

CO2 Handout

CO2.R:

```
library(nlme)
CO2[1:5,]
plot(CO2,outer=~Treatment*Type,layout=c(4,1))
m1CO2.lis <- nlsList(uptake~SSasypOff(conc,th1,th2,th3),data=CO2)
m1CO2.lis

m1CO2.nlme <- nlme(m1CO2.lis)
# The above call to nlme with input m1CO2.lis is a succinct way to accomplish the
# following
# model specification:
# m1CO2.nlme <- nlme(uptake ~ SSasypOff(conc,th1,th2,th3),data=CO2,
# fixed= th1+th2+th3 ~ 1, random= th1+th2+th3 ~ 1, start=c(mean(coef(m1CO2.lis)[,1]),
# mean(coef(m1CO2.lis)[,2]), mean(coef(m1CO2.lis)[,3]) ))

m1CO2.nlme

m2CO2.nlme <- update( m1CO2.nlme, random= th1+th2 ~ 1)
m2CO2.nlme
anova(m1CO2.nlme,m2CO2.nlme) # remember, this LRT statistics isn't really chi^2, so
# the p
# value here is overestimated
plot(m2CO2.nlme,id=.05,cex=.8,adj=-.5)

m2CO2.nlmeRE <- ranef( m2CO2.nlme, augFrame=T)
m2CO2.nlmeRE

plot(m2CO2.nlmeRE,form = ~ Type*Treatment)

t(cbind(CO2$Type,CO2$Treatment,model.matrix(~Type*Treatment,data=CO2)))

m3CO2.nlme <- update(m2CO2.nlme, fixed=list(th1 + th2 ~ Type*Treatment, th3 ~ 1),
start = c(32.41,0,0,0,-4.56,0,0,0, 49.34) )
summary(m3CO2.nlme)

anova( m3CO2.nlme, Terms= 2:4 ) # tests significance of Type *Treatment terms in
# asymptote
anova( m3CO2.nlme, Terms= 6:8 ) # tests significance of Type *Treatment terms in th2

#Alternatively, LRTs could be used here as follows:

m3aCO2.nlme <- update(m2CO2.nlme, fixed=list(th1 ~1, th2 ~ Type*Treatment, th3 ~ 1),
start = c(32.41,-4.56,0,0,0, 49.34) )
m3bCO2.nlme <- update(m2CO2.nlme, fixed=list(th1 ~ Type*Treatment, th2+th3 ~ 1),
start = c(32.41,0,0,0,-4.56, 49.34) )
anova(m3CO2.nlme,m3aCO2.nlme)# tests significance of Type *Treatment terms in
# asymptote
anova(m3CO2.nlme,m3bCO2.nlme)# tests significance of Type *Treatment terms in th2

# after adding covariates, one or more random effects may no longer be needed
# a rough guide to which random effect is relatively small is to compare the random
# effect's sd with the absolute value of the corresponding fixed effect. Here, based
# on
# m3CO2.nlme we have 2.3496/32.3425=.073 (7.3%) for th1 and .07961/4.5095=.017 (1.7%)
# for th2. Therefore, we consider first dropping the random effect corresponding to
# th2:

m4CO2.nlme <- update(m3CO2.nlme,random= th1 ~ 1)
```

```
anova(m3CO2.nlme,m4CO2.nlme) # remember, this LRT statistics isn't really chi^2, so
  the p
                                # value here is overestimated

# now test for necessity of random effect in th1:
m4coef <- fixef(m4CO2.nlme)
m4coef
m5CO2.gnls <- gnls(uptake~ SSasymptOff(conc,th1,th2,th3),data=CO2,
  params=list(th1+th2~Type*Treatment,th3~1),start=fixef(m4CO2.nlme))
anova(m4CO2.nlme,m5CO2.gnls) # remember, this LRT statistics isn't really chi^2, so
  the p
                                # value here is overestimated

summary(m4CO2.nlme)
plot(augPred(m4CO2.nlme,level=0:1),layout=c(6,2))
```

