Package ‘UnitLevelNonlin’

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Title Implements certain unit-level nonlinear models

Version 0.0.0.9000

Description This package implements small area prediction for a unit-level lognormal model and a unit-level gamma-Poisson model.

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Encoding UTF-8

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RoxygenNote 7.1.2

Imports lme4,
stats

Suggests knitr,
rmarkdown

VignetteBuilder knitr

R topics documented:

`SAEPoissonMean` *Small area inference for a unit-level gamma-Poisson model*

Description

Small area inference for a unit-level gamma-Poisson model

Usage

```
SAEPoissonMean(ys, xs, areafacsamp, xN, areafacpop, sampindex)
```

Arguments

`ys`	a numeric vector containing the collected counts
`xs`	the matrix of covariates for sampled elements that does not contain an intercept
`areafacsamp`	a vector of area labels for the sample
`xN`	the matrix of covariates for population elements that does not contain an intercept
`areafacpop`	a vector of area labels for the population
`sampindex`	indexes of sampled elements

Value

a list with four components: parest = estimators of fixed parameters, pred = predictors, g1hat = estimate of leading term in MSE, g2hat = estimate of second term in MSE

Examples

```
#### Simulate population:
N <- 10000
mux <- 0.5; sdx <- 1
D <- 100
Nis <- rep(100,D)
f <- 0.05
nis <- Nis*f
xN1 <- rnorm(N, mean = mux, sd = sdx)
xN2 <- rnorm(N, mean = mux, sd = sdx)
beta1 <- 2
muxN <- exp(beta1*xN1/4 + beta1*xN2/4)
uD <- rgamma(D, shape = 5, rate = 2)
names(uD) <- 1:D
areafacpop <- rep(1:D, Nis)
meanyN <- muxN*uD[as.character(areafacpop)]
yN <- rpois(N, lambda = meanyN)
indexpop <- 1:N
ybarNipop <- tapply(yN, areafacpop, mean)
sampindex <-  as.vector(sapply(1:D, function(i){ sample(indexpop[areafacpop == i],
     size = nis[i], replace = FALSE) }) )
xN <- cbind(xN1, xN2)
ys <- yN[sampindex]
xs <- xN[sampindex,]
areafacsamp <- areafacpop[sampindex]
```

`unitLN` *Small area inference for the unit-level lognormal model*

Description

Small area inference for the unit-level lognormal model

Usage

```
unitLN(yspos, Xs, Xpop, areafacpop, areafacsamp, sampindex)
```

Arguments

`yspos`	a numeric vector with the positive (not log transformed) response variables
`Xs`	the matrix of covariates for sampled elements that does not contain an intercept
`Xpop`	the matrix of covariates for the full population that does not contain an intercept
`areafacpop`	a vector of area labels for the full population
`areafacsamp`	a vector of area labels for the sample
`sampindex`	the vector of sampled index values

Value

a list with predictions and MSE estimates

Examples

```
beta0 <- log(0.5)
beta1 <- 1
beta2 <- 2
D <- 60
Nis <- c(100, 200, 500)
Nis <- rep(Nis, each = D/length(Nis))
N <- sum(Nis)
x1 <- rnorm(N)
x2 <- rnorm(N)
areafacpop <- rep(1:D, Nis)
sigma2b <- 0.5
sigma2e <- 1
bi <- rnorm(D, mean = 0, sd = sqrt(sigma2b))
ei <- rnorm(N, mean = 0, sd = sqrt(sigma2e))
names(bi) <- as.character(1:D)
y <- exp(beta0 + beta1*x1 + beta2*x2 + bi[as.character(areafacpop)] + ei)
samplist <- sapply(1:D, function(i){sample( (1:N)[areafacpop == i],
size = 0.1*Nis[i], replace = FALSE)})
sampindex <- unlist(samplist)
areafacsamp <- areafacpop[sampindex]
ys <- y[sampindex]
Xpop <- cbind(x1, x2)
Xs <- Xpop[sampindex,]
popindex <- 1:N
unitLN(ys, Xs, Xpop,  areafacpop, areafacsamp, sampindex)
```

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