Chapter 6: Multivariate Fay-Herriot model with missing dependent variables (MMFH)

Anna-Lena Wölwer

Description

The theoretical basis of the *Multivariate Fay-Herriot model with missing dependent variables (MMFH)* model and the presented code is given in Chapter 6 of the dissertation *Model-Based Prediction and Estimation Using Incomplete Survey Data* by *Anna-Lena Wölwer*, which is available as an open-source document here *XXXXX insert OPUS link here*.

This folder contains files `MMFH_gen_dat_m3.R` and `MMFH_fitting.R`, both of which contain executable functions which are illustrated in the following. `MMFH_gen_dat_m3.R` contains functions for generating data according to MMFH models. `MMFH_fitting.R` contains a function for fitting a MMFH model (parameter estimation, predictions, analytical MSE estimates).

Libraries

For the examples, we use the following libraries.

```
library(Matrix)
library(mvtnorm)
library(reshape2)
library(ggplot2)
library(sae)
```

```
Lade nötiges Paket: MASS
```

```
Lade nötiges Paket: lme4
```

Short overview of the R codes in this folder

```
source(paste0(getwd(), "/MMFH_gen_dat_m3.R"))
```

The file comes with two functions for generating data according to a MMFH model with $m = 3$ dependent variables (therefore the *_m3* in the name). The code contains comments on the inputs of the functions.

Function `f_prep_MMFH_m3` is used to generate all quantities which are typically considered to be fixed in model-based small area simulation studies like the matrix of auxiliary information. For a simulation study, we would execute this function only once. The function takes as input all parameters of a multivariate Fay-Herriot model like the fixed effects, the variance components, and the number of domains.

Function `f_gen_MMFH_m3` is used to generate all quantities which are typically considered random in model-based small area simulation studies like the random effects and sampling errors. For a simulation study, we would execute this function in each Monte Carlo iteration. The function takes as input all quantities generated by function `f_prep_MMFH_m3` as well as the inputs of `f_prep_MMFH_m3`.

```
source(paste0(getwd(), "/MMFH_fitting.R"))
```

The file contains function `f_MMFH`. The code contains comments on the inputs of the function.

Function `f_MMFH` is used to fit a MMFH model to input data. This includes the estimation of the model fixed effects (β) and variance components (θ) via Fisher-Scoring, either based on maximum likelihood (ML) or restricted maximum likelihood (REML). Furthermore, based on the parameter estimates, the model returns estimates of the random effects, the synthetic predictions ($X\beta$) and the EBPs. In addition, the MSE estimates are given.

Although in this file we only cover the case of $m = 3$ dependent variables, function `f_MMFH` works for an arbitrary number of $m \geq 2$ dependent variables.

Generate example data

Generate the fixed quantities of a MMFH model including randomly generated auxiliary information (documentation of required inputs in `MMFH_gen_dat_m3.R`).

Set input quantities

```
m = 3 # total number of variables of interest, number of dependent variables
D = 100 # total number of domains
v_ref = c(2,3,4) # variances of random effects of the 3 variables
```

```
cor_ref = c(.2,.3,.4) # correlations of random effects
v_rer = c(2.5,3.5,4.5) # variances of sampling errors of the 3 variables
cor_rer = c(.15,.25,.35) # correlations of sampling errors
beta = list(c(1.5, 2.5), # list, for each variable: vector of fixed effects
            c(2.3,3.3,4.3),
            c(4.1,3.1,2.1, 2.2))
range_aux = c(10, 100) # range of the uniform distribution from which auxiliary informatio
perc_mis = c(5, 5, 2) # percentage of missing domain information per variable
```

Generate data

```
d_fix <- f_prep_MMFH_m3(seed = 56)
names(d_fix)
```

```
 [1] "m"         "D"         "v_ref"     "cor_ref"   "v_rer"     "cor_rer"
 [7] "beta"      "range_aux" "seed"      "m"         "V_ed"      "V_ud"
[13] "x"
```

Use `f_gen_MMFH_m3` to generate the model information which typically varies between Monte Carlo iterations. That is, the generation of the dependent variables. The function allows to set certain values as missing, input `perc_mis` determines the number of domains for which the survey information of the three dependent variables is missing. Note that in this code the missing dependent variables are non-overlapping. That is, there is maximum one missing dependent variable per domain. This, however, can easily be changed in the code.

```
d_var <- f_gen_MMFH_m3( x = d_fix$x,
                        beta = d_fix$beta,
                        V_ud = d_fix$V_ud,
                        V_ed = d_fix$V_ed,
                        seed = 67,
                        verbose = TRUE )
```

```
Generated number of missing y values (non-overlapping over the 100 domains) for the three dep
```

```
str(d_var)
```

```
List of 3
 $ y_true: num [1:100, 1:3] 68.4 220.7 188.4 136.4 202.9 ...
 $ y_obs : num [1:100, 1:3] 68.4 219.8 187.6 138.1 205.2 ...
 $ y_mis : num [1:100, 1:3] NA NA NA NA NA ...
```

`y_true` are the (according to the model) true values of the dependent variables, `y_obs` are the survey estimates of the dependent variables, `y_mis` are the survey estimates, which we consider to be available, some of which are missing (determined by `perc_mis` in `f_gen_MMFH_m3`). The missing mechanism is *missing completely at random* (MCAR).

