixef(mF)[2]

## TreatmentExp
##      1.011793

fixef(mF)[3]

## HabitatB
##      0.676039

```

```

# Calculation of the variance in fitted values
VarF <- var(Fixed)

VarF

## [1] 0.3709611

```

```
# An alternative way for getting the same result  
VarF <- var(as.vector(fixef(mF) %*% t(getME(mF, "X"))))
```

$$R_{\text{GLMM}(m)}^2 = \frac{\sigma_f^2}{\sigma_f^2 + \sum_{l=1}^u \sigma_l^2 + \sigma_e^2 + \sigma_d^2}, \quad \text{eqn 29}$$

Figure 1:

$$R_{\text{GLMM}(c)}^2 = \frac{\sigma_f^2 + \sum_{l=1}^u \sigma_l^2}{\sigma_f^2 + \sum_{l=1}^u \sigma_l^2 + \sigma_e^2 + \sigma_d^2}. \quad \text{eqn 30}$$

Figure 2:

```
# R2GLMM(m) - marginal R2GLMM
# see Equ. 29 and 30 and Table 2
VarF/(VarF + VarCorr(mF)$Container[1] + VarCorr(mF)$Population[1] + pi^2/3)
## [1] 0.07765834
```

```
VarCorr(mF)$Container[1]
## [1] 0.00579262
VarCorr(mF)$Population[1]
## [1] 1.110213
```

```
# R2GLMM(c) - conditional R2GLMM for full model
# Equ. XXX, XXX
(VarF + VarCorr(mF)$Container[1] + VarCorr(mF)$Population[1])/
  (VarF + VarCorr(mF)$Container[1] + VarCorr(mF)$Population[1] + pi^2/3)
## [1] 0.311287
```

Literatur

Nakagawa, Shinichi, Holger Schielzeth, and Robert B. O’Hara. 2013. “A General and Simple Method for Obtaining R2 from Generalized Linear Mixed-Effects Models.” *Methods in Ecology and Evolution* 4 (2): 133–42. doi:10.1111/j.2041-210x.2012.00261.x.

Binary and proportion data		
Link function	Logit link	Probit link
Distribution-specific variance	$\pi^2/3$	1
Model specification	$Y_{ijk} = \text{Binomial}(m_{ijk}, p_{ijk}),$ $\text{link}(p_{ijk}) = \beta_0 + \sum_{h=1}^p \beta_h x_{hijk} + \gamma_k + \alpha_{jk} + e_{ijk}$ $\gamma_k \sim \text{Gaussian}(0, \sigma_\gamma^2)$ $\alpha_{jk} \sim \text{Gaussian}(0, \sigma_\alpha^2)$ $e_{ijk} \sim \text{Gaussian}(0, \sigma_e^2)$	
Description	Y_{ijk} is the number of ‘successes’ in m_{ijk} trials by the j th individual in the k th group at the i th occasion (for binary data, m_{ijk} is 1), p_{ijk} is the underlying (latent) probability of success for the j th individual in the k th group at the i th occasion (for binary data, σ_e^2 is 0).	
Marginal R^2 ($R_{\text{GLMM}(m)}^2$)	$R_{\text{logit}(m)}^2 = \frac{\sigma_f^2}{\sigma_f^2 + \sigma_\gamma^2 + \sigma_\alpha^2 + \sigma_e^2 + \pi^2/3}$	$R_{\text{probit}(m)}^2 = \frac{\sigma_f^2}{\sigma_f^2 + \sigma_\gamma^2 + \sigma_\alpha^2 + \sigma_e^2 + 1}$
Conditional R^2 ($R_{\text{GLMM}(c)}^2$)	$R_{\text{logit}(c)}^2 = \frac{\sigma_f^2 + \sigma_\gamma^2 + \sigma_\alpha^2}{\sigma_f^2 + \sigma_\gamma^2 + \sigma_\alpha^2 + \sigma_e^2 + \pi^2/3}$	$R_{\text{probit}(c)}^2 = \frac{\sigma_f^2 + \sigma_\gamma^2 + \sigma_\alpha^2}{\sigma_f^2 + \sigma_\gamma^2 + \sigma_\alpha^2 + \sigma_e^2 + 1}$

Figure 3: