# Supplementary file 3: annotated R-script for lme-AIC/logLikelihood analysis for demographic article-level metrics

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If necessary, install the package `nlme`

```r
install.packages("nlme")
```

Load the package:

```r
library(nlme)
```

Upload data file for demographic proportions

```r
demographic <- read.csv("TableS3_proportions.csv",stringsAsFactors = FALSE)
names(demographic)
```

```
## [1] "Predatory."
## [2] "Journal"
## [3] "X.a..Prop.developing.prim.authors"
## [4] "X.b..Prop.developing.corr.authors"
## [5] "X.c..Prop.developing.other.authors"
## [6] "X.d..Prop.statistics.reported"
## [7] "X.e..Prop.stats.adequate"
```

Arcsine transform the proportion data

```r
demographic$arcProp.developing.corr.authors <- asin(demographic$X.b..Prop.developing.corr.authors)
demographic$arcProp.developing.other.authors <- asin(demographic$X.c..Prop.developing.other.authors)
```

lme and AIC/logLikelihood for effect of journal [random] and journal type [fixed] on proportion of corresponding authors from developing countries

```r
demo.lme<-lme(arcProp.developing.corr.authors~Predatory.,random=~1|Journal,data=demographic)
anova(demo.lme)
```

```
##             numDF denDF  F-value p-value
## (Intercept)     1    10 76.14131  <.0001
## Predatory.      1    10  5.55180  0.0402
```

```r
demo.gls<-gls(arcProp.developing.corr.authors~Predatory.,data=demographic)
anova(demo.lme,demo.gls)
```

```
##          Model df      AIC      BIC    logLik   Test      L.Ratio p-value
## demo.lme     1  4 15.86477 17.07511 -3.932387
## demo.gls     2  3 13.86477 14.77253 -3.932387 1 vs 2 1.776357e-15       1
```

lme and AIC/logLikelihood for effect of journal [random] and journal type [fixed] on proportion of additional authors from developing countries

```r
demo2.lme<-lme(arcProp.developing.other.authors~Predatory.,random=~1|Journal,data=demographic)
anova(demo2.lme)
```

```
##             numDF denDF  F-value p-value
## (Intercept)     1    10 59.75029  <.0001
## Predatory.      1    10  2.37068  0.1547
```

```
demo3.gls<-gls(arcProp.developing.other.authors~Predatory.,data=demographic)
anova(demo2.lme,demo3.gls)
```

```
##           Model df      AIC      BIC    logLik   Test L.Ratio p-value
## demo2.lme     1  4 18.64552 19.85586 -5.322761
## demo3.gls     2  3 16.64552 17.55328 -5.322761 1 vs 2       0       1
```