

Getting started with the glmmADMB package

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1  maybe don't want to depend on cacheSweave?

> library(MASS)
> epil2 <- transform(epil, Base = log(base/4), Age = log(age),
  Visit = scale(period, center = TRUE, scale = 5))

> library(glmmADMB)

> fm <- glmm.admb(y ~ Base * trt + Age + Visit + (Visit | subject),
  data = epil2, family = "nbinom")

> fm2 <- glmm.admb(y ~ Base * trt + Age + Visit + (1 | subject),
  data = epil2, family = "nbinom")

> summary(glm(y ~ lbase * trt + lage + V4, family = poisson, data = epil),
  cor = FALSE)
> epil3 <- subset(epil, period == 1)
> epil3["period"] <- rep(0, 59)
> epil3["y"] <- epil3["base"]
> epil["time"] <- 1
> epil3["time"] <- 4
> epil3 <- rbind(epil, epil3)
> epil3$pred <- unclass(epil3$trt) * (epil3$period > 0)
> epil3$subject <- factor(epil3$subject)
> epil3 <- aggregate(epil3, list(epil3$subject, epil3$period >
  0), function(x) if (is.numeric(x)) sum(x) else x[1])
> epil3$pred <- factor(epil3$pred, labels = c("base", "placebo",
  "drug"))
> contrasts(epil3$pred) <- structure(contr.sdif(3), dimnames = list(NULL,
  c("placebo-base", "drug-placebo")))
> summary(glm(y ~ pred + factor(subject) + offset(log(time)), family = poisson,
  data = epil3), cor = FALSE)
> summary(glmmPQL(y ~ lbase * trt + lage + V4, random = ~1 | subject,
  family = poisson, data = epil))
> summary(glmmPQL(y ~ pred, random = ~1 | subject, family = poisson,
  data = epil3))
```