Robust Small Area Estimation: a Vignette

Tobias Schoch*

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Contents

*Contact: Tobias Schoch, University of Applied Sciences Northwestern Switzerland, Riggenbachstrasse 16, CH-4600 Olten, Switzerland; e-mail: tobias.schoch@fhnw.ch; phone: +41 62 286 01 47.

1 Introduction

The `rsae` package offers functions to estimate

- model A, area-level SAE model, aka Fay-Herriot model,
- model B, basic unit-level SAE model,

by either maximum likelihood or robust methods. The classification of the models (A or B) follows the proposal of Rao (2003). Currently, the package includes the following robust (i.e. bounded-influence estimating equation) methods for model A:

- Huber-type M-estimation, using a slight generalization of Huber's Proposal 2 to estimate the variance components; cf., Richardson and Welsh (1995), Sinha and Rao (2009), Schoch (2011),
- variance estimation and MSPE estimation (parametric bootstrap; see Sinha and Rao (2009))

(Robust estimating methods for model type "a" will be released in the near future)
NOTE: In order to use the full functionality of **rsae**, I recommend to install the **robustbase** package.

2 Getting started

I will not attempt to provide another introduction to `R`. There are several excellent resources intended to accomplish this task.

Once `R` is running, the installation of additional packages is straightforward. A platform-independent way to install the `rsae` package is to type

```
> install.package("rsae")
```

in the console (note that the character "`>`" is not part of the command; it denotes the command prompt of the command-line interface, indicating that `R` is ready to read your commands). Provided your computer has a proper internet connection (and you have sufficient writing permissions on your system), the installation of the package should proceed automatically (at least on Windows and Apple computers, because binary sources are available from CRAN). On POSIX compliant OS, e.g., AIX, HP-UX, Solaris, etc. and mostly POSIX-compliant systems such as Linux, OpenSolaris, etc. installation is more involved (see Appendix C for more details on the installation process).

Once the `rsae` package is installed, we need to load it to the current session.[1]

```
> library(rsae)
```

The model fitting exercise with `rsae` takes alway three (or more) steps. Namely,

[1] Note that we have to load a package in every session where we need its functionality, whereas installation is needed a single time on your computer.

- setting up a `saemodel`, given some data,
- fitting the `saemodel` by robust methods,
- (robustly) predicting the random effects and the area-specific means, given the robustly fitted model.

These steps will be discussed in subsequent Sections.

3 Setting up a model

First of all, we have to set up a model. We use the `landsat` data from Battese et al. (1988), the landmark paper on the basic unit-level SAE model (here: units=segments, each about 250 hectares; areas=Counties). Those readers who are not familiar with the `landsat` can type `help(landsat)` in the `R` console in order to get a description of the data.

3.1 Exploring the data

First, we have to load the `landsat` data into the workspace.

```
> data(landsat)
```

Next, we will explore the data. The `names` command reports the names of the variables in the `landsat` data.

```
> names(landsat)
```

```
 [1] "SegmentsInCounty"   "SegementID"         "HACorn"
 [4] "HASoybeans"         "PixelsCorn"         "PixelsSoybeans"
 [7] "MeanPixelsCorn"     "MeanPixelsSoybeans" "outlier"
[10] "CountyName"
```

Get a table (i.e., an aggregation) of the variable `CountyName`.

```
> table(landsat$CountyName)
```

```
Cerro Gordo    Hamilton       Worth    Humboldt    Franklin  Pocahontas
          1           1           1           2           3           3
  Winnebago      Wright     Webster     Hancock     Kossuth      Hardin
          3           3           4           5           5           6
```

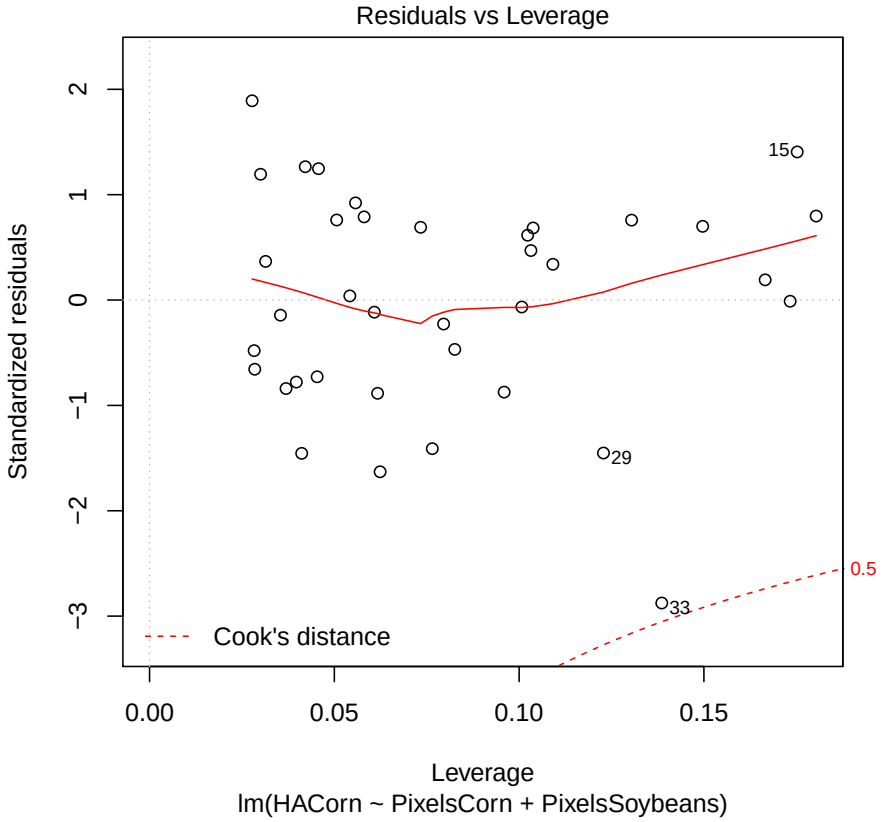
So, there are twelve areas – the smallest areas (Cerro Gordo, Hamilton, and Worth) contain one unit, the largest area, Hardin, involves six units.

Next, we want to have a look at observations no. 30 to 35 and some interesting variables.

```
> landsat[30:35, c("HACorn", "PixelsCorn", "PixelsSoybeans", "CountyName", "outlier")]
```

```
   HACorn PixelsCorn PixelsSoybeans CountyName outlier
30 122.66        342            182    Kossuth   FALSE
31 104.21        294            179    Kossuth   FALSE
32  88.59        220            262     Hardin   FALSE
33  88.59        340             87     Hardin    TRUE
34 165.35        355            160     Hardin   FALSE
35 104.00        261            221     Hardin   FALSE
```

Note that I added the variable `outlier` to the original data. This variable flags observation no. 33 as outlier. This is in line with Battese et al. (1988), who indicate that for both observations no. 32 and 33, the interviewed farm operators reported for `HACorn` the same value. Despite the same number of estimated hectares under corn (i.e., 88.59), the readings for `PixelsCorn` are very different for obs. no. 32 and 33. To be precise, we would call observation no. 33 a leverage point rather than an outlier.



The following figure is a display of the (standardized) residuals of the linear model against the leverage. Note that obs. no. 33 is very close the the bound on the values of Cook's distance.

```
>    linmodel <- lm(HACorn ~ PixelsCorn + PixelsSoybeans, data = landsat)
>    plot(linmodel, 5)
```

Note that Sinha and Rao (2009), on the other hand, included this bad leverage point in their simulation exercise and obtained completely different estimates.

3.2 We set up our first model

Having explored the data, we consider setting up the model. The (first of their) model writes (Battese et al., 1988)

$$HACorn_{i,j} = \alpha + \beta_1 \cdot PixelsCorn_{i,j} + \beta_2 \cdot PixelsSoybeans_{i,j} + u_i + e_{i,j},$$

where $j = 1, \ldots, n_i$, $i = 1, \ldots, 12$.

The `rsae` package provides the function `saemodel` to set up a model. The model is specified by mainly three arguments: (1) the `formula` argument defines the fixed-effect part (the $\sim$ operator separates dependent and independent variables), (2) the `area` argument specifies the area-level random effect (here, the variable `CountyName` serves as area identifier; note the leading $\sim$ operator), (3) the `data` argument specifies the data (a `data.frame`). The only "difficulty" here is that we use `data=subset(landsat, subset=(outlier==FALSE))` to include only non-outlying observations, instead of `data=landsat`. We call our model `bhfmodel` (Batteese, Harter, and Fuller).

```
> bhfmodel <- saemodel(formula=HACorn ~ PixelsCorn + PixelsSoybeans,
+                      area=~CountyName,
+                      data=subset(landsat, subset=(outlier==FALSE)))
```

(Note that in `R`, a `formula object` (evaluated by `model.frame` and `model.matrix`) contains always an intercept term. In the case we want to fit the above model without an intercept, we have to change the RHS of the formula part to look like this: `-1 + PixelsCorn + PixelsSoybeans`).

Suppose we have generated several different models (e.g., using different independent variables), and they all reside in the current workspace. It may be difficult to figure out which of them is the `bhfmodel` (except you you have adopted unique naming conventions). For situations like this, type the name of the model to get some information.

```
> bhfmodel

SAE MODEL TYPE: B (J.N.K. Rao's classification)
---
FIXED EFFECTS: HACorn ~ (Intercept) + PixelsCorn + PixelsSoybeans
AREA-SPECIFIC RANDOM EFFECTS: CountyName
```

If you need to know more about a particular model, you may use the `summary` method.

```
> summary(bhfmodel)

Model summary:
saemodel(formula = HACorn ~ PixelsCorn + PixelsSoybeans, area = ~CountyName,
    data = subset(landsat, subset = (outlier == FALSE)))
```

```
---
No. of areas:  12
No. of obs.:  36
Smallest area:  1  units
Largest area:  5  units
```

The important thing to note is that `summary` reminds you of the fact that the model was generated using only non-outlying observations.

4 (Robust) Estimation

Having set up our model, we consider estimating the parameters of the Gaussian core model by different methods. All fitting is done using the following workhorse function

```
fitsaemodel(method, model, ...)
```

Depending on the arguments delivered, `fitsaemodel` decides what method to use. The decision is based on the `method` argument.

4.1 Maximum likelihood estimation

To start with, we compute the usual maximum likelihood (ML) estimates. Therefore, we call `fitsaemodel` with `method="ml"` (the ML methods does not need any additional [...] arguments).

```
> mlfit <- fitsaemodel("ml", bhfmodel)
```

Type name of the fit, i.e. `mlfit`, to get a display of the model fit.

```
> mlfit

ESTIMATES OF SAE-MODEL (model type B)
Method:  Maximum likelihood estimation
---
Fixed effects
Model: HACorn ~ (Intercept) + PixelsCorn + PixelsSoybeans
  Coefficients:
   (Intercept)      PixelsCorn  PixelsSoybeans
     50.967557        0.328581       -0.133710
---
Random effects
  Model: ~1| CountyName
           (Intercept)  Residual
Std. Dev.  11.0028      11.7181
---
Number of Observations:  36
Number of Areas:  12
```

Note that the layout of the output is similar to the one of the `lme` (linear mixed-effects model) function in the `nlme` package (cf. Pinheiro et al., 2011). In particular, the output on the random-effects part mimicks what the `print` methods reports for `lme` (i.e., `~1|Countyname`).

