Just Another Gibbs Sampler: JAGS

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Agenda

Introduction

- JAGS is a program to perform inference for Bayesian Hierarchical models. It was proposed by Martyn Plummer in 2003 as an alternative to the BUGS software;
- The Gibbs Sampler function of JAGS is the ARMS, which is flexible for dealing with univariate target densities;
- The main advantages of JAGS, compared to BUGS, is the programming language and its interfaces with other software, such as R and Python;
- Also, JAGS does not require the specification of the conditional distributions.

Introduction

- Although JAGS is a really useful software to learn, there are few good examples online that explain both theory and code;
- The goals of this project were:
  - Learn how to use JAGS to perform Bayesian modelling and;
  - Write new codes;
- Basically, JAGS requires only the sampling distribution and the prior distribution for each parameter.

Introduction

```
model {
# Likelihood
    for (i in 1:n) {
        y[i] ~ dnorm(mu[i], precision)
        mu[i] <- alpha + beta * x
    }
# Prior distributions
    alpha ~ dnorm(0.0, 1.0E-3)
    beta ~ dnorm(0.0, 1.0E-3)
    aux <- dgamma(0.001, 0.001)
    precision ~ 1.0/ aux
}
```

R scripts

- Our main contributions were to add **mathematical details** and provide **real datasets examples** for **5** R scripts;
- The models involved were:
  - Random effect model;
  - Multivariate Normal model;
  - Beta regression;
  - Time series Beta Auto-Regressive model of order 1 and;
  - Mixture model.

R script - Beta regression

Let $\{Y_i\}_{i=1}^{n}$ be independent and identically distributed random variables and $X_i = (1, x_{i,1}, ..., x_{i,1})$ a line vector with all covariates of the individual i. We assume that Y_i is distributed according to a Beta distribution, denoted by $Y_i \sim \text{Beta}(\mu, \phi)$, which may be written in the form

$$f(Y_i|\mu, \phi) = \frac{\Gamma(\phi)\Gamma(\mu\phi)}{\Gamma((1-\mu)\phi)} Y_i^{\mu\phi-1}(1-Y_i)^{(1-\mu)/\phi},$$

where $0 < Y_i < 1$, $\mathbb{E}(Y_i) = \mu$, $\mathbb{V}(Y_i) = \mu(1-\mu)/(1+\phi)$, $0 < \mu < 1$ and $\phi > 0$. Thus, it is possible to model $g(\mu) = X_i\boldsymbol{\beta}$, where $g(\cdot)$ is the link function that maps the unit interval into $\mathbb{R}$.

This parametrization was proposed by Ferrari and Cribari-Neto (2004).

R script - Beta regression

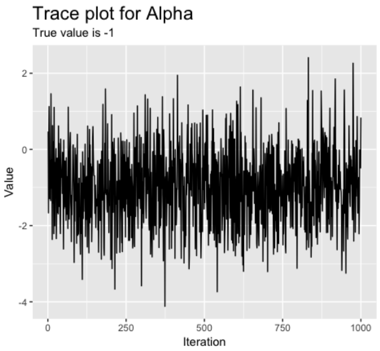
```
model
{
  # Likelihood
  for (t in 1:T) {
  y[t] ~ dbeta(a[t], b[t])
  a[t] <- mu[t] * phi
  b[t] <- (1 - mu[t]) * phi
  logit(mu[t]) <- alpha + beta * x[t]
  }
  # Priors
  alpha ~ dnorm(0, 10^-2)
  beta ~ dnorm(0, 10^-2)
  phi ~ dunif(0, 10)
}
```

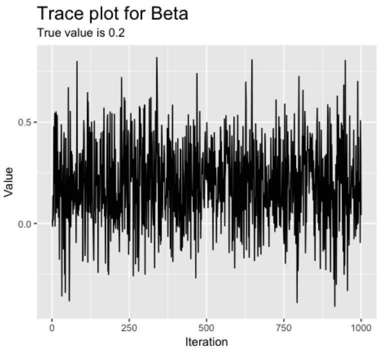
R script - Beta regression

```r
library(datasets)
head(attenu)

#Set up the data
acc=with(attenu,list(y=attenu$accel
                     ,T=nrow(attenu)))

# Set up jags model
jags_model=jags(acc,
                parameters.to.save = model_parameters,
                model.file = textConnection(model_code),
                n.chains=4,
                n.iter=1000,
                n.burnin=200,
                n.thin=2)
# Plot the jags output
print(jags_model)
```

R script - Beta regression

Simulation results for Beta regression, where three parameters were consider. The true values were set in $\alpha = -1$, $\beta = 0.2$ and $\phi = 5$.





Python scripts

- 3 Python scripts were created providing **mathematical details** and **simulated and real datasets examples**;
- The models involved were:
  - Bayesian linear regression;
  - Logistic regression;
  - Beta regression.

Python script - Logistic regression

The logistic regression model assumes that a sequence of independent and identically distributed random variables $\{Y_i\}_1^n$ has a Binomial distribution, denoted by $Y_i \sim \text{Binomial}(p_i)$, in the form of

$$f(Y_i|p_i) = \binom{n}{Y_i} p_i^{Y_i}(1-p_i)^{1-Y_i},$$

where $Y_i \in \{0,1\}$, $\log(\frac{p_i}{1-p_i}) = X_i\beta$, $X_i = (1, x_{i,1}, ..., x_{i,1})$ is the line vector of covariates associated to the individual i and β is the vector of unknown parameters.

Python script - Logistic regression

```
model
{
  # Likelihood
  for (t in 1:n) {
  y[t] ~ dbin(p[t], 1)
  logit(p[t]) <- beta_0 + beta_1 * x_1[t] +
                 beta_2 * x_2[t]
  }

  # Priors
  beta_0 ~ dnorm(0.0,0.01)
  beta_1 ~ dnorm(0.0,0.01)
  beta_2 ~ dnorm(0.0,0.01)
}
```

Python script - Logistic regression

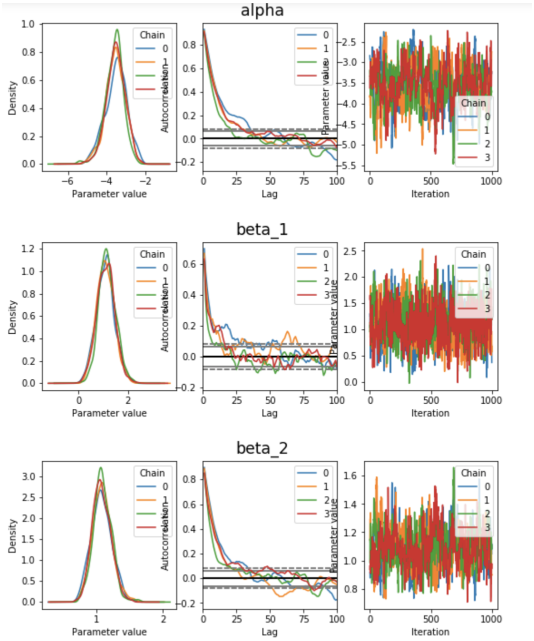
The data obtained for this section was adapted from data used to model logistic regression of moth mortalities when exposed to identical doses of a particular insecticide;

- Response variable: denotes the number of deaths observed in each batch;
- X_1 it is defined as the sexcode (i.e male or female);
- X_2 it is defined as the dose administered to each moth.

Python script - Logistic regression

```python
# Set up the data
model = pyjags.Model(code, data=dict(T = T, y = y,
                                     x_1 = x_1,
                                     x_2 = x_2, K = 1))

# Number of iterations to remove at start
model.sample(200, vars=[])

# Choose the parameters to watch and iterations:
samples = model.sample(1000, vars=['alpha', 'beta_1',
                                   'beta_2'])

print(jags_model)
```

Python script - Logistic regression



New models

Here we present 3 new models that we implemented both in R and Python;

The models are:

- Poisson regression model;
- Exponential survival model;
- Gaussian Mixture model.

Poisson regression model

A random variable Y is said to have a Poisson distribution with parameter λ if it takes integers $y = 0, 1, 2 \ldots$ with probability mass function

$$P(Y = y) = \frac{exp\{-\lambda\}\lambda^y}{y!},$$

where $\lambda > 0$. This mean can be modelled via a link function passed in a systematic component. For the Poisson regression case, the most widely used link function is the natural log, resulting in a equation that has the form

$$log(\hat{\lambda}) = \beta_0 + \beta_1\phi(x_1) + \cdots + \beta_n\phi(x_n).$$

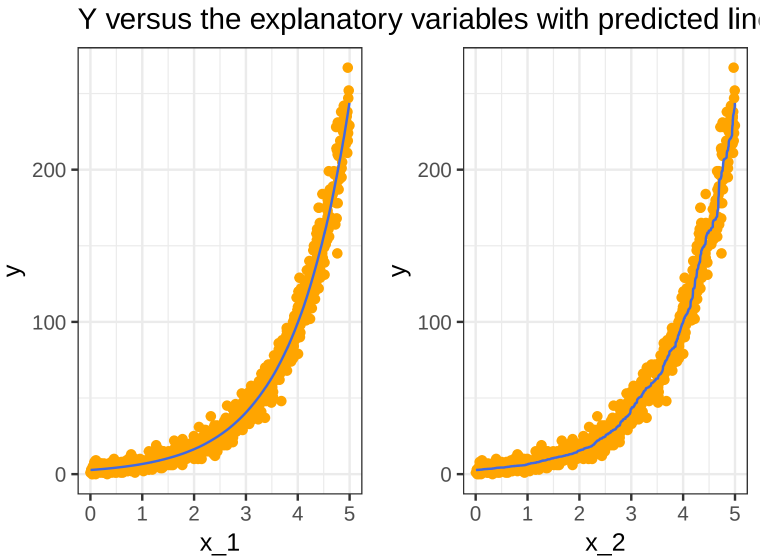
Poisson regression model

```
model
{
  # Likelihood
  for (i in 1:T) {
    y[i] ~ dpois(p[i])
    log(p[i]) <- alpha + beta_1 * x_1[i] +
                         beta_2 * x_2[i]
  }
  # Priors
  alpha ~ dnorm(0.0, 0.01)
  beta_1 ~ dnorm(0.0, 0.01)
  beta_2 ~ dnorm(0.0, 0.01)
}
'
```

Poisson regression model

```r
Simulate data -----------------------

# Some R code to simulate data from the Poisson model
T = 1000
set.seed(123)
x_1 = sort(runif(T, 0, 5))
x_2 = sort(runif(T, 0, 5))
alpha = 1
beta_1 = 1.2
beta_2 = -0.3
mu = alpha + beta_1 * x_1 + beta_2 * x_2
lambda = exp(mu)
y = rpois(n = T, lambda = lambda)
```

Poisson regression model



Exponential Survival models

In survival analysis, we are usually interested in modelling the time until a certain event occurs. Let T be a random variable representing the survival times of individuals in some population.

$$F(t) = P(T \leq t) = \int_0^t f(u)du$$

Survival data is also often censored. In this case, the likelihood is written as

$$L(t) = \prod_{i=1}^{n} [f(t_i)]^{\delta_i} [S(t_i)]^{1-\delta_i},$$

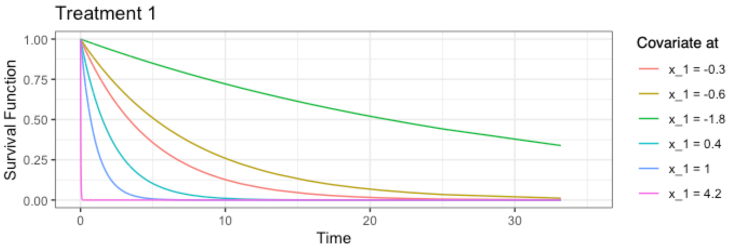
where δ_i is the indicator variable that takes 1 for the failures and 0 for censored observations. We consider for the failure time the Exponential distribution, given by

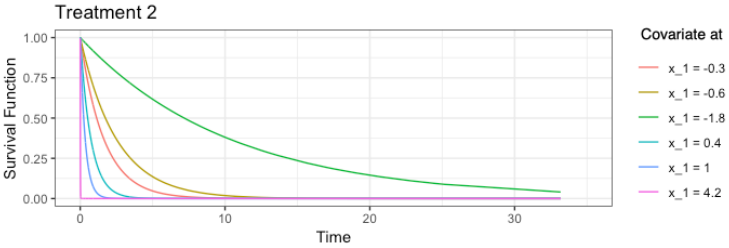
$$f(t) = \frac{1}{\alpha} exp\Big\{ -\frac{t}{\alpha} \Big\}, \quad \alpha > 0.$$

