A WinBUGS Program

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# Meta-analysis of TG5 data.
# Code by Kerrie Mengersen, Daniel Burrell and
# Ian Wood, 2005.
#
# Combine multiple study observations to obtain
# single study-level effects. Combine study-level
# effects to obtain breed-level effects. Combine
# breed-level effects to estimate overall effect.

model{
    # Combine study 1 observations into one study-
    # level effect. Similarly combine study 4
    # observations into one study-level effect.

    for ( i in 1:16)
    {
        precY[i] <- tauY/(SE[i]*SE[i])
        Y[i] ~ dnorm(mu.s[study[i]], precY[i])
    }

    # Generate the 11 study-level effects, mu.s
    for ( j in 1:11 )
    {
        precmu.s[j] <- alpha*Ws[j]*taumu.s
        mu.s[j] ~ dnorm(mu.b[breed[j]], precmu.s[j])
    }

    # Generate the 4 breed-level effects, mu.b
    for ( k in 1:4 )
    {
        precmu.b[k] <- alpha*Wb[k]*taumu.b
        mu.b[k] ~ dnorm(mu, precmu.b[k])
    }
    mu ~ dnorm(0, 1.0E-6)

    # Determine probability of positive association
    # between marbling and more T alleles overall
    # and for each breed.
    mup <- step(mu)
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    mun <- step(-mu)
    for ( k in 1:4 )
    {
        mubp[k] <- step(mu.b[k])
        mubn[k] <- step(-mu.b[k])
    }

    # Posterior predictive checks:
    # generate 16 predicted Y values from model
    # on each Gibbs sampling sweep.
    # Results analysed using R on CODA output.
    for ( i in 1:16)
    {
        Ysim[i] ~ dnorm(mu.s[study[i]], precY[i])
    }

    # Setting up precisions
    tauYtop ~ dchisqr(dfY)
    tauY <- tauYtop/dfY
    taumu.s.top ~ dchisqr(dfmu.s)
    taumu.s <- taumu.s.top/dfmu.s
    taumu.b.top ~ dchisqr(dfmu.b)
    taumu.b <- taumu.b.top/dfmu.b
}

# Initial values for variables in MCMC runs
list( mu = 0,mu.b=c(0, 0, 0, 0),
mu.s = c(0, 0, 0, 0, 0, 0, 0, 0, 0,0,0) )

# Data sets:

# CCvCT (0 vs 1) with prior weights:
list(   dfY = 200,
        dfmu.s = 10,
        dfmu.b = 3,
        Y =  c(0.14,-0.54,-0.26,-0.1,-0.07,-0.01,0.07,
             -0.1,-0.25,-0.25,-0.09,-0.15,-0.01,-0.05,
              -0.15,-0.08),
        SE = c(0.1,0.23,0.16,0.11,0.2,0.05,0.18,0.11,
               0.13,0.09,0.14,0.19,0.1,0.1,0.12,0.09),
        study = c(1,2,3,4,5,6,1,4,4,7,8,9,1,4,10,11),
```

```
        breed = c(1,2,2,3,2,1,1,1,4,2,2),
        Ws = c(0.7508,0.991,0.9234,0.891,0.8754,0.613,
               0.805,0.9666,0.2155,0.998,0.9105),
        Wb = c(1,1,1,1),
        alpha = 100)

# TTvCT (2 vs 1) with prior weights:
list(   dfY = 100,
        dfmu.s = 10,
        dfmu.b = 3,
        Y =  c(0.13,0.15,0.22,0.24,0.29,0.24,0.01,
              -0.22,0.06,0.11,0.18,-0.95,0.07,-0.02,
               0.12,0.04),
        SE = c(0.23,0.18,0.23,0.21,0.14,0.14,0.46,0.2,
           0.25,0.18,0.21, 0.59,0.21,0.18,0.13,0.07),
        study = c(1,2,3,4,5,6,1,4,4,7,8,9,1,4,10,11),
        breed = c(1,2,2,3,2,1,1,1,4,2,2),
        Ws = c(0.7508,0.991,0.9234,0.891,0.8754,0.613,
               0.805,0.9666,0.2155,0.998,0.9105),
        Wb = c(1,1,1,1),
        alpha=100)

# TTvCC (2 vs 0) with prior weights:
list(   dfY = 130,
        dfmu.s = 10,
        dfmu.b = 3,
        Y =  c(-0.01,0.69,0.48,0.34,0.36,0.25,-0.06,
               -0.12,0.31,0.36,0.27,-0.80,0.08,0.03,
                0.27,0.12),
        SE = c(0.25,0.29,0.28,0.24,0.24,0.15,0.49,
               0.23,0.28,0.20,0.25,0.62,0.23,0.21,
               0.18,0.11),
        study = c(1,2,3,4,5,6,1,4,4,7,8,9,1,4,10,11),
        breed = c(1,2,2,3,2,1,1,1,4,2,2),
        Ws = c(0.7508,0.991,0.9234,0.891,0.8754,0.613,
               0.805,0.9666,0.2155,0.998,0.9105),
        Wb = c(1,1,1,1),
        alpha=100)

## Recessivity assumption:
# CCvCT (0 vs 1) with prior weights for complete
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```
# T recessivity:
list(   dfY = 200,
        dfmu.s = 10,
        dfmu.b = 3,
        Y =  c(0.14,-0.54,-0.26,-0.1,-0.07,-0.01,0.07,
             -0.1,-0.25,-0.25,-0.09,-0.15,-0.01,-0.05,
              -0.15,-0.08),
        SE = c(0.1,0.23,0.16,0.11,0.2,0.05,0.18,0.11,
               0.13,0.09,0.14,0.19,0.1,0.1,0.12,0.09),
        study = c(1,2,3,4,5,6,1,4,4,7,8,9,1,4,10,11),
        breed = c(1,2,2,3,2,1,1,1,4,2,2),
        Ws = c(0.235,0.8393,0.4546,0.3984,0.9928,
            0.1377,0.2875,0.5563,0.013,0.7043,0.4309),
        Wb = c(1,1,1,1),
        alpha=100)

# TTvCT (2 vs 1) with prior weights for complete
# T recessivity:
list(   dfY = 100,
        dfmu.s = 10,
        dfmu.b = 3,
        Y =  c(0.13,0.15,0.22,0.24,0.29,0.24,0.01,
              -0.22,0.06,0.11,0.18,-0.95,0.07,-0.02,
               0.12,0.04),
        SE = c(0.23,0.18,0.23,0.21,0.14,0.14,0.46,
               0.2,0.25,0.18,0.21,0.59,0.21,0.18,
               0.13,0.07),
        study = c(1,2,3,4,5,6,1,4,4,7,8,9,1,4,10,11),
        breed = c(1,2,2,3,2,1,1,1,4,2,2),
        Ws = c(0.235,0.8393,0.4546,0.3984,0.9928,
            0.1377,0.2875,0.5563,0.013,0.7043,0.4309),
        Wb = c(1,1,1,1),
        alpha=100)

# TTvCC (2 vs 0) with prior weights for complete
# T recessivity:
list(   dfY = 130,
        dfmu.s = 10,
        dfmu.b = 3,
        Y =  c(-0.01,0.69,0.48,0.34,0.36,0.25,-0.06,
               -0.12,0.31,0.36,0.27,-0.80,0.08,0.03,
```

```
        0.27,0.12),
SE = c(0.25,0.29,0.28,0.24,0.24,0.15,0.49,
       0.23,0.28,0.20,0.25,0.62,0.23,0.21,
       0.18,0.11),
study = c(1,2,3,4,5,6,1,4,4,7,8,9,1,4,10,11),
breed = c(1,2,2,3,2,1,1,1,4,2,2),
Ws = c(0.235,0.8393,0.4546,0.3984,0.9928,
    0.1377,0.2875,0.5563,0.013,0.7043,0.4309),
Wb = c(1,1,1,1),
alpha=100)
```