Bayesian Analysis For Cure Rate Model Under GEV with COM-Poisson Regression

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Abstract

This project introduces the log maxima generalized extreme value (GEV) distribution to analyze right-censored survival data with a cure fraction. The proposed GEV model can lead to very flexible hazard functions. We also propose a more general count data distribution–Conway Maxwell Poisson (Com-Poisson distribution) to describe the count data in the survival model. The advantage of COM-Poisson is that it can be able to handle both underdispersion and overdispersion through controlling one special parameter in the distribution. A problem in sampling COM-Poisson is the calculation of the normalized constant for which doesn't have a closed form so that there is no accurate estimate for the constant. So an alternative sampling method–Exchange algorithm instead of the common used MCMC sampling (i.e. Metropolis sampling) will be used in this project. The exchange sampling is specifically illustrated in this project and implemented through a simulation.

Keywords: Cure Rate Model; Maxima GEV Distribution; COM-Poisson Distribution; Exchange Algorithm; MCMC sampling.

1 Introduction

Cure rate models have been used for the survival data for various types of cancers. The standard cure rate model $S(t) = \pi + (1-\pi)S^*(t)$ where a fraction π of the population is considered "cured" and $1-\pi$ is non-cured, and $S^*(t)$ denotes the survival function for non-cured group in this population. The former standard cure rate model $S(t) = \pi+(1-\pi)S^*(t)$ has several drawbacks, i.e, we might get the improper posterior distributions for many types of non-informative improper priors. Therefore different types of cure rate models (Chen et al. (1999)) are introduced, for example, the Gamma and Weibull distributions. The hazard function, however, often is not monotone. In Roy and Dey (2014), it proved that the maxima GEV for $\log T$, where T is the failure time/survival time for a subject, can be fit to flexible hazard functions through controlling the shape parameters. The variable N_i, which is the number of clonogenic cells for the ith subjects ($i = 1, \ldots, n$), being described by the simple Poisson distribution in Chen et al. (1999), however, usually encounters the overdispersion or underdispersion. By incorporating a new parameter which controls the amount of dispersion, the N_i is following the COM-Poisson (Shmueli et al. (2005)) which will illustrate N_i's better in overdispersion and underdispersion. N_i is not observed and considered to be a latent variable. The usual MCMC algorithm is not able to compute the accept ratio due to the normalized constant of COM-Poisson. Therefore, the exchange algorithm (Chanialidis et al. (2018)) is deployed, incorporating the density of auxiliary data sampled from the distribution estimated at the value of parameters from proposed distribution. With all assumptions satisfied, the posterior distribution for the parameters can be derived and based on which the Bayesian MCMC sampling will be performed.

In section 2, we will discuss the strengths and drawbacks of the previous work, and also we will provide the definition and derivation for the standard survival model. In section 3, we will introduce the cure model under standard log GEV for maxima and the COM-Poisson regression models under a Bayesian frame work and how to construct the exchange algorithm to perform the sampling. Section 4 shows the results of recovery work of these methods applied to a simulated data set.

2 Previous Work

In the previously popular standard cure rate model (Berkson and Gage (1952)), the survival function can be written as $S(t) = \pi + (1-\pi)S^*(t)$ where a fraction π of the population

are considered "cured" and $1-\pi$ is non-cured, and $S^*(t)$ denotes the survival function for non-cured group in this population. The common choices for $S^*(t)$ are Weibull and Gamma distributions. However, there are some disadvantages of the standard cure rate model,

- It doesn't have a proportional hazard structure, which may be desirable for survival models.
- The computation is time-consuming and we might get improper posterior distributions for many types of non-informative priors. Therefore, we cannot perform Bayesian analysis under this case.

Therefore, an alternative cure rate model has been rised by Yakovlev et al. (1993), and a Bayesianc formulation of this model is by *Chenet al.* (1999), which can be derived as follows:

- N: the number of clonogenic cells and is following Poisson (θ) distribution.
- $\mathbf{Z}$: the incubation time for the N cells, and $\mathbf{Z} = (Z_1, \ldots, Z_N)$.
- $T = \min(Z_1, \ldots, Z_N)$, and $P(Z_0 = \infty) = 1$.
- The survival function for the population is

$$\begin{aligned} S(t) &= P(\text{no cancer by time t}) = P(N=0) + P(Z_1 > t, \ldots, Z_N > t, N \geq 1) \\ &= \exp(-\theta) + \sum_{j=1}^{\infty} S(t)^j \frac{\theta^j}{j!} \exp(-\theta) \\ &= \exp(-\theta + \theta S(t)) \end{aligned}$$

  The cure rate is given by $P(N=0) = \exp(-\theta) = \lim_{t\to\infty} S(t)$.

The alternative model even through solves some problems in the previous model, it still has some drawbacks:

- The survival models do not include flexible hazard functions.
- The number of clonogenic cells N is assumed to be Poisson for simplicity and ease of implementation, however, the Poisson model usually fails to capture the phenomenon of dispersion, especially when the mean and variance differ significantly.

Therefore, a new cure rate model and a more flexible count distribution should be considered to overcome the drawbacks discussed above.