Exponential Survival models

```
model
{
  # Likelihood
  for (i in 1:T) {
    mu[i] = exp(beta_1 * x_1[i] + beta_2 * x_2[i])
    t[i] ~ dexp(mu[i] * lambda_0)
  }
  # Priors
  lambda_0 ~ dgamma(1, 1)
  beta_1 ~ dnorm(0.0, 0.01)
  beta_2 ~ dnorm(0.0, 0.01)
}
'
```

Exponential Survival models





Gaussian Mixture model

The mixture model is viewed hierarchically: the observations y are modeled conditionally on the vector z, having z itself a probabilistic specification.

$$p(y_i|\theta, \lambda) = \lambda_1 f(y_i|\theta_i) + \cdots + \lambda_H f(y_i|\theta_H),$$

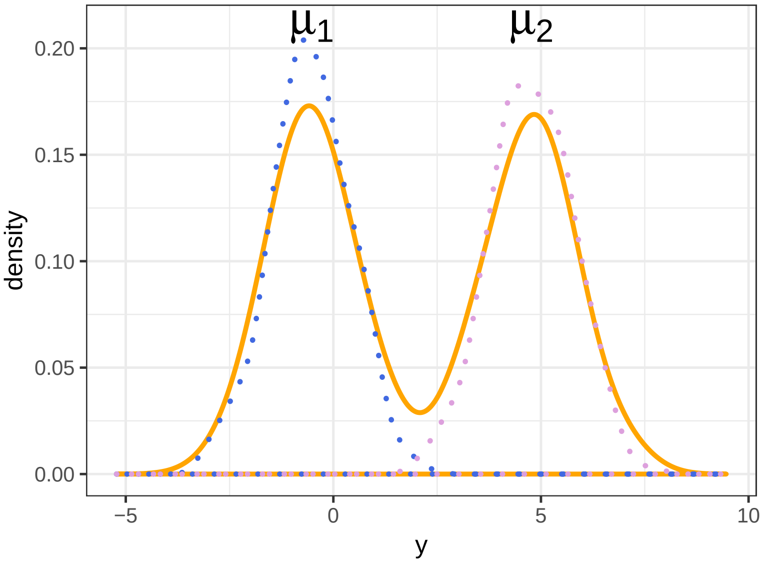
where the vector $\lambda = (\lambda_1, \ldots, \lambda_H)$ represents the proportions of the population taken as being drawn from each $f_h(y_i|\theta_h)$ distribution, for $h = 1, \ldots, H$, also that $\sum_{h=1}^{H} \lambda_h = 1$. Usually, the mixture components are assumed to be part of the same parametric family, such as the Gaussian, but with different parameter vectors. The unobserved variables is written as

$$z_{ih} = \begin{cases} 1, & \text{of the } i\text{th unite is drawn from the } h\text{th component} \\ 0, & \text{otherwise} \end{cases}$$

Gaussian Mixture model

```
model {
  # Likelihood:
  for(i in 1:N) {
    y[i] ~ dnorm(mu[i] , 1/sigma_inv)
    mu[i] <- mu_clust[clust[i]]
    clust[i] ~ dcat(lambda_clust[1:Nclust])
  }
  # Prior:
  sigma_inv ~ dgamma( 0.01 ,0.01)
  mu_clust[1] ~ dnorm(0, 10)
  mu_clust[2] ~ dnorm(5, 10)

  lambda_clust[1:Nclust] ~ ddirch(ones)
}
```

Gaussian Mixture model



Final remarks

- This project we learned how to use JAGS to perform Bayesian analysis;
- We had some challenges: i) JAGS was new for whole the group; ii) Difficulties to run the package **pyjags**;
- Our contributions were to provide mathematical details and codes for existing and new models. In the end, we produced:
  - 8 R scripts (3 new);
  - 3 Python scripts (all of them new);
- As future work other models can be implemented, such as other GLMs, Geostatistical models, more complex Survival models and other GLMMs with/without longitudinal structure.

Acknowledgments

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Science Foundation Ireland sfi For what's next

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