A Bayesian hierarchical model for related densities using Pólya trees

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Abstract

Bayesian hierarchical models are used to share information between related samples and obtain more accurate estimates of sample-level parameters, common structure, and variation between samples. When the parameter of interest is the distribution or density of a continuous variable, a hierarchical model for continuous distributions is required. A number of such models have been described in the literature using extensions of the Dirichlet process and related processes, typically as a distribution on the parameters of a mixing kernel. We propose a new hierarchical model based on the Pólya tree, which allows direct modeling of densities and enjoys some computational advantages over the Dirichlet process. The Pólya tree also allows more flexible modeling of the variation between samples, providing more informed shrinkage and permitting posterior inference on the dispersion function, which quantifies the variation among sample densities. We also show how the model can be extended to cluster samples in situations where the observed samples are believed to have been drawn from several latent populations.

1 Introduction

Many statistical applications deal with learning and comparing the distributions of two or more related samples. We may be interested in learning how samples are similar or testing whether they are distinguishably different from each other. Because distributions are complex infinite-dimensional objects, classical approaches work with low-dimensional parameterizations of the distribution. Analysis of variance, for example, reduces distributions to a mean and variance, which are sufficient under the assumption of normality. A wide range of other parametric models within both the Bayesian and frequentist inferential frameworks use other parameterizations of the distribution to reduce the dimensionality of the problem. Classical nonparametric approaches use features of the samples such as medians (Westenberg, 1948), rank-based scores (Wilcoxon, 1945), or summaries of the empirical distribution functions, as in the Kolmogorov-Smirnov (Kolmogorov, 1933) and Cramér-von Mises tests (Anderson, 1962).
A number of Bayesian nonparametric approaches embrace the infinite-dimensional nature of the problem using extensions of Dirichlet processes. The Hierarchical Dirichlet process (Beal et al., 2002; Teh et al., 2006) builds a hierarchical model using the Dirichlet process, allowing it to share information between samples. The Nested Dirichlet process of Rodríguez et al. (2008) takes a different approach, using a Dirichlet process as the base measure of a second Dirichlet process. This induces clustering in the samples, with samples in a cluster being modeled with a single density. Müller et al. (2004) model each sample density as a mixture of two components: one Dirichlet process mixture of Gaussians representing common structure between samples, and a second Dirichlet process mixture of Gaussians representing the idiosyncratic structure of the given sample. A variety of other dependent Dirichlet Processes (MacEachern, 1999) have been described in the literature. Teh and Jordan (2010) give an overview of hierarchical models based on the Dirichlet process.

While the Dirichlet process has been the basis of most of the work in this area, work has also been done on hierarchical extensions of other priors. For example, Teh (2006) defines a Hierarchical Pitman-Yor process, taking advantage of the more flexible clustering structure of the Pitman-Yor process over the Dirichlet process. Camerlenghi et al. (2017) consider hierarchical models based on Normalized Random Measures (Barrios et al., 2013), which includes both the Dirichlet process and the Pitman-Yor process as special cases.

An alternative approach for modeling densities within the Bayesian nonparametric framework is to use a model derived from Pólya trees (Freedman, 1963). Pólya trees are a class of tail-free prior in which an infinite recursive binary partition is placed on the sample space, and probability mass assigned to the elements of the partition by a corresponding infinite sequence of Beta-distributed random variables. A special case gives the familiar Dirichlet process (Ferguson, 1973), but the Pólya tree family is considerably more flexible. With appropriate specification of the prior parameters, the Pólya tree assigns probability 1 to the set of absolutely continuous distributions (Ferguson, 1974). This property allows it to be used to directly model probability densities without the encumbrance of a mixing kernel.

The Pólya tree model allows tractable computation of the marginal likelihood, which has made it popular in Bayesian hypothesis testing of nonparametric density models. Examples include Berger and Guglielmi (2001); Ma and Wong (2011); Chen and Hanson (2014); Holmes et al. (2015); Soriano and Ma (2017); Filippi and Holmes (2017). These approaches are unsatisfactory when estimation and prediction rather than formal hypothesis testing are of primary interest. Statisticians have recognized the benefits of partial shrinkage as far back as Stein’s shrinkage estimator for the mean of a multivariate normal distribution (Stein, 1956). We may expect that related samples will have similar but not identical distributions. In this situation, neither independence nor a single common distribution are appropriate models. A partial shrinkage model allows borrowing of information across samples while preserving between-sample variation.

Within the Bayesian inference framework, partial shrinkage is naturally achieved with a hierarchical model. While a simple hierarchy of Pólya trees is possible and is described herein, we build on the richer Adaptive Pólya tree model of Ma (2017). This model allows us to learn the concentration parameters of the Pólya tree, rather than fixing them in the prior. In contrast to Dirichlet process-based models, the richer structure of the Pólya tree allows us to model both the means and the between-group variation of the densities in a fully nonparametric manner. This not only improves the estimation of the distributions, but also
allows us to perform inference on how the variation between groups differs over the sample space.

In Section 2 we describe the model and contrast it with several existing models. We discuss Bayesian posterior inference and computation in Section 3. In Section 4 we give theoretical grounding for the appropriateness of the method. Section 5 describes two ways in which the model allows us to go beyond the capabilities of existing models. We show simulation results in Section 6 and demonstrate application to real data in Section 7. Finally, we conclude with some discussion in Section 8.

2 Model

2.1 Reviewing the Pólya tree construction

We begin with a brief sketch of the Pólya tree; the reader interested in the mathematical details should refer to [Mauldin et al. (1992); Lavine (1992, 1994)]. Applications of the Pólya tree are discussed in, for example, [Hanson and Johnson (2002); Walker et al. (1999)]. The Pólya tree consists of an infinite recursive partition $\mathcal{A}$ of the sample space and a corresponding infinite sequence of Beta-distributed random variables which assign mass to the various regions $A \in \mathcal{A}$ of the partition. Figure 1 illustrates the partitioning sequentially. In this illustration our sample space is the interval $(0, 1]$ on the real line, and our prior mean, shown in the first pane, is the uniform distribution on that interval. At each level of the recursive partition we cut each region in half at the midpoint. Although arbitrary partitions may be used, the dyadic partition described here is convenient and is often used as a default partition in the absence of a compelling reason to use a different one. Other partitions may be more convenient in the presence, for example, of censored data [Mulleire and Walker, 1997]. The second pane shows the result after the first cut and mass allocation, in this case the majority of the mass having been allocated to the right-hand side. In the next step we cut each of the two regions from the second pane in half again, and assign the probability mass to each to its children according to a Beta-distributed random variable. This results in four regions, shown in the third pane, which are again cut and mass distributed in the fourth pane. The process continues indefinitely.

We denote the Pólya tree prior as $Q \sim PT(Q_0, \nu)$, where $Q_0$ is the centering distribution and $\nu$ is an (infinite dimensional) concentration parameter describing how much $Q$ is expected to vary from $Q_0$. The parameters of the sequence of Beta distributions from which the mass allocations are drawn are derived very simply from $Q_0$ and $\nu$. For an arbitrary region $A$ belonging to the recursive partition $\mathcal{A}$, the fraction of the mass allocated to the left child $A_\ell$ of $A$ is given by the random variable

$$\theta(A) \sim \text{Beta}(\theta_0(A)\nu(A), (1 - \theta_0(A))\nu(A)),$$

where $\theta_0(A) = Q_0(A_\ell)/Q_0(A)$, with the remainder of the mass allocated to the right child $A_r$. $Q_0$ thus determines the mean of the mass allocations (and hence the expectation of the resulting density), while $\nu = \{\nu(A) : A \in \mathcal{A}\}$ controls the variation of the mass allocations, and hence the dispersion of $Q$ around $Q_0$. Alternatively, $\nu$ controls the strength of the shrinkage of the posterior mean density from the empirical process towards $Q_0$. With an
appropriate choice of $\nu$, the Pólya tree prior almost surely generates an absolutely continuous distribution [Kraft, 1964].

