

# Models

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```
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
## v dplyr      1.1.4      v readr      2.1.5
## v forcats    1.0.0      v stringr   1.5.1
## v ggplot2    3.5.1      v tibble    3.2.1
## v lubridate  1.9.3      v tidyr     1.3.1
## v purrr      1.0.2
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()     masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```
library(readxl)
library(ggplot2)
library(emmeans)
```

```
## Welcome to emmeans.
## Caution: You lose important information if you filter this package's results.
## See '? untidy'
```

```
library(ordinal)
```

```
##
## Attaching package: 'ordinal'
##
## The following object is masked from 'package:dplyr':
##
##     slice
```

```
library(nlme)
```

```
##
## Attaching package: 'nlme'
##
## The following object is masked from 'package:dplyr':
##
##     collapse
```

```
library(glmmTMB)
library(brms)
```

```
## Loading required package: Rcpp
## Loading 'brms' package (version 2.22.0). Useful instructions
## can be found by typing help('brms'). A more detailed introduction
## to the package is available through vignette('brms_overview').
##
## Attaching package: 'brms'
##
## The following object is masked from 'package:glmmTMB':
##
##     lognormal
##
## The following object is masked from 'package:stats':
##
##     ar
```

```
library(multgee)
```

```
## Loading required package: gnm
```

```
library(lme4)
```

```
## Loading required package: Matrix
##
## Attaching package: 'Matrix'
##
## The following objects are masked from 'package:tidyr':
##
##     expand, pack, unpack
##
## Attaching package: 'lme4'
##
## The following object is masked from 'package:brms':
##
##     ngrps
##
## The following object is masked from 'package:nlme':
##
##     lmList
```

```
library(geepack)
```

## Purpose

This file will be used to compare different models for each CT feature

## Reading in Data

### Tree-in-bud

```
# Read in each rater's sheet
vh_tib <- read_excel('C:/Users/Eddie/OneDrive/Desktop/BIOSTAT/Thesis/Thesis/DataProcessed/2025.2.4.xlsx'
  mutate(rater = "VH")

jw_tib <- read_excel('C:/Users/Eddie/OneDrive/Desktop/BIOSTAT/Thesis/Thesis/DataProcessed/2025.2.4.xlsx'
  mutate(rater = "JW")

tib <- bind_rows(vh_tib, jw_tib)
```

### Large Nodules

```
# Read in each rater's sheet
vh_ln <- read_excel('C:/Users/Eddie/OneDrive/Desktop/BIOSTAT/Thesis/Thesis/DataProcessed/2025.2.4.xlsx'
  mutate(rater = "VH")

jw_ln <- read_excel('C:/Users/Eddie/OneDrive/Desktop/BIOSTAT/Thesis/Thesis/DataProcessed/2025.2.4.xlsx'
  mutate(rater = "JW")

ln <- bind_rows(vh_ln, jw_ln)
```

### Ground-glass Opacities

```
# Read in each rater's sheet
vh_ggo <- read_excel('C:/Users/Eddie/OneDrive/Desktop/BIOSTAT/Thesis/Thesis/DataProcessed/2025.2.4.xlsx'
  mutate(rater = "VH")

jw_ggo <- read_excel('C:/Users/Eddie/OneDrive/Desktop/BIOSTAT/Thesis/Thesis/DataProcessed/2025.2.4.xlsx'
  mutate(rater = "JW")

ggo <- bind_rows(vh_ggo, jw_ggo)
```

### Consolidations

```
# Read in each rater's sheet
vh_cons <- read_excel('C:/Users/Eddie/OneDrive/Desktop/BIOSTAT/Thesis/Thesis/DataProcessed/2025.2.4.xlsx'
  mutate(rater = "VH")

jw_cons <- read_excel('C:/Users/Eddie/OneDrive/Desktop/BIOSTAT/Thesis/Thesis/DataProcessed/2025.2.4.xlsx'
  mutate(rater = "JW")

cons <- bind_rows(vh_cons, jw_cons)
```

## Bronchiectasis

```
# Read in each rater's sheet
vh_branch <- read_excel('C:/Users/Eddie/OneDrive/Desktop/BIOSTAT/Thesis/Thesis/DataProcessed/2025.2.4.xls')
mutate(rater = "VH")

jw_branch <- read_excel('C:/Users/Eddie/OneDrive/Desktop/BIOSTAT/Thesis/Thesis/DataProcessed/2025.2.4.xls')
mutate(rater = "JW")

branch <- bind_rows(vh_branch, jw_branch)
```

## Atelectasis

```
# Read in each rater's sheet
vh_atel <- read_excel('C:/Users/Eddie/OneDrive/Desktop/BIOSTAT/Thesis/Thesis/DataProcessed/2025.2.4.xls')
mutate(rater = "VH")

jw_atel <- read_excel('C:/Users/Eddie/OneDrive/Desktop/BIOSTAT/Thesis/Thesis/DataProcessed/2025.2.4.xls')
mutate(rater = "JW")

atel <- bind_rows(vh_atel, jw_atel)
```

## Thin-wall Cavity

```
# Read in each rater's sheet
vh_thin <- read_excel('C:/Users/Eddie/OneDrive/Desktop/BIOSTAT/Thesis/Thesis/DataProcessed/2025.2.4.xls')
mutate(rater = "VH")

jw_thin <- read_excel('C:/Users/Eddie/OneDrive/Desktop/BIOSTAT/Thesis/Thesis/DataProcessed/2025.2.4.xls')
mutate(rater = "JW")

thin <- bind_rows(vh_thin, jw_thin)
```

## Thick-wall Cavity

```
# Read in each rater's sheet
vh_thick <- read_excel('C:/Users/Eddie/OneDrive/Desktop/BIOSTAT/Thesis/Thesis/DataProcessed/2025.2.4.xls')
mutate(rater = "VH")

jw_thick <- read_excel('C:/Users/Eddie/OneDrive/Desktop/BIOSTAT/Thesis/Thesis/DataProcessed/2025.2.4.xls')
mutate(rater = "JW")

thick <- bind_rows(vh_thick, jw_thick)
```

## Models

### Tree-in-bud

```
#make sure everything is in correct format
tib$Value <- ordered(tib$Value, levels = c(0,1,2,3))
tib$Attribute <- factor(tib$Attribute, levels = c("RUL", "RML", "RLL", "LUS", "LLS", "LLL"))
tib$newID <- factor(tib$newID)
tib$rater <- factor(tib$rater)

#model 1 - lobe and rater as fixed effects and random int
tib_mod1 <- clmm(
  Value ~ Attribute + rater + (1 | newID),
  data = tib
)

summary(tib_mod1)
```

```
## Cumulative Link Mixed Model fitted with the Laplace approximation
##
## formula: Value ~ Attribute + rater + (1 | newID)
## data:    tib
##
## link threshold nobs logLik   AIC      niter    max.grad cond.H
## logit flexible  1464 -1251.20 2522.41 830(5715) 2.28e-03 5.2e+01
##
## Random effects:
## Groups Name          Variance Std.Dev.
## newID (Intercept) 3.887      1.971
## Number of groups: newID 161
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## AttributeRML    0.2234     0.1988   1.123 0.261254
## AttributeRLL    0.5813     0.1970   2.950 0.003176 **
## AttributeLUS   -1.2542     0.2054  -6.108 1.01e-09 ***
## AttributeLLS   -0.2069     0.1985  -1.042 0.297183
## AttributeLLL    0.3660     0.1984   1.845 0.065020 .
## raterVH         0.5376     0.1389   3.871 0.000109 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Threshold coefficients:
##      Estimate Std. Error z value
## 0|1  -1.6399     0.2230  -7.355
## 1|2   2.5052     0.2334  10.732
## 2|3   5.3019     0.3038  17.450
```

```
#compute pairwise comparisons
emm <- emmeans(tib_mod1, ~ Attribute, type = "link")
pairs(emm)
```

```
## contrast estimate    SE df z.ratio p.value
```

```
## RUL - RML    -0.223 0.199 Inf  -1.123 0.8718
## RUL - RLL    -0.581 0.197 Inf  -2.950 0.0374
## RUL - LUS     1.254 0.205 Inf   6.108 <.0001
## RUL - LLS     0.207 0.198 Inf   1.042 0.9036
## RUL - LLL    -0.366 0.198 Inf  -1.845 0.4366
## RML - RLL    -0.358 0.198 Inf  -1.812 0.4580
## RML - LUS     1.478 0.208 Inf   7.099 <.0001
## RML - LLS     0.430 0.200 Inf   2.151 0.2612
## RML - LLL    -0.143 0.199 Inf  -0.716 0.9800
## RLL - LUS     1.836 0.209 Inf   8.792 <.0001
## RLL - LLS     0.788 0.199 Inf   3.966 0.0010
## RLL - LLL     0.215 0.196 Inf   1.097 0.8829
## LUS - LLS    -1.047 0.205 Inf  -5.110 <.0001
## LUS - LLL    -1.620 0.209 Inf  -7.761 <.0001
## LLS - LLL    -0.573 0.200 Inf  -2.867 0.0477
##
## Results are averaged over the levels of: rater
## P value adjustment: tukey method for comparing a family of 6 estimates
```

## Large Nodules

```
#make sure everything is in correct format
ln$Value <- as.numeric(as.character(ln$Value))
ln_clean <- ln %>% filter(Value %in% c(0, 1))
ln$Attribute <- factor(ln$Attribute, levels = c("RUL", "RML", "RLL", "LUS", "LLS", "LLL"))
ln$newID <- factor(ln$newID)
ln$rater <- factor(ln$rater)

#model 1 - lobe and rater as fixed effects and random int
ln_mod1 <- glmer(Value ~ Attribute + rater + (1 | newID),
  data = ln_clean,
  family = binomial(link = "logit"))
summary(ln_mod1)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula: Value ~ Attribute + rater + (1 | newID)
## Data: ln_clean
##
##      AIC      BIC   logLik deviance df.resid
##    851.7    894.0   -417.8   835.7     1454
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.4246 -0.2332 -0.1783 -0.0946  6.1055
##
## Random effects:
## Groups Name          Variance Std.Dev.
## newID (Intercept) 3.354      1.831
## Number of obs: 1462, groups: newID, 161
##
```

```
## Fixed effects:
##           Estimate Std. Error z value Pr(>|z|)
## (Intercept) -2.41194    0.30940  -7.796 6.41e-15 ***
## AttributeLLS -1.50418    0.36752  -4.093 4.26e-05 ***
## AttributeLUS -1.59640    0.37537  -4.253 2.11e-05 ***
## AttributeRLL -0.09297    0.29192   -0.318    0.750
## AttributeRML -1.50417    0.36752  -4.093 4.26e-05 ***
## AttributeRUL -0.17204    0.29343   -0.586    0.558
## raterVH      -0.23740    0.23577   -1.007    0.314
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##           (Intr) AttLLS AttLUS AttRLL AttRML AttRUL
## AttributLLS -0.299
## AttributLUS -0.289  0.332
## AttributRLL -0.457  0.388  0.380
## AttributRML -0.299  0.337  0.332  0.388
## AttributRUL -0.446  0.389  0.381  0.485  0.389
## raterVH      -0.193  0.010  0.011  0.007  0.010  0.002
```

```
#compute pairwise comparisons
emm <- emmeans(ln_mod1, ~ Attribute, type = "link")
pairs(emm)
```

```
## contrast estimate SE df z.ratio p.value
## LLL - LLS 1.50e+00 0.368 Inf 4.093 0.0006
## LLL - LUS 1.60e+00 0.375 Inf 4.253 0.0003
## LLL - RLL 9.30e-02 0.292 Inf 0.318 0.9996
## LLL - RML 1.50e+00 0.368 Inf 4.093 0.0006
## LLL - RUL 1.72e-01 0.293 Inf 0.586 0.9920
## LLS - LUS 9.22e-02 0.430 Inf 0.215 0.9999
## LLS - RLL -1.41e+00 0.370 Inf -3.813 0.0019
## LLS - RML -3.30e-06 0.423 Inf 0.000 1.0000
## LLS - RUL -1.33e+00 0.370 Inf -3.597 0.0044
## LUS - RLL -1.50e+00 0.378 Inf -3.979 0.0010
## LUS - RML -9.22e-02 0.430 Inf -0.215 0.9999
## LUS - RUL -1.42e+00 0.378 Inf -3.767 0.0023
## RLL - RML 1.41e+00 0.370 Inf 3.813 0.0019
## RLL - RUL 7.91e-02 0.297 Inf 0.266 0.9998
## RML - RUL -1.33e+00 0.370 Inf -3.596 0.0044
##
## Results are averaged over the levels of: rater
## Results are given on the log odds ratio (not the response) scale.
## P value adjustment: tukey method for comparing a family of 6 estimates
```

## Ground-glass Opacities

```
#make sure everything is in correct format
ggo$Value <- ordered(ggo$Value, levels = c(0,1,2,3))
ggo$Attribute <- factor(ggo$Attribute, levels = c("RUL", "RML", "RLL", "LUS", "LLS", "LLL"))
ggo$newID <- factor(ggo$newID)
```

```
ggo$rater <- factor(ggo$rater)
```

```
#model 1 - lobe and rater as fixed effects and random int
```

```
ggo_mod1 <- clmm(
  Value ~ Attribute + rater + (1 | newID),
  data = ggo
)
```

```
summary(ggo_mod1)
```

```
## Cumulative Link Mixed Model fitted with the Laplace approximation
```

```
##
```

```
## formula: Value ~ Attribute + rater + (1 | newID)
```

```
## data:      ggo
```

```
##
```

```
## link threshold nobs logLik AIC      niter      max.grad cond.H
```

```
## logit flexible 1463 -520.04 1060.07 712(3481) 3.38e-04 8.7e+01
```

```
##
```

```
## Random effects:
```

```
## Groups Name      Variance Std.Dev.
```

```
## newID (Intercept) 4.244      2.06
```

```
## Number of groups: newID 161
```

```
##
```

```
## Coefficients:
```

```
##      Estimate Std. Error z value Pr(>|z|)
```

```
## AttributeRML -0.3838      0.3329 -1.153  0.249
```

```
## AttributeRLL  0.4662      0.3013  1.547  0.122
```

```
## AttributeLUS -0.1413      0.3210 -0.440  0.660
```

```
## AttributeLLS -0.4351      0.3342 -1.302  0.193
```

```
## AttributeLLL  0.1019      0.3150  0.323  0.746
```

```
## raterVH       0.2339      0.2027  1.154  0.248
```

```
##
```

```
## Threshold coefficients:
```

```
##      Estimate Std. Error z value
```

```
## 0|1  3.3437      0.3122 10.71
```

```
## 1|2  6.4286      0.4277 15.03
```

```
## 2|3  7.6695      0.5497 13.95
```

```
## (1 observation deleted due to missingness)
```

```
#compute pairwise comparisons
```

```
emm <- emmeans(ggo_mod1, ~ Attribute, type = "link")
```

```
pairs(emm)
```

```
## contrast estimate      SE df z.ratio p.value
```

```
## RUL - RML  0.3838 0.333 Inf  1.153 0.8590
```

```
## RUL - RLL -0.4662 0.301 Inf -1.547 0.6334
```

```
## RUL - LUS  0.1413 0.321 Inf  0.440 0.9979
```

```
## RUL - LLS  0.4351 0.334 Inf  1.302 0.7842
```

```
## RUL - LLL -0.1019 0.315 Inf -0.323 0.9995
```

```
## RML - RLL -0.8499 0.319 Inf -2.661 0.0832
```

```
## RML - LUS -0.2425 0.337 Inf -0.719 0.9797
```

```
## RML - LLS  0.0513 0.349 Inf  0.147 1.0000
```



```
## RML - LLL -0.4856 0.332 Inf -1.464 0.6870
## RLL - LUS 0.6074 0.306 Inf 1.983 0.3519
## RLL - LLS 0.9013 0.321 Inf 2.810 0.0558
## RLL - LLL 0.3643 0.299 Inf 1.219 0.8276
## LUS - LLS 0.2938 0.338 Inf 0.869 0.9540
## LUS - LLL -0.2431 0.319 Inf -0.761 0.9739
## LLS - LLL -0.5370 0.333 Inf -1.613 0.5901
##
## Results are averaged over the levels of: rater
## P value adjustment: tukey method for comparing a family of 6 estimates
```

## Consolidations

```
#make sure everything is in correct format
cons$Value <- ordered(cons$Value, levels = c(0,1,2,3))
cons$Attribute <- factor(cons$Attribute, levels = c("RUL", "RML", "RLL", "LUS", "LLS", "LLL"))
cons$newID <- factor(cons$newID)
cons$rater <- factor(cons$rater)

#model 1 - lobe and rater as fixed effects and random int
cons_mod1 <- clmm(
  Value ~ Attribute + rater + (1 | newID),
  data = cons
)

summary(cons_mod1)
```

```
## Cumulative Link Mixed Model fitted with the Laplace approximation
##
## formula: Value ~ Attribute + rater + (1 | newID)
## data: cons
##
## link threshold nobs logLik AIC niter max.grad cond.H
## logit flexible 1464 -956.14 1932.29 737(2940) 9.12e-04 5.2e+01
##
## Random effects:
## Groups Name Variance Std.Dev.
## newID (Intercept) 1.987 1.409
## Number of groups: newID 161
##
## Coefficients:
## Estimate Std. Error z value Pr(>|z|)
## AttributeRML 0.19877 0.20722 0.959 0.337447
## AttributeRLL -0.50246 0.21427 -2.345 0.019028 *
## AttributeLUS -1.47097 0.23996 -6.130 8.79e-10 ***
## AttributeLLS -0.04054 0.20780 -0.195 0.845330
## AttributeLLL -0.78502 0.21890 -3.586 0.000336 ***
## raterVH -0.15844 0.15012 -1.055 0.291212
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Threshold coefficients:
```

```
##      Estimate Std. Error z value
## 0|1    0.4193     0.1927   2.176
## 1|2    4.0826     0.2619  15.589
## 2|3    6.6375     0.5492  12.087
```

```
#compute pairwise comparisons
emm <- emmeans(cons_mod1, ~ Attribute, type = "link")
pairs(emm)
```

```
## contrast estimate      SE df z.ratio p.value
## RUL - RML -0.1988 0.207 Inf -0.959 0.9307
## RUL - RLL 0.5025 0.214 Inf 2.345 0.1762
## RUL - LUS 1.4710 0.240 Inf 6.130 <.0001
## RUL - LLS 0.0405 0.208 Inf 0.195 1.0000
## RUL - LLL 0.7850 0.219 Inf 3.586 0.0045
## RML - RLL 0.7012 0.214 Inf 3.279 0.0133
## RML - LUS 1.6697 0.241 Inf 6.942 <.0001
## RML - LLS 0.2393 0.207 Inf 1.157 0.8573
## RML - LLL 0.9838 0.219 Inf 4.495 0.0001
## RLL - LUS 0.9685 0.243 Inf 3.984 0.0010
## RLL - LLS -0.4619 0.214 Inf -2.159 0.2573
## RLL - LLL 0.2826 0.223 Inf 1.265 0.8040
## LUS - LLS -1.4304 0.240 Inf -5.963 <.0001
## LUS - LLL -0.6860 0.246 Inf -2.793 0.0586
## LLS - LLL 0.7445 0.219 Inf 3.404 0.0087
##
## Results are averaged over the levels of: rater
## P value adjustment: tukey method for comparing a family of 6 estimates
```

## Bronchiectasis

```
#make sure everything is in correct format
branch$Value <- ordered(branch$Value, levels = c(0,1,2,3))
branch$Attribute <- factor(branch$Attribute, levels = c("RUL", "RML", "RLL", "LUS", "LLS", "LLL"))
branch$newID <- factor(branch$newID)
branch$rater <- factor(branch$rater)

#model 1 - lobe and rater as fixed effects and random int
branch_mod1 <- clmm(
  Value ~ Attribute + rater + (1 | newID),
  data = branch
)

summary(branch_mod1)
```

```
## Cumulative Link Mixed Model fitted with the Laplace approximation
##
## formula: Value ~ Attribute + rater + (1 | newID)
## data:      branch
##
## link threshold nobis logLik AIC niter max.grad cond.H
```

```
## logit flexible 1464 -1385.34 2790.67 763(4527) 1.86e-03 4.9e+01
##
## Random effects:
## Groups Name Variance Std.Dev.
## newID (Intercept) 3.988 1.997
## Number of groups: newID 161
##
## Coefficients:
## Estimate Std. Error z value Pr(>|z|)
## AttributeRML 1.3352 0.1925 6.937 4.00e-12 ***
## AttributeRLL -0.2240 0.1890 -1.185 0.23583
## AttributeLUS -1.7670 0.2075 -8.517 < 2e-16 ***
## AttributeLLS 0.6070 0.1876 3.235 0.00122 **
## AttributeLLL -0.7735 0.1944 -3.980 6.91e-05 ***
## raterVH 1.2279 0.1396 8.793 < 2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Threshold coefficients:
## Estimate Std. Error z value
## 0|1 -0.9978 0.2167 -4.604
## 1|2 2.4363 0.2274 10.715
## 2|3 4.2675 0.2554 16.707

#compute pairwise comparisons
emm <- emmeans(bronch_mod1, ~ Attribute, type = "link")
pairs(emm)

## contrast estimate SE df z.ratio p.value
## RUL - RML -1.335 0.192 Inf -6.937 <.0001
## RUL - RLL 0.224 0.189 Inf 1.185 0.8440
## RUL - LUS 1.767 0.207 Inf 8.517 <.0001
## RUL - LLS -0.607 0.188 Inf -3.235 0.0154
## RUL - LLL 0.774 0.194 Inf 3.980 0.0010
## RML - RLL 1.559 0.194 Inf 8.039 <.0001
## RML - LUS 3.102 0.220 Inf 14.081 <.0001
## RML - LLS 0.728 0.187 Inf 3.884 0.0014
## RML - LLL 2.109 0.202 Inf 10.427 <.0001
## RLL - LUS 1.543 0.206 Inf 7.475 <.0001
## RLL - LLS -0.831 0.188 Inf -4.408 0.0002
## RLL - LLL 0.550 0.194 Inf 2.833 0.0524
## LUS - LLS -2.374 0.211 Inf -11.248 <.0001
## LUS - LLL -0.994 0.208 Inf -4.786 <.0001
## LLS - LLL 1.381 0.195 Inf 7.070 <.0001
##
## Results are averaged over the levels of: rater
## P value adjustment: tukey method for comparing a family of 6 estimates
```

## Atelectasis

```
#make sure everything is in correct format
atel$Value <- ordered(atel$Value, levels = c(0,1,2,3))
```

```

atel$Attribute <- factor(atel$Attribute, levels = c("RUL", "RML", "RLL", "LUS", "LLS", "LLL"))
atel$newID <- factor(atel$newID)
atel$rater <- factor(atel$rater)

#model 1 - lobe and rater as fixed effects and random int
atel_mod1 <- clmm(
  Value ~ Attribute + rater + (1 | newID),
  data = atel
)

summary(atel_mod1)

```

```

## Cumulative Link Mixed Model fitted with the Laplace approximation
##
## formula: Value ~ Attribute + rater + (1 | newID)
## data:    atel
##
## link threshold nobs logLik AIC      niter      max.grad cond.H
## logit flexible  1464 -814.68 1649.35 717(4325) 5.26e-04 7.1e+01
##
## Random effects:
## Groups Name      Variance Std.Dev.
## newID (Intercept) 2.306    1.519
## Number of groups: newID 161
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## AttributeRML    2.3755     0.2524   9.414 < 2e-16 ***
## AttributeRLL   -1.1306     0.3281  -3.446  0.00057 ***
## AttributeLUS   -0.9873     0.3218  -3.068  0.00215 **
## AttributeLLS    1.8745     0.2444   7.671  1.7e-14 ***
## AttributeLLL   -0.8749     0.3103  -2.820  0.00480 **
## raterVH         0.1221     0.1741   0.701  0.48302
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Threshold coefficients:
##      Estimate Std. Error z value
## 0|1    2.3050     0.2507   9.196
## 1|2    4.5289     0.3016  15.014
## 2|3    5.2631     0.3250  16.194

```

```

#compute pairwise comparisons
emm <- emmeans(atel_mod1, ~ Attribute, type = "link")
pairs(emm)

```

```

## contrast estimate    SE  df z.ratio p.value
## RUL - RML   -2.376 0.252 Inf  -9.414 <.0001
## RUL - RLL    1.131 0.328 Inf   3.446 0.0075
## RUL - LUS    0.987 0.322 Inf   3.068 0.0262
## RUL - LLS   -1.875 0.244 Inf  -7.671 <.0001
## RUL - LLL    0.875 0.310 Inf   2.820 0.0544
## RML - RLL    3.506 0.322 Inf  10.900 <.0001

```

```
## RML - LUS      3.363 0.313 Inf  10.759 <.0001
## RML - LLS      0.501 0.197 Inf   2.545 0.1113
## RML - LLL      3.250 0.302 Inf  10.765 <.0001
## RLL - LUS     -0.143 0.371 Inf  -0.386 0.9989
## RLL - LLS     -3.005 0.314 Inf  -9.584 <.0001
## RLL - LLL     -0.256 0.361 Inf  -0.709 0.9810
## LUS - LLS     -2.862 0.305 Inf  -9.390 <.0001
## LUS - LLL     -0.112 0.356 Inf  -0.316 0.9996
## LLS - LLL      2.749 0.294 Inf   9.364 <.0001
##
## Results are averaged over the levels of: rater
## P value adjustment: tukey method for comparing a family of 6 estimates
```

## Thin-wall Cavity

```
#make sure everything is in correct format
thin$Value <- as.numeric(as.character(thin$Value))
thin$Attribute <- factor(thin$Attribute, levels = c("RUL", "RML", "RLL", "LUS", "LLS", "LLL"))
thin$newID <- factor(thin$newID)
thin$rater <- factor(thin$rater)

#model 1 - lobe and rater as fixed effects and random int
thin_mod1 <- glmer(Value ~ Attribute + rater + (1 | newID),
  data = thin,
  family = binomial(link = "logit"))
summary(thin_mod1)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula: Value ~ Attribute + rater + (1 | newID)
## Data: thin
##
##      AIC      BIC   logLik deviance df.resid
##    282.4    324.6   -133.2   266.4     1451
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.7394 -0.0189 -0.0170 -0.0102  3.3083
##
## Random effects:
## Groups Name             Variance Std.Dev.
## newID  (Intercept) 29.64      5.444
## Number of obs: 1459, groups: newID, 161
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -7.30572    1.08801  -6.715 1.88e-11 ***
## AttributeRML -1.77456    0.75606  -2.347  0.0189 *
## AttributeRLL -0.67017    0.62980  -1.064  0.2873
## AttributeLUS -0.57806    0.62793  -0.921  0.3573
## AttributeLLS -2.11079    0.82407  -2.561  0.0104 *
```

```
## AttributeLLL -1.35510    0.70863 -1.912    0.0558 .
## raterVH      -0.08215    0.53753 -0.153    0.8785
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##          (Intr) AttRML AttRLL AttLUS AttLLS AttLLL
## AttributRML -0.077
## AttributRLL -0.161  0.393
## AttributLUS -0.182  0.384  0.447
## AttributLLS -0.069  0.332  0.359  0.354
## AttributLLL -0.111  0.364  0.408  0.405  0.339
## raterVH     -0.217 -0.032 -0.031 -0.001 -0.001 -0.001
```

```
#compute pairwise comparisons
```

```
emm <- emmeans(thin_mod1, ~ Attribute, type = "link")
pairs(emm)
```

```
## contrast estimate SE df z.ratio p.value
## RUL - RML 1.7746 0.756 Inf 2.347 0.1754
## RUL - RLL 0.6702 0.630 Inf 1.064 0.8956
## RUL - LUS 0.5781 0.628 Inf 0.921 0.9414
## RUL - LLS 2.1108 0.824 Inf 2.561 0.1069
## RUL - LLL 1.3551 0.709 Inf 1.912 0.3945
## RML - RLL -1.1044 0.771 Inf -1.433 0.7071
## RML - LUS -1.1965 0.776 Inf -1.543 0.6364
## RML - LLS 0.3362 0.915 Inf 0.368 0.9991
## RML - LLL -0.4195 0.827 Inf -0.507 0.9959
## RLL - LUS -0.0921 0.661 Inf -0.139 1.0000
## RLL - LLS 1.4406 0.839 Inf 1.718 0.5198
## RLL - LLL 0.6849 0.731 Inf 0.937 0.9370
## LUS - LLS 1.5327 0.841 Inf 1.823 0.4507
## LUS - LLL 0.7770 0.732 Inf 1.061 0.8968
## LLS - LLL -0.7557 0.886 Inf -0.853 0.9574
##
## Results are averaged over the levels of: rater
## Results are given on the log odds ratio (not the response) scale.
## P value adjustment: tukey method for comparing a family of 6 estimates
```

```
#model 2 - lobe as fixed effect, rater as random effect and random int
```

```
thin_mod2 <- glmer(Value ~ Attribute + (1 | newID) + (1 | rater),
  data = thin,
  family = binomial(link = "logit"))
summary(thin_mod2)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula: Value ~ Attribute + (1 | newID) + (1 | rater)
## Data: thin
##
## AIC      BIC    logLik deviance df.resid
## 282.4    324.7  -133.2   266.4    1451
```

```
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.7033 -0.0186 -0.0173 -0.0100  3.3759
##
## Random effects:
##   Groups Name            Variance Std.Dev.
##   newID   (Intercept) 2.988e+01 5.4664091
##   rater   (Intercept) 5.279e-08 0.0002298
## Number of obs: 1459, groups: newID, 161; rater, 2
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -7.3432     1.0616  -6.917  4.6e-12 ***
## AttributeRML  -1.7785     0.7559  -2.353   0.0186 *
## AttributeRLL  -0.6733     0.6298  -1.069   0.2850
## AttributeLUS  -0.5782     0.6280  -0.921   0.3572
## AttributeLLS  -2.1112     0.8241  -2.562   0.0104 *
## AttributeLLL  -1.3554     0.7087  -1.913   0.0558 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) AttRML AttRLL AttLUS AttLLS
## AttributRML -0.086
## AttributRLL -0.172  0.392
## AttributLUS -0.187  0.384  0.447
## AttributLLS -0.072  0.332  0.359  0.354
## AttributLLL -0.114  0.364  0.408  0.405  0.339
```

## Thick-wall Cavity

