Dependent Random Density Functions with Common Atoms and Pairwise Dependence

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Abstract

The paper is concerned with constructing pairwise dependence between \( m \) random density functions each of which is modeled as a mixture of Dirichlet process model. The key to this is how to create dependencies between random Dirichlet processes. The present paper adopts a plan previously used for creating pairwise dependence, with the simplification that all random Dirichlet processes share the same atoms. Our contention is that for all dependent Dirichlet process models, common atoms are sufficient.

We show that by adopting common atoms, it is possible to compute the \( L_p \) distances between all pairs of random probability measures.

Keywords: Bayesian nonparametric inference; Dependent Dirichlet process; \( L_p \) distance; Mixture of Dirichlet process; Pairwise dependence.

1. Introduction. There has been substantial recent interest in the construction of dependent probability measures. We first restrict our thoughts to dependence between two random probability measures, \( P_1 \) and \( P_2 \), though for the paper we are concerned with creating (pairwise) dependence between \( m \) probability measures. To complete the motivation, the typical scenario in which such measures are employed is with mixture models, generating random densities \( f_1 \) and \( f_2 \), whereby

\[
f_1(x) = \int_{\Theta} K(x|\theta) P_1(d\theta) \quad \text{and} \quad f_2(x) = \int_{\Theta} K(x|\theta) P_2(d\theta)
\]

The marginal models for each \( f_j \) are a random density function based on the benchmark mixture of Dirichlet process model (Lo, 1984); so that each \( P_j \) is a Dirichlet process (Ferguson, 1973), and \( K(x|\theta) \) is a density function for each \( \theta \in \Theta \). The reason for dependence is that it is thought that properties of \( f_1 \) and \( f_2 \) are similar in some way; for example the means are similar, or it is thought the distance between them is small, in that they resemble each other.
We can write each $P_j$ using the constructive definition of the Dirichlet process given in Sethuraman (1994); so that

$$P_j = \sum_{k=1}^{\infty} w_{jk} \delta_{\theta_{jk}}$$

where we write $\theta_j = (\theta_{jk})_{k=1}^{\infty}$, being independent and identically distributed from some fixed distribution $P_0(\theta)$, with density function $p_0(\theta)$. And we write $w_j = (w_{jk})_{k=1}^{\infty}$; a stick-breaking process, so if all the $(z_{jk})_{k=1}^{\infty}$ are independent and identically distributed from the beta$(1,c)$ distribution, for some $c > 0$, then $w_{j1} = z_{j1}$ and, for $k > 1$,

$$w_{jk} = z_{jk} \prod_{j<l}(1 - z_{jl}).$$

In applications, the $P_1$ and $P_2$ can be made dependent in a variety of ways. The modeling of dependent random Dirichlet processes has been the focus of much recent research in Bayesian nonparametrics; following original developments in MacEachern (1999). More recent work is to be found in De Iorio et al. (2004), Griffin and Steel (2006), Dunson and Park (2008) and summaries in Hjort et al. (2010). The use of the Dependent Dirichlet process arises mostly in regression problems where a random measure $P_z$ is constructed for each covariate $z$ and is of the type

$$P_z = \sum_{k=1}^{\infty} w_k(z) \delta_{\theta_k(z)},$$

where $(w_k(z), \theta_k(z))$ are processes of weights and atoms.

On the other hand, the work reported here is about modeling a finite number of densities, equivalent to the regression model with a finite number of fixed covariates. Previous work related to this type of structure is to be found in Müller et al. (2004) and Bulla et al. (2009), and more recently Hatjispyros et al. (2011), Kolossiatis et al. (2013) and Griffin et al. (2013). These papers model an arbitrary but finite number of random distribution functions, $(P_1, \ldots, P_m)$ via a common component and an index specific idiosyncratic component. That is, the basic idea is to model

$$P_j = p_j P_0 + (1 - p_j) P_j^*$$

where $P_0$ is the common component to all other distributions and $(P_j^*)$ are the idiosyncratic parts, unique to each $P_j$, $p_j \in (0,1)$. And $(P_0, P_j^*)$ are modeled as mutually independent mixture of Dirichlet process models, or based on some other stick-breaking process (Ishwaran and James, 2001) or normalized random measure as in the case of Griffin et al. (2013). In all these cases the (random) atoms for the underlying Dirichlet process are unique to each $j$.

The present paper is concerned with constructing $P_j$ so that there is a unique common component for each pair $(P_j, P_{j'})$ with $j \neq j'$. This allows arbitrary pairwise dependence between any two $P_j$ and $P_{j'}$. The details of this idea for the case $m = 2$ were presented in Hatjispyros et al. (2011). Our numeric results target the key $m = 3$ case, which essentially gives access to arbitrary values of $m$. It is clear that $m = 2$ is a straightforward special case.
Moreover, our thesis is that when constructing e.g. \( P_1 \) and \( P_2 \), it is sufficient to create a dependence between the weights and to take \( \theta_1 = \theta_2 \). That is, it is sufficient for the random probability measures \( P_1 \) and \( P_2 \) to have the same atoms. We demonstrate this sufficiency throughout the paper.

The key to the understanding of this idea is quite straightforward. From a fixed set of random atoms obtained for one probability measure, another probability measure can be obtained by reassigning the weights to these same atoms. It should be clear that varying weights can provide probability measures which are either remarkably close, when weights are similar, to probability measures which are far apart, when the weights are dissimilar.

It is less interpretable to have both varying weights and atoms. For if the weights are similar, there is nothing to be said about the closeness of the distributions as the ultimate picture will depend on the atoms. And we decide to make the atoms similar and allow the weights to vary so that with the same atoms we can easily compute distances between the two measures. We will look at this in Section 2.

We will demonstrate the idea using a dependent model suggested by Hatjispyros et al. (2011) for constructing pairwise dependence for the finite set of densities \((f_1, \ldots, f_m)\) where each \( f_j \) is a random density function. The idea is that from each density we observe independent data sets, yet the densities from which they come share common features. For example, they may all have similar tail behaviour or even have common variances, and so on. Hence, it is imperative to model in the prior an arbitrary level of dependence between each pair \((f_j, f_k)\), for each \( j \neq k \). The key is to construct the prior model in such a way that for every pair there is a “common” part and a “difference” part, to be explained more explicitly in due course.

