MOSAIC$_\text{bioacc}$ REPORT

2021-05-12

This report is provided by the MOSAIC$_\text{bioacc}$ application available here:
https://mosaic.univ-lyon1.fr/bioacc

Contact: sandrine.charles@univ-lyon1.fr

MOSAIC$_\text{bioacc}$ uses the JAGS (version 4.3.0) and R (version 4.0.2) software, and in particular packages RJags (version 4.10), jagsUI (version 1.5.1) and Shiny (version 1.6.0).

The MOSAIC$_\text{bioacc}$ application is a turn-key web tool providing bioaccumulation factors (BCF/BSAF/BMF) from a toxicokinetic (TK) model fitted to accumulation-depuration data. It is designed to fulfil the requirements of regulators when examining applications for market authorization of active substances.

Data summary

File used: Gammarus_prochloraz_1d_Rosch2017.txt

Exposure: 100 $\mu g.mL^{-1}$

Accumulation phase duration: 1 days

Number of replicates: NA

Times: 0, 0.0164934384389481, 0.0167837229554734, 0.0781129244468574, 0.0819394021646935, 0.111310917336771, 0.130469695427453, 0.263314445990115, 0.263420003996125, 0.399193989225543, 0.430359990499779, 0.731939213668254, 0.747746525068141, 1.00224687755648, 1.00177186652944, 1.00163991902193, 1.01641803986322, 1.01472911176707, 1.0435464474076, 1.05740093569632, 1.0992810745805, 1.08323625766709, 1.17285500476896, 1.12648865062938, 1.45503794433323, 1.30496084928955, 1.30477612277904, 1.45437820679567, 1.75392543834847, 3.1030359236514

Exposure routes: water

Elimination routes: excretion

Bayesian inference

Three MCMC chains were used to estimate model parameters.

Number of iterations: 29968

Thin: 8

TK Model

The TK model used for these calculations was:

$$\frac{dC_p(t)}{dt} = k_{uw} \times c_w - (k_{ee}) \times C_p(t) \quad for\ 0 \leq t \leq t_c$$

$$\frac{dC_p(t)}{dt} = -(k_{ee}) \times C_p(t) \quad for\ t > t_c$$

with:

t: time (expressed in days)

t_c: duration of the accumulation phase (expressed in days)

$C_p(t)$: internal concentration of the parent compound at time (expressed in $\mu g.g^{-1}$)

k_{ee}: elimination rates of excretion (expressed per days $^{-1}$)

c_w: exposure concentration of water route (expressed in $\mu g.mL^{-1}$)

k_{uw}: uptake rate of water exposure (expressed per days $^{-1}$)
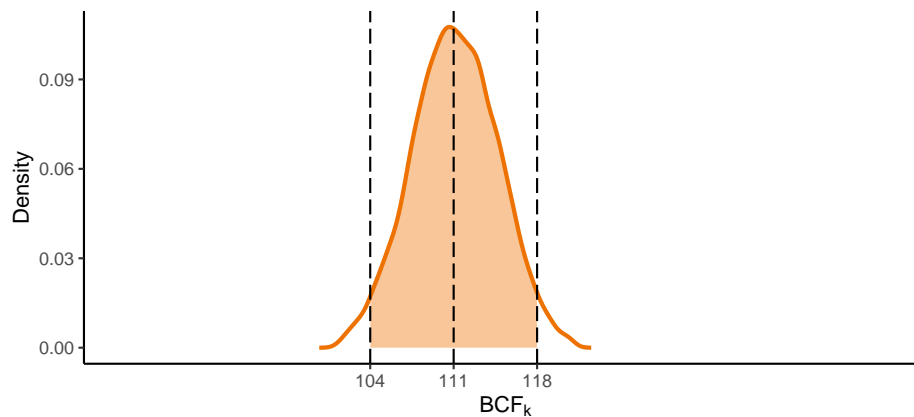
Bioaccumulation factor calculation

Calculations

$$BCF_k = \frac{k_{uw}}{k_{ee}}$$

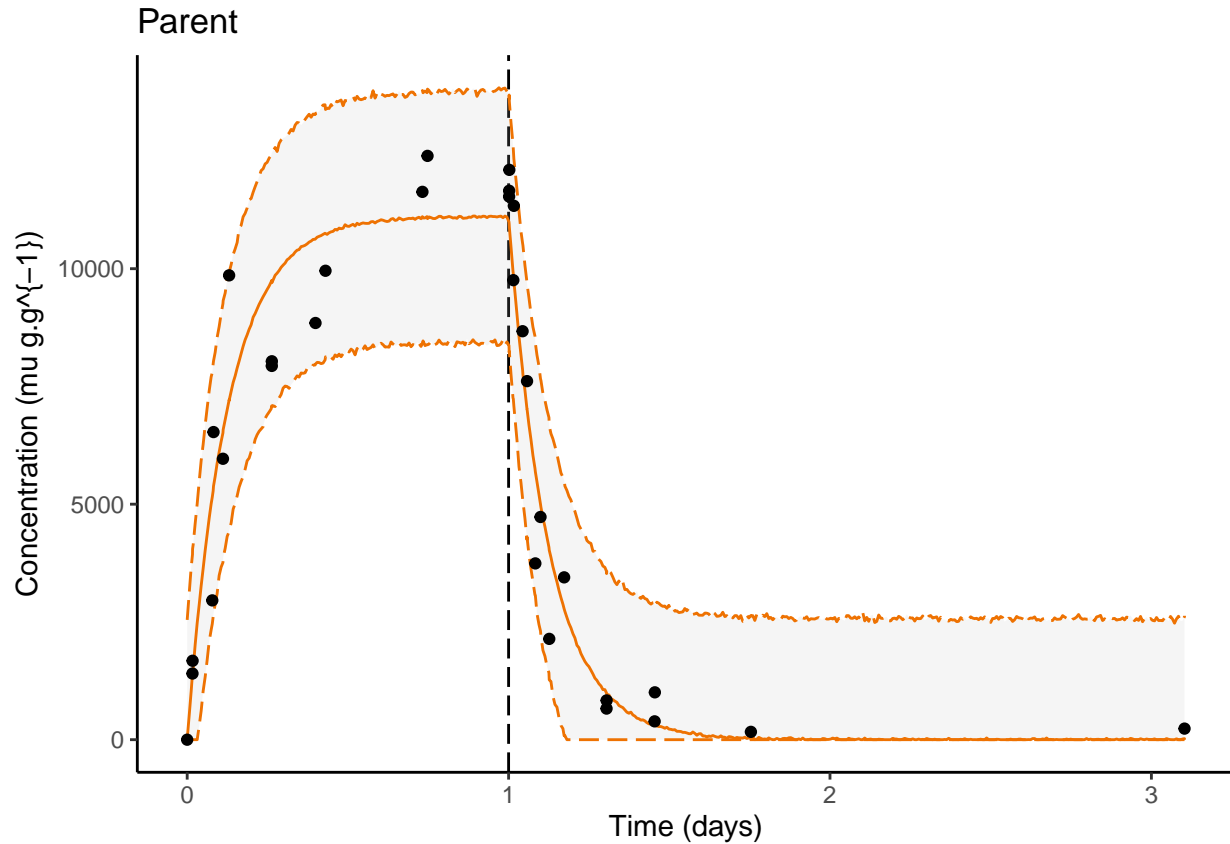$$BCF_{ss} = \frac{C_p(t_c)}{c_w}$$

Bioconcentration factor (BCF)

BCF_k plot

BCF summary

	2.5%	50%	97.5%	CV
BCFk	104	111	118	0.032

Fitting results

Fit plot

Parent

Quantiles of estimated parameters

	2.5%	50%	97.5%	
k_{uw}	720.9	886.8	1090	d^{-1}
k_{ee}	6.53	7.977	9.785	d^{-1}
σ_p	985	1269	1717	$\mu g.g^{-1}$

Goodness-of-fit criteria

Posterior Predictive Check

The PPC shows the observed values against their corresponding estimated predictions (black dots), along with their 95% credible interval (vertical segments). If the fit is correct, we expect to see 95% of the data within the intervals. Ideally observations and predictions should coincide, so we would expect to see black dots along the first bisector y = x (plain black line). The 95% credible intervals are colored in green if they

overlap this line, in red otherwise.

Parent compound:

percentage of data in CI:

100% (29/29)
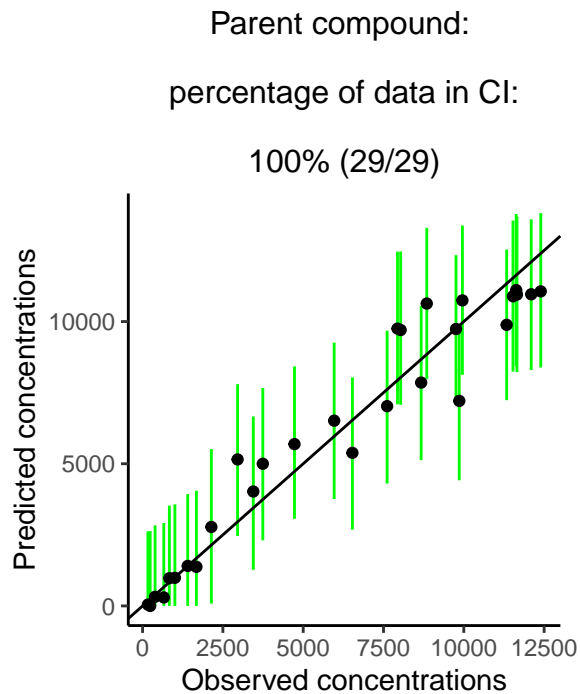
Priors and posteriors

The prior distribution is represented by the gray area and the posterior distribution by the orange area. The accuracy of the model parameter estimation can be visualized by comparing prior and posterior distributions: the overall expectation is to get a narrower posterior distribution compared to the prior one, what reflects that data contributed enough to precisely estimate parameters.
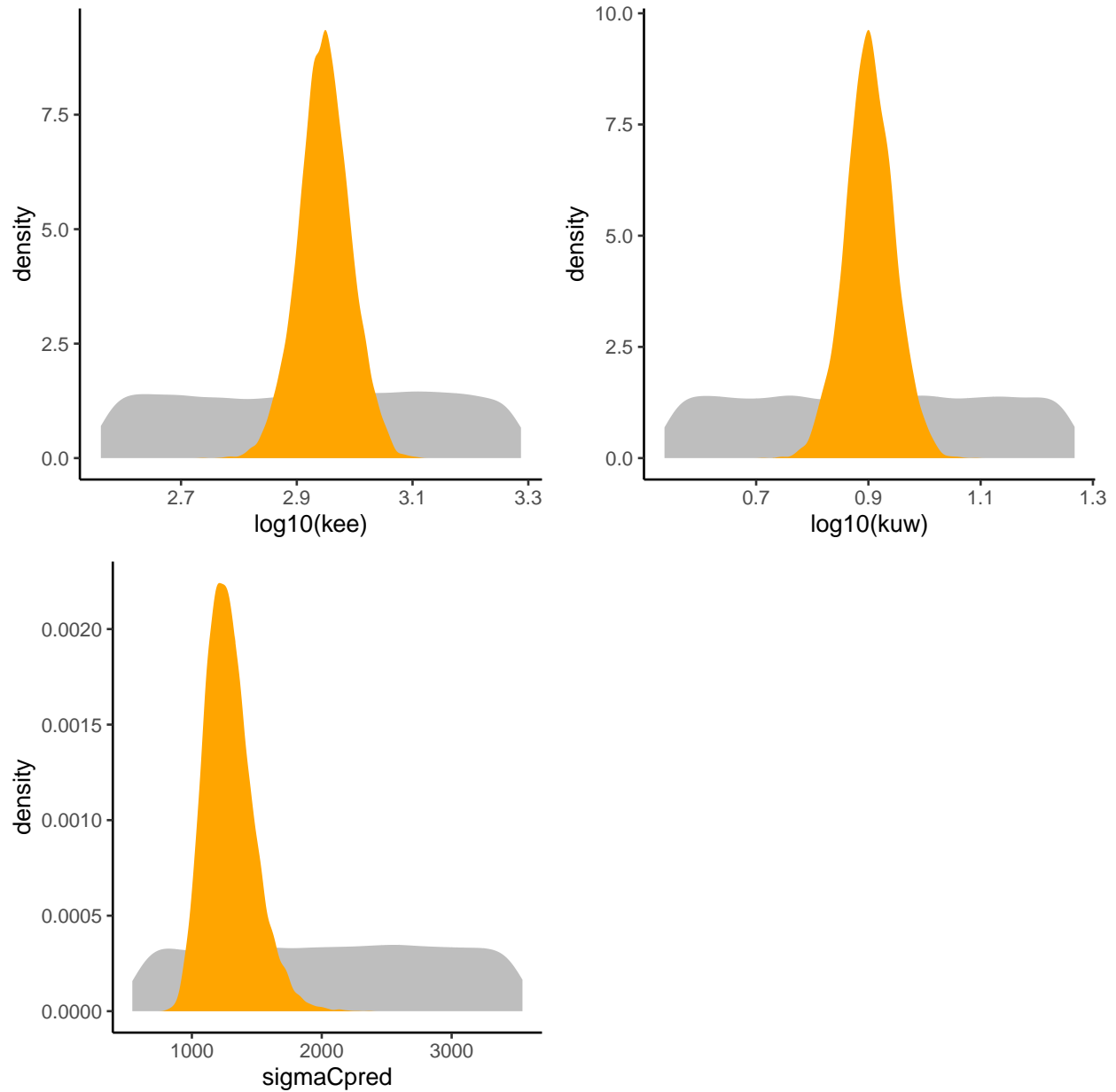
Correlation between parameters