Output from CO2.R:

```
> library(nlme)
> CO2[1:5,]
Grouped Data: uptake ~ conc | Plant
  Plant  Type  Treatment  conc  uptake
1   Qn1 Quebec nonchilled   95   16.0
2   Qn1 Quebec nonchilled  175   30.4
3   Qn1 Quebec nonchilled  250   34.8
4   Qn1 Quebec nonchilled  350   37.2
5   Qn1 Quebec nonchilled  500   35.3
> plot(CO2,outer=~Treatment*Type,layout=c(4,1))
> mlCO2.lis <- nlsList(uptake~SSasypOff(conc,th1,th2,th3),data=CO2)
> mlCO2.lis
Call:
  Model: uptake ~ SSasypOff(conc, th1, th2, th3) | Plant
  Data: CO2

Coefficients:
      th1      th2      th3
Qn1 38.13978 -4.380647  51.22324
Qn2 42.87169 -4.665728  55.85816
Qn3 44.22800 -4.486118  54.64958
Qc1 36.42873 -4.861741  31.07538
Qc3 40.68370 -4.945218  35.08889
Qc2 39.81950 -4.463838  72.09422
Mn3 28.48285 -4.591566  46.97188
Mn2 32.12827 -4.466157  56.03863
Mn1 34.08481 -5.064579  36.40805
Mc2 13.55520 -4.560851  13.05675
Mc3 18.53506 -3.465158  67.84877
Mc1 21.78723 -5.142256 -20.39998

Degrees of freedom: 84 total; 48 residual
Residual standard error: 1.79822
>
> mlCO2.nlme <- nlme(mlCO2.lis)
> # The above call to nlme with input mlCO2.lis is a succinct way to accomplish the
  following
> # model specification:
> # mlCO2.nlme <- nlme(uptake ~ SSasypOff(conc,th1,th2,th3),data=CO2,
> # fixed= th1+th2+th3 ~ 1, random= th1+th2+th3 ~ 1,
  start=c(mean(coef(mlCO2.lis)[,1]),
> # mean(coef(mlCO2.lis)[,2]), mean(coef(mlCO2.lis)[,3]) ))
>
> mlCO2.nlme
Nonlinear mixed-effects model fit by maximum likelihood
  Model: uptake ~ SSasypOff(conc, th1, th2, th3)
  Data: CO2
  Log-likelihood: -201.3106
  Fixed: list(th1 ~ 1, th2 ~ 1, th3 ~ 1)
      th1      th2      th3
32.473902 -4.636174 43.546754

Random effects:
  Formula: list(th1 ~ 1, th2 ~ 1, th3 ~ 1)
  Level: Plant
  Structure: General positive-definite, Log-Cholesky parametrization
      StdDev      Corr
th1      9.5105877  th1  th2
th2      0.1285620 -0.162
th3     10.3742988  1.000 -0.140
Residual 1.7665298
```

```

Number of Observations: 84
Number of Groups: 12
>
> m2CO2.nlme <- update( m1CO2.nlme, random= th1+th2 ~ 1)
> m2CO2.nlme
Nonlinear mixed-effects model fit by maximum likelihood
  Model: uptake ~ SSasymptOff(conc, th1, th2, th3)
  Data: CO2
  Log-likelihood: -202.7583
  Fixed: list(th1 ~ 1, th2 ~ 1, th3 ~ 1)
           th1      th2      th3
32.411764 -4.560265 49.343573

Random effects:
  Formula: list(th1 ~ 1, th2 ~ 1)
  Level: Plant
  Structure: General positive-definite, Log-Cholesky parametrization
           StdDev   Corr
th1      9.6593926 th1
th2      0.1995124 -0.777
Residual 1.8079224

Number of Observations: 84
Number of Groups: 12
> anova(m1CO2.nlme,m2CO2.nlme) # remember, this LRT statistics isn't really chi^2, so
  the p
      Model df      AIC      BIC    logLik    Test L.Ratio p-value
m1CO2.nlme   1 10 422.6212 446.9293 -201.3106
m2CO2.nlme   2  7 419.5167 436.5324 -202.7583 1 vs 2 2.89549  0.408
> # value here is overestimated
> plot(m2CO2.nlme,id=.05,cex=.8,adj=-.5)
>
> m2CO2.nlmeRE <- ranef( m2CO2.nlme, augFrame=T)
> m2CO2.nlmeRE
           th1      th2      Type Treatment conc uptake
Qn1  6.1715987  0.048361985  Quebec nonchilled  435 33.22857
Qn2 10.5325882 -0.172842971  Quebec nonchilled  435 35.15714
Qn3 12.2180908 -0.057987100  Quebec nonchilled  435 37.61429
Qc1  3.3521234 -0.075586358  Quebec chilled  435 29.97143
Qc3  7.4743083 -0.192416381  Quebec chilled  435 32.58571
Qc2  7.9284657 -0.180323624  Quebec chilled  435 32.70000
Mn3 -4.0733486  0.033449394  Mississippi nonchilled  435 24.11429
Mn2 -0.1419773  0.005645756  Mississippi nonchilled  435 27.34286
Mn1  0.2406596 -0.193859245  Mississippi nonchilled  435 26.40000
Mc2 -18.7991627  0.319367709  Mississippi chilled  435 12.14286
Mc3 -13.1168244  0.299428913  Mississippi chilled  435 17.30000
Mc1 -11.7865217  0.166761922  Mississippi chilled  435 18.00000
>
> plot(m2CO2.nlmeRE,form = ~ Type*Treatment)
>
> t(cbind(CO2$Type,CO2$Treatment,model.matrix(~Type*Treatment,data=CO2)))
           1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18
(Intercept)  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1
TypeMississippi  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0
Treatmentchilled  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0
TypeMississippi:Treatmentchilled  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0
           19 20 21 22 23 24 25 26 27 28 29 30 31 32 33
(Intercept)  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1

