

Last time we fit an interaction model to this data, allowing the effect of treatment to differ depending on what the subject's natural coping style was. Here's the output:

```
> pp <- read.delim("http://rem.ph.ucla.edu/rob/mld/data/tabdelimiteddata/pain.txt")
> pp <- subset(pp, !is.na(l2paintol))
> pp$trt <- as.character(pp$treatment)
> pp$trt[pp$trial < 4] <- "baseline"
> pp$trt <- factor(pp$trt, levels = c("baseline", "attend", "distract",
+   "no directions"))
> m3 <- lme(l2paintol ~ cs * trt, random = ~1 | id, data = pp)
> summary(m3)
```

```
...
Random effects:
  Formula: ~1 | id
          (Intercept) Residual
StdDev:   0.8909409 0.5858537
```

```
Fixed effects: l2paintol ~ cs * trt
              Value Std.Error DF   t-value p-value
(Intercept)   4.532592 0.1693017 175 26.772276 0.0000
csdistracter   0.478031 0.2393500  62  1.997206 0.0502
trtattend      0.108192 0.2116055 175  0.511289 0.6098
trtdistract    0.038954 0.2116055 175  0.184088 0.8542
trtno directions -0.108203 0.2125829 175 -0.508990 0.6114
csdistracter:trtattend -0.459945 0.2992544 175 -1.536971 0.1261
csdistracter:trtdistract  0.537127 0.2924447 175  1.836679 0.0680
csdistracter:trtno directions -0.373634 0.3026533 175 -1.234529 0.2187
...
```

We discussed what the various  $\alpha$  parameters meant in this parameterization, and also what the corresponding  $X_i$  matrices were for several subjects.

**Comparing the interaction model with the additive model:** We might be interested in knowing if there was any evidence for an interaction; we could test this by comparing the model with the interaction and the model without the interaction. We use the ML method because we are comparing models with different fixed effects but the same random effects.

```
> m2 <- lme(l2paintol ~ cs + trt, random = ~1 | id, data = pp)
> m2ML <- update(m2, method = "ML")
> m3ML <- update(m3, method = "ML")
> anova(m2ML, m3ML)
```

	Model	df	AIC	BIC	logLik	Test	L.Ratio	p-value
	m2ML	1	7 592.1204	616.6292	-289.0602			
	m3ML	2	10 590.6603	625.6728	-285.3301	1 vs 2	7.460178	0.0586

What do we conclude?

Continuing from last class, what hypothesis tests might we be interested in this case?

What linear combinations of the  $\alpha$  parameters would we use for testing them?

**The group means:** (For space, some code is omitted; it's all available on the website.)

```
> K3
```

```
  [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8]
AB   1   0   0   0   0   0   0   0
DB   1   1   0   0   0   0   0   0
AA   1   0   1   0   0   0   0   0
AD   1   0   0   1   0   0   0   0
AN   1   0   0   0   1   0   0   0
DA   1   1   1   0   0   1   0   0
DD   1   1   0   1   0   0   1   0
DN   1   1   0   0   1   0   0   1
```

```
> t3 <- glht(m3, linfct = K3)
```

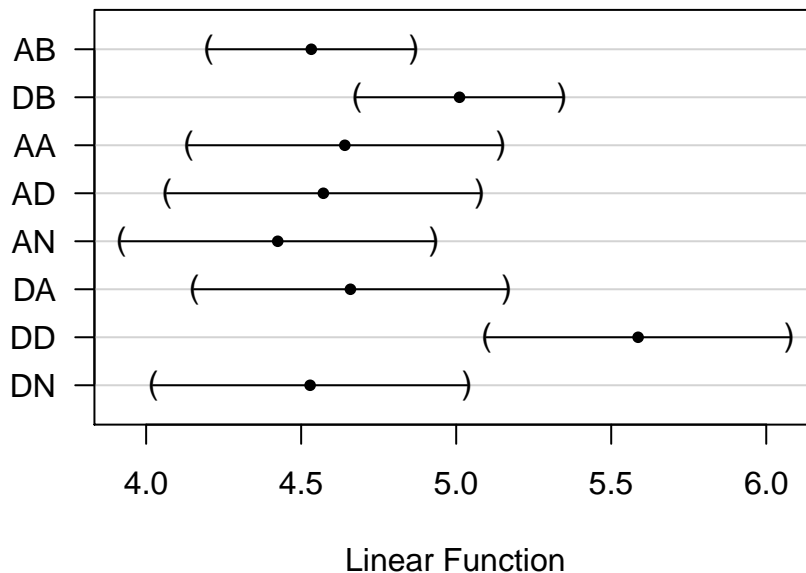
```
> sum.t3 <- summary(t3, test = adjusted(type = "none"))
```

```
> ci.t3 <- confint(t3, calpha = qnorm(1 - 0.05/2))
```

```
      est   se    t in seconds: est  lwr  upr
AB 4.53 0.169 26.8          23.1 18.4 29.1
DB 5.01 0.169 29.6          32.2 25.6 40.6
AA 4.64 0.257 18.0          24.9 17.6 35.4
AD 4.57 0.257 17.8          23.8 16.8 33.7
AN 4.42 0.258 17.2          21.5 15.1 30.5
DA 4.66 0.257 18.1          25.3 17.8 35.8
DD 5.59 0.249 22.4          48.1 34.3 67.4
DN 4.53 0.258 17.5          23.1 16.3 32.8
```

```
> plot(confint(t3, calpha = qnorm(1 - 0.05/2)))
```