3 Model Description and Methods

3.1 Cure Rate Model under log Maxima Generalized Extreme Value Distribution

Suppose that $Y_1, \ldots, Y_n \overset{i.i.d}{\sim} F(y)$ and let $M_n = \max\{Y_1, \ldots, Y_n\}$. If there exits a non-degenerate distribution function $G(x)$ and a pair of sequence $a_n > 0$ and b_n such that

$$\lim_{n\to\infty} P\{\frac{M_n - b_n}{a_n} \leq x\} = G(x)$$

on all points in the continuity set of $G(x)$, then $G(x)$ is a generalized extreme value distribution for maxima (denote as MGEV distribution).

$$G(x) = \begin{cases} \exp\left\{-(1+\xi\frac{x-\mu}{\sigma})_+^{-\frac{1}{\xi}}\right\} & \text{if } \xi > 0 \text{ or } \xi < 0 \\ \exp\left\{-\exp(-\frac{x-\mu}{\sigma})\right\} & \text{if } \xi = 0 \end{cases}$$

Furthermore, if we assume that $\log T$ is following a MGEV distribution, then $T \sim \log MGEV$. The cdf, suvival function and pdf of T are:

$$F_M(t|\xi) = \exp\left\{-(1+\xi\log t)^{-\frac{1}{\xi}}\right\} \tag{1}$$

$$S_M(t|\xi) = 1 - \exp\left\{-(1+\xi\log t)^{-\frac{1}{\xi}}\right\} \tag{2}$$

$$f_M(t|\xi) = \frac{\exp\left\{-(1+\xi\log t)^{-\frac{1}{\xi}}\right\}}{y_i(1+\xi\log t)^{\frac{1}{\xi}+1}} \tag{3}$$

for $t > \exp(-\frac{1}{\xi})$ if $\xi > 0$ or $t < \exp(-\frac{1}{\xi})$ if $\xi < 0$.

Suppose that we have n subject and N_i denote the clonogenic cells for the ith subject. We assume that N_i's, the unobserved count data, are independent COM-Poisson distribution with parameters μ_i and ν_i, $i = 1, \ldots, n$, for which can be able to handle both of

overdispersion and underdisperion. If we let t_i denote the failure time and be right-censored, and let c_i be the censoring time and we observe that $y_i = \min(t_i, c_i)$, where the censoring indicator $\delta_i = I(t_i < c_i)$. Incubation time y_i for the N_i cells $\overset{i.i.d}{\sim} F(\cdot|\xi), i = 1, \ldots, n$. $F(\cdot|\xi)$ is the cdf of log MGEV distribution with shape parameter ξ. The complete data is given by $\mathbf{D} = (n, \mathbf{y}, \boldsymbol{\delta}, \mathbf{N})$, where $\mathbf{y} = (y_1, \ldots, y_n)$, and $\delta = (\delta_1, \ldots, \delta_n)$, $\mathbf{N} = (N_1, \ldots, N_n)$. The complete data likelihood function of the parameters $(\boldsymbol{\theta}, \boldsymbol{\nu}, \xi)$ can be written as (Chen et al. (1999)):

$$L(\boldsymbol{\theta}, \boldsymbol{\nu}, \xi|\mathbf{D}) = \prod_{i=1}^{n} S(y_i|\xi)^{N_i - \delta_i} (N_i f(y_i|\xi))^{\delta_i} \times \exp\left\{ \sum_{i=1}^{n} N_i \log(\theta_i) - \log(N_i!) - \log(Z(\theta_i, \nu_i)) \right\}$$

with

$$P(N_i = n) = \frac{\theta_i^n}{n!} \frac{1}{Z(\theta_i, \nu_i)}, n = 0, 1, \ldots, \text{where} \quad Z(\theta_i, \nu_i) = \sum_{j=0}^{\infty} \frac{\theta_i^j}{(j!)^{\nu_i}} \tag{4}$$

for $\theta_i > 0$ and $\nu_i \geq 0$. If we incorporate the covariates through θ_i, ν_i, for each subject i, let $\mathbf{x}_i' = [1, x_{i1}, \ldots, x_{ip}]$ be the $p \times 1$ vector of covariates, $\boldsymbol{\beta} = (\beta_0, \beta_1, \ldots, \beta_p)$ and $\boldsymbol{\gamma} = (\gamma_0, \gamma_1, \ldots, \gamma_p)$ be the corresponding coefficients, $\log(\theta_i) = x_i'\boldsymbol{\beta}$ and $\log(\nu_i) = -x_i'\boldsymbol{\gamma}$.We can directly derive the posterior distribution of ξ and N_i:

$$\begin{aligned}
\pi(\xi|\mathbf{D}, \boldsymbol{\beta}, \boldsymbol{\gamma}) &\propto f(\mathbf{D}|\xi) \times \pi(\xi) \\
&\propto \prod_{i=1}^{n} S(y_i|\xi)^{N_i - \delta_i} (N_i f(y_i|\xi))^{\delta_i} \times \pi(\xi) \\
\pi(N_i|\mathbf{D}_{obs}, \boldsymbol{\beta}, \boldsymbol{\gamma}, \xi) &\propto S(y_i|\xi)^{N_i - \delta_i} (N_i f(y_i|\xi))^{\delta_i} \frac{(\mathbf{x}_i'\boldsymbol{\beta})^{N_i}}{N_i!} \frac{1}{Z(\mathbf{x}_i'\boldsymbol{\beta}, \mathbf{z}_i'\boldsymbol{\gamma})} \pi(\boldsymbol{\beta}, \boldsymbol{\gamma})
\end{aligned}$$

Since the posterior distribution of parameter ξ has no closed form, so a standard MCMC sampling, Metropolis-Hastings algorithm will be deployed to sample ξ. However, the only problem is to sample $\boldsymbol{\beta}, \boldsymbol{\gamma}$ since the normalized constant $Z(\theta_i, \nu_i)$ has no closed form so that it's difficult to calculate.

