

dirichletprocess: An R Package for Fitting Complex Bayesian Nonparametric Models

Gordon J. Ross

School of Mathematics
University of Edinburgh
Gordon.Ross@ed.ac.uk

Dean Markwick

Department of Statistical Science
University College London
dean.markwick.15@ucl.ac.uk

Abstract

The **dirichletprocess** package implements a software framework for creating R objects that represent Dirichlet processes. Such processes are used in non-parametric statistics and can be applied to density estimation, cluster analysis and hierarchical prior specification. Our package provides the necessary tooling to achieve such tasks but with the flexibility to allow the user to move beyond the default implementations and extend the software using their own mixture kernels or alternative sampling algorithms. As such the user can perform their statistical task using our Dirichlet process objects as non-parametric building blocks.

Keywords: dirichlet process, bayesian inference, nonparametric statistics, R.

1. Introduction

Many applications of statistical theory involve parametric specifications of the probability distributions of interest – that observations are generated by Normal distributions, that group-level fixed effects can be modeled by Gamma distributions, and so on. However in some situations there will be insufficient prior information and data to justify parametric assumptions. In this case, non-parametric methods allow a more flexible and robust specification of distributions which allows their essential features to be ‘learned from the data’ rather than specified in advance.

While frequentist nonparametrics has a long history, Bayesian nonparametrics was a relatively dormant field until the mid 1990s. Although much of the theory of nonparametric priors had been worked out in previous decades ([Ferguson 1973](#)), computational issues prevented their widespread adoption. This changed with the development of posterior simulation methods such as Metropolis-Hastings ([Hastings 1970](#)) and the Gibbs sampler ([Geman and Geman 1984](#)) which were first applied to the task of nonparametric density estimation using Dirichlet process mixtures in a seminal paper by [Escobar and West \(1995\)](#). This kick started research into Bayesian non-parametrics, which has now become one of the most popular research areas in the statistics and machine learning literature. While there are now several widely used models within the field of Bayesian nonparametrics including the Gaussian process, Beta process and Polya trees, the Dirichlet process mixture model (DPMM) has been the most popular due to its wide applicability and elegant computational structure.

At the most basic level, the DPMM can be viewed as an infinite dimensional mixture model which represents an unknown density $f(y)$ as:

$$f(y) = \int k(y | \theta) p(\theta | G) d\theta, \quad G \sim \text{DP}(\alpha, G_0), \quad (1)$$

where $k(\cdot | \theta)$ denotes the mixture kernel, and the mixing distribution G is assigned a non-parametric Dirichlet process prior with a base measure G_0 and concentration parameter α . In the most widely used DPMM, the mixture kernel is taken to be Gaussian so that $\theta = (\mu, \sigma^2)$ and $k(y | \theta) = N(\mu, \sigma^2)$ with a conjugate Normal-Inverse-Gamma specification for G_0 . The infinite dimensional nature of such a model makes it capable of approximating any continuous distribution to an arbitrary degree of accuracy.

The use of DPMMs is not restricted to simply estimating the density of observed data. Instead, the DPMM can be used at any level in a hierarchical model where it is considered necessary to represent a density non-parametrically due to a lack of knowledge about its parametric form. For example, consider a case where there are J groups of observations, with observations in each group j following a Gaussian distribution with a group-specific mean μ_j and a common variance σ^2 . To share information across groups, the means μ_j are assumed to be exchangeable and given a prior $p(\mu_j)$. If $y_{i,j}$ denotes the i^{th} observation in group j , then the model is:

$$\begin{aligned} y_{i,j} &\sim N(y_{i,j} | \mu_j, \sigma^2), \\ \mu_j &\sim f(\mu_j | \theta). \end{aligned}$$

This model is an example of **partial pooling**, where the inference for each mean μ_j is based on the means of each of the other $J-1$ groups, allowing information to be shared across groups. As a biased estimation technique, it is related to methods such as the Lasso estimator, and usually results in more accurate estimation than estimating each group mean separately. However, completing the model specification requires choosing a form for the distribution of group means $f(\mu_j | \theta)$, which is made more difficult since the group means may not be observable with a high degree of accuracy, particularly when the number of observations is small. In this case, using a non-parametric DPMM specification for $f(\mu_j | \theta)$ would avoid the risks of potentially specifying an inappropriate parametric form.

Typically when working with DPMMs, the posterior distributions are analytically intractable, so inference instead usually involved computational simulation. A variety of simulation algorithms based around Gibbs sampling and Metropolis-Hastings have been developed to draw samples from DPMM posterior distributions, which can then be used for inference. As such, the widespread adoption of DPMMs has to some extent been held back by the level of statistical and programming literacy required to implement use them. The purpose of the **dirichletprocess** package is to provide a unified implementation of these simulation algorithms for a very wide class of DP mixture models which makes it easy to incorporate DPMMs into hierarchical models

The design philosophy of the **dirichletprocess** package is the polar opposite of the existing **DPpackage** R package which also provides an implementation of DPMMs. The purpose of **DPpackage** is to give a fast implementation of several common tasks where DPs are used, such as density estimation using Gaussian mixtures, and a variety of specific regression models. While this package is very useful in these situations, it cannot be used for any applications

of DPs which do not fall into one of the pre-specified tasks incorporated in the package, or use mixture kernels other than those provided.

In contrast, the purpose of the **dirichletprocess** package is not to automate a pre-specified range of tasks, but instead to represent DPMMs as objects in R so that they can be used as building blocks inside user-specified hierarchical models. The target audience is hence users who are working with (possibly hierarchical) models which uses a DPMM at some stage, and who hence require a DPMM implementation which can be used as a part of a more general model estimation scheme. As such, the number of tasks which can be achieved using the **dirichletprocess** is quite large, although the trade-off is that the functions in this package will be a lot slower than the highly efficient ones in **DPpackage** when it comes to the specific models which it implements.

Key features of the **dirichletprocess** package include:

- An implementation of DP mixture models for various types of mixture kernel including the Gaussian, Beta, Multivariate Normal and Weibull.
- Implementation of DP posterior sampling algorithms in both the conjugate and non-conjugate cases.
- A object-based interface which allows the user to work directly with DP objects in R so that they can be incorporated into hierarchical models.

The latter point should hopefully make the package especially flexible and useful.

For the user already well versed in the mathematics behind Dirichlet processes, Section 2 can be skipped as Section 3 shows how the package can be used in R without any knowledge of the underlying algorithms.

1.1. A Technical Note

The ultimate purpose of this package is to represent Dirichlet process mixture models as objects in R, so that they can be manipulated and used as building blocks. At the time of writing, R currently features three separate object systems (S3, S4 and RC) designed to allow object-orientated programming. This package uses S3. There are two motivations for this design choice which in my opinion outweigh any advantages that come from using any of other of the R object systems.

1. Speed. While R is an excellent programming language which makes carrying out high level statistical analysis easy, its slow speed remains a bottleneck particularly in tasks such as Gibbs Sampling and Monte Carlo Markov Chain (MCMC) sampling which are inherently sequential and cannot be vectorized. While the base R system is already slow, the S4 and Reference Class (RC) object systems suffer from further performance hits since they must search for the correct method for each function evaluation (Wickham 2014). S3 suffers a similar slowdown but to a lesser extent. The price we pay in speed we make up for in code comprehension and ease of development.
2. Ease-of-use. A key feature of this package is that users can themselves specify new DP mixture types if the package does not implement the precise specification they desire. The object systems S4 and RC are geared towards intermediary/advanced R

programmers and can scare novices. The design philosophy of this package required users to be able override the behaviour of DP objects and create new mixture types without needing to learn the intricacies of any particular object system. The chosen representation where DP objects are simple S3 structures does not require the user to learn anything about the more obscure intricacies of R objects, and instead they can focus purely on writing the R functions to implement the DP mathematics.

2. Background information

It is commonly required to learn the unknown probability distribution F which generated the observations y_1, \dots, y_n . In parametric Bayesian inference, F is assumed to belong to a known family of distributions (such as the Normal or Exponential) with an associated parameter vector θ of finite length and which much be estimated. This leads to the model:

$$\begin{aligned} y_i &\sim F(y_i \mid \theta), \\ \theta &\sim p(\theta \mid \gamma), \end{aligned}$$

where $p(\theta \mid \gamma)$ denotes the prior distribution and γ is a prior parameter. The task of inference then involves finding an appropriate value for θ , which is equivalent to choosing which member of the specified family of distributions gives the best fit to the data.

In practice however, it may not be clear how to choose an appropriate parametric family of distributions for F . If the wrong family is chosen, then conclusions based on the estimated model may be highly misleading. For example, if it is assumed that F has a Normal distribution with unknown parameters $\theta = (\mu, \sigma^2)$ when in fact the true F is heavy-tailed, this can lead to severe underestimation of the probability of extreme events occurring (Coles 2001).

This problem can be avoided by using a nonparametric prior specification which puts positive prior mass on the whole space of probability densities rather than on a subspace spanned by the finite-length parameter vector θ . This allows the estimated F to adapt to the data, rather than being restricted to a particular family of distributions such as the Normal or Exponential. The Dirichlet process (DP) is one of the most widely used Bayesian nonparametric priors, due to its flexibility and computational simplicity. Our aim in this section is not to give a full treatment of the Dirichlet processes, and a reader unfamiliar with them should refer to a standard reference such as Antoniak (1974). Instead we will only focus on describing the properties of the DP that are directly relevant to their implementation in the **dirichletprocess** package.

The basic DP model has the form:

$$\begin{aligned} y_i &\sim F, \\ F &\sim \text{DP}(\alpha, G_0), \end{aligned}$$

here G_0 is known as the **base measure** and encapsulates any prior knowledge that might be known about F . Specifically, it can be shown that $\mathbb{E}[F \mid G_0, \alpha] = G_0$. The concentration parameter α specifies the prior variance and controls the relative contribution that the prior and data make to the posterior, as the following result shows.

Key Property 1: The DP is a conjugate prior in the following sense: if $y_1, \dots, y_n \sim F$ and $F \sim \text{DP}(\alpha, G_0)$, then:

$$F \mid y_1, \dots, y_n \sim \text{DP} \left(\alpha + n, \frac{\alpha G_0 + \sum_{i=1}^n \delta_{y_i}}{\alpha + n} \right),$$

where δ_{y_i} denotes a point-mass at y_i . In other words, the posterior distribution of F is a weighted sum of the base measure G_0 and the empirical distribution of the data, with the weighting controlled by α .