```

```

TypeMississippi      0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
Treatmentchilled    0 0 0 1 1 1 1 1 1 1 1 1 1 1 1
TypeMississippi:Treatmentchilled 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
34 35 36 37 38 39 40 41 42 43 44 45 46 47 48
1 1 1 1 1 1 1 1 1 1 2 2 2 2 2
2 2 2 2 2 2 2 2 2 1 1 1 1 1 1
(Intercept)        1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
TypeMississippi    0 0 0 0 0 0 0 0 0 1 1 1 1 1 1
Treatmentchilled   1 1 1 1 1 1 1 1 1 0 0 0 0 0 0
TypeMississippi:Treatmentchilled 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
49 50 51 52 53 54 55 56 57 58 59 60 61 62 63
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
(Intercept)        1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
TypeMississippi    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Treatmentchilled   0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
TypeMississippi:Treatmentchilled 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
64 65 66 67 68 69 70 71 72 73 74 75 76 77 78
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
(Intercept)        1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
TypeMississippi    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Treatmentchilled   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
TypeMississippi:Treatmentchilled 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
79 80 81 82 83 84
2 2 2 2 2 2
2 2 2 2 2 2
(Intercept)        1 1 1 1 1 1
TypeMississippi    1 1 1 1 1 1
Treatmentchilled   1 1 1 1 1 1
TypeMississippi:Treatmentchilled 1 1 1 1 1 1

```

```

>
> m3CO2.nlm2 <- update(m2CO2.nlm2, fixed=list(th1 + th2 ~ Type*Treatment, th3 ~ 1),
+ start = c(32.41,0,0,0,-4.56,0,0,0, 49.34) )
> summary(m3CO2.nlm2)

```

Nonlinear mixed-effects model fit by maximum likelihood

Model: uptake ~ SSasymptOff(conc, th1, th2, th3)

Data: CO2
AIC BIC logLik
388.418 420.0186 -181.209

Random effects:

Formula: list(th1 ~ 1, th2 ~ 1)
Level: Plant
Structure: General positive-definite, Log-Cholesky parametrization

	StdDev	Corr
th1.(Intercept)	2.34968044	t1.(I)
th2.(Intercept)	0.07960365	-0.92
Residual	1.79195661	

Fixed effects: list(th1 + th2 ~ Type * Treatment, th3 ~ 1)

	Value	Std.Error	DF	t-value	p-value
th1.(Intercept)	41.81757	1.562449	64	26.76411	0.0000
th1.TypeMississippi	-10.53049	2.208351	64	-4.76848	0.0000
th1.Treatmentchilled	-2.96941	2.213206	64	-1.34168	0.1844
th1.TypeMississippi:Treatmentchilled	-10.89927	3.112280	64	-3.50202	0.0008
th2.(Intercept)	-4.55726	0.096292	64	-47.32747	0.0000
th2.TypeMississippi	-0.10411	0.121685	64	-0.85554	0.3954
th2.Treatmentchilled	-0.17124	0.111962	64	-1.52947	0.1311
th2.TypeMississippi:Treatmentchilled	0.74124	0.221716	64	3.34317	0.0014
th3	50.50779	4.364865	64	11.57144	0.0000

Correlation:

t1.(I) th1.TM th1.Tr t1.TM: t2.(I) th2.TM

```

th1.TypeMississippi          -0.703
th1.Treatmentchilled        -0.701  0.496
th1.TypeMississippi:Treatmentchilled  0.497 -0.709 -0.711
th2.(Intercept)              -0.627  0.415  0.407 -0.278
th2.TypeMississippi          0.458 -0.680 -0.322  0.482 -0.535
th2.Treatmentchilled         0.500 -0.351 -0.717  0.509 -0.594  0.445
th2.TypeMississippi:Treatmentchilled -0.262  0.375  0.362 -0.547  0.365 -0.553
th3                           -0.086  0.014  0.001  0.019  0.590 -0.033
                                th2.Tr t2.TM:

```

```

th1.TypeMississippi
th1.Treatmentchilled
th1.TypeMississippi:Treatmentchilled
th2.(Intercept)
th2.TypeMississippi
th2.Treatmentchilled
th2.TypeMississippi:Treatmentchilled -0.511
th3                                -0.057  0.140