### 2.2 The Hierarchical Pólya Tree

It is conceptually straightforward to extend the Pólya tree to a hierarchical model. Let $X_1, \ldots, X_k$ be $k$ samples arising from related distributions on a complete, separable space $\Omega$. For ease of exposition we again use $\Omega = (0, 1]$, though like the Pólya tree the model can be applied to more general sample spaces. We model these samples as coming from $k$ exchangeable distributions $Q_i$, which are centered at a common underlying measure $Q$, itself unknown. Applying Pólya tree priors to both $Q$ and the $Q_i$ gives us the hierarchical model

$$
\begin{align*}
X_{ij} | Q_i & \sim Q_i \\
Q_i | Q & \sim \text{PT}(Q, \tau) \\
Q & \sim \text{PT}(Q_0, \nu).
\end{align*}
$$

Here $Q_0$ is the overall prior mean, $\tau$ controls the variation among samples around the common structure $Q$, and $\nu$ controls the variation of the common structure from $Q_0$, which determines the smoothness of $Q$. This model, which we call the Hierarchical Pólya tree, allows nonparametric estimation of the sample distributions $Q_i$ and the common structure $Q$. The Hierarchical Pólya tree model is illustrated in Figure 2. The first row shows the upper level of the hierarchy, which like the basic Pólya tree illustrated in Figure 1 is centered at the uniform distribution on $(0, 1]$. The second row shows the lower level of the hierarchy, the individual group distributions $Q_i$ conditioned on $Q$. They follow exactly the same Pólya tree construction, but each cut is centered on the corresponding cut from $Q$, rather than on the uniformed distribution. $Q$ captures the common structure of the groups, while the $Q_i$ model the idiosyncratic structure of each group.

The hierarchy of Pólya trees translates directly to the decomposed space as a hierarchical model for Beta random variables. For an arbitrary region $A \in \mathcal{A}$, we have

$$
\begin{align*}
\theta_i(A) | \theta(A) & \sim \text{Beta}(\theta(A)\tau(A), (1 - \theta(A))\tau(A)) \\
\theta(A) & \sim \text{Beta}(\theta_0(A)\nu(A), (1 - \theta_0(A))\nu(A)).
\end{align*}
$$

Figure 1: An illustration of the recursive partitioning and probability allocation of the standard Pólya tree.
The representation of the hierarchy of Pólya trees as a hierarchy of Beta random variables allows tractable posterior inference, as described in Section 3.

### 2.3 The Stochastically Increasing Shrinkage prior on dispersion

The Pólya tree’s concentration parameter is traditionally set to increase with depth at a predetermined rate to ensure absolute continuity, with a constant multiplicative term to control the overall level of variation which may be treated as a tuning parameter (as in Berger and Guglielmi (2001)) or have a prior placed on it. Hanson (2006) discusses some of the necessary considerations when placing a prior on this parameter. However, Ma (2017) shows that putting a flexible nonparametric prior on the concentration parameter allows the Pólya tree to learn the true distribution more accurately, particularly when the smoothness of the underlying density varies over the sample space. We can extend the Hierarchical Pólya tree model by placing priors on both concentration parameters. In addition to more accurate inference on $Q$ and the $Q_i$, putting a prior distribution on $\tau$ allows us to learn the variation between samples in a nonparametric way. That is, we can estimate a posterior dispersion function which summarizes the variability between sample densities at any given point in the sample space. Dispersion can be measured in a variety of ways; in Section 5.1 we show how to derive the posterior mean variance of the densities and interpret a standardized version using the coefficient of variation to correct for the height of the density. Nonparametric inference on the variation between samples across the sample space is made possible by the flexibility of the Pólya tree model. We contrast how several other models treat between-sample variation in Section 2.5.

