```
library(simstudy)
library(rstan)
library(data.table)

defS <- defData(varname = "a.k", formula = 3, variance = 2, id = "study")
defS <- defData(defS, varname = "d.0", formula = 3, dist = "nonrandom")
defS <- defData(defS, varname = "v.k", formula = 0, variance = 6, dist=
"normal")
defS <- defData(defS, varname = "s2.k", formula = 16, variance = .2, dist =
"gamma")
defS <- defData(defS, varname = "size.study", formula = ".3;.5;.2", dist =
"categorical")
defS <- defData(defS, varname = "n.study",
    formula = "(size.study==1) * 20 + (size.study==2) * 40 + (size.study==3) *
60",
    dist = "poisson")

defI <- defDataAdd(varname = "y", formula = "a.k + x * (d.0 + v.k)", variance =
"s2.k")

RNGkind(kind = "L'Ecuyer-CMRG")
set.seed(12764)

ds <- genData(12, defS)

dc <- genCluster(ds, "study", "n.study", "id", )
dc <- trtAssign(dc, strata = "study", grpName = "x")
dc <- addColumns(defI, dc)

d.obs <- dc[, .(study, id, x, y)]
```

Build the Stan model

There are multiple ways to estimate a `Stan` model in `R`, but I choose to build the Stan code directly rather than using the `brms` or `rstanarm` packages. In the Stan code, we need to define the data structure, specify the parameters, specify any transformed parameters (which are just a function of the parameters), and then build the model – which includes laying out the prior distributions as well as the likelihood.

In this case, the model is slightly different from what was presented in the context of a mixed effects model. This is the mixed effects model:

$$
y_{ik} = \alpha_k + \delta_k x_{ik} + e_{ik} \\
\\
\delta_k = \delta_0 + v_k \\
e_{ik} \sim N(0, \sigma_k^2), v_k \sim N(0,\tau^2)
$$

In this Bayesian model, things are pretty much the same:

$$
y_{ik} \sim N(\alpha_k + \delta_k x_{ik}, \sigma_k^2) \\
\\
\delta_k \sim N(\Delta, \tau^2)
$$

The key difference is that there are prior distributions on Δ and τ, introducing an additional level of uncertainty into the estimate. I would expect that the estimate of the overall treatment effect Δ will have a wider 95% CI (credible interval in this context) than the 95% CI (confidence interval) for δ_0 in the mixed effects model. This added measure of uncertainty is a strength of the Bayesian approach.

```
data {
  int N;               // number of observations
  int K;               // number of studies
  real y[N];                    // vector of continuous outcomes
  int kk[N];   // study for individual
  int x[N];    // treatment arm for individual
}

parameters {
  vector[K] beta;              // study-specific intercept
  vector[K] delta;             // study effects
  real sigma[K];       // sd of outcome dist - study specific
  real Delta;                  // average treatment effect
  real  tau;           // variation of treatment effects
}

transformed parameters{

  vector[N] yhat;

  for (i in 1:N)
      yhat[i] = beta[kk[i]] + x[i] * delta[kk[i]];
}

model {

  // priors

  sigma ~ normal(0, 2.5);
  beta ~ normal(0, 10);

  tau ~ normal(0, 2.5);
  Delta ~ normal(0, 10);
  delta ~ normal(Delta, tau);


  // outcome model

  for (i in 1:N)
    y[i] ~ normal(yhat[i], sigma[kk[i]]);
}
```

Generate the posterior distributions

With the model in place, we transform the data into a `list` so that Stan can make sense of it:

```
N <- nrow(d.obs)                                ## number of observations
K <- dc[, length(unique(study))]                ## number of studies
y <- d.obs$y                                    ## vector of continuous outcomes
kk <- d.obs$study                               ## study for individual
x <- d.obs$x                                    ## treatment arm for individual

ddata <- list(N = N, K = K, y = y, kk = kk, x = x)
```

And then we compile the Stan code:

```
rt <- stanc("model.stan")
sm <- stan_model(stanc_ret = rt, verbose=FALSE)
```

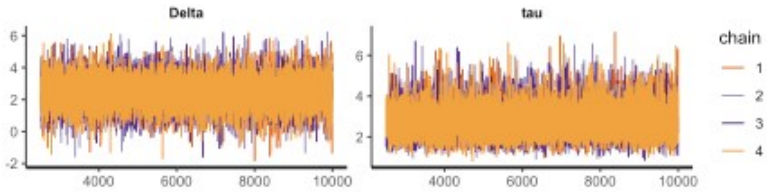
Finally, we can sample data from the posterior distribution:

```
fit <-  sampling(sm, data=ddata, seed = 3327, iter = 10000, warmup = 2500,
                 control=list(adapt_delta=0.9))
```

Check the diagonstic plots

Before looking at any of the output, it is imperative to convince ourselves that the MCMC process was a stable one. The *trace* plot is the most basic way to assess this. Here, I am only showing these plots for \(\Delta\) and \(\tau\), but the plots for the other parameters looked similar, which is to say everything looks good:

```
pname <- c("Delta", "tau")
stan_trace(object = fit, pars = pname)
```



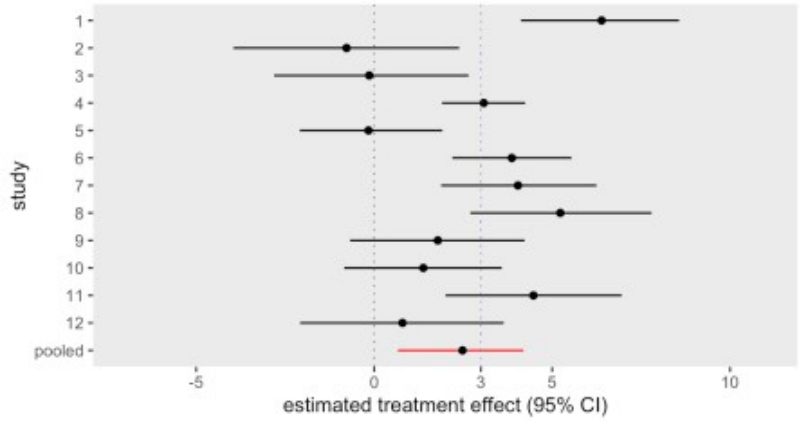
Look at the results

It is possible to look inspect the distribution of any or all parameters. In this case, I am particularly interested in the treatment effects at the study level, and overall. That is, the focus here is on \(\Delta\), \(\delta_k\), and \(\tau\).

```
pname <- c("delta", "Delta","tau")
print(fit, pars=pname, probs = c(0.05, 0.5, 0.95))
```

```
## Inference for Stan model: model.
## 4 chains, each with iter=10000; warmup=2500; thin=1;
## post-warmup draws per chain=7500, total post-warmup draws=30000.
##
##            mean se_mean   sd    5%   50%  95% n_eff Rhat
## delta[1]   6.39    0.01 1.13  4.51  6.41 8.22 29562    1
## delta[2]  -0.78    0.01 1.62 -3.45 -0.78 1.85 28188    1
## delta[3]  -0.14    0.01 1.39 -2.37 -0.16 2.18 28909    1
## delta[4]   3.08    0.00 0.59  2.09  3.08 4.05 34277    1
## delta[5]  -0.16    0.01 1.01 -1.77 -0.18 1.52 27491    1
## delta[6]   3.87    0.00 0.86  2.47  3.87 5.27 35079    1
## delta[7]   4.04    0.01 1.11  2.21  4.03 5.87 32913    1
## delta[8]   5.23    0.01 1.29  3.12  5.23 7.36 33503    1
## delta[9]   1.79    0.01 1.25 -0.27  1.78 3.82 30709    1
## delta[10]  1.38    0.01 1.12 -0.46  1.38 3.21 30522    1
## delta[11]  4.47    0.01 1.25  2.43  4.47 6.54 34573    1
## delta[12]  0.79    0.01 1.45 -1.60  0.80 3.16 33422    1
## Delta      2.48    0.00 0.89  1.01  2.50 3.89 31970    1
## tau        2.72    0.00 0.71  1.72  2.64 4.01 24118    1
##
## Samples were drawn using NUTS(diag_e) at Sat Jun 27 15:47:15 2020.
## For each parameter, n_eff is a crude measure of effective sample size,
## and Rhat is the potential scale reduction factor on split chains (at
## convergence, Rhat=1).
```

The forest plot is quite similar to the one based on the mixed effects model, though as predicted, the 95% CI is considerably wider:



As a comparison, here is the plot from the mixed effects model estimated using the `nlme` package in the previous post. The bootstrapped estimates of uncertainty at the study level are quite close to the Bayesian measure of uncertainty; the difference really lies in the uncertainty around the global estimate.