### 95% confidence level



The group changes from baseline:

```
> K4
```

```
      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8]
AA-AB    0    0    1    0    0    0    0    0
AD-AB    0    0    0    1    0    0    0    0
AN-AB    0    0    0    0    1    0    0    0
DA-DB    0    0    1    0    0    1    0    0
DD-DB    0    0    0    1    0    0    1    0
DN-DB    0    0    0    0    1    0    0    1
```

```
> t4 <- glht(m3, linfct = K4)
```

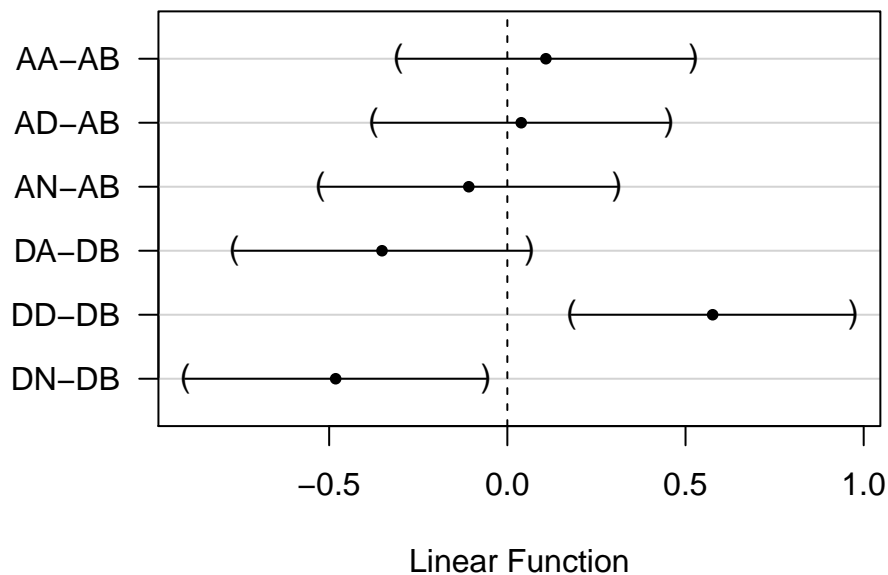
```
> sum.t4 <- summary(t4, test = adjusted(type = "none"))
```

```
> ci.t4 <- confint(t4, calpha = qnorm(1 - 0.05/2))
```

	est	se	t	in seconds:	est	lwr	upr
AA-AB	0.1082	0.212	0.511		1.078	0.809	1.44
AD-AB	0.0390	0.212	0.184		1.027	0.771	1.37
AN-AB	-0.1082	0.213	-0.509		0.928	0.695	1.24
DA-DB	-0.3518	0.212	-1.662		0.784	0.588	1.04
DD-DB	0.5761	0.202	2.854		1.491	1.133	1.96
DN-DB	-0.4818	0.215	-2.237		0.716	0.534	0.96

```
> plot(ci.t4)
```