The layout of the paper is as follows. In Section 2 we provide some preliminary findings concerned with the evaluation of distances between probability measures being generated. This is possible when atoms are common to each distribution. In section 3 we describe the model of interest and introduce the latent variables which will form the basis of the Gibbs sampler which is described in Section 4. Section 5 contains a numerical illustration involving a real data set and finally Section 6 concludes with a summary and future work.

2. Preliminaries. Given the common atoms for \( P_1 \) and \( P_2 \) we can easily compute distances between them and also between the corresponding mixed density functions. So, for suitable sets \( A \),

\[
|P_1(A) - P_2(A)| = \sum_{\theta_j \in A} |w_{1j} - w_{2j}|.
\]

Therefore, for the total variation distance between \( P_1 \) and \( P_2 \) we have

\[
d(P_1, P_2) = \sup_A |P_1(A) - P_2(A)| = \sup_J |W_{1j} - W_{2j}|,
\]
where, for example,

$$W_{1J} = \sum_{j \in J} w_{1j},$$

where $J$ is an index set. This is simple to interpret but impossible to obtain and control if the atoms are not identical. In fact, if the atoms are disjoint for each measure, close weights, even identical weights, says nothing about how close the two measures are to each other. We believe equal atoms is fundamental as a consequence.

We can formalize the idea of using common atoms and the sufficiency of this by considering the following

**Lemma 1:** We consider the densities $f_0(x) = \sum_{j=1}^{\infty} q_j K(x | \theta_j)$ and $f_1(x) = \sum_{j=1}^{\infty} w_j K(x | \psi_j)$ where the $(\theta_j)$, $(\psi_j)$ and $(w_j)$ are fixed, and the $(\theta_j)$ are dense in $\Theta$. Then we can find $(q_j)$ such that the $L_1$-distance between $f_0$ and $f_1$ can be made arbitrarily small.

**Proof:** Because the $(\theta_j)$ are dense in $\Theta$, for any $j$ and any $\epsilon_j > 0$, we can find $l(j)$ and $\theta_{l(j)}$ such that

$$d_1(K(\cdot | \psi_j), K(\cdot | \theta_{l(j)})) < \epsilon_j.$$

We assume without loss of generality that $l(j)$ is one to one, for $j \in \mathbb{N}$. Then, we put $q_{l(j)} = w_j$, and for the remaining indices we set $q_k = 0$. Thus, we have that $\sum_{j=1}^{\infty} q_{l(j)} = \sum_{j=1}^{\infty} w_j = 1$. Hence,

$$d_1(f_0, f_1) = \int_X \left| \sum_{j=1}^{\infty} w_j \{K(x | \psi_j) - K(x | \theta_{l(j)})\} \right| \, dx$$

$$\leq \sum_{j=1}^{\infty} w_j d_1(K(\cdot | \psi_j), K(\cdot | \theta_{l(j)})) \leq \sum_{j=1}^{\infty} w_j \epsilon_j.$$

Now choose $(\epsilon_j)$ such that, for any $\epsilon > 0$, we have

$$\sum_{j=1}^{\infty} w_j \epsilon_j < \epsilon,$$

and the lemma follows.

Thus, even though atoms are fixed across densities, as long as they form a dense set, we can approximate arbitrarily accurately any density with any atoms.

Hence, we can obtain weights to allow this distance to be either 0, the weights coincide, or to be 1. A dependent prior for $(w_1, w_2)$ can be used to provide a small distance between $P_1$ and $P_2$ if that is what is required. This is not so obvious to achieve if the atoms are dissimilar. Moreover, if atoms are dissimilar computing the informative distances is not possible and one is left with computing objects such as

$$\text{Cov}(P_1(A), P_2(A)),$$

which, although it provides some insight on the dependence between $P_1$ and $P_2$, is not the appropriate learning tool for the similarity between two random densities. Clearly, in that
case the total variation distance (or the $L_2$ distance between densities) is a more appropriate measure.

We now turn to looking at a distance between $f_1$ and $f_2$, and for ease of computation we make this the $L_2$ distance,

$$d_2(f_1, f_2) = \int_X (f_1(x) - f_2(x))^2 \, dx.$$  

**Lemma 2:** We consider the random mixtures $f_i(x) = \sum_{j=1}^{\infty} w_{ij} K(x|\theta_j)$, $i = 1, 2$ with $\theta_j$ independent, coming from the base measure $P_0$ for all $k \geq 1$, then

$$\mathbb{E} \left[ d_2(f_1, f_2) \mid w_1, w_2 \right] = (\alpha - \beta) \sum_{j=1}^{\infty} (w_{1j} - w_{2j})^2,$$

where $\alpha = \mathbb{E} \left\{ \int_X K(x|\theta_j)^2 \, dx \right\}$ and $\beta = \mathbb{E} \left\{ \int_X K(x|\theta_j)K(x|\theta_k) \, dx \right\}$.

**Proof:** It is that

$$d_2(f_1, f_2) = \int_X \left\{ \sum_{j=1}^{\infty} (w_{1j} - w_{2j}) K(x|\theta_j) \right\}^2 \, dx$$

$$= \sum_{j=1}^{\infty} \Phi_j^2 (w_{1j} - w_{2j})^2 + \sum_{j \neq k} \Phi_{jk} (w_{1j} - w_{2j})(w_{1k} - w_{2k}),$$

where

$$\Phi_j^2 = \int_X K(x|\theta_j)^2 \, dx \quad \text{and} \quad \Phi_{jk} = \int_X K(x|\theta_j)K(x|\theta_k) \, dx.$$  

