Tutorial 12: Bayesian analysis of a hierarchical non-linear model for PRRS data

Required files: `Tutorial12.R`, `cplot.R`, `a1chain.rdata`, `b1chain.rdata`, `c1chain.rdata`

In this tutorial we will analyse the Bayesian estimates of individual parameters of the Woods function, obtained using 15 pigs of the PRRS infection experiment. These estimates are based on the hierarchical non-linear model described in the lecture.

Use the script `Tutorial12.R` to run the code required to answer the questions of this session

Question 1: Use step 1 of the `R` script to plot the viraemia profiles of 15 pigs from the sample. How do the viraemia of the different pigs vary? Particularly, how different are the viraemia profiles of pigs 6 and 13?

Posterior distribution of the parameters

To make inferences about the individual parameters of the Woods function for each pig, we will use the chains from an MCMC algorithm developed to sample from the posterior distributions associated with the hierarchical non-linear model described in the lecture.

Question 2: Use step 2 of the `R` script to plot the posterior distribution of the parameters of the Woods function for pigs 6 and 13. Based on these posteriors, how different are the estimated Woods functions for these two pigs?

Question 3: How do the parameter estimates vary among all 15 pigs? Analyse the posterior means and 95% credible intervals of the Woods function parameters for each pig to answer this question (Use step 3 of the `R` script).

Now plot the viraemia profiles for each pig along with estimates of the Woods function and its associated 95% credibility intervals (the shaded region in the resulting plots). Use step 4 of the `R` script.

Question 4: Based on the estimated Wood function for each pig, can we say that the proposed hierarchical non-linear model fits the data well? Why?