

Robust Small Area Estimation: a Vignette

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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 \(1986\)](#), [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)
```

¹Note 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.

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

- 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, Harter, and Fuller \(1988\)](#), 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

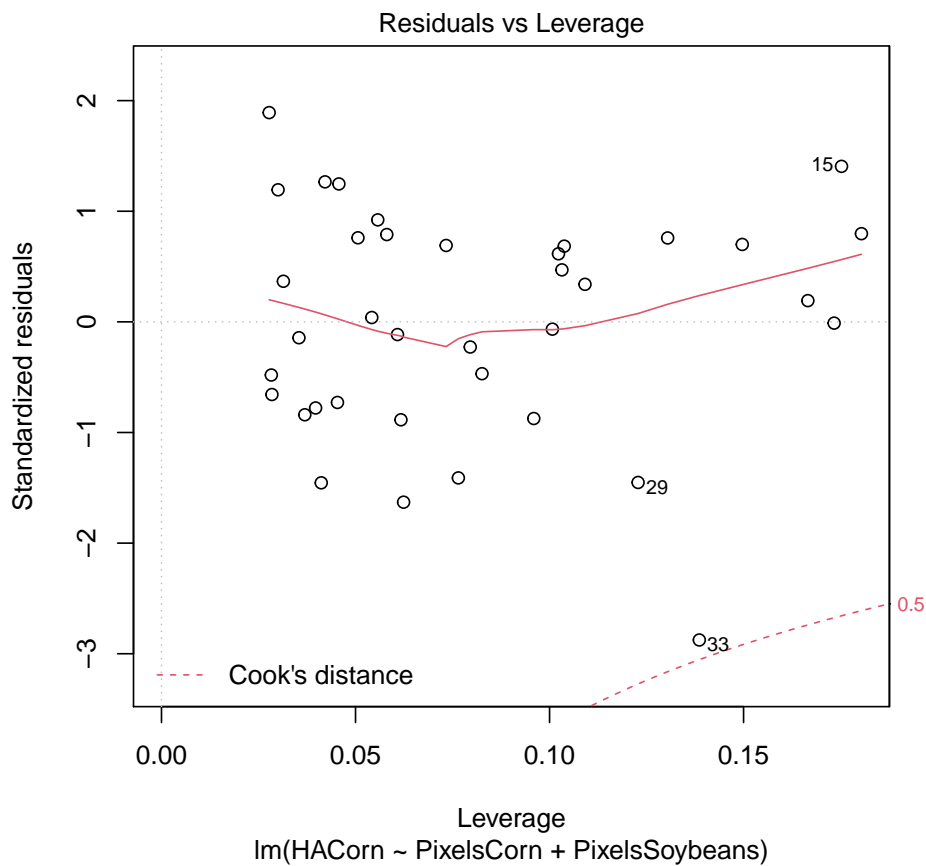
So, there are twelve areas – the smallest areas (Cerro Gordo, Hamilton, and Worth) contain one unit, the largest area, Hardin, involves six units.

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 $j = 1, \dots, n_i$, $i = 1, \dots, 12$.

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 `~` 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 `~` 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` (Battese, 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 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(bhfmmodel)
```

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", bhfmmodel)
```

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, Bates, Default, and Sarkar, 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 not 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. Nonetheless, 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,

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

where $x_{i,j} \sim N(0, 1)$, $e_{i,j} \sim N(0, 1)$, $\beta = (1, 1)^T$, $n_i = n = 10$, $\forall i = 1, \dots, 10$ (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`)

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

and consider the following model fit

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

```
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 response variable is supposed to be uncontaminated 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 -estimation 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 (uncontaminated) 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 ranef 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 Croux, Todorov, Ruckstuhl, Salibian-Barrera, Verbeke, Koller, Maechler, 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-specific 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, Cantoni, Copt, and Victoria-Feser \(113–114 2009\)](#). 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 `bhfmmodel` 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
```

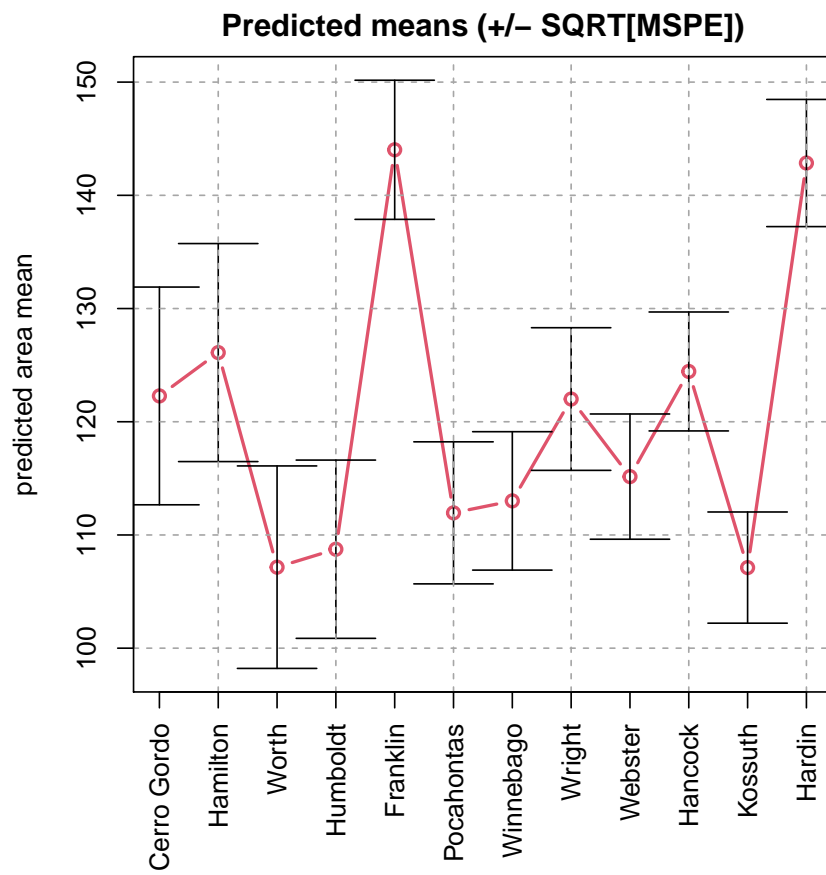
Robustly Estimated/Predicted Area-Level Means:

	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 bootstrap replicates)

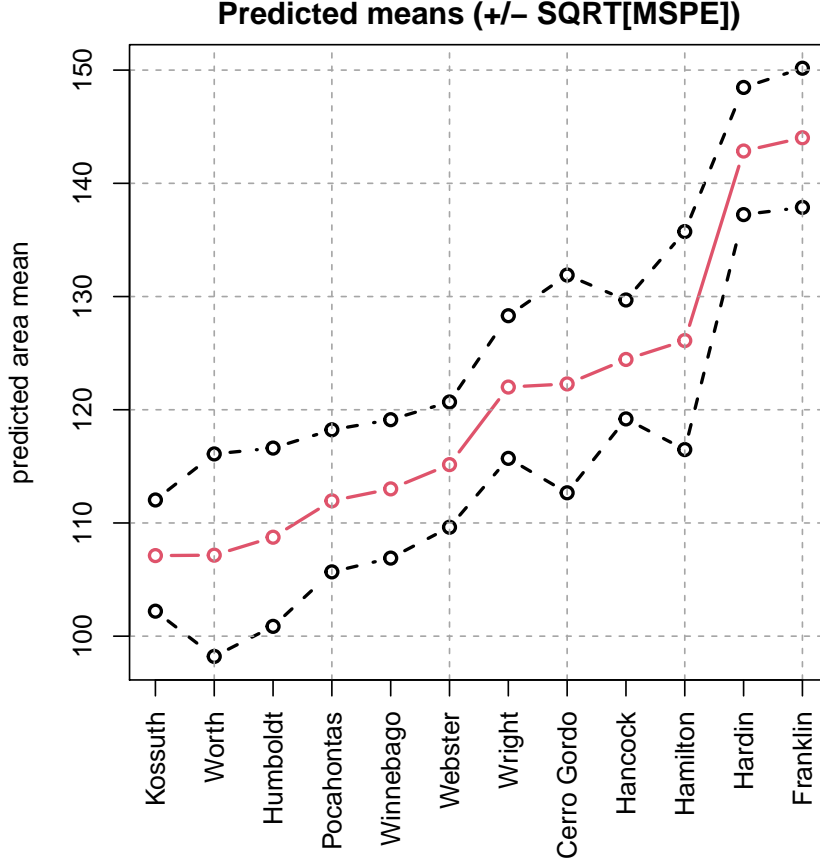
and a visual display of the predicted county means

