

refitME: Tutorial for fitting measurement error models using Monte Carlo Expectation Maximization in R

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This tutorial documents fitting an MCEM algorithm via the `refitME` R-package. For more specific details see: *refitME: Measurement Error Modelling using Monte Carlo Expectation Maximization in R*. Also, see `?refitME` for further details on the fitting function, input arguments and output.

Example 1: A simple GLM example taken from Carroll *et al.* (2006).

We use the Framingham heart study data set. In addition to the naive model, we also fit a `simex` model and compare it with MCEM. Computational times for both models are also reported.

Load data and R-packages.

```
suppressWarnings(suppressMessages(library(refitME)))
suppressWarnings(suppressMessages(library(simex)))

set.seed(2020)

data(Framinghamdata)
```

Fit the naive model.

The first stored variable `w1` is the error contaminated variable used in the analysis.

```
glm_naiv <- glm(Y ~ w1 + z1 + z2 + z3, x = TRUE, family = binomial,
               data = Framinghamdata)
```

Setup all tuning parameters and variables.

```
W <- as.matrix(Framinghamdata$w1) # Matrix of error-contaminated covariate.
sigma.sq.u <- 0.01259/2 # ME variance, obtained from Carroll et al. (2006) monograph.
B <- 100 # The number of Monte Carlo replication values/SIMEX simulations.
```

Fit the SIMEX model.

```
start <- Sys.time()
glm_simex <- simex(glm_naiv, SIMEXvariable = c("w1"),
                  measurement.error = cbind(sqrt(sigma.sq.u)), B = B) # SIMEX.
end <- Sys.time()
t1 <- difftime(end, start, units = "secs")
comp.time <- c(t1)
```

Fit the MCEM model.

```
start <- Sys.time()
glm_MCEM <- refitME(glm_naiv, sigma.sq.u, W, B)
```

```
## [1] "One specified error-contaminated covariate."
## [1] "convergence :-)"
## [1] 5
```

```
end <- Sys.time()
t2 <- difftime(end, start, units = "secs")
comp.time <- c(comp.time, t2)
```

Report model estimates and compare computational times.

```
est.beta <- rbind(coef(glm_naiv), coef(glm_simex), coef(glm_MCEM))
est.beta.se <- rbind(sqrt(diag(vcov(glm_naiv))),
                    sqrt(diag(glm_simex$variance.jackknife)), sqrt(diag(vcov(glm_MCEM))))
row.names(est.beta) = row.names(est.beta.se) <- c("Naive GLM", "SIMEX", "MCEM")
colnames(est.beta) = colnames(est.beta.se) <- c("(Intercept)", "SBP", "chol. level",
                                                "age", "smoke")
round(est.beta, digits = 3)
```

```
##           (Intercept)   SBP chol. level   age smoke
## Naive GLM      -14.951 1.707         0.008 0.055 0.592
## SIMEX          -15.919 1.947         0.008 0.053 0.598
## MCEM           -16.059 1.955         0.008 0.056 0.594
```

```
round(est.beta.se, digits = 3) # Standard error estimates.
```

```
##           (Intercept)   SBP chol. level   age smoke
## Naive GLM         1.900 0.418         0.002 0.012 0.250
## SIMEX             2.043 0.456         0.002 0.012 0.251
## MCEM              2.185 0.487         0.002 0.012 0.250
```

```
names(comp.time) <- c("SIMEX", "MCEM")
comp.time # SIMEX and MCEM.
```

```
## Time differences in secs
##      SIMEX      MCEM
## 8.135574 4.861159
```

Example 2: A GAM example taken from Ganguli *et al.* (2005).

The Milan mortality air pollution data set. Here, we fit GAM models via the `mgcv` package where one covariate (daily total suspended particles measurements) is error-contaminated.

Load data and R-packages.

```
suppressWarnings(suppressMessages(library(refitME)))

set.seed(2020)

data(milan.mort)
dat.air <- milan.mort
```

Setup all variables.

```
Y <- dat.air[, 6] # Mortality counts.
n <- length(Y)

z1 <- (dat.air[, 1])
z2 <- (dat.air[, 4])
z3 <- (dat.air[, 5])
w1 <- log(dat.air[, 9])
dat <- data.frame(cbind(Y, z1, z2, z3, w1))
```

Fit the naive model.

```
gam_naiv <- gam(Y ~ s(w1) + s(z1, k = 25) + s(z2) + s(z3), family = "poisson", data = dat)
```

Fit the MCEM model.

