



Analyses for CNM study 1

R packages used

```
library(nlme) # for lme(), gls(), intervals()
```

Data

All the data cleanup and preparation was done on a separate R script, “data cleanup.R”.

```
source("data cleanup.r")
```

```
## Warning: package 'lubridate' was built under R version 3.5.3
```

```
##
```

```
## Attaching package: 'lubridate'
```

```
## The following object is masked from 'package:base':
```

```
##
```

```
##     date
```

```
##
```

```
## Attaching package: 'reshape'
```

```
## The following object is masked from 'package:lubridate':
```

```
##
```

```
##     stamp
```

The data was converted to long format, that is, each row is a partner/relationship from a participant. To compare models using a likelihood ratio test, models must be generated using the same dataset, so to avoid potential comparison issues caused by missing data, only complete data subsets were used on each analysis.

Checking the need for mixed effects models

Defining variables in a complete dataset:

```
vars <- c("Respondent.ID", "avoidance", "anxiety", "satisfaction", "hierarchy")
data <- na.omit(study1.long[vars])
dv1 <- data$avoidance
dv2 <- data$anxiety
dv3 <- data$satisfaction
iv <- data$hierarchy
id <- data$Respondent.ID
```

Checking whether a random-intercept model is an improvement over a fixed intercept one:

```
# Intercept only models, using general least squares (gls)
i1 <- gls(dv1 ~ 1, method = "REML", na.action=na.exclude)
i2 <- gls(dv2 ~ 1, method = "REML", na.action=na.exclude)
i3 <- gls(dv3 ~ 1, method = "REML", na.action=na.exclude)

# Random intercept only models, using linear mixed effects (lme)
ri1 <- lme(dv1 ~ 1, random = list(id = pdSymm(form = ~ 1)),
           method="REML", na.action=na.exclude)
ri2 <- lme(dv2 ~ 1, random = list(id = pdSymm(form = ~ 1)),
           method="REML", na.action=na.exclude)
```



```
ri3 <- lme(dv3 ~ 1, random = list(id = pdSymm(form = ~ 1)),
          method="REML", na.action=na.exclude)

anova(i1, ri1)

##      Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## i1      1  2 1713.504 1722.171 -854.7521
## ri1     2  3 1702.758 1715.758 -848.3789 1 vs 2 12.74626 4e-04

anova(i2, ri2)

##      Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## i2      1  2 1969.847 1978.514 -982.9236
## ri2     2  3 1924.692 1937.692 -959.3462 1 vs 2 47.15476 <.0001

anova(i3, ri3)

##      Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## i3      1  2 3006.037 3014.703 -1501.018
## ri3     2  3 2973.114 2986.114 -1483.557 1 vs 2 34.92231 <.0001
```

The random-intercept models significantly improve the fixed-intercept ones. This confirms the appropriateness of using linear mixed effects models.

Variability in within-participant anxiety, avoidance, and relationship satisfaction by hierarchy type

Step 1: Look at hierarchy type only

To test whether the within-participant variability in avoidance, anxiety, and relationship satisfaction differed by hierarchy type, we compared (via likelihood ratio test) two linear mixed effects models for each outcome variable: one which assumed a homogeneous variance across hierarchical and non-hierarchical groups and one which assumed heterogeneous variance. Both models had a random intercept and no fixed effects.

Options used in the nlme::lme() function:

`random = list(id = pdSymm(form = ~ 1))`, which is the same as `random = ~ 1|id`, sets the random effects to be structured as a positive-definite symmetric matrix; it assumes homogeneous between-subject variance.

`random = list(id = pdDiag(form = ~ iv))` sets the random effects to be structured as a diagonal matrix; it assumes heterogeneous between-subject variance across the levels of iv (hierarchical and non-hierarchical groups).

`weights = varIdent(form = ~ 1 | iv)` sets heterogeneous within-participant variance for levels of iv (hierarchical and non-hierarchical groups)

`method = "REML"` Restricted Maximum Likelihood (REML) is used if fixed effects don't change between models to be compared. If fixed effects change, we use "ML", Maximum Likelihood.

```
wsh1 <- lme(dv1 ~ 1, random = list(id = pdSymm(form = ~ 1)),
           weights = varIdent(form = ~ 1 | iv),
           method="REML")
wsh2 <- lme(dv2 ~ 1, random = list(id = pdSymm(form = ~ 1)),
           weights = varIdent(form = ~ 1 | iv),
           method="REML")
wsh3 <- lme(dv3 ~ 1, random = list(id = pdSymm(form = ~ 1)),
           weights = varIdent(form = ~ 1 | iv),
```



```
method="REML")
anova(ri1,wsh1)
```

```
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## ri1      1  3 1702.758 1715.758 -848.3789
## wsh1      2  4 1693.915 1711.248 -842.9576 1 vs 2 10.84263 0.001
```

```
anova(ri2,wsh2)
```

```
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## ri2      1  3 1924.692 1937.692 -959.3462
## wsh2      2  4 1915.984 1933.317 -953.9919 1 vs 2 10.70866 0.0011
```

```
anova(ri3,wsh3)
```

```
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## ri3      1  3 2973.114 2986.114 -1483.557
## wsh3      2  4 2970.761 2988.094 -1481.380 1 vs 2 4.353521 0.0369
```

Hierarchy type is related to within-participant variability in avoidance, anxiety, and satisfaction.

```
summary(wsh1)
```

```
## Linear mixed-effects model fit by REML
## Data: NULL
##      AIC      BIC    logLik
## 1693.915 1711.248 -842.9576
##
## Random effects:
## Formula: ~1 | id
##      (Intercept) Residual
## StdDev: 0.3974177 0.9113319
##
## Variance function:
## Structure: Different standard deviations per stratum
## Formula: ~1 | iv
## Parameter estimates:
## NonHierarchical Hierarchical
##      1.000000      1.251087
## Fixed effects: dv1 ~ 1
##      Value Std.Error DF t-value p-value
## (Intercept) 2.06933 0.05022416 339 41.20188 0
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -1.7133403 -0.7427639 -0.2162893 0.5643724 4.6181998
##
## Number of Observations: 564
## Number of Groups: 225
```

```
summary(wsh2)
```

```
## Linear mixed-effects model fit by REML
## Data: NULL
##      AIC      BIC    logLik
## 1915.984 1933.317 -953.9919
##
```



```
## Random effects:
## Formula: ~1 | id
##      (Intercept) Residual
## StdDev:   0.7732425 1.009965
##
## Variance function:
## Structure: Different standard deviations per stratum
## Formula: ~1 | iv
## Parameter estimates:
## NonHierarchical   Hierarchical
##      1.000000      1.266016
## Fixed effects: dv2 ~ 1
##      Value Std.Error   DF  t-value p-value
## (Intercept) 2.227602 0.0705765 339 31.56294      0
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -2.4747354 -0.5595333 -0.3092204  0.5039857  3.4660662
##
## Number of Observations: 564
## Number of Groups: 225
```

```
summary(wsh3)
```

```
## Linear mixed-effects model fit by REML
## Data: NULL
##      AIC      BIC   logLik
## 2970.761 2988.094 -1481.38
##
## Random effects:
## Formula: ~1 | id
##      (Intercept) Residual
## StdDev:   1.717406 2.776182
##
## Variance function:
## Structure: Different standard deviations per stratum
## Formula: ~1 | iv
## Parameter estimates:
## NonHierarchical   Hierarchical
##      1.000000      1.158269
## Fixed effects: dv3 ~ 1
##      Value Std.Error   DF  t-value p-value
## (Intercept) 20.04605 0.1710055 339 117.2246      0
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -3.6367692 -0.5945878  0.1165595  0.6878617  1.9789642
##
## Number of Observations: 564
## Number of Groups: 225
```

The within-participant standard deviations for avoidance, anxiety, and relationship satisfaction were higher in the hierarchical group by 25%, 26%, and 16% respectively.

Estimated weight and standard deviations for non-hierarchical and hierarchical groups:



```
summary(wsh1)$sigma # avoidance, non-hierarchical

## [1] 0.9113319
summary(wsh1)$sigma*coef(wsh1$modelStruct$varStruct, uncons=FALSE)

## Hierarchical
##      1.140155
summary(wsh2)$sigma # anxiety, non-hierarchical

## [1] 1.009965
summary(wsh2)$sigma*coef(wsh1$modelStruct$varStruct, uncons=FALSE)

## Hierarchical
##      1.263554
summary(wsh3)$sigma # satisfaction, non-hierarchical

## [1] 2.776182
summary(wsh3)$sigma*coef(wsh1$modelStruct$varStruct, uncons=FALSE)

## Hierarchical
##      3.473245
Confidence intervals:
intervals(wsh1, level = 0.95, which = "all")

## Approximate 95% confidence intervals
##
## Fixed effects:
##           lower    est.    upper
## (Intercept) 1.970539 2.06933 2.16812
## attr("label")
## [1] "Fixed effects:"
##
## Random Effects:
## Level: id
##           lower    est.    upper
## sd((Intercept)) 0.285393 0.3974177 0.5534154
##
## Variance function:
##           lower    est.    upper
## Hierarchical 1.095153 1.251087 1.429223
## attr("label")
## [1] "Variance function:"
##
## Within-group standard error:
##           lower    est.    upper
## 0.8312993 0.9113319 0.9990696
intervals(wsh2, level = 0.95, which = "all")

## Approximate 95% confidence intervals
##
## Fixed effects:
```



```
##               lower      est.      upper
## (Intercept) 2.088779 2.227602 2.366425
## attr("label")
## [1] "Fixed effects:"
##
## Random Effects:
##   Level: id
##               lower      est.      upper
## sd((Intercept)) 0.6461323 0.7732425 0.9253584
##
## Variance function:
##               lower      est.      upper
## Hierarchical 1.09994 1.266016 1.457167
## attr("label")
## [1] "Variance function:"
##
## Within-group standard error:
##       lower      est.      upper
## 0.9156106 1.0099647 1.1140421
```

```
intervals(wsh3, level = 0.95, which = "all")
```

```
## Approximate 95% confidence intervals
##
## Fixed effects:
##               lower      est.      upper
## (Intercept) 19.70968 20.04605 20.38241
## attr("label")
## [1] "Fixed effects:"
##
## Random Effects:
##   Level: id
##               lower      est.      upper
## sd((Intercept)) 1.394681 1.717406 2.114808
##
## Variance function:
##               lower      est.      upper
## Hierarchical 1.009026 1.158269 1.329587
## attr("label")
## [1] "Variance function:"
##
## Within-group standard error:
##       lower      est.      upper
## 2.522023 2.776182 3.055953
```

Exploratory - checked whether a heterogeneous between-subjects variance model improved the heterogeneous within-subjects variance model:

```
bsh1 <- lme(dv1 ~ 1, random = list(id = pdDiag(form = ~ iv)),
            weights = varIdent(form = ~ 1 | iv),
            method="REML")
bsh2 <- lme(dv2 ~ 1, random = list(id = pdDiag(form = ~ iv)),
            weights = varIdent(form = ~ 1 | iv),
            method="REML")
bsh3 <- lme(dv3 ~ 1, random = list(id = pdDiag(form = ~ iv)),
            weights = varIdent(form = ~ 1 | iv),
```



```

        method="REML")
anova(wsh1,bsh1)

##          Model df          AIC          BIC    logLik    Test      L.Ratio p-value
## wsh1         1  4 1693.915 1711.248 -842.9576
## bsh1         2  5 1695.915 1717.582 -842.9576 1 vs 2 2.484712e-07 0.9996

anova(wsh2,bsh2)

##          Model df          AIC          BIC    logLik    Test      L.Ratio p-value
## wsh2         1  4 1915.984 1933.317 -953.9919
## bsh2         2  5 1917.983 1939.650 -953.9916 1 vs 2 0.0004971541 0.9822

anova(wsh3,bsh3)

##          Model df          AIC          BIC    logLik    Test      L.Ratio p-value
## wsh3         1  4 2970.761 2988.094 -1481.38
## bsh3         2  5 2972.761 2994.427 -1481.38 1 vs 2 2.926199e-07 0.9996

```

No significant improvement.

