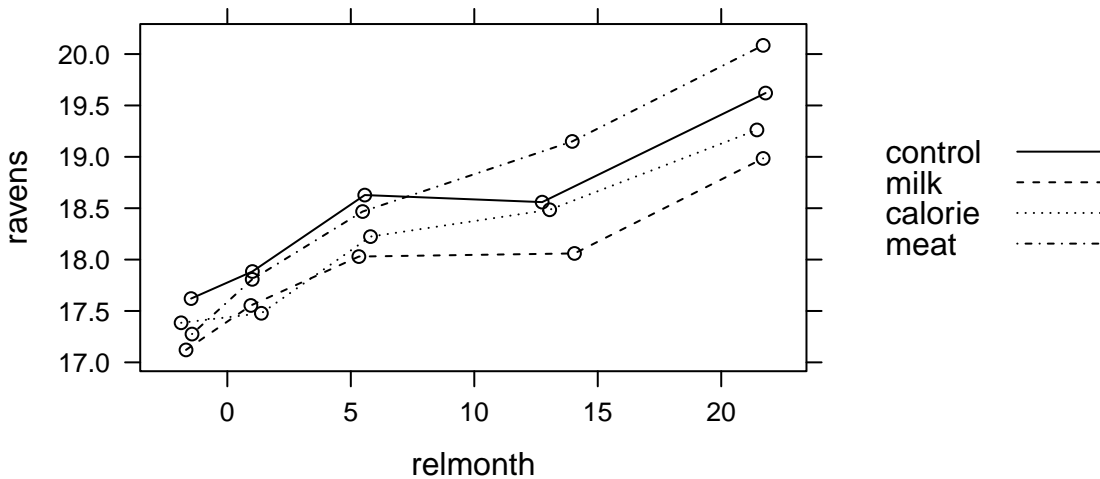


Time as Linear Effect, different by Treatment?

See page 212, section 7.3.4.

Finally, we could include time as linear effect, and see how it differs by treatment.

Here's a plot of those means.



```
> m1 <- lme(ravens ~ relmonth + relmonth:trt, random = ~1 | id,
+ data = r1)
> summary(m1)
```

```
...
Random effects:
Formula: ~1 | id
(Intercept) Residual
StdDev:    1.571213 2.394095
```

```
Fixed effects: ravens ~ relmonth + relmonth:trt
              Value Std.Error DF t-value p-value
(Intercept)  17.597612 0.09398886 2017 187.23083 0.0000
relmonth      0.087214 0.01044508 2017  8.34976 0.0000
relmonth:trtmilk -0.026361 0.01435383 2017 -1.83651 0.0664
relmonth:trtcalorie -0.008877 0.01466419 2017 -0.60538 0.5450
relmonth:trtmeat  0.030606 0.01466966 2017  2.08632 0.0371
...
```

```
> m0 <- lme(ravens ~ relmonth, random = ~1 | id, data = r1)
> m0b <- update(m0, method = "ML")
> m1b <- update(m1, method = "ML")
> anova(m0b, m1b)
```

Model	df	AIC	BIC	logLik	Test	L.Ratio	p-value
m0b	1	4	12325.86	12349.25	-6158.932		
m1b	2	7	12315.14	12356.06	-6150.570	1 vs 2	16.72284 8e-04

Here are slopes:

```
> K1
```

```
      [,1] [,2] [,3] [,4] [,5]
control slope  0  1  0  0  0
milk slope    0  1  1  0  0
calorie slope  0  1  0  1  0
meat slope    0  1  0  0  1
```

```
> t1 <- glht(m1, linfct = K1)
```

```
> summary(t1, test = adjusted(type = "none"))
```