```
> plot(pr)
```

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

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



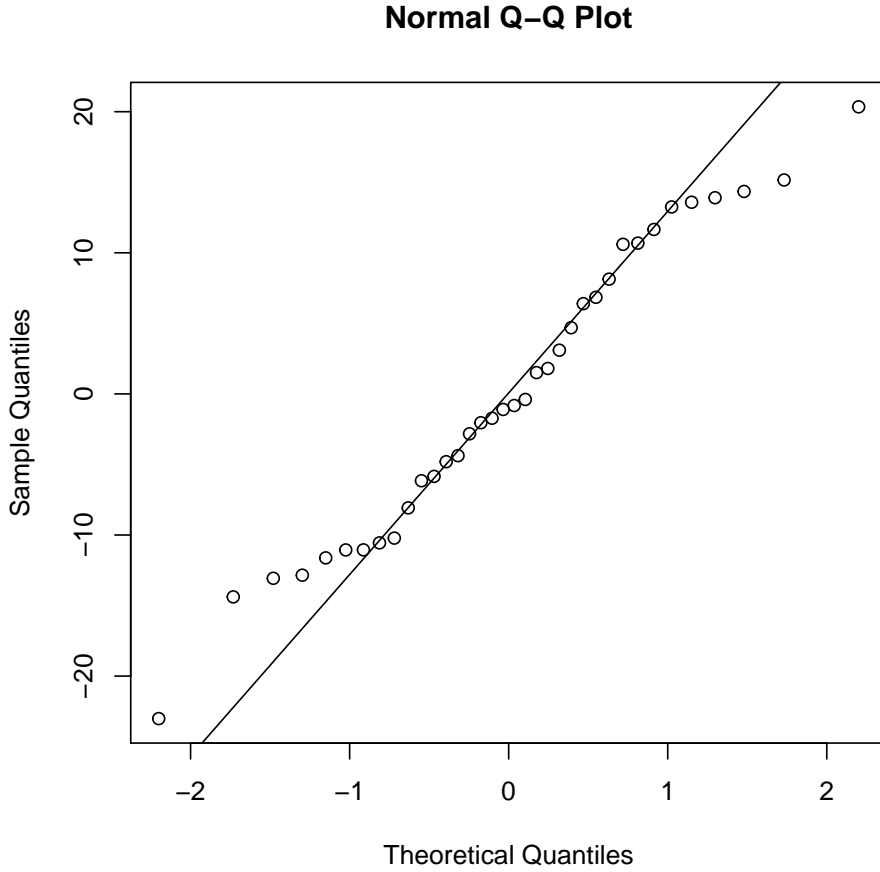
Once the area-specific random effects have been predicted (by means of robust methods), we can have a look at the residuals. Note that the residuals are given by

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

where the superscript R highlights the fact that robust estimates/predictions are used. Obviously, since the residuals depend on \hat{u}_i^R (which 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 available having estimated the fixed- and random-effects parameters.

The residual 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

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

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

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

and

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

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

The default values of `makedata` for balanced data, i.e., $n_i = n, \forall i = 1, \dots, g$ 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 (through 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 identifiers (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 $nsize^T = (n_1, \dots, n_5) = (5, 2, 3, 4, 1)^T$. (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.
```

Ein BibTeX-eintrag für LaTeX Benutzer ist

```
@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(landsat, subset=(outlier==FALSE)), method="ML")

```

```

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 `FORTTRAN 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 `FORTTRAN` compilers supported by R, and in what order they are selected if you have several compilers. Therefore, any compatible `FORTTRAN` 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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