Step 2: add control variables

We first checked which potential control variables are related to the within-participant variability in the outcomes:

```

cvs.num <- c("rel.length.c", "age.c", "incomeperPPL.c") # numerical vars
cvs.cat <- c("N.Partners.3levels", "gender", "orientation.binary",
            "race.binary", "children.binary", "education.3levels",
            "marital.status", "cohab", "coparent") # categorical vars
cvs <- c(cvs.num, cvs.cat)

```

Numerical variables:

```

for(x in cvs.num){ # numerical vars
  data <- na.omit(study1.long[c(vars,x)])
  print(x)
  cv <- data[[x]]
  dv1 <- data$avoidance
  dv2 <- data$anxiety
  dv3 <- data$satisfaction
  iv <- data$hierarchy
  id <- data$Respondent.ID
  m1 <- lme(dv1 ~ 1, random = list(id = pdSymm(form = ~ 1)),
            method="REML")
  m2 <- lme(dv2 ~ 1, random = list(id = pdSymm(form = ~ 1)),
            method="REML")
  m3 <- lme(dv3 ~ 1, random = list(id = pdSymm(form = ~ 1)),
            method="REML")
  mcv1 <- lme(dv1 ~ 1, random = list(id = pdSymm(form = ~ 1)),
              #weights = varFixed(~cv),
              #weights = varPower(1,~cv),
              weights = varExp(1,~cv),
              method="REML",
              control=lmeControl(opt = "optim"
                                #returnObject=TRUE
                                )

```



```

)
mcv2 <- lme(dv2 ~ 1, random = list(id = pdSymm(form = ~ 1)),
  #weights = varFixed(~cv),
  #weights = varPower(1,~cv),
  weights = varExp(1,~cv),
  method="REML",
  control=lmeControl(opt = "optim"
    #returnObject=TRUE
  )
)
mcv3 <- lme(dv3 ~ 1, random = list(id = pdSymm(form = ~ 1)),
  #weights = varFixed(~cv),
  #weights = varPower(1,~cv),
  weights = varExp(1,~cv),
  method="REML",
  control=lmeControl(opt = "optim"
    #returnObject=TRUE
  )
)
a1 <- anova(m1,mcv1); a2 <- anova(m2,mcv2); a3 <- anova(m3,mcv3);
print(a1); print(a2); print(a3);
}

```

```

## [1] "rel.length.c"
##      Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## m1         1  3 1686.358 1699.325 -840.1789
## mcv1        2  4 1670.893 1688.183 -831.4465 1 vs 2 17.46479 <.0001
##      Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## m2         1  3 1900.927 1913.895 -947.4634
## mcv2        2  4 1898.419 1915.710 -945.2098 1 vs 2 4.507312 0.0338
##      Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## m3         1  3 2945.399 2958.367 -1469.699
## mcv3        2  4 2945.262 2962.552 -1468.631 1 vs 2 2.137014 0.1438
## [1] "age.c"
##      Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## m1         1  3 1702.758 1715.758 -848.3789
## mcv1        2  4 1717.480 1734.813 -854.7398 1 vs 2 12.72168 4e-04
##      Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## m2         1  3 1924.692 1937.692 -959.3462
## mcv2        2  4 1971.141 1988.475 -981.5708 1 vs 2 44.44913 <.0001
##      Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## m3         1  3 2973.114 2986.114 -1483.557
## mcv3        2  4 3009.368 3026.701 -1500.684 1 vs 2 34.25337 <.0001
## [1] "incomeperPPL.c"
##      Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## m1         1  3 1332.046 1344.273 -663.0233
## mcv1        2  4 1340.895 1357.197 -666.4475 1 vs 2 6.848584 0.0089
##      Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## m2         1  3 1494.572 1506.798 -744.2859
## mcv2        2  4 1534.143 1550.445 -763.0717 1 vs 2 37.57165 <.0001
##      Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## m3         1  3 2307.176 2319.402 -1150.588
## mcv3        2  4 2336.047 2352.348 -1164.023 1 vs 2 26.87112 <.0001

```




Categorical variables:

```
for(x in cvs.cat){ # categorical vars
  data <- na.omit(study1.long[c(vars,x)])
  print(x)
  cv <- data[[x]]
  dv1 <- data$avoidance
  dv2 <- data$anxiety
  dv3 <- data$satisfaction
  iv <- data$hierarchy
  id <- data$Respondent.ID
  m1 <- lme(dv1 ~ 1, random = list(id = pdSymm(form = ~ 1)),
    method="REML")
  m2 <- lme(dv2 ~ 1, random = list(id = pdSymm(form = ~ 1)),
    method="REML")
  m3 <- lme(dv3 ~ 1, random = list(id = pdSymm(form = ~ 1)),
    method="REML")
  mcv1 <- lme(dv1 ~ 1, random = list(id = pdSymm(form = ~ 1)),
    weights = varIdent(form = ~1|cv),
    method="REML")
  mcv2 <- lme(dv2 ~ 1, random = list(id = pdSymm(form = ~ 1)),
    weights = varIdent(form = ~1|cv),
    method="REML")
  mcv3 <- lme(dv3 ~ 1, random = list(id = pdSymm(form = ~ 1)),
    weights = varIdent(form = ~1|cv),
    method="REML")
  print(anova(m1,mcv1))
  print(anova(m2,mcv2))
  print(anova(m3,mcv3))
}
```

```
## [1] "N.Partners.3levels"
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m1      1  3 1702.758 1715.758 -848.3789
## mcv1    2  5 1683.952 1705.618 -836.9759 1 vs 2 22.80603 <.0001
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m2      1  3 1924.692 1937.692 -959.3462
## mcv2    2  5 1928.644 1950.310 -959.3219 1 vs 2 0.04867099 0.976
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m3      1  3 2973.114 2986.114 -1483.557
## mcv3    2  5 2967.545 2989.211 -1478.772 1 vs 2 9.56959 0.0084
## [1] "gender"
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m1      1  3 1409.988 1422.414 -701.9941
## mcv1    2  5 1400.180 1420.890 -695.0898 1 vs 2 13.80854 0.001
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m2      1  3 1591.117 1603.543 -792.5583
## mcv2    2  5 1593.515 1614.225 -791.7574 1 vs 2 1.601779 0.4489
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m3      1  3 2462.146 2474.572 -1228.073
## mcv3    2  5 2463.782 2484.492 -1226.891 1 vs 2 2.364013 0.3067
## [1] "orientation.binary"
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m1      1  3 1392.963 1405.357 -693.4815
## mcv1    2  4 1390.362 1406.887 -691.1812 1 vs 2 4.600673 0.032
```



```
##      Model df      AIC      BIC    logLik    Test    L.Ratio p-value
## m2      1  3 1565.982 1578.376 -779.9909
## mcv2     2  4 1567.586 1584.111 -779.7930 1 vs 2 0.3957323 0.5293
##      Model df      AIC      BIC    logLik    Test    L.Ratio p-value
## m3      1  3 2431.052 2443.446 -1212.526
## mcv3     2  4 2433.049 2449.574 -1212.524 1 vs 2 0.003576701 0.9523
## [1] "race.binary"
##      Model df      AIC      BIC    logLik    Test    L.Ratio p-value
## m1      1  3 1405.787 1418.200 -699.8935
## mcv1     2  4 1407.786 1424.337 -699.8930 1 vs 2 0.001065629 0.974
##      Model df      AIC      BIC    logLik    Test    L.Ratio p-value
## m2      1  3 1578.72 1591.134 -786.3602
## mcv2     2  4 1580.15 1596.701 -786.0749 1 vs 2 0.5705183 0.4501
##      Model df      AIC      BIC    logLik    Test    L.Ratio p-value
## m3      1  3 2448.825 2461.238 -1221.412
## mcv3     2  4 2450.171 2466.722 -1221.086 1 vs 2 0.6534813 0.4189
## [1] "children.binary"
##      Model df      AIC      BIC    logLik    Test    L.Ratio p-value
## m1      1  3 1409.988 1422.414 -701.9941
## mcv1     2  4 1410.788 1427.357 -701.3942 1 vs 2 1.1998 0.2734
##      Model df      AIC      BIC    logLik    Test    L.Ratio p-value
## m2      1  3 1591.117 1603.543 -792.5583
## mcv2     2  4 1592.304 1608.872 -792.1521 1 vs 2 0.8123354 0.3674
##      Model df      AIC      BIC    logLik    Test    L.Ratio p-value
## m3      1  3 2462.146 2474.572 -1228.073
## mcv3     2  4 2462.592 2479.160 -1227.296 1 vs 2 1.553942 0.2126
## [1] "education.3levels"
##      Model df      AIC      BIC    logLik    Test    L.Ratio p-value
## m1      1  3 1389.832 1402.213 -691.9160
## mcv1     2  5 1393.791 1414.425 -691.8953 1 vs 2 0.04152336 0.9795
##      Model df      AIC      BIC    logLik    Test    L.Ratio p-value
## m2      1  3 1569.435 1581.816 -781.7175
## mcv2     2  5 1572.252 1592.886 -781.1259 1 vs 2 1.183284 0.5534
##      Model df      AIC      BIC    logLik    Test    L.Ratio p-value
## m3      1  3 2419.608 2431.988 -1206.804
## mcv3     2  5 2422.550 2443.185 -1206.275 1 vs 2 1.05754 0.5893
## [1] "marital.status"
##      Model df      AIC      BIC    logLik    Test    L.Ratio p-value
## m1      1  3 1702.758 1715.758 -848.3789
## mcv1     2  4 1700.197 1717.530 -846.0986 1 vs 2 4.560775 0.0327
##      Model df      AIC      BIC    logLik    Test    L.Ratio p-value
## m2      1  3 1924.692 1937.692 -959.3462
## mcv2     2  4 1923.451 1940.784 -957.7255 1 vs 2 3.241416 0.0718
##      Model df      AIC      BIC    logLik    Test    L.Ratio p-value
## m3      1  3 2973.114 2986.114 -1483.557
## mcv3     2  4 2974.251 2991.584 -1483.126 1 vs 2 0.8632052 0.3528
## [1] "cohab"
##      Model df      AIC      BIC    logLik    Test    L.Ratio p-value
## m1      1  3 1702.758 1715.758 -848.3789
## mcv1     2  5 1684.597 1706.263 -837.2983 1 vs 2 22.16132 <.0001
##      Model df      AIC      BIC    logLik    Test    L.Ratio p-value
## m2      1  3 1924.692 1937.692 -959.3462
## mcv2     2  5 1918.558 1940.224 -954.2790 1 vs 2 10.13439 0.0063
##      Model df      AIC      BIC    logLik    Test    L.Ratio p-value
```



```
## m3      1  3 2973.114 2986.114 -1483.557
## mcv3    2  5 2976.225 2997.891 -1483.112 1 vs 2 0.8894541 0.641
## [1] "coparent"
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m1      1  3 1702.758 1715.758 -848.3789
## mcv1    2  5 1702.606 1724.272 -846.3028 1 vs 2 4.152251 0.1254
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m2      1  3 1924.692 1937.692 -959.3462
## mcv2    2  5 1923.902 1945.568 -956.9509 1 vs 2 4.790579 0.0911
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m3      1  3 2973.114 2986.114 -1483.557
## mcv3    2  5 2976.507 2998.174 -1483.254 1 vs 2 0.6068902 0.7383
```

After adjusting p-values for multiple comparisons, the following variables were related to within-participant variance:

Avoidance - relationship length, number of partners, gender, and cohabitation.

Anxiety - cohabitation

Satisfaction - number of partners

Model selection for within-participant variability in avoidance

Strategy: start with a model that includes hierarchy (variable of interest), relationship length, number of partners, gender, and cohabitation status. Then perform model selection through a backwards elimination process.

Model with 4 control variables:

```
cv5.avoid <- c("rel.length.c", "N.Partners.3levels", "gender", "cohab")
data <- na.omit(study1.long[c(vars, cv5.avoid)])
dv <- data$avoidance
iv <- data$hierarchy
id <- data$Respondent.ID
cv1 <- data[[cv5.avoid[1]]]
cv4 <- data[[cv5.avoid[2]]]
cv5 <- data[[cv5.avoid[3]]]
cv11 <- data[[cv5.avoid[4]]]

mcv4 <- lme(dv ~ 1, random = list(id = pdSymm(form = ~ 1)),
  weights = varComb(
    varIdent(form = ~ 1 | iv),
    varExp(1, ~cv1), # length
    varIdent(form = ~ 1 | cv4), # number of partners
    varIdent(form = ~ 1 | cv5), # gender
    varIdent(form = ~ 1 | cv11) # cohab
  ),
  method="REML")
aic3 <- numeric() # vector that will store AIC values for later comparison
mcv3 <- lme(dv ~ 1, random = list(id = pdSymm(form = ~ 1)),
  weights = varComb(
    varIdent(form = ~ 1 | iv),
    #varExp(1, ~cv1), # length
    varIdent(form = ~ 1 | cv4), # number of partners
    varIdent(form = ~ 1 | cv5), # gender
```



```

        varIdent(form = ~ 1 | cv11) # cohab
    ),
    method="REML")
a1 <- anova(mcv3,mcv4)
aic3[1] <- a1$AIC[2]-a1$AIC[1] # AIC of full minus reduced model

mcv3 <- lme(dv ~ 1, random = list(id = pdSymm(form = ~ 1)),
    weights = varComb(
        varIdent(form = ~ 1 | iv),
        varExp(1, ~cv1), # 1 length
        #varIdent(form = ~ 1 | cv4), # number of partners
        varIdent(form = ~ 1 | cv5), # gender
        varIdent(form = ~ 1 | cv11) # cohab
    ),
    method="REML")
a4 <- anova(mcv3,mcv4)
aic3[2] <- a4$AIC[2]-a4$AIC[1] # AIC of full minus reduced model

mcv3 <- lme(dv ~ 1, random = list(id = pdSymm(form = ~ 1)),
    weights = varComb(
        varIdent(form = ~ 1 | iv),
        varExp(1, ~cv1), # length
        varIdent(form = ~ 1 | cv4), # number of partners
        #varIdent(form = ~ 1 | cv5), # gender
        varIdent(form = ~ 1 | cv11) # cohab
    ),
    method="REML")
a5 <- anova(mcv3,mcv4)
aic3[3] <- a5$AIC[2]-a5$AIC[1] # AIC of full minus reduced model

mcv3 <- lme(dv ~ 1, random = list(id = pdSymm(form = ~ 1)),
    weights = varComb(
        varIdent(form = ~ 1 | iv),
        varExp(1, ~cv1), # length
        varIdent(form = ~ 1 | cv4), # number of partners
        varIdent(form = ~ 1 | cv5) # gender
        #varIdent(form = ~ 1 | cv11) # cohab
    ),
    method="REML")
a11 <- anova(mcv3,mcv4)
aic3[4] <- a11$AIC[2]-a11$AIC[1] # AIC of full minus reduced model

print(aic3)

```

```
## [1] -7.743088 -12.856747 -4.240881 -2.824791
```

** Eliminate cohabitation - it improves the model with 3 control variables, but not by much (after adjusting for multiple testing, improvement is not significant) **

