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Simulation Tools for Small Area Estimation: Introducing the R-package saeSim

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Abstract

The abstract of the article in English

Keywords: package, small area estimation, reproducible research, simulation, R.

1. Introduction

The demand for reliable small area statistics from sample surveys has been substantial grown over the last decades due to their use in public and private sectors. In this paper we present a framework for simulation studies inside the field of small area estimation. This tool might be useful for the prospective researcher or data analyst to provide reproducible research.

Reproducible research has become a widely discussed topic in many academic areas. For instance in the field of statistics, many mostly open-source tools like the R-language (R Core Team 2014) and LaTeX, dynamic reporting packages like knitr (Yihui 2013), sweave (Leisch 2002) and more recently rmarkdown (Allaire, McPherson, Xie, Wickham, Cheng, and Allen 2014), make the integration of text and source code for statistical analysis possible. Publishing source-code and data alongside in an article draws special attention to authoring the analysis. However, the requirements for source code are different from the written words in the article itself.

> *Instead of imagining that our main task is to instruct a computer what to do, let us concentrate rather on explaining to human beings what we want a computer to do.* (Knuth 1992, p.99)

Next to the combination of text and source code, reproducible research aims that the full output of the academic research which is the paper combined with the full computational environment like data and source code, is available. However, real data is often very sensitive and governed by strictly confidentiality rules. Synthetic data generation mechanisms (Kolb 2013) can be used to provide safe data which is publicly available to enable the community to reproduce the analysis and results. Burgard, Kolb, and Münnich (2014) interpreted this as an open research philosophy. Such synthetic data sets can be used to test newly proposed statistical methods in a close-to-reality framework/ simulation. This may provide valuable insights about the quality of the introduced methods in a controlled environment under different scenarios. In general, statistical simulation studies are divided in the literature into two concepts:

- Design-based: The simulation study is based on true or synthetic data of a fixed population. Then, samples are selected repeatedly from the underlying finite population and different estimation methods are applied in each replication. The obtained estimates are compared to the true values of the population, for instance, in terms of relative bias (RB) or relative root mean squared error (RRMSE).

- Model-based: The simulation study uses data drawn from certain distributions. In each iteration, the population is generated from a model and a sample is selected according to a specific sampling scheme. The sample is used to estimate the quantity of interest and quality measures (like RB and RRMSE) are derived.

Further discussion regarding model- and design-based simulations is available in Münnich, Schürle, Bihler, Boonstra, Knotterus, Nieuwenbroek, Haslinger, Laaksonen, Eckmair, Quatember, Wagner, Renfer, Oetliker, and Wiegert (2003), Salvati, Chandra, Giovanna-Ranalli, and Chambers (2010) or Alfons, Templ, and Filzmoser (2010).

However, simulation studies are often presented very briefly in academic articles without providing enough details about the underlying structure of the study. Alfons *et al.* (2010) provide a framework (simFrame) which helps the prospective researcher or data analyst to conduct simulation studies in a reproducible environment. The R-package simFrame (Alfons *et al.* 2010) is an object-oriented tool for statistical simulation studies based on S4 classes. It includes a wide range of different features (like data generation, sampling schemes, outlier contamination mechanisms and missing values) to conduct simulation studies. simFrame was originally developed for simulations in the context of survey statistics but is now designed to be as general as possible (cf. Alfons *et al.* 2010).

Survey statistics are used, for example, in order to deliver specific indicators as a basis for economic and political decision processes. Especially regional or group-specific comparisons are of interest (cf. Schmid and Münnich 2014). Surveys which shall provide the sufficient data for these regional indicators, however, are generally designed for larger areas (NUTS 1-2 level). Hence, sample information on more detailed levels, like NUTS3, is hardly available so that classical estimation methods (direct estimators) may lead to high variances of the estimates (cf. Ghosh and Rao 1994). In this case, small area estimation methods may reveal highly improved results for the target estimates. Small area estimation has become more and more attractive over the last decade:

> *In 2002, small area estimation (SAE) was flourishing both in research and applications, but my own feeling then was that the topic has been more or less exhausted in terms of research and that it will just turn into a routine application in sample survey practice. As the past 9 years show, I was completely wrong; not only is the research in this area accelerating, but it now involves some of the best known statisticians...* Pfeffermann (2013)

However, the empirical part is also often presented very briefly in the context of small area estimation. Thus, there is a need to have a suited framework to guarantee the reproducibility of analysis. To the best of our knowledge, there is not any R-package or framework adjusted for the special case of small area estimation which provides a simulation environment.

