Model

We create a linear model with a logit link for the outcomes y using infant-specific intercept and slope parameters. Note that the times are the same 7 times for each infant so we can index t from 1 to 7 only. We use $\log(t)$ as our predictor in the linear model. You can take the log of the 7 times in `R` and pass that as data to JAGS or you can pass the times and take logs in JAGS.

Each infant will then have their own value of α and β:

`Y`[i,j] ~dnorm(mu[i,j], tau)
`mu`[i,j] = alpha[i] + beta[i]*(logt[j]-mean(logt[]))

These are then modelled as coming from a common hierarchical prior (one for α and one for β):

`alpha`[i] ~dnorm(alpha0,taua)
`beta`[i] ~dnorm(beta0,taub)

You then need to set the prior on τ and the hyper-priors on $\alpha_0, \beta_0, \tau_\alpha, \tau_\beta$. As suggested, you can take these to be independent and using Jeffreys' priors we get uniform priors for α_0, β_0 and $\propto \frac{1}{\phi*}$ for each of the variance parameters (inverses of each of the above 3 precision parameters). See `hepatitis.model` for full model specification.

Mean of Intercept $\boldsymbol{\alpha}$ and Slope $\boldsymbol{\beta}$

If you calculate the mean of the $\boldsymbol{\alpha}$ across all 52 infants and then take the mean of this across MCMC iterations then this is of course equal to the mean of all $\boldsymbol{\alpha}$ across infants and MCMC iterations (same goes for $\boldsymbol{\beta}$). However, when we want to get the credible intervals for the across-infant means of these coefficients then this is not some function of the credible intervals for each $\boldsymbol{\alpha}$ or $\boldsymbol{\beta}$. We need to calculate the mean at each iteration and then get the credible interval of those values. This can be done in the model file (see `hepatitis.model`) or in `R` if you prefer.

You can use `HPDinterval` (assuming you used coda.samples to generate the MCMC samples) for the Credible Intervals. Again, see `hepatitis.model` and `hepatitis.R` for this.

Checking Convergence (and mixing)

To check for convergence you should have used gelman.diag and gelman.plot. In hierarchical models such as these convergence can be an issue. For simplicity I'll focus on the two across-infant means $\bar{\boldsymbol{\alpha}}$ and $\bar{\boldsymbol{\beta}}$ and the 3 variance parameters $\phi, \phi_\alpha, \phi_\beta$.

After $1,000$ iterations, the BGR statistics look good (close to or equal to 1). However the BGR plots don't look very convincing. Setting $10,000$ MCMC iterations helps.

`acfplot(hep.samps)` shows thinning to about every 10th iteration is required for the variance terms and the $\bar{\boldsymbol{\beta}}$ terms to create independent samples, but this wasn't explicitly asked for in the Lab Sheet.