Taking expectations over the atoms but keeping the weights fixed, we have

$$\mathbb{E} \left[ d_2(f_1, f_2) \mid w_1, w_2 \right] = \alpha \sum_{j=1}^{\infty} (w_{1j} - w_{2j})^2 + \beta \sum_{j \neq k} (w_{1j} - w_{2j})(w_{1k} - w_{2k})$$

$$= (\alpha - \beta) \sum_{j=1}^{\infty} (w_{1j} - w_{2j})^2 + \beta \mathcal{S},$$

where

$$\mathcal{S} = \sum_{j=1}^{\infty} (w_{1j} - w_{2j})^2 + 2 \sum_{j < k} (w_{1j} - w_{2j})(w_{1k} - w_{2k}), \quad \alpha = \mathbb{E} \left( \Phi_j^2 \right) \quad \text{and} \quad \beta = \mathbb{E} \left( \Phi_{jk} \right),$$

and note that $\alpha - \beta = \int_X \text{Var} \left\{ K(x|\theta_j) \right\} \, dx > 0$. Now it is very easy to show that $\mathcal{S} = 0$ by utilizing the identities

$$\sum_{j=1}^{\infty} w_{ij}^2 + 2 \sum_{j < k} w_{ij} w_{ik} = 1,$$

and

$$\sum_{j=1}^{\infty} w_{1j} w_{2j} + \sum_{j < k} w_{1j} w_{2k} + \sum_{j < k} w_{2j} w_{1k} = 1,$$

and the lemma follows.

So, again, crucial distances can be understood solely through the weights.
If we are now interested in creating dependent weights for \( f_1 \) and \( f_2 \) (which will allow extensions to a larger number of densities with pairwise dependence), then we construct weights of the type
\[
w_{1j} = pw_{11j} + (1 - p)w_{12j} \quad \text{and} \quad w_{2j} = qw_{21j} + (1 - q)w_{22j},
\]
with \( w_{12j} = w_{21j} \). This gives a common part to \( f_1 \) and \( f_2 \), via a common part to \( P_1 \) and \( P_2 \), and we can write
\[
P_1 = \sum_j w_{1j} \delta_{\theta_j} \quad \text{and} \quad P_2 = \sum_j w_{2j} \delta_{\theta_j},
\]
due to the common atoms.

On the other hand, in Hatjispyros et al. (2011) the model was described as
\[
P_1 = pP_{11} + (1 - p)P_{12} \quad \text{and} \quad P_2 = qP_{21} + (1 - q)P_{22}
\]
with \( P_{12} = P_{21} \). It had to be like this due to the uncommon atoms of \( P_{11}, P_{12} \) and \( P_{22} \), i.e.
\[
P_{jl} = \sum_{k=1}^{\infty} w_{jlk} \delta_{\theta_{jlk}}.
\]
The details of the model where random probability measures share common atoms is now described in Section 3.

3. The model. We start off by describing the model as it was in Hatjispyros et al. (2011) and then proceed to detail the simplifications when atoms are common. So, we have the set of random density functions generated via
\[
f_j(x|\mathbb{P}_{j1}, \ldots, \mathbb{P}_{jm}) = \sum_{l=1}^{m} p_{jl} g_{jl}(x|\mathbb{P}_{jl}), \quad 1 \leq j \leq m,
\]
where \( \sum_{l=1}^{m} p_{jl} = 1 \). The random densities satisfy \( g_{jl} = g_{lj} \) and are independent mixtures of Dirichlet process models; so that
\[
g_{jl}(x) = g(x|\mathbb{P}_{jl}) = \int_{\Theta} K(x|\theta) \mathbb{P}_{jl}(d\theta),
\]
for some kernel density \( K(\cdot|\cdot) \) and \( \{\mathbb{P}_{jl} : 1 \leq j, l \leq m\} \) form a matrix of random distributions with \( \mathbb{P}_{jl} = \mathbb{P}_{lj} \) for \( j > l \) and each other element is an independent Dirichlet process. Equivalently, the random densities \( (f_j) \) are dependent mixtures of the dependent random measures
\[
Q_j(d\theta) = \sum_{l=1}^{m} p_{jl} \mathbb{P}_{jl}(d\theta), \quad 1 \leq j \leq m.
\]
In matrix notation
\[
Q = A 1, \quad A = \mathcal{W} \otimes \mathcal{P},
\]
where \( \mathcal{W} = (p_{jl}) \) is the matrix of weights and \( \mathcal{P} = (\mathbb{P}_{jl}) \) is the symmetric matrix of the independent Dirichlet measures.
We can write each $\mathbb{P}_{jl}$ using the constructive definition of the Dirichlet process given in Sethuraman (1994); so that, and now adopting common atoms for all probability measures,

$$\mathbb{P}_{jl} = \sum_{k=1}^{\infty} w_{jlk} \delta_{\theta_k}$$

where we write $\vartheta = (\theta_k)_{k=1}^{\infty}$, being independent and identically distributed from some fixed distribution $P_0(\theta)$, with density function $p_0(\theta)$, and we write $w_{jl} = (w_{jlk})_{k=1}^{\infty}$; being a stick-breaking process; so if all the $(z_{jlk})$ are independent and identically distributed from the beta$(1,c)$ distribution, for some $c > 0$, then $w_{j1} = z_{j1}$ and, for $k > 1$,

$$w_{jlk} = z_{jlk} \prod_{r<k} (1 - z_{jlr}).$$

Hence, we can write

$$g_{jl}(x|w_{jl}, \vartheta) = \sum_{k=1}^{\infty} w_{jlk} K(x|\theta_k),$$

and

$$f_j(x|(w_{j1}, \ldots, w_{jm}), \vartheta) = \sum_{k=1}^{\infty} \left\{ \sum_{l=1}^{m} p_{jl} w_{jlk} \right\} K(x|\theta_k).$$

We could write this as

$$f_j(x|(w_{j1}, \ldots, w_{jm}), \vartheta) = \sum_{k=1}^{\infty} w_{jk} K(x|\theta_k)$$

and to create a pairwise dependence it is necessary to include the other weights for each other density $f_j$. This at least to us only seems possible by taking

$$w_{jk} = \sum_{l=1}^{m} p_{jl} w_{jlk}$$

for some weights $(p_{jl})$. And the common component is worked out by taking $w_{jlk} = w_{ljk}$. There is no unidentifiability here because we have $w_{jlk} = w_{ljk}$ and it is this feature which is creating the dependence between the densities $(f_1, \ldots, f_m)$.