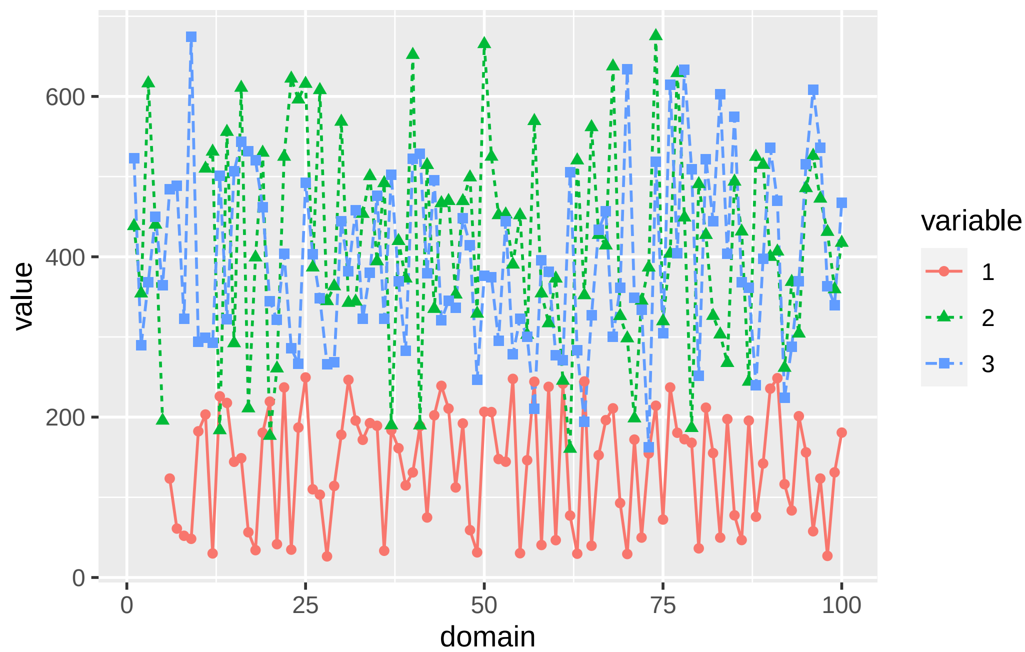
Have a look at the generated dependent variables.

```r
d_plot <- reshape2::melt(d_var$y_mis)
d_plot$Var2 <- factor(d_plot$Var2)
colnames(d_plot) <- c("domain", "variable", "value")
```

```r
ggplot2::ggplot(d_plot,
                aes(x = domain, y = value, group = variable,
                    color = variable, fill = variable,
                    shape = variable, lty = variable)) +
  geom_line() +
  geom_point()
```

```
Warning: Removed 5 row(s) containing missing values (geom_path).
```

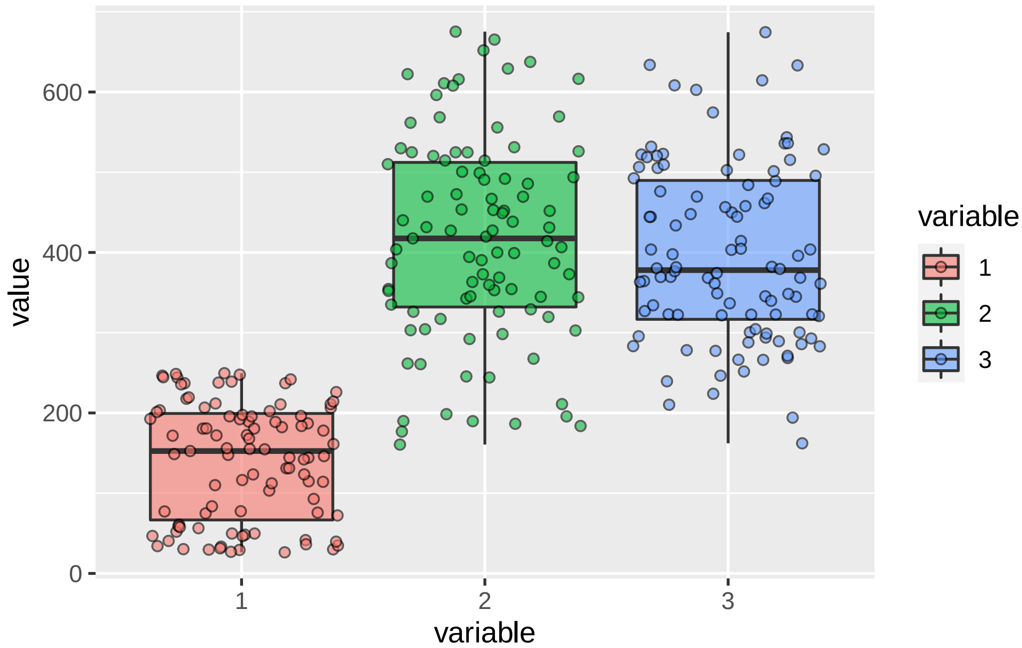
```
Warning: Removed 10 rows containing missing values (geom_point).
```




```r
ggplot2::ggplot(d_plot,
                aes(x = variable, y = value,
                    fill = variable)) +
  geom_boxplot(alpha = .6) +
  geom_jitter(pch = 21, alpha = .6)
```

```
Warning: Removed 10 rows containing non-finite values (stat_boxplot).
```

```
Warning: Removed 10 rows containing missing values (geom_point).
```