To learn more about the fit, we may call the `summary` method. In particular, the model summary supplies us with inferential statistics of fixed effects.

```
> summary(mlfit)

ESTIMATION SUMMARY
Method:  Maximum likelihood estimation
---
Fixed effects
                    Value  Std.Error    t-value df    p-value
(Intercept)    50.9675570 23.4750890  2.1711337 22   0.040984 *
PixelsCorn      0.3285805  0.0479840  6.8477166 22 7.0475e-07 ***
PixelsSoybeans -0.1337099  0.0530628 -2.5198431 22   0.019502 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

4.1.1 When the ML estimator does not converge

Now, we deliberately set the number of outer-loop iterations to one, in order to show the model report, when the algorithm fails to converge.

```
> failconvg <- fitsaemodel("ml", bhfmodel, niter=1)
```

Here is the report

```
> failconvg

THE METHOD DID NOT CONVERGE!
---
  1) use convergence() of your fitted model to learn more
  2) study the documentation using the command ?fitsaemodel
  3) you may call fitsaemodel with 'init' equal to (either) 'lts'
     or 's' (this works also for ML, though it may no be very efficient)
  4) if it still does not converge, the last resort is to modify
     'acc' and/or 'niter' (and hope and pray)
```

Obviously, `niter=1` is a bad choice. Nontheless, we follow the hint and call the `convergence` method:

```
> convergence(failconvg)

CONVERGENCE REPORT
NOTE: ALGORITHM DID NOT CONVERGE!
---
```

```
User specified number of iterations (niter) and
numeric precision (acc):

                 niter  acc
overall loop     1e+00  1e-05
fixeff           2e+02  1e-05
residual var     2e+02  1e-05
area raneff var  1e+02  1e-05
---
Number of runned EE-specific iterations in each
call (given the user-defined specs), reported for
each of the  1 overall iterations separately:

   fixeff  residual var  area raneff var
1   2       2            18
```

Now, it may happen that the ML-method of `fitsaemodel` does not converge (even if the parameters have not been modified). A remedy is to initialize the ML method by a regression S-estimator (sic!), calling `fitsaemodel` with `init="s"`. Obviously, this approach is not optimal in terms of computing time. Nonetheless, by this specification, `fitsaemodel` enters the "safe mode" of robust Huber-type M-estimation and applies several checks whether the algorithm behaves well (these checks are ignored in the default mode).

4.1.2 When the mixed linear model is not appropriate

Suppose that our data do not have area-specific variation. Notably, we shall generate data based on the linear model,

$$y_{i,j} = (1,\ x_{i,j})^T \boldsymbol{\beta} + e_{i,j}, \tag{1}$$

where $x_{i,j} \sim N(0,1)$, $e_{i,j} \sim N(0,1)$, $\boldsymbol{\beta} = (1,1)^T$, $n_i = n = 10$, $\forall i = 1, \ldots, 10$ (balanced data). The following code generates the data.

```
> set.seed(12345)
> n <- 200; beta <- c(1, 1)
> cst <- rep(1, n)
> x <- rnorm(n)
> y <- as.matrix(cbind(cst, x)) %*% beta + rnorm(n)
> areaid <- rep(1:10, each=10)
> df <- data.frame(y=y, x=x, areaid=areaid)
```

The OLS fit of our linear model is

```
> lm(y ~ x, data=df)

Call:
lm(formula = y ~ x, data = df)
```

```
Coefficients:
(Intercept)            x
      1.080        1.034
```

Then, we set up the `saemodel` with the identical data (i.e., `df`)

```
> fakemlm <- saemodel(y ~ x, area=~areaid, data=df)
```

and consider the following model fit

```
> fitsaemodel("ml", fakemlm)
```

```
ESTIMATES OF SAE-MODEL (model type B)
Method:  Maximum likelihood estimation
---
Fixed effects
Model: y ~ (Intercept) + x
  Coefficients:
(Intercept)            x
    1.07965      1.03365
---
Random effects
  Model: ~1| areaid
---
NOTE THAT THE VARIANCE OF THE AREA-LEVEL RANDOM
EFFECT IS ALMOST ZERO! DO YOU REALLY NEED THE
RANDOM EFFECT? IF SO, GO AHEAD. HOWEVER, YOU
SHOULD CONSIDER FITTING A (ROBUST) GLS MODEL.
---
           (Intercept)  Residual
Std. Dev.  0.000000     0.955232
---
Number of Observations:  200
Number of Areas:  10
```

The report indicates that the random-effect variance is close to zero or equal to zero. Therefore, the MLM model is not appropriate.

4.2 Huber-type M-estimation

Huber-type M-estimation is the recommended estimation method for situations where the response variable is supposed to be (moderately) contaminated. The M-estimators downweight the influence of outlying observations (in the vector of responses) on the estimates. Notably, they bound the influence of outliers. But, no attempt is made to limit the effect of leverage points (see above). In principle, one may adapt generalized regression M-estimators (GM) to the family of linear mixed-level models in order to deal with influential observations/leverage (i.e., to bound also the influence of the design matrix). This has been done by Richardson (1997). However, in terms of numerical properties,

the Schweppe- and Mallows-type weighted GM-estimators turned out to be extremely unstable (Richardson, 1995). Therefore, we propose to use the S-estimator (with constrained parameter space) if the data are heavily contaminated and/or contain influential observations/leverage (see below).

Next, we discuss two different fitting modes for the Huber-type M-estimation method.

- If the reponse variable is supposed to be uncontamined or contaminated by only a couple of outliers, I recommend to use the (very fast) **default mode**.
- If the response variable is moderately contaminated and/or if the **default-mode algorithm failed to converge**, I recommend the **safe mode**.

4.2.1 Default mode

The default-mode setup of the Huber-type M-estmation exercise is

```
> huberfit <- fitsaemodel("huberm", bhfmodel, k=1.5)
```

where `k` denotes the robustness-tuning constant of the Huber ψ-function ($0 < k \leq \infty$; note that (in the limit) $k = \infty$ leads to the ML estimates). (**NOTE:** that in the simple location-scale model, the choice of `k=1.345` leads to estimates which feature an asymptotic relative efficiency w.r.t. the ML estimate of approx. 95% at the true (uncontamined) Gaussian core model. This property does **not** directly carry over to the estimates of mixed-linear models!)

```
> huberfit
```

```
ESTIMATES OF SAE-MODEL (model type B)
Method:  Huber-type M-estimation
Robustness tuning constant: k =  1.5
---
Fixed effects
Model: HACorn ~ (Intercept) + PixelsCorn + PixelsSoybeans
  Coefficients:
   (Intercept)      PixelsCorn  PixelsSoybeans
     50.284889        0.328453       -0.139159
---
Random effects
  Model: ~1| CountyName
           (Intercept)  Residual
Std. Dev.  11.9537      12.3639
---
Number of Observations:  36
Number of Areas:  12
```

To learn more about the fit, we shall call the `summary` method.

```
> summary(huberfit)
```

```
ESTIMATION SUMMARY
Method:  Huber-type M-estimation
Robustness tuning constant:  k  =  1.5
---
Fixed effects
                    Value  Std.Error    t-value df    p-value
(Intercept)    50.2848895 24.8465096  2.0238211 22   0.055301 .
PixelsCorn      0.3284534  0.0507730  6.4690607 22 1.6536e-06 ***
PixelsSoybeans -0.1391587  0.0561777 -2.4771135 22   0.021409 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
---
Degree of downweighting/winsorization:

                 sum(wgt)/n
fixeff           0.984130
residual var     0.972323
area raneff var  0.984131
```

The output is by default separated into 2 blocks when the algorithm converged.

- Block 1 reports some inferential statistics of the fixed-effects part.
- Block 2 reports the degree of down-weighting outlying residuals at the final iteration. The degree of down-weighting is reported for all estimating equations (EE) separately. In general $d = 1$, if no down-weighting took place. Conversely, the smaller d, the more outlying residuals have been down-weighted (and/or the same outliers are heavier down-weighted).

In addition, the `convergence` method supplies us with a report on the convergence of the method.

```
> convergence(huberfit)

CONVERGENCE REPORT
---
User specified number of iterations (niter) and
numeric precision (acc):

                 niter  acc
overall loop     4e+01  1e-05
fixeff           2e+02  1e-05
residual var     2e+02  1e-05
area raneff var  1e+02  1e-05
---
Number of runned EE-specific iterations in each
call (given the user-defined specs), reported for
each of the  11 overall iterations separately:
```

```
    fixeff  residual var  area raneff var
1    3      10            19
2    9      10            13
3   11       7            12
4    4       7            12
5    8       6            12
6    6       5            12
7    5       4            12
8    4       3            12
9    3       3            12
10   2       2            12
11   1       1            12
```

It consist of the following blocks:

- Block 1 reports the default or user-specified max number of iterations, `niter`, and the numeric tolerance, `acc`, used in the termination rule of the algorithms.
- Block 2 reports the number of iterations that each of the estimating equation–specific (EE-specific) loops (aka inner loops) and the overall loop (aka outer loop) used to conform to the termination rule. Each row in the table represents a single run of the overall loop. In the example, the algorithm needed 7 overall loops. The entries of a row refer to the EE-specific number of iterations in a particular overall loop.

  It is evident that the number of (inner-loop) iterations for `fixeff` and `residual var` become smaller, the higher the number of outer/overall loops. This is not (and will never be) the case for `area raneff var` because it is obtained using a different optimization method.

  In general, we can feel confident if the number of inner-loop iterations decrease (in the case of `fixeff` and `residual var`). However, there are situations where the algorithm converges perfectly without featuring such a nice decrease in the number of inner-loop iterations.

4.2.2 Safe mode

The safe mode should be used when the data are supposed to be moderately contaminated and/or the algorithm in default mode failed to converge. The safe-mode algorithm is initialized by a high-breakdown-point regression estimator. However, it is only safe up to a certain degree of contamination (i.e., breakdown-point is rather low for M-estimators). In the presence of too many outliers, the M-estimator will break down.

NOTICE: in order to use the safe-mode functions, you need the **robustbase** package (Rousseeuw et al., 2011).

The safe mode is entered if one specifies (in `fitsaemodel`) either

- `init = "lts"` for initializing the method by a fast-LTS regression estimator (Rousseeuw, 1984; Rousseeuw and Van Driessen, 2006),
- `init = "s"` for initializing the method by a regression S-estimator (Rousseeuw and Yohai, 1984; Salibian-Barrera and Yohai, 2006).

(Also, the safe mode uses a couple of tests to check whether the estimates at consecutive iterations behave well. Notably, it prevents cycling estimates (i.e., the situation when the algorithm is trapped in a flip-flop), which typically occurs for very small robustness-tuning constants).

In general, the results of `fitsaemodel` with either `init = "s"` or `init = "lts"` are the same. For data with more than 50,000 observations, `init="s"` is considerably faster. The call is

```
> fitsaemodel("huberm", bhfmodel, k=1.2, init="s")

ESTIMATES OF SAE-MODEL (model type B)
Method:  Huber-type M-estimation
Robustness tuning constant: k =  1.2
---
Fixed effects
Model: HACorn ~ (Intercept) + PixelsCorn + PixelsSoybeans
  Coefficients:
   (Intercept)      PixelsCorn  PixelsSoybeans
     57.134292        0.312452       -0.161064
---
Random effects
  Model: ~1| CountyName
           (Intercept)  Residual
Std. Dev.  13.0714      12.9421
---
Number of Observations:  36
Number of Areas:  12
```

Also, we can get more information calling the `summary` method.

4.3 S-estimation

[has to be written]

5 Robust prediction

Once the parameters of the Gaussian core model have been estimated robustly, we consider (robustly) predicting the random effects. Sinha and Rao (2009) proposed to solve the robustified mixed model equations (Fellner, 1986) by a Newton-Raphson-type updating scheme that is obtained from a Taylor-series expansion of the robustified mixed model equations. Consequently, computation is very involved.

However, Schoch (2011) showed that robust predictions of the area-specifc means can be obtained far more easily by means of the robust predictor of random effects due to Copt and Victoria-Feser (2009); see also Heritier et al. (113–114 2009). Namely, since the robustly estimated parameters of the core Gaussian model determine the model completely, prediction is straightforward.

The workhorse function for (robust) prediction is given by

```
robpredict(fit, areameans=NULL, k=NULL, reps=NULL)
```

where `fit` is a fitted model (an object produced by `fitsaemodel`), `k` is the robustness-tuning constant (of the Huber ψ-function) for robust prediction. By default `k` is `NULL` which means that the procedure takes the same `k` as has been used for estimating the parameters of the core model. The robustness-tuning constant `k` does not necessarily be the same as the one used in `fitsaemodel`. Further, choosing `k` sufficiently large (e.g., `k=20000` should work in (almost) all situations), `robpredict` produces the usual EBLUP predictions. If `areameans=NULL` (the default setting), the prediction is based on the same data that have been used for the model fitting exercise (i.e., within-sample prediction). However, in the SAE context, we are usually interested in (robustly) predicting the small-area means. Therefore, we deliver the area-specific population means through `areameans`.

In addition, the `robpredict` function can compute area-specific mean squared prediction errors (MSPE) by means of a (robust) parametric bootstrap method; see Sinha and Rao (2009). In order to obtain MSPE, we need to specify the number of bootstrap replicates, `reps`.

NOTICE: I recommend to start with relatively small values of `reps`, e.g., `reps=100`, since large values of `reps` are associated with a large computational effort. Once you get an intuition of how much time the algorithm consumes, you can try larger values of `reps`.

In the `landsat` example, the county-specific population means of pixels of the segments under corn and soybeans are recorded in the variables `MeanPixelsCorn` and `MeanPixelsSoybeans`, respectively. Note that each sample segment in a particular county has assigned the county-specific mean (in the `landsat` data). Therefore, each population mean of the variables `MeanPixelsCorn` and `MeanPixelsSoybeans` occurs n_i times. The unique county-specific population means are obtained using

```
> d <- unique(landsat[-33, c("MeanPixelsCorn", "MeanPixelsSoybeans", "CountyName")])
> d <- cbind(rep(1,12), d)
> rownames(d) <- d$CountyName
> d <- d[,1:3]
```

Let us have a look at `d`.

```
> d
```

```
             rep(1, 12) MeanPixelsCorn MeanPixelsSoybeans
Cerro Gordo           1         295.29              189.70
Hamilton              1         300.40              196.65
Worth                 1         289.60              205.28
Humboldt              1         290.74              220.22
```

```
Franklin             1         318.21             188.06
Pocahontas           1         257.17             247.13
Winnebago            1         291.77             185.37
Wright               1         301.26             221.36
Webster              1         262.17             247.09
Hancock              1         314.28             198.66
Kossuth              1         298.65             204.61
Hardin               1         325.99             177.05
```

The first column of `d` is a dummy variable (the `bhfmodel` has an intercept term). The second and third column represent the county-specific population means of segments under corn and soybeans (the rows of the above table are labeled with the county names).

Next, we consider predicting the random and fixed effects and the county means. Note that we do not explicitly specify `k`. This means that the procedure uses the same `k` as the one that has been used for robust estimation (here, the model has been estimated by `method="ml"` which is equivalent to $k = \infty$). MSPE is obtained using 500 bootstrap replicates.

```
> pr <- robpredict(mlfit, areameans=d, reps=500)

0   10   20   30   40   50   60   70   80   90   100
|----|----|----|----|----|----|----|----|----|----|
**************************************************
DONE
```

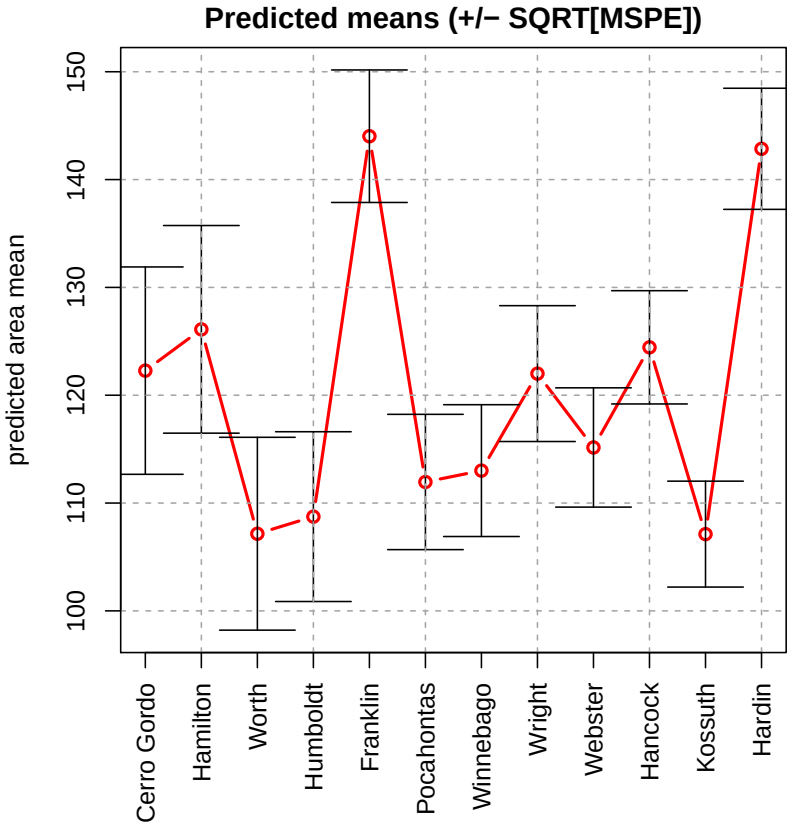
The results are

```
> pr

Robustly Estimated/Predicted Area-Level Means:
             raneff   fixeff   area mean  MSPE
Cerro Gordo   -0.348  122.629  122.281     92.470
Hamilton       2.731  123.379  126.110     92.716
Worth        -11.522  118.677  107.154     79.980
Humboldt      -8.313  117.053  108.741     61.997
Franklin      13.641  130.380  144.021     37.772
Pocahontas     9.529  102.425  111.954     39.358
Winnebago     -9.043  122.052  113.009     37.365
Wright         1.648  120.358  122.006     39.693
Webster       11.082  104.073  115.155     30.596
Hancock       -3.229  127.671  124.442     27.591
Kossuth      -14.621  121.740  107.119     24.116
Hardin         8.445  134.408  142.853     31.536
(MSPE: 500 boostrap replicates)
```

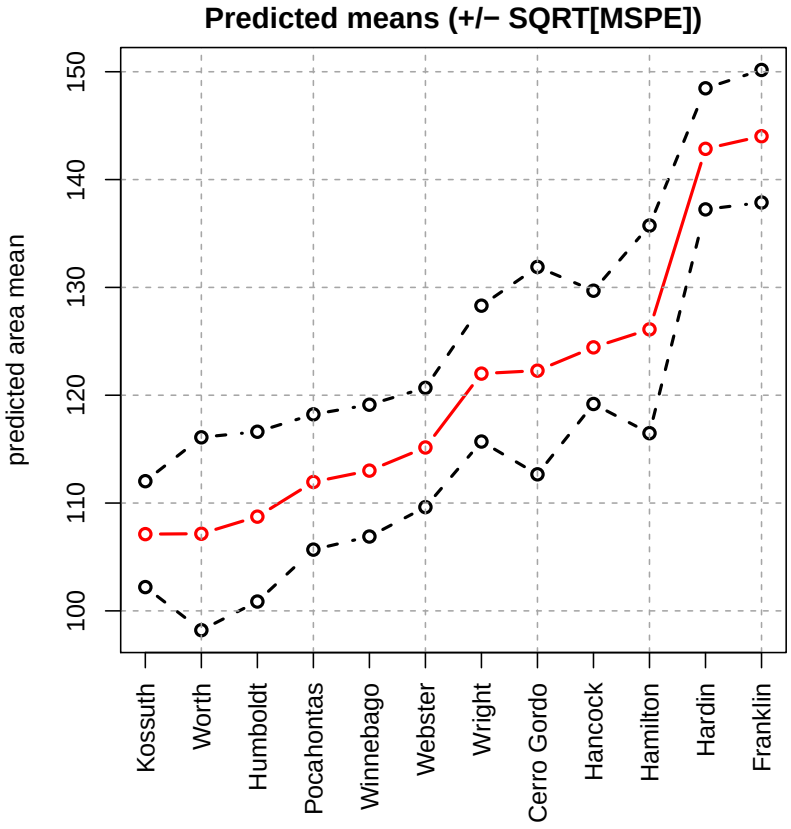
and a visual display of the predicted county means

```
> plot(pr)
```



another plot, but with lines; here the predicted means are sorted in ascending order

```
> plot(pr, type="l", sort="means")
```



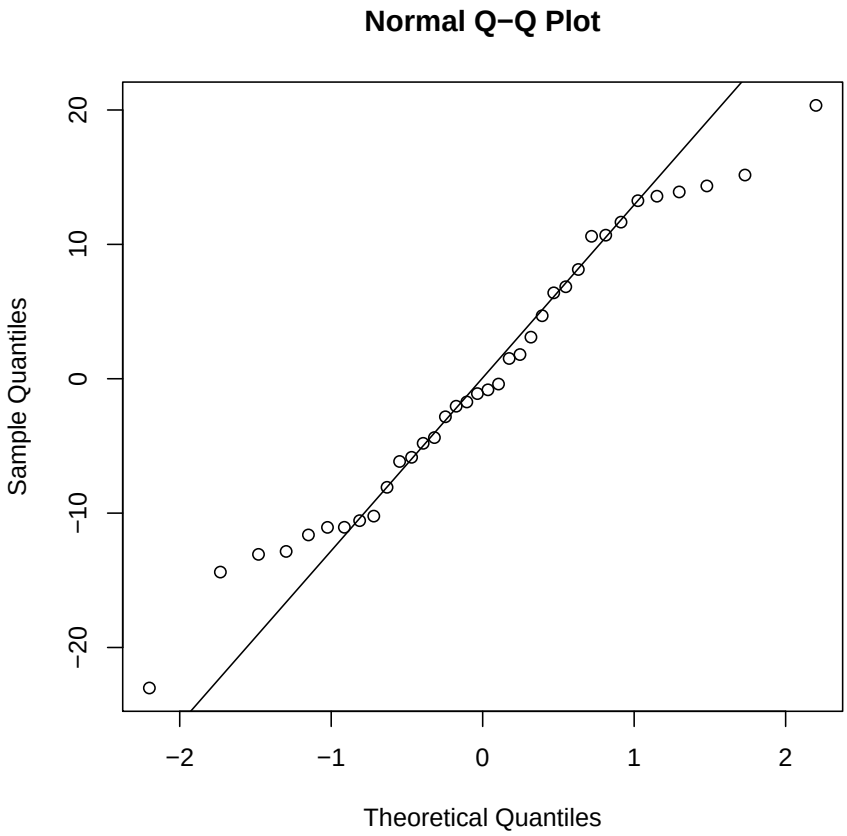
Once the area-specific random effects have been predicted (by means of robust methods), we can have a look at the residuals. Note that the residuals are given by

$$r_{i,j} = y_{i,j} - \mathbf{x}_{i,j}^T \hat{\boldsymbol{\beta}}^R - \hat{u}_i^R, \tag{2}$$

where the superscript R highlights the fact that robust estimates/predictions are used. Obviously, since the residuals depend on $\hat{u}_i^R$ (which is depends itself on the user-specified robustness-tuning constant), a residual analysis can only take place subsequent to robustly predicting u_i. This is contrast to the standard ML (or REML) case where $\hat{u}_i$ is readily availabe having estimated the fixed- and random-effects parameters.

The residualy may be used for an `QQ-plot`. (Note that `bhfmodel` is not optimal in terms of the tail behavior of the residuals)

```
> res <- residuals(pr)
> qqnorm(res)
> qqline(res)
```



6 Utility functions

6.1 Synthetic data generation

The `rsae` package is shipped with a device to generate synthetic data (balanced and unbalanced) of basic unit-level model. This tool is particularly useful when comparing the behavior of different methods (e.g., in simulation studies) because it enables the user to generate data tailored for specific problems. In particular, `makedata` is able to generate outlier-contaminated data.

6.1.1 Uncontaminated data

The core model is given by

$$y_{i,j} = \alpha + \mathbf{x}_{i,j}^T \boldsymbol{\beta} + u_i + e_{i,j}, \quad j = 1, \ldots, n_i, \quad i = 1, \ldots, g, \tag{3}$$

where $y_{i,j}$ is the response variable, $\mathbf{x}_{i,j}$ is a p-vector of design variables, u_i is an area-specific random effect, and $e_{i,j}$ is a model error. The total number of observations is $n = \sum_{i=1}^{g} n_i$. Moreover, we assume that u_i and $e_{i,j}$ are independent and that

$$\mathbf{x}_{i,j} \sim MVN(\mathbf{0}, \mathbf{I}_p), \tag{4}$$

and

$$e_{i,j} \sim N(0, v_e), \quad u_i \sim N(0, v_u), \tag{5}$$

where $\mathbf{I}_i$ is the $(p \times p)$ identity matrix, $j = 1, \ldots, n_i$; $i = 1, \ldots, g$.

The default values of `makedata` for balanced data, i.e., $n_i = n, \forall i = 1, \ldots, g$ are reported in Table 1.

Table 1: Default setup of `makedata` (balanced data)

n	g	v_e	v_u	α	β
4	20	1	1	1	1

Now, call the `makedata` function

```
> mymodel <- makedata()
```

to generate the data. Note that `makedata` has been called without arguments, implying that all arguments are given by the default value. However, you are well advised to specify the random seed (default: `seed=1024`) to meet our needs. Otherwise, your computer generates the same random numbers every time `makedata()` is called.

By typing the name of the generated model (here `mymodel`) in the console, we obtain (trough the `print` method) some characteristics of the synthetic data. This feature is particularly useful if we have several different models in the workspace (and have some troubles figuring out what the models actually do).

```
> mymodel
```

```
SAE MODEL TYPE: B (J.N.K. Rao's classification)
DATA: Synthetic, simulated data
MODEL:
   y_ij = intercept + sum_k[ beta_k * x_kij] + v_i + e_ij
 with
   each x_kij ~ N(0, 1), k=1,...,2
   v_i ~  N(0, 1)
   e_ij ~ N(0, 1)
```

In addition, there is a `summary` method.