```

```

Standardized Within-Group Residuals:
      Min      Q1      Med      Q3      Max
-2.86200009 -0.49444089 -0.04219099  0.56603935  3.04071100

```

Number of Observations: 84

Number of Groups: 12

>

```
> anova( m3CO2.nlme, Terms= 2:4 ) # tests significance of Type *Treatment terms in
asymptote
```

```
F-test for: th1.Type, th1.Treatment, th1.Type:Treatment
```

```
  numDF denDF  F-value p-value
1      3     64 49.91221 <.0001
```

```
> anova( m3CO2.nlme, Terms= 6:8 ) # tests significance of Type *Treatment terms in th2
```

```
F-test for: th2.Type, th2.Treatment, th2.Type:Treatment
```

```
  numDF denDF  F-value p-value
1      3     64 4.199872  0.0089
```

>

```
> #Alternatively, LRTs could be used here as follows:
```

>

```
> m3aCO2.nlme <- update(m2CO2.nlme, fixed=list(th1 ~1, th2 ~ Type*Treatment, th3 ~ 1),
+ start = c(32.41,-4.56,0,0,0, 49.34) )
```

```
> m3bCO2.nlme <- update(m2CO2.nlme, fixed=list(th1 ~ Type*Treatment, th2+th3 ~ 1),
+ start = c(32.41,0,0,0,-4.56, 49.34) )
```

```
> anova(m3CO2.nlme,m3aCO2.nlme)# tests significance of Type *Treatment terms in
asymptote
```

```

      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
m3CO2.nlme    1 13 388.4180 420.0186 -181.2090
m3aCO2.nlme    2 10 414.7932 439.1014 -197.3966 1 vs 2 32.37523 <.0001

```

```
> anova(m3CO2.nlme,m3bCO2.nlme)# tests significance of Type *Treatment terms in th2
```

```

      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
m3CO2.nlme    1 13 388.4180 420.0186 -181.2090
m3bCO2.nlme    2 10 393.6765 417.9847 -186.8383 1 vs 2 11.25857 0.0104

```

>

```
> # after adding covariates, one or more random effects may no longer be needed
> # a rough guide to which random effect is relatively small is to compare the random
> # effect's sd with the absolute value of the corresponding fixed effect. Here, based
on
```

```
> # m3CO2.nlme we have 2.3496/32.3425=.073 (7.3%) for th1 and .07961/4.5095=.017
(1.7%)
```

```
> # for th2. Therefore, we consider first dropping the random effect corresponding to
th2:
```