From the error message, you can see that there are (as we wanted) missing values in the dependent variables. Furthermore, you can play around with the parameters of the data generation and see how the outcomes of the sampling estimates change.

The number of domains with missing values of variables 1, 2, and 3 is

```
colSums(is.na(d_var$y_mis))
```

```
[1] 5 5 0
```

Function f_MMFH

Set some of the function inputs.

```
method <- "REML" # REML or ML in Fisher-Scoring
# method <- "ML"
verbose <- TRUE # print intermediate outputs
eps <- 1e-8 # convergence tolerance
maxiter <- 100 # maximum number of iterations of Fisher-Socring
```

Fit a MMFH model to survey estimates `d_var$y_mis` (documentation of required input in `MMFH_fitting.R`).

```r
res_MMFH <- f_MMFH(y           = d_var$y_mis,
                   x           = d_fix$x,
                   V_ed        = d_fix$V_ed,
                   theta       = NULL,
                   theta_start = NULL,
                   method      = method,
                   eps         = eps,
                   maxiter     = maxiter,
                   verbose     = TRUE)
```

```
 iter            loglike lambda  var_1  var_2  var_3 rho_12 rho_13 rho_23  v1.x1  v1.x2  v2.
    0           -421.986     NA  1.976  1.823  3.991  0.021  0.055 -0.053  1.329  2.501  2.7
    1           -419.142      1  1.985  1.823  3.980  0.084  0.301  0.460  1.375  2.500  2.5
    2           -419.136      1  1.996  1.821  3.947  0.104  0.304  0.446  1.372  2.500  2.6
    3           -419.136      1  1.996  1.821  3.949  0.103  0.305  0.447  1.372  2.500  2.6
    4           -419.136      1  1.996  1.821  3.949  0.103  0.305  0.447  1.372  2.500  2.6
    5           -419.136      1  1.996  1.821  3.949  0.103  0.305  0.447  1.372  2.500  2.6
    6           -419.136      1  1.996  1.821  3.949  0.103  0.305  0.447  1.372  2.500  2.6
    7           -419.136      1  1.996  1.821  3.949  0.103  0.305  0.447  1.372  2.500  2.6
    8           -419.136      1  1.996  1.821  3.949  0.103  0.305  0.447  1.372  2.500  2.6
    9           -419.136      1  1.996  1.821  3.949  0.103  0.305  0.447  1.372  2.500  2.6
```

With `verbose = TRUE`, the model returns the intermediate parameter estimates.