```
> summary(mymodel)
```

```
Model summary:
makedata()
---
No. of areas:  20
No. of obs.:  80
Balanced data, each area has  4  units
```

6.1.2 Contaminated data

The `makedata` allows to draw the model errors $e_{i,j}$ and/or random effects u_i from a (contamination) mixture distribution.
Contamination of the law of $e_{i,j}$

```
> makedata(ve.epsilon=0.1)

SAE MODEL TYPE: B (J.N.K. Rao's classification)
DATA: Synthetic, simulated data
MODEL:
   y_ij = intercept + sum_k[ beta_k * x_kij] + v_i + e_ij
 with
   each x_kij ~ N(0, 1), k=1,...,2
   v_i ~  N(0, 1)
   e_ij ~ (0.9)*N(0, 1) + 0.1*N(0, 41)
```

Contamination of the law of u_j

```
> makedata(vu.epsilon=0.1)

SAE MODEL TYPE: B (J.N.K. Rao's classification)
DATA: Synthetic, simulated data
MODEL:
   y_ij = intercept + sum_k[ beta_k * x_kij] + v_i + e_ij
 with
   each x_kij ~ N(0, 1), k=1,...,2
   v_i ~ (0.9)*N(0, 1) + 0.1*N(0, 41)
   e_ij ~ N(0, 1)
```

and both

```
> makedata(vu.epsilon=0.1, ve.epsilon=0.1)

SAE MODEL TYPE: B (J.N.K. Rao's classification)
DATA: Synthetic, simulated data
MODEL:
   y_ij = intercept + sum_k[ beta_k * x_kij] + v_i + e_ij
 with
   each x_kij ~ N(0, 1), k=1,...,2
   v_i ~ (0.9)*N(0, 1) + 0.1*N(0, 41)
   e_ij ~ (0.9)*N(0, 1) + 0.1*N(0, 41)
```

It goes without saying that we may change other parameters of the `makedata` function. For instance, we may generate contaminated, unbalanced data; see below.

6.1.3 Unbalanced data

Further, we can generate unbalanced data very easily. First, we have to set both arguments `n` and `g` in `makedata` equal to `NULL` (since `n` is not a constant for unbalanced data). Next, we have to tell `makedata` to produce unbalanced data on grounds of a vector of area idetifiers (ID; all units in a particular area are assigned an area-specific identifier code). By way of example, suppose we want to generate 16 units that reside in 5 areas. The following code snippet defines the vector identifiers.

```
> my_area_id = c(1,1,1,1,1,2,2,3,3,3,4,4,4,4,4,5)
```

Thus, the vector of area size is $nsize^T = (n_1, \ldots, n_5) = (5, 2, 3, 4, 1)^T$. (Note that the IDs do not have to be sorted (as in the display); any permutation of the IDs is a valid argument. The number of areas is determined from the number of unique elements.)

The data are generated by the following command.

```
> mymodelub <- makedata(n=NULL, g=NULL, areaID=my_area_id)
```

A About rsae

```
> citation("rsae")

To cite package 'rsae' in publications use:

  Tobias Schoch (2014). rsae: Robust Small Area Estimation. R package
  version 0.1-5.

A BibTeX entry for LaTeX users is

  @Manual{,
    title = {rsae: Robust Small Area Estimation},
    author = {Tobias Schoch},
    year = {2014},
    note = {R package version 0.1-5},
  }
```

B Comparing the ML estimates of `rsae` with those of `nlme`

For ease of comparability, we report (again) the maximum likelihood estimates obtained by `fitsaemodel`.

```
> fitsaemodel("ml", bhfmodel)

ESTIMATES OF SAE-MODEL (model type B)
Method:  Maximum likelihood estimation
---
Fixed effects
```

```
Model: HACorn ~ (Intercept) + PixelsCorn + PixelsSoybeans
  Coefficients:
   (Intercept)      PixelsCorn  PixelsSoybeans
     50.967557        0.328581       -0.133710
---
Random effects
  Model: ~1| CountyName
           (Intercept)  Residual
Std. Dev.  11.0028      11.7181
---
Number of Observations:  36
Number of Areas:  12
```

These results are equal to those of the `lme` function in the **nlme** package (which may be called the industrial standard).

```
> require(nlme)
> nlme::lme(HACorn ~ PixelsCorn + PixelsSoybeans, random=~1|CountyName, data=subset(lan

Linear mixed-effects model fit by maximum likelihood
  Data: subset(landsat, subset = (outlier == FALSE))
  Log-likelihood: -147.0126
  Fixed: HACorn ~ PixelsCorn + PixelsSoybeans
   (Intercept)     PixelsCorn PixelsSoybeans
    50.9675892      0.3285805     -0.1337102

Random effects:
 Formula: ~1 | CountyName
        (Intercept) Residual
StdDev:    11.00298 11.71806

Number of Observations: 36
Number of Groups: 12
```

C Package installation on Linux systems

In this section, I give some details on the installation of `rsae` on a Linux powered system. These details essentially summarize my experience with `openSUSE 11.4` on a `x86_64` platform. Some of the details carry directly over to other (mostly-) POSIX-compliant systems, others do not. It is up to the user to modify these hints to fit on his/her system. Note the following:

- Make sure that you have installed `R-devel` (or `r-base-dev`) in addition to `R-base`; see R-admin (2011, chapters 2, 6 and Appendix A.1)
- The `rsae` package contains `FORTRAN 90` code that must be compiled (and linked to `R`'s `BLAS` and `LAPACK`) at installation. The code has been written and tested

for `gfortran` (v. 4.5-1). The code does not use (to the best of my knowledge) any compiler-specific code. See R-admin (2011, Appendix B.8) for more details on `FORTRAN` compilers supported by `R`, and in what order they are selected if you have several compilers. Therefore, any compatible `FORTRAN` compiler should work. However, I highly recommend to use `gfortran`. (Note that if the `C` compiler that your current `R` installation knows of is `gcc 4` [the command `R CMD config CC` tells you what `R` uses; then check the version `gcc -v`], it will automatically choose `gfortran`)

- you need the system tool `GNU make`. By default, most Linux distributions are delivered with a copy of `make`, whereas `openSUSE 11.4` is not. You thus have to grab a version from the internet. See R-admin (2011, Appendix B.5) for more on `make`.

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