

saeSim: Simulation Tools for Small Area Estimation

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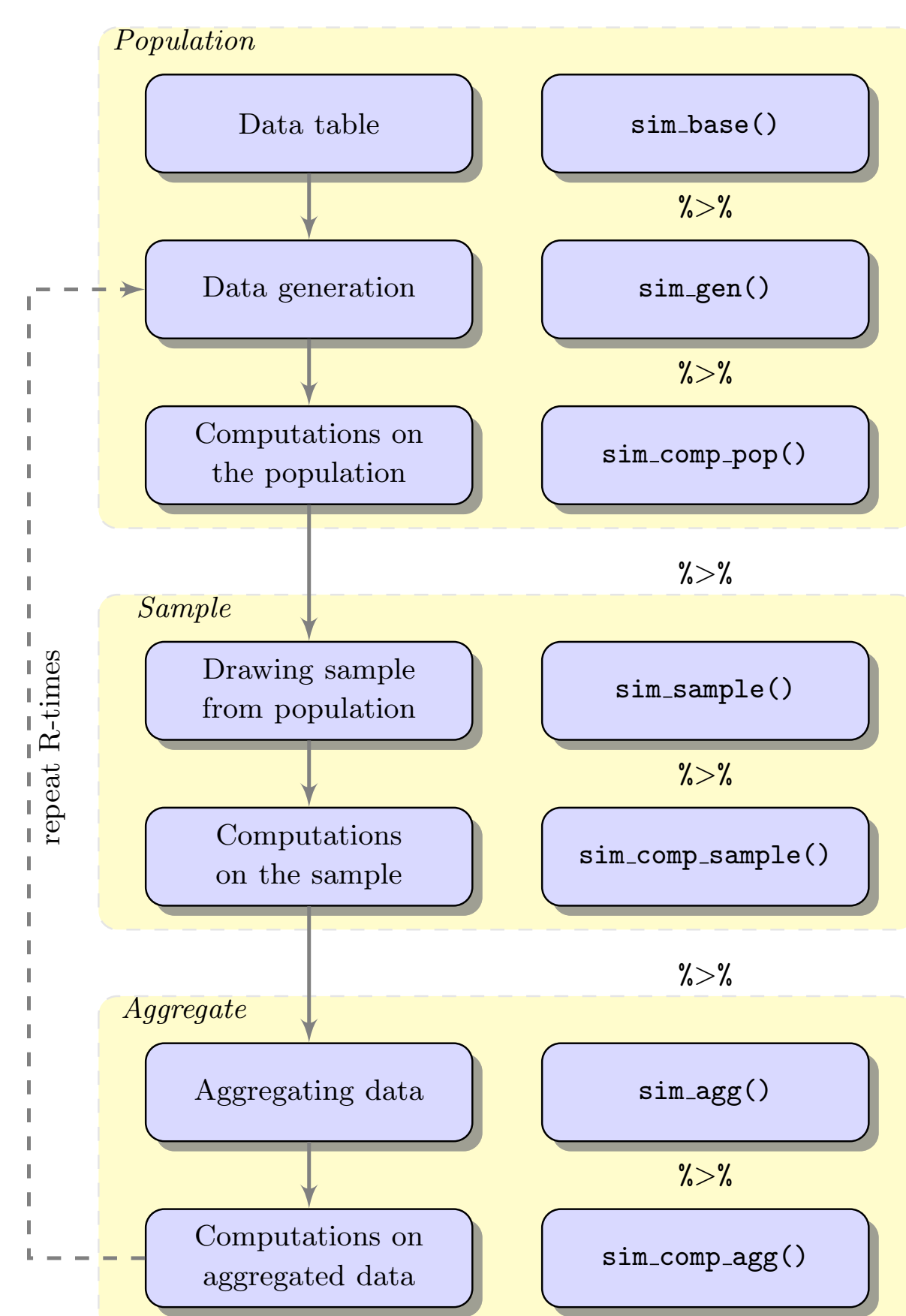
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Introduction

With this package we provide tools for the composition of simulation studies in the context of small area estimation. We want to support and encourage the publication of source code by providing a standardised set of tools for the community.