3.2 COM-Poisson Regression and Exchange Algorithm

Assume N_i's are independent Conway–Maxwell–Poisson (COM-Poisson) distribution with equation (4). ν governs the amount of dispersion:overdispersion ($\nu < 1$) and the underdis-

persion ($\nu > 1$)

$$\begin{cases} \nu = 1 & \text{Poisson} \\ \nu = 0, \theta < 1 & \text{Geometric} \\ \nu \to \infty \ \text{ with probability} \frac{\theta}{1+\theta} & \text{Bernoulli} \end{cases}$$

If we incorporate the covariates through θ_i, ν_i, for each subject i, let $\mathbf{x}_i' = [1, x_{i1}, \ldots, x_{ip}]$ be the $p \times 1$ vector of covariates, $\boldsymbol{\beta} = (\beta_0, \beta_1, \ldots, \beta_p)$ and $\boldsymbol{\gamma} = (\gamma_0, \gamma_1, \ldots, \gamma_p)$ be the corresponding coefficients and through the log link functions, $\log(\theta_i) = x_i'\boldsymbol{\beta}$ and $\log(\nu_i) = -x_i'\boldsymbol{\gamma}$. Rewrite the parameters as $\mu_i = (\theta_i, \nu_i)'$ and $\theta_i = \eta(\beta, x_i) = \exp(x_i'\beta)$, $\nu_i = \eta(\gamma, x_i) = \exp(-x_i'\gamma)$ be the link functions, and rewrite the pmf $P(N_i = n_i) = \frac{h(n_i|\mu_i)}{Z_h(\mu_i)}$. The Bayesian parameter inference for β and γ in COM-Poisson regression models is a doubly-intractable problem, so the direct application of a standard MCMC methods is infeasible. For example, a Metropolis algorithm requires the calculation of the intractable ratios $\left\{ \frac{Z_h(\mu_i)}{Z_h(\mu_i^*)} \right\}_{i=1}^{n}$ if it proposes a move from μ_i to μ_i^*. Now the acceptance ratio becomes

$$\rho(\mu, \mu^*) = \min \left\{ 1, \frac{\prod_{i=1}^{n} \frac{h(n_i|\mu_i^*)}{Z_h(\mu_i^*)}}{\prod_{i=1}^{n} \frac{h(n_i|\mu_i)}{Z_h(\mu_i)}} \frac{q(\mu^*, \mu)\pi(\mu^*)}{q(\mu, \mu^*)\pi(\mu)} \right\}.$$

Even through Shmueli et al. (2004) proposed an approximations by a truncated sum $Z_h(\mu_i) = \sum_{i=1}^{k} q_h(n|\mu_i)$ to estimate the normalized constant, there still exists some bias in the acceptance ratio.

The exchange algorithm proposed by Benson and Friel (2017) can solve this problem by augmenting the doubly-intractable posterior with auxiliary data. Same with standard Metropolis, the exchange algorithm update the parameter from the current state μ to proposed state μ^* using the proposal distribution $q(\mu, \mu^*)$, but in addition the posterior is augmented with n auxiliary draws $N^* = (n_1^*, \ldots, n_n^*)$ generated from the likelihood estimated at the values of the parameters μ^* which are just proposed from the proposal distribution. Therefore, the augmented posterior can be written as

$$\pi(\beta, \beta^*, \mathbf{n}^*|\mathbf{n}) \propto h(\mathbf{n}|\boldsymbol{\mu})\pi(\beta)q(\beta, \beta^*)h(\mathbf{n}^*|\boldsymbol{\mu}^*)$$

The acceptance ratio for the augmented posterior is now calculated as

$$\rho_{exchange}(\beta,\beta^*) = \min\left\{1, \frac{\prod_{i=1}^n \frac{h(n_i|\mu_i^*)}{Z_h(\mu_i^*)}}{\prod_{i=1}^n \frac{h(n_i|\mu_i)}{Z_h(\mu_i)}} \frac{q(\beta^*,\beta)\pi(\beta^*)}{q(\beta,\beta^*)\pi(\beta)} \frac{\prod_{n=1}^n \frac{h(n_i^*|\mu_i)}{Z_h(\mu_i)}}{\prod_{n=1}^n \frac{h(n_i^*|\mu_i')}{Z_h(\mu_i')}}\right\}$$

$$= \min\left\{1, \frac{\prod_{i=1}^n h(n_i|\mu_i^*)q(\beta^*,\beta)\pi(\beta^*)\prod_{i=1}^n h(n_i^*|\mu_i)}{\prod_{i=1}^n h(n_i|\mu_i)q(\beta,\beta^*)\pi(\beta)\prod_{i=1}^n h(n_i^*|\mu_i^*)} \frac{\cancel{\prod_i \frac{1}{Z_h(\mu_i^*)}} \cancel{\prod_i \frac{1}{Z_h(\mu_i)}}}{\cancel{\prod_i \frac{1}{Z_h(\mu_i)}} \cancel{\prod_i \frac{1}{Z_h(\mu_i^*)}}}\right\}$$

