

MOSAIC_{bioacc} REPORT

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This report is provided by the MOSAIC_{bioacc} application available here:
<https://mosaic.univ-lyon1.fr/bioacc>

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MOSAIC_{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_{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: Perca_SAmPAP_45d_Gaillard2017_muscles.txt

Exposure: 1.631 $\mu g.g^{-1}$

Accumulation phase duration: 45 days

Number of replicates: 1

Times: 0, 1.2012012012012, 3.36336336336336, 9.36936936936936, 18.2582582582582, 28.1081081081081, 37.2372372372372, 43.003003003003, 45.1651651651651, 46.1261261261261, 48.2882882882882, 58.1381381381381, 67.027027027027, 79.9999999999999

Exposure routes: food

Elimination routes: excretion biotransformation

Bayesian inference

Three MCMC chains were used to estimate model parameters.

Number of iterations: 243490

Thin: 65

TK Model

The TK model used for these calculations was:

$$\frac{dC_p(t)}{dt} = k_{uf} \times c_f - (k_{ee} + k_{m1}) \times C_p(t) \quad \text{for } 0 \leq t \leq t_c$$

$$\frac{dC_p(t)}{dt} = - (k_{ee} + k_{m1}) \times C_p(t) \quad \text{for } t > t_c$$

$$\frac{dC_{m1}(t)}{dt} = k_{m1} \times C_p(t) - k_{em1} \times C_{m1}(t)$$

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 $\mu g \cdot g^{-1}$)

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

c_f : exposure concentration of food route (expressed in $\mu g \cdot g^{-1}$)

k_{uf} : uptake rate of food exposure (expressed per days $^{-1}$)

$C_{m\ell}(t)$: internal concentration of metabolite ℓ (expressed in $\mu g \cdot g^{-1}$)

ℓ : index of metabolites, $\ell = 1 \dots L$ with L total number of metabolites

$k_{m\ell}$: metabolization rate of metabolite ℓ (expressed per days $^{-1}$)

$k_{em\ell}$: elimination rates of metabolite ℓ (expressed per days $^{-1}$)