Note this will take a fair while to run if B is large (consider decreasing B if you want a rough answer).

```
sigma.sq.u <- 0.0915 # This gives a reliability ratio of 0.7.  
rel.rat <- round((1 - sigma.sq.u/var(dat$w1))*100, digits = 0)  
  
W <- as.matrix(w1)  
  
gam_MCEM1 <- refitME(gam_naiv, sigma.sq.u, W)
```

```
## [1] "One specified error-contaminated covariate."  
## [1] "convergence :-)"  
## [1] 14
```

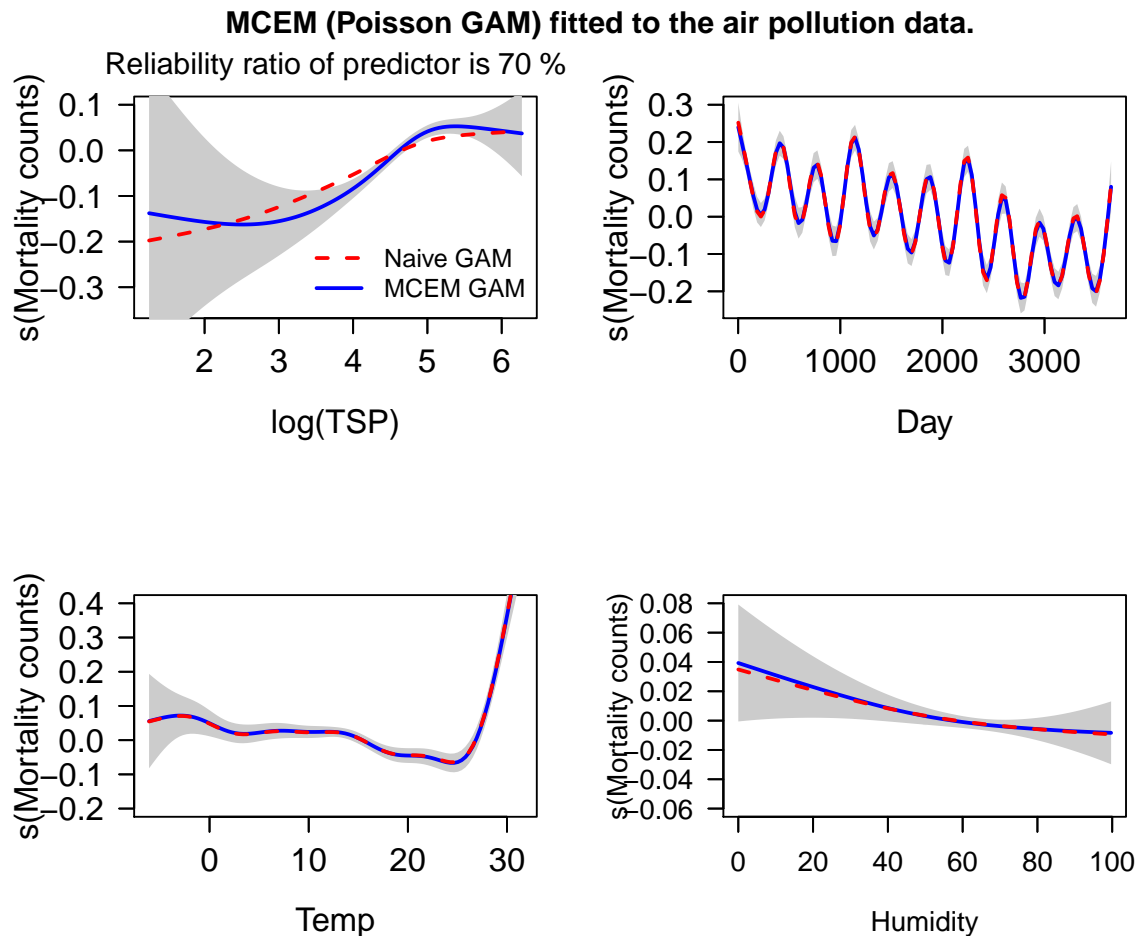


Figure 1: *Plots of smooths against covariate. TSP (top left is the error contaminated variable).*

Example 3: A point-process model using presence-only data

We use the *Corymbia eximia* presence-only data set from Renner and Warton (2013). Here, we fit a naive models point-process model (PPM) and an MCEM PPM.

Load data and R-packages.

```
suppressWarnings(suppressMessages(library(refitME)))

data(Corymbiaeximiadata)

dat <- Corymbiaeximiadata
```

Setup all variables.

```
Y <- dat$Y.obs

Rain <- dat$Rain
D.Main <- dat$D.Main
MNT <- dat$MNT

p.wt <- rep(1.e-6, length(Y))
p.wt[Y == 0] <- 1

X <- cbind(rep(1, length(Y)), poly(MNT, degree = 2, raw = TRUE),
           poly(Rain, degree = 2, raw = TRUE),
           poly(sqrt(D.Main), degree = 2, raw = TRUE))

colnames(X) <- c("(Intercept)", "X1", "X2", "Z1", "Z2", "Z3", "Z4")

dat1 <- data.frame(cbind(Y, p.wt, X))
colnames(dat1)[1:2] <- c("Y", "p.wt")
```

