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 code is available in the file `Saramago_BUGS_code.txt`.

- Can you see what has been omitted?

3. Running the model

- Run the model using the `bugs()` command and inspect the output.
- Has the MCMC converged?
- Write some additional BUGS and R code to return the hazard ratios.
- What is the conclusion?