- The field of Small Area Estimation is concerned with the development and application of statistical methods to report statistics for small domains. *Small* refers to the small number of sampled units within groups.
- Model and design based simulation studies have been used to introduce new methods to the field.
- Although we have small area estimation in mind, the framework may prove useful for the composition of micro simulations in general.
- The package highlights a specific way to map a simulation study into R, namely in terms of a pipeline where a data frame is modified in each step.
- With this package the composition of a simulation study is reduced to *chaining the steps together*.



Data generation

saeSim provides several functions to make the composition and generation of synthetic population data more efficient.

- You can use predefined generators, e.g. for spatially correlated variates, or include univariate random number generators from R.
- sim.gen defines the position in the chain. gen.generic controls the generation process and accepts any random number generator as argument. Also we defined shortcuts like sim.gen.generic to be less verbose.
- In the following you see a definition for drawing numbers from a linear mixed model. The response is constructed with an R expression and set by sim.resp.eq.

```
setup <- sim_base() %>% # default with 100 areas (domains) and 100 units each
sim_gen(gen_generic(rnorm, sd = 4, name = "x")) %>%
sim_gen(gen_generic(rnorm, sd = 4, name = "e")) %>%
sim_gen(gen_generic(rnorm, sd = 2, groupVars = "idD", name = "v")) %>%
sim_resp_eq(y = 100 + 2 * x + v + e)
setup
```

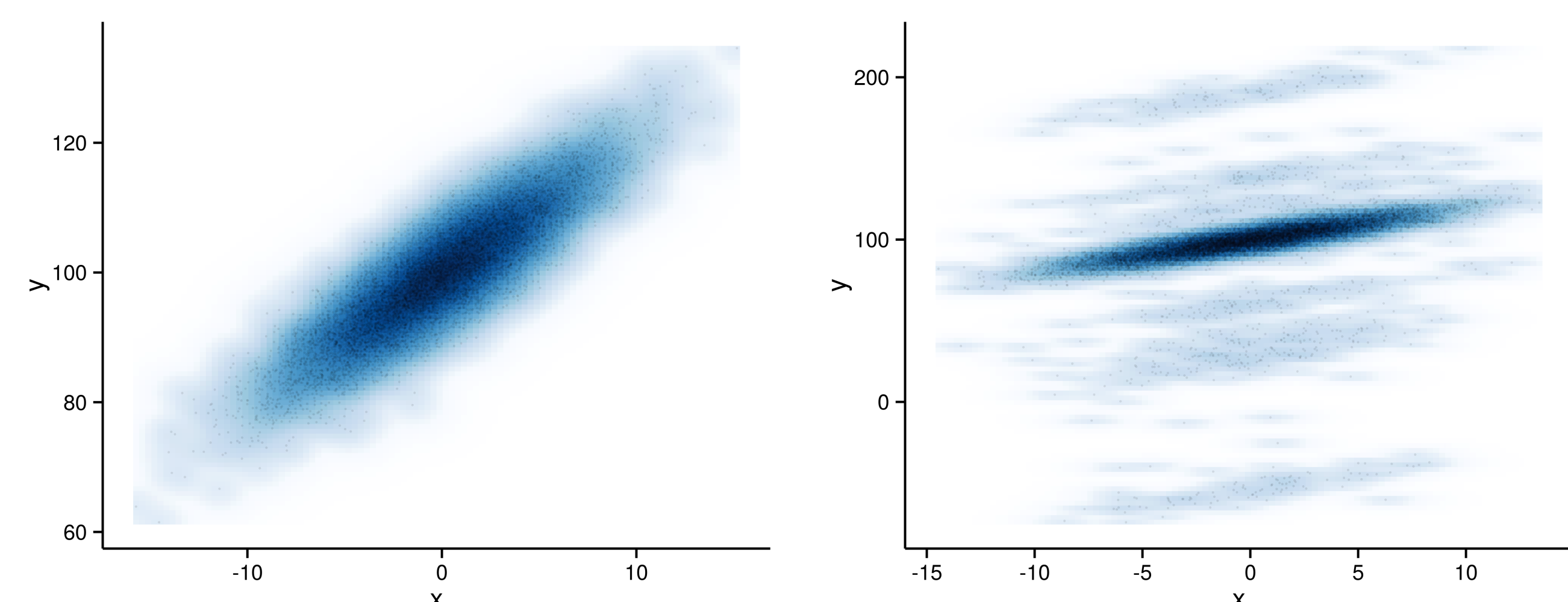
```
##
## # data.frame [10,000 x 6]
##   idD idU      x      e      v      y
##   <int> <int>   <dbl>   <dbl>   <dbl>   <dbl>
## 1     1     1  3.9462670  1.841257  2.443888 112.17768
## 2     1     2 -5.7587514  7.802529  2.443888  98.72891
## 3     1     3  0.7469758 -1.089258  2.443888 102.84858
## 4     1     4 -5.2633582  3.373478  2.443888  95.29065
## 5     1     5 -1.8117415  8.351238  2.443888 107.17164
## 6     1     6 -1.3475448  1.510108  2.443888 101.25891
## # ... with 9,994 more rows
```

Outliers

Outliers can be added to the data generation. sim.gen.cont provides the interface to control the degree and level of contamination.

- Set the frequency or probability for adding contaminated observations.
- You can choose between unit and area level outliers, i.e. *outlying* units or groups in the data.

```
setupCont <- setup %>%
sim_gen_cont(gen_generic(rnorm, sd = 50, name = "e"), 0.01, "unit") %>%
sim_gen_vc(sd = 50, areaVar = "idD", nCont = 0.1, type = "area")
autoplot(setup)
autoplot(setupCont)
```



Parallel computations

Simulation studies are embarrassingly parallel. For parallel computations we utilize parallelMap which makes it easy to switch between different parallel back-ends in R, e.g. multicore, socket, MPI and BatchJobs.

- To start the simulation use the function sim and specify the number of runs.
- To start the simulation in parallel define the mode and number of cpus.
- Packages and also objects can be loaded on all nodes with extra arguments to sim.
- Here we perform 16 runs on 4 cores. sim always returns a list and we combine the results directly using rbind.all.

```
sim(setup, R = 16, mode = "socket", cpus = 4) %>% dplyr::bind_rows() %>% dim()
## Starting parallelization in mode=socket with cpus=4.
## Mapping in parallel: mode = socket; cpus = 4; elements = 16.
## Stopped parallelization. All cleaned up.
## [1] 160000      8
```