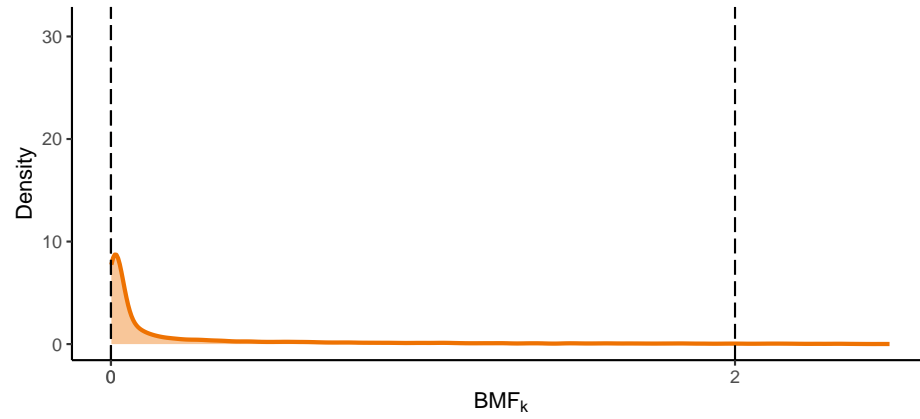
Bioaccumulation factor calculation

Calculations

$$BMF_k = \frac{k_{uf}}{k_{ee} + k_{m1}}$$

$$BMF_{ss} = \frac{C_p(t_c)}{c_f}$$

BMF_k plot

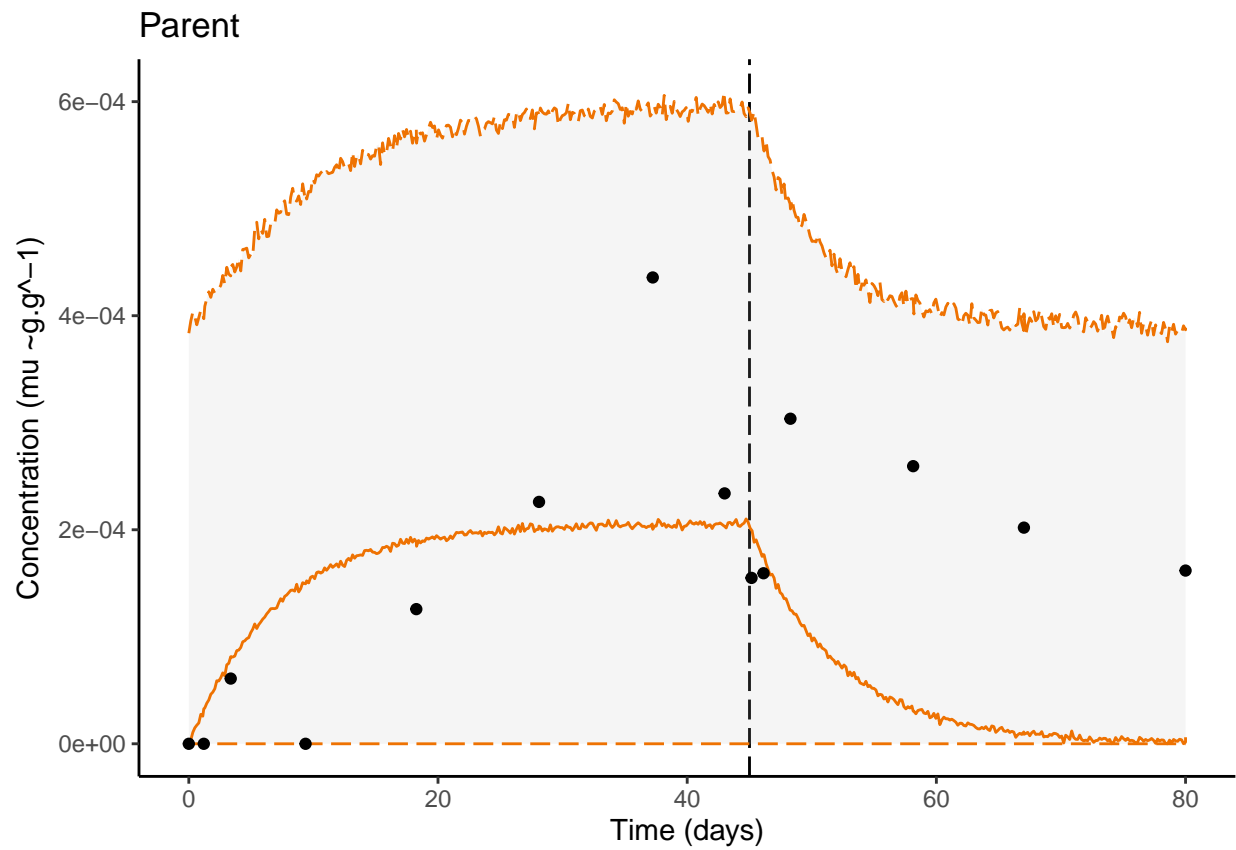