The aim of this article is to inform the prospective researcher or data analyst of a new R-package (simFrame) which supports the process of making simulation studies reproducible and offers a *human-readable* interface in the field of small area estimation. To be more precise, the package has three main objectives: First, provide tools for data generation which are reproducible. Second, unify the process of simulation studies. Third, make the source-code of simulation studies available, such that it supports the conducted research in a transparent manner.

The paper is organised as follows. In Section 2 we give a short introduction to small area estimation focusing mainly on unit-level (Battese, Harter, and Fuller 1988) and area-level models (Fay and Herriot 1979). Section 3 introduces a framework for simulation studies and how it is supported by the R-package saeSim. To illustrate some of the features of the package we present a case study in Section 4. We conclude the paper in Section 5 by summarising the main findings and by providing some avenues for further research.

SONSTIGER TEXT: The objective of small area estimation is to produce reliable statistics (means, quantiles, proportions, etc.) for domains where little or no sampled units are available. Groups may be areas or other entities, for example defined by socio-economic characteristics. New statistical methods are applied in model-based and design-based simulation studies. Considering the demands for reproducible research we propose a framework for simulation studies inside the field of small area estimation.

2. Small area estimation

The objective of small area estimation is to produce reliable statistics (means, quantiles, proportions, etc.) for domains where little or no sampled units are available. Groups may be areas or other entities, for example defined by socio-economic characteristics. The demand for such estimators is rising as they are used for fund allocation, educational and health programs (Pfeffermann 2013). As direct estimation of such statistics are considered to be unreliable, methods in small area estimation try to improve the domain predictions by borrowing strength from neighboured or *similar* domains. This can be achieved by using additional information from census data to assist the prediction for non-sampled domains or domains with little information. For the purpose of this article we will introduce two basic models frequently used in small area estimation, the unit-level model introduced by Battese *et al.* (1988) and the area-level model introduced by Fay and Herriot (1979).

The unit level model (Battese *et al.* 1988) can be expressed as:

$$\begin{aligned} y_{ij} = &\; x_{ij}^\top\beta + v_i + e_{ij} \\ v_i \overset{iid}{\sim} &\; N(0, \sigma_v^2) \\ e_{ij} \overset{iid}{\sim} &\; N(0, \sigma_e^2) \end{aligned}$$

where $i = 1, \ldots, D$ and $j = 1, \ldots, n_i$. y_{ij} is the the dependent variable for domain i and unit j, and x_{ij} the corresponding auxiliary information for that unit. Furthermore v and e are independent. This model can be seen as a linear mixed model from which the best linear unbiased predictor (BLUP) can be derived and is used for the domain prediction (Rao 2003).

Due to reasons of confidentiality unit-level information is not always available. Instead only aggregates, or rather the direct estimators may be supplied. However, these direct estimations are known to be unreliable, hence in such situations area-level models can be valuable. The area-level model introduced by Fay and Herriot (1979) is build on a sampling model:

$$y_i = \mu_i + e_i,$$

where y_i is a direct estimator of a statistic of interest μ_i for an area i with $i = 1, \ldots, D$ and D being the total number of areas. The sampling error e_i is assumed to be independent and normally distributed with known variances $\sigma_{e,i}^2$, i.e. $e_i|\mu_i \sim N(0, \sigma_{e,i}^2)$. The model is modified with the linking model by assuming a linear relationship between the true area statistic μ_i and some auxiliary variables x_i:

$$\mu_i = x_i^\top\beta + v_i,$$

with $i = 1, \ldots, D$. Note that x_i is a vector containing area-level (aggregated) information for P variables and β is a vector $(1 \times P)$ of regression coefficients describing the (linear) relationship. The model errors v_i are assumed to be independent and normally distributed, i.e. $v_i \sim N(0, \sigma_v^2)$. Furthermore e_i and v_i are assumed to be independent. Combining the sampling and linking model leads to:

$$y_i = x_i^\top \beta + v_i + e_i. \quad (1)$$

Model 1 is effectively a random-intercept model where the distribution of the error term e_i is heterogeneous and known.

3. A simulation framework

In our opinion simulation studies can best be summarised when understood as a process of data manipulation. Thus the main focus of saeSim is to define the steps in that process which can then be *cleanly* defined and repeated. Before we go into any detail of the functionality of the package we will discuss the process behind simulation studies and later how saeSim maps this process into R.