A simple approach is to put independent priors on the variance of each Beta random variable. However, we expect spatial structure in the dispersion function—locations near each other in the sample space are likely to have similar levels of variation. The variance of the Beta distributions is generally expected to be smaller at deeper levels of the partition, but the decay in the variance may be heterogeneous over the sample space depending on the local smoothness of the densities. While the recursive partitioning allows independent priors to capture some spatial structure, we can do better by introducing dependency between regions in the partition. Ma (2017) introduces Markov dependency on the concentration parameter, following the tree topology.
The Stochastically Increasing Shrinkage (SIS) prior introduces a state variable \( S(A) \) supported on a finite set of integers \( 1, \ldots, I \), corresponding to decreasing prior variance and increasing shrinkage for the Beta random variables. In particular, the last state \( I \) corresponds to complete shrinkage or zero variance, which is achieved through fixing \( \nu(A) \) at \( \infty \) when \( S(A) = I \). For example, we may have \( S(A) \in \{1, 2, 3, 4\} \) with \( S(A) = i \) implying \( \nu(A) \sim F_i \) with the \( F_i \) stochastically ordered \( F_1 \prec F_2 \prec F_3 \prec F_4 \) and \( F_4 \) being a point mass at infinity. The number of states and the corresponding distributions can be chosen to balance the flexibility and computational complexity of the model. A simple way to enforce such a stochastic ordering is through partitioning the support of the concentration parameter \( \nu(A) \) into disjoint intervals. Given these latent states, the SIS prior adopts a transition probability matrix for \( S(A) \mid S(\text{Par}(A)) \), denoted \( \Gamma(A) \). Ma (2017) discusses several prior possibilities for this transition matrix. We adopt the recommendation given there to use an exponential kernel for the transition probabilities. The resulting transition matrix can be given as

\[
\Gamma(A) = \begin{bmatrix}
\frac{1}{\sum_{i=0}^{I-1} e^{\beta i}} & \frac{e^{\beta}}{\sum_{i=0}^{I-1} e^{\beta i}} & \cdots & \frac{e^{\beta(I-1)}}{\sum_{i=0}^{I-1} e^{\beta i}} \\
0 & \frac{1}{\sum_{i=0}^{I-2} e^{\beta i}} & \cdots & \frac{e^{\beta(I-2)}}{\sum_{i=0}^{I-2} e^{\beta i}} \\
\vdots & \vdots & \ddots & \vdots \\
0 & 0 & \cdots & 1
\end{bmatrix}.
\]

This upper-triangular transition probability matrix induces stochastically increasing shrinkage, and ensures that the model generates absolutely continuous densities (see Theorem 1). The parameter \( \beta \) controls the stickiness of the transition; that is, larger values of beta correspond to a stronger dependence in the shrinkage state between adjacent nodes in the Pólya Tree. \( \beta \) can be set equal to zero, in which case the transition is uniform between the states with shrinkage no less than the current node. We denote the SIS prior

\[ \nu \sim \text{SIS}(\Gamma). \]

Figure 3 illustrates the SIS prior in action. As you move down to finer resolutions the shrinkage state tends to increase, eventually reaching complete shrinkage. Because the transitions are stochastic and the state of each node can be learned from the data, the amount of shrinkage or prior variance can vary over the sample space to capture large smooth features in one part of the sample space and smaller scale features in another part. This allows the resulting density to have heterogeneous smoothness across the sample space.
2.4 The Hierarchical Adaptive Pólya Tree

Having described the SIS prior, we can adopt this prior for the concentration parameters $\tau$ and $\nu$, and write the complete model as follows:

$$
X_{ij} \mid Q_i \overset{\text{ind}}{\sim} Q_i \\
Q_i \mid Q, \tau \overset{\text{iid}}{\sim} PT(Q, \tau) \\
Q \mid \nu \sim PT(Q_0, \nu) \\
\tau \sim SIS(\Gamma_\tau) \\
\nu \sim SIS(\Gamma_\nu).
$$

We call this model the Hierarchical Adaptive Pólya Tree (HAPT). In contrast to existing models, this specification allows fully nonparametric inference on both the densities and the variation between densities. The inclusion of the SIS priors allows the model to adapt the level of shrinkage or information borrowing in different parts of the sample space to more accurately capture the densities of each group, rather than using fixed uniform shrinkage. Figure 4 shows a graphical representation of the model.
Figure 4: A graphical representation of the model. The boxes outline the parts of the model whose posteriors are computed with each of the three strategies described in Section 3.1. From left to right: The posterior of the $Q_i$ conditional on other parameters is conjugate and can be integrated out numerically; the posterior of $Q, \nu, \tau$ conditional on $S_\nu$ and $S_\tau$ is approximated using quadrature; and the posterior of $S_\nu$ and $S_\tau$ is computed using HMM methods.

2.4.1 Choice of prior parameters
The Hierarchical Adaptive Pólya Tree has three prior parameters for which values must be chosen. The most straightforward is the prior mean measure $Q_0$, which we typically choose from a parametric family. Some consideration must be given to the choice of the SIS prior parameters $\Gamma_\tau$ and $\Gamma_\nu$.

Ma (2017) recommends an empirical Bayes approach to setting the $\beta$ parameters, and where computationally feasible we may also recommend this approach. When the dataset is quite large or HAPT is embedded in a larger algorithm, as in Section 5.2, empirical Bayes estimation may not be practical. Based on our experience the model fit is not very sensitive to reasonable variation in this parameter; we suggest default values of $\beta = 1$ for both $\Gamma_\tau$ and $\Gamma_\nu$.

2.5 Comparison to existing models
The most prominent existing nonparametric models for estimation of related distributions are based on the Dirichlet process, including the Hierarchical Dirichlet process (HDP) (Teh et al., 2006), Nested Dirichlet process (NDP) (Rodríguez et al., 2008; Rodríguez and Dunson, 2014), and the hierarchical mixture of common and idiosyncratic Dirichlet process model of Müller, Quintana, and Rosner (MQR) (Müller et al., 2004). The Hierarchical Adaptive Pólya tree enjoys several advantages over these methods:

1. Nonparametric estimation of between-sample variation. The HDP and NDP have a single concentration parameter that controls the dependence between samples. MQR has one parameter per sample that controls what proportion of the sample is explained by common structure and how much by idiosyncratic structure.

In contrast, HAPT places a fully nonparametric prior on the variation between samples,
which allows it to learn spatially heterogeneous variation between samples. Indeed, the variation between samples at different locations of the sample space may be of primary interest in some scientific applications: learning where common structure is largely preserved between samples and where distributions vary widely may point the way to understanding important underlying phenomena.

2. **Computation.** HDP, NDP, and MQR all rely on MCMC methods to draw from the posterior. The Hierarchical Adaptive Pólya tree is not fully conjugate, but the necessary integration can be split into low-dimensional integrals and approximated extremely quickly using adaptive quadrature methods, without concerns about Markov chain convergence. See Section 3.1 for details.

3. **Interpretability.** HAPT provides an easily interpretable estimate of the common structure: The posterior estimate of $Q$ is both the estimate of the mean density across samples, and the expected value of the posterior predictive for a new sample. In contrast, the HDP estimates a discrete instead of continuous distribution, and the NDP does not provide any estimate of common structure. MQR provides an estimate of common structure, but it is neither the mean of sample distributions nor a posterior predictive estimate. Interpretation of the common structure in the MQR model is most straightforward if variation between samples involves contamination of an underlying distribution by an idiosyncratic process for each sample.

Other existing models based on Normalized Random Measures (Regazzini et al., 2003) or more generally Poisson-Kingman models (Pitman, 2003), including the Hierarchical Pitman-Yor model (Teh, 2006) are subject, to various extents, to limitations similar to those of the models based on the Dirichlet process. Recent works such as Griffin et al. (2013); Griffin and Leisen (2017); Camerlenghi et al. (2017); Camerlenghi et al. (2018) provide more flexible means to modeling the dependency among multiple samples than the classical models, but the aforementioned benefits of the Pólya tree remain even in view of these state-of-the-art