

Importance of individual to phenological responses of individuals in tissue analysis

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1 Startup

First off, grab the two main libraries for mixed-effects models in R and the experimental data.

```
> options(stringsAsFactors = FALSE)
> setwd("~/Documents/git/projects/treegarden/genetics/analyses")
> library(nlme)
> library(lme4)
> alldater <- read.csv("output/indforGBS.csv", header=TRUE)
```

Since not all individuals received the three chilling treatments, subset to only the no-additional-chilling treatment (which all individuals were in).

```
> daterch0 <- subset(alldater, chill=="chill0")
```

2 With nlme

Fit two basic mixed-effects models, one considering **site** and one considering **individual** as the varying random effect; note that both include **species** as an additional random effect.

```
> lme.mod.sp.ind <- lme(lday~warm*photo, random = list(ind=~1, sp=~1), data=daterch0,
+   na.action=na.exclude)
> lme.mod.sp.site <- lme(lday~warm*photo, random = list(site=~1, sp=~1), data=daterch0,
+   na.action=na.exclude)
```

Now look at the output of the models. We see that with individual in the model we get mildly stronger photoperiod and temperature and interaction effects.

```
> summary(lme.mod.sp.ind)
```

Linear mixed-effects model fit by REML

Data: daterch0

	AIC	BIC	logLik
	2639.539	2666.3	-1312.77

Random effects:

Formula: ~1 | ind
(Intercept)

StdDev: 9.418006

Formula: ~1 | sp %in% ind

```

      (Intercept) Residual
StdDev:    9.418001 8.081702

Fixed effects: lday ~ warm * photo
              Value Std.Error DF   t-value p-value
(Intercept) 181.21222 16.441506 242  11.021631  0e+00
warm         -6.59709  0.923338 242  -7.144824  0e+00
photo        -7.83998  1.590948 242  -4.927867  0e+00
warm:photo    0.31988  0.089777 242   3.563047  4e-04
Correlation:
      (Intr) warm  photo
warm      -0.987
photo     -0.978  0.972
warm:photo 0.968 -0.981 -0.990

Standardized Within-Group Residuals:
      Min      Q1      Med      Q3      Max
-3.91013968 -0.58505260  0.02522124  0.54156647  2.65967148

Number of Observations: 342
Number of Groups:
      ind sp %in% ind
      97      97

> summary(lme.mod.sp.site)

Linear mixed-effects model fit by REML
Data: daterch0
      AIC      BIC    logLik
2563.461 2590.222 -1274.731

Random effects:
Formula: ~1 | site
      (Intercept)
StdDev: 0.002405337

Formula: ~1 | sp %in% site
      (Intercept) Residual
StdDev:    13.17339 9.106168

Fixed effects: lday ~ warm * photo
              Value Std.Error DF   t-value p-value
(Intercept) 177.03711 18.294051 319   9.677305  0.000
warm         -6.45654  1.017946 319  -6.342718  0.000
photo        -7.60251  1.755387 319  -4.330956  0.000
warm:photo    0.30910  0.099122 319   3.118359  0.002
Correlation:
      (Intr) warm  photo
warm      -0.977
photo     -0.968  0.972
warm:photo 0.958 -0.981 -0.990

Standardized Within-Group Residuals:

```

	Min	Q1	Med	Q3	Max
	-4.31574968	-0.58520426	-0.02882628	0.55103469	3.28243199

Number of Observations: 342

Number of Groups:

site	sp	%in%	site
2			20

3 With lme4

The above models are run from package `nlme` which does not easily allow crossed and nested random effects together. And crossed and nested random effects are what we have so let's try the most correct models using the `lme4` package. Here we can look at the same design as the two models above plus a model with both `individual` and `site` (where `individual` is nested within `site`, which is our design).

```
> mod.site.sp <- lmer(lday~warm*photo + (1/sp) + (1/site), data=daterch0,
+   na.action=na.exclude)
> mod.sp.ind <- lmer(lday~warm*photo + (1/sp) + (1/ind), data=daterch0,
+   na.action=na.exclude)
> mod.site.sp.ind <- lmer(lday~warm*photo + (1/sp) + (1/site/ind), data=daterch0,
+   na.action=na.exclude)
```

When we look at the summary of the models we see that `site` explains so little that the models with `individual`, whether nested within `site` or not, are effectively identical.

```
> summary(mod.site.sp) # site explains nada!
```

```
Linear mixed model fit by REML ['lmerMod']
Formula: lday ~ warm * photo + (1 | sp) + (1 | site)
Data: daterch0
```

REML criterion at convergence: 2525

Scaled residuals:

	Min	1Q	Median	3Q	Max
	-4.5067	-0.5964	0.0029	0.5141	3.1119

Random effects:

Groups	Name	Variance	Std.Dev.
sp	(Intercept)	177.8	13.334
site	(Intercept)	0.0	0.000
Residual		84.0	9.165

Number of obs: 342, groups: sp, 10; site, 2

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	175.00104	18.55168	9.433
warm	-6.34310	1.01946	-6.222
photo	-7.40886	1.75799	-4.214
warm:photo	0.29867	0.09932	3.007

Correlation of Fixed Effects:

(Intr)	warm	photo
--------	------	-------

```

warm      -0.964
photo     -0.955  0.972
warm:photo 0.945 -0.981 -0.990

```

```

> # so the below models are identical (wow)
> summary(mod.sp.ind)

```

```

Linear mixed model fit by REML ['lmerMod']
Formula: lday ~ warm * photo + (1 | sp) + (1 | ind)
Data: daterch0

```

REML criterion at convergence: 2505.3

Scaled residuals:

	Min	1Q	Median	3Q	Max
	-4.4827	-0.5881	0.0363	0.4778	2.9141

Random effects:

Groups	Name	Variance	Std.Dev.
ind	(Intercept)	20.07	4.480
sp	(Intercept)	175.04	13.230
Residual		65.33	8.083

Number of obs: 342, groups: ind, 97; sp, 10

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	177.98778	16.68911	10.665
warm	-6.48757	0.91067	-7.124
photo	-7.66842	1.56977	-4.885
warm:photo	0.31149	0.08864	3.514

Correlation of Fixed Effects:

	(Intr)	warm	photo
warm	-0.958		
photo	-0.949	0.972	
warm:photo	0.939	-0.981	-0.990

```

> summary(mod.site.sp.ind)

```

```

Linear mixed model fit by REML ['lmerMod']
Formula: lday ~ warm * photo + (1 | sp) + (1 | site/ind)
Data: daterch0

```

REML criterion at convergence: 2505.3

Scaled residuals:

	Min	1Q	Median	3Q	Max
	-4.4827	-0.5881	0.0363	0.4778	2.9141

Random effects:

Groups	Name	Variance	Std.Dev.
ind:site	(Intercept)	20.07	4.480
sp	(Intercept)	175.04	13.230

```

site      (Intercept)    0.00    0.000
Residual                65.33    8.083
Number of obs: 342, groups: ind:site, 97; sp, 10; site, 2

```

Fixed effects:

```

              Estimate Std. Error t value
(Intercept) 177.98778   16.68911  10.665
warm         -6.48757    0.91067   -7.124
photo        -7.66842    1.56977   -4.885
warm:photo    0.31149    0.08864    3.514

```

Correlation of Fixed Effects:

```

              (Intr) warm  photo
warm          -0.958
photo         -0.949  0.972
warm:photo    0.939 -0.981 -0.990

```

So the good news is that individual matters some. If you look at the variance it's not so much compared to species but it seems a good amount, especially compared to site.