Practical: Network meta-analysis with time to event data alongside count data

1. Introduction

A small number of data from the case study of compression systems aiming to deliver high compression to promote venous leg ulcer healing, from Saramago (2014). They are saved in `part 2/practical/tte_counts_input_data.RData` and created at the top of the analysis `R` script. The data include the following variables:

- `treat`: treatment arm (coded 1,2)
- `baseline`: reference treatment code,
- `t.obs`: time to event in months (under censoring)
- `t.cens`: time of censoring in months,
- `n.subjects`: Number of participants in IPD
- `n.treat`: Number of treatments
- `a.id` : study number
- `a.treat` : treatment arm code (coded from 1 to number of treatments),
- `r` : number of events in trial arm
- `n` : number of patients in trial arm
- `a.base` : reference treatment code
- `a.time` : follow-up time of trial
- `n.agg.trials` : Number of AD studies
- `n.agg.arms` : Number of AD study arms

The `R` script `tte_counts_script.R` guides you through the analysis.

2. BUGS code

Look at the BUGS code in the file `tte_counts_BUGS_code.txt`. This is a simplified version of the original model from Saramago (2014). The original coded is available in the file `Saramago_BUGS_code.txt`.

- Can you see what has been omitted/changed?
  - *Centres and other covariates*, requiring addition parameters in the regression terms
  - *Additional IPD data set.* In the paper there were two IPD data sets. The model for each of these was coded separately. This could have been handled more generically but included additional indexes, so that in future this could have handled any number of IPD studies. Because this code was written specific to this analysis and there were only two data sets this was fine but further duplication is not recommended.
  - *Weibull survival distribution.* This required an extra hyper-parameter `shape` in comparison the exponential distribution, which also needed a prior distribution specifying.

3. Running the model

- Run the model using the `bugs()` command and inspect the output.
- Has the MCMC converged? Look at the trace plots for the "hairy caterpillar". What is the effective sample size?
- Write some additional BUGS and R code to return the hazard ratios.

```
for (k in 2:n.treat) {
  hr <- exp(d[k])
}
```

and don't forget to include the additional parameter in the list of monitored parameters to return i.e. `parameters = c("d", "hr")`.

- What is the conclusion? The HR is about 0.7 indicating that the alternative treatment (2) rates the rate of occurrence of events.