Fit the naive (PPM) model.

```
PPM_naiv1 <- glm(Y/p.wt ~ X1 + X2 + Z1 + Z2 + Z3 + Z4, family = "poisson",
                 weights = p.wt, data = dat1)
```

Fit the MCEM PPM.

```
sigma.sq.u <- 0.25  
  
W <- dat$MNT # Measured with error.  
  
PPM_MCEM1 <- refitME(PPM_naiv1, sigma.sq.u, W)  
  
## [1] "One specified error-contaminated covariate."  
## [1] "convergence :-)"  
## [1] 5
```

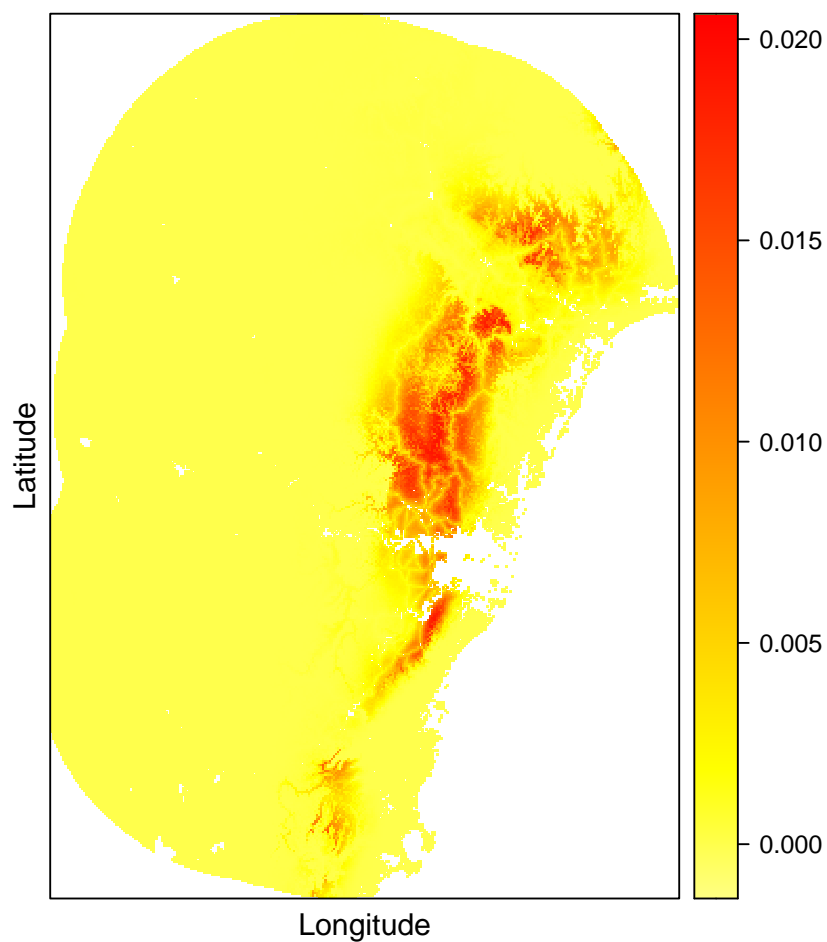


Figure 2: Plot of predicted presences of *Corymbia eximia* using presence-only data when fitting the MCEM model. Here the max temperature covariate is assumed to be error-contaminated.

Example 4: A VGAM example using the *Prinia flaviventris* capture-recapture data.

We use the *Prinia flaviventris* capture-recapture data set from Hwang, Huang and Wang (2007). Here, we fit naive `vglm` and `vgam` capture-recapture models, and the MCEM capture-recapture model. For all models we used the `posbinomial()` family provided in `VGAM`.

Load data and R-packages.

```
suppressWarnings(suppressMessages(library(refitME)))
suppressMessages(library(VGAM))
data(Priniadata)
```

Setup all variables.

```
tau <- 17 # No. of capture occasions.
w1 <- Priniadata$w1
```

Fit the naive `vglm` and `vgam` capture-recapture models.

```
CR_naiv1 <- vglm(cbind(cap, noncap) ~ w1,
                 VGAM::posbinomial(omit.constant = TRUE, parallel = TRUE ~ w1),
                 data = Priniadata, trace = FALSE)
CR_naiv2 <- vgam(cbind(cap, noncap) ~ s(w1, df = 2),
                 VGAM::posbinomial(omit.constant = TRUE, parallel = TRUE ~ s(w1, df = 2)),
                 data = Priniadata, trace = FALSE)
```

Fit the MCEM capture-recapture model.

```
sigma.sq.u <- 0.37/var(w1) # ME variance.
B <- 100
CR_MCEM <- refitME(CR_naiv2, sigma.sq.u, B)
```

```
## [1] "convergence :-)"
## [1] 8
```