The cancellation of the normalizing constants in the acceptance ratio above is due to the *exchange* of parameters (μ_i, μ_I^*) associated with the data $\mathbf{N} = (n_1, ..., n_n)$ and the auxiliary data $\mathbf{N}^* = (n_1^*, ..., n_n^*)$, the auxiliary being discarded after each move. The acceptance ratio for the exchange algorithm becomes

$$a = \min\left\{1, \frac{\{\prod_i h_{\mu^*}(n_i)\}\,\pi(\beta^*)\pi(\gamma^*)\,\{\prod_i h_{\mu}(n_i^*)\}}{\{\prod_i h_{\mu}(n_i)\}\,\pi(\beta)\pi(\gamma)\,\{\prod_i h_{\mu^*}(n_i^*)\}}\right\}$$

The standard Metropolis-Hastings to sample ξ and N_i's and the Exchange algorithms for $\boldsymbol{\beta}$ and $\boldsymbol{\gamma}$ will be applied to a simulated data set.

4 Simulation and Recovery Work

In this project, we simulate a right-censored data set and the process is given below:

Step 1. Let the sample size $n = 1000$, and suppose that we have one covariate: the age the patients which is randomly sampled with replacement from 1 to 100 and then standardized this variable. The $n \times 2$ design matrix $\mathbf{X} = [\mathbf{1}, \text{standardized age}]$ and also set $\beta = (1, 0.2)'$ and $\gamma = (0.5, -0.3)' \Rightarrow \theta_i = \exp(X_i'\beta)$ and $\nu_i = \exp(-x_i'\gamma)$. For every $i = 1, ...n$ we draw a sample from CMP(θ_i, ν_i), denoted by N_i. And get N_i samples from the distribution log MGEV($\mu = 0$, $\sigma = 1$, $\xi = 0.3$), denote the samples as $Z_{i1}, ..., Z_{i,N_i}$. Set $t_i = \min(Z_{i1}, ..., Z_{i,N_i})$ and $t_i = \infty$ if $N_i = 0$.

Step 2. For every $i = 1, ...n$ we draw a sample from CMP(θ_i, ν), denoted by N_i. And get N_i samples from the distribution log MGEV($\mu = 0$, $\sigma = 1$, $\xi = 0.3$), denote the samples as $Z_{i1}, ..., Z_{i,N_i}$. Set $t_i = \min(Z_{i1}, ..., Z_{i,N_i})$ and $t_i = \infty$ if $N_i = 0$.

Step 3. Let $y_i = \min(t_i, c_i)$ and $\delta_i = I(t_i < c_i)$ where c_i is the censoring time and chosen to be a constant so that the censoring percentage to be 28%.

Step 4. We include the covariates in the model and perform a Bayesian analysis. The multivariate normal $\mathbf{N}_2(\mathbf{0}, 100 \times \mathbf{I})$ are assigned to both $\boldsymbol{\beta}$ and $\boldsymbol{\gamma}$, and the proper prior on ξ

is $\pi(\xi) = \text{Uniform}(-1, 1)$. In this process, $20,000$ MCMC iterations are used for sampling the posterior estimation of the parameters and the burn-in is set to be $1,000$. We use trace plots, autocorrelations to check the convergence in the MCMC sampler.

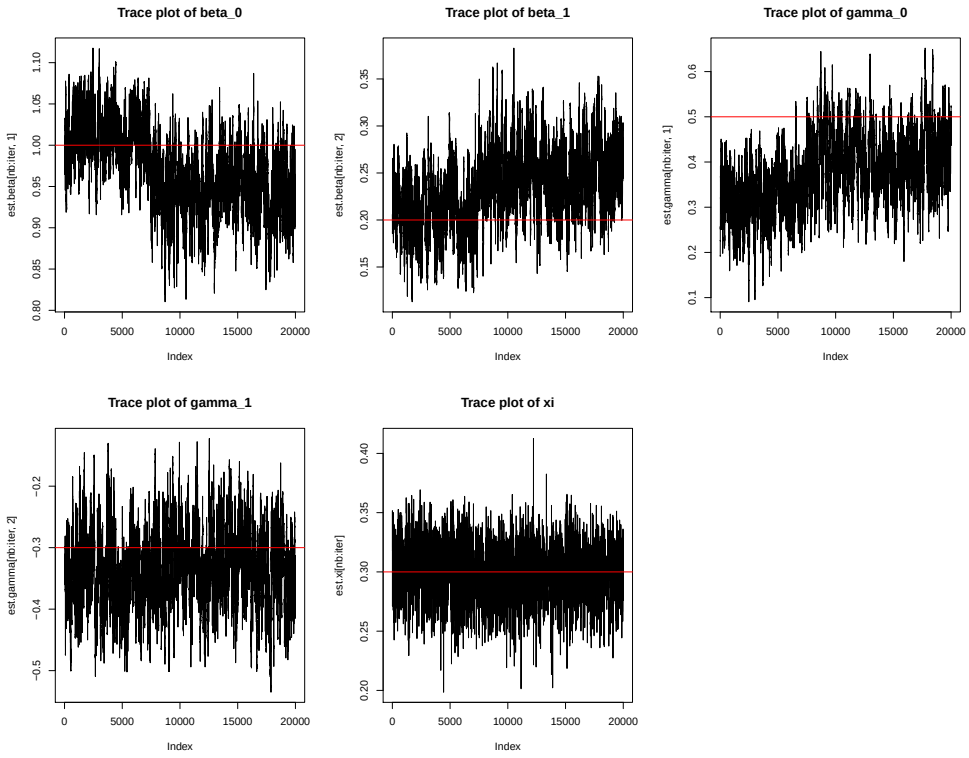

Figure 1: The trace plots for the parameters

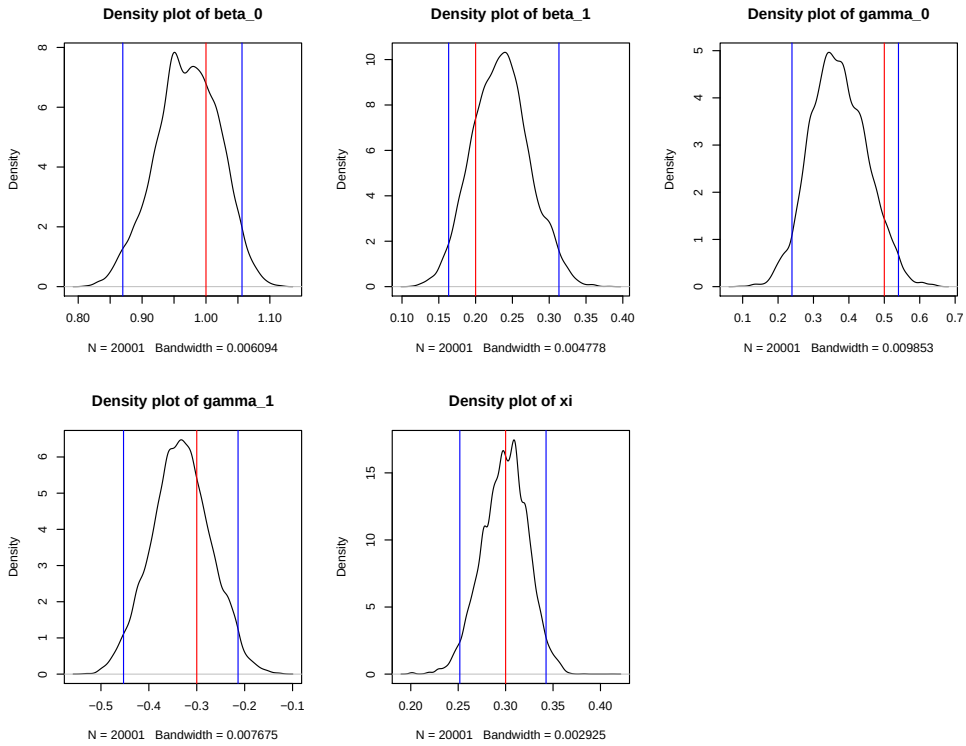

Figure 2: The density plots for the parameters

The trace plots for γ_1 and ξ seem to be mixing well, while there is a slight trend for other parameters, which might be due to the autocorrelation between states. Therefore, the thinning process would be taken to remove the strong autocorrelation. We can pick one sample for every 150 step.

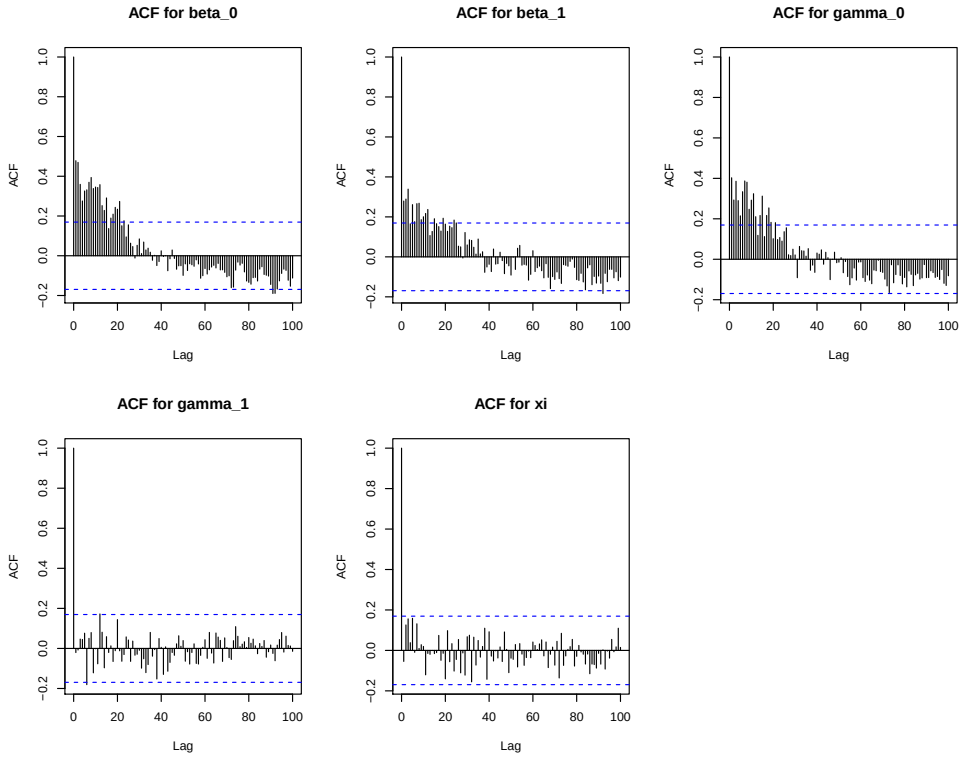

Figure 3: The density plots for the parameters

We also run the simulation for 10 times. Finally, 10 out 10 times the true values for the parameters are falling into the 95% HPD intervals.

Parameters					
	β_0	β_1	γ_0	γ_1	ξ
True	1	0.2	0.5	-0.3	0.3
Posterior Mean	0.971	0.234	0.372	-0.33	0.296
95% HPD lower	0.87	0.163	0.24	-0.453	0.252
95% HPD upper	1.06	0.313	0.54	-0.214	0.33

The averaged HPD 95% interval for the sampled parameters are calculated and can be see in table 4. And we can see that the true values are all within the HPD intervals and the posterior means are very close to the true values. Therefore, the sampling work is very stable and the recovery work performs well.

5 Conclusions

- In this project, a computationally MCMC algorithm for COM-Poisson regression is presented to explain the count data in the cure rate model. Therefore, both of the survival function and the count data can be flexible to to general cases. It also displayed how the exchange algorithm worked, combined with the standard MCMC algorithm. Finally, the simulation results showed that those algorithm could recovery the true setups very well.

- The special MCMC sampling-Exchange algorithm nested with Metropolis algorithm works well in the simulated data set, further, those algorithms will be applied to describe the real data set. Meanwhile, the efficiency would also be a concentration in the future work.

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A R code for project

```
rm(list = ls())
set.seed(123457)

###=================================
#simulation
###=================================
#install.packages("'COMPoissonReg")

install.packages("devtools")
library(devtools)
install_github("cchanialidis/combayes")
library(combayes)

install.packages("evd")
library(evd)

library(purrr)

library(MASS)

install.packages("MCMCglmm")
library(MCMCglmm)

install.packages("mvnfast")
library(mvnfast)
install.packages("truncnorm")
library(truncnorm)

##HPD interval function
HPDinterval.mcmc < function(obj, prob = 0.95, ...)
{
```

```
  obj <- as.matrix(obj)
  vals <- apply(obj, 2, sort)
  if (!is.matrix(vals)) stop("obj must have nsamp > 1")
  nsamp <- nrow(vals)
  npar <- ncol(vals)
  gap <- max(1, min(nsamp - 1, round(nsamp * prob)))
  init <- 1:(nsamp - gap)
  inds <- apply(vals[init + gap, ,drop=FALSE] - vals[init , ,drop=FALSE],
                2, which.min)
  ans <- cbind(vals[cbind(inds, 1:npar)],
               vals[cbind(inds + gap, 1:npar)])
  dimnames(ans) <- list(colnames(obj), c("lower", "upper"))
  attr(ans, "Probability") <- gap/nsamp
  ans
}

#=============================================
####simulation for y, delta and N
#=============================================
n = 1000  #sample size
beta.true = c(1, 0.2); gamma.true <- c(0.5, 0.3)

x_age <sample(c(1:100), 1000, replace = TRUE)

x1 <- scale(x_age)
x< cbind(rep(1, n), x1)

gamma.true <- c(0.5, 0.3)

theta <- exp(tcrossprod(x, t(beta.true)))
eta <- exp(tcrossprod( x, t(gamma.true)))

summary(eta)
```

```
N < rcmpois(mu=theta ,nu=eta ,n=1)

N <rpois(n, lambda = theta)

xi.true < 0.3
summary(N)
y < rep(NA, 1000)
delta < rep(NA, 1000)
c1 = sample(seq(1.1, 1.4, 0.001), 1000, replace = T)
rate < NULL

for (i in 1:n){

  if(N[i] ==0)
  {
    y[i] < c1[i];
    delta[i] < 0
  }else{
    g1 < rgev(N[i], loc=0, scale=1, shape=xi.true)
    z1 < exp(g1);  t1 < min(z1) ; y[i] < min(t1, c1[i])
    delta[i] < ifelse(t1 < c1[i], 1, 0)

  }
}
rate1 = length(which(delta == 0))/n
rate < c(rate, rate1)
rate #around 0.28


#=============================
###MCMC to sample parameters
#=============================
```

```
ns < 20000
nb < 1000
iter < ns+nb

p < dim(x)[2]

#parameter space
est.beta  < matrix(0,nrow=iter,ncol=p)
est.gamma < matrix(0,nrow=iter,ncol=p)
est.xi  < matrix(0,nrow=iter,ncol=1)
est.dev < matrix(0,nrow=iter,ncol=1)

#generate initial values
beta_current < est.beta[1, ]  <  as.vector(rmvn(1,mu=c(1, 1),sigma=diag(2)*
gamma_current < est.gamma[1, ] <  as.vector(rmvn(1,mu=c(0.5, 0.5),sigma=di
est.xi[1] < runif(1, min=1, max = 1)

beta.prior < c(1, 0.5)
gamma.prior < c(0.7, 0.7)

sig_beta < diag(p)*100
sig_gamma < diag(p)*100
mean_beta < rep(0, p)
mean_gamma < rep(0, p)

mu_current < exp(tcrossprod(x, t(beta_current)))
nu_current < exp(tcrossprod( x, t(gamma_current)))

N < rcmpois(mu=mu_current ,nu=nu_current,n=1)

#the accept ratio to move
accept_exchange_func < function(N,mu_new,nu_new,mu,nu, log_u){
  N_can < rcmpois(mu=mu_new,nu=nu_new,n=1)
```

```
  log_likeli_ratio <- (sum(dcmpois(N,mu=mu_new,nu=nu_new,log=TRUE,unnormalise
                           dcmpois(N,mu=mu,nu=nu,log=TRUE,unnormalised=TRUE)
                      +sum( dcmpois(N_can,mu=mu_new,nu=nu_new,log=TRUE,unno
                           +dcmpois(N_can,mu=mu,nu=nu,log=TRUE,unnormalised=
  list(accept=log_likeli_ratio>log_u,details=list())
}

#likelihood function for xi and N
log.lik <- function(y, xi, N, delta, mu, nu){
  post.N1<NULL
  for (i in 1:length(N)){
    if(N[i]==0){
      post.N1[i] <- 1
    }else{
      post.N1[i] <- ((pgev(log(y[i]), loc=0, scale=1, shape=xi, lower.tail =
    }
  }
  post.N2 <- ifelse(post.N1 < 0.0001, 0.0001, post.N1)
  post.N <- ifelse(post.N2 == 0.9999, 0.9999, post.N2)

  log_likeli_xi <- sum(log(post.N))+ log(dunif(xi, min=1,max=1))
  #log(dnorm(xi, mean=xi.true, sd=1))

  log_likeli_N <- sum(log(post.N)+
                      dcmpois(N, mu=mu,nu=nu,log=TRUE,unnormalised=TRUE)+
                      dcmpois(N, mu=exp(tcrossprod(x, t(beta.prior))),
                              nu=exp( tcrossprod(x, t(gamma.prior))), log=T
  loglike <- sum(log(post.N)+dcmpois(N, mu=mu,nu=nu,log=TRUE,unnormalised=TRU
  list(post.xi=log_likeli_xi,post.N = log_likeli_N , loglike = loglike, deta
}

#deviance
est.dev[1] <  2*log.lik(y, est.xi[1], N, delta, mu_current, nu_current)$logl
```

```
accept_beta  < 0
accept_gamma < 0
accept.xi < 0
accept.N < 0

pb < utils::txtProgressBar(min=1, max=iter, style=3)
for (l in 2:iter){
  #N.can < rpois(1000, lambda = 3)
  N.can < rcmpois(mu=exp(tcrossprod(x, t(beta.true))),nu=exp( tcrossprod(x,
  frac < log.lik(y=y, xi=est.xi[l 1], N=N.can, delta=delta, mu=exp(tcrosspro
                         nu=exp( tcrossprod(x, t(est.gamma[l 1, ])))))$post.N
                log.lik(y=y, xi=est.xi[l 1],N=N, delta=delta, mu=exp(tcrosspr
                           nu=exp( tcrossprod(x, t(est.gamma[l 1, ])))))$post.N

  if(log(runif(1)) < frac){N=N.can}else{N=N;accept.N = accept.N+1}

  for (i in 1:p){

    par_candidate < as.vector(rmvn(1,mu=c(beta_current[i],gamma_current[i]),
                              sigma=diag(p)*0.002))
    beta_candidate < beta_current
    beta_candidate[i] < as.vector(par_candidate[1])
    gamma_candidate < gamma_current
    gamma_candidate[i] < as.vector(par_candidate[2])

    log_u < (log(runif(1)) + dmvn(beta_current,mu=mean_beta,sigma=sig_beta,l
               dmvn(beta_candidate,mu=mean_beta,sigma=sig_beta,log=TRUE)
             + dmvn(gamma_current,mu=mean_gamma,sigma=sig_gamma,log=TRUE)
               dmvn(gamma_candidate,mu=mean_gamma,sigma=sig_gamma,log=TRUE)

    mu_candidate < exp(tcrossprod(x, t(beta_candidate)))
    nu_candidate <  exp( tcrossprod(x, t(gamma_candidate)))
```

```
  if(accept_exchange_func(N=N,mu_new=mu_candidate,
                          nu_new=nu_candidate,mu=mu_current,
                          nu=nu_current,log_u=log_u)$accept){
    beta_current < beta_candidate
    mu_current   < mu_candidate
    gamma_current < gamma_candidate
    nu_current   < nu_candidate

  }
}

##sample two parameters
beta_candidate < as.vector(c(rnorm(1, mean=beta_current[1], sd=0.002),
                             rnorm(1, mean=beta_current[2], sd=0.002)))
mu_candidate < exp(tcrossprod(x, t(beta_candidate)))
nu_candidate < nu_current

log_u <(log(runif(1))+dmvn(beta_current,mu=mean_beta,sigma=sig_beta,log=TR
        dmvn(beta_candidate,mu=mean_beta,sigma=sig_beta,log=TRUE))

if(accept_exchange_func(N=N,mu_new=mu_candidate,nu_new=nu_candidate,mu=mu_c
                        nu=nu_current,log_u=log_u)$accept){
  beta_current < beta_candidate
  mu_current   < mu_candidate
  accept_beta < accept_beta+1
}

##sample gamma
gamma_candidate < as.vector(c(rnorm(1, mean=gamma_current[1], sd=0.002),
                              rnorm(1, mean=gamma_current[2], sd=0.002)))
