Stuff from Gustaf Granath, Stephane Laurent, and Jeff Morris:
Simulate data:

```
> set.seed(666)
> sims <- function(I, J, sigmab0, sigmaw0){
+     Mu <- rnorm(I, mean=0, sd=sigmab0)
+     y <- c(sapply(Mu, function(mu) rnorm(J, mu, sigmaw0)))
+     data.frame(y=y, group=gl(I,J))
+ }
> I <- 4 # number of groups
> J <- 50 # number of repeats per group
> sigmab0 <- sqrt(2) # between standard deviation
> sigmaw0 <- sqrt(3) # within standard deviation
> ##Only 4 groups with variance = 2
> dat.sim <- sims(I, J, sigmab0, sigmaw0)
> library(lme4)
> mod <- lmer(y ~1 + (1|group), dat.sim)

> nsim <- 1e4
> ## library(lme4.0)
> ## mod2 <- lmer(y ~1 + (1|group), dat.sim)
> ## set.seed(101)
> ## mcmcsamp_t1 <- system.time(mcmcsampdat1 <- mcmcsamp(mod2, n=nsim))
> ## save("mcmcsampdat1","mcmcsamp_t1",file="mcmcsampdat.RData")
> load(system.file("vignettedata","mcmcsampdat.RData",package="lme4"))
> v1 <- get_mcvars(mod2,mcmcsampdat1)

> Vpop2=as.numeric(nsum)
> for (i in 1:nsum) {
+     dat2<-simulate(mod)
+     model2<-refit(mod, dat2)
+     Vpop2[i]=VarCorr( model2)$group[1]
+ }
> den <- data.frame(y = c(v1$mcmc[,1], Vpop2 ),
+              met = rep(c("mcmcsamp","parametric boot"), each=nsum) )

> library(lattice)
> densityplot(~ y, data=den, groups = met, xlim = c(-1,10),
+             main="Simulated data - between groups (n=4) variance = 2",
```

```
+             plot.points = TRUE, xlab = "VAR(group)", auto.key =
+             list(space = "right"))
> trellis.focus("panel", 1, 1, highlight = FALSE)
> panel.abline(v = VarCorr(mod)$group[1] )
> trellis.unfocus()
```

From Jeff Morris:

> A simple balanced nested design.
>
> The odd behavior is that the mcmcsamp estimates of the variance components move away from the actual variance component estimates on sample 2 and stay away. Bootstrap works fine.
>
> And do either of you see any issues with using the bootstrap approach to get confidence intervals for the sum of the three components? That is, get the total variance based on the sum of the three components at each iteration and go from there. Nlme won't do it for me and can't use Satterthwaites with REMLs that I can see.

```
> calcium <- read.table(system.file("vignettedata","calcium.txt",
+                                   package="lme4"),header=TRUE)
> lmer(Calcium~1+(1|Plant/Leaf),data=calcium)
```