To avoid cluttering up the notation, at this point we adopt a simpler notation for the random densities $f_j$; namely, from now on, we denote $f_j(x|(w_{j1}, \ldots, w_{jm}), \vartheta)$ by $f_j(x)$.

Given mutually independent observations $x = (x_{ji})$ for $j = 1, \ldots, m$ and $i = 1, \ldots, n_j$, our method of inference will be the Gibbs sampler and we will rely crucially on slice latent variables (Walker (2007), Kalli et al. (2010)); so for each $f_j$ we introduce the latent variables $u_j = (u_{ji})_{i=1}^{n_j}$ such that the joint density of $u_{ji}$ with $x_{ji}$ is given by

$$f_j(x_{ji}, u_{ji}) = \sum_{l=1}^{m} p_{jl} \sum_{k=1}^{\infty} 1(u_{ji} < w_{jlk}) K(x_{ji}|\theta_k).$$  (2)
This augmented scheme is at the core of our sampling methodology. It essentially shifts the problem from one of sampling from a mixture with an infinite number of components to actually having to deal with only a finite number of them. It can be readily verified that the sets

\[ A_{w_{jl}}(u_{ji}) = \{ k \in \mathbb{N} : u_{ji} < w_{jlk} \}, \]

with \( w_{jl} = w_{lj} \), are finite.

This means, and this will become clearer later on, that for each pair \((j,l)\) only a finite number of the \((\theta_k)\) and \(w_{jl} = (w_{jlk})_{k=1}^{\infty}\) are needed in each iteration of the Gibbs sampler.

We can then express the \(f_j\) \(u_j\)-augmented random densities in (2) as follows:

\[ f_j(x_{ji}, u_{ji}) = \sum_{l=1}^{m} p_{jl} \sum_{k \in A_{w_{jl}}(u_{ji})} K(x_{ji} | \theta_k), \quad 1 \leq i \leq n_j. \]

We now introduce latent variables \(\delta = (\delta_{ji})_{i=1}^{n_j}\) selecting the mixture and \(d = (d_{ji})_{i=1}^{n_j}\) selecting the component within the mixture from which the observations come; so for each \(i = 1, \ldots, n_j\) we have

\[ f_j(x_{ji}, u_{ji}, d_{ji} | \delta_{ji}) = \prod_{r=1}^{m} \mathbf{1}(u_{ji} < w_{jrd_{ji}})^{\delta_{ji}} K(x_{ji} | \theta_{d_{ji}}) \]

with \(\delta_{ji} = (\delta_{ji}^1, \ldots, \delta_{ji}^m)\) and \(\Pr(\delta_{ji} = \hat{e}_l) = p_{jl}\), where \(\hat{e}_l\) denotes the usual basis vector having its only nonzero component equal to 1 at position \(l\).

Hence, for a sample of size \(n_1\) from \(f_1\), a sample of size \(n_2\) from \(f_2\), etc., a sample of size \(n_m\) from \(f_m\) we can write the full likelihood as a multiple product:

\[ f(x, u, d | \delta) = \prod_{j=1}^{m} \prod_{i=1}^{n_j} \prod_{l=1}^{m} \mathbf{1}(u_{ji} < w_{jld_{ji}})^{\delta_{ji}} K(x_{ji} | \theta_{d_{ji}}). \]

It will be reinforcing our intuition, and will make the Gibbs sampling algorithmic steps, as well as the dependencies between variables, much clearer if we express the model concisely in a hierarchical fashion using the auxiliary variables and the stick breaking representation. We thus have, for \(j = 1 \ldots, m\) and \(i = 1, \ldots, n_j\),

\[ x_{ji}, u_{ji} | d_{ji}, \delta_{ji}, \theta_{d_{ji}}, (w_{jrd_{ji}})_{r=1}^{m} \sim \prod_{r=1}^{m} K(x_{ji} | \theta_{d_{ji}}) \{ \mathcal{U}(u_{ji} | 0, w_{jrd_{ji}}) \}^{\delta_{ji}} \]

\(\Pr(d_{ji} = k | w_{ji}, \delta_{ji} = \hat{e}_l) = w_{jlk}\)

\(\Pr(\delta_{ji} = \hat{e}_l) = p_{jl}\)

\(w_{jlk} = z_{jlk} \prod_{r<k} (1 - z_{jlr}), \quad z_{jlk} \sim \text{beta}(1, c), \quad \theta_k \sim p_0, \quad k \in \mathbb{N},\)

where \(\mathcal{U}(u|\alpha, \beta)\) is the uniform density over the interval \((\alpha, \beta)\).
It is also clear, by construction, that we can by choice of the \((p_{j1}, \ldots, p_{jm-1})\) and the \((g_{ji})\) arrange for \(f_j\) and \(f_l\) to be as close or as far apart as desired with respect to the \(L_2\) metric.

4. The Gibbs sampler. We are now ready to describe the Gibbs sampler and the full conditional densities for estimating the model, having completed the model by assuming that the prior for \((p_{j1}, \ldots, p_{jm-1})\) for \(j = 1, \ldots, m\) is Dirichlet with fixed parameters \((a_{j1}, \ldots, a_{jm})\) i.e.

\[
\pi(p_{j1}, \ldots, p_{jm-1}) \propto p_{j1}^{a_{j1}-1} \cdots p_{jm-1}^{a_{jm-1}-1} (1 - p_{j1} - \cdots - p_{jm-1})^{a_{jm}-1}.
\]

At each iteration we will sample variables,

\[
\begin{align*}
    w_{jlk}, & \quad 1 \leq j \leq l \leq m, 1 \leq k \leq N^*, \\
    u_{ji}, d_{ji}, & \quad 1 \leq j \leq m, 1 \leq i \leq n_j, \\
    p_{ji}, & \quad 1 \leq j \leq m, 1 \leq l \leq m - 1,
\end{align*}
\]

with \(N^*\) almost surely finite. In the sequel we will see how to obtain \(N^*\).