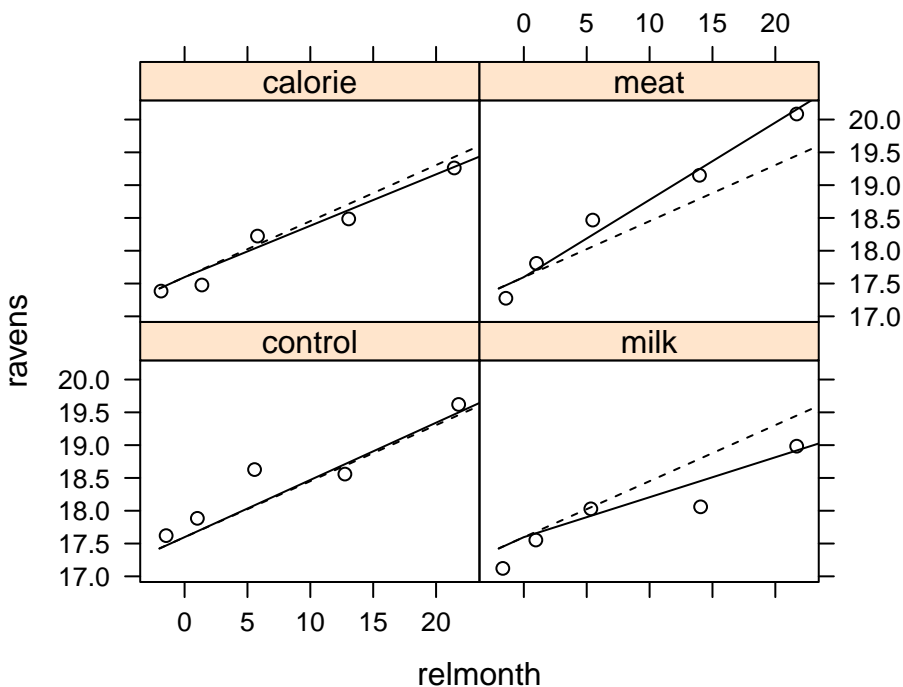
Simultaneous Tests for General Linear Hypotheses

```
Fit: lme.formula(fixed = ravens ~ relmonth + relmonth:trt, data = r1,
  random = ~1 | id)
```

Linear Hypotheses:

	Estimate	Std. Error	z value	Pr(> z)
control slope == 0	0.08721	0.01045	8.350	< 2e-16
milk slope == 0	0.06085	0.01017	5.983	2.19e-09
calorie slope == 0	0.07834	0.01060	7.388	1.49e-13
meat slope == 0	0.11782	0.01065	11.068	< 2e-16

(Adjusted p values reported -- none method)



dashed: same slope (model m0)
 solid: different slopes (model m1)

Here are some pairwise comparisons:

```
> K2
```

	[,1]	[,2]	[,3]	[,4]	[,5]
meat-control	0	0	0	0	1
meat-calorie	0	0	0	-1	1
meat-milk	0	0	-1	0	1
control-calorie	0	0	0	-1	0
control-milk	0	0	-1	0	0
calorie-milk	0	0	-1	1	0

```
> t2 <- glht(m1, linfct = K2)
```

```
> summary(t2)
```

Simultaneous Tests for General Linear Hypotheses

```
Fit: lme.formula(fixed = ravens ~ relmonth + relmonth:trt, data = r1,
  random = ~1 | id)
```

Linear Hypotheses:

	Estimate	Std. Error	z value	Pr(> z)
meat-control == 0	0.030606	0.014670	2.086	0.1574
meat-calorie == 0	0.039483	0.014472	2.728	0.0324
meat-milk == 0	0.056967	0.014194	4.013	<0.001
control-calorie == 0	0.008877	0.014664	0.605	0.9304
control-milk == 0	0.026361	0.014354	1.837	0.2560
calorie-milk == 0	0.017484	0.014136	1.237	0.6033

(Adjusted p values reported -- single-step method)

More models...

A jump instead of different slopes

```
> m2 <- lme(ravens ~ relmonth + trt, random = ~1 | id, data = r1)
> summary(m2)
```

...

Random effects:

```
Formula: ~1 | id
          (Intercept) Residual
StdDev:    1.572384 2.396820
```

Fixed effects: ravens ~ relmonth + trt

	Value	Std.Error	DF	t-value	p-value
(Intercept)	17.564231	0.11061467	2017	158.78754	0.0000
relmonth	0.083930	0.00625354	2017	13.42125	0.0000
trtmilk	-0.191384	0.18040095	2017	-1.06088	0.2889
trtcalorie	-0.056763	0.18139233	2017	-0.31293	0.7544
trtmeat	0.501268	0.18661056	2017	2.68617	0.0073

...

A jump and different slopes

```
> m3 <- lme(ravens ~ relmonth * trt, random = ~1 | id, data = r1)
> summary(m3)
```

...

Random effects:

```
Formula: ~1 | id
          (Intercept) Residual
StdDev:    1.573776 2.394358
```

Fixed effects: ravens ~ relmonth * trt

	Value	Std.Error	DF	t-value	p-value
(Intercept)	17.555883	0.11204185	2014	156.69041	0.0000
relmonth	0.087780	0.01047686	2014	8.37847	0.0000
trtmilk	0.063103	0.21651687	2014	0.29145	0.7707
trtcalorie	-0.017256	0.22202421	2014	-0.07772	0.9381
trtmeat	0.256695	0.22692062	2014	1.13121	0.2581
relmonth:trtmilk	-0.028356	0.01667856	2014	-1.70016	0.0893
relmonth:trtcalorie	-0.007367	0.01732321	2014	-0.42529	0.6707
relmonth:trtmeat	0.020355	0.01725639	2014	1.17956	0.2383

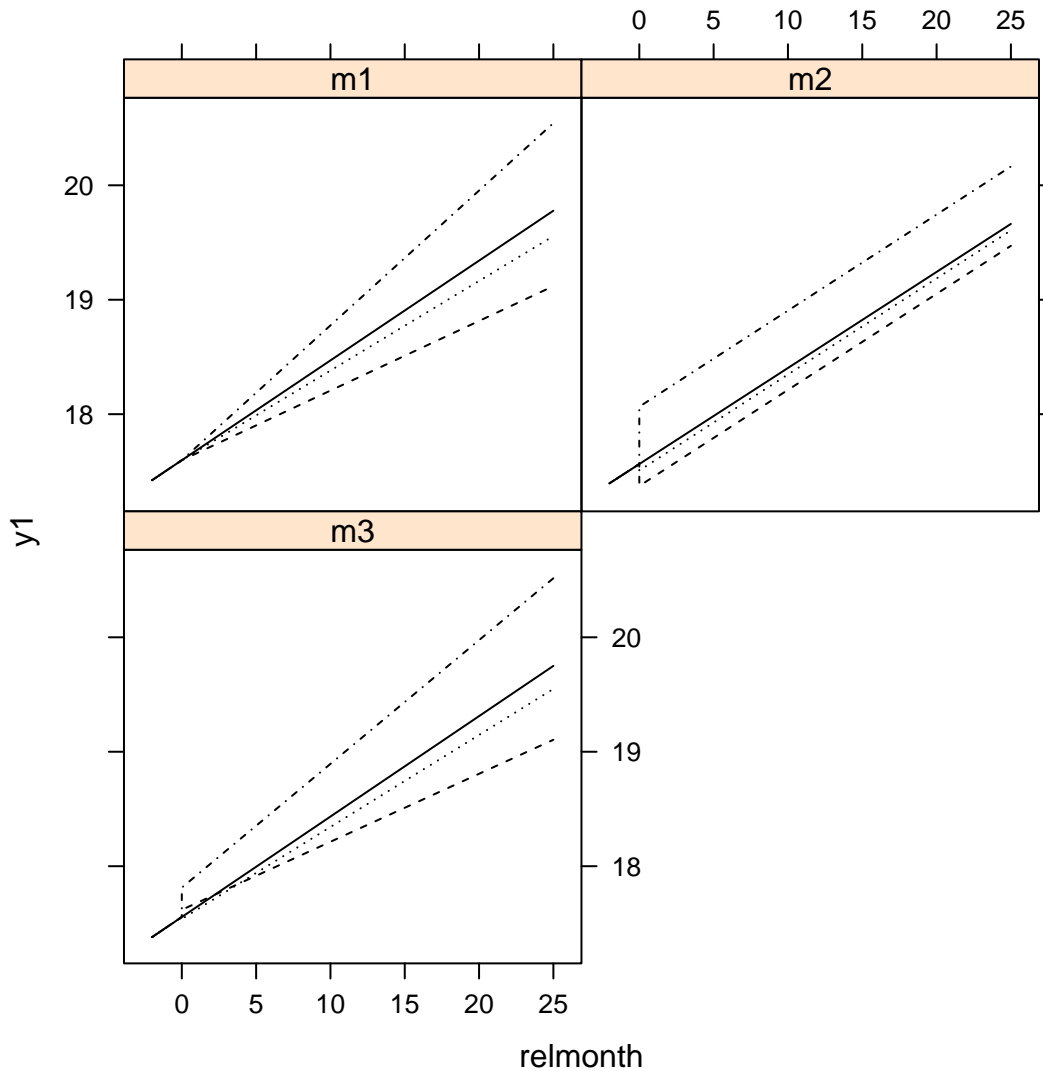
...

```
> m2b <- update(m2, method = "ML")
> m3b <- update(m3, method = "ML")
> anova(m0b, m1b, m2b, m3b)
```