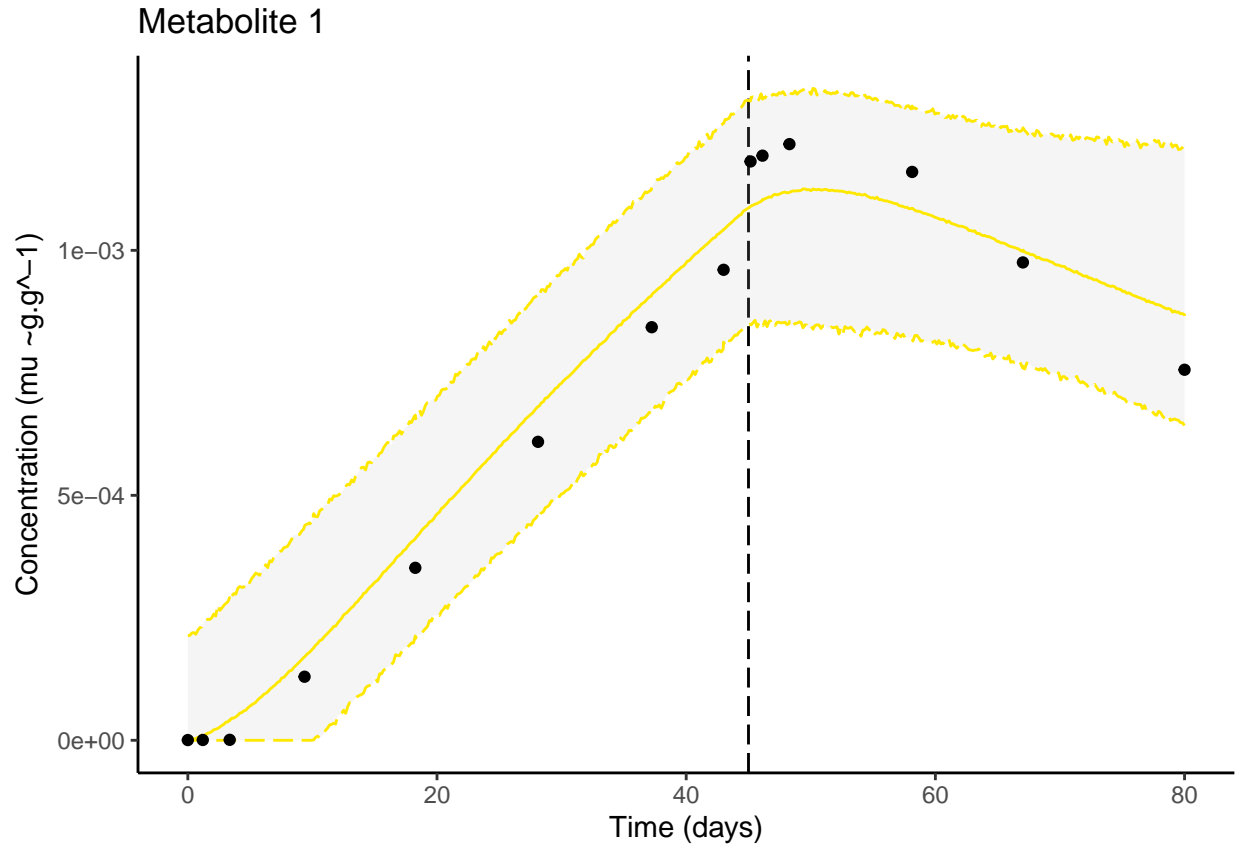
BMF summary

	2.5%	50%	97.5%	CV
BMFk	0	0	2	Inf

Fitting results

Fit plot





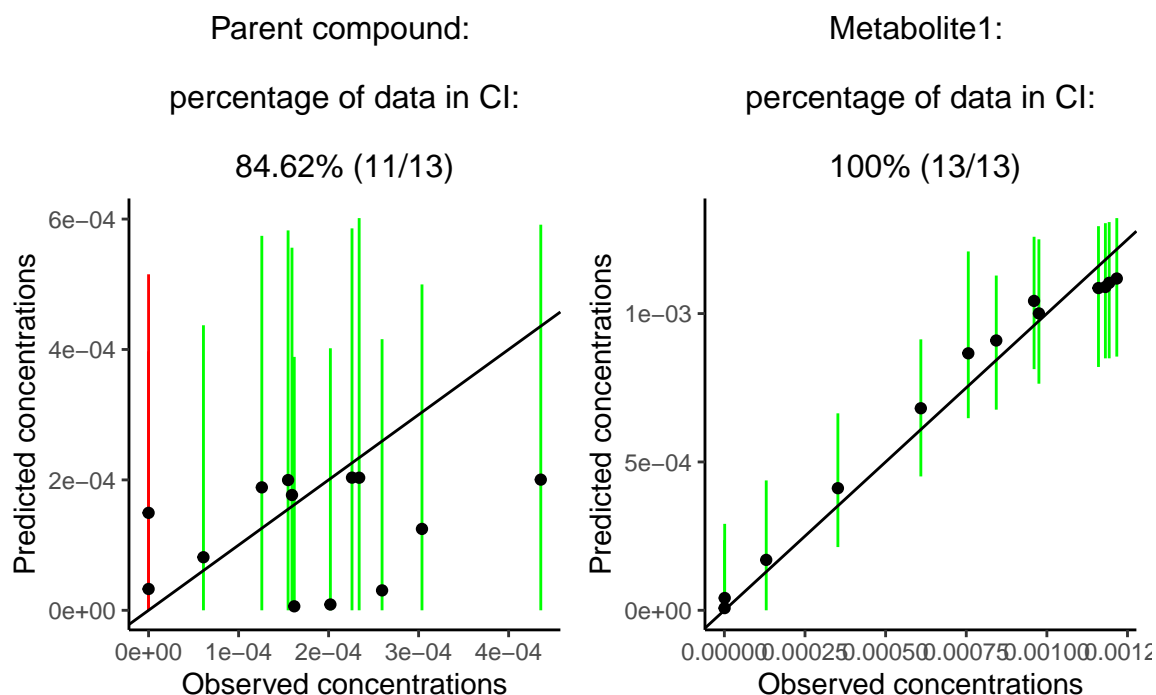
Quantiles of estimated parameters

	2.5%	50%	97.5%	
k_{uf}	1.397e-05	2.281e-05	0.0001066	d^{-1}
k_{ee}	1.245e-05	0.001115	1136	d^{-1}
k_{m1}	0.1045	0.1572	46050	d^{-1}
k_{em1}	2.627e-05	0.01226	0.01959	d^{-1}
σ_p	0.000106	0.0001714	0.0003227	$\mu g.g^{-1}$
σ_{met1}	5.106e-05	8.849e-05	0.0001841	$\mu g.g^{-1}$

Goodness-of-fit criteria

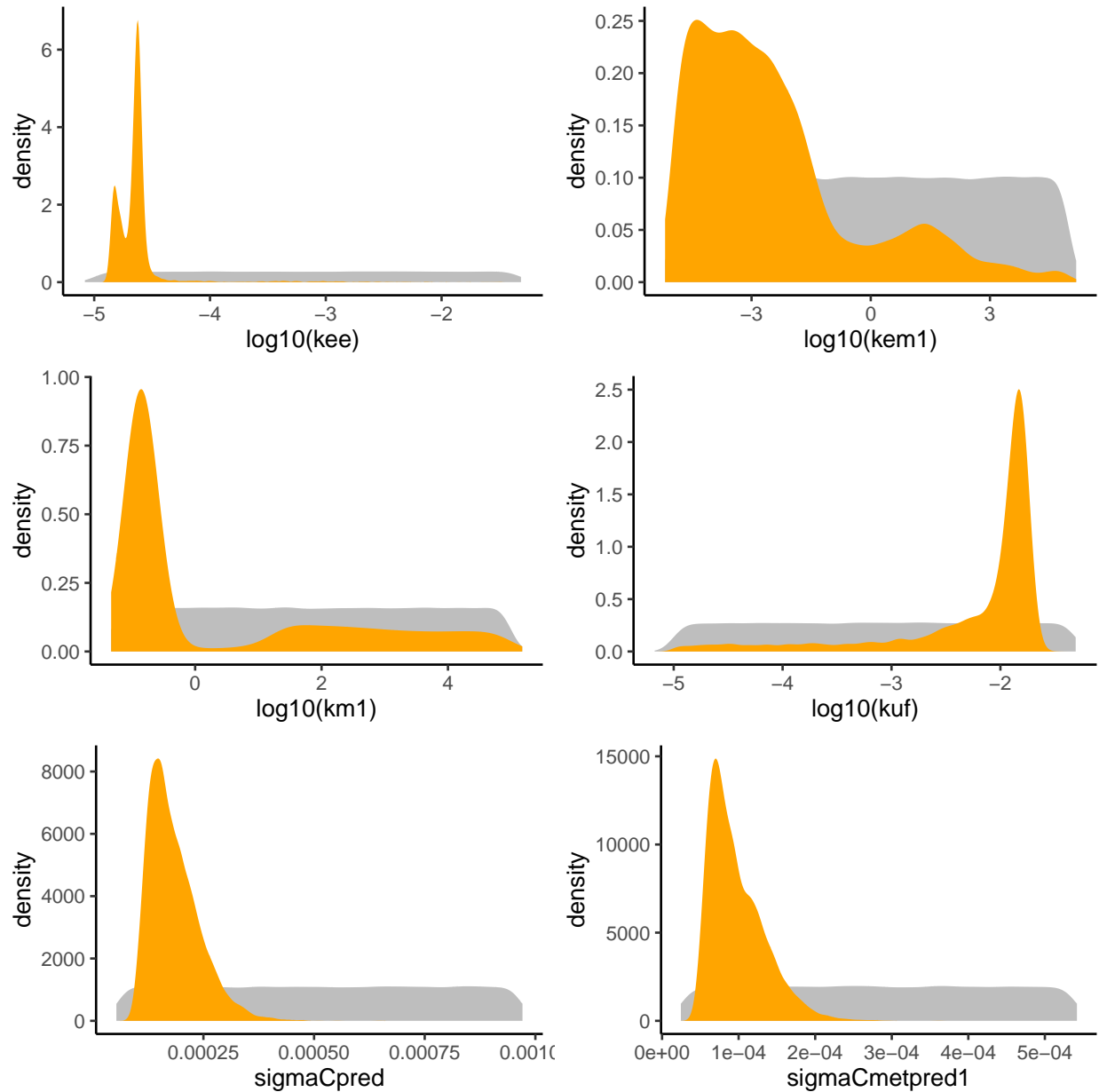
Posterior Predictive Check

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.



Priors and posteriors

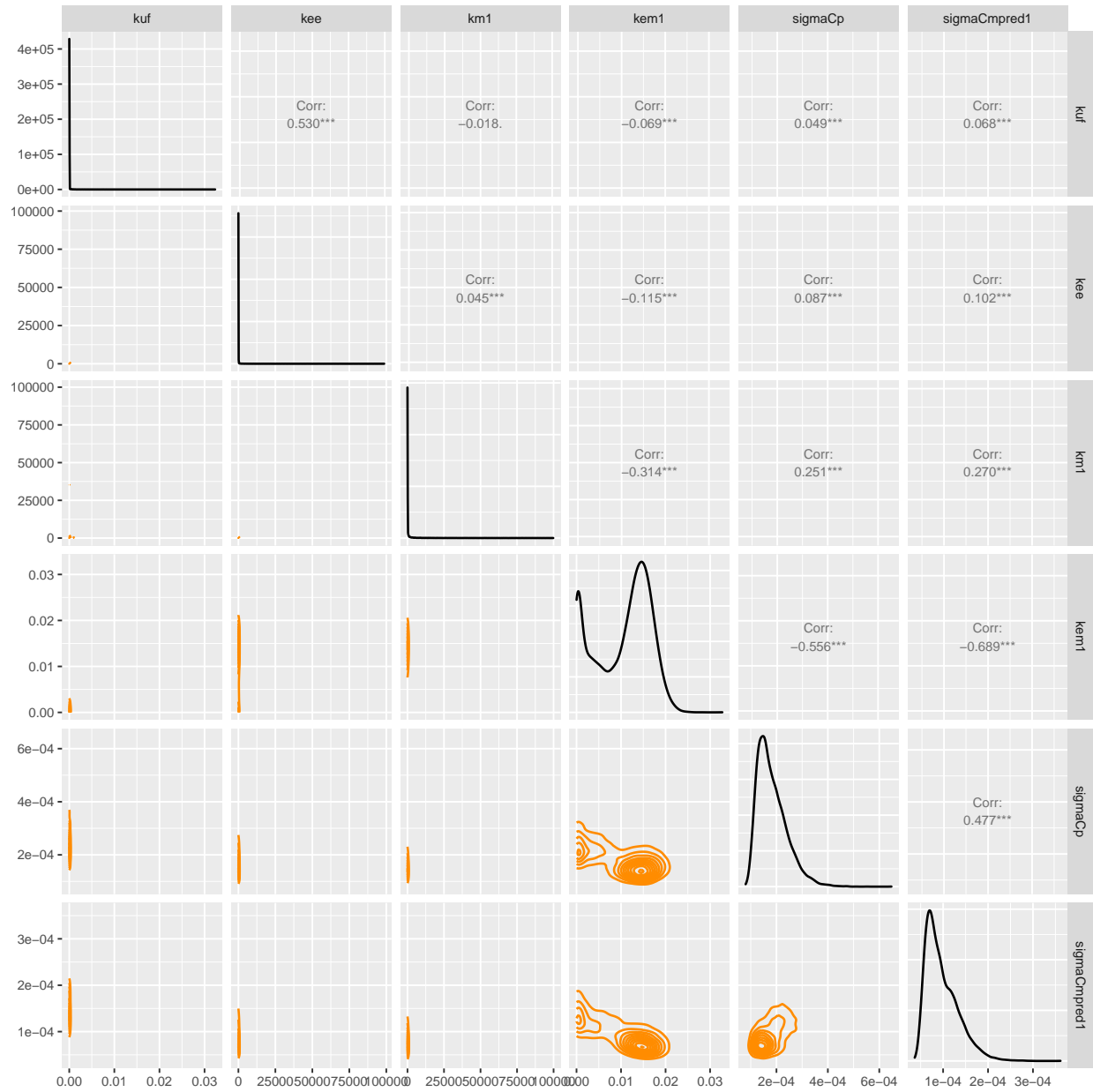
The prior distribution is represented by the gray area and the posterior distribution by the orange area. The accuracy of the model parameter estimation can be visualized by comparing prior and posterior distributions: the overall expectation is to get a narrower posterior distribution compared to the 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 checked 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
kuf	1.296951
kee	1.308201
km1	1.410858
kem1	3.065156
sigmaCpred	1.829955
sigmaCmetpred1	2.045064

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.

$$\text{WAIC} = -399.3$$

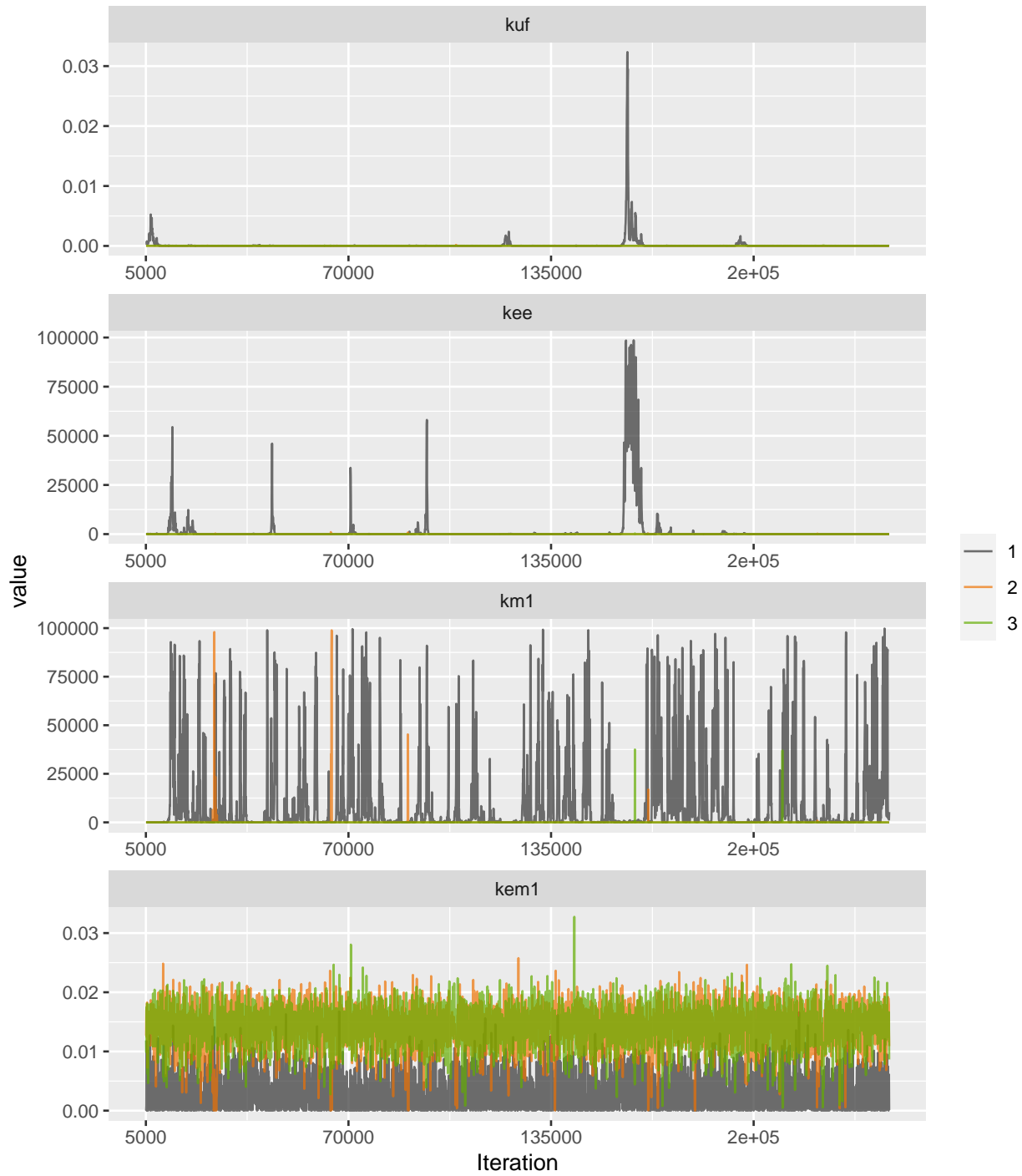
Deviance Information Criterion

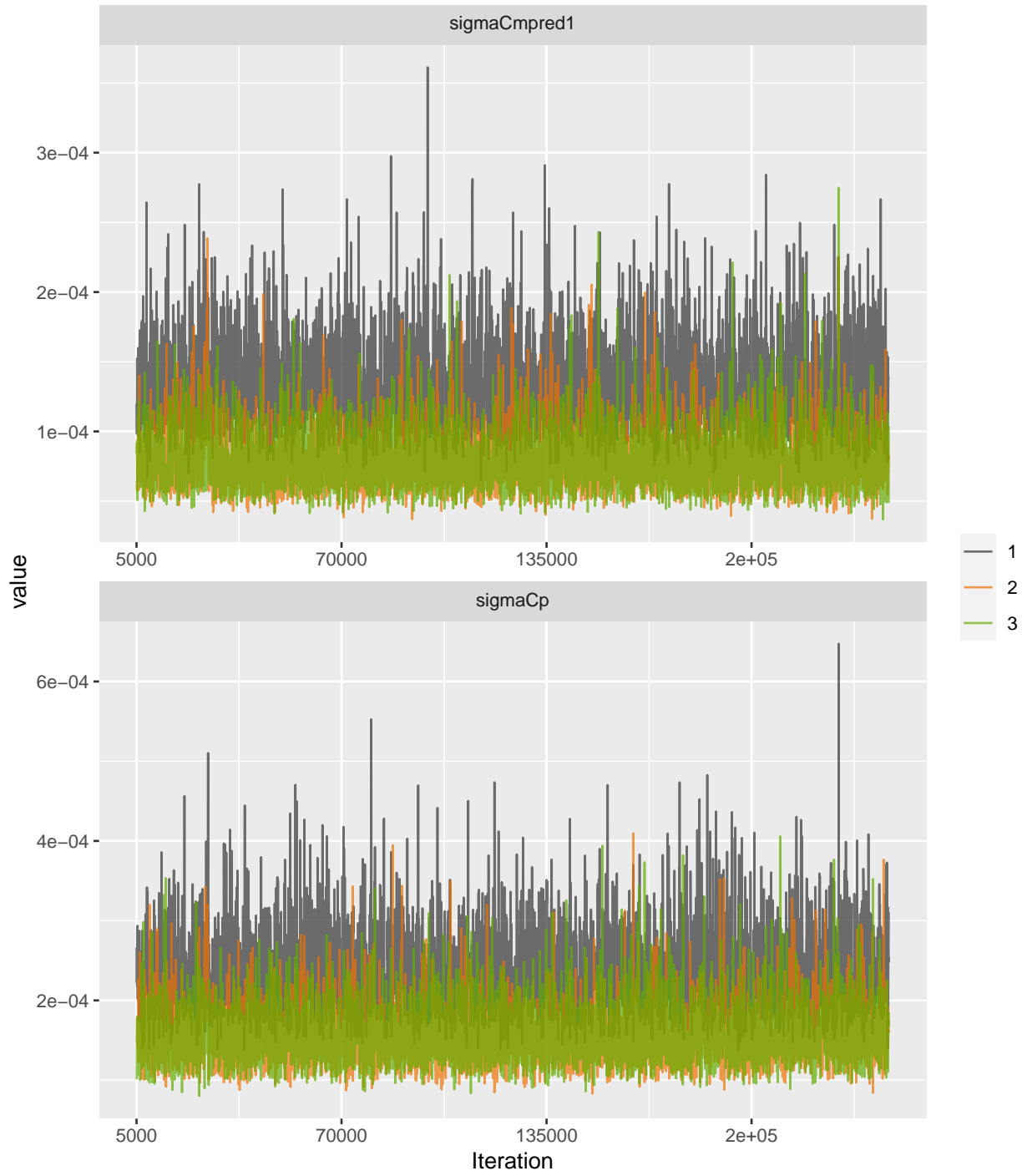
This criteria, denoted DIC, is a penalized deviance statistics accounting for the number of parameters for use in model comparison for a same dataset (e.g., with or without k_{ee}). Sub-models with lower DIC values will be preferred.

$$\text{DIC} = -385.1966$$

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	expf	replicate	concm1
0.0000	0.000000000000	1.631	1	0.0000
1.2012	0.000000000000	1.631	1	0.0000
3.3634	0.00006094562	1.631	1	0.0000
9.3694	0.000000000000	1.631	1	0.0001
18.2583	0.00012582363	1.631	1	0.0004
28.1081	0.00022601434	1.631	1	0.0006
37.2372	0.00043573354	1.631	1	0.0008
43.0030	0.00023395805	1.631	1	0.0010
45.1652	0.00015500756	1.631	1	0.0012
46.1261	0.00015933452	1.631	1	0.0012
48.2883	0.00030374170	1.631	1	0.0012
58.1381	0.00025940685	1.631	1	0.0012
67.0270	0.00020198593	1.631	1	0.0010
80.0000	0.00016185967	1.631	1	0.0008