epil R Documentation

Seizure Counts for Epileptics

Description

Thall and Vail (1990) give a data set on two-week seizure counts for 59 epileptics. The number of seizures was recorded for a baseline period of 8 weeks, and then patients were randomly assigned to a treatment group or a control group. Counts were then recorded for four successive two-week periods. The subject's age is the only covariate.

Usage

epil

Format

```
This data frame has 236 rows and the following 9 columns:
```

```
the count for the 2-week period.

trt

treatment, "placebo" or "progabide".

base

the counts in the baseline 8-week period.

age

subject's age, in years.

V4

0/1 indicator variable of period 4.

subject

subject

subject number, 1 to 59.

period

period, 1 to 4.
```

log-counts for the baseline period, centred to have zero mean.

log-ages, centred to have zero mean.

Source

Thall, P. F. and Vail, S. C. (1990) Some covariance models for longitudinal count data with over-dispersion. *Biometrics* **46**, 657–671.

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth Edition. Springer.

Examples

```
summary(glm(y \sim lbase*trt + lage + V4, family = poisson,
            data = epil), cor = FALSE)
epil2 <- epil[epil$period == 1, ]</pre>
epil2["period"] <- rep(0, 59); epil2["y"] <- epil2["base"]</pre>
epil["time"] <- 1; epil2["time"] <- 4</pre>
epil2 <- rbind(epil, epil2)</pre>
epil2$pred <- unclass(epil2$trt) * (epil2$period > 0)
epil2$subject <- factor(epil2$subject)</pre>
epil3 <- aggregate(epil2, list(epil2$subject, epil2$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),</pre>
    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))
```