Should one more variable be eliminated?

```

mcv3 <- lme(dv ~ 1, random = list(id = pdSymm(form = ~ 1)),
    weights = varComb(
        varIdent(form = ~ 1 | iv),

```



```

        varExp(1, ~cv1), # length
        varIdent(form = ~ 1 | cv4), # number of partners
        varIdent(form = ~ 1 | cv5) # gender
    ),
    method="REML")
aic2 <- numeric() # vector that will store AIC values for later comparison
mcv2 <- lme(dv ~ 1, random = list(id = pdSymm(form = ~ 1)),
    weights = varComb(
        varIdent(form = ~ 1 | iv),
        #varExp(1, ~cv1), # length
        varIdent(form = ~ 1 | cv4), # number of partners
        varIdent(form = ~ 1 | cv5) # gender
    ),
    control=lmeControl(opt = "optim"
        #opt = "nlminb"
        #returnObject=TRUE
    ),
    method="REML")
a1 <- anova(mcv2,mcv3)
aic2[1] <- a1$AIC[2]-a1$AIC[1] # AIC of full minus reduced model

mcv2 <- lme(dv ~ 1, random = list(id = pdSymm(form = ~ 1)),
    weights = varComb(
        varIdent(form = ~ 1 | iv),
        varExp(1, ~cv1), # length
        #varIdent(form = ~ 1 | cv4), # number of partners
        varIdent(form = ~ 1 | cv5) # gender
    ),
    method="REML")
a4 <- anova(mcv2,mcv3)
aic2[2] <- a4$AIC[2]-a4$AIC[1] # AIC of full minus reduced model

mcv2 <- lme(dv ~ 1, random = list(id = pdSymm(form = ~ 1)),
    weights = varComb(
        varIdent(form = ~ 1 | iv),
        varExp(1, ~cv1), # length
        varIdent(form = ~ 1 | cv4) # number of partners
        #varIdent(form = ~ 1 | cv5) # gender
    ),
    method="REML")
a5 <- anova(mcv2,mcv3)
aic2[3] <- a5$AIC[2]-a5$AIC[1] # AIC of full minus reduced model

print(aic2)

```

```
## [1] -18.23048 -19.85542 -3.83260
```

**** Remove gender - only a small improvement,non-significant after correcting p-value for multiple testing ****

```

aic1 <- numeric()
mcv2 <- lme(dv ~ 1, random = list(id = pdSymm(form = ~ 1)),
    weights = varComb(
        varIdent(form = ~ 1 | iv),
        varExp(1, ~cv1), # length
        varIdent(form = ~ 1 | cv4) # number of partners
    )

```



```

    ),
    method="REML")
mcv1 <- lme(dv ~ 1, random = list(id = pdSymm(form = ~ 1)),
  weights = varComb(
    varIdent(form = ~ 1 | iv),
    #varExp(1, ~cv1), # length
    varIdent(form = ~ 1 | cv4) # number of partners
  ),
  method="REML")
a <- anova(mcv1, mcv2)
aic1[1] <- a$AIC[2] - a$AIC[1]
print(a)

```

```

##      Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## mcv1      1  6 1363.722 1388.496 -675.8608
## mcv2      2  7 1343.368 1372.272 -664.6842 1 vs 2 22.35324 <.0001

```

```

mcv1 <- lme(dv ~ 1, random = list(id = pdSymm(form = ~ 1)),
  weights = varComb(
    varIdent(form = ~ 1 | iv),
    varExp(1, ~cv1) # length
    #varIdent(form = ~ 1 | cv4) # number of partners
  ),
  method="REML")
a <- anova(mcv1, mcv2)
aic1[2] <- a$AIC[2] - a$AIC[1]
print(a)

```

```

##      Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## mcv1      1  5 1371.442 1392.088 -680.7212
## mcv2      2  7 1343.368 1372.272 -664.6842 1 vs 2 32.07405 <.0001

```

Both variables improve the model.

Final model for within-participant avoidance:

```

var.avoidance <- lme(dv ~ 1, random = list(id = pdSymm(form = ~ 1)),
  weights = varComb(
    varIdent(form = ~ 1 | iv),
    varExp(1, ~cv1), # length
    varIdent(form = ~ 1 | cv4) # number of partners
  ),
  method="REML")
summary(var.avoidance)

```

```

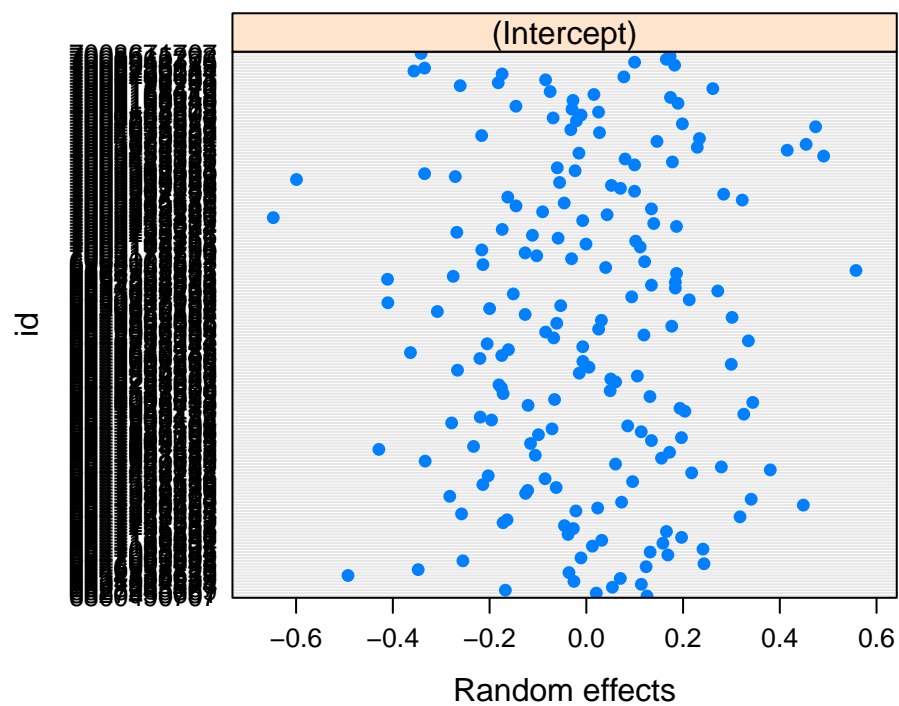
## Linear mixed-effects model fit by REML
## Data: NULL
##      AIC      BIC    logLik
## 1343.368 1372.272 -664.6842
##
## Random effects:
## Formula: ~1 | id
##      (Intercept) Residual
## StdDev:  0.3738431  1.12048
##

```

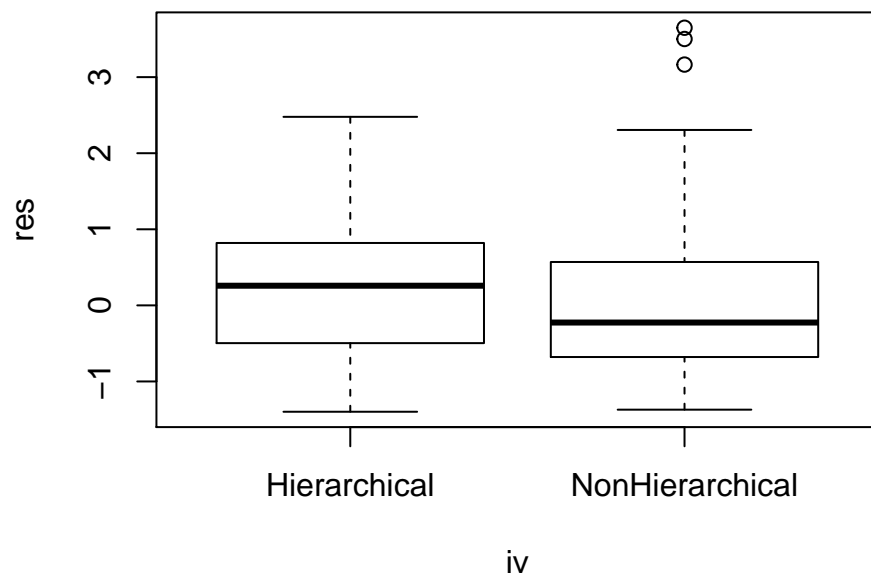


```
## Combination of variance functions:
## Structure: Different standard deviations per stratum
## Formula: ~1 | iv
## Parameter estimates:
## NonHierarchical    Hierarchical
##      1.000000      1.298594
## Structure: Exponential of variance covariate
## Formula: ~cv1
## Parameter estimates:
##      expon
## -0.04278682
## Structure: Different standard deviations per stratum
## Formula: ~1 | cv4
## Parameter estimates:
##      >3      3      2
## 1.0000000 0.8949208 0.6129545
## Fixed effects: dv ~ 1
##      Value Std.Error DF t-value p-value
## (Intercept) 1.853254 0.04848691 274 38.22174      0
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -1.39799056 -0.63526356 -0.05280845  0.77141668  3.64912238
##
## Number of Observations: 460
## Number of Groups: 186

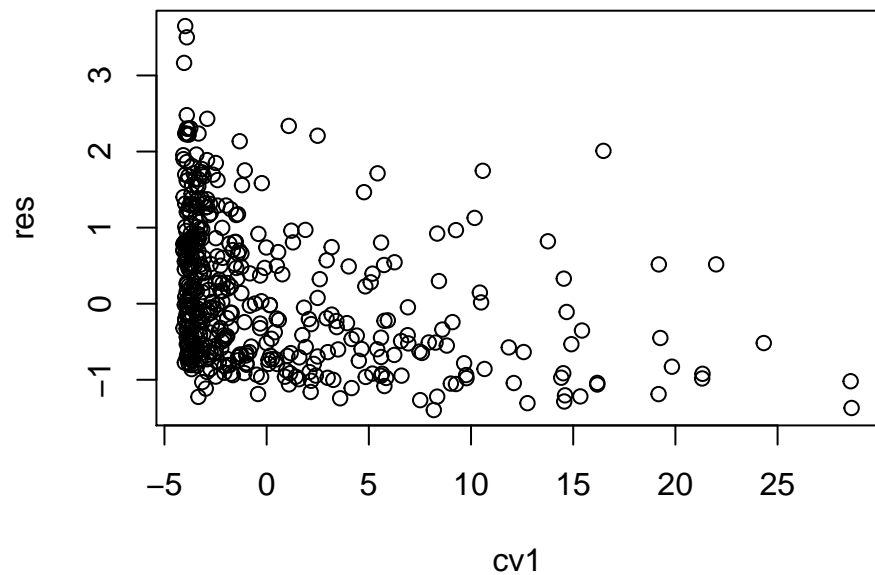
res <- resid(var.avoidance, type = "pearson")
fit <- fitted(var.avoidance, level=0)
plot(ranef(var.avoidance, level = 1))
```



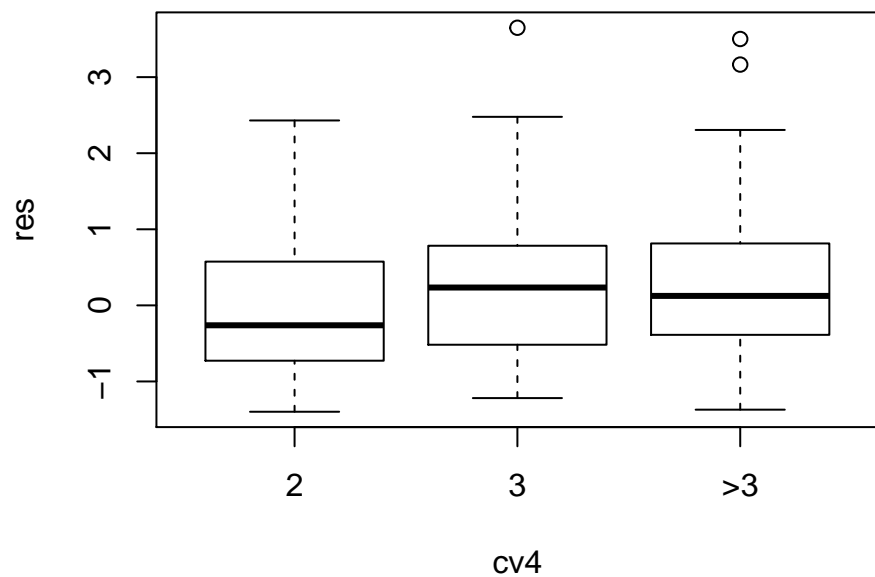
```
plot(res ~ iv)
```



```
plot(res ~ cv1)
```

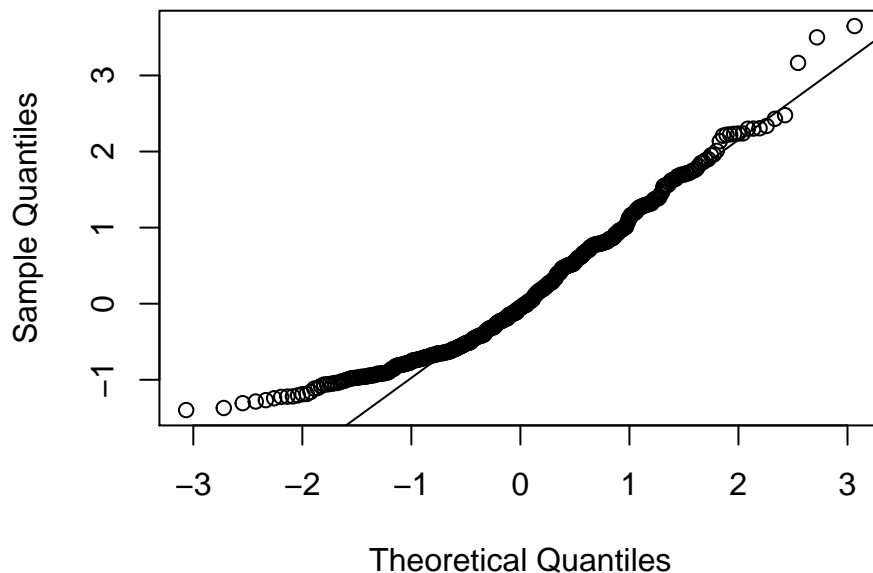
```
plot(res ~ cv4)
```



```
qqnorm(res)  
qqline(res)
```



Normal Q-Q Plot



Model selection - Within-participant variability in anxiety

Check whether adding cohabitation to a model with hierarchy type improves the model

```
data <- na.omit(study1.long[c(vars,"cohab")])
dv <- data$satisfaction
iv <- data$hierarchy
id <- data$Respondent.ID
cv <- data[["cohab"]]
mcv1 <- lme(dv ~ 1, random = list(id = pdSymm(form = ~ 1)),
            weights = varIdent(form = ~ 1 | cv), # cohab
            method="ML")
m0 <- lme(dv ~ 1, random = list(id = pdSymm(form = ~ 1)),
          weights = varComb(
            varIdent(form = ~ 1 | iv),
            varIdent(form = ~ 1 | cv) # cohab
          ),
          method="ML")
a <- anova(m0,mcv1)
print(a)
```

##	Model	df	AIC	BIC	logLik	Test	L.Ratio	p-value
##	m0	1 6	2971.743	2997.753	-1479.872			
##	mcv1	2 5	2974.534	2996.209	-1482.267	1 vs 2	4.790989	0.0286

In a model with heterogeneous within-participant variance by hierarchy type, cohabitation is no longer significantly associated with within-participant variability (after adjusting significance for multiple testing).



