BUGS

Kidney: Weibull regression with random efects

McGilchrist and Aisbett (1991) analyse time to first and second recurrence of infection in kidney patients on dialysis using a Cox model with a multiplicative frailty parameter for each individual. The risk variables considered are age, sex and underlying disease (coded other, GN, AN and PKD). A portion of the data are shown below.

Patient Number	Recurrence time t	Event (2 = cens)	Age at time t	Sex (1 = female)	Disease (0 = other; 1 = GN 2 = AN; 3 = PKD)
1	8,16	1,1	28,28	0	0
2	23,13	1,2	48,48	1	1
3	22,28	1,1	32,32	0	0
4	447,318	1,1	31,32	1	0
.....					
35	119,8	1,1	22,22	1	1
36	54,16	2,2	42,42	1	1
37	6,78	2,1	52,52	1	3
38	63,8	1,2	60,60	0	3

We have analysed the same data assuming a parametric Weibull distribution for the survivor function, and including an additive random effect b_i for each patient in the exponent of the hazard model as follows

$$t_{ij} \sim \text{Weibull}(r, \mu_{ij}) \quad i = 1,...,38;\ j = 1,2$$

$$\log\mu_{ij} = \alpha + \beta_{age}AGE_{ij} + \beta_{sex}SEX_i + \beta_{disease1}DISEASE_{i1} + \beta_{disease2}DISEASE_{i2} + \beta_{disease3}DISEASE_{i3} + b_i$$

$$b_i \sim \text{Normal}(0, \tau)$$

where AGE_{ij} is a continuous covariate, SEX_i is a 2-level factor and $DISEASE_{ik}$ (k = 1,2,3) are dummy variables representing the 4-level factor for underlying disease. Note that the the survival distribution is a truncated Weibull for censored observations as discussed in the mice example. The regression coefficients and the precision of the random effects τ are given independent ``non-informative" priors, namely

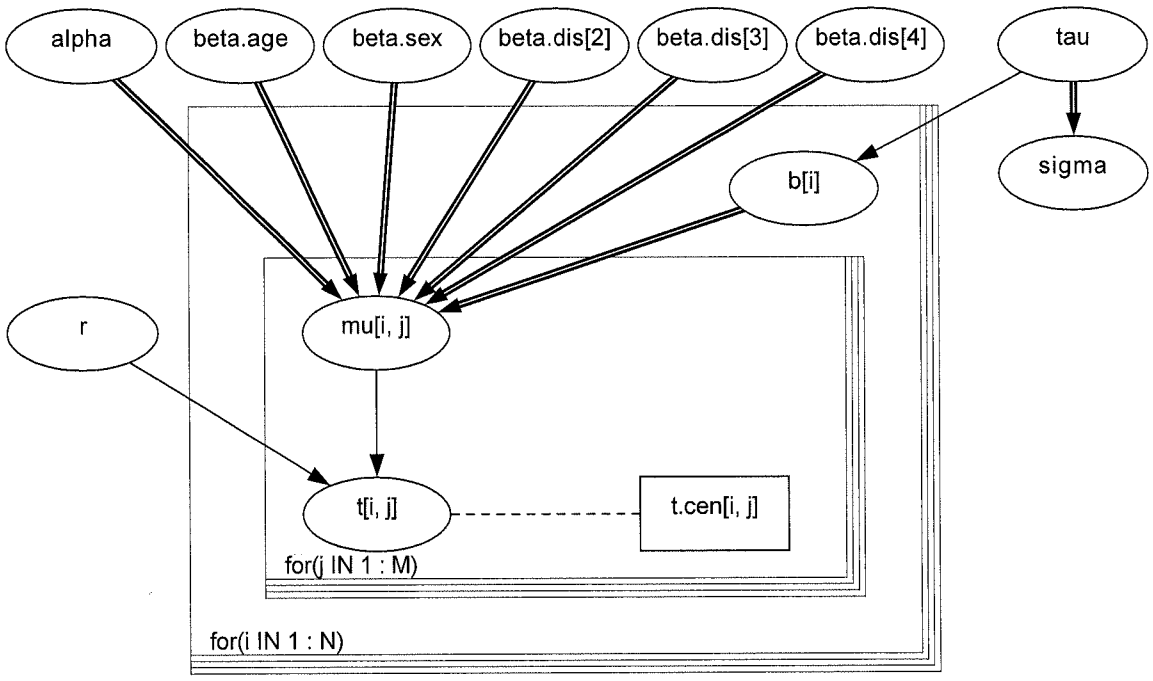
$$b_k \sim \text{Normal}(0, 0.0001)$$

$$\tau \sim \text{Gamma}(0.0001, 0.0001)$$

The shape parameter of the survival distribution r is given a Gamma(1, 0.0001) prior which is slowly decreasing on the positive real line.

The graphical model and *BUGS* language are given below.