The DP is a prior distribution over the space of probability distributions. As such, samples from a DP are probability distributions. The stick-breaking representation first introduced by [Sethuraman \(1994\)](#) shows what such samples look like:

Key Property 2: Suppose that $F \sim \text{DP}(\alpha, H)$ is a random probability distribution sampled from a DP prior. Then with probability 1, F can be written as:

$$F = \sum_{k=1}^{\infty} w_k \delta_{\phi_k}, \quad \phi_k \sim G_0$$

where

$$w_k = z_k \prod_{i=1}^{k-1} (1 - z_i), \quad z_i \sim \text{Beta}(1, \alpha).$$

In other words, random probability distributions can be sampled from a DP by first drawing a collection of samples z_i from a Beta distribution, transforming these to produce the weights $\{w_i\}$, and then drawing the associated atoms from G_0 . Note that in order for F to be a true from a DP, an infinite number of such weights and atoms must be drawn. However in practice, the above summation can be truncated with only a finite number N of draws, while still providing a very good approximation.

By combining Key Properties 1 and 2, we can sample a DP from its posterior distribution $F \mid y_1, \dots, y_n$ as follows:

Key Property 3: If $y_1, \dots, y_n \sim F$ and $F \sim \text{DP}(\alpha, G_0)$ then we can draw a sample probability distribution from the posterior $F \mid y_1, \dots, y_n$ as follows:

$$F = \sum_{k=1}^N w_k \delta_{\phi_k}, \quad \phi_k \sim \frac{\alpha G_0 + \sum_{i=1}^n \delta_{y_i}}{\alpha + n},$$

where

$$w_k = z_k \prod_{i=1}^{k-1} (1 - z_i), \quad z_i \sim \text{Beta}(1, \alpha + n).$$

2.1. Dirichlet process Mixtures

The stick breaking representation in Key Property 2 above shows that probability distributions sampled from a DP are discrete with probability 1. As such, the DP is not an appro-

priate prior for F when F is continuous. As such, it is usual to adopt the following mixture specification instead, which we will call the Dirichlet process mixture model (DPMM):

$$\begin{aligned} y_i &\sim k(y_i \mid \theta_i), \\ \theta_i &\sim F, \\ F &\sim \text{DP}(\alpha, G_0). \end{aligned} \tag{2}$$

In other words, F has a DP prior as before, but rather than the data y_i being drawn from F , it is instead the mixture parameters θ which are draws from F . These θ values then act as the parameters of a parametric kernel function $k(\cdot)$, which is usually continuous. The most commonly used example is the Gaussian mixture model where $\theta_i = (\mu_i, \sigma_i^2)$ so that $k(y_i \mid \theta_i) = N(y_i \mid \mu_i, \sigma_i^2)$.

The key point here is that since F is discrete, two independent draws θ_i, θ_j from F can have identical values with a non-zero probability. As such, the DPMM can be seen as sorting the data into clusters, corresponding to the mixture components. The above model can hence be written equivalently as the following mixture model, which is infinite dimensional can hence be viewed as a generalization of the finite mixture models commonly used in non-parametric statistics:

$$\begin{aligned} y_i &\sim G, \\ G &= \int k(y_i \mid \theta) F(\theta) d\theta, \\ F &\sim \text{DP}(\alpha, \theta). \end{aligned} \tag{3}$$

When the DPMM is used in practice, interest may focus on several different parameters of the posterior distribution. In some cases, the primary object of interest will be the n θ_i parameters from Equation 2 which are associated with the n observations. This is particularly the case in clustering applications, where the goal is to assign similar observations to the same cluster (i.e. to identical values of θ). However in other situations it will be the distribution F which is of primary interest, with the θ_i parameters integrated out. The **dirichletprocess** package returns posterior samples of all these quantities, so that the user can decide which are most relevant.

Posterior inference in the **dirichletprocess** package is based around the Chinese Restaurant Process sampler (Neal 2000). This is a Gibbs-style algorithm based on the DPMM representation in Equation 2 above, and draws samples of $\theta_1, \dots, \theta_n$ from their posterior with the distribution F integrated out.

Key Property 4: Let θ_{-i} denote the set of θ values with θ_i excluded, i.e. $\theta_{-i} = (\theta_1, \dots, \theta_{i-1}, \theta_{i+1}, \dots, \theta_n)$. Then the posterior distribution for θ_i conditional on the other model parameters is:

$$\begin{aligned} p(\theta_i \mid \theta_{-i}, y_{1:n}, \alpha, G_0) &= \sum_{j \neq i} q_{i,j} \delta(\theta_j) + r_i H_i, \\ q_{i,j} &= b k(y_i, \theta_j), \quad r_i = b \alpha \int k(y_i, \theta) dG_0(\theta) \end{aligned}$$

where b is set such that $\sum_{j \neq i} q_{i,j} + r_i = 1$ and H_i is the posterior distribution of θ based off of the prior base measure G_0 .

Based on this result, Gibbs sampling is used to repeatedly draw each value of θ_i in turn from its posterior distribution, with all other variables held constant. An important distinction needs to be made between the **conjugate** case where the G_0 base measure is the conjugate prior for θ with respect to the kernel $k(\cdot)$, and the **non-conjugate** case where there is not a closed form for the posterior distribution. In the conjugate case, the integral in Key Property 4 can be computed analytically and the resulting distribution is simply the predictive distribution. In this case, the θ_i values can be sampled directly from their true posterior distribution.

In the non-conjugate case things are slightly more difficult, and the integral in Key Property 4 cannot be evaluated. As such, numerical techniques must be used instead, which will typically result in slower computation. The **dirichletprocess** package handles the non-conjugate case by using “Algorithm 8” from (Neal 2000), which is one of the most widely used techniques for performing this sampling.

In both the conjugate and non-conjugate cases, the Gibbs sampling is conceptually similar, with the new values of θ_i being proposed sequentially from their respective posterior distributions. However in practice, this can result in poor mixing of the Gibbs sampler. One approach to speed up convergence is to add in additional update of the θ_i values at the end of the sampling. For each cluster and its associated data points we update the cluster parameter using the posterior distribution.

For simple density estimation and non-hierarchical predictive tasks, having a posterior sample of $\theta_{1:n}$ will be sufficient for inference, and the distribution F is not of any intrinsic interest. However when the DP is used as part of a hierarchical model such as in the regression and point process examples we discuss later, it is also necessary to have samples from the posterior distribution of F . These can be obtained using the following property:

Key Property 5: Given the model from Eq. (2) let $\theta_1, \dots, \theta_n$ be a sample from the posterior $p(\theta_{1:n} \mid y_{1:n}, \alpha, G_0)$ drawn using the CRP sampler. Then, $p(F \mid \theta_{1:n}, y_{1:n}, \alpha, G_0) = p(F \mid \theta_{1:n}, \alpha, G_0)$ is conditionally independent of $y_{1:n}$. As such, $\theta_{1:n}$ can be considered as an i.i.d sample from F , and so F can be sampled from its posterior distribution using Key Property 3 above:

$$F = \sum_{i=1}^N w_i \delta_{\theta_i}, \quad w_i \sim \text{Beta}(\alpha + n, 1), \quad \phi_i \sim G_0 + \sum_{i=1}^n \delta_{y_i}$$

2.2. Hyperparameter Inference

In the above discussion, we assumed that the concentration parameter α and base measure G_0 were constant. However in practice, better results can often be obtained if they are also learned from the data.

Inferring the Concentration Parameter

Following West (1992) we use a $\text{Gamma}(a, b)$ prior for α . The corresponding posterior distribution depends only on the number of unique values of $\theta_{1:n}$. More specifically, given the model in Equation (2) let $\theta_1, \dots, \theta_n$ denote a sample from the posterior $p(\theta_{1:n} \mid y_{1:n}, \alpha, G_0)$. Suppose that there are k unique values in this sample. Then a sample from $p(\alpha \mid \theta_{1:n}, y_{1:n}, G_0)$ can be obtained as follows:

- Simulate a random number z from a $\text{Beta}(\alpha + 1, n)$ distribution
- Define $\tilde{\pi}_1 = a + k + 1$ and $\tilde{\pi}_2 = n(b - \log(z))$, then define $\pi = \tilde{\pi}_1 / (\tilde{\pi}_1 + \tilde{\pi}_2) \in [0, 1]$
- With probability π , draw a value of α from a $\text{Gamma}(a + k, b - \log(z))$ distribution, and with probability $(1 - \pi)$ draw it from a $\text{Gamma}(a + k - 1, b - \log(z))$ distribution instead.

When fitting a DP the value of α can be easily inferred and sampled by default in the **dirichletprocess** package.

Inferring the Base Measure

The base measure G_0 can be parameterised with values γ which themselves are also random and from some distribution $p(\gamma)$. By placing a prior distribution on the parameters of the base measure this allows for the DP to adapt to the data and ensure that the fitting algorithms converge to the stationary distributions quicker

$$\begin{aligned}\phi_i &| \gamma \sim G_0, \\ \gamma &\sim p(\gamma), \\ \gamma &| \phi_i \sim H,\end{aligned}$$

where H is the posterior distribution. If we chose our $p(\gamma)$ such that it is conjugate to the posterior, we can directly sample from the posterior distribution, otherwise, a Metropolis Hastings step is include in the computation.

2.3. Implemented Mixture Models

As we will discuss, one of the strengths of the **dirichletprocess** package is that it allows users to specify DPMS using whichever choices of the kernel k and base measure G_0 they please. However for ease of use, we have implemented certain choices of k and G_0 directly in the package.

Gaussian Mixture Model

The Gaussian distribution is the most commonly used mixture model. In this case, $\theta = (\mu, \sigma^2)$ for the mean and variance. The kernel is:

$$k(y_i | \theta) = N(y_i | \mu, \sigma^2) = \frac{1}{\sqrt{2\pi\sigma^2}} \exp\left(\frac{-(y - \mu)^2}{2\sigma^2}\right). \quad (4)$$

The conjugate prior for θ is the Normal-Gamma distribution, with parameters $\gamma = (\mu_0, k_0, \alpha_0, \beta_0)$

$$G_0(\theta | \gamma) = N\left(\mu | \mu_0, \frac{\sigma^2}{k_0}\right) \text{Inv-Gamma}\left(\sigma^2 | \alpha_0, \beta_0\right). \quad (5)$$

the default setting of the parameters is $\mu_0 = 0, \sigma_0^2 = 1, \alpha_0 = 1, \beta_0 = 1$. We recommenced rescaling our data y such that its mean is 0 and standard deviation is 1. This leads to the default parameterisation of G_0 being uninformative.

Since this prior is conjugate, the predictive distribution for a new observation \hat{y} can be found analytically, and is a location/scale Student-t distribution:

$$p(\tilde{y} | \gamma) = \int k(\hat{y} | \theta) p(\theta | G_0) d\theta = \frac{1}{\tilde{\sigma}} \text{Student-t} \left(\frac{\tilde{y} - \tilde{\mu}}{\tilde{\sigma}} | \tilde{v} \right), \quad (6)$$

where $\tilde{v} = 2\alpha_0$, $\tilde{\mu} = \mu_0$, $\tilde{\sigma} = \sqrt{\frac{\beta_0(k_0+1)}{\alpha_0 k_0}}$.