A. We start with initial \(\{d_{ji}, \delta_{ji}\}\) for \(j = 1, \ldots, m\) and \(i = 1, \ldots, n_j\), and \((p_{ji})\) for \(j = 1, \ldots, m\) and \(l = 1, \ldots, m - 1\). The first task is to generate the \((w_{jlk}, \theta_k)\). We will do this by sampling from the conditional distribution with the \((u_{ji})\) for \(j = 1, \ldots, m\) and \(i = 1, \ldots, n_j\) integrated out. Then standard results, see Kalli et al. (2010), give

\[
\pi(z_{jlk} | \cdots) = \text{beta}\left(1 + \sum_{i=1}^{n_j} 1(d_{ji} = k, \delta_{ji} = \hat{e}_j), c + \sum_{i=1}^{n_j} 1(d_{ji} > k, \delta_{ji} = \hat{e}_j)\right),
\]

also for \(j \neq l\) we have

\[
\pi(z_{jlk} | \cdots) = \text{beta}\left(1 + \sum_{i=1}^{n_j} 1(d_{ji} = k, \delta_{ji} = \hat{e}_l), c + \sum_{i=1}^{n_j} 1(d_{ji} = k, \delta_{li} = \hat{e}_j) + \sum_{i=1}^{n_l} 1(d_{li} > k, \delta_{li} = \hat{e}_l)\right).
\]

The \(\delta\)'s and \(d\)'s will only enter the equation for \(j \leq M = \max_{i,j} \{d_{ji}\}\). For \(j > M\) we take all the \((z_{jlk})\) independently from \(\text{beta}(1, c)\) and take the \((\theta_k)\) independently from \(p_0\). The \(z\)'s yield the \((w_{jlk})\) according to the stick-breaking formula.

B. Here we describe how to sample the \((\theta_k)\) for \(k \leq M\). We have for \(1 \leq j \leq m\)

\[
\pi(\theta_k | \cdots) \propto p_0(\theta_k) \prod_{j=1}^{m} \prod_{i=1, d_{ji} = k}^{n_j} K(x_{ji} | \theta_k). \tag{5}
\]

C. Before we concern ourselves with how many of the \(z\)'s and \(\theta\)'s to sample beyond \(M\), we sample the \((u_{ji})\). From the likelihood one has

\[
\pi(u_{ji} | \cdots) \propto \prod_{l=1}^{m} 1(u_{ji} < w_{jld_{ji}})^{d_{ji}},
\]
where \( w_{jld_j} = w_{jld_j} \) when \( j > l \). So, if \( \delta_{ji} = \hat{e}_l \) we take \( u_{ji} \) uniform from \((0, w_{jld_j})\). For example, when \( m = 3 \) we have for \( 1 \leq i \leq n_1 \),

\[
\pi(u_{1i} \ldots) = \begin{cases} 
\mathcal{U}(0, w_{1ld_1}) & \delta_{1i} = \hat{e}_1 \\
\mathcal{U}(0, w_{2ld_1}) & \delta_{1i} = \hat{e}_2 \\
\mathcal{U}(0, w_{3ld_1}) & \delta_{1i} = \hat{e}_3,
\end{cases}
\]

and so on.

**D.** We now proceed to sample the rest of the \((w_{jlk})\) and \((\theta_k)\). Let \( N_{jl} \) be the smallest integer \( N \) for which

\[
\sum_{k=1}^{N} w_{jlk} > 1 - u_{jl}^*,
\]

where for \( j = l \) we have

\[
u_{jj}^* = \min\{u_{ji}\}, \quad j = 1, \ldots, m,
\]

also for \( 1 \leq j < l \leq m \) we have

\[
u_{jl}^* = \min\{\min\{u_{ji}\}, \min\{u_{li}\}\}.
\]

This then implies that we must sample, in order to sample the \((d_{ji}, \delta_{ji})\), the rest of \((w_{jlk}, \theta_k)\) from the prior for \( k = M + 1, \ldots, N^* \) where \( N^* = \max_{jl} \{N_{jl}\} \).

**E.** We now concentrate on sampling the \((d_{ji}, \delta_{ji})_{i=1}^{\tau_j} \). To do this we first need to explicitly find the constraint sets in relations (3) and (4) then for \( 1 \leq j \leq m, \ 1 \leq l \leq m \) and \( 1 \leq i \leq n_j \) the likelihood expression gives

\[
\Pr(d_{ji} = k, \delta_{ji} = \hat{e}_l \ldots) \propto p_{ji} \mathbf{1} (k \in A_{w_{jl}}(u_{ji})) K(x_{ji}|\theta_k),
\]

where \( p_{jm} = 1 - \sum_{r=1}^{m-1} p_{jr} \) and \( w_{jl} = w_{lj} \). Also we have

\[
\Pr(d_{ji} = k, \delta_{ji} = \hat{e}_l \ldots) = \frac{p_{ji} K(x_{ji}|\theta_k)}{\sum_{s \in A_{w_{jl}}(u_{ji})} K(x_{ji}|\theta_s)}, \quad k \in A_{w_{jl}}(u_{ji}).
\]

Now it is clear that for each \((j, i)\) we can sample the \( \{d_{ji}, \delta_{ji}\} \) together as a block.

**F.** It is also easily seen that the full conditional for each \((p_{j1}, \ldots, p_{jm-1})\) is a Dirichlet distribution, namely for \( j = 1, \ldots, m \) we have

\[
\pi(p_{j1}, \ldots, p_{jm-1} | \ldots) \propto p_{j1}^{\alpha_j + \sum_{i=1}^{n_1} 1(\delta_{ji} = \hat{e}_l)^{-1} \ldots p_{jm-1}^{\alpha_{jm-1} + \sum_{i=1}^{n_{m-1}} 1(\delta_{ji} = \hat{e}_{m-1})^{-1}}
\]

\[
\times (1 - p_{j1} - \ldots - p_{jm-1})^{\alpha_j + \sum_{i=1}^{n_{m}} 1(\delta_{ji} = \hat{e}_{m})^{-1}}. \tag{6}
\]

We can use the output at each iteration of the Gibbs sampler, after a sensible burn-in time period, to sample from the densities \((f_{1}, \ldots, f_{m})\). So we sample independently \((x_{j,n_j+1})\) from the densities based on the current parameter values of each density. This would then involve, for each \( j \), sampling the component \( l \) according to the probabilities \((p_{j1}, \ldots, p_{jm-1})\) and then sampling \( x_{j,n_j+1} \) from the \( K(\cdot|\theta_k) \) where \( k \) is chosen according to the probabilities \((w_{jlk})\). These
collection of samples collected over the course of the Gibbs sampler can be used to provide estimates for the \( m \) densities.

