

## Pediatric Pain data

```
> pp <- read.delim("http://rem.ph.ucla.edu/rob/mld/data/tabdelimiteddata/pain.txt")
> pp$trt <- as.character(pp$treatment)
> pp$trt[pp$trial <= 3] <- "baseline"
> pp$trt <- factor(pp$trt, levels = c("baseline", "attend", "distract",
+   "no directions"))
> pp <- subset(pp, !is.na(pp$l2paintol))
```

## A couple models

```
> m1 <- gls(l2paintol ~ trt * cs, data = pp, correlation = corCompSymm(form = ~1 |
+   id), weights = varIdent(form = ~1 | trial))
> m2 <- lme(l2paintol ~ trt * cs, data = pp, random = ~1 | id,
+   weights = varIdent(form = ~1 | trial))
```

## Why aren't they the same?

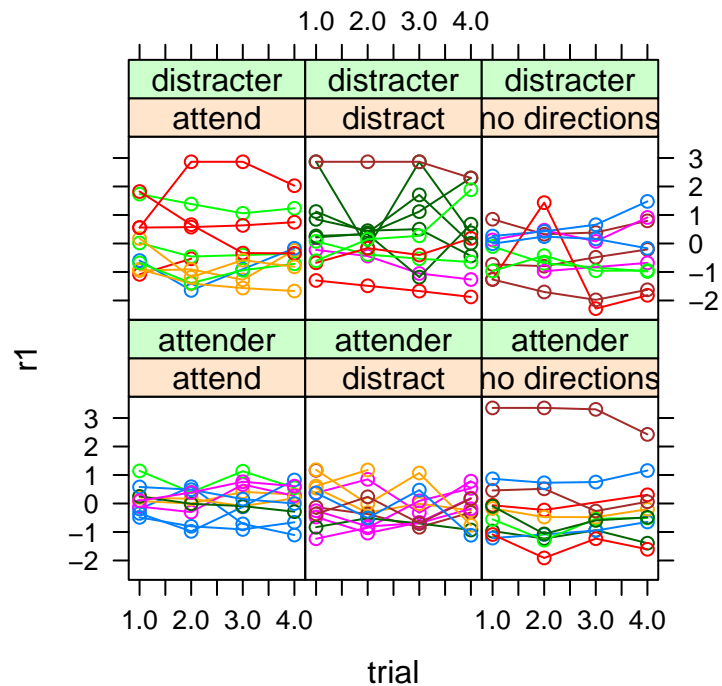
```
> anova(m1, m2)
```

	Model	df	AIC	BIC	logLik
m1	1	13	606.4179	651.5027	-290.2090
m2	2	13	605.1748	650.2596	-289.5874

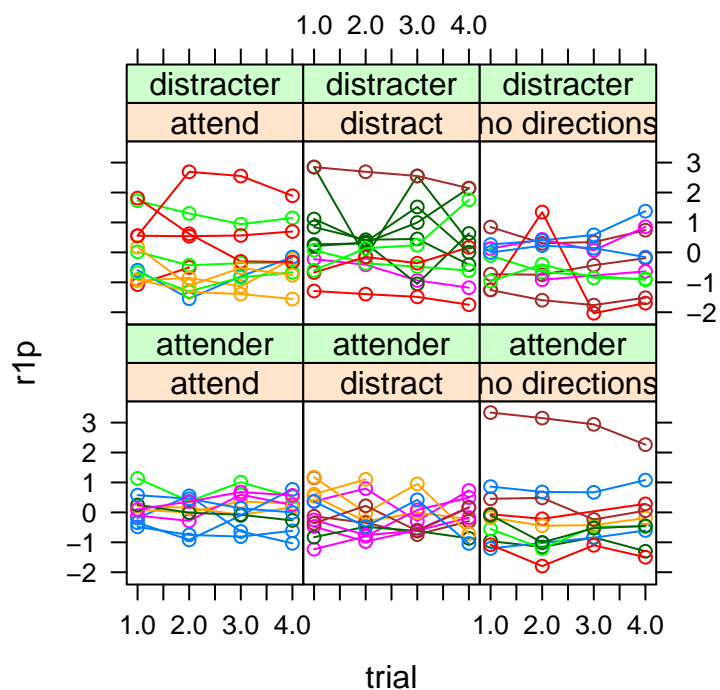
## Getting Residuals from a GLS

```
> r1 <- residuals(m1)
> r1p <- residuals(m1, type = "pearson")

> plot(xyplot(r1 ~ trial | treatment * cs, group = id, type = "b",
+ data = pp))
```



```
> plot(xyplot(r1p ~ trial | treatment * cs, group = id, type = "b",
+ data = pp))
```