Finally the posterior distribution is also a Normal Inverse Gamma distribution due to the conjugacy of the prior

$$\begin{aligned} p(\theta | y, \gamma) &= N(\mu | \mu_n, \frac{\sigma^2}{k_0 + n}) \text{Inv-Gamma}(\sigma^2 | \alpha_n, \beta_n), \\ \mu_n &= \frac{\kappa_0 \mu_0 + n \bar{y}}{k_0 + n}, \\ \alpha_n &= \alpha_0 + \frac{n}{2}, \\ \beta_n &= \beta_0 + \frac{1}{2} \sum_{i=1}^n (y_i - \bar{y})^2 + \frac{\kappa_0 n (\bar{y} - \mu_0)^2}{2(\kappa_0 + n)}. \end{aligned}$$

Multivariate Gaussian Mixture Model

The multivariate Gaussian mixture model is the most widely used non-parametric modeling approach for multivariate data. It is also heavily used in clustering applications (Maceachern and MÅijller 1998). For the unknown parameters we have $\theta = (\boldsymbol{\mu}, \Lambda)$ for d dimensional data $\boldsymbol{\mu}$ is a column vector of length d and Λ is a $d \times d$ dimensional matrix

$$k(y_i | \theta) = \frac{|\lambda|^{\frac{1}{2}}}{2\pi^{-\frac{d}{2}}} \exp \left(-\frac{1}{2} (y_i - \boldsymbol{\mu})^\top \Lambda (y_i - \boldsymbol{\mu}) \right). \quad (7)$$

For the prior choice we use a multivariate normal distribution for $\boldsymbol{\mu}$ and Wishart distribution for Λ

$$G_0(\boldsymbol{\mu}, \Lambda | \boldsymbol{\mu}_0, \kappa_0, \nu_0, T_0) = N(\boldsymbol{\mu} | \boldsymbol{\mu}_0, (\kappa_0 \Lambda)^{-1}) \text{Wi}_{\nu_0}(\Lambda | T_0), \quad (8)$$

where $\boldsymbol{\mu}_0$ is the mean vector of the prior, κ_0, ν_0 are single values and T is a matrix. The default prior parameters are set as $\boldsymbol{\mu} = \mathbf{0}, T = \mathbf{I}, \kappa_0 = 0, \nu_0 = 1$.

This prior choice is conjugate to the posterior, therefore the posterior distribution can be expressed analytically

$$\begin{aligned} p(\theta | y_i) &= N(\boldsymbol{\mu} | \boldsymbol{\mu}_n, (\kappa_n \Lambda_n)^{-1}) \text{Wi}(\Lambda | \nu_n, T_n), \\ \boldsymbol{\mu}_n &= \frac{\kappa_0 \boldsymbol{\mu}_0 + n \bar{\mathbf{y}}}{k + n}, \\ \kappa_n &= \kappa_0 + n, \\ \nu_n &= \nu_0 + n, \\ T_n &= T_0 + \sum_{i=1}^n (y_i - \bar{\mathbf{y}})(y_i - \bar{\mathbf{y}})^\top + \frac{\kappa_0 n}{\kappa_0 + n} (\boldsymbol{\mu}_0 - \bar{\mathbf{y}})(\boldsymbol{\mu}_0 - \bar{\mathbf{y}})^\top. \end{aligned}$$

Again, as this is a conjugate mixture we can write the predictive function for some new data \hat{y}

$$p(\hat{y} | \mathbf{y}) = \frac{1}{\pi^{\frac{nd}{2}}} \frac{\Gamma_d(\frac{\nu_n}{2})}{\Gamma_d(\frac{\nu_0}{2})} \frac{|T_0|^{\frac{\nu_0}{2}}}{|T_n|^{\frac{\nu_n}{2}}} \left(\frac{\kappa_0}{\kappa_n} \right)^{\frac{d}{2}}. \quad (9)$$

Beta Mixture Model

Dirichlet process mixtures of Beta distributions have been considered by [Kottas \(2006a\)](#) for the non-parametric estimation of continuous distributions that are defined on a bounded interval, $[0, T]$. For ease of interpretation, we follow their parameterisation of the Beta distribution in terms of its mean and standard deviation, In this case, $\theta = (\mu, \nu)$ with a known parameter T . The mixture kernel is:

$$k(y_i | \theta) = \text{Beta}(y_i | \mu, \nu, T) = \frac{y^{\frac{\mu\nu}{T}-1} (T-y)^{\nu(1-\frac{\mu}{T})-1}}{\text{B}(\frac{\mu\nu}{T}, \nu(1-\frac{\mu}{T})) T^{\nu-1}}. \quad (10)$$

There is no conjugate prior for the mixture kernel. Instead, the **dirichletprocess** package uses the (non-conjugate) prior from [Kottas \(2006a\)](#) where

$$G_0(\mu, \nu | T, \alpha_0, \beta_0) = U(\mu | 0, T) \text{Inv-Gamma}(\nu | \alpha_0, \beta_0). \quad (11)$$

To sample from the posterior distribution we use the Metropolis Hastings algorithm. With the parameters $\alpha_0 = 2, \beta_0 = 8$ as the default. However, there is also the ability to place a prior distribution on β_0 and update the prior parameter with each iteration. For this we use a default prior distribution of

$$\beta_0 \sim \text{Gamma}(a, b), \quad (12)$$

with $a = 1, b = 0.125$ by default.

Weibull Mixture Model

The Weibull distribution has strictly positive support it is mainly used for positive only data modeling. Furthermore, it is ubiquitously used in survival analysis. Mixture of Weibull distributions have been considered by [Kottas \(2006a\)](#) for a variety of survival applications. The parameters of the Weibull distribution are the shape a and scale b

$$k(y_i | \theta) = \text{Weibull}(y | a, b) = \frac{a}{b} y^{a-1} \exp\left(-\frac{y^a}{b}\right), \quad (13)$$

where $\theta = (a, b)$.

We use a non-conjugate Uniform Inverse Gamma distribution for the unknown parameters

$$G_0(a, b | \phi, \alpha, \beta) = U(a | 0, \phi) \text{Inv-Gamma}(b | \alpha, \beta), \quad (14)$$

by default ϕ, α and β do not have assigned values. Instead, we place priors on ϕ and β and update with each fitting procedure, α remains fixed. For ϕ we use a Pareto distribution as our prior as this is conjugate to the Uniform distribution.

$$\begin{aligned}
a_i &\sim U(0, \phi), \\
\phi &\sim \text{Pareto}(x_m, k), \\
\phi \mid a_i &\sim \text{Pareto}(\max\{a_i, x_m\}, k + n),
\end{aligned}$$

by default $x_m = 6, k = 2$ which is an infinite variance prior distribution.

As b is from a Inverse Gamma distribution with fixed shape α it has a conjugate prior which is the Gamma distribution.

$$\begin{aligned}
b_i &\sim \text{Inv-Gamma}(\alpha, \beta), \\
\beta &\sim \text{Gamma}(\alpha_0, \beta_0), \\
\beta \mid b &\sim \text{Gamma}\left(\alpha_0 + n\alpha, \beta_0 + \sum_{i=1}^n \frac{1}{b_i}\right),
\end{aligned}$$

with α fixed by the user and $\alpha_0 = 1, \beta_0 = 0.5$ by default. This prior on β with $\alpha_0 = 1$ is a conventional distribution with mean $\frac{1}{\beta_0}$ which allows for the user to decide how disperse the prior needs to be. As this is a non-conjugate model we must use a Metropolis Hastings step to sample from the posterior distribution.

3. Package Overview

The **dirichletprocess** package contains implementations of a variety of Dirichlet process mixture models for nonparametric Bayesian analysis. Unlike several other R packages, the emphasis is less on providing a set of functions which completely automate routine tasks (e.g. density estimation or linear regression) and more on providing an abstract data type representation of Dirichlet process objects which allow them to be used as building blocks within hierarchical models.

To illustrate how the package is meant to be used, and how it differs from other R packages, consider the task of density estimation. We wish to estimate the density of data generated from the Student-t distribution but with a mixture of Gaussian distributions.

```

R> y <- rt(200, 3) + 2 #generate sample data
R> dp <- DirichletProcessGaussian(y)
R> dp <- Fit(dp, 1000, progressBar = FALSE)

```

The function `DirichletProcessGaussian` is the creator function for a mixture model of one dimensional Gaussians. Which leads to the creation of the object `dp`. We use the function `Fit` to infer the cluster parameters by performing a Chinese Restaurant Sample for 1000 iterations. This returns the object `dp` updated with the MCMC samples of the cluster parameters, `dp$clusterParameterChains`, the weights associated with cluster parameters, `dp$weights` and the samples of the concentration parameter α , `dp$alphaChain`. Using the `Fit` function the details of the sampling are removed from the user and this provides an ‘out-of-the-box’ method to easily fit a Dirichlet process to data. Only a specification of the type of mixture model is needed.

The **dirichletprocess** package currently provides the following features:

- Implementations of Dirichlet process mixture models using Gaussian, Beta, and Weibull mixture kernels.
- Implementation of various schemes for re-sampling
- Access to samples from the Dirichlet process in both marginal form, as well as in (truncated) stick-breaking form
- A flexible way for the user to add new Dirichlet process models which are not currently implemented in the package, and yet still use the re-sampling functions from the package. To illustrate this, Section 4.2 shows how simple it is to create a Dirichlet process mixture model with Poisson and Gamma distribution kernels, even though this is not implemented in the package.
- An ability to plot the likelihood, posterior and credible intervals of a Dirichlet process using `plot`.

All of the above features will be demonstrated in the following examples.

Nonparametric Density Estimation

The most simple application of DPMs is to estimate the distribution of independent and identically distributed observations y_1, \dots, y_n , where:

$$y_i \sim F$$

$$F = \sum_{i=1}^n \pi_i k(y_i | \theta_i)$$

where k is some density function parameterised by θ_i and n is some unknown amount of clusters. The most widely used specification is the Gaussian mixture kernel with a Normal-Inverse Gamma base measure G_0 , which is described more fully in Section 3.

As an example we use the waiting times between eruptions of the Old Faithful volcano. This dataset is available within R and called `faithful`. We transform the waiting times to be zero mean and unit standard deviation and proceed to fit a DPMM with the default settings. We then model the waiting times as a mixture of normal distributions

$$y_i \sim F,$$

$$F = \sum_{i=1}^n \pi_i k(y_i | \theta_i) \quad \theta_i = \{\mu_i, \sigma_i^2\},$$

$$\theta_i \sim G$$

$$G \sim DP(\alpha, G_0),$$

where $k(y_i | \theta)$ is the standard normal probability density and G_0 is the base measure as in Section 2.3.

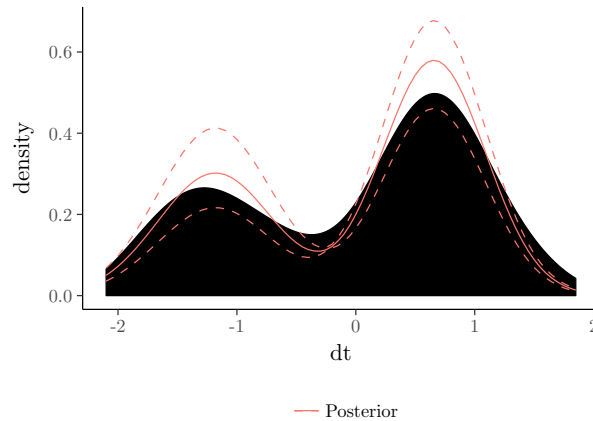


Figure 1: Old Faithful waiting times density estimation with a DPMM of Gaussians.

```
R> its <- 500
R> faithfulTransformed <- faithful$waiting - mean(faithful$waiting)
R> faithfulTransformed <- faithfulTransformed/sd(faithful$waiting)
R> dp <- DirichletProcessGaussian(faithfulTransformed)
R> dp <- Fit(dp, its)
R> plot(dp)
```

The resulting fit from the model is shown in Figure 1. The multi-modal nature has been successfully captured a property that a singular distribution would not find.

After running the `Fit` function, the DP object contains 3 MCMC parameter chains by default:

- A list containing the samples of the cluster parameters ϕ_i .
- A list containing the weights associated with each cluster parameter w_i .
- A numeric vector of the samples of α .

Using these quantities, the user can then perform the appropriate analysis.

For most users the `Fit` function is sufficient for practical purposes. However, for the more advanced users who wish to alter how they fit the `dirichletprocess` object there are a number of functions available to help.

By default, the `Fit` function updates the cluster allocation, the cluster parameters and then the α parameter. In some rare cases, updating α every iteration can delay convergence. Instead, the user can instead choose to update α every 10 iterations.

```
R> dp <- DirichletProcessGaussian(y)
R> samples <- list()
R> for(s in seq_len(1000)){
+   dp <- ClusterComponentUpdate(dp)
+   dp <- ClusterParameterUpdate(dp)
+ }
```

```

+   if(s %% 10 == 0) {
+       dp <- UpdateAlpha(dp)
+   }
+   samples[[s]] <- list()
+   samples[[s]]$phi <- dp$clusterParameters
+   samples[[s]]$weights <- dp$weights
+ }

```

By manually calling `ClusterComponentUpdate`, `ClusterParameterUpdate` and `UpdateAlpha` the user has control over the MCMC routine. The function `ClusterComponentUpdate` updates the allocation of all data points y_i to a cluster parameter θ_i using the Chinese Restaurant Process sampler. The function `ClusterParameterUpdate` updates each θ_i by drawing from the posterior distribution of the parameter using all the data associated to that cluster parameter. Finally, `UpdateAlpha` samples a new value of α from its posterior distribution using the method outlined in Section 2.2

The key point of the **dirichletprocess** package which the above code highlights is that a) the user controls when to re-sample the DP parameters, and b) the current sample is contained in the DP object and ready for inspection at any point in the code. This allows DP objects to be used as building blocks within hierarchical models.

3.1. Density Estimation on Bounded Intervals

In some situations it will be necessary to estimate densities on bounded intervals. For example, it might be known that the observations y_i are restricted to lie within the interval $[0, 1]$. In this case, a mixture of Gaussian distributions is inappropriate, since this will assign positive probability to the whole real line. An alternative specification is a mixture of Beta distributions, since the Beta distribution only has positive mass in $[0, 1]$. The full model is the same as in the previous example but replacing k with the Beta distribution.

```

R> y <- c(rbeta(150, 1, 3), rbeta(150, 7, 3)) #generate sample data
R> dp <- DirichletProcesBeta(y, 1)
R> dp <- Fit(dp, 1000)

```

Figure 2 shows the resulting likelihood and posterior draws of the fit to the simulated data.

Estimation of an Inhomogeneous Poisson Process Intensity Function

One practical application of Beta mixture models is the estimation of an inhomogeneous Poisson process intensity function. A Poisson process is a collection of points in space distributed with rate λ . In the inhomogeneous case, the intensity is dependent on time and as such the number of events in some window $[0, T]$ can be written as

$$N \sim \text{Poisson}(\lambda(t)). \quad (15)$$

In parametric estimation, a functional form of $\lambda(t)$ would be constructed i.e. $\alpha_0 + \alpha t$ and the parameters $\{\alpha_0, \alpha\}$ would be estimated. However, the accuracy of such a method would be dependent on correctly identifying the parametric form of $\lambda(t)$. With the non-parametric methods that a DPMM provides, such assumptions can be ignored and an intensity function

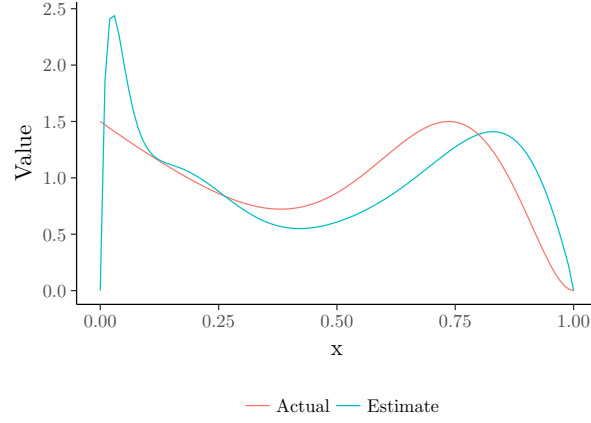


Figure 2: Estimated generating density using a Beta Dirichlet process mixture model.

can be built without the need to specify a parametric form. Firstly, we assume that $\lambda(t) = \lambda_0 h(t)$ where $\int_0^T h(t)dt = 1$, i.e. the intensity rate can be decomposed into an amplitude λ_0 controlling the number of events and a density $h(t)$ controlling the distribution of the events over $[0, T]$. To infer the value of λ_0 a conjugate Gamma prior can be used and thus the posterior distribution can be directly sampled.

The model for estimating (t) can be written as

$$\begin{aligned}\lambda(t) &= \sum_{i=1}^N w_i k(t \mid \theta_i), \\ \theta_i &\sim G, \\ G &\sim \text{DP}(\alpha, G_0),\end{aligned}$$

where $k(t \mid \theta)$ and G_0 are the default implementation of the Beta mixture model shown in Section 2.3.

In this toy example we simulate a Poisson process with $\lambda(t) = \sin^2\left(\frac{t}{50}\right)$.

```
R> y <- cumsum(runif(1000))
R> pdf <- function(x) sin(x/50)^2
R> accept_prob <- pdf(y)
R> pts <- sample(y, 500, prob=accept_prob)
```

We then estimate this intensity function using a mixture of Beta distributions that span the full length of the time elapsed.

```
R> dpBeta <- DirichletProcessBeta(pts, max(pts)*1.01)
R> dpBeta <- Fit(dpBeta, 1000)
```

From Figure 3 we can see that the true intensity function has been recovered using the mixture of Beta distributions.

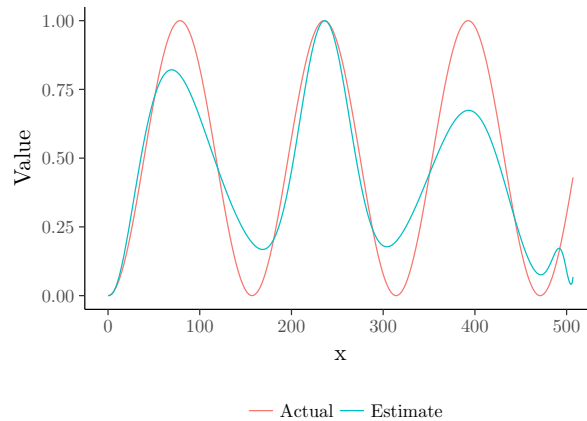


Figure 3: Estimated intensity function using a DPMM of generalised Beta distribution

3.2. Cluster Analysis

For any Dirichlet model, each data point y_i is assigned a cluster parameter θ_i . The collection of unique values of cluster parameters θ_i^* allows for a natural way of grouping the data and hence the Dirichlet process is an effective way of performing cluster analysis. For multidimensional data it is most common to use a mixture of multivariate normal distributions to cluster the observations into appropriate groups. In the **dirichletprocess** package, the clustering labels is available at each fitting iteration and available to the user as `dp$clusterLabels`.

To demonstrate this we simulate some test data from two multivariate Gaussian distributions and fit a Dirichlet mixture with default parameterisation. The full model can be written as

$$\begin{aligned} y_i &\sim N(\boldsymbol{\mu}_i, \Sigma_i), \\ \theta_i &= \{\boldsymbol{\mu}_i, \Sigma_i\}, \\ \theta_i &\sim G, \\ G &\sim \text{DP}(\alpha, G_0), \end{aligned}$$

where the prior parameters of G_0 take on their default value as shown in Section 2.3. We will be using the cluster labels to indicate which group each data point belongs to.

We simulate data from two different Gaussian distributions.

```
R> y <- rmvnorm(30, c(7, 10), diag(2) - 0.1)
R> y <- rbind(y, rmvnorm(30, c(1, 2), diag(2) + 0.1))
```

We form the `dirichletprocess` object and extract the initial cluster labels to a separate dataframe for plotting purposes.

```
R> dp <- DirichletProcessMvnormal(y)
R> initialDF <- data.frame(x=y[, 1], y=y[, 2],
+                          label = dp$clusterLabels,
+                          fit = "Initial")
R> dp <- Fit(dpobj, 250)
```

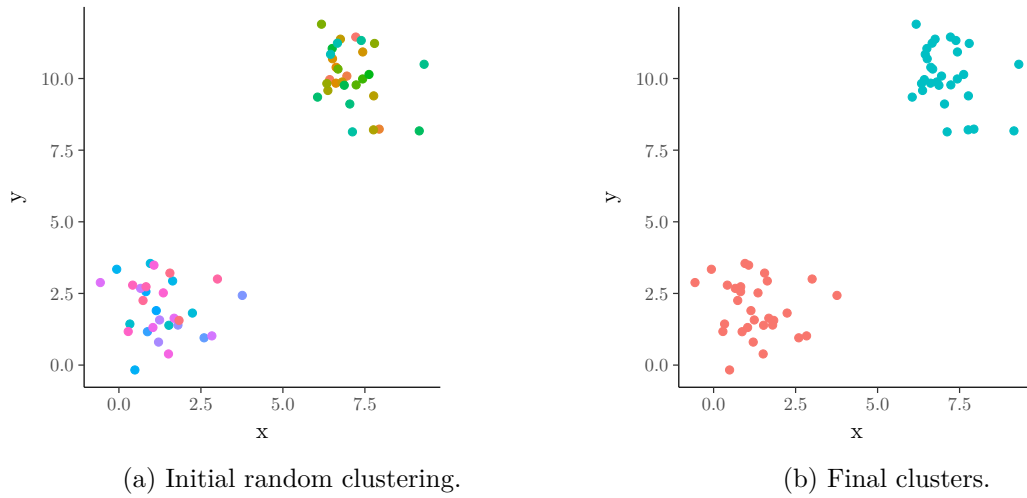



Figure 4: The starting clusters compared to the final clusters showing that the two groups have been identified.

```
R> finalDF <- data.frame(x=y[, 1], y=y[, 2],
+                        label = dp$clusterLabels,
+                        fit = "Final")
```

When analysing the results of the fit we are interested in the final Gibbs sample of the cluster labels and how it has changed from the initial labelling. Using the cluster label to assign a colour to each datapoint we can easily see the distinct clusters that form.