5. Comparing PDDP and CAPDDP priors – Numerical Illustrations

In this section we compare the pairwise dependent Dirichlet process (PDDP) and the common atoms pairwise dependent Dirichlet process (CAPDDP) models. We present two simulated and one real data example with \( m = 3 \). For the choice of kernel we have a normal model \( K(x|\theta) = N(x|\theta) \), where \( \theta = (\mu, \lambda) \) and \( \lambda \) is the precision. The prior for the means and the precisions for both PDDP and CAPDDP models will be independent normals \( N(0, s^{-1}) \) and gammas \( Ga(\epsilon, \epsilon) \), respectively, i.e. \( P_0(d\mu, d\lambda) = N(\mu|0, s^{-1}) Ga(\lambda|\epsilon, \epsilon) \, d\mu \, d\lambda \). Attempting a noninformative prior specification, we took in all our numerical experiments \( s = 0.001 \) and \( \epsilon = 0.001 \). The concentration parameter is everywhere constant and has been set to \( c = 1 \). Our only change, across examples, will be the value of the hyperparameter \( (\alpha_{ji}) \) of the selection probabilities.

Our finding is that the massive extra cost of more parameters and the essentially equivalent predictive performance of the models combined with the lack of availability of the computation of distances, puts the PDDP model at a significant disadvantage to the CAPDDP model.

**First simulated data example:** We simulated three data sets, of sizes \( n_1 = 80 \), \( n_2 = 30 \) and \( n_3 = 80 \), independently from

\[
\begin{align*}
x_{1i} &\sim f_1(x) = \text{Ga}(2 - x|2, 1), \quad 1 \leq i \leq n_1 \\
x_{2i} &\sim f_2(x) = N(x|0, 2), \quad 1 \leq i \leq n_2 \\
x_{3i} &\sim f_3(x) = \text{Ga}(x + 2|2, 1), \quad 1 \leq i \leq n_3.
\end{align*}
\]

In both cases, when atoms are common (CAPDDP) and when atoms are unequal (PDDP), the hyperparameters in relation (6) of the Dirichlet priors for the mixing weights are given by \( \alpha_{ji} = 1(j \neq i) + 3 \, 1(j = i) \). We sample 70,000 points from the predictives after a burn-in of 10,000.

The following results are presented in Figures 1,2,3,4:

1. In 1(a), 1(b) and 1(c) the true densities, as well as the kernel density estimates based on samples of the first 40,000 points after the burn-in period for the PDDP and CAPDDP models, are superimposed over the corresponding data sets. We note the similarity of the posterior predictive estimates of the densities \( f_1, f_2 \) and \( f_3 \).

2. In 1(d), 1(e) and 1(f) the histograms of the predictive samples coming from the PDDP model along with the associated KDE curves.

3. In 1(g), 1(h) and 1(i) the corresponding predictive samples and KDE curves of the CAPDDP model.
4. In 2(a), 2(b) and 2(c) the histograms of the sampled values of the conditional expectations of the $L_2$ distances via

$$E\left[d_2(f_j, f_i) \mid w_j, w_i, N^*\right] \propto \sum_{k=1}^{N^*} (w_{jk} - w_{ik})^2, \quad 1 \leq j < i \leq 3,$$

where

$$w_{1k} = p_{11}w_{11k} + p_{12}w_{12k} + (1 - p_{11} - p_{12})w_{13k},$$
$$w_{2k} = p_{21}w_{21k} + p_{22}w_{22k} + (1 - p_{21} - p_{22})w_{23k},$$
$$w_{3k} = p_{31}w_{31k} + p_{32}w_{32k} + (1 - p_{31} - p_{32})w_{33k}.$$  

5. In 2(d), 2(e) and 2(f) the running averages of the associated expected $L_2$ distances

$$d_{ji} = E\left[d_2(f_j, f_i)\right], \quad 1 \leq j < i \leq 3.$$

Our numerical approximations after 50,000 iterations are $d_{12} \propto 0.0969$, $d_{23} \propto 0.0970$ and $d_{13} \propto 0.2555$. These values exhibit the same features as the $L_2$ distances of the true densities given in relations (7)

$$d_2(f_1, f_2) = d_2(f_2, f_3) = \frac{1}{4} + \frac{1}{2\sqrt{2\pi}} - \frac{2}{e\sqrt{\pi}} \approx 0.0346,$$
$$d_2(f_1, f_3) = \frac{64}{3}e^{-4} \approx 0.1093.$$

6. In 3(a), 3(b) and 3(c) the histograms of the $p$-values of the Anderson–Darling two-sample test between 700 samples of size 100 coming from the PDDP and CAPDDP models. The test rejects 267 samples out of 700 of the $f_1$-predictive, rejects 234 samples out of 700 of the $f_2$-predictive and 263 samples out of 700 of the $f_3$-predictive.

7. In 4(a), 4(b) the histograms of the $p$-values of one-sample Anderson–Darling tests. In 4(a) we test 700 samples of size 100 against the hypothesis that the samples from the $f_2$-PDDP-predictive are coming from a normal with mean 0 and variance 2. The rejection rate is 242/700. The rejection rate is smaller for the corresponding $f_2$-CAPDDP-predictive, namely 216/700.