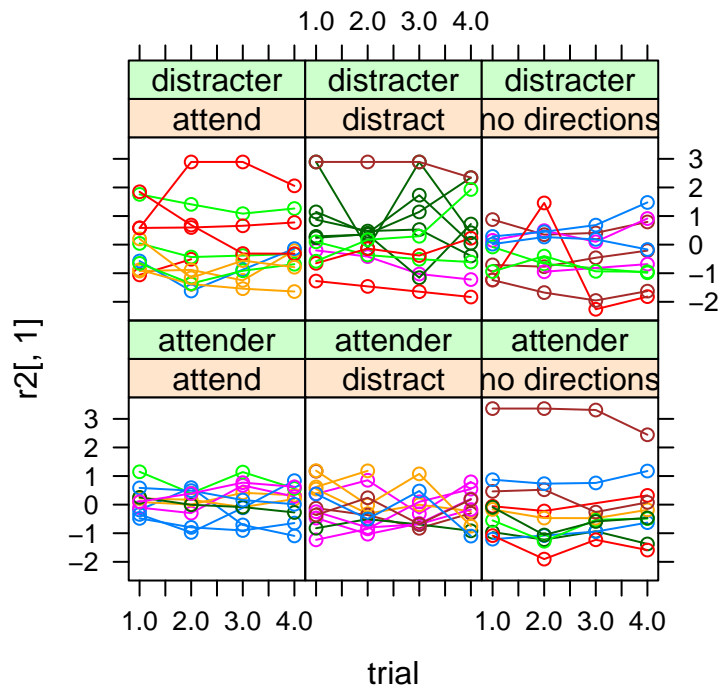
## Getting Residuals from an LME

```
> r2 <- residuals(m2, level = 0:1)
> head(r2)
```

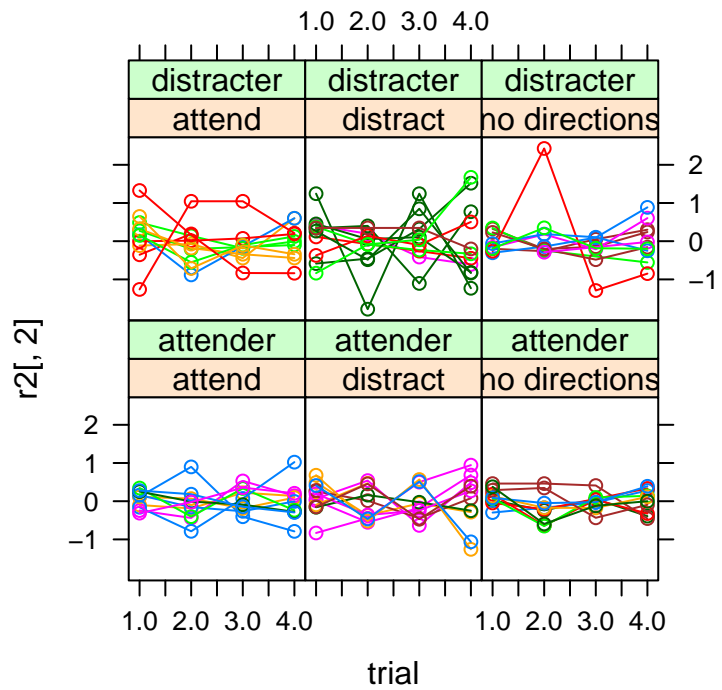
	fixed	id
1	-0.1851701	0.11820852
2	0.5957683	0.89914694
3	-0.7093026	-0.40592396
4	-1.0929422	-0.78956353
5	-0.9612741	0.02227418
6	-1.2243085	-0.24076023

```
> r2p <- residuals(m2, level = 0:1, type = "pearson")
```

```
> plot(xyplot(r2[, 1] ~ trial | treatment * cs, group = id, type = "b",
+ data = pp))
```



```
> plot(xyplot(r2[, 2] ~ trial | treatment * cs, group = id, type = "b",
+ data = pp))
```



## Plotting Random Effects

```
> m3 <- lme(l2paintol ~ trt * cs, data = pp, random = ~trial |  
+ id, weights = varIdent(form = ~1 | trial))  
> p1 <- plot(ranef(m2))  
> p2 <- plot(ranef(m3))  
> plot(c(RI = p1, RIAS = p2, layout = c(3, 1)))
```