>

```
> m4CO2.nlme <- update(m3CO2.nlme,random= th1 ~ 1)
```

```
> anova(m3CO2.nlme,m4CO2.nlme) # remember, this LRT statistics isn't really chi^2, so
the p
```

```

      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
m3CO2.nlme    1 13 388.4180 420.0186 -181.2090
m4CO2.nlme    2 11 387.0552 413.7942 -182.5276 1 vs 2 2.637221 0.2675
>
> # value here is overestimated
>
> # now test for necessity of random effect in th1:
> m4coef <- fixef(m4CO2.nlme)
> m4coef
      th1.(Intercept)          th1.TypeMississippi
      41.85406331          -10.56657039
th1.Treatmentchilled th1.TypeMississippi:Treatmentchilled
      -2.94957184          -10.90069619
      th2.(Intercept)          th2.TypeMississippi
      -4.57241024          -0.09656911
th2.Treatmentchilled th2.TypeMississippi:Treatmentchilled
      -0.17096784          0.71723763
      th3
      50.12288837
> m5CO2.gnls <- gnls(uptake~ SSasymptOff(conc,th1,th2,th3),data=CO2,
+   params=list(th1+th2~Type*Treatment,th3~1),start=fixef(m4CO2.nlme))
> anova(m4CO2.nlme,m5CO2.gnls) # remember, this LRT statistics isn't really chi^2, so
the p
      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
m4CO2.nlme    1 11 387.0552 413.7942 -182.5276
m5CO2.gnls    2 10 418.3440 442.6522 -199.1720 1 vs 2 33.28885 <.0001
>
> # value here is overestimated
>
> summary(m4CO2.nlme)
Nonlinear mixed-effects model fit by maximum likelihood
Model: uptake ~ SSasymptOff(conc, th1, th2, th3)
Data: CO2
      AIC      BIC    logLik
387.0552 413.7942 -182.5276

Random effects:
Formula: th1 ~ 1 | Plant
      th1.(Intercept) Residual
StdDev:      2.063599 1.836172

Fixed effects: list(th1 + th2 ~ Type * Treatment, th3 ~ 1)
      Value Std.Error DF  t-value p-value
th1.(Intercept)      41.85406  1.411576  64  29.65058  0.0000
th1.TypeMississippi -10.56657  1.994065  64  -5.29901  0.0000
th1.Treatmentchilled -2.94957  2.000419  64  -1.47448  0.1453
th1.TypeMississippi:Treatmentchilled -10.90070  2.808000  64  -3.88201  0.0002
th2.(Intercept)     -4.57241  0.085233  64 -53.64576  0.0000
th2.TypeMississippi -0.09657  0.102861  64  -0.93883  0.3513
th2.Treatmentchilled -0.17097  0.090413  64  -1.89096  0.0632
th2.TypeMississippi:Treatmentchilled  0.71724  0.204411  64   3.50881  0.0008
th3                  50.12289  4.515320  64  11.10063  0.0000

Correlation:
      t1.(I) th1.TM th1.Tr t1.TM: t2.(I) th2.TM
th1.TypeMississippi -0.702
th1.Treatmentchilled -0.699  0.495
th1.TypeMississippi:Treatmentchilled  0.496 -0.710 -0.712
th2.(Intercept)     -0.265  0.151  0.140 -0.085
th2.TypeMississippi  0.167 -0.280 -0.115  0.198 -0.465
th2.Treatmentchilled  0.193 -0.133 -0.289  0.204 -0.550  0.417
th2.TypeMississippi:Treatmentchilled -0.098  0.143  0.128 -0.223  0.328 -0.508
th3                  -0.099  0.016  0.001  0.021  0.685 -0.038
th2.Tr t2.TM:

th1.TypeMississippi
th1.Treatmentchilled

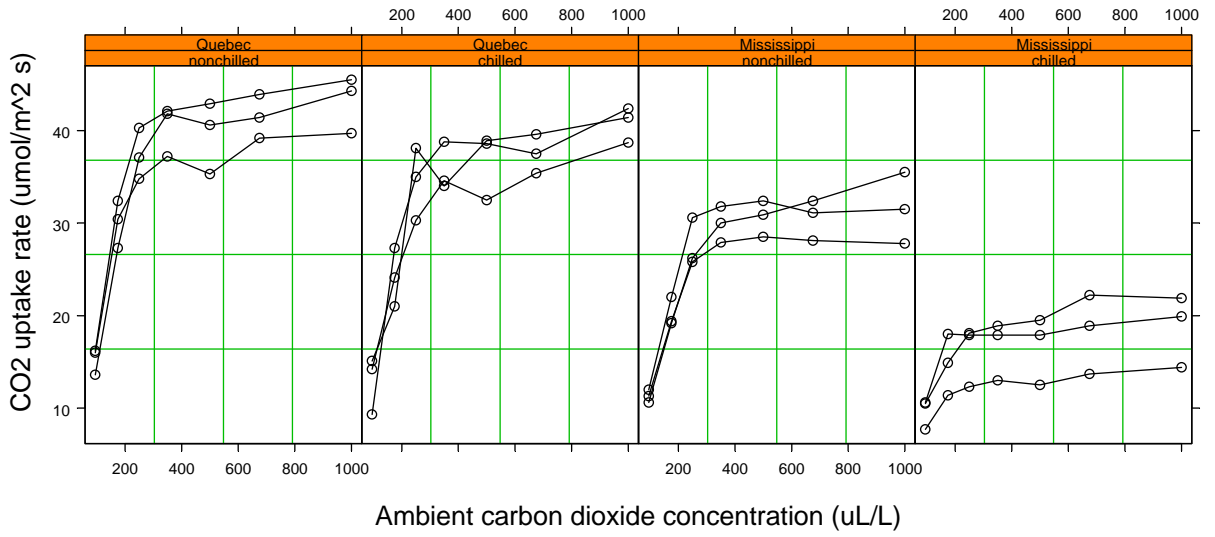
```