See the model output.

```r
str(res_MMFH)
```

```
List of 2
 $ est:List of 4
  ..$ ebp  : num [1:100, 1:3] 66.8 221.1 188.9 139 202.1 ...
  .. ..- attr(*, "dimnames")=List of 2
  .. .. ..$ : chr [1:100] "1" "2" "3" "4" ...
  .. .. ..$ : chr [1:3] "v1" "v2" "v3"
  ..$ ref  : num [1:100, 1:3] 0.0265 -0.0519 0.5524 0.4887 0.6061 ...
  .. ..- attr(*, "dimnames")=List of 2
  .. .. ..$ : chr [1:100] "1" "2" "3" "4" ...
  .. .. ..$ : chr [1:3] "v1" "v2" "v3"
```

```
  ..$ Xbeta: num [1:100, 1:3] 66.8 221.1 188.4 138.5 201.5 ...
  .. ..- attr(*, "dimnames")=List of 2
  .. .. ..$ : chr [1:100] "1" "2" "3" "4" ...
  .. .. ..$ : chr [1:3] "v1" "v2" "v3"
  ..$ fit  :List of 6
  .. ..$ method    : chr "REML"
  .. ..$ covergence: logi TRUE
  .. ..$ iterations: num 9
  .. ..$ estcoef   :'data.frame':   9 obs. of  4 variables:
  .. .. ..$ beta     : num [1:9] 1.37 2.5 2.6 3.3 4.29 ...
  .. .. ..$ std_error: num [1:9] 0.45706 0.00724 0.75001 0.00824 0.00895 ...
  .. .. ..$ tvalue   : num [1:9] 3 345.37 3.47 400.6 479.42 ...
  .. .. ..$ pvalue   : num [1:9] 0.00268 0 0.00052 0 0 ...
  .. ..$ refvar    : Named num [1:6] 1.996 1.821 3.949 0.103 0.305 ...
  .. .. ..- attr(*, "names")= chr [1:6] "var_1" "var_2" "var_3" "rho_12" ...
  .. ..$ goodness  : Named num -419
  .. .. ..- attr(*, "names")= chr "ll"
 $ mse: num [1:100, 1:6] 2.01 2.07 2.37 2.23 2.42 ...
  ..- attr(*, "dimnames")=List of 2
  .. ..$ : chr [1:100] "1" "2" "3" "4" ...
  .. ..$ : chr [1:6] "v1" "cov12" "cov13" "v2" ...
```

The function returns the parameters estimates, EBPs, predictions of random effects, synthetic predictions, and MSE estimates.

Compare MMFH fitting algorithm to sae::eblupFH (for univariate FH models)

We make an example to compare the MMFH output to the output of a (univariate) Fay-Herriot model using function `sae::mseFH`.

```r
# Calculate (univariate) Fay-Herriot models with function mseFH from the sae package
res_FH <- list()
for (k in 1:m) {
  a_tmp <- which(!is.na(d_var$y_mis[,k]))
  res_FH[[k]] <- sae::mseFH(d_var$y_mis[,k][a_tmp] ~ -1 + d_fix$x[[k]][a_tmp,],
                            vardir = sapply(d_fix$V_ed[a_tmp], function (d){ d[k,k] }),
                            method = method,
                            PRECISION = eps,
                            MAXITER = maxiter)
}
```

For illustration, we choose variable 1.

```r
# For variable 1: Get FH results
k = 1
a_tmp <- which(!is.na(d_var$y_mis[,k]))
eblup_tmp <- rep(NA, D)
mse_tmp <- rep(NA, D)
eblup_tmp[which(!is.na(d_var$y_mis[,k]))] <- as.vector(res_FH[[k]]$est$eblup)
mse_tmp[which(!is.na(d_var$y_mis[,k]))] <- as.vector(res_FH[[k]]$mse)
```

Compare the EBPs:

```r
cbind("true" = d_var$y_true[,k],
      "FH_EBLUP" = eblup_tmp,
      "FH_SYN" = as.vector(d_fix$x[[k]] %*% res_FH[[k]]$est$fit$estcoef[,1]),
      "MMFH" = res_MMFH$est$ebp[,k])[1:10,]
```

```
        true  FH_EBLUP    FH_SYN      MMFH
1   68.38396        NA  66.77100  66.84720
2  220.71834        NA 221.12334 221.08786
3  188.39494        NA 188.32858 188.90442
4  136.44930        NA 138.50444 139.02736
5  202.94951        NA 201.46048 202.08717
6  122.66383 123.49433 123.56519 123.49003
7   60.69563  61.41211  61.73316  61.41823
8   50.28309  49.73459  47.91795  49.80205
9   48.79156  48.38538  48.50245  48.43657
10 181.52393 180.76330 179.52180 180.74569
```

Exemplary for the first 10 domains, you can see the true values of the dependent variables in the first column. Furthermore, column 2 shows the FH EBLUPs (*FH_EBLUP*). For domains 1 to 5, the survey estimates were considered missing. Therefore, the FH model cannot be used to calculated EBLUPs and only return synthetic predictions *FH_SYN*. In addition, column 4 gives the EBPs of the MMFH model. With the MMFH model, we can calculate EBPs also for the domains with missing values of variable 1 as the model uses the correlations of the variable to variables 2 and 3 in a multivariate model.

Compare the MSE estimates:

```r
cbind("FH" = mse_tmp,
      "MMFH" = res_MMFH$mse[,"v1"])[1:10,]
```

```
         FH     MMFH
1        NA 2.005688
2        NA 2.067900
3        NA 2.367980
4        NA 2.225455
5        NA 2.424869
6  1.177989 1.137820
7  1.194565 1.156174
8  1.201212 1.378379
9  1.200909 1.157729
10 1.181551 1.266511
```

Also for the MSE, only the MMFH model can give estimates for domains 1 to 5, for whcih the survey direct estimates are considered missing.