Figure 4 shows how the data points have successfully found their true clusters. After initially being assigned random cluster allocations, colourised in Figure 4a the data is separated into the correct clusters as shown in Figure 4b. Whilst this example only shows two dimensions, the code is generalised to work with as many dimensions as necessary.

3.3. Modifying the Observations

In some applications of Dirichlet processes the data being used can change from iteration to iteration. For example for a full data set $\mathbf{y} = y_1, \dots, y_n$ you may observe at different intervals different samples of this full data set y^* . When fitting a DP object we provide the appropriate function `ChangeObservations` to change the observations between iterations.

This function takes the new data, predicts what clusters from the previous fitting the new data belongs to and updates the clustering labels and parameters accordingly. A modified object with the new data associated to clusters and the function `Fit` is ready to be used to sample the cluster parameters and weights again.

Example: Priors in Hierarchical Models

One application of observations changing with each iteration is using a Dirichlet process as a prior for a parameter in a hierarchical model. An example of hierarchical modelling comes from Gelman, Carlin, Stern, and Rubin (2014) involving tumour risk in rats for 71 experiments. We extend this application by including a Dirichlet process as the prior choice.

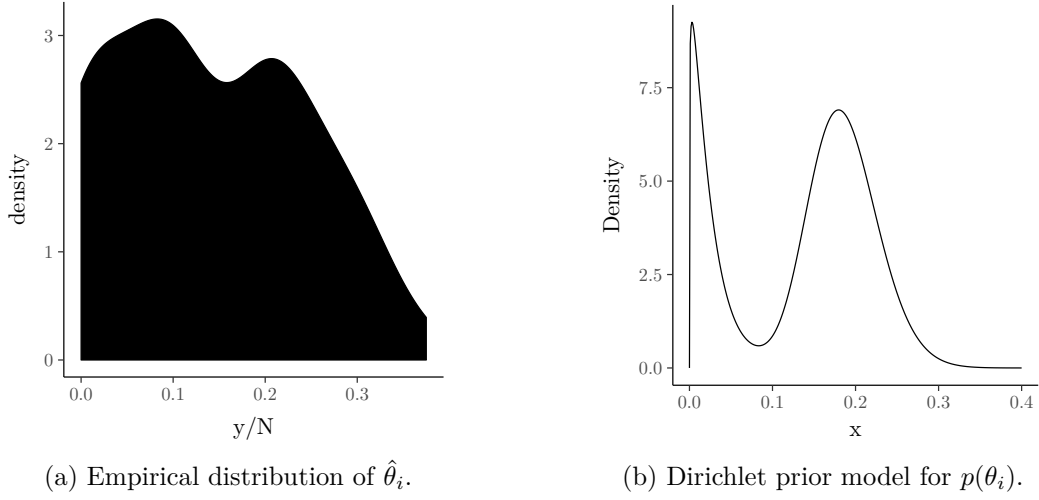


Figure 5: Rat tumour risk empirical density and fitted prior distribution.

A naive approach would model each experiment as a Binomial draw with unknown θ_i and known N_i . A Beta distribution is the conjugate prior for the Binomial distribution and would be used as the prior on θ :

$$\begin{aligned} y_i \mid \theta_i, N_i &\sim \text{Binomial}(N_i, \theta_i), \\ \theta_i &\sim \text{Beta}(\alpha, \beta). \end{aligned}$$

However, Figure 5a shows the empirical distribution of $\hat{\theta}_i = \frac{y_i}{N_i}$. This distribution shows hints of bimodality, something that a single Beta distribution cannot capture and hence the prior choice of $p(\theta_i)$ is dubious. An alternative procedure is to instead use a nonparametric prior on the θ'_i s. Since these parameters are constrained to lie between 0 and 1, one choice might be a Dirichlet process mixture of Beta distributions. This leads to the following model

$$\begin{aligned} y_i \mid \theta_i, N_i &\sim \text{Binomial}(N_i, \theta_i), \\ \theta_i &\sim \text{Beta}(\alpha_i, \beta_j), \\ \alpha_i, \beta_i &\sim F, \\ F &\sim DP(\alpha, G_0), \end{aligned}$$

where α and G_0 follow the default implementations of the **dirichletprocess** package. We then implement this model using the **dirichletprocess** functions as follows:

```

R> numSamples = 200
R> thetaDirichlet <- matrix(nrow=numSamples, ncol=nrow(rats))
R> dpobj <- DirichletProcessBeta(rats$y/rats$N,
+   maxY=1, g0Priors = c(2, 150),
+   mhStep=c(0.25, 0.25), hyperPriorParameters = c(1, 1/150))
R> dpobj <- Fit(dpobj, 10)
R> clusters <- dpobj$clusterParameters
R> a <- clusters[[1]] * clusters[[2]]
R> b <- (1 - clusters[[1]]) * clusters[[2]]
R> for(i in seq_len(numSamples)){
+
+   posteriorA <- a[dpobj$clusterLabels] + rats$y
+   posteriorB <- b[dpobj$clusterLabels] + rats$N - rats$y
+   thetaDirichlet[i, ] <- rbeta(nrow(rats), posteriorA, posteriorB)
+
+   dpobj <- ChangeObservations(dpobj, theta_dir[i, ])
+   dpobj <- Fit(dpobj, 5)
+   clusters <- dpobj$clusterParameters
+
+   a <- clusters[[1]] * clusters[[2]]
+   b <- (1 - clusters[[1]]) * clusters[[2]]
+ }

```

Plotting the resulting estimation in Figure 5b reveals a more suitable prior. This confirms what we saw from the empirical distribution that the data is bi-modal.

3.4. Hierarchical Dirichlet process

A hierarchical Dirichlet process can be used for grouped data. Each dataset is modelled using Dirichlet process but where the base measure itself is also a Dirichlet process. Mathematically this can be expressed as

$$\begin{aligned}
 x_{ij} &\sim F(\theta_{ij}), \\
 \theta_{ij} &\sim G_j, \\
 G_j &\sim \text{DP}(\alpha, G_0), \\
 G_0 &\sim \text{DP}(\gamma, H),
 \end{aligned}$$

for each dataset $j = 1, \dots, n$ with data x_{1j}, \dots, x_{Nj} there is a separate Dirichlet process generating the required parameters θ_{ij} . Using the stick breaking construction, we can express

G_0 as an infinite sum (Key Property 2), the same procedure can be applied to the G_j measures

$$\begin{aligned} G_j &= \sum_{i=1}^{\infty} \pi_{jk} \delta_{\phi_k}, \quad \phi_k \sim H, \\ \pi'_{jk} &= \text{Beta} \left(\alpha \beta_k, \alpha \left(1 - \sum_{l=1}^k \beta_l \right) \right), \quad \pi_{jk} = \pi'_{jk} \prod_{l=1}^{k-1} (1 - \pi'_{jl}), \\ \beta'_k &\sim \text{Beta}(1, \gamma), \quad \beta_k = \beta'_k \prod_{l=1}^{k-1} (1 - \beta'_l), \end{aligned}$$

we call H the global distribution and each G_j the local distribution for further details see [Teh, Jordan, Beal, and Blei \(2005\)](#).

To fit a hierarchical Dirichlet process, Algorithm 8 from Neal is used as detailed in Section 2.1. Each datapoint x_{ij} is further assigned as label k_{ij} which indicates which global parameter ϕ_k it is assigned. Then for each global parameter, we can update its value by drawing from its posterior distribution, using all the data available across the data sets

$$\phi_k \mid x_{ij} = h(\phi_k) \prod_{k_{ij}=k} f(x_{ij} \mid \phi_k), \quad (16)$$

where h is the density of the global distribution H and f is the density of the mixing distribution F . From these updated parameters a new G_j can be drawn using for each j using Key Property 5.

For a hierarchical DP model each individual concentration parameter α can be inferred using the above algorithm without modification for each individual dataset. For the top level concentration parameter γ , the number of unique cluster parameters across all the individual G_j 's is used for n in the sampling of γ .

In this example we create two synthetic data sets and fit a Hierarchical Dirichlet process to demonstrate the use of such a tool. In this case we are fitting a Beta Dirichlet mixture model and therefore simulate from a Beta distribution

$$\begin{aligned} y_1 &\sim \text{Beta}(0.25, 5) + \text{Beta}(0.75, 6), \\ y_2 &\sim \text{Beta}(0.25, 5) + \text{Beta}(0.4, 10), \end{aligned}$$

as we can see, there is a common group of parameters between the two datasets. First we simulate the two data sets.

```
R> mu <- c(0.25, 0.75, 0.4)
R> tau <- c(5, 6, 10)
R> a <- mu * tau
R> b <- (1 - mu) * tau
R> y1 <- c(rbeta(100, a[1], b[1]), rbeta(100, a[2], b[2]))
R> y2 <- c(rbeta(100, a[1], b[1]), rbeta(100, a[3], b[3]))
```

We then use the appropriate constructor functions to build a hierarchical Dirichlet object with uninformative priors for the global base distribution and fit for 5000 iterations.

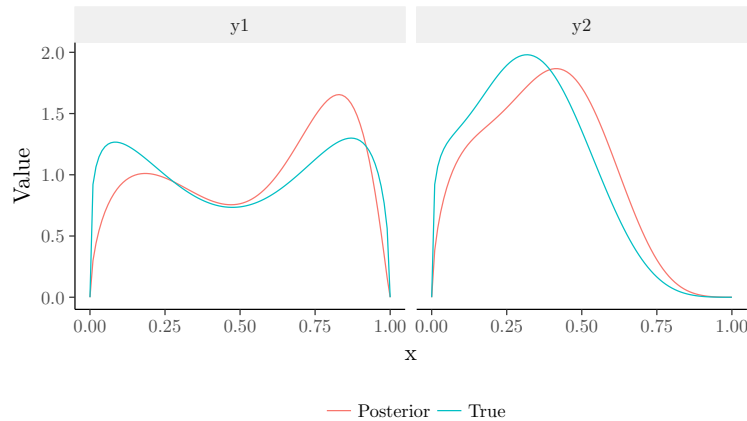


Figure 6: Hierarchical Beta Dirichlet process mixture results.

```
R> dpobjlist <- DirichletProcessHierarchicalBeta(list(y1, y2), maxY=1,
+ hyperPriorParameters = c(1, 0.01), mhStepSize = c(0.1, 0.1),
+ gammaPriors = c(2, 4), alphaPriors = c(2, 4))
R> dpobjlist <- Fit(dpobjlist, 5000, TRUE)
```

The resulting G_j 's are plotted in Figure 6. When we look at the final sample of the cluster parameters we find that they share a common cluster as expected.

4. Advanced Features

The material in this section can largely be skipped as long as the user is getting good results from the **dirichletprocess** package using the default specifications. However inevitably problems will arise due to (e.g.) the default hyper parameters being inadequate for a particular data set, or the sampler seeming not to converge due to bad initial default parameter values. In this case, the user will need to know what is going on under the hood so that they can change the default settings to better suited values, or otherwise modify the internal sampling procedure. We have done our best to ensure that this will usually only require changing a small number of the parameters which control the sampling behaviour, but understanding what needs to be changed (and why) requires some understanding of how the objects are constructed.

4.1. Structure of a DP Object: The Gory Details

The DP is an S3 object. All DPs have the following fields and available which are defined upon construction and do not ever change. When using the DP objects implemented in this package, these will be set by the constructor functions and so can largely be ignored for the default mixture models.

A DP object is defined by its kernel mixing distribution. Each mixing distribution has the following functions and fields associated with its class

- `Likelihood(...)`: a function which specifies the density of the mixture kernel $k(y | \theta)$.

- **PriorDraw(...)**: a function which returns a random sample of size n from the DP base measure G_0 .
- **g0Priors**: a list of parameters for the base measure G_0 .

For a conjugate mixing distribution the posterior distribution of θ is tractable and can be sampled from directly and the marginal distribution of the data can also be evaluated. Therefore two functions are needed to complete the specification of a conjugate mixture model:

- **PosteriorDraw(...)**: a function that returns a sample of size n given data y from the posterior distribution of θ , i.e. a sample from the distribution of $p(\theta | y)$.
- **Predictive(...)**: a function that returns the value of the marginal distribution of the data $f(y) = \int k(y, \theta) dG()$. The Chinese Restaurant Sampling can now be carried out using ‘Algorithm 4’ from [Neal \(2000\)](#).

For a non-conjugate mixing distribution we can no longer directly sample from the posterior distribution $p(\theta | x)$ or calculate the marginal distribution of the data. Instead the Metropolis-Hastings algorithm is used to sample from the distribution $p(\theta | x)$ [Hastings \(1970\)](#). The Metropolis-Hastings algorithm works by generating a candidate parameter θ^{i+1} and accepting this candidate value as a sample from the posterior with probability proportional to $\frac{k(y|\theta^{i+1})p(\theta^{i+1})}{k(y|\theta^i)p(\theta^i)}$. Typically, the candidate parameter is distributed as $\theta_{i+1} \sim N(\theta_i, h^2)$. From this, the non-conjugate mixture model requires 2 additional functions an extra parameter to be defined.

- **PriorDensity(...)**: a function which evaluates $p(\theta)$ which is the DP base measure G_0 for a given θ .
- **mhParameterProposal(...)**: a function that returns a candidate parameter to be evaluated for the Metropolis-Hastings algorithm.
- **mhStepSize**: h , the size of the step to make when proposing a new parameter for the Metropolis Hastings algorithm.

Now Chinese Restaurant Sampling can be performed using ‘Algorithm 8’ ([Neal 2000](#)).

Once the appropriate mixing distribution is defined we can create a **dirichletprocess** object which contains the data, the mixing distribution object and the parameter α . Then the rest of **dirichletprocess** class functions are available.

By using the default constructor functions **DirichletProcessBeta/Gaussian/Mvnormal/Weibull** the base measure prior parameters are chosen to be non-informative, see Section for [2.3](#) for the specific values of the prior parameters.

4.2. Creating New Dirichlet process Mixture Types

The **dirichletprocess** package currently implements Dirichlet process mixture models using Gaussian, Beta and Weibull kernels. While these kernels should be appropriate for most applications, there will inevitably be times when a user wants to fit a DP model for a kernel which has not been implemented, or otherwise wants to do something complex with a DP which goes beyond the scope of this package. To anticipate this, we have tried to make it

easy to construct your own mixture models and reuse the implemented algorithms for fitting a Dirichlet process.

The functions in the package are designed to work on S3 R objects, where each object represents a type of Dirichlet process mixture (e.g Gaussian or Beta). In order to create new types of Dirichlet process mixtures, the user must create a new S3 object type which encapsulates his model and ensure that its specifications correspond to those of the package. If this is done, then all the package functions for re-sampling/prediction/etc should continue work on the new DP type. This means that the package can hopefully be used for DP applications that we did not consider when writing it, while saving the user from having to write their own functions for re-sampling and fitting.

To illustrate how this works, this section will work through an extended example of how to create a new S3 type which represents a DP mixture model not implemented in the **dirichletprocess** package. We will explain how the S3 objects are constructed in detail so that the user will be able to create their own.

Conjugate Mixture

Suppose we have a particular scenario that requires a Dirichlet process mixture of Poisson distributions. The Poisson distribution has a conjugate prior of the Gamma distribution therefore it is trivial for a user to write their own mixing distribution.

Firstly, we start with the likelihood of the Poisson distribution

$$k(x | \theta) = \frac{\theta^x \exp(-\theta)}{x!},$$

as there is only one free parameter for the Poisson distribution the parameter list θ if of length 1.

```
Likelihood.poisson <- function(mdobj, x, theta){
  return(as.numeric(dpois(x, theta[[1]])))
}
```

We then write the random prior draw function which draws a value of θ from the base measure G_0 . The conjugate prior to the Poisson distribution is the Gamma distribution

$$G_0 \sim \text{Gamma}(\alpha_0, \beta_0).$$

```
PriorDraw.poisson <- function(mdobj, n){
  draws <- rgamma(n, mdobj$priorParameters[1], mdobj$priorParameters[2])
  theta <- list(array(draws, dim=c(1,1,n)))
  return(theta)
}
```

The prior parameters α_0, β_0 are stored in the mixing distribution object `mdobj`.

We then write the `PosteriorDraw` function to sample from the posterior distribution of θ . Again, as the base measure G_0 is conjugate this is a direct sample from the posterior distribution

$$\theta | x \sim \text{Gamma}(\alpha_0 + \sum_{i=1}^n x_i, \beta_0 + n),$$

using the inbuilt `rgamma` function this is trivial.

```

PosteriorDraw.poisson <- function(mdobj, x, n=1){
  priorParameters <- mdobj$priorParameters
  lambda <- rgamma(n, priorParameters[1] + sum(x), priorParameters[2] + nrow(x))
  return(list(array(lambda, dim=c(1,1,n))))
}

```

Finally the marginal distribution of the data $f(y)$ can be evaluated as it is a conjugate mixture model and translated into the appropriate R function:

```

Predictive.poisson <- function(mdobj, x){
  priorParameters <- mdobj$priorParameters
  pred <- numeric(length(x))
  for(i in seq_along(x)){
    alphaPost <- priorParameters[1] + x[i]
    betaPost <- priorParameters[2] + 1
    pred[i] <- (priorParameters[2] ^ priorParameters[1]) / gamma(priorParameters[1])
    pred[i] <- pred[i] * gamma(alphaPost) / (betaPost^alphaPost)
    pred[i] <- pred[i] * (1 / prod(factorial(x[i])))
  }
  return(pred)
}

```

With these functions written for the Poisson mixture model we now need to use the `MixingDistribution` constructor function to create a new object that can be used by the Dirichlet process constructor function, `DirichletProcessCreate`.

```
poisMd <- MixingDistribution("poisson", priorParameters = c(1, 1), "conjugate")
```

This is now ready to be used in a `dirichletprocess` object. To demonstrate we simulate some test data and fit a Dirichlet process with our new mixing distribution.

```

R> y <- c(rpois(150, 3), rpois(150, 10))
R> dp <- DirichletProcessCreate(y, poisMd)
R> dp <- Initialise(dp)
R> dp <- Fit(dp, 1000)

```

As Figure 7 shows, the true generating function has been recovered. This shows how easy it is for the user to create their own mixture models using the `dirichletprocess` package.

Nonconjugate Mixture

Suppose that a particular application requires a Dirichlet process mixture of Gamma distributions. As the Gamma distribution does not have a conjugate prior distribution additional steps must be taken when creating the necessary functions.

Firstly we must write the likelihood function, as the Gamma distribution has two parameters α, β the list θ will also have two components. The density of the Gamma distribution can be written as

$$k(y \mid \alpha, \beta) = \frac{\beta^\alpha}{\Gamma(\alpha)} y^{\alpha-1} e^{-\beta y},$$

which can be easily translated using `dgamma` in R.

