Try Bayesian Survival Analysis using the JACC study data (Bayesian Survival Analysis presentations)

Chaochen Wang | Aichi Medical University 2020-01-12

Parametric Survival Analysis Model (in a Bayesian way)

- We chose Weibull model to describe the survival data we have.
- Weibull model is both a proportional hazard model and a accelerated failure time (AFT) model. The relationship between the acceleration factor and log hazard ratio:

Weibull Survival funciton in a proportional hazard way expression is: ${}_{\alpha}{}^{\rm T}$

$$S(t|\mathbf{x}) = \exp\{-\lambda t^{\kappa} e^{\beta_{\mathbf{PH}}^{\mathbf{T}}}\}$$

Weibull Survival function in a AFT way expression is:

$$S(t|\mathbf{x}) = \exp\{-\lambda t^{\kappa} e^{\kappa \beta_{\mathbf{AFT}}^{\mathbf{T}}}\}$$

```
\exp(\beta_{PH}^T) = \exp(\kappa \beta_{AFT}^T)
```

An example of a crude Weibull model using the JAGS program in R:

```
jacc.weibull.model <- function() {</pre>
  for(i in 1:39386){
    \# sAge[i] \leftarrow (Age[i] - mean(Age[])) / sd(Age[])
    is.censored[i] ~ dinterval(t[i], c[i])
    t[i] ~ dweib(shape, lambda[i])
    lambda[i] <- exp(-mu[i] * shape)</pre>
    mu[i] <- beta[1] + beta[2]*equals(Mlkfre[i], 2) +</pre>
      beta[3]*equals(Mlkfre[i], 3) + beta[4] * equals(Mlkfre[i], 4) +
      beta[5] * equals(Mlkfre[i], 5) # +
      # beta[6] * sAge[i]
    ### calculate log-likelihoods
    \# y[i] \leftarrow ifelse(is.censored[i], c[i], t[i])
    # loglik[i] <- log(ifelse(is.censored[i],</pre>
                        exp(-lambda[i] * (y[i] ^ shape)),
                     shape * lambda[i] * (y[i] ^ (shape - 1)) * exp(-lambda[i] * (y[i] ^ shape))))
  }
  ## priors for betas
  for(j in 1:5){
    beta[j] ~ dnorm(0, 0.001)
  }
  ### prior for shape
```

```
shape ~ dgamma(.001, .001)
  ### Generated values
  AFT[2] <- exp(beta[2])
  HR[2] <- exp(shape * beta[2])</pre>
  p.crit[2] \leftarrow step(1 - HR[2])
  AFT[3] <- exp(beta[3])
  HR[3] <- exp(shape * beta[3])</pre>
  p.crit[3] \leftarrow step(1 - HR[3])
  AFT[4] <- exp(beta[4])
  HR[4] <- exp(shape * beta[4])</pre>
  p.crit[4] \leftarrow step(1 - HR[4])
  AFT[5] <- exp(beta[5])
  HR[5] <- exp(shape * beta[5])</pre>
  p.crit[5] \leftarrow step(1 - HR[5])
}
  You can use the following codes to run the above model (careful
about the cost of time):
library(R2jags) #conect to jags sampling engine in R
jagsfit <- jags.parallel(data = JACCdata,</pre>
                            parameters.to.save = c("beta[5]", "HR[5]", "AFT[5]"),
                            #add more variables if you want to check more
                            n.iter = 10000,
                            n.burnin = 2500,
                            n.chains = 3,
                            model.file = jacc.weibull.model)
```

Check model fitting:

