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Appendix A

Guide to R functions

To examine the Markov chain Monte Carlo (MCMC) output of the computer program **Siena** (Snijders, Steglich, Schweinberger, and Huisman, 2006) for maximum likelihood (ML) and Bayesian estimation, the R functions `siena_mle` and `siena_bayes` can be used, respectively. The R functions input files generated by **Siena** and output, among other things, trace plots and MCMC lag 1, . . . , 100 autocorrelations of sampled entities (see Chapters 4 and 5), and, in the Bayesian case, in addition 95% posterior intervals, histograms, and Gaussian kernel density estimates of the marginal posterior densities of the parameters.

The R functions `siena_mle` and `siena_bayes` can be downloaded from the website <http://stat.gamma.rug.nl/stocnet>, and can be used in R as follows:

(1) Load the R function:

- ML estimation: `source("siena_mle.r")`.
- Bayesian estimation: `source("siena_bayes.r")`.

(2) Call the R function:

- ML estimation: `siena_mle(project_name, full_output, no_random_effects, no_actors)`.
- Bayesian estimation: `siena_bayes(project_name, full_output, no_random_effects, no_actors)`.

The arguments are:

- `project_name` (string): the name of the **Siena** project that is to be examined; note that calling `siena_mle` or `siena_bayes` presumes that **Siena** carried out ML or Bayesian estimation of the project `project_name`, respectively.

- `full_output` (0 or 1): 1 indicates that the full output is desired, while 0 indicates that selected output is desired.
- `no_random_effects` (non-negative integer): the number of actor-dependent weights (parameters) in the model.
- `no_actors` (positive integer): the number of actors.

Examples are provided by `siena_mle("alcohol", 1, 3, 50)` and `siena_bayes("alcohol", 1, 3, 50)`.