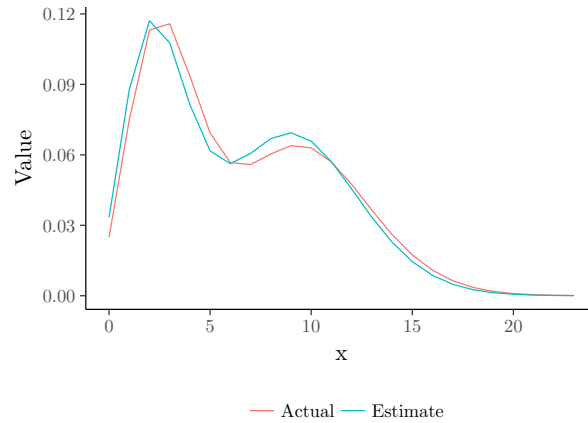


Figure 7: The true and estimated distributions from the Poisson mixture model.

```
Likelihood.gamma <- function(mdobj, x, theta){
  return(as.numeric(dgamma(x, theta[[1]], theta[[2]])))
}
```

We now need the function to draw random parameters from the base measure G_0 . For the parameters of the Gamma distribution we will be using a prior distribution of an Exponential distribution

$$\alpha \sim \text{Exp}(\alpha_0),$$

$$\beta \sim \text{Exp}(\beta_0).$$

```
PriorDraw.gamma <- function(mdobj, n=1){
  theta <- list()
  theta[[1]] = array(rexp(n, mdobj$priorParameters[1]), dim=c(1,1, n))
  theta[[2]] = array(rexp(n, mdobj$priorParameters[2]), dim=c(1,1, n))
  return(theta)
}
```

Now as we are drawing from the posterior distribution using the Metropolis-Hastings algorithm, we also need a function that calculates the prior density for a given α, β .

```
PriorDensity.gamma <- function(mdobj, theta){
  priorParameters <- mdobj$priorParameters
  thetaDensity <- dexp(theta[[1]], priorParameters[1])
  thetaDensity <- thetaDensity * dexp(theta[[2]], priorParameters[2])
  return(as.numeric(thetaDensity))
}
```

Finally, the Metropolis Hastings algorithm also needs a function that perturbs the parameters to explore the posterior distribution. As for the Gamma distribution the parameters $\alpha, \beta > 0$ we must constrain our proposals. This is achieved by taking the absolute value of a standard normal perturbation.

$$\begin{aligned}\alpha^{i+1} &= |\alpha^i + h \cdot \eta|, \\ \eta &\sim N(0, 1), \\ \beta^{i+1} &= |\beta^i + h \cdot \zeta|, \\ \zeta &\sim N(0, 1).\end{aligned}$$

Again this is easy to translate into R:

```
MhParameterProposal.gamma <- function(mdobj, oldParams){
  mhStepSize <- mdobj$mhStepSize
  newParams <- oldParams
  newParams[[1]] <- abs(oldParams[[1]] + mhStepSize[1]*rnorm(1))
  newParams[[2]] <- abs(oldParams[[2]] + mhStepSize[2]*rnorm(1))
  return(newParams)
}
```

We can now construct our mixing distribution object using the constructor function `MixingDistribution`. The arguments of this function specify the prior parameters α_0, β_0 and set the scale h at which the new parameter proposals are made using the parameter `mhStepSize`.

```
gammaMd<- MixingDistribution("gamma", priorParameters = c(0.1, 0.1),
  "nonconjugate", mhStepSize=c(0.1, 0.1))
```

The *dirichletprocess* object can now be created and fit to some test data. As it is a new type of mixture, it must be initialised.

```
R> y <- c(rgamma(100, 2, 4), rgamma(100, 6, 3))
R> dp <- DirichletProcessCreate(y, gammaMd)
R> dp <- Initialise(dp)
R> dp <- Fit(dp, 1000)
```

From Figure 8 we can see that the true distribution has been correctly identified.

4.3. Resampling Component Indexes and Parameters

When calling the `Fit` function on a DP object the component indexes and parameters are resampled following Algorithm 4 for the conjugate case and Algorithm 8 for the non-conjugate case from Neal (2000). For both types of DP mixture the two functions that do the majority of the work are `ClusterComponentUpdate` and `ClusterParameterUpdate`.

In a conjugate DPMM new component indexes and new cluster parameters are drawn directly from the predictive and posterior distributions making the algorithm very efficient. In such case, the only option available to users is to change the prior parameters of the base distribution G_0 . Ensuring that the base distribution is correctly parameterised with sensible values for the underlying data will provide optimal performance for the fitting algorithm.

However, in a non-conjugate case new cluster components are proposed from the chosen prior distribution and new cluster parameters are sampled using the Metropolis Hastings

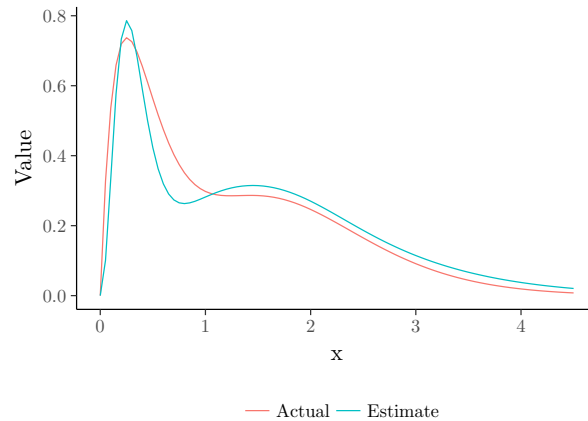


Figure 8: The results of implementing the new Gamma mixture model.

algorithm to obtain a posterior sample. By using the Metropolis Hastings algorithm, the parameters in question are proposed using a random walk but constrained to the particular support of the parameter. For example, the parameters in a Weibull distribution are strictly positive, therefore the random walk is restricted to fall on the positive real line. An ill proposed prior distribution can severely effect the convergence of the fitting process. The parameter `mhStepSize` in the constructor function for a non-conjugate mixture controls the scale of new parameter proposals for the random walk. When creating a new DP object, the constructor function has a flag `verbose` that outputs an estimated acceptance ratio, for optimal performance of the Metropolis Hastings algorithm this value should be around 0.234 (Gelman, Roberts, Gilks, and others 1996). Therefore the user should adjust `mhStepSize` to reach this value. As with the conjugate case, care must be taken to ensure that the base measure is well suited for the data.

Overriding Default Behaviour

For both conjugate and non-conjugate mixture models, the user can write their own `ClusterComponentUpdate` and `ClusterParameterUpdate` functions to override the default behaviour. The user can still benefit from the other S3 methods and structures implemented in `dirichletprocess` but with their custom sampling schemes.

For the non-conjugate mixture models there is a further option available to change the component index and parameter re-sampling. In Algorithm 8 of Neal (2000) each datapoint can form a new cluster with parameter drawn from the base measure, these proposals are called ‘auxiliary’ variables and m are drawn for each data point. By default $m = 3$. However this can be changed in the `Initialise(dp, ..., m=m)` function. Using more auxiliary variables can lead to more changes in the component indexes and greater exploration of the base measure but at the cost of computational time.

4.4. Resampling the Base Measure, G_0

It is desirable that the user knows how to best set the parameters of the base measure to correctly represent the underlying data. However, whilst desirable this is not always practical.

In which case **dirichletprocess** offers functionality to use hyper-prior parameters on G_0 and update them with each iteration.

For the mixing distributions that allow for re-sampling of the base measure, it is simple to include the flag `Fit(dp, ..., updatePrior=TRUE)`. At each fitting iteration the base measure with variable parameters will be updated based on the current cluster parameters. For details on the exact specification of the hyper-prior distributions for each implemented mixture kernel see Section 2.3. If a user wishes to change the default prior on the hyper parameters then it is as simple as changing the `PriorParametersUpdate` function for the mixing distribution object.

4.5. Component Prediction

Given a fitted DP object and some new data \hat{y} to predict the cluster labels of the new data we use the command `ClusterLabelPredict`. Using the appropriate algorithm for a conjugate or non-conjugate mixture model the cluster label probabilities are calculated from the new data \hat{y} , these probabilities are then sampled once to obtain a cluster label. It is these cluster labels that are returned with the appropriate cluster parameters.

4.6. Stick Breaking Representation

The stick breaking representation of a Dirichlet process allows for easy posterior inference using Key Property 3 and 5 (Section 2). In the **dirichletprocess** package drawing from the posterior is easily achieved using both `PosteriorClusters` and `PosteriorFunction` depending on users need.

- **PosteriorClusters**: Returns the posterior clusters ϕ_k and weights w_k as a list for the user.
- **PosteriorFunction**: Draws the posterior clusters and uses the likelihood function of the mixing distribution to return a function with appropriate posterior weights and parameters. This is a sample of the measure F for models of the form in Eq. (2).

Example: Point Process Intensity Estimation

We refer back to the example in Section 3.1.1 where we estimated the intensity function of an inhomogeneous Poisson process and now demonstrate an alternate method.

In the previous method, we resampled the cluster assignments and parameters with each iteration before plotting the final sample as our estimate for $\lambda(t)$. In this example, we will instead be estimating $\lambda(t)$ with each iteration and using it to update the data. The full model can be written as

$$\begin{aligned} N &\sim \text{Poisson}(\lambda(t)), \\ \lambda(t) &= \int k(t \mid \theta) dF, \\ F &\sim \text{DP}(\alpha, G_0), \end{aligned}$$

where k and G_0 are as per Section 2.3 for the Beta distribution mixture models. We sample the posterior distribution of G using Key Property 5 (Section 2) which states that a sample

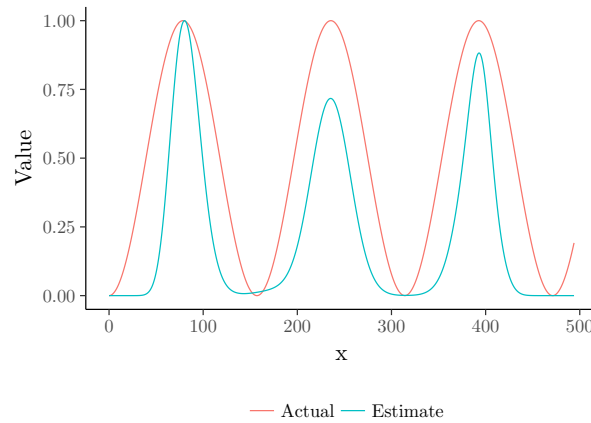


Figure 9: Estimation of the inhomogeneous Poisson process using stick breaking.

of G can be drawn independently of the data using the stick breaking representation of the data and the model parameters θ .

In this toy model we simulate 500 event times using the same intensity function as in Section 3.1.1. But instead of passing the full data set into the Dirichlet process object, we just use a random sample of 100 of these event times.

```
R> y <- cumsum(runif(1000))
R> pdf <- function(x) sin(x/50)^2
R> accept_prob <- pdf(y)
R> pts <- sample(y, 500, prob=accept_prob)
```

We then fit the Dirichlet process, draw a posterior sample of the intensity function $\hat{\lambda}(t)$ and sample 150 new points from the full data set with probabilities proportional to $\hat{\lambda}(t)$. The Dirichlet process object is then modified with the new data and the process is repeated.

```
R> dp <- DirichletProcessBeta(sample(pts, 100), maxY = max(pts)*1.01,
+ alphaPrior = c(2, 0.01))
R> dp <- Fit(dp, 100, TRUE)
R> for(i in seq_len(2000)){
+   lambdaHat <- PosteriorFunction(dp)
+   newPts <- sample(pts, 150, prob=lambdaHat(pts))
+   newPts[is.infinite(newPts)] <- 1
+   newPts[is.na(newPts)] <- 0
+   dp <- ChangeObservations(dp, newPts)
+   dp <- Fit(dp, 2, TRUE)
+ }
```

Figure 9 shows the true intensity function is being recovered even though the full dataset is never observed.

4.7. Working with Censored Observations

The following example is intended to illustrate how simple the **dirichletprocess** package makes it for the user to extend Dirichlet process mixture modeling to situations which are not directly supported by the package.