mu_candidate < mu_current
nu_candidate < exp( tcrossprod(x, t(gamma_candidate)))
```

```
log_u < (log(runif(1))+ dmvn(gamma_current ,mu=mean_gamma, sigma=sig_gamma, l
          dmvn(gamma_candidate ,mu=mean_gamma, sigma=sig_gamma, log=TRUE))

if(accept_exchange_func(N=N,mu_new=mu_candidate ,nu_new=nu_candidate ,
                        mu=mu_current ,nu=nu_current ,log_u=log_u)$accept){
  gamma_current < gamma_candidate
  nu_current    < nu_candidate

  accept_gamma < accept_gamma+1
}

est.beta[l,] < beta_current; est.gamma[l,] < gamma_current
##sample xi
#mu_update < exp(tcrossprod(x, t(est.beta[l,])))
#nu_update < exp(tcrossprod( x, t(est.gamma[l,])))
#N < rcmpois(mu=mu_update, nu=nu_update , n=1)

xi.can < rnorm(1, mean= est.xi[l 1], sd = 0.2) #runif(1, min = 1, max =
#0.5*runif(1, min = 1, max = 1)
#rnorm(1, mean= est.xi[l 1], sd = 1)
#a < pnorm(0, mean = est.xi[l 1], sd = 0.01)
#b < runif(1, 0, 1 a)
#xi.can < qnorm(a+b, mean = est.xi[l 1], sd = 0.01)
#xi.can < rgamma(1, shape = 2, scale = 0.3)
xi.frac < log.lik(y=y, xi=xi.can, N=N, delta=delta ,mu=exp(tcrossprod(x, t(
                  nu=exp( tcrossprod(x, t(est.gamma[l, ])))))$post.xi
  log.lik(y=y, xi=est.xi[l 1], N=N, delta=delta ,mu=exp(tcrossprod(x, t(est.
          nu=exp( tcrossprod(x, t(est.gamma[l, ])))))$post.xi
#frac < min(1, xi.frac)
if(log(runif(1)) < xi.frac){
  est.xi[l] =xi.can
  accept.xi =accept.xi +1
}else{est.xi[l] = est.xi[l 1]}
```

```
  est.dev[1] <- 2*log.lik(y, est.xi[l], N, delta,
                          mu=exp(tcrossprod(x, t(est.beta[l,]))), nu=exp( to

  utils::setTxtProgressBar(pb, l)
}
close(pb)


nb=1000
colMeans(est.beta[ c(1:nb), ])
colMeans(est.gamma[ c(1:nb), ])

mean(est.xi[ c(1:nb)])

acfs <- seq(nb, iter, 150)

windows()
par(mfrow=c(2,3))
plot(est.beta[nb:iter ,1], type="l", main="Trace plot of beta_0")
abline(h=beta.true[1], col="red")
plot(est.beta[nb:iter ,2], type="l", main="Trace plot of beta_1")
abline(h=beta.true[2], col="red")

plot(est.gamma[nb:iter,1], type="l", main="Trace plot of gamma_0")
abline(h=gamma.true[1], col="red")
plot(est.gamma[nb:iter,2], type="l", main="Trace plot of gamma_1")
abline(h=gamma.true[2], col="red")

plot(est.xi[nb:iter], type="l", main="Trace plot of xi")
abline(h=xi.true, col="red")

acf(est.beta[acfs,1], lag.max = 100, main="ACF for beta_0")
```

```
acf(est.beta[acfs,2], lag.max = 100, main="ACF for beta_1")
acf(est.gamma[acfs,1], lag.max = 100, main="ACF for gamma_0")
acf(est.gamma[acfs,2], lag.max = 100, main="ACF for gamma_1")
acf(est.xi[acfs], lag.max = 100, main="ACF for xi")

HPDbeta < HPDinterval.mcmc(est.beta[3000:iter, ], prob=0.95)
HPDgamma < HPDinterval.mcmc(est.gamma[3000:iter, ], prob=0.95)
HPDxi < HPDinterval.mcmc(est.xi[3000:iter], prob=0.95)

plot(density(est.beta[nb:iter ,1]), type="l", main="Density plot of beta_0")
abline(v=beta.true[1], col="red")
abline(v=HPDbeta[1, ], col = "blue")

plot(density(est.beta[nb:iter ,2]), type="l", main="Density plot of beta_1")
abline(v=beta.true[2], col="red")
abline(v=HPDbeta[2, ], col = "blue")

plot(density(est.gamma[nb:iter ,1]), type="l", main="Density plot of gamma_0"
abline(v=gamma.true[1], col="red")
abline(v=HPDgamma[1, ], col = "blue")

plot(density(est.gamma[nb:iter ,2]), type="l", main="Density plot of gamma_1"
abline(v=gamma.true[2], col="red")
abline(v=HPDgamma[2, ], col = "blue")

plot(density(est.xi[nb:iter]), type="l", main="Density plot of xi")
abline(v=xi.true, col="red")
abline(v=HPDxi, col = "blue")

est.beta.mean <colMeans(est.beta[acfs, ])
est.gamma.mean < colMeans(est.gamma[acfs, ])
est.xi.mean < mean(est.xi[acfs])
```

```
devtheta.mean <- 2*log.lik(y, est.xi.mean, N, delta,
                           mu=exp(tcrossprod(x, t(est.beta.mean))), nu=exp(

devhat <- mean(est.dev[acfs])

DIC.mean <- 2*devhat devtheta.mean

DIC.mean

save(est.beta, file="est_beta_comp.RDATA")
save(est.gamma, file="est_gamma_comp.RDATA")
save(est.xi, file="est_xi_comp.RDATA")
save(est.dev, file="est_dev_comp.RDATA")
effectiveSize(est.beta[acfs, ])
```