Simulation studies in small area estimation address three different levels, the population, the sample and data on aggregated level, as illustrated in figure 1. The **population-level** defines the data on which a study is conducted and may be a true population, synthetic population data or randomly generated variates from a model. We see three different point of views to define a population. First *design-based*, which means that a simulation study is based on true or synthetic data of *one* population. Second a *semi-model-based* point of view, where only one population is drawn from a model and is fixed in the whole simulation study. And third, *model-based* studies which have changing random populations drawn from a model.

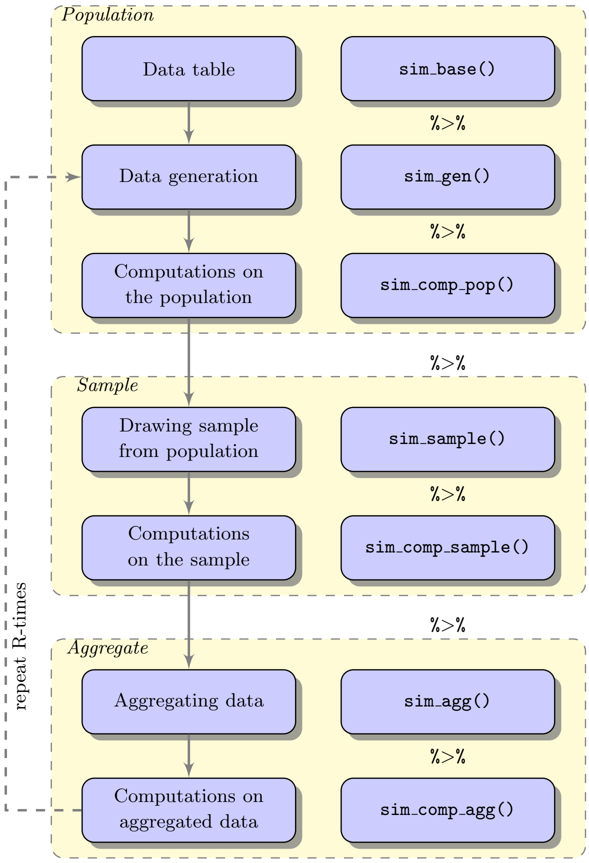


Figure 1: Process of simulation.

The scope of this article is not not to promote any of those viewpoints, but simply to identify the similarity in them. The *base* (first component in figure 1) of any simulation study is a data table, the question is, if this data is *fixed* or *random* over the course of the simulation. Or from a more technical point of view, is the data generation (the second step in figure 1) repeated in each simulation run or omitted?

Depending on the choice of a fixed or random population it is necessary to recompute the population domain-statistics like domain means and variances, or other statistics of interest (third component in figure 1).

The **sample-level** is when domain predictions are conducted for unit-level models. Independently of how the population is treated, fixed or random, this phase consists of two steps, first drawing a sample, and second conducting computations on the samples (fourth and fifth component in figure 1). Given a sample, design or model based small area methods are applied. Of interest are estimated parameters, which can be estimated model parameters or domain predictions as well as measures of uncertainty for the estimates.

As the sample-level is when unit-level models are applied, the **aggregate-level** is when area-level models are applied (the seventh and last component in figure 1). Area-level models in small area estimation typically only use information available for domains (in contrast to units). Thus, the question for simulation studies for area-level methods is, if the data is generated on unit-level and used after the aggregation (sixth component in figure 1) or if the data is generated directly on area-level, i.e. drawn from an area-level model. Depending on whether unit-level data and sampling are part of the simulation the aggregate-level follows the generation of the population or is based on the aggregated sample. Again, we do not promote a specific viewpoint but simply allow steps in the process of simulation to be omitted.

Depending on the topic of research steps in this simulation framework can be more relevant than others or completely irrelevant. We see these steps more as a complete list of phases one can encounter, thus single components can be omitted if not relevant in specific applications. For example *data generation* is not relevant if you have population data, or the *sample-level* is not used, when the sample is directly drawn from the model.

From this considerations, saeSim maps the different steps into R. Two layers with separate responsibilities need to be discussed. The first is *how* different simulation components can be combined, and the second *when* or in which order they are applied. Regarding the first, in saeSim we put a special emphasis on the interface of each component, which is to use functions which take a data.frame as argument and have a data.frame as return value. This is a widely used approach for data manipulation and promoted recently in the package dplyr (Wickham and Francois 2014). This definition of interfaces, the return value of one component is the input of the next, is also used in saeSim.