```
#make sure everything is in correct format
thick$Value <- as.numeric(as.character(thick$Value))
thick$Attribute <- factor(thick$Attribute, levels = c("RUL", "RML", "RLL", "LUS", "LLS", "LLL"))
thick$newID <- factor(thick$newID)
thick$rater <- factor(thick$rater)

#model 1 - lobe and rater as fixed effects and random int
thick_mod1 <- glmer(Value ~ Attribute + rater + (1 | newID),
  data = thick,
  family = binomial(link = "logit"))
summary(thick_mod1)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula: Value ~ Attribute + rater + (1 | newID)
## Data: thick
##
##      AIC      BIC    logLik deviance df.resid
##    459.3    501.7   -221.7    443.3     1455
```

```

##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.3835 -0.0436 -0.0127 -0.0064  7.3517
##
## Random effects:
##   Groups Name            Variance Std.Dev.
##   newID  (Intercept) 34.18      5.846
## Number of obs: 1463, groups: newID, 161
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -5.9512     0.9287  -6.408 1.47e-10 ***
## AttributeRML  -4.0559     0.7015  -5.782 7.40e-09 ***
## AttributeRLL  -1.9291     0.4954  -3.894 9.84e-05 ***
## AttributeLUS  -2.7587     0.5532  -4.987 6.14e-07 ***
## AttributeLLS  -4.0557     0.7016  -5.781 7.43e-09 ***
## AttributeLLL  -2.6024     0.5409  -4.812 1.50e-06 ***
## raterVH       -0.1305     0.4197  -0.311  0.756
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) AttRML AttRLL AttLUS AttLLS AttLLL
## AttributRML  0.165
## AttributRLL  0.150  0.406
## AttributLUS  0.176  0.405  0.485
## AttributLLS  0.165  0.358  0.406  0.405
## AttributLLL  0.174  0.407  0.490  0.477  0.407
## raterVH      -0.215 -0.014 -0.020 -0.019 -0.014 -0.019

#compute pairwise comparisons
emm <- emmeans(thick_mod1, ~ Attribute, type = "link")
pairs(emm)

## contrast estimate SE df z.ratio p.value
## RUL - RML  4.055886 0.702 Inf  5.782 <.0001
## RUL - RLL  1.929101 0.495 Inf  3.894 0.0014
## RUL - LUS  2.758720 0.553 Inf  4.987 <.0001
## RUL - LLS  4.055749 0.702 Inf  5.781 <.0001
## RUL - LLL  2.602447 0.541 Inf  4.812 <.0001
## RML - RLL -2.126785 0.675 Inf -3.152 0.0202
## RML - LUS -1.297166 0.696 Inf -1.865 0.4239
## RML - LLS -0.000137 0.795 Inf  0.000 1.0000
## RML - LLL -1.453438 0.690 Inf -2.107 0.2835
## RLL - LUS  0.829619 0.535 Inf  1.552 0.6305
## RLL - LLS  2.126648 0.675 Inf  3.152 0.0202
## RLL - LLL  0.673346 0.525 Inf  1.284 0.7942
## LUS - LLS  1.297029 0.696 Inf  1.865 0.4241
## LUS - LLL -0.156273 0.559 Inf -0.279 0.9998
## LLS - LLL -1.453302 0.690 Inf -2.107 0.2836
##
## Results are averaged over the levels of: rater
## Results are given on the log odds ratio (not the response) scale.

```



## P value adjustment: tukey method for comparing a family of 6 estimates

## Statistical Model Notation

$\lambda_{ijkl} = \log\left(\frac{P(\text{Score}_{ijk} \leq l | b_i, b_k)}{1 - P(\text{Score}_{ijk} \leq l | b_i, b_k)}\right) = \alpha_l + \beta_1(\text{lobe}_j) + \beta_2(\text{rater}_k) + b_i + b_k$ , where  $i = \text{subject}$ ,  $j = \text{lobe}$ ,  $k = \text{rater}$ ,  $l = \text{score level}$ ,  $b_i \sim N(0, \sigma_{\text{subject}}^2)$ , and  $b_k \sim N(0, \sigma_{\text{rater}}^2)$ . Thus we have  $ICC = \frac{\sigma_{\text{subject}}^2}{\sigma_{\text{subject}}^2 + \sigma_{\text{rater}}^2}$