Model selection - Within-participant variability in relationship satisfaction

Check whether adding number of partners to a model with hierarchy type improves the model

```
data <- na.omit(study1.long[c(vars,"N.Partners.3levels")])
dv <- data$satisfaction
iv <- data$hierarchy
id <- data$Respondent.ID
cv <- data[["N.Partners.3levels"]]
mcv1 <- lme(dv ~ 1, random = list(id = pdSymm(form = ~ 1)),
            weights = varIdent(form = ~ 1 | cv), # number of partners
            method="ML")
m0 <- lme(dv ~ 1, random = list(id = pdSymm(form = ~ 1)),
            weights = varComb(
              varIdent(form = ~ 1 | iv),
              varIdent(form = ~ 1 | cv) # number of partners
            ),
            method="ML")
a <- anova(m0,mcv1)
print(a)
```

##	Model	df	AIC	BIC	logLik	Test L.Ratio	p-value
##	m0	1 6	2963.177	2989.187	-1475.589		
##	mcv1	2 5	2965.826	2987.501	-1477.913	1 vs 2 4.649	0.0311

In a model with heterogeneous within-participant variance by hierarchy type, number of partners is no longer significantly associated with within-participant variability (after adjusting significance for multiple testing).

Avoidance, Anxiety, and relationship satisfaction by hierarchy type

Here we use the same variance models from the previous analyses and add fixed effects to it.

Avoidance

Step 1: add hierarchy type to model from previous analysis

```
data <- na.omit(study1.long[c(vars,cvs.avoid[1],cvs.avoid[4])])
dv <- data$avoidance
iv <- data$hierarchy
id <- data$Respondent.ID
cv1 <- data[[cvs.avoid[1]]] # rel. length
cv4 <- data[[cvs.avoid[4]]] # number of partners

m.avoid <- lme(dv ~ 1, random = list(id = pdSymm(form = ~ 1)),
              weights = varComb(
                varIdent(form = ~ 1 | iv),
                varExp(1, ~cv1), # length
                varIdent(form = ~ 1 | cv4) # number of partners
              ),
              method="ML")

m.avoid.h <- lme(dv ~ iv, random = list(id = pdSymm(form = ~ 1)),
                weights = varComb(
                  varIdent(form = ~ 1 | iv),
                  varExp(1, ~cv1), # length
```



```

        varIdent(form = ~ 1 | cv4) # number of partners
    ),
    method="ML")
print(anova(m.avoid, m.avoid.h))

```

```

##           Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## m.avoid      1  7 1640.424 1670.694 -813.2117
## m.avoid.h    2  8 1631.897 1666.492 -807.9485 1 vs 2 10.52637  0.0012

```

Adding hierarchy type as a fixed effect improved the variance-only model for avoidance.

Step 2: control variables

Checking which potential control variables are related to avoidance:

```

for(x in cvs){
  if(x != "rel.length.c" & x != "N.Partners.3levels"){
    data <- na.omit(study1.long[c(vars,"rel.length.c","N.Partners.3levels"),x])
  } else {
    data <- na.omit(study1.long[c(vars,"rel.length.c","N.Partners.3levels")])
  }
  print(x)
  dv <- data$avoidance
  iv <- data$hierarchy
  id <- data$Respondent.ID
  cv1 <- data$rel.length.c
  cv4 <- data$N.Partners.3levels
  cv <- data[[x]]
  m1 <- lme(dv ~ 1, random = list(id = pdSymm(form = ~ 1)),
    weights = varComb(
      varIdent(form = ~ 1 | iv),
      varExp(1, ~cv1), # length
      varIdent(form = ~ 1 | cv4) # number of partners
    ),
    method="ML")
  mcv <- lme(dv ~ cv, random = list(id = pdSymm(form = ~ 1)),
    weights = varComb(
      varIdent(form = ~ 1 | iv),
      varExp(1, ~cv1), # length
      varIdent(form = ~ 1 | cv4) # number of partners
    ),
    method="ML")
  a1 <- anova(m1,mcv)
  print(a1)
}

```

```

## [1] "rel.length.c"
##           Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## m1          1  7 1631.025 1661.296 -808.5127
## mcv         2  8 1571.818 1606.413 -777.9089 1 vs 2 61.20755 <.0001
## [1] "age.c"
##           Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## m1          1  7 1631.025 1661.296 -808.5127
## mcv         2  8 1630.423 1665.018 -807.2116 1 vs 2 2.602187  0.1067
## [1] "incomeperPPL.c"

```



```

##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m1      1  7 1264.281 1292.727 -625.1405
## mcv     2  8 1265.613 1298.123 -624.8065 1 vs 2 0.668069 0.4137
## [1] "N.Partners.3levels"
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m1      1  7 1631.025 1661.296 -808.5127
## mcv     2  9 1621.103 1660.023 -801.5516 1 vs 2 13.92204 9e-04
## [1] "gender"
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m1      1  7 1339.151 1368.069 -662.5753
## mcv     2  9 1341.357 1378.538 -661.6783 1 vs 2 1.793924 0.4078
## [1] "orientation.binary"
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m1      1  7 1327.215 1356.073 -656.6077
## mcv     2  8 1329.213 1362.193 -656.6064 1 vs 2 0.002461753 0.9604
## [1] "race.binary"
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m1      1  7 1335.926 1364.814 -660.9630
## mcv     2  8 1337.913 1370.928 -660.9564 1 vs 2 0.01326144 0.9083
## [1] "children.binary"
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m1      1  7 1339.151 1368.069 -662.5753
## mcv     2  8 1335.830 1368.879 -659.9147 1 vs 2 5.321132 0.0211
## [1] "education.3levels"
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m1      1  7 1318.133 1346.944 -652.0666
## mcv     2  9 1319.947 1356.991 -650.9737 1 vs 2 2.185764 0.3352
## [1] "marital.status"
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m1      1  7 1631.025 1661.296 -808.5127
## mcv     2  8 1574.408 1609.003 -779.2040 1 vs 2 58.61739 <.0001
## [1] "cohab"
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m1      1  7 1631.025 1661.296 -808.5127
## mcv     2  9 1571.167 1610.086 -776.5835 1 vs 2 63.8583 <.0001
## [1] "coparent"
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m1      1  7 1631.025 1661.296 -808.5127
## mcv     2  9 1605.653 1644.572 -793.8263 1 vs 2 29.3727 <.0001

```

The following variables were related to avoidance: relationship length, number of partners, marital status, cohabitation, and coparenting. PS: After adjusting for multiple testing, children ($p=0.02$) is not a significant predictor.

Model selection strategy: start with a model that includes hierarchy (iv of interest), relationship length, number of partners, marital status, cohabitation status, and coparenting status, all as fixed effects variables. Then perform model selection through a backwards elimination process.

```

cvs.avoid.fix <- c("rel.length.c", "N.Partners.3levels",
                  "marital.status", "cohab", "coparent")
data <- na.omit(study1.long[c(vars,cvs.avoid.fix)])
dv <- data$avoidance
iv <- data$hierarchy
id <- data$Respondent.ID
cv1 <- data$rel.length.c

```



```

cv4 <- data$N.Partners.3levels
cv10 <- data$marital.status
cv11 <- data$cohab
cv12 <- data$coparent
aic0 <- numeric()
m0 <- lme(dv ~ iv + cv1 + cv4 + cv10 + cv11 + cv12,
          random = list(id = pdSymm(form = ~ 1)),
          weights = varComb(
            varIdent(form = ~ 1 | iv),
            varExp(1, ~cv1), # length
            varIdent(form = ~ 1 | cv4) # number of partners
          ),
          method="ML")

print(cvs.avoid.fix[1])

## [1] "rel.length.c"

m <- update(m0, .~. -cv1)
a <- anova(m,m0)
diff <- a$AIC[2] - a$AIC[1]
aic0[1] <- diff
print(a)

##      Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## m         1 15 1542.469 1607.334 -756.2343
## m0        2 16 1534.467 1603.656 -751.2333 1 vs 2 10.00203 0.0016

print(cvs.avoid.fix[2])

## [1] "N.Partners.3levels"

m <- update(m0, .~. -cv4)
a <- anova(m,m0)
diff <- a$AIC[2] - a$AIC[1]
aic0[2] <- diff
print(a)

##      Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## m         1 14 1534.653 1595.194 -753.3266
## m0        2 16 1534.467 1603.656 -751.2333 1 vs 2 4.186693 0.1233

print(cvs.avoid.fix[3])

## [1] "marital.status"

m <- update(m0, .~. -cv10)
a <- anova(m,m0)
diff <- a$AIC[2] - a$AIC[1]
aic0[3] <- diff
print(a)

##      Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## m         1 15 1533.913 1598.779 -751.9567
## m0        2 16 1534.467 1603.656 -751.2333 1 vs 2 1.446788 0.229

print(cvs.avoid.fix[4])

```



```
## [1] "cohab"
m <- update(m0, .~. -cv11)
a <- anova(m,m0)
diff <- a$AIC[2] - a$AIC[1]
aic0[4] <- diff
print(a)
```

```
##      Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## m         1 14 1540.894 1601.436 -756.4472
## m0        2 16 1534.467 1603.656 -751.2333 1 vs 2 10.42784 0.0054
```

```
print(cvs.avoid.fix[5])
```

```
## [1] "coparent"
```

```
m <- update(m0, .~. -cv12)
a <- anova(m,m0)
diff <- a$AIC[2] - a$AIC[1]
aic0[5] <- diff
print(a)
```

```
##      Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## m         1 14 1530.730 1591.271 -751.3651
## m0        2 16 1534.467 1603.656 -751.2333 1 vs 2 0.2637 0.8765
```

```
print(aic0)
```

```
## [1] -8.0020353 -0.1866934 0.5532116 -6.4278388 3.7363000
```

** Eliminate coparenting - it does not improve model with 4 control variables and increases AIC the most **

```
cvs.avoid.fix <- c("rel.length.c", "N.Partners.3levels",
                  "marital.status", "cohab")
aic0 <- numeric()
data <- na.omit(study1.long[c(vars,cvs.avoid.fix)])
dv <- data$avoidance
iv <- data$hierarchy
id <- data$Respondent.ID
cv1 <- data$rel.length.c
cv4 <- data$N.Partners.3levels
cv10 <- data$marital.status
cv11 <- data$cohab
aic1 <- numeric()
m0 <- lme(dv ~ iv + cv1 + cv4 + cv10 + cv11,
          random = list(id = pdSymm(form = ~ 1)),
          weights = varComb(
            varIdent(form = ~ 1 | iv),
            varExp(1, ~cv1), # length
            varIdent(form = ~ 1 | cv4) # number of partners
          ),
          method="ML")
print(cvs.avoid.fix[1])
```

```
## [1] "rel.length.c"
```



```
m <- update(m0, .~. -cv1)
a <- anova(m,m0)
diff <- a$AIC[2] - a$AIC[1]
aic0[1] <- diff
print(a)
```

```
##      Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## m         1 13 1540.177 1596.394 -757.0886
## m0        2 14 1530.730 1591.271 -751.3651 1 vs 2 11.44684 7e-04
```

```
print(cvs.avoid.fix[2])
```

```
## [1] "N.Partners.3levels"
```

```
m <- update(m0, .~. -cv4)
a <- anova(m,m0)
diff <- a$AIC[2] - a$AIC[1]
aic0[2] <- diff
print(a)
```

```
##      Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## m         1 12 1530.774 1582.667 -753.3873
## m0        2 14 1530.730 1591.271 -751.3651 1 vs 2 4.044229 0.1324
```

```
print(cvs.avoid.fix[3])
```

```
## [1] "marital.status"
```

```
m <- update(m0, .~. -cv10)
a <- anova(m,m0)
diff <- a$AIC[2] - a$AIC[1]
aic0[3] <- diff
print(a)
```

```
##      Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## m         1 13 1530.151 1586.368 -752.0755
## m0        2 14 1530.730 1591.271 -751.3651 1 vs 2 1.420667 0.2333
```

```
print(cvs.avoid.fix[4])
```

```
## [1] "cohab"
```

```
m <- update(m0, .~. -cv11)
a <- anova(m,m0)
diff <- a$AIC[2] - a$AIC[1]
aic0[4] <- diff
print(a)
```

```
##      Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## m         1 12 1537.077 1588.970 -756.5386
## m0        2 14 1530.730 1591.271 -751.3651 1 vs 2 10.34701 0.0057
```

```
print(aic0)
```

```
## [1] -9.44684043 -0.04422927 0.57933324 -6.34700617
```

```
** Eliminate marital status - it does not improve model with 3 control variables and increases AIC the most
**
```




```

cvs.avoid.fix <- c("rel.length.c", "N.Partners.3levels", "cohab")
aic0 <- numeric()
data <- na.omit(study1.long[c(vars,cvs.avoid.fix)])
dv <- data$avoidance
iv <- data$hierarchy
id <- data$Respondent.ID
cv1 <- data$rel.length.c
cv4 <- data$N.Partners.3levels
cv11 <- data$cohab
aic1 <- numeric()
m0 <- lme(dv ~ iv + cv1 + cv4 + cv11,
          random = list(id = pdSymm(form = ~ 1)),
          weights = varComb(
            varIdent(form = ~ 1 | iv),
            varExp(1, ~cv1), # length
            varIdent(form = ~ 1 | cv4) # number of partners
          ),
          method="ML")

print(cvs.avoid.fix[1])