**Second simulated data example:** We have simulated independently two groups of data sets, the “large” group

$$G_1 = \left\{ (x_{11i})_{i=1}^{300}, (x_{2i})_{i=1}^{300}, (x_{3i})_{i=1}^{300} \right\},$$

and the “small” group

$$G_2 = \left\{ (x_{1i})_{i=1}^{120}, (x_{2i})_{i=1}^{60}, (x_{3i})_{i=1}^{120} \right\},$$
from the normal 3-mixtures

\[ x_{1i} \sim f_1(x) = \frac{1}{3} N(x | -10, 1) + \frac{1}{3} N(x | -20, 1) + \frac{1}{3} N(x | 20, 1) \]

\[ x_{2i} \sim f_2(x) = \frac{1}{3} N(x | -20, 1) + \frac{1}{3} N(x | 0, 1) + \frac{1}{3} N(x | 30, 1) \]  \hspace{1cm} (10)

\[ x_{3i} \sim f_3(x) = \frac{1}{3} N(x | 20, 1) + \frac{1}{3} N(x | 30, 1) + \frac{1}{3} N(x | 10, 1). \]

In both cases, CAPDDP and PDDP, the hyperparameters in relation (10) of the Dirichlet priors for the mixing weights \( p_{ji} \) are \( \alpha_{ji} = 1 \). We sample 70,000 points from the predictives after a burn-in of 10,000.

The following results are presented in Figure 5:

1. In 5(a)–5(c) the \( f_j \)-CAPDDP-predictives for the large group of data sets \( G_1 \). As it can be seen they predict very effectively the true densities apart from the nearly discernible small bumps in the areas around the modes of the 3-mixtures. Such mass dislocations can occur as well during the computation of the \( f_j \)-PDDP-predictives but they quickly disappear as the MCMC evolves. In the common atoms case such mass dislocations need a very large number of iterations to completely disappear.

2. In 5(d)–5(f) the KDE curves of the distributions of the conditional expectations of the \( L_2 \) distances. As it can be seen, due to the large sample size, these are tight and centered about the same value \( d_{ji} \approx 0.44 \).

3. In 5(g)–5(i) the \( f_j \)-CAPDDP-predictives for the small group of data sets \( G_2 \), which is a reduction of the \( G_1 \) group. Here the mass dislocations expand due to the small sample sizes. Nevertheless all the \( L_2 \) conditional expectation distributions, remain centered to \( d_{ji} \approx 0.4 \). We observe that the variance has been increased considerably purely due to the smaller sample sizes. Note that the \( L_2 \) distances of the true densities given in relations (10) are

\[ d_2(f_1, f_2) = d_2(f_1, f_3) = d_2(f_2, f_3) \approx 0.125. \]

Real data example: The data set is to be found at [http://lib.stat.cmu.edu/datasets/pbcseq](http://lib.stat.cmu.edu/datasets/pbcseq) and involves data from 312 individuals. We take the observation as SGOT (serum glutamic-oxaloacetic transaminase) level, just prior to liver transplant or death or the last observation recorded, under three conditions on the individual

1. The individual is dead without transplantation.
2. The individual had a transplant.
3. The individual is alive without transplantation.
We normalize the means of all three data sets to zero. Since it is reasonable to assume the densities for the observations are similar for the three categories (especially for the last two), we adopt the model proposed in this paper with \( m = 3 \). The number of transplanted individuals is small (sample size of 28) so it is reasonable to borrow strength for this density from the other two. We took the hyperparameters of the Dirichlet priors for the mixing weights \( (p_{ji}) \) are for \( 1 \leq i, j \leq 3 \)

\[
\alpha_{ji} = \begin{cases} 
10 & \text{if } j = i = 1 \text{ or } j = i = 3 \\
1 & \text{elsewhere}.
\end{cases}
\]

We sample 50,000 points from the predictives after a burn-in of 10,000.

The following results are presented in Figure 6:

1. In 6(a)–6(c). The histograms for the three data sets along with the superimposed predictive density curves of the \( f_j \)-PDDP (solid) and \( f_j \)-CAPDDP (dashed).

2. In 6(d)–6(f) the approximate densities of the 50,000 sampled values of the conditional expectations of the \( L_2 \) distances.

   We note how the distribution of \( \mathbb{E}[d_2(f_2, f_3) | w_2, w_3, N^*] \) concentrates near zero, and the similarity of the distributions of \( \mathbb{E}[d_2(f_1, f_2) | w_1, w_2, N^*] \) and \( \mathbb{E}[d_2(f_1, f_3) | w_1, w_3, N^*] \).

3. In 6(g)–6(i) the running averages.

General distinctive features between the CAPDDP and the PDDP models include:

1. The average number of clusters during CAPDDP computations is larger than the average number of clusters in PDDP computations. A detailed comparison between the numerical approximations of the average number of clusters, for both the CAPDDP and the PDDP case, can be found in Table 1 where we compare the average number of clusters coming from the three numerical examples.

2. Borrowing of strength, seems to be sometimes weaker for the undersampled data set in the CAPDDP case. A detailed comparison on the borrowing of strength for the second predictive in the three numerical examples can be found in Table 2. The larger the predictive running average for the \( p_{22} \) selection probability is, the weaker the borrowing of strength between the second data set and the other two covariate data sets.

6. Discussion. We have shown when constructing pairwise dependent random densities, for the purposes of borrowing strength, the random Dirichlet processes used to effect this can be taken to have identical atoms. Random probability measures can be constructed by adapting the weights to these atoms and can provide arbitrary degrees of proximity; from identical to far apart. These distances can be readily evaluated precisely because they have identical atoms and hence share the same supports. Also the time complexity difference between the two
algorithms is substantial. Let $\Delta T$ be the time complexity difference between the PDDP and the CAPDDP algorithms based on a single sweep of the associated Gibbs samplers. Then it is not difficult to verify that

$$\Delta T \propto \left( \frac{m(m+1)}{2} - 1 \right) N^* \sum_{j=1}^{m} n_j,$$

where $N^*$ is a Poisson random variable with mean $c \log(1/u^*)$ and $u^*$ being the global minimum of the auxiliary variables $u_{ji}$ for $1 \leq j \leq m$ and $1 \leq i \leq n_j$ (Muliere, Tardella 1998). This time complexity difference is due to the fact that in the uncommon atom case we have to sample the posterior locations of $m(m+1)/2$ different random measures.