Graphical model for kidney example:



BUGS *language for kidney example*

```
model
{
    for (i in 1:N) {
        for (j in 1:M) {
# Survival times bounded below by censoring times:
            t[i,j] ~ dweib(r,mu[i,j]) I(t.cen[i,j],);
            log(mu[i,j]) <- alpha + beta.age*age[i,j]
                + beta.sex *sex[i]
                + beta.dis[disease[i]] + b[i];
        }
# Random effects:
        b[i] ~ dnorm(0.0, tau)
    }
# Priors:
    alpha ~ dnorm(0.0, 0.0001);
    beta.age ~ dnorm(0.0, 0.0001);
    beta.sex ~ dnorm(0.0, 0.0001);
#   beta.dis[1] <- 0;  # corner-point constraint
    for(k in 2 : 4) {
        beta.dis[k] ~ dnorm(0.0, 0.0001);
        }
    tau ~ dgamma(1.0E-3, 1.0E-3);
    r ~ dgamma(1.0, 1.0E-3);
    sigma <- 1/sqrt(tau); # s.d. of random effects
}
```

```
Data ⇨list(N = 38, M = 2,
t = structure(
.Data = c(  8,  16,
   23,  NA,
   22,  28,
  447, 318,
        30,  12,
        24, 245,
         7,   9,
       511,  30,
        53, 196,
        15, 154,
         7, 333,
       141,  NA,
        96,  38,
        NA,  NA,
       536,  NA,
        17,  NA,
       185, 177,
       292, 114,
        NA,  NA,
        15,  NA,
       152, 562,
       402,  NA,
        13,  66,
        39,  NA,
        12,  40,
        NA, 201,
       132, 156,
        34,  30,
         2,  25,
       130,  26,
        27,  58,
        NA,  43,
       152,  30,
       190,  NA,
       119,   8,
        NA,  NA,
        NA,  78,
        63,  NA), .Dim = c(38, 2)),
t.cen = structure(
.Data = c(  0,    0,
         0,   13,
         0,    0,
         0,    0,
         0,    0,
         0,    0,
         0,    0,
         0,    0,
         0,    0,
         0,    0,
         0,    0,
         0,    0,
         0,    8,
         0,    0,
       149,   70,
         0,   25,
         0,    4,
         0,    0,
         0,    0,
        22,  159,
         0,  108,
         0,    0,
         0,   24,
         0,    0,
         0,   46,
         0,    0,
       113,    0,
         0,    0,
```

```
        0,   0,
        0,   0,
        0,   0,
        0,   0,
        5,   0,
        0,   0,
        0,   5,
        0,   0,
       54,  16,
        6,   0,
        0,   8), .Dim = c(38, 2)),
  age = structure(
.Data = c(28,  28,
       48,  48,
       32,  32,
       31,  32,
       10,  10,
       16,  17,
       51,  51,
       55,  56,
       69,  69,
       51,  52,
       44,  44,
       34,  34,
       35,  35,
       42,  42,
       17,  17,
       60,  60,
       60,  60,
       43,  44,
       53,  53,
       44,  44,
       46,  47,
       30,  30,
       62,  63,
       42,  43,
       43,  43,
       57,  58,
       10,  10,
       52,  52,
       53,  53,
       54,  54,
       56,  56,
       50,  51,
       57,  57,
       44,  45,
       22,  22,
       42,  42,
       52,  52,
       60,  60), .Dim = c(38, 2)),
    beta.dis = c(0, NA, NA, NA),
   sex = c(0, 1, 0, 1, 0, 1, 0, 1, 1, 0, 1, 1, 1, 1, 1,
0, 1, 1, 1, 1, 0, 1, 1, 1, 0, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1, 1, 1, 0),
disease = c(1, 2, 1, 1, 1, 1, 2, 2, 3, 2, 3, 1, 3, 3, 1, 3, 1, 1,2, 1, 4, 1, 3, 3,
          3, 3, 2, 3, 2, 2, 3, 3, 4, 2, 1, 1, 4, 4))⇦
```

Inits ⇨list(beta.age = 0, beta.sex = 0, beta.dis=c(NA,0,0,0),
alpha = 0, r=1, tau=0.3)⇦

Results

A 1000 update burn in followed by a further 10000 updates gave the parameter estimates

node	mean	sd	MC error	2.5%	median	97.5%	start	sample
alpha	-4.6	0.8962	0.07002	-6.541	-4.541	-3.065	1001	10000
beta.age	0.003027	0.01475	9.703E-4	-0.02411	0.002423	0.03368	1001	10000
beta.dis[2]	0.1329	0.5393	0.02148	-0.9443	0.1276	1.237	1001	10000
beta.dis[3]	0.6444	0.5301	0.02364	-0.4158	0.6428	1.711	1001	10000
beta.dis[4]	-1.168	0.8335	0.03382	-2.772	-1.182	0.5535	1001	10000
beta.sex	-1.938	0.4854	0.02524	-2.952	-1.917	-1.033	1001	10000
r	1.215	0.1623	0.01293	0.9275	1.204	1.536	1001	10000
sigma	0.6374	0.357	0.02847	0.04597	0.653	1.322	1001	10000