```

```
## [1] "rel.length.c"
```

```

m <- update(m0, .~. -cv1)
a <- anova(m,m0)
diff <- a$AIC[2] - a$AIC[1]
aic0[1] <- diff
print(a)

```

```

##      Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## m         1 12 1554.472 1606.364 -765.2361
## m0        2 13 1530.151 1586.368 -752.0755 1 vs 2 26.32116 <.0001

```

```
print(cvs.avoid.fix[2])
```

```
## [1] "N.Partners.3levels"
```

```

m <- update(m0, .~. -cv4)
a <- anova(m,m0)
diff <- a$AIC[2] - a$AIC[1]
aic0[2] <- diff
print(a)

```

```

##      Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## m         1 11 1530.866 1578.434 -754.4328
## m0        2 13 1530.151 1586.368 -752.0755 1 vs 2 4.714721 0.0947

```

```
print(cvs.avoid.fix[3])
```

```
## [1] "cohab"
```

```

m <- update(m0, .~. -cv11)
a <- anova(m,m0)
diff <- a$AIC[2] - a$AIC[1]
aic0[3] <- diff
print(a)

```



```
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m        1 11 1542.581 1590.148 -760.2902
## m0       2 13 1530.151 1586.368 -752.0755 1 vs 2 16.42951   3e-04
```

```
print(aic0)
```

```
## [1] -24.321164 -0.714721 -12.429509
```

**** Eliminate number of partners - it has a small, non-significant improvement in the model ****

```
cvs.avoid.fix <- c("rel.length.c", "cohab")
aic0 <- numeric()
data <- na.omit(study1.long[c(vars,cvs.avoid.fix)])
dv <- data$avoidance
iv <- data$hierarchy
id <- data$Respondent.ID
cv1 <- data$rel.length.c
cv11 <- data$cohab
aic1 <- numeric()
m0 <- lme(dv ~ iv + cv1 + cv11,
          random = list(id = pdSymm(form = ~ 1)),
          weights = varComb(
            varIdent(form = ~ 1 | iv),
            varExp(1, ~cv1), # length
            varIdent(form = ~ 1 | cv4) # number of partners
          ),
          method="ML")
```

```
print(cvs.avoid.fix[1])
```

```
## [1] "rel.length.c"
```

```
m <- update(m0, .~. -cv1)
a <- anova(m,m0)
diff <- a$AIC[2] - a$AIC[1]
aic0[1] <- diff
print(a)
```

```
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m        1 10 1554.021 1597.265 -767.0105
## m0       2 11 1530.866 1578.434 -754.4328 1 vs 2 25.15542  <.0001
```

```
print(cvs.avoid.fix[2])
```

```
## [1] "cohab"
```

```
m <- update(m0, .~. -cv11)
a <- anova(m,m0)
diff <- a$AIC[2] - a$AIC[1]
aic0[2] <- diff
print(a)
```

```
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m        1  9 1547.867 1586.786 -764.9335
## m0       2 11 1530.866 1578.434 -754.4328 1 vs 2 21.00124  <.0001
```

```
print(aic0)
```

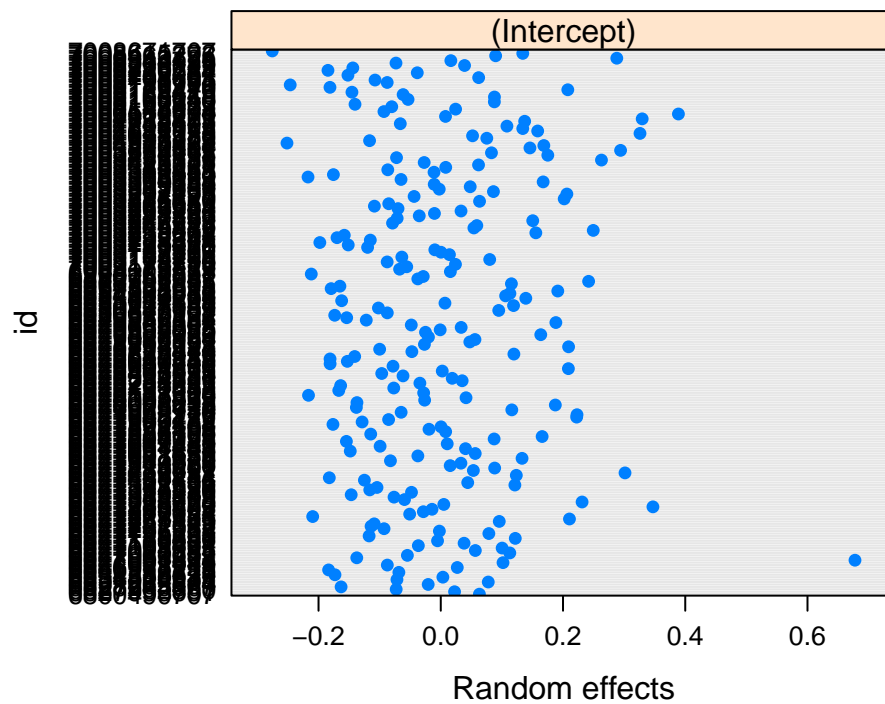
```
## [1] -23.15542 -17.00124
```



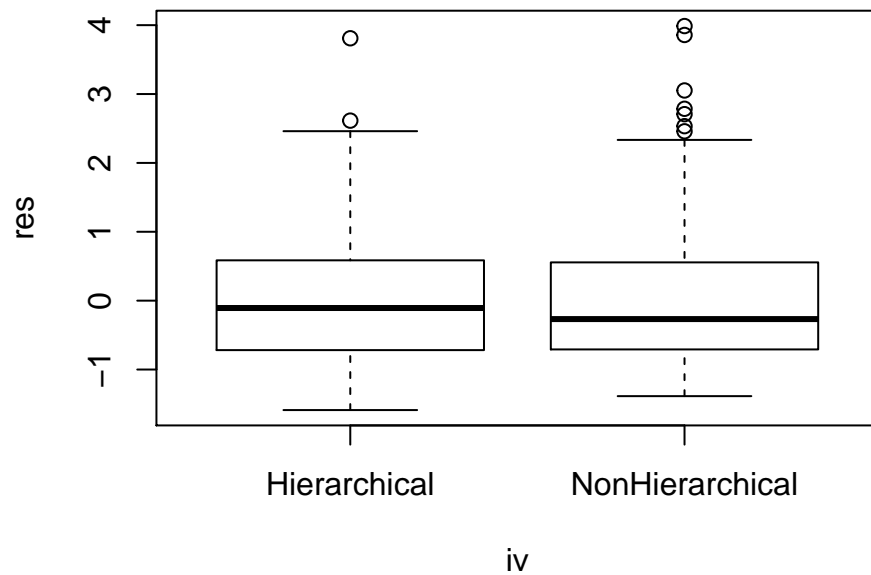
**** Keep length of relationship and cohabitation status - both significantly improve the model ****

Residual plots:

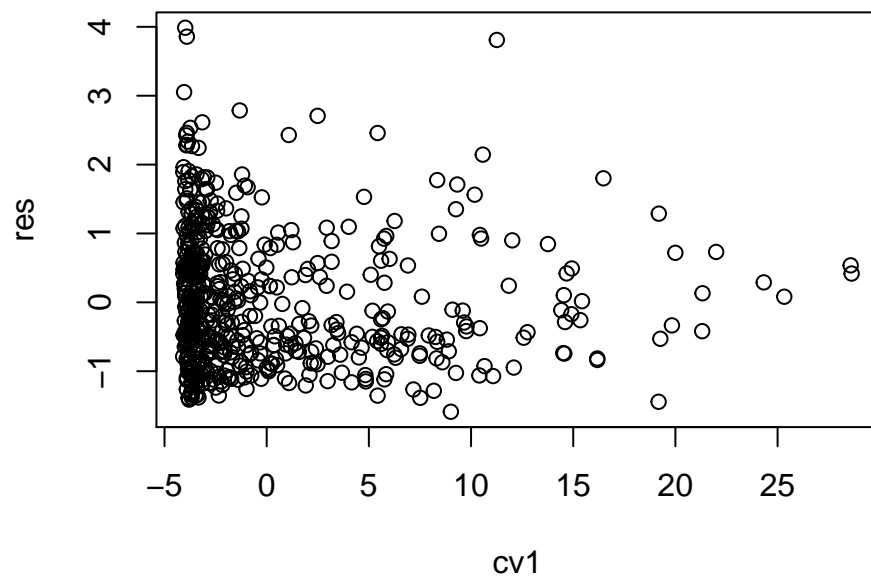
```
res <- resid(m0, type = "pearson")
fit <- fitted(m0, level=0)
plot(ranef(m0, level = 1))
```



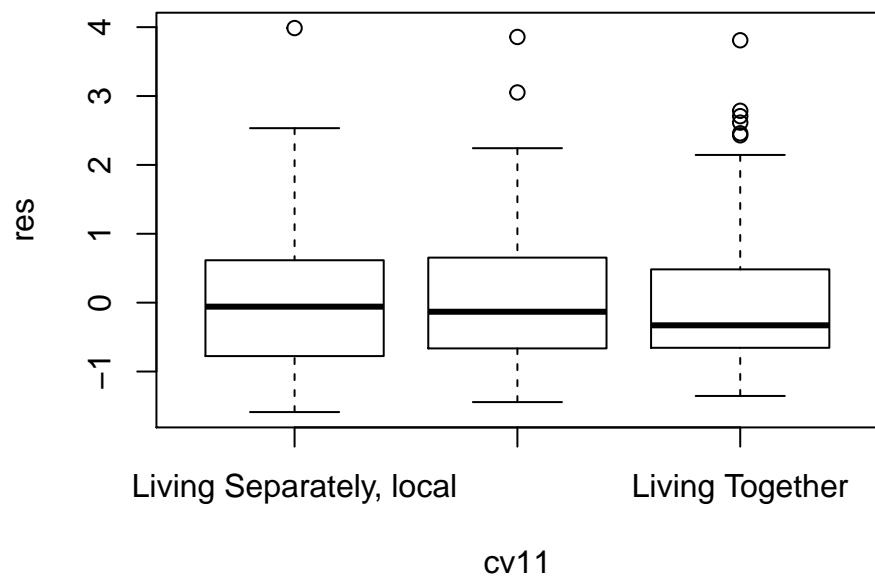
```
plot(res ~ iv)
```



```
plot(res ~ cv1)
```

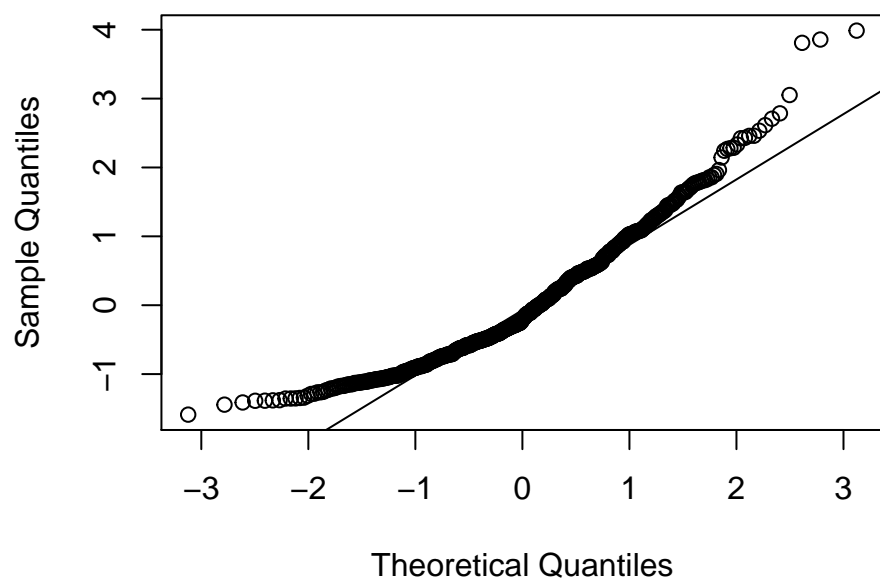


```
plot(res ~ cv11)
```



```
qqnorm(res)  
qqline(res)
```

Normal Q-Q Plot





Anxiety

Step 1: add hierarchy type to model from previous analysis

```

data <- na.omit(study1.long[vars])
dv <- data$anxiety
iv <- data$hierarchy
id <- data$Respondent.ID

m.anx <- lme(dv ~ 1, random = list(id = pdSymm(form = ~ 1)),
             weights = varIdent(form = ~ 1 | iv),
             method="ML")

m.anx.h <- lme(dv ~ iv, random = list(id = pdSymm(form = ~ 1)),
              weights = varIdent(form = ~ 1 | iv),
              method="ML")

print(anova(m.anx, m.anx.h))

```

##	Model	df	AIC	BIC	logLik	Test	L.Ratio	p-value
##	m.anx	1 4	1912.517	1929.858	-952.2586			
##	m.anx.h	2 5	1900.972	1922.647	-945.4857	1 vs 2	13.54583	2e-04

Adding hierarchy type as a fixed effect improved the variance model (no fixed effects) for anxiety.