Model	df	AIC	BIC	logLik	Test	L.Ratio	p-value
m0b	1	4	12325.86	12349.25	-6158.932		
m1b	2	7	12315.14	12356.06	-6150.570	1 vs 2	16.722836
m2b	3	7	12320.67	12361.59	-6153.336		
m3b	4	10	12319.78	12378.24	-6149.891	3 vs 4	6.889961

```
> anova(m1b, m3b)
```

Model	df	AIC	BIC	logLik	Test	L.Ratio	p-value
m1b	1	7	12315.14	12356.06	-6150.570		
m3b	2	10	12319.78	12378.24	-6149.891	1 vs 2	1.359755



Including sex...

Slope depends on sex; effect of treatment doesn't though

```
> s1 <- lme(ravens ~ relmonth + relmonth:trt + sex * relmonth,
+         random = ~1 | id, data = r1)
> summary(s1)
```

...

Random effects:

```
Formula: ~1 | id
          (Intercept) Residual
StdDev:    1.550071 2.389807
```

Fixed effects: ravens ~ relmonth + relmonth:trt + sex * relmonth

	Value	Std.Error	DF	t-value	p-value
(Intercept)	17.419794	0.13491708	2016	129.11482	0.0000
relmonth	0.071220	0.01199129	2016	5.93935	0.0000
sexboy	0.341871	0.18625719	532	1.83548	0.0670
relmonth:trtmilk	-0.027303	0.01430085	2016	-1.90918	0.0564
relmonth:trtcalorie	-0.009746	0.01460880	2016	-0.66714	0.5048
relmonth:trtmeat	0.031691	0.01461771	2016	2.16797	0.0303
relmonth:sexboy	0.030482	0.01123819	2016	2.71238	0.0067

...

Slope and effect of treatment depend on sex

```
> s2 <- lme(ravens ~ relmonth + relmonth:trt + sex * relmonth +
+         relmonth:trt:sex, random = ~1 | id, data = r1)
> summary(s2)
```

...

Random effects:

```
Formula: ~1 | id
          (Intercept) Residual
StdDev:    1.552237 2.389325
```