Survival analysis is an area of statistics concerned with analysing the duration of time before an event happens such as a failure in a mechanical system or a death in a biological context. We are concerned with constructing a survival function which as the name indicates shows how the probability of not experiencing the event changes with time. Survival data is often generated by observational studies which result in censoring. In the context of medical statistics, censoring occurs due to finite time periods of the studies. When analysing the effects of medical treatments patients events can be censored for a variety of reasons. This is a missing data problem as we no longer know the exact time at which an event occurred, just that it occurred before or after a specific time. Right censoring is when a patient is yet to be effected by the event after a study ends. Left censoring is when it is not known exactly when the event occurred, just that it occurred before the study started. To deal with this censored information we must adapt our likelihoods.

One approach for modeling such data non parametrically is a Dirichlet process mixture of Weibull distributions. The **dirichletprocess** package does not directly support the analysis of censored data – as stated throughout, the purpose of the package is not to provide the user with a small number of functions for solving predefined problems, but instead to make it easy to use Dirichlet process mixtures in a wide variety of contexts. As such, it is very simple for the user to extend the functionality of the package to allow for censoring.

Example: Censored Observations

For the data we replicate the work of [Kottas \(2006b\)](#) and use leukaemia remission times taken from [Lawless \(2011\)](#). This dataset contains two groups of censored observations and we wish to investigate the impact two different treatments have on leukaemia remission times. We fit a censored Weibull DP model to each of the data sets and compare the survival functions. The full model can be written as

$$\begin{aligned} y_i &\sim \text{Weibull}(y_i \mid a_i, b_i), \\ a_i, b_i &\sim G, \\ G &\sim \text{DP}(\alpha, G_0), \end{aligned}$$

where the Weibull density and G_0 follow the form shown in [Section 2.3](#).

Censored data can come in the form of two columns - the time it takes for the event to occur and an indicator variable; 1 for a right censored observation, 0 otherwise. Therefore the density of the Weibull distribution can be written as

$$\begin{aligned} k(y \mid a, b) &= \frac{a}{b} y^{a-1} \exp\left(-\frac{y^a}{b}\right) \quad \text{for uncensored,} \\ k(y \mid a, b) &= 1 - \exp\left(-\frac{y^a}{\lambda}\right) \quad \text{for censored.} \end{aligned}$$

Therefore we must translate this likelihood into the appropriate function for the **dirichletprocess** package.

```

Likelihood.weibullcens <- function(mdobj, x, theta){
  alpha = theta[[1]][,,drop=TRUE]
  lambda = theta[[2]][,,drop=TRUE]

  y <- as.numeric(
    lambda^(-1) * alpha * x[,1]^(alpha-1) * exp(-lambda^(-1) * x[, 1]^alpha))
  y_cens <- as.numeric(1 - exp(-x[,1]^alpha / lambda))

  if(nrow(x) == 1){
    if(x[,2] == 0) return(y)
    if(x[,2] == 1) return(y_cens)
  }
  else{
    y_ret <- y
    y_ret[x[, 2] == 1] <- y_cens[x[, 2]==1]
    return(y_ret)
  }
}

```

We now wish to create two different `MixingDistribution` objects for each of the data sets. Again we use the `MixingDistribution` constructor function and provide the resulting object with a custom class.

```

mdobjA <- MixingDistribution("weibullcens", c(1,2,0.5), "nonconjugate",
  mhStepSize=c(0.11,0.11), hyperPriorParameters=c(2.222, 2, 1, 0.05))
mdobjB <- MixingDistribution("weibullcens", c(1,2,0.5), "nonconjugate",
  mhStepSize=c(0.11,0.11), hyperPriorParameters=c(2.069, 2, 1, 0.08))

class(mdobjA) <- c("list", "weibullcens", "weibull", "nonconjugate")
class(mdobjB) <- c("list", "weibullcens", "weibull", "nonconjugate")

```

We can easily use this modified mixture model for our censored data. The sampling is then carried out as normal with no other changes needed. The default functions available for the Weibull mixture model are applied to our custom `dirichletprocess` object.

```

R> dpA <- DirichletProcessCreate(data_a, mdobjA, c(2, 0.9))
R> dpA <- Initialise(dpA)
R> dpB <- DirichletProcessCreate(data_b, mdobjB, c(2, 0.9))
R> dpB <- Initialise(dpB)
R> dpA <- Fit(dpA, 500, TRUE)
R> dpB <- Fit(dpB, 500, TRUE)

```

Using the fitted values we can easily extract the estimate density of the survival times using the weights and cluster parameters. The survival function is calculated as $S(y) = 1 - \exp(-\frac{y^a}{b})$. The resulting density and survival estimate is shown in Figure 10 which correctly replicate the findings of Kottas (2006b).

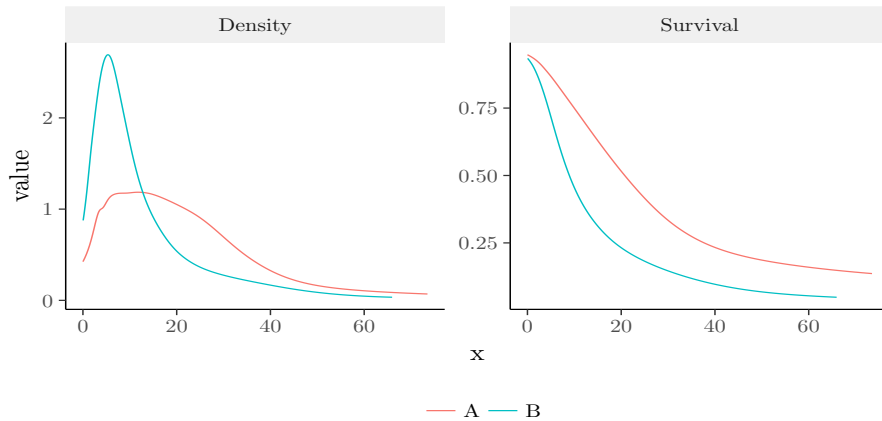


Figure 10: Point estimates for the survival and density functions of the two treatments.

To fully understand what has happened here, it is vital to understand that the DP is defined by its base likelihood and G_0 distribution. In creating a new mixing distribution of class `weibullcens` and `weibull` we are able to include the new likelihood but retain all the previous functions of a Weibull DP mixture. This makes it trivial to define your own likelihoods based off the foundations laid in the different classes available.

Computational details

The results in this paper were obtained using R 3.4.2 with the `dirichletprocess` 0.1.1 package. R itself and all packages used are available from the Comprehensive R Archive Network (CRAN) at <https://CRAN.R-project.org/>.

Acknowledgements

We thank Gianluca Baio and Federico Ricciardi for their helpful comments in the development of this package and vignette.

References

- Antoniak CE (1974). “Mixtures of Dirichlet Processes with Applications to Bayesian Non-parametric Problems.” *The Annals of Statistics*, **2**(6), 1152–1174. ISSN 0090-5364. URL <http://www.jstor.org/stable/2958336>.
- Coles S (2001). *An Introduction to Statistical Modeling of Extreme Values*. Springer Series in Statistics. Springer London, London. ISBN 978-1-84996-874-4 978-1-4471-3675-0. URL <http://link.springer.com/10.1007/978-1-4471-3675-0>.
- Escobar MD, West M (1995). “Bayesian Density Estimation and Inference Using Mixtures.” *Journal of the American Statistical Association*, **90**(430), 577–588. ISSN 0162-1459. doi:

- 10.1080/01621459.1995.10476550. URL <http://www.tandfonline.com/doi/abs/10.1080/01621459.1995.10476550>.
- Ferguson TS (1973). “A Bayesian Analysis of Some Nonparametric Problems.” *The Annals of Statistics*, **1**(2), 209–230. ISSN 0090-5364, 2168-8966. doi:10.1214/aos/1176342360. URL <http://projecteuclid.org/euclid.aos/1176342360>.
- Gelman A, Carlin JB, Stern HS, Rubin DB (2014). *Bayesian data analysis*, volume 2. Chapman & Hall/CRC Boca Raton, FL, USA.
- Gelman A, Roberts GO, Gilks WR, others (1996). “Efficient Metropolis jumping rules.”
- Geman S, Geman D (1984). “Stochastic Relaxation, Gibbs Distributions, and the Bayesian Restoration of Images.” *IEEE Transactions on Pattern Analysis and Machine Intelligence*, **PAMI-6**(6), 721–741. ISSN 0162-8828. doi:10.1109/TPAMI.1984.4767596.
- Hastings WK (1970). “Monte Carlo Sampling Methods Using Markov Chains and Their Applications.” *Biometrika*, **57**(1), 97–109. ISSN 0006-3444. doi:10.2307/2334940. URL <http://www.jstor.org/stable/2334940>.
- Kottas A (2006a). “Dirichlet process mixtures of beta distributions, with applications to density and intensity estimation.” In *Workshop on Learning with Nonparametric Bayesian Methods, 23rd International Conference on Machine Learning (ICML)*.
- Kottas A (2006b). “Nonparametric Bayesian survival analysis using mixtures of Weibull distributions.” *Journal of Statistical Planning and Inference*, **136**(3), 578–596. ISSN 0378-3758. doi:10.1016/j.jspi.2004.08.009. URL <http://www.sciencedirect.com/science/article/pii/S0378375804003465>.
- Lawless JF (2011). *Statistical models and methods for lifetime data*, volume 362. John Wiley & Sons.
- Maceachern SN, Mäijller P (1998). “Estimating Mixture of Dirichlet Process Models.” *Journal of Computational and Graphical Statistics*, **7**(2), 223–238. ISSN 1061-8600, 1537-2715. doi:10.1080/10618600.1998.10474772. URL <http://www.tandfonline.com/doi/abs/10.1080/10618600.1998.10474772>.
- Neal RM (2000). “Markov Chain Sampling Methods for Dirichlet Process Mixture Models.” *Journal of Computational and Graphical Statistics*, **9**(2), 249–265. ISSN 1061-8600, 1537-2715. doi:10.1080/10618600.2000.10474879. URL <http://www.tandfonline.com/doi/abs/10.1080/10618600.2000.10474879>.
- Sethuraman J (1994). “A constructive definition of Dirichlet priors.” *Statistica sinica*, pp. 639–650.
- Teh YW, Jordan MI, Beal MJ, Blei DM (2005). “Sharing clusters among related groups: Hierarchical Dirichlet processes.” In *Advances in neural information processing systems*, pp. 1385–1392.
- West M (1992). *Hyperparameter estimation in Dirichlet process mixture models*. Duke University ISDS Discussion Paper\# 92-A03.

Wickham H (2014). *Advanced r*. CRC Press.

Affiliation:

Gordon J. Ross

School of Mathematics

University of Edinburgh

James Clerk Maxwell Building

Edinburgh, UK

E-mail: Gordon.Ross@ed.ac.uk

URL: <http://gordonjross.co.uk/>

and

Dean Markwick

Department of Statistical Science

University College London

1-19 Torrington Place

London, UK

E-mail: dean.markwick.15@ucl.ac.uk