Understanding a simulation as a process of manipulating one data object, see the second column in figure 1 how the different steps in a simulation can be accessed. It is important to note that the functions in figure 1 control the process, the second layer, i.e. *when* components are applied. Each of these functions take a simulation setup object to be modified and a function with the discussed interface as arguments. Hence a simulation setup is a collection of functions to be applied in a certain sequence. Also the second-layer functions have a defined interface: a sim_setup as input to be modified and a sim_setup as output. Thus, components can be chained together using the *pipe operator* (%>%) from the package magrittr (Bache and Wickham 2014).

With saeSim we want to contribute tools for simulation studies in the field of small area estimation. We see the need for sharing tools for data generation and simulation amongst the scientific community and thus defined an interface for these tools as well as a platform to make them accessible. By defining the steps behind a simulation we hope to promote a reasonable way to communicate them alongside publications and during research. In the next section we will present a case study and focus more on the concrete functionality provided by the package.

4. Case study

Braking the responsibility into what is applied and when it is applied addresses several aspects of reproducibility. First, by defining the interface between all components, it is easy to combine them in any combination and thus easy to share and reuse. Second, by controlling when components are applied we avoid the necessity of control structures in syntax and emphasise on the definition of components. The following example shows these aspects of the package using a predefined simulation setup:

```
> setup1 <- sim_base_lm() %>% sim_sample(sample_number(5))
> setup2 <- sim_base_lm() %>% sim_sample(sample_fraction(0.05))
```

Without knowing anything about the setup defined in sim_base_lm we can see that setup1 and setup2 only differ in the applied sampling scheme. sim_sample is responsible to control when a function is applied (after the population-level) and sample_number(5) and sample_fraction(0.05) define the explicit way of drawing samples. The pipe operator %>% is used to add new components to the setup. As said before the composition of a simulation in that manner will focus on the definition of components and hide control structures. The next example will repeat the simulation stored in setup1 two times. The results are returned in a list of data.frames which have five rows as we sample 5 observations:

```
> setup1 %>% sim(R = 2) %>% sapply(nrow)
```

```
[1] 5 5
```

As a side remark: The pipe operator, %>%, is designed to make otherwise nested expressions more readable as a line can be read from left to right, instead of inside out (Bache and Wickham 2014). As a minimal example see the following lines which are equivalent:

```
> sum(1:10)
```

```
[1] 55
```

```
> 1:10 %>% sum
```

```
[1] 55
```

4.1. Model-based simulation

The first task for the model-based simulation is to generate the data under the model:

$$y_i = 100 + 2 \cdot x_i + v_i + e_i$$

where $x_i \overset{iid}{\sim} N(0, 4^2)$, $v_i \overset{iid}{\sim} N(0, 1)$ and $e_i \overset{indep}{\sim} N(0, \sigma_i^2)$ with $\sigma_i^2 = 0.1, 0.2, \ldots, 4$ and $i = 1, \ldots, 40$ as index for the domains. Also are x_i, v_i and e_i independent from each other. The starting point is always a data table as *base-component*, in this case just with an id variable named idD and constructed with the function base_id. Any random number generator in R can be used, however we have a strictly *normal* model, for which some predefined functions can be used.

```
> library(saeSim)
```

```
> setup <- base_id(nDomains = 40, nUnits = 1) %>%
+   sim_gen_x(mean = 0, sd = 4) %>%
+   sim_gen_v(mean = 0, sd = 1)
> setup
```

```
  idD          x          v
1   1 -2.5058152 -0.1645236
2   2  0.7345733 -0.2533617
3   3 -3.3425144  0.6969634
4   4  6.3811232  0.5566632
5   5  1.3180311 -0.6887557
6   6 -3.2818735 -0.7074952
```

Note that if you print a simulation setup to the console, as in the above example, one simulation run is performed and only the first rows of the resulting data table are printed. This enables interactivity with the object itself, however it hides that the setup object is a collection of functions to be called. The error component e_i in the model has different variances which is not covered by a predefined function. Thus, as a *generator* function we will define a function which takes a data.frame as input and returns it after adding a variable named vardir with the variances and the variable e with the generated random numbers:

```
> gen_e <- function(dat) {
+   dat$vardir <- seq(0.1, 4, length.out = nrow(dat))
+   dat$e <- rnorm(nrow(dat), sd = sqrt(dat$vardir))
+   dat
+ }
> setup <- setup %>% sim_gen(gen_e)
> setup

  idD          x          v vardir          e
1   1 -2.2746749 -0.5059575    0.1  0.1344285
2   2 -0.5407145  1.3430388    0.2 -0.1067262
3   3  4.7123480 -0.2145794    0.3  0.5797550
4   4 -6.0942672 -0.1795565    0.4  0.5606229
5   5  2.3757848 -0.1001907    0.5 -0.4378710
6   6  1.3318015  0.7126663    0.6  1.7088396
```