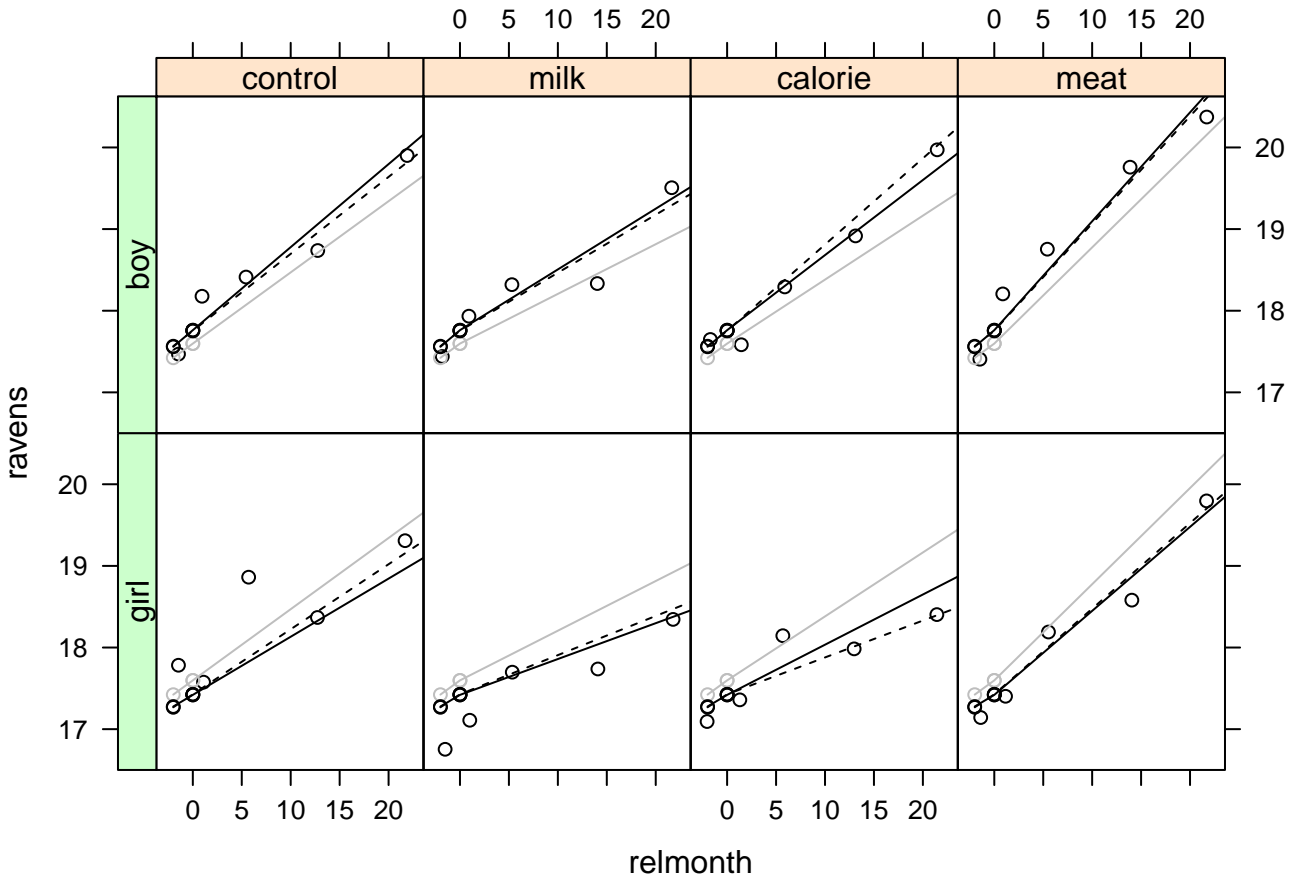
Fixed effects: ravens ~ relmonth + relmonth:trt + sex * relmonth + relmonth:trt:sex

	Value	Std.Error	DF	t-value	p-value
(Intercept)	17.427227	0.13515290	2013	128.94453	0.0000
relmonth	0.079653	0.01516616	2013	5.25204	0.0000
sexboy	0.326980	0.18681517	532	1.75028	0.0806
relmonth:trtmilk	-0.031678	0.02096755	2013	-1.51082	0.1310
relmonth:trtcalorie	-0.034497	0.02147413	2013	-1.60647	0.1083
relmonth:trtmeat	0.025219	0.02093748	2013	1.20449	0.2285
relmonth:sexboy	0.014589	0.02085719	2013	0.69948	0.4843
relmonth:trtmilk:sexboy	0.008521	0.02867447	2013	0.29717	0.7664
relmonth:trtcalorie:sexboy	0.045885	0.02930283	2013	1.56588	0.1175
relmonth:trtmeat:sexboy	0.011934	0.02925395	2013	0.40795	0.6834

...

```
> s1b <- update(s1, method = "ML")
> s2b <- update(s2, method = "ML")
> anova(m1b, s1b, s2b)
```

	Model	df	AIC	BIC	logLik	Test	L.Ratio	p-value
m1b	1	7	12315.14	12356.06	-6150.570			
s1b	2	9	12299.61	12352.22	-6140.804	1 vs 2	19.532098	0.0001
s2b	3	12	12302.70	12372.85	-6139.351	2 vs 3	2.907099	0.4062



gray: model m1 from before; no difference between sexes
 black: model s1; effect of treatment on slope is the same between sexes
 dashed: model s2; effect of treatment on slope is different between sexes