We can also extend this principle to regression scenarios whereby densities $(f_j)$ are characterized by covariates $z$. We can still adopt the idea of common atoms by designing

$$f_z(x) = \int K(x|\theta) P_z(d\theta)$$

where

$$P_z(d\theta) = \sum_{k=1}^{\infty} w_k(z) \delta_{\theta_k}(d\theta).$$

So as before we would have

$$f_z(x) = \sum_{k=1}^{\infty} w_k(z) K(x|\theta_k)$$

and the covariate dependent weights will adapt the weights on the atoms to change the shape of the density. This could be densities which are far apart, based on a covariate pair which are far apart, or densities close to each other when the covariates are close. Indeed this is a simpler version of many Bayesian nonparametric regression models which typically include $z$ in $K(x|z,\theta)$ and have $\theta_k(z)$. We believe these extras are unnecessary.

To conform with our model described in Section 3 we could now take

$$w_k(z) = \int p(s,z) w_k(s,z) ds$$

with $w_k(z,s) = w_k(s,z)$ and $\int p(s,z) ds = 1$ for all $z$. So, for each $(s,z)$, for $s \geq z$, $(w_k(s,z))$ is a stick-breaking set of weights, mutually independent over $(s \geq z)$, and for each $z$, $(p(\cdot,z))$ is a Dirichlet process, mutually independent over $(z)$.

This is not as complicated as it looks, essentially we would replace a finite $m$ with $m = +\infty$. So if covariates are from the set $(z_1, z_2, z_3, \ldots)$ then we would model

$$f_j(x) = f_{z_j}(x) = \sum_{k=1}^{\infty} \sum_{l=1}^{\infty} p_{jl} w_{jk} K(x|\theta_k).$$

Of course, in practice, only a finite number of covariates would be observed.

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| Data sets and sample sizes | Model | Predictive 1 | Predictive 2 | Predictive 3 |
|---------------------------|-------|--------------|--------------|--------------|
| gamma-normal-gamma | CAPDDP | 3.075 | 4.456 | 4.044 |
| $n_1 = 100 \ n_2 = 50 \ n_3 = 100$ | PDDP | 1.571 | 1.079 | 2.183 |
| normal 3-mixtures | CAPDDP | 4.861 | 4.773 | 3.154 |
| $n_1 = 120 \ n_2 = 60 \ n_3 = 120$ | PDDP | 3.090 | 3.041 | 3.062 |
| real example | CAPDDP | 5.045 | 6.178 | 4.328 |
| $n_1 = 143 \ n_2 = 28 \ n_3 = 139$ | PDDP | 3.090 | 3.041 | 3.062 |

Table 2: Running averages for the selection probabilities in predictive $f_2$.

| Data sets and sample sizes | Model | $p_{21}$ | $p_{22}$ | $p_{23}$ |
|---------------------------|-------|----------|----------|----------|
| gamma-normal-gamma | CAPDDP | 0.343 | 0.301 | 0.356 |
| $n_1 = 100 \ n_2 = 50 \ n_3 = 100$ | PDDP | 0.484 | 0.167 | 0.349 |
| normal 3-mixtures | CAPDDP | 0.146 | 0.702 | 0.152 |
| $n_1 = 120 \ n_2 = 60 \ n_3 = 120$ | PDDP | 0.359 | 0.405 | 0.236 |
| real example | CAPDDP | 0.341 | 0.325 | 0.334 |
| $n_1 = 143 \ n_2 = 28 \ n_3 = 139$ | PDDP | 0.305 | 0.328 | 0.366 |
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Figure 1: (a), (b), (c): histograms for the three data sets. (d), (e), (f): predictives for $f_1$, $f_2$ and $f_3$ in the case of the uncommon atoms model PDDP. (g), (h), (i): the corresponding predictives for the case of the common atoms model CAPDDP. In both cases the prior specifications are the same, $c = 1$, $\epsilon = 0.001$ and $\tau = 0.001$. The hyperparameters in relation (6) of the Dirichlet priors are equal to $\alpha_{ji} = 1(j \neq i) + 31(j = i)$. 
Figure 2: Histograms of the conditional expectations a), b), c) and of the running averages d), e), f) of the $L_2$ distances from the CAPDDP model. The same prior specifications apply as in Figure 1.
Figure 3: Histograms of p-values for 2-sample Anderson–Darling tests. Test of 700 pairs of predictive samples of size 100, coming from the PDDP and CAPDDP models, respectively. Burn-in period of 30,000.

Figure 4: Histograms of p-values from 1-sample Anderson–Darling tests, between $f_2$–predictive and $N(0, 2)$. (a), (b): test of 700 pairs of predictive samples of size 100, coming from the PDDP and CAPDDP model, respectively. Burn-in period of 10,000.
Figure 5: Predictives for $f_1$, $f_2$ and $f_3$ coming from the CAPDDP model and expected $L_2$ distances, for different sample sizes. (a)–(f): equal sample sizes $n_1 = n_2 = n_3 = 300$. (g)–(l): the initial sample is reduced to size $n_1 = n_3 = 120$ and $n_2 = 60$. In both cases the prior specifications are the same, $c = 0.1$, $\epsilon = 0.001$ and $\tau = 0.001$. The hyperparameters in relation (6) of the Dirichlet priors are equal to $\alpha_{ji} = 1$. Burn-in period of 10,000.
Figure 6: (a), (b), (c): histograms for the three real data sets with the CAPDDP and PDDP density estimations superimposed. (d), (e), (f): the associated expected pairwise $L_2$ distances $L_2 CE(f_i, f_j)$. (g), (h), (i): the running averages corresponding to the expected pairwise distances $RAV L_2 CE (f_i, f_j)$. In all cases the prior specifications are the same, $c = 1$, $\epsilon = 0.001$ and $\tau = 0.001$. The hyperparameters in relation (6) of the Dirichlet priors are $\alpha_{ji} = 1$, for all $1 \leq j, i \leq 3$. Burn-in period of 10,000.