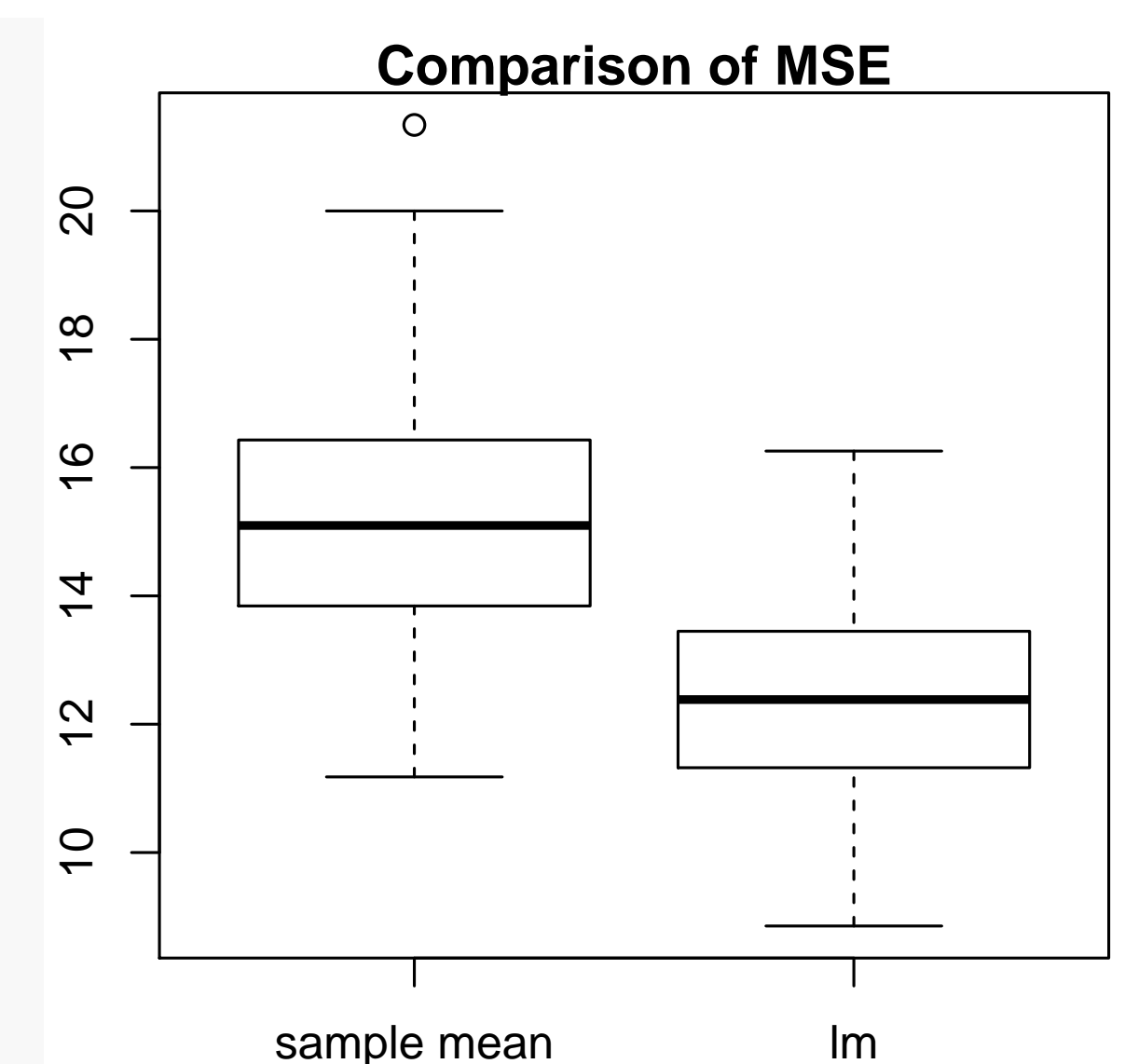
Extensions

To make saeSim more than just a tool for data generation define your own components and arrange them in the process.

- This is a complete example beginning with data generation, followed by simple random sampling in each domain and completing with a comparison of the mean squared error of the sample mean and the average of a linear predictor in each domain.
- Here we define comp_lm to use a linear model to predict the area means. The data is aggregated for each domain by the aggregation function sim.agg.
- At this time we do not see the need to provide tools for further reshaping and aggregation of results. Instead we rely on existing packages like dplyr which is used after the call to sim.

```
comp_lm <- function(dat) {
  dat$lm <- predict(lm(y ~ x, data = dat))
  dat
}

simDat <- setup %>% sim_sample() %>%
sim_comp_popMean() %>%
sim_comp_sample(comp_lm) %>%
sim_agg() %>% sim(R = 100) %>%
bind_rows() %>% group_by(idD) %>%
summarise(
  MSE_direct = mean((y - popMean)^2),
  MSE_lm = mean((lm - popMean)^2)
)
boxplot(simDat$MSE_direct, simDat$MSE_lm,
names = c("sample mean", "lm"),
main = "Comparison of MSE")
```



Design and naming

You do not have to redefine, reuse instead!

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

- setup1 and setup2 only differ in the specific way samples are drawn.
- sim.sample inserts the sampling function at the appropriate position in the process.
- For every step in the process tools are named using the corresponding prefix, e.g. gen.generic for data generation or sample.fraction for drawing samples.

Remarks

- We hope to encourage the small area estimation community to contribute and publish the code of simulation studies alongside articles.
- saeSim is a suggestion how such studies can be conducted. The design aims to use common tools and to remove control structures from the code. At the same time we encourage the definition of short and self contained functions as *components*.
- The package is not complete. If you have suggestions you are welcome to contribute to <https://github.com/wahani/saeSim>.

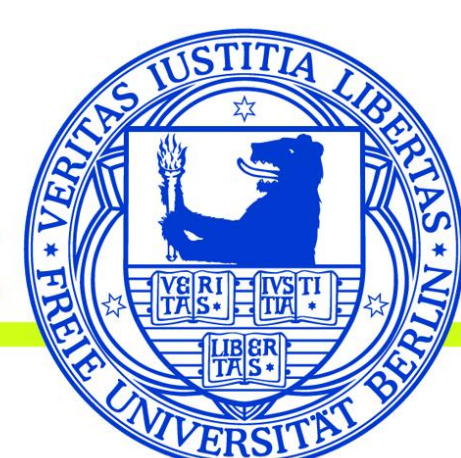
References

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