Step 2: control variables

Checking which potential control variables are related to anxiety:

```

for(x in cvs){
  data <- na.omit(study1.long[c(vars,x)])
  print(x)
  dv <- data$anxiety
  iv <- data$hierarchy
  id <- data$Respondent.ID
  cv <- data[[x]]
  m1 <- lme(dv ~ 1, random = list(id = pdSymm(form = ~ 1)),
            weights = varIdent(form = ~ 1 | iv),
            method="ML")
  mcv <- lme(dv ~ cv, random = list(id = pdSymm(form = ~ 1)),
            weights = varIdent(form = ~ 1 | iv),
            method="ML")
  a <- anova(m1,mcv)
  print(a)
}

```

##	[1]	"rel.length.c"						
##	Model	df	AIC	BIC	logLik	Test	L.Ratio	p-value
##	m1	1 4	1889.623	1906.921	-940.8116			
##	mcv	2 5	1853.985	1875.606	-921.9923	1 vs 2	37.63856	<.0001

##	[1]	"age.c"						
##	Model	df	AIC	BIC	logLik	Test	L.Ratio	p-value
##	m1	1 4	1912.517	1929.858	-952.2586			
##	mcv	2 5	1913.950	1935.626	-951.9751	1 vs 2	0.5670111	0.4514

##	[1]	"incomeperPPL.c"						
##	Model	df	AIC	BIC	logLik	Test	L.Ratio	p-value



```
## m1      1  4 1488.719 1505.030 -740.3597
## mcv     2  5 1490.355 1510.744 -740.1777 1 vs 2 0.364047  0.5463
## [1] "N.Partners.3levels"
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m1      1  4 1912.517 1929.858 -952.2586
## mcv     2  6 1914.753 1940.763 -951.3764 1 vs 2 1.764562  0.4138
## [1] "gender"
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m1      1  4 1581.768 1598.345 -786.8839
## mcv     2  6 1583.705 1608.570 -785.8526 1 vs 2 2.062734  0.3565
## [1] "orientation.binary"
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m1      1  4 1558.268 1574.802 -775.1341
## mcv     2  5 1556.183 1576.850 -773.0913 1 vs 2 4.085704  0.0432
## [1] "race.binary"
##      Model df      AIC      BIC    logLik    Test      L.Ratio p-value
## m1      1  4 1569.976 1586.536 -780.9881
## mcv     2  5 1571.976 1592.675 -780.9880 1 vs 2 0.0002802241  0.9866
## [1] "children.binary"
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m1      1  4 1581.768 1598.345 -786.8839
## mcv     2  5 1583.352 1604.073 -786.6760 1 vs 2 0.4157617  0.5191
## [1] "education.3levels"
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m1      1  4 1560.868 1577.384 -776.4339
## mcv     2  6 1563.118 1587.892 -775.5587 1 vs 2 1.750394  0.4168
## [1] "marital.status"
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m1      1  4 1912.517 1929.858 -952.2586
## mcv     2  5 1884.621 1906.296 -937.3104 1 vs 2 29.89654  <.0001
## [1] "cohab"
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m1      1  4 1912.517 1929.858 -952.2586
## mcv     2  6 1873.617 1899.628 -930.8086 1 vs 2 42.90002  <.0001
## [1] "coparent"
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m1      1  4 1912.517 1929.858 -952.2586
## mcv     2  6 1905.634 1931.644 -946.8169 1 vs 2 10.88358  0.0043
```

The following variables were related to anxiety: relationship length, sexual orientation, marital status, cohabitation, co-parenting.

Model selection strategy: start with a model that includes hierarchy (iv of interest), relationship length, sexual orientation, marital status, cohabitation, co-parenting, all as fixed effects variables. Then perform model selection through a backwards elimination process.

```
cvs.anx.fix <- c("rel.length.c", "orientation", "marital.status", "cohab", "coparent")
data <- na.omit(study1.long[c(vars,cvs.anx.fix)])
dv <- data$anxiety
iv <- data$hierarchy
id <- data$Respondent.ID
cv1 <- data$rel.length.c
cv6 <- data$orientation
cv10 <- data$marital.status
cv11 <- data$cohab
```



```

cv12 <- data$coparent
aic0 <- numeric()
m0 <- lme(dv ~ iv + cv1 + cv6 + cv10 + cv11 + cv12,
          random = list(id = pdSymm(form = ~ 1)),
          weights = varIdent(form = ~ 1 | iv),
          method="ML")

print(cvs.anx.fix[1])

## [1] "rel.length.c"

m <- update(m0, .~. -cv1)
a <- anova(m,m0)
diff <- a$AIC[2] - a$AIC[1]
aic0[1] <- diff
print(a)

##      Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## m        1 17 1521.022 1591.253 -743.5111
## m0       2 18 1517.847 1592.209 -740.9235 1 vs 2 5.175343 0.0229

print(cvs.anx.fix[2])

## [1] "orientation"

m <- update(m0, .~. -cv6)
a <- anova(m,m0)
diff <- a$AIC[2] - a$AIC[1]
aic0[2] <- diff
print(a)

##      Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## m        1 11 1513.181 1558.624 -745.5903
## m0       2 18 1517.847 1592.209 -740.9235 1 vs 2 9.333689 0.2296

print(cvs.anx.fix[3])

## [1] "marital.status"

m <- update(m0, .~. -cv10)
a <- anova(m,m0)
diff <- a$AIC[2] - a$AIC[1]
aic0[3] <- diff
print(a)

##      Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## m        1 17 1516.114 1586.345 -741.0571
## m0       2 18 1517.847 1592.209 -740.9235 1 vs 2 0.2672973 0.6052

print(cvs.anx.fix[4])

## [1] "cohab"

m <- update(m0, .~. -cv11)
a <- anova(m,m0)
diff <- a$AIC[2] - a$AIC[1]
aic0[4] <- diff
print(a)

```




```
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m        1 16 1526.345 1592.444 -747.1723
## m0       2 18 1517.847 1592.209 -740.9235 1 vs 2 12.49774 0.0019
```

```
print(cvs.anx.fix[5])
```

```
## [1] "coparent"
```

```
m <- update(m0, .~. -cv12)
a <- anova(m,m0)
diff <- a$AIC[2] - a$AIC[1]
aic0[5] <- diff
print(a)
```

```
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m        1 16 1515.306 1581.406 -741.6530
## m0       2 18 1517.847 1592.209 -740.9235 1 vs 2 1.459097 0.4821
```

```
print(aic0)
```

```
## [1] -3.175343 4.666311 1.732703 -8.497738 2.540903
```

**** Eliminate coparenting - it does not improve model with 4 control variables and increases AIC the most ****

```
cvs.anx.fix <- c("rel.length.c", "orientation", "marital.status", "cohab")
data <- na.omit(study1.long[c(vars,cvs.anx.fix)])
dv <- data$anxiety
iv <- data$hierarchy
id <- data$Respondent.ID
cv1 <- data$rel.length.c
cv6 <- data$orientation
cv10 <- data$marital.status
cv11 <- data$cohab
aic0 <- numeric()
m0 <- lme(dv ~ iv + cv1 + cv6 + cv10 + cv11,
          random = list(id = pdSymm(form = ~ 1)),
          weights = varIdent(form = ~ 1 | iv),
          method="ML")
```

```
print(cvs.anx.fix[1])
```

```
## [1] "rel.length.c"
```

```
m <- update(m0, .~. -cv1)
a <- anova(m,m0)
diff <- a$AIC[2] - a$AIC[1]
aic0[1] <- diff
print(a)
```

```
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m        1 15 1517.321 1579.289 -743.6602
## m0       2 16 1515.306 1581.406 -741.6530 1 vs 2 4.014495 0.0451
```

```
print(cvs.anx.fix[2])
```

```
## [1] "orientation"
```

```
m <- update(m0, .~. -cv6)
a <- anova(m,m0)
```



```
diff <- a$AIC[2] - a$AIC[1]
aic0[2] <- diff
print(a)
```

```
##      Model df      AIC      BIC   logLik   Test  L.Ratio p-value
## m        1  9 1510.106 1547.287 -746.053
## m0       2 16 1515.306 1581.406 -741.653 1 vs 2 8.800016 0.2673
```

```
print(cvs.anx.fix[3])
```

```
## [1] "marital.status"
```

```
m <- update(m0, .~. -cv10)
a <- anova(m,m0)
diff <- a$AIC[2] - a$AIC[1]
aic0[3] <- diff
print(a)
```

```
##      Model df      AIC      BIC   logLik   Test  L.Ratio p-value
## m        1 15 1513.449 1575.418 -741.7248
## m0       2 16 1515.306 1581.406 -741.6530 1 vs 2 0.1435067 0.7048
```

```
print(cvs.anx.fix[4])
```

```
## [1] "cohab"
```

```
m <- update(m0, .~. -cv11)
a <- anova(m,m0)
diff <- a$AIC[2] - a$AIC[1]
aic0[4] <- diff
print(a)
```

```
##      Model df      AIC      BIC   logLik   Test  L.Ratio p-value
## m        1 14 1523.208 1581.045 -747.6041
## m0       2 16 1515.306 1581.406 -741.6530 1 vs 2 11.90224 0.0026
```

```
print(aic0)
```

```
## [1] -2.014495  5.199984  1.856493 -7.902243
```

```
** Eliminate orientation - it does not improve a model with 3 control variables and it increases AIC the most
**
```

```
cvs.anx.fix <- c("rel.length.c", "marital.status", "cohab")
data <- na.omit(study1.long[c(vars,cvs.anx.fix)])
dv <- data$anxiety
iv <- data$hierarchy
id <- data$Respondent.ID
cv1 <- data$rel.length.c
cv10 <- data$marital.status
cv11 <- data$cohab
aic0 <- numeric()

m0 <- lme(dv ~ iv + cv1 + cv10 + cv11,
          random = list(id = pdSymm(form = ~ 1)),
          weights = varIdent(form = ~ 1 | iv),
          method="ML")
```



```
print(cvs.anx.fix[1])

## [1] "rel.length.c"
m <- update(m0, .~. -cv1)
a <- anova(m,m0)
diff <- a$AIC[2] - a$AIC[1]
aic0[1] <- diff
print(a)

##      Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## m         1  8 1835.759 1870.354 -909.8798
## m0        2  9 1831.461 1870.380 -906.7305 1 vs 2 6.298463 0.0121

print(cvs.anx.fix[2])

## [1] "marital.status"
m <- update(m0, .~. -cv10)
a <- anova(m,m0)
diff <- a$AIC[2] - a$AIC[1]
aic0[2] <- diff
print(a)

##      Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## m         1  8 1829.702 1864.297 -906.8510
## m0        2  9 1831.461 1870.380 -906.7305 1 vs 2 0.2410078 0.6235

print(cvs.anx.fix[3])

## [1] "cohab"
m <- update(m0, .~. -cv11)
a <- anova(m,m0)
diff <- a$AIC[2] - a$AIC[1]
aic0[3] <- diff
print(a)

##      Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## m         1  7 1838.741 1869.012 -912.3707
## m0        2  9 1831.461 1870.380 -906.7305 1 vs 2 11.28028 0.0036

print(aic0)

## [1] -4.298463  1.758992 -7.280277

** Eliminate marital status **

cvs.anx.fix <- c("rel.length.c", "cohab")
data <- na.omit(study1.long[c(vars,cvs.anx.fix)])
dv <- data$anxiety
iv <- data$hierarchy
id <- data$Respondent.ID
cv1 <- data$rel.length.c
cv11 <- data$cohab
aic0 <- numeric()

m0 <- lme(dv ~ iv + cv1 + cv11,
          random = list(id = pdSymm(form = ~ 1)),
```



```
weights = varIdent(form = ~ 1 | iv),
method="ML")

print(cvs.anx.fix[1])

## [1] "rel.length.c"
m <- update(m0, .~. -cv1)
a <- anova(m,m0)
diff <- a$AIC[2] - a$AIC[1]
aic0[1] <- diff
print(a)

##      Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## m        1  7 1840.053 1870.323 -913.0264
## m0       2  8 1829.702 1864.297 -906.8510 1 vs 2 12.35068 4e-04

print(cvs.anx.fix[2])

## [1] "cohab"
m <- update(m0, .~. -cv11)
a <- anova(m,m0)
diff <- a$AIC[2] - a$AIC[1]
aic0[2] <- diff
print(a)

##      Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## m        1  6 1840.161 1866.108 -914.0808
## m0       2  8 1829.702 1864.297 -906.8510 1 vs 2 14.45945 7e-04

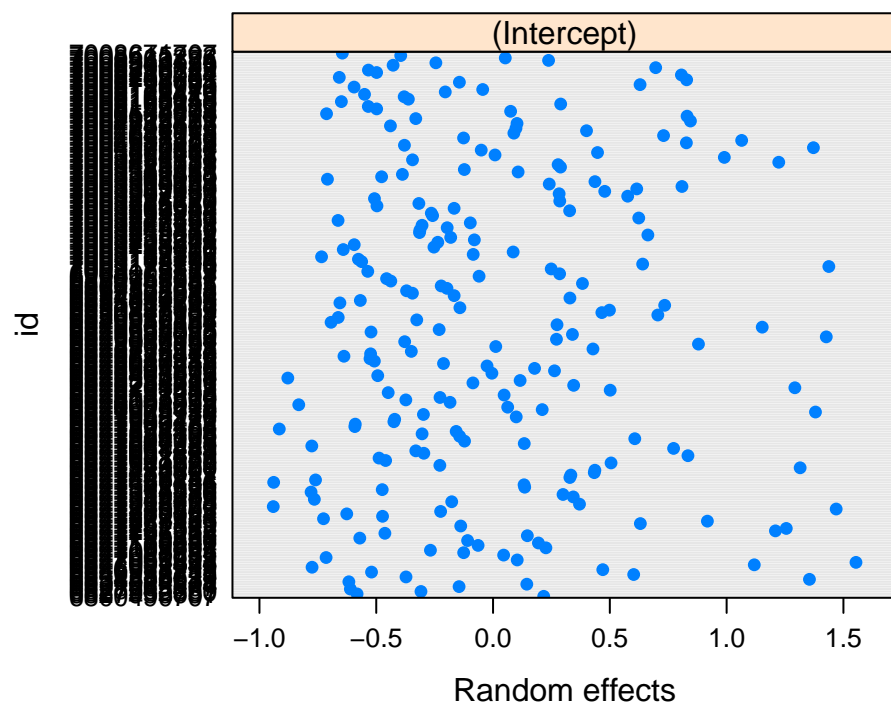
print(aic0)

## [1] -10.35068 -10.45945

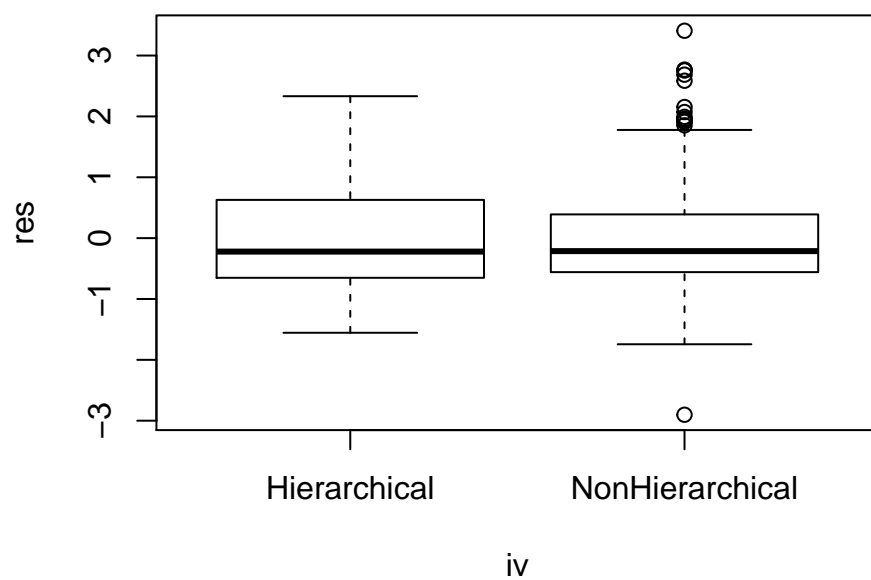
** Keep relationship length and cohabitation **

Residual plots:

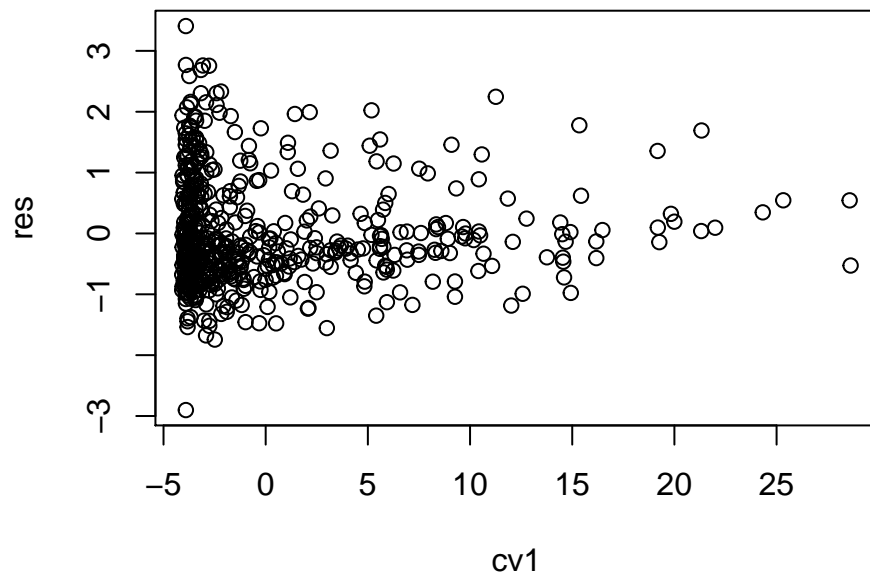
res <- resid(m0, type = "pearson")
fit <- fitted(m0, level=0)
plot(ranef(m0, level = 1))
```