### 95% confidence level



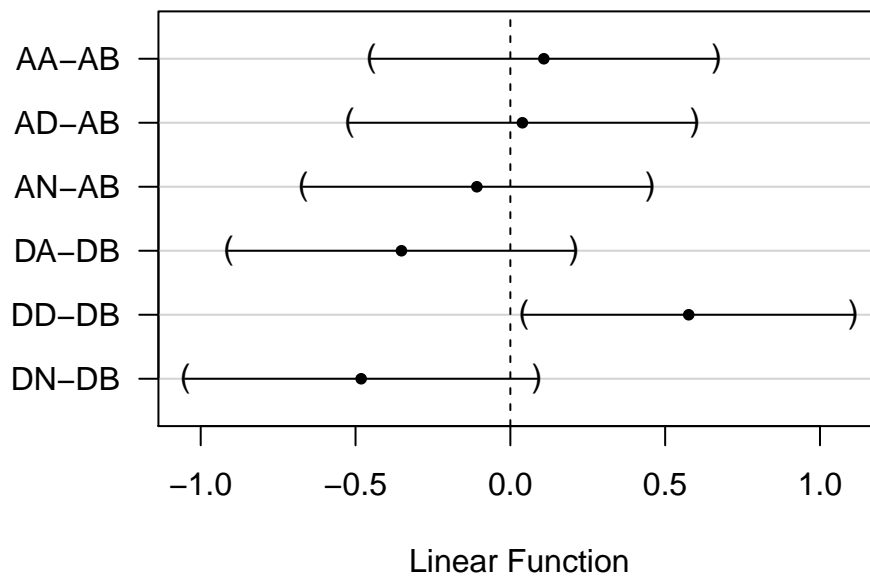
**But wait, we are doing six tests!**

Most straightforward way to do correction is with “Bonferroni” method; just divide the desired significance level by the number of tests (here, 6).

```
> sum.t4 <- summary(t4, test = adjusted(type = "bonferroni"))
> ci.t4 <- confint(t4, calpha = qnorm(1 - 0.05/2/6))
```

	est	se	t	in seconds:	est	lwr	upr
AA-AB	0.1082	0.212	0.511		1.078	0.732	1.59
AD-AB	0.0390	0.212	0.184		1.027	0.698	1.51
AN-AB	-0.1082	0.213	-0.509		0.928	0.629	1.37
DA-DB	-0.3518	0.212	-1.662		0.784	0.532	1.15
DD-DB	0.5761	0.202	2.854		1.491	1.031	2.16
DN-DB	-0.4818	0.215	-2.237		0.716	0.483	1.06

```
> plot(ci.t4)
```

**95% confidence level**

## Tests between treatments, after correcting for baseline:

```
> K3b
```

```
      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8]
DA v DN   0   0   1   0  -1   1   0  -1
DD v DN   0   0   0   1  -1   0   1  -1
DA v DD   0   0   1  -1   0   1  -1   0
AA v AN   0   0   1   0  -1   0   0   0
AD v AN   0   0   0   1  -1   0   0   0
AA v AD   0   0   1  -1   0   0   0   0
DA v AA   0   0   0   0   0   1   0   0
DA v AD   0   0   1  -1   0   1   0   0
DD v AD   0   0   0   0   0   0   1   0
DD v AA   0   0  -1   1   0   0   1   0
DA v AN   0   0   1   0  -1   1   0   0
DD v AN   0   0   0   1  -1   0   1   0
AA v DN   0   0   1   0  -1   0   0  -1
AD v DN   0   0   0   1  -1   0   0  -1
DN v AN   0   0   0   0   0   0   0   1
```

```
> t3b <- glht(m3, linfct = K3b)
```

```
> sum.t3b <- summary(t3b, test = adjusted(type = "bonferroni"))
```

```
> ci.t3b <- confint(t3b, calpha = qnorm(1 - 0.05/2/15))
```

```
      est    se      t    pval in seconds: est    lwr    upr
DA v DN  0.1301 0.300  0.433 1.00000      1.094 0.594 2.02
DD v DN  1.0579 0.293  3.605 0.00468      2.082 1.146 3.78
DA v DD -0.9278 0.291 -3.190 0.02136      0.526 0.291 0.95
AA v AN  0.2164 0.298  0.725 1.00000      1.162 0.633 2.13
AD v AN  0.1472 0.298  0.493 1.00000      1.107 0.603 2.03
AA v AD  0.0692 0.298  0.233 1.00000      1.049 0.572 1.92
DA v AA -0.4599 0.299 -1.537 1.00000      0.727 0.395 1.34
DA v AD -0.3907 0.299 -1.306 1.00000      0.763 0.415 1.40
DD v AD  0.5371 0.292  1.837 0.99386      1.451 0.800 2.63
DD v AA  0.4679 0.292  1.600 1.00000      1.383 0.763 2.51
DA v AN -0.2436 0.300 -0.812 1.00000      0.845 0.459 1.55
DD v AN  0.6843 0.293  2.334 0.29376      1.607 0.885 2.92
AA v DN  0.5900 0.302  1.954 0.76061      1.505 0.814 2.78
AD v DN  0.5208 0.302  1.725 1.00000      1.435 0.776 2.65
DN v AN -0.3736 0.303 -1.235 1.00000      0.772 0.417 1.43
```

```
> plot(ci.t3b)
```

**95% confidence level**