If you want to see the coloured matrix giving a summary of parameter correlations, you need to import the corresponding figure directly from the application, page bottom, section "Downloads", then choose Download an output and select "GOF" then "parameter correlation". You can select the output format you prefer.

Correlations between parameters are visualized by projecting the joint posterior distribution in a plot matrix with planes of parameter pairs (lower triangular elements), marginal posterior distribution of each model parameter (diagonal), and Pearson correlation coefficients (upper triangular elements). Correlations are expected to be low (reflected by "potatoid" shapes of density lines in orange); a leaning elliptical shape translates high correlations (positive if leaning to the right, negative if leaning to the left).
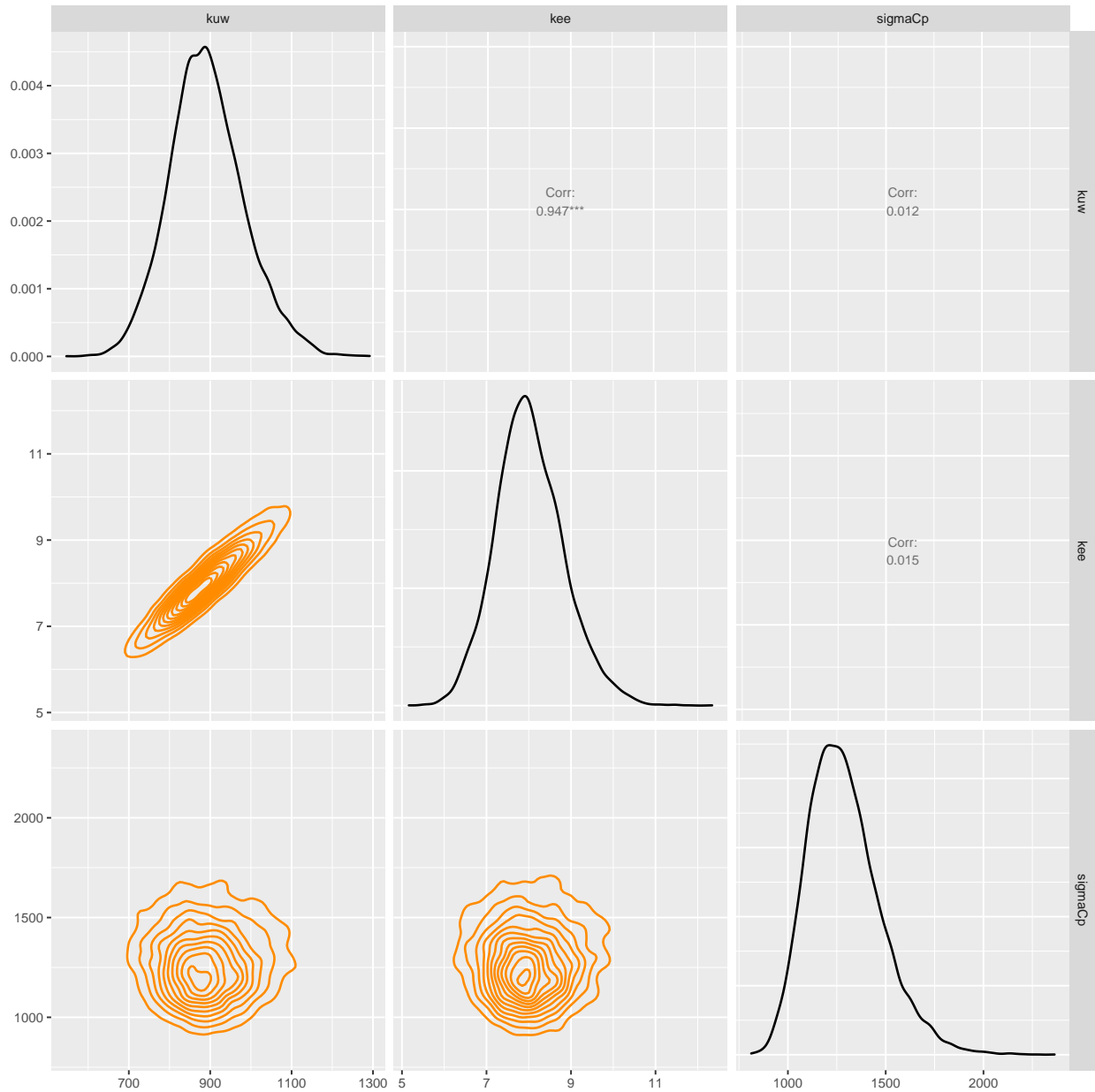
Potential Scale Reduction Factors