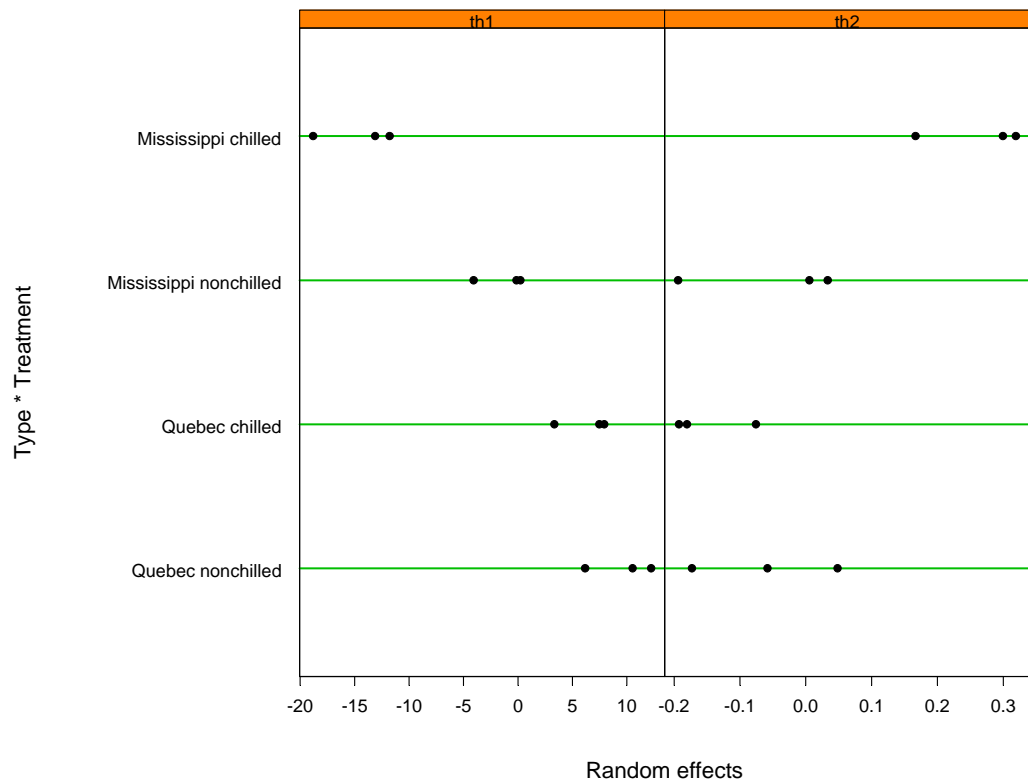
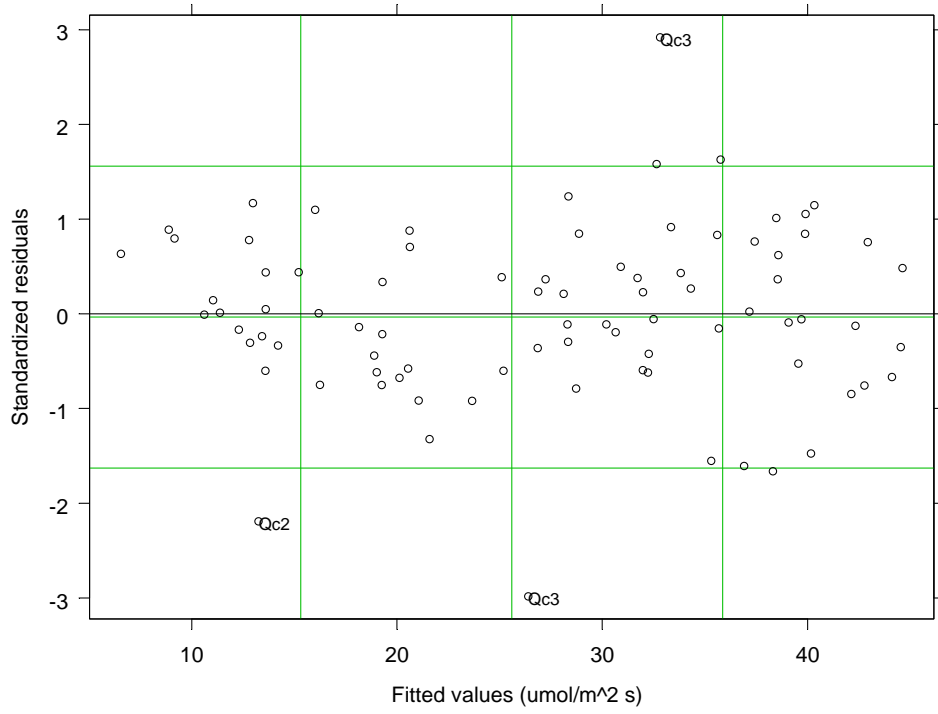
```
th1.TypeMississippi:Treatmentchilled
th2.(Intercept)
th2.TypeMississippi
th2.Treatmentchilled
th2.TypeMississippi:Treatmentchilled -0.451
th3 -0.073 0.156

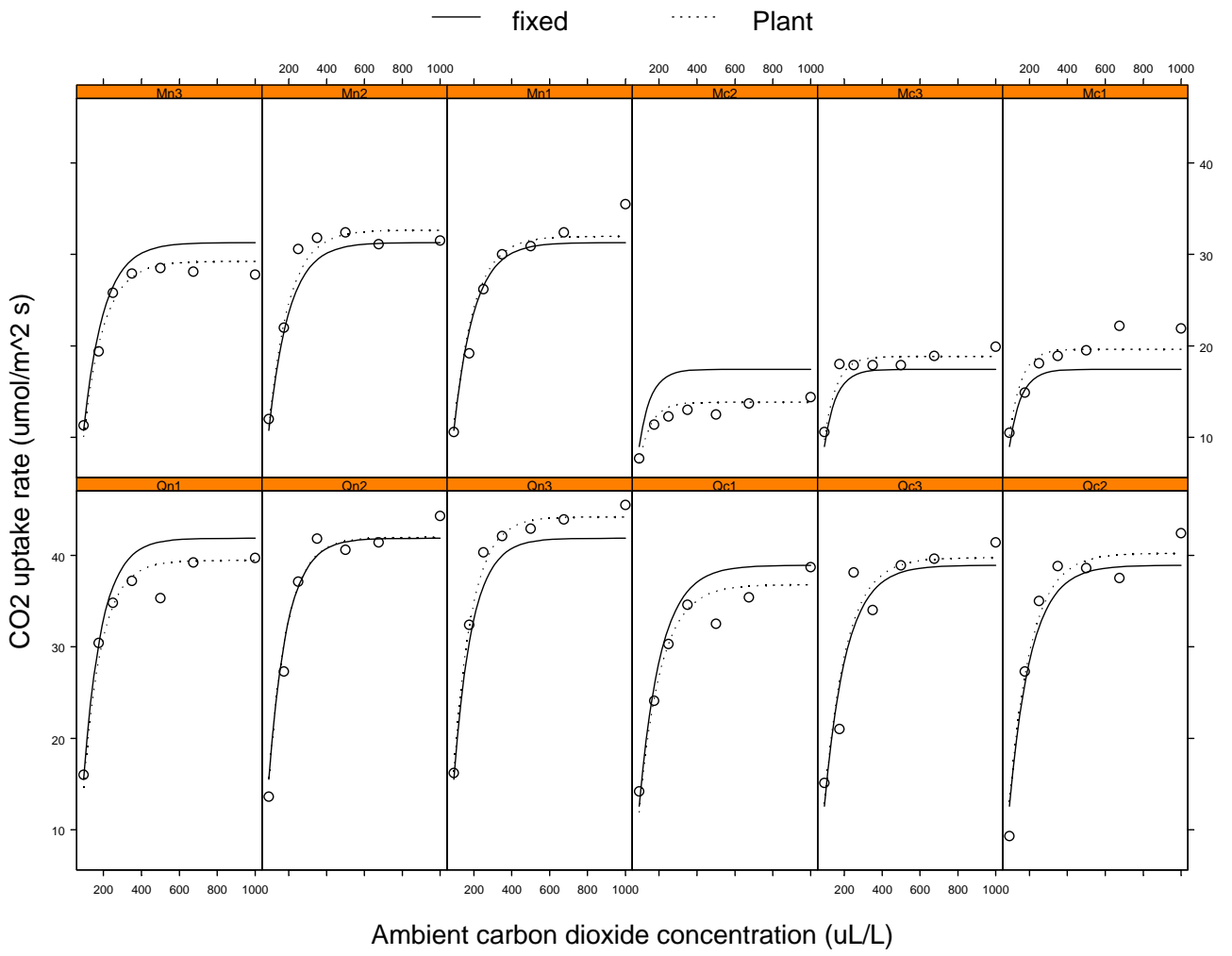
Standardized Within-Group Residuals:
      Min      Q1      Med      Q3      Max
-2.90872164 -0.45013350 -0.04087351 0.58512285 2.90637173

Number of Observations: 84
Number of Groups: 12
> plot(augPred(m4CO2.nlme,level=0:1),layout=c(6,2))
>
>
```