The last step in data generation is to construct the response variable which will be named y and added to the data. Also we will add the *true* area statistic under the model to the data:

```
> setup <- setup %>%
+   sim_resp_eq(y = 100 + 2 * x + v + e) %>%
+   sim_comp_pop(comp_var(trueStat = y - e))
```

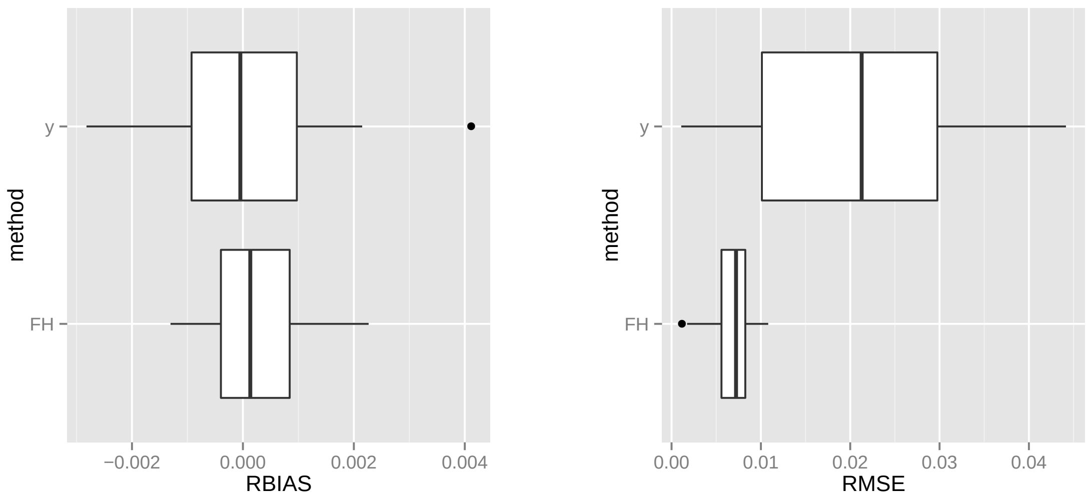
Not all necessary functions can be provided by the package. As said before, one of the main objectives was to define the interface between components. To add the area-level predictions from a Fay-Herriot model we need to define a function for that. The function takes a data.frame as input and returns the modified version. Here we use the function eblupFH from the package sae (Molina and Marhuenda 2013) to estimate the EBLUP under the FH model. Finally we add comp_FH to the process:

```
> library(sae)

> comp_FH <- function(dat) {
+   modelFH <- eblupFH(y ~ x, vardir, data = dat)
+   dat$FH <- modelFH$eblup
+   dat
+ }
> setup <- setup %>% sim_comp_agg(comp_FH)
> setup

  idD         x          v vardir          e         y  trueStat        FH
1   1  1.637607  0.7073107    0.1  0.1258998 104.10843 103.98253 104.06121
2   2  6.755493  1.0341077    0.2 -0.1822523 114.36284 114.54509 114.23876
3   3  6.346354  0.2234804    0.3  0.7253263 113.64151 112.91619 113.45213
4   4 -1.323631 -0.8787076    0.4 -0.4434978  96.03053  96.47403  96.45416
5   5 -9.140942  1.1629646    0.5 -0.4105563  82.47052  82.88108  82.46045
6   6  9.990646 -2.0001649    0.6 -0.7754272 117.20570 117.98113 118.08379
```

The object setup stores all necessary information to run one iteration of the simulation. To start more repetitions, sim is called, which will return $R = 100$ (as the number of repetitions) data.frames containing the simulated data from each iteration as a list. We use rbind_all from the package dplyr to append the resulting list:

```
> library(dplyr)

> simResults <- sim(setup, R = 100) %>% rbind_all
> simResults %>% select(idD, idR, simName, trueStat, y, FH)

Source: local data frame [4,000 x 6]

   idD idR simName  trueStat         y        FH
1    1   1         107.87088 108.21065 108.30528
2    2   1         113.29033 114.13809 113.80733
3    3   1         105.88208 105.55180 105.63108
4    4   1          84.61171  84.36450  84.63272
5    5   1         103.68692 103.39260 103.42371
6    6   1         104.26130 103.97032 103.79131
7    7   1          97.85114  97.54439  97.43298
8    8   1         101.93187 101.66741 101.49500
9    9   1          92.51517  93.88300  93.67397
10  10   1         104.07055 103.37302 104.01407
.. ... ...     ...       ...       ...       ...
```

An additional variable idR is automatically added as an ID-variable for the iteration as well as a variable simName which purpose is to distinguish between scenarios, should there be more than one. At this time we do not provide further tools to process the resulting data. As it is a data.frame many packages for processing that data are available in R, in this case dplyr (Wickham and Francois 2014) and reshape2 (Wickham 2007) have been used. The Rmd-file for this article can be checked for further detail, thus we do not see need to provide further tools from here on.



(a) (b)

Figure 2: RBIAS and RMSE for the conducted model-based simulation

4.2. Design-based simulation

In the design-based simulation we want to illustrate the use of saeSim when starting from data of a population. For this purpose we use a synthetic population generated from Austrian EU-SILC (European Union Statistics on Income and Living Conditions) data. We use this data to illustrate the functionality of the package, the data consists of 25 thousand households and does not represent the true population size of Austria. It is published alongside the R-package simFrame (Alfons *et al.* 2010) where it is used as example data. To keep this study as simple as possible, we further restrict the data for the main income holder and will only use some of the provided auxiliary information.

```
> data(eusilcP, package = "simFrame")
> simDat <- eusilcP %>%
+   mutate(agesq = age^2, eqIncome = as.numeric(eqIncome)) %>%
+   filter(main) %>%
+   select(region, eqIncome, age, agesq, gender)
> head(simDat)

         region eqIncome age agesq gender
1 Upper Austria 11128.45  25   625   male
2        Styria 19694.85  53  2809   male
3        Styria  5066.24  30   900 female
4 Upper Austria 31480.01  32  1024   male
5        Vienna 17813.40  77  5929 female
6 Lower Austria 13501.53  35  1225   male
```

For the purpose of the design-based case study we want to apply the earlier introduced BHF estimator which is implemented in the R-package sae (Molina and Marhuenda 2013). The function we use, eblupBHF, expects three data objects to produce the predictions. The sampled data, the population means of the auxiliary variables and the population sizes in each domain. To store these informations and make them available during the simulation we attach them as attributes to the population data. There are other options but setting attributes to the processed data is supported in the package and presents a very flexible form of processing data on different aggregation levels.

```
> attr(simDat, "popMeans") <- group_by(simDat, region) %>%
+   summarise(age = mean(age),
+             agesq = mean(agesq),
+             genderFemale = mean(as.integer(gender) - 1),
+             trueStat = mean(eqIncome))
> attr(simDat, "popMeans")

Source: local data frame [9 x 5]

         region      age    agesq genderFemale trueStat
1    Burgenland 54.50063 3269.677    0.3366708 22005.42
2 Lower Austria 51.95259 3009.934    0.3777874 19813.37
3        Vienna 46.98310 2486.448    0.4662797 20395.84
4     Carinthia 51.81428 2995.735    0.3540337 19486.18
5        Styria 50.64087 2886.845    0.3573538 19335.39
6 Upper Austria 50.18644 2795.804    0.3443871 20517.29
7      Salzburg 51.44943 2965.268    0.4189108 19890.33
8         Tyrol 51.76707 2995.451    0.3975648 19350.89
9    Vorarlberg 49.06904 2697.382    0.3583756 22156.12

> attr(simDat, "popN") <- group_by(simDat, region) %>% summarise(N = n())
> attr(simDat, "popN")
```

```
Source: local data frame [9 x 2]

         region    N
1    Burgenland  799
2 Lower Austria 4619
3        Vienna 5857
4     Carinthia 1723
5        Styria 3386
6 Upper Austria 4071
7      Salzburg 1671
8         Tyrol 1889
9    Vorarlberg  985
```

Before we come to the estimation configuration, the first step is to add a sampling scheme. As stated earlier, the starting point of a simulation setup is to provide a data.frame as *base-component* which, in this case, is the population data. Then the sampling component is added, in which we define to draw 10 per cent of the observations from each domain with simple random sampling.

```
> setup <- simDat %>%
+   sim_sample(sample_fraction(0.1, groupVars = "region"))
> setup

      region eqIncome age agesq gender
1 Burgenland 23572.28  67  4489   male
2 Burgenland 24056.37  26   676   male
3 Burgenland 21613.73  46  2116   male
4 Burgenland 11750.30  40  1600   male
5 Burgenland  9664.08  80  6400 female
6 Burgenland 19369.91  63  3969 female
```