Convergence of the MCMC chains can be check with the Gelman-Rubin diagnostic expressed with the potential scale reduction factor (PSRF). Approximate convergence is diagnosed when the PSRF is below 1.01.

	PSRF
kuw	0.9999466
kee	0.9999317
sigmaCpred	1.000886

Watanabe–Akaike information criterion

Information criteria offer a computationally appealing way of estimating the generalization performance of the model. A fully Bayesian criterion is the widely applicable information criterion (WAIC) by Watanabe a penalized deviance statistics accounting for the uncertainty in the parameters and can be used also for singular models. WAIC is widely used in model comparison for a same dataset (e.g., with or without k_{ee}). Sub-models with lower WAIC values will be preferred.

WAIC = 499.4

Deviance Information Criterion

This criteria, denoted DIC, is a penalized deviance statistics accounting for the number of parameters for use in model comparison for a same dataset (e.g., with or without k_{ee}). Sub-models with lower DIC values will be preferred.

DIC = 499.5261

Traces of MCMC iterations

A traceplot is an essential plot for assessing convergence and diagnosing of MCMC chains. It shows the time series of the sampling process leading to the posterior distribution. Different colors are used for each of the chains (here 3) to assess within-chain convergence.
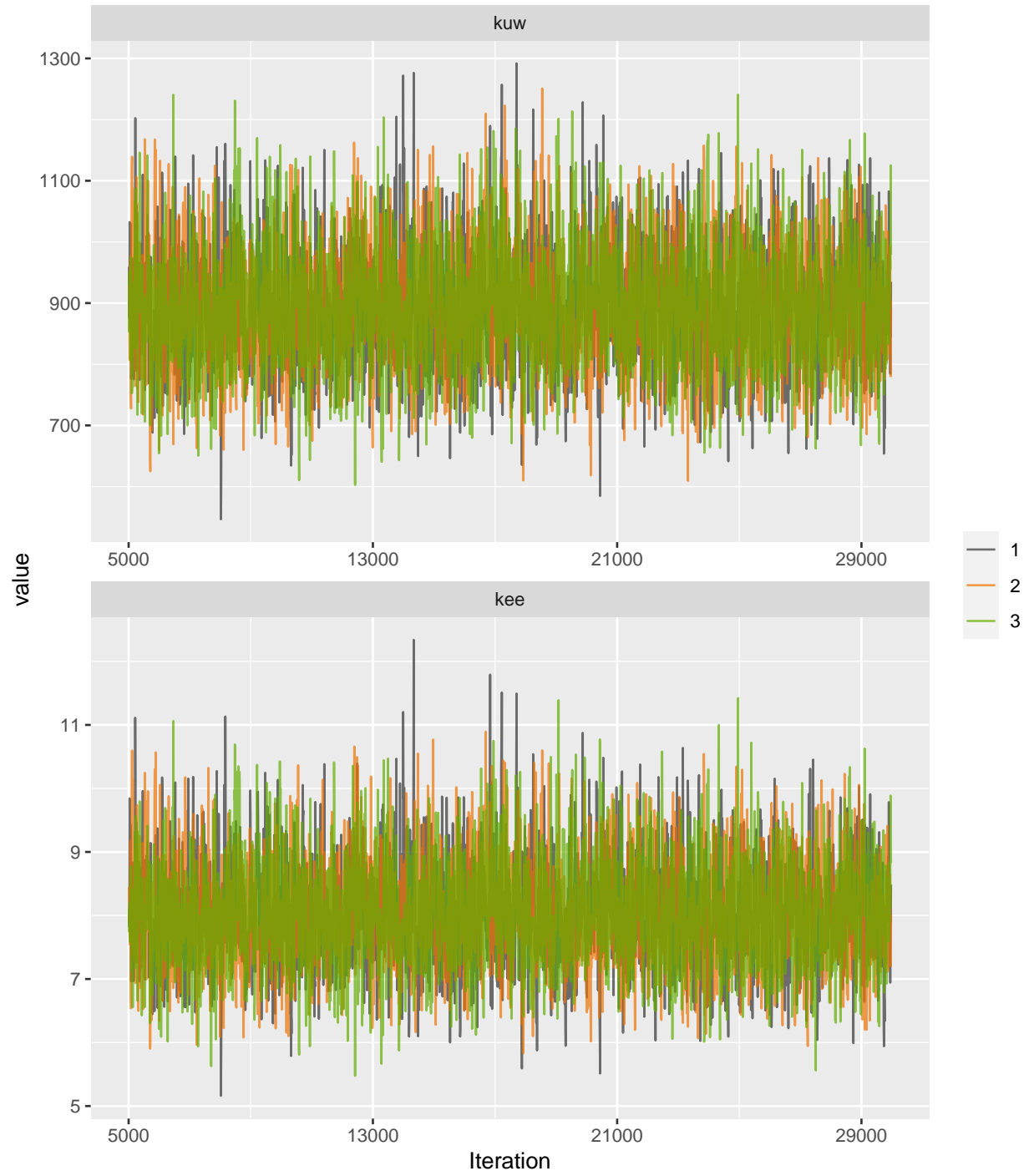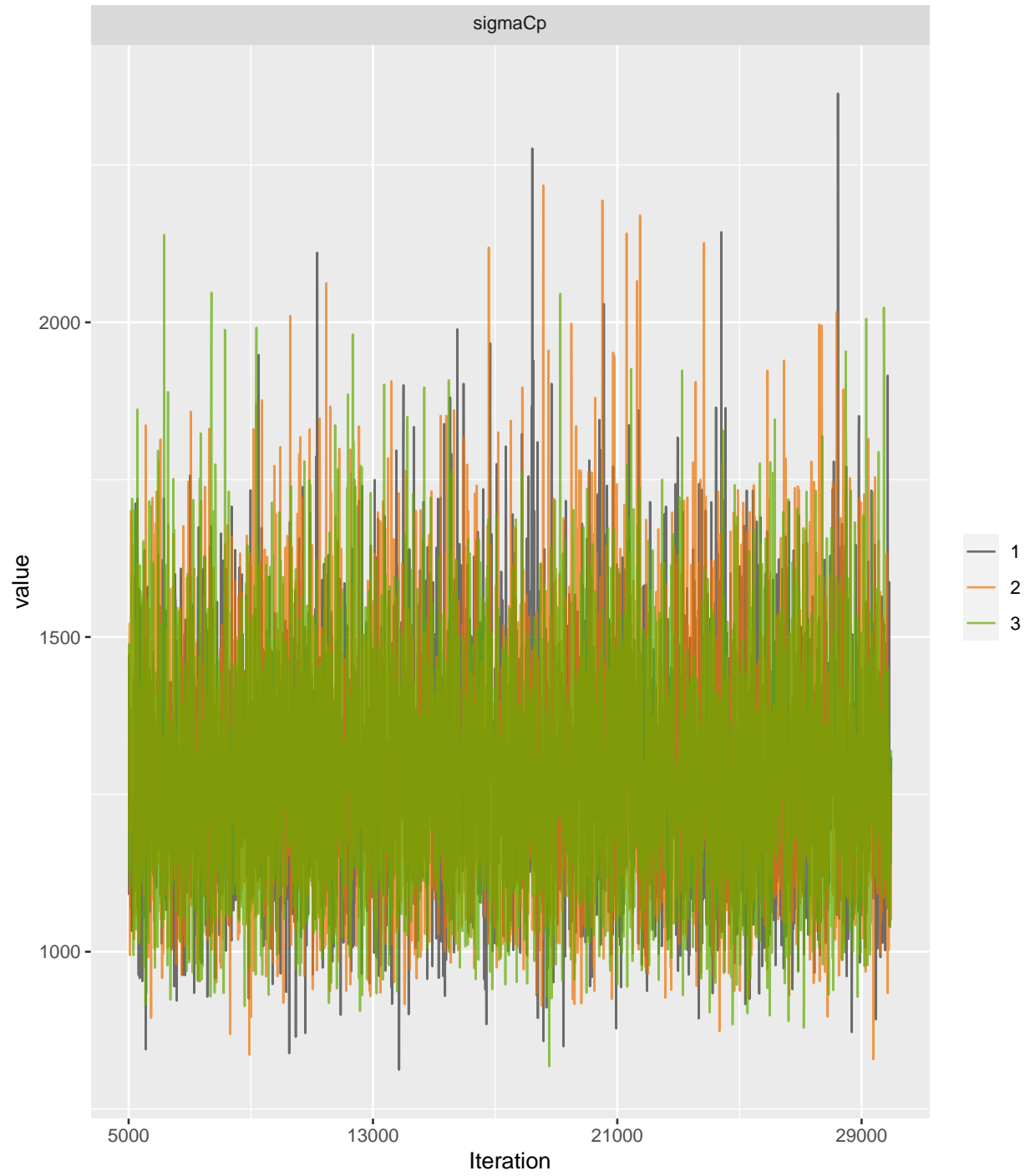
Data Table

time	conc	expw	replicate
0.0000	0.0000	100	1
0.0165	1404.9243	100	1
0.0168	1676.0500	100	2
0.0781	2957.5242	100	1
0.0819	6531.4544	100	2
0.1113	5964.4496	100	1
0.1305	9858.7483	100	2
0.2633	7935.7453	100	1
0.2634	8034.3365	100	2
0.3992	8847.2387	100	1
0.4304	9956.2839	100	2
0.7319	11631.2783	100	1
0.7477	12395.3072	100	2
1.0022	12098.6364	100	2
1.0018	11654.9761	100	1
1.0016	11531.7371	100	2
1.0164	11334.5020	100	1
1.0147	9757.0432	100	2
1.0435	8672.4347	100	1
1.0574	7612.5267	100	2
1.0993	4728.5764	100	1
1.0832	3742.7174	100	2
1.1729	3446.6272	100	1
1.1265	2140.4525	100	2
1.4550	1005.4928	100	1
1.3050	833.4860	100	2
1.3048	660.9515	100	1
1.4544	389.2979	100	2
1.7539	166.4122	100	1
3.1030	235.6055	100	1