Plots from CO2.R:







CO2.sas:

```
options ls=78 pageno=1 nodate;
```

```
data one;
```

```
  infile 'n:\courses\stat8230\Fall09\nlmeCO2.dat' firstobs=2;
```

```
  input obsno  Plant $  Type $  Treat $  conc uptake ;
```

```
  xtype= 0*(type='Quebec')+1*(type='Mississ');
```

```
  xtrt= 0*(treat='nonchill')+1*(treat='chill');
```

```
  xtrttype=xtype*xtrt;
```

```
run;
```

```
proc sort;
```

```
  by plant;
```

```
run;
```

```
proc nlmixed data=one method=gauss;
```

```
  parms th10=42 th11=-10 th12=-3 th13=-11 th20=-4.6 th21=-.1 th22=-.2
```

```
        th23=.7 th3=50 sig2=4 psill=3.5;
```

```
  th1=th10+th11*xtype+th12*xtrt+th13*xtrttype+b;
```

```
  th2=th20+th21*xtype+th22*xtrt+th23*xtrttype;
```

```
  mean= th1*(1-exp(-exp(th2)*(conc-th3)));
```

```
  model uptake ~ normal(mean,sig2);
```

```
  random b ~ normal( 0, psill ) subject=plant;
```

```
run;
```