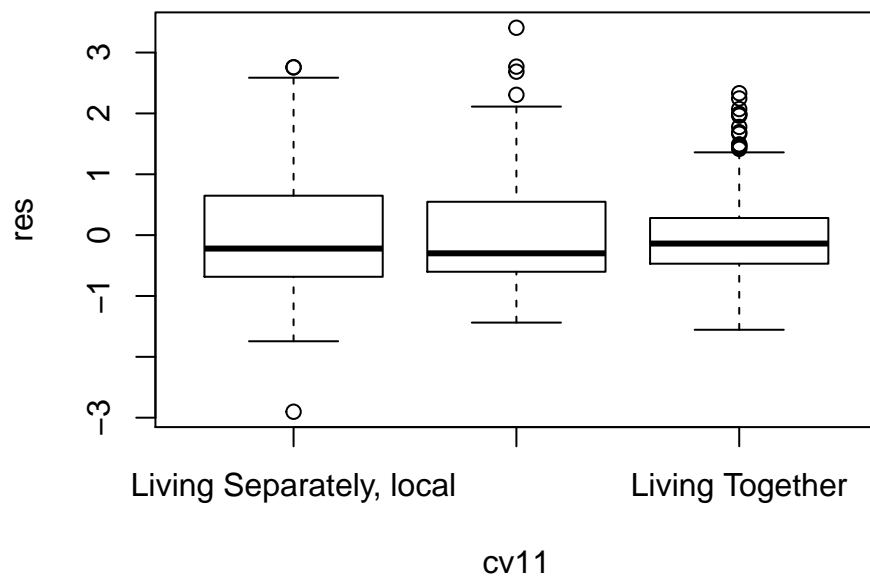
```
plot(res ~ iv)
```



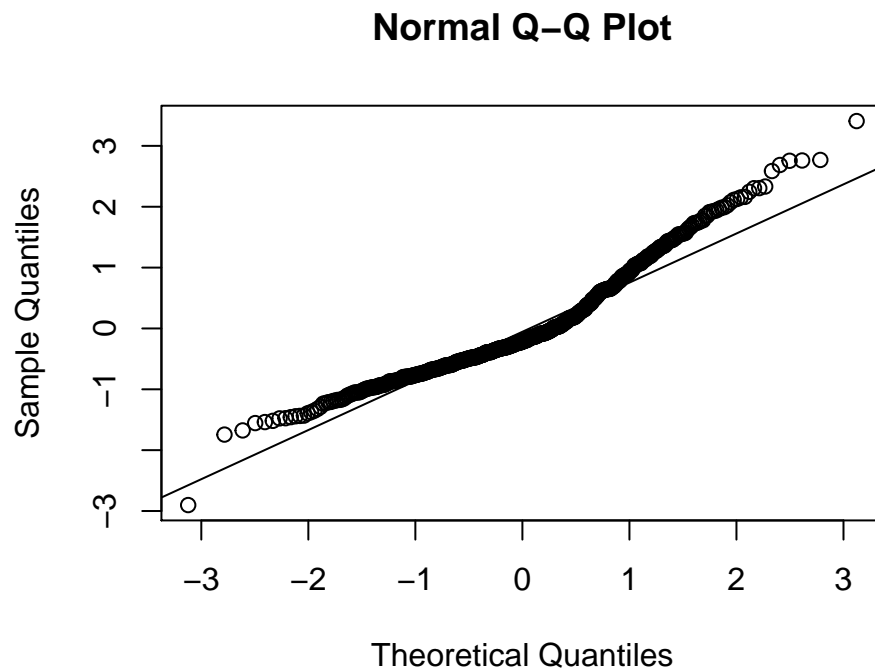
```
plot(res ~ cv1) # rel. length
```



```
plot(res ~ cv1) # cohab
```



```
qqnorm(res)  
qqline(res)
```



Satisfaction

Step 1: add hierarchy type to model from previous analysis

```
data <- na.omit(study1.long[vars])
dv <- data$satisfaction
iv <- data$hierarchy
id <- data$Respondent.ID

m.sat <- lme(dv ~ 1, random = list(id = pdSymm(form = ~ 1)),
            weights = varIdent(form = ~ 1 | iv),
            method="ML")

m.sat.h <- lme(dv ~ iv, random = list(id = pdSymm(form = ~ 1)),
              weights = varIdent(form = ~ 1 | iv),
              method="ML")

print(anova(m.sat, m.sat.h))
```

##	Model	df	AIC	BIC	logLik	Test L.Ratio	p-value
##	m.sat	1	4	2969.064	2986.405	-1480.532	
##	m.sat.h	2	5	2956.329	2978.004	-1473.165	1 vs 2 14.7354 1e-04

Adding hierarchy type as a fixed effect improved the variance model (no fixed effects) for satisfaction.

Step 2: control variables

Checking which potential control variables are related to satisfaction:



```

for(x in cvs){
  data <- na.omit(study1.long[c(vars,x)])
  print(x)
  dv <- data$satisfaction
  iv <- data$hierarchy
  id <- data$Respondent.ID
  cv <- data[[x]]
  m1 <- lme(dv ~ 1, random = list(id = pdSymm(form = ~ 1)),
            weights = varIdent(form = ~ 1 | iv),
            method="ML")
  mcv <- lme(dv ~ cv, random = list(id = pdSymm(form = ~ 1)),
            weights = varIdent(form = ~ 1 | iv),
            method="ML")
  a <- anova(m1,mcv)
  print(a)
}

```

```

## [1] "rel.length.c"
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m1      1  4 2941.305 2958.602 -1466.652
## mcv     2  5 2930.017 2951.638 -1460.008 1 vs 2 13.28801 3e-04
## [1] "age.c"
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m1      1  4 2969.064 2986.405 -1480.532
## mcv     2  5 2970.799 2992.474 -1480.399 1 vs 2 0.2653941 0.6064
## [1] "incomeperPPL.c"
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m1      1  4 2306.772 2323.083 -1149.386
## mcv     2  5 2308.769 2329.158 -1149.385 1 vs 2 0.002634695 0.9591
## [1] "N.Partners.3levels"
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m1      1  4 2969.064 2986.405 -1480.532
## mcv     2  6 2965.087 2991.097 -1476.543 1 vs 2 7.977476 0.0185
## [1] "gender"
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m1      1  4 2461.340 2477.917 -1226.670
## mcv     2  6 2460.173 2485.039 -1224.087 1 vs 2 5.166593 0.0755
## [1] "orientation.binary"
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m1      1  4 2430.531 2447.065 -1211.266
## mcv     2  5 2430.610 2451.276 -1210.305 1 vs 2 1.921985 0.1656
## [1] "race.binary"
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m1      1  4 2448.238 2464.797 -1220.119
## mcv     2  5 2450.140 2470.840 -1220.070 1 vs 2 0.09763496 0.7547
## [1] "children.binary"
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m1      1  4 2461.340 2477.917 -1226.670
## mcv     2  5 2460.307 2481.028 -1225.153 1 vs 2 3.033148 0.0816
## [1] "education.3levels"
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m1      1  4 2419.185 2435.701 -1205.592
## mcv     2  6 2421.665 2446.439 -1204.833 1 vs 2 1.519473 0.4678
## [1] "marital.status"

```




```
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m1      1  4 2969.064 2986.405 -1480.532
## mcv     2  5 2960.798 2982.473 -1475.399 1 vs 2 10.26638 0.0014
## [1] "cohab"
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m1      1  4 2969.064 2986.405 -1480.532
## mcv     2  6 2956.537 2982.548 -1472.269 1 vs 2 16.52699 3e-04
## [1] "coparent"
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m1      1  4 2969.064 2986.405 -1480.532
## mcv     2  6 2962.505 2988.515 -1475.252 1 vs 2 10.55977 0.0051
```

The following variables were related to anxiety: relationship length, marital status, cohabitation, co-parenting.

Model selection strategy: start with a model that includes hierarchy (iv of interest), relationship length, marital status, cohabitation, co-parenting, all as fixed effects variables. Then perform model selection through a backwards elimination process.

```
cvs.sat.fix <- c("rel.length.c", "marital.status", "cohab", "coparent")
data <- na.omit(study1.long[c(vars,cvs.sat.fix)])
dv <- data$satisfaction
iv <- data$hierarchy
id <- data$Respondent.ID
cv1 <- data$rel.length.c
cv10 <- data$marital.status
cv11 <- data$cohab
cv12 <- data$coparent
aic0 <- numeric()
m0 <- lme(dv ~ iv + cv1 + cv10 + cv11 + cv12,
          random = list(id = pdSymm(form = ~ 1)),
          weights = varIdent(form = ~ 1 | iv),
          method="ML")

print(cvs.sat.fix[1])
```

```
## [1] "rel.length.c"
m <- update(m0, .~. -cv1)
a <- anova(m,m0)
diff <- a$AIC[2] - a$AIC[1]
aic0[1] <- diff
print(a)
```

```
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m      1 10 2918.595 2961.839 -1449.298
## m0     2 11 2918.783 2966.351 -1448.391 1 vs 2 1.8124 0.1782

print(cvs.sat.fix[2])
```

```
## [1] "marital.status"
m <- update(m0, .~. -cv10)
a <- anova(m,m0)
diff <- a$AIC[2] - a$AIC[1]
aic0[2] <- diff
print(a)
```

```
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
```



```
## m      1 10 2916.783 2960.027 -1448.392
## m0     2 11 2918.783 2966.351 -1448.391 1 vs 2 0.0003488189 0.9851
```

```
print(cvs.sat.fix[3])
```

```
## [1] "cohab"
```

```
m <- update(m0, .~. -cv11)
a <- anova(m,m0)
diff <- a$AIC[2] - a$AIC[1]
aic0[3] <- diff
print(a)
```

```
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m       1   9 2918.967 2957.886 -1450.483
## m0      2  11 2918.783 2966.351 -1448.391 1 vs 2 4.184037 0.1234
```

```
print(cvs.sat.fix[4])
```

```
## [1] "coparent"
```

```
m <- update(m0, .~. -cv12)
a <- anova(m,m0)
diff <- a$AIC[2] - a$AIC[1]
aic0[4] <- diff
print(a)
```

```
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## m       1   9 2915.791 2954.711 -1448.896
## m0      2  11 2918.783 2966.351 -1448.391 1 vs 2 1.008725 0.6039
```

```
print(aic0)
```

```
## [1] 0.1876002 1.9996512 -0.1840373 2.9912755
```

**** Eliminate coparenting - it does not improve model with 4 control variables and increases AIC the most ****

```
cvs.sat.fix <- c("rel.length.c", "marital.status", "cohab")
data <- na.omit(study1.long[c(vars,cvs.sat.fix)])
dv <- data$satisfaction
iv <- data$hierarchy
id <- data$Respondent.ID
cv1 <- data$rel.length.c
cv10 <- data$marital.status
cv11 <- data$cohab
aic0 <- numeric()
m0 <- lme(dv ~ iv + cv1 + cv10 + cv11,
          random = list(id = pdSymm(form = ~ 1)),
          weights = varIdent(form = ~ 1 | iv),
          method="ML")
```

```
print(cvs.sat.fix[1])
```

```
## [1] "rel.length.c"
```

```
m <- update(m0, .~. -cv1)
a <- anova(m,m0)
diff <- a$AIC[2] - a$AIC[1]
aic0[1] <- diff
```



```
print(a)
```

	Model	df	AIC	BIC	logLik	Test	L.Ratio	p-value
## m	1	8	2916.591	2951.186	-1450.295			
## m0	2	9	2915.791	2954.711	-1448.896	1 vs 2	2.799484	0.0943

```
print(cvs.sat.fix[2])
```

```
## [1] "marital.status"
```

```
m <- update(m0, .~. -cv10)
a <- anova(m,m0)
diff <- a$AIC[2] - a$AIC[1]
aic0[2] <- diff
print(a)
```

	Model	df	AIC	BIC	logLik	Test	L.Ratio	p-value
## m	1	8	2913.801	2948.396	-1448.900			
## m0	2	9	2915.791	2954.711	-1448.896	1 vs 2	0.009129234	0.9239

```
print(cvs.sat.fix[3])
```

```
## [1] "cohab"
```

```
m <- update(m0, .~. -cv11)
a <- anova(m,m0)
diff <- a$AIC[2] - a$AIC[1]
aic0[3] <- diff
print(a)
```

	Model	df	AIC	BIC	logLik	Test	L.Ratio	p-value
## m	1	7	2916.701	2946.972	-1451.351			
## m0	2	9	2915.791	2954.711	-1448.896	1 vs 2	4.909633	0.0859

```
print(aic0)
```

```
## [1] -0.7994839 1.9908708 -0.9096331
```

```
** Eliminate marital status **
```

```
cvs.sat.fix <- c("rel.length.c", "cohab")
data <- na.omit(study1.long[c(vars,cvs.sat.fix)])
dv <- data$satisfaction
iv <- data$hierarchy
id <- data$Respondent.ID
cv1 <- data$rel.length.c
cv11 <- data$cohab
aic0 <- numeric()
```

```
m0 <- lme(dv ~ iv + cv1 + cv11,
  random = list(id = pdSymm(form = ~ 1)),
  weights = varIdent(form = ~ 1 | iv),
  method="ML")
```

```
print(cvs.sat.fix[1])
```

```
## [1] "rel.length.c"
```



```
m <- update(m0, .~. -cv1)
a <- anova(m,m0)
diff <- a$AIC[2] - a$AIC[1]
aic0[1] <- diff
print(a)
```

```
##      Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## m        1  7 2916.617 2946.888 -1451.309
## m0       2  8 2913.801 2948.396 -1448.900 1 vs 2 4.816656 0.0282
```

```
print(cvs.sat.fix[2])
```

```
## [1] "cohab"
```

```
m <- update(m0, .~. -cv11)
a <- anova(m,m0)
diff <- a$AIC[2] - a$AIC[1]
aic0[2] <- diff
print(a)
```

```
##      Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## m        1  6 2915.594 2941.541 -1451.797
## m0       2  8 2913.801 2948.396 -1448.900 1 vs 2 5.793781 0.0552
```

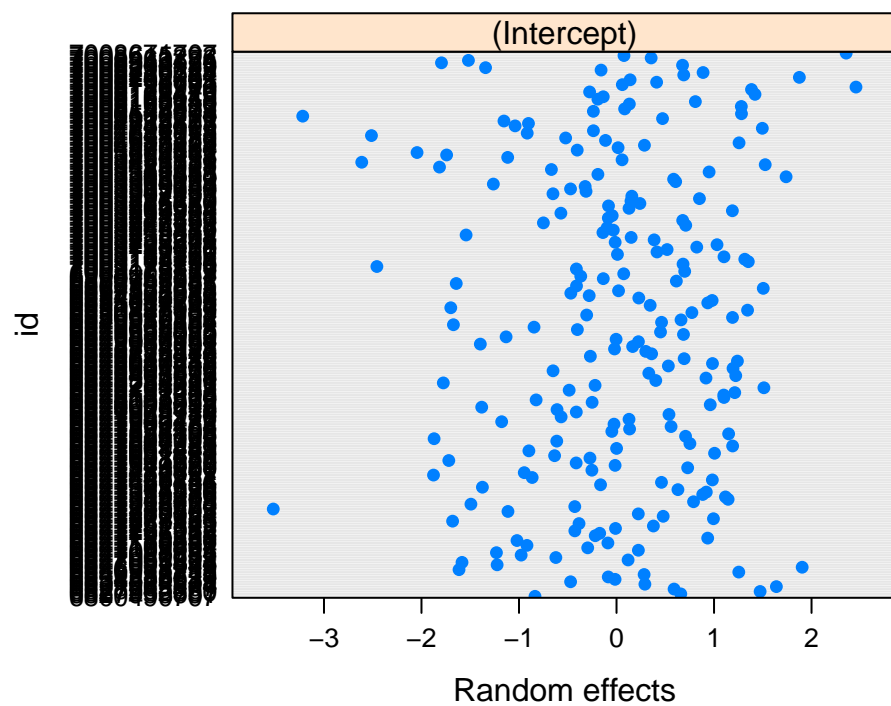
```
print(aic0)
```

```
## [1] -2.816656 -1.793781
```

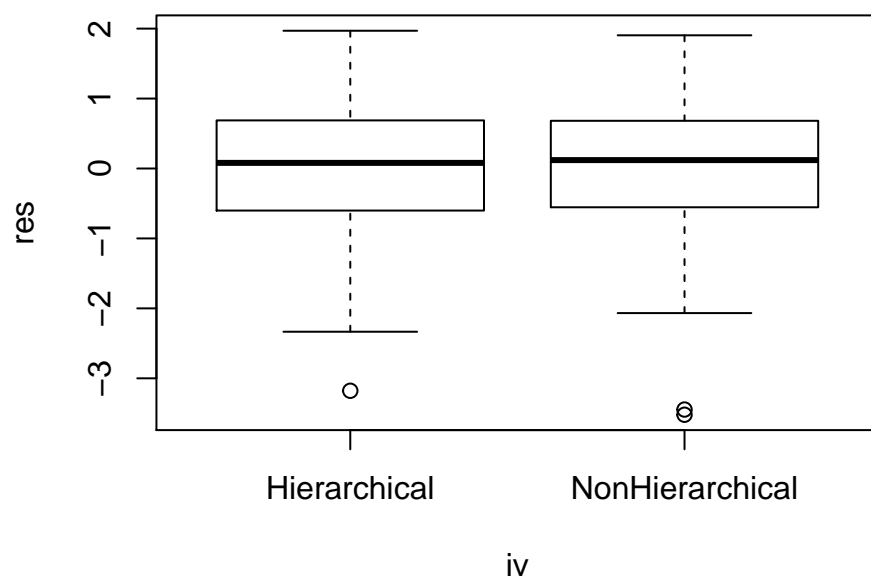
```
** Keep relationship length and cohabitation **
```

Residual plots:

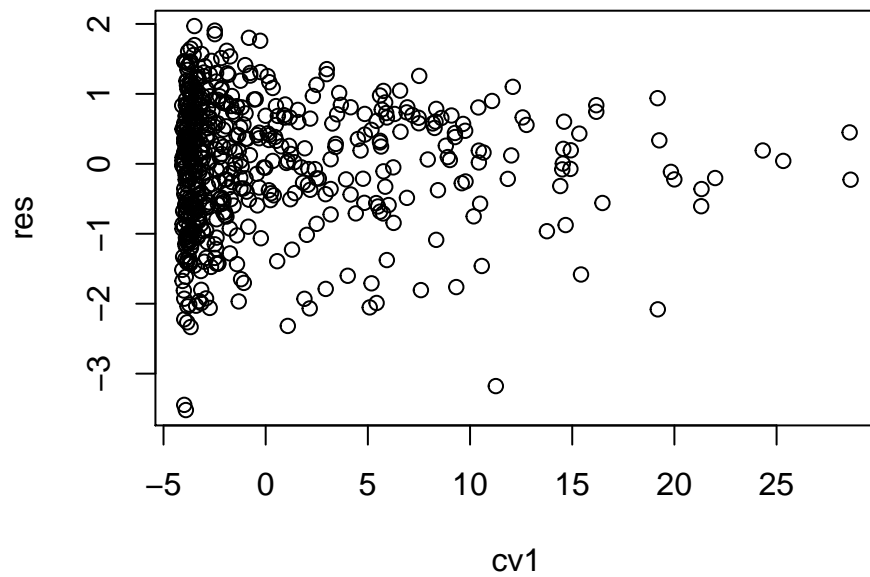
```
res <- resid(m0, type = "pearson")
fit <- fitted(m0, level=0)
plot(ranef(m0, level = 1))
```



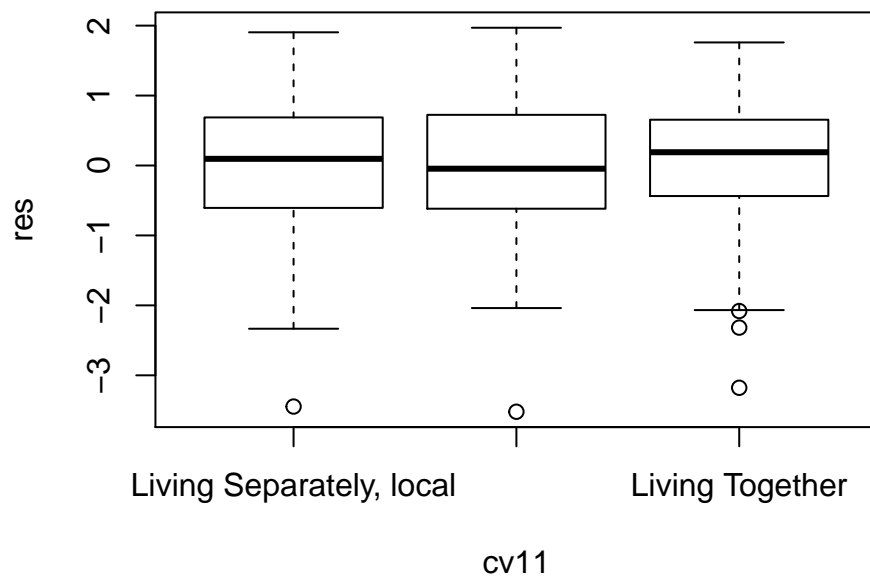
```
plot(res ~ iv)
```



```
plot(res ~ cv1) # rel. length
```



```
plot(res ~ cv11) # cohab
```



```
qqnorm(res)  
qqline(res)
```