What now needs to be done, is to define the components which add the desired estimates to the data. Here we will compute the mean of income in each domain as the direct estimator and the EBLUP under the BHF model. Although this could be done in one step, we will separate the two computations to illustrate how to combine several estimations and define each component independent of one another. This focus on the definition of each component and meeting the convention of the defined interface is the intended approach. It will automatically organise the simulation and each component is arranged using the simulation framework. Hence, we will define two functions, one for adding the direct estimates and one for adding the EBLUP.

```
> comp_direct <- function(dat) {
+   attr(dat, "sampleMean") <-
+     dat %>% group_by(region) %>% summarise(direct = mean(eqIncome))
+   dat
+ }
> comp_BHF <- function(dat) {
+   popMeans <- select(attr(dat, "popMeans"), -trueStat)
+   modelBHF <-
+     eblupBHF(eqIncome ~ age + agesq + gender, region, meanxpop = popMeans,
+              popnsize = attr(dat, "popN"), data = dat)
+   attr(dat, "BHF") <- modelBHF$eblup
+   dat
+ }
```

Another positive aspect of the above definitions is, that each step is relatively small and the purpose clearly defined, which will make them easy to understand, modify and reproduce. Finally we will combine the simulation results in an *aggregation-component*, possibly followed by the application of area-level models but skipped in this example. The result of this aggregation step will be a data.frame with one row for each region.

```
> agg_results <- function(dat) {
+   cbind(attr(dat, "sampleMean"),
+         BHF = attr(dat, "BHF")$eblup,
+         trueStat = attr(dat, "popMeans")$trueStat)
+ }
```

To combine the simulation setup and the defined components we arrange them using the function sim_comp_sample to ensure that the direct estimator and the EBLUP is computed on the sampled data, and sim_agg to add the above aggregation step.

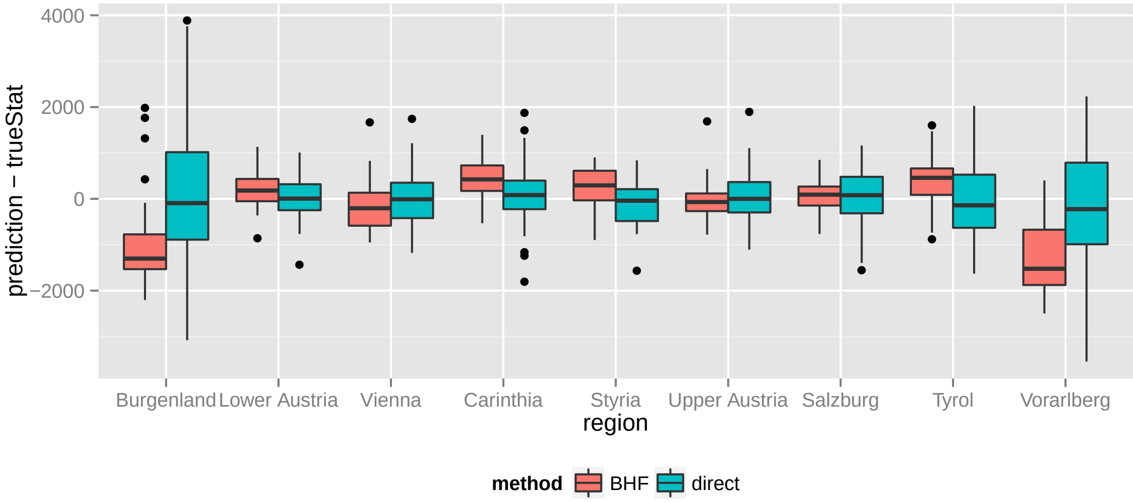
```
> setup <- setup %>%
+   sim_comp_sample(comp_BHF) %>%
+   sim_comp_sample(comp_direct) %>%
+   sim_agg(agg_results)
> setup

         region   direct      BHF trueStat
1    Burgenland 21933.95 21255.53 22005.42
2 Lower Austria 18885.08 19036.29 19813.37
3        Vienna 20734.08 20720.48 20395.84
4     Carinthia 19211.55 19377.21 19486.18
5        Styria 18704.75 18955.96 19335.39
6 Upper Austria 20636.94 20504.37 20517.29
```

To repeat the simulation R times the simulation setup can be passed to the function sim, the resulting list is directly combined using rbind_all.

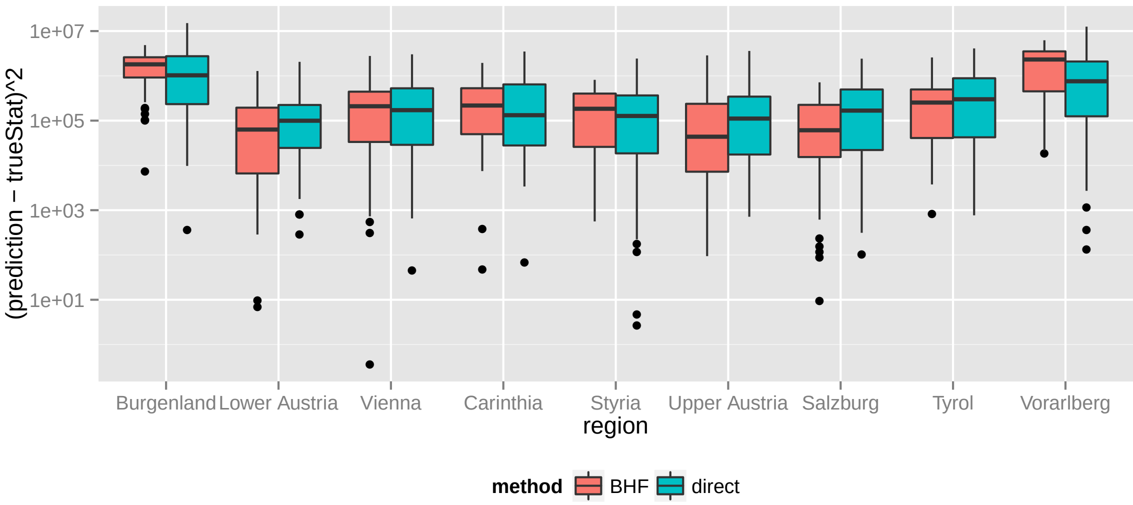
```
> simResults <- setup %>% sim(R = 50) %>% rbind_all
> simResults

Source: local data frame [450 x 6]

          region   direct      BHF trueStat idR simName
1     Burgenland 23083.61 20800.15 22005.42   1
2  Lower Austria 20414.91 20264.56 19813.37   1
3         Vienna 20756.78 20422.85 20395.84   1
4      Carinthia 19581.64 19912.43 19486.18   1
5         Styria 19443.11 19757.42 19335.39   1
6  Upper Austria 20417.38 20356.38 20517.29   1
7       Salzburg 19900.44 20009.83 19890.33   1
8          Tyrol 18493.29 19540.25 19350.89   1
9     Vorarlberg 21166.20 20444.35 22156.12   1
10    Burgenland 21340.42 20510.92 22005.42   2
..           ...      ...      ...      ... ...     ...
```

To further process the simulation results we present two graphics, using the package ggplot2 (Wickham 2009) and reshape2 (Wickham 2007).

```
> ggDat <- melt(simResults,
+               id.vars = c("region", "trueStat"),
+               measure.vars = c("BHF", "direct"),
+               variable.name = "method",
+               value.name = "prediction")

> ggplot(ggDat, aes(x = region, y = prediction - trueStat, fill = method)) +
+   geom_boxplot() + theme(legend.position = "bottom")
```




```
> ggplot(ggDat, aes(x = region, y = (prediction - trueStat)^2, fill = method)) +
+   geom_boxplot() + scale_y_log10() + theme(legend.position = "bottom")
```



5. Outlook

With saeSim have three objects, making simulation tools available and reusable, unify the process behind simulations and third assist the researcher to design her code in a transparent way. By providing the package we not only want to make our own tools available but also open it for contributions. The package source is available on CRAN `somewhere` and the repository for development at `https://github.com/wahani/saeSim` where tools may be submitted.

Apart from the availability of specific utility functions, we hope to promote and support the design of source code for simulation studies. One aspect is the design of simulations as processes of data, which changes the Use this package to share and publish simulation studies alongside papers. Contribute to the package to make your ideas available. Contribute to the package and make your whole simulation study available.

- Link to simFrame
- Package Features
  - outliers
  - sampling
  - non-linear models
- How to contribute?
- parallel computations
- Process the results of a simulation

6. TODO

- Chapter 3 + 4 - what will happen in these chapters?
- kein RBIAS + RRMSE in model-based
- Einleitung 4.2 was ist das ziel der design-basierten simulation
- Conclusion

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