Output from CO2.sas:

The SAS System

1

The NL MIXED Procedure

Specifications

Data Set	WORK.ONE
Dependent Variable	uptake
Distribution for Dependent Variable	Normal
Random Effects	b
Distribution for Random Effects	Normal
Subject Variable	Plant
Optimization Technique	Dual Quasi-Newton
Integration Method	Adaptive Gaussian Quadrature

Dimensions

Observations Used	84
Observations Not Used	0
Total Observations	84
Subjects	12
Max Obs Per Subject	7
Parameters	11
Quadrature Points	1

Parameters

th10	th11	th12	th13	th20	th21	th22	th23
42	-10	-3	-11	-4.6	-0.1	-0.2	0.7

Parameters

th3	sig2	psi11	NegLogLike
50	4	3.5	183.824519

Iteration History

Iter	Calls	NegLogLike	Diff	MaxGrad	Slope
1	4	183.387266	0.437253	2.862998	-169.327
2	6	183.328045	0.059221	1.344453	-0.0218
3	8	183.287856	0.040189	6.428232	-0.02925
4	10	182.735958	0.551898	1.540587	-0.37297
5	11	182.717733	0.018225	0.691183	-0.02766
6	12	182.712342	0.005391	2.134704	-0.01294
7	14	182.692426	0.019916	0.409779	-0.02624
8	16	182.65139	0.041036	0.915862	-0.01214
9	18	182.639338	0.012051	0.513377	-0.00948

The NL MIXED Procedure

Iteration History

Iter	Calls	NegLogLike	Diff	MaxGrad	Slope
10	20	182.598927	0.040411	0.332902	-0.01286
11	22	182.597102	0.001825	0.189378	-0.00316
12	23	182.594196	0.002906	1.077225	-0.00064
13	25	182.569016	0.025179	3.462089	-0.00622
14	26	182.533415	0.035601	0.677214	-0.02764
15	28	182.532449	0.000966	0.111109	-0.00183
16	30	182.532378	0.000071	0.21259	-0.00004
17	33	182.52991	0.002469	0.555997	-0.0001
18	34	182.526166	0.003743	0.100477	-0.00305
19	36	182.52593	0.000236	0.008738	-0.00046
20	38	182.525928	2.132E-6	0.013756	-1.35E-6

NOTE: GCONV convergence criterion satisfied.

Fit Statistics

-2 Log Likelihood	365.1
AIC (smaller is better)	387.1
AICC (smaller is better)	390.7
BIC (smaller is better)	392.4

Parameter Estimates

Parameter	Estimate	Standard		t Value	Pr > t	Alpha	Lower
		Error	DF				
th10	41.8268	1.3355	11	31.32	<.0001	0.05	38.8873
th11	-10.4974	1.8863	11	-5.57	0.0002	0.05	-14.6490
th12	-2.8833	1.8932	11	-1.52	0.1560	0.05	-7.0503
th13	-11.0100	2.6594	11	-4.14	0.0016	0.05	-16.8632
th20	-4.5749	0.08081	11	-56.61	<.0001	0.05	-4.7527

Parameter Estimates

Parameter	Upper	Gradient
th10	44.7663	-0.00292
th11	-6.3457	0.006329
th12	1.2837	0.00409
th13	-5.1568	-0.00876
th20	-4.3970	0.006182

The NL MIXED Procedure

Parameter Estimates

Parameter	Estimate	Standard Error	DF	t Value	Pr > t	Alpha	Lower
th21	-0.09846	0.09633	11	-1.02	0.3287	0.05	-0.3105
th22	-0.1721	0.08530	11	-2.02	0.0687	0.05	-0.3598
th23	0.7137	0.2061	11	3.46	0.0053	0.05	0.2602
th3	49.9958	4.3098	11	11.60	<.0001	0.05	40.5099
sig2	3.3711	0.5615	11	6.00	<.0001	0.05	2.1352
psi11	4.2734	2.0034	11	2.13	0.0563	0.05	-0.1360

Parameter Estimates

Parameter	Upper	Gradient
th21	0.1136	0.004096
th22	0.01567	-0.01376
th23	1.1672	-0.00141
th3	59.4816	0.000859
sig2	4.6069	0.000044
psi11	8.6829	0.002308