

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

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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 an accelerated failure time (AFT) model. The relationship between the acceleration factor and log hazard ratio:

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

Weibull Survival function in a proportional hazard way expression is:

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

Weibull Survival function in an AFT way expression is:

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

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

```
jacc.weibull.model <- function() {  
  for(i in 1:39386){  
    # sAge[i] <- (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)  
    mu[i] <- beta[1] + beta[2]*equals(Mlffre[i], 2) +  
      beta[3]*equals(Mlffre[i], 3) + beta[4] * equals(Mlffre[i], 4) +  
      beta[5] * equals(Mlffre[i], 5) # +  
      # beta[6] * sAge[i]  
  
    ### calculate log-likelihoods  
    # y[i] <- ifelse(is.censored[i], c[i], t[i])  
    # loglik[i] <- log(ifelse(is.censored[i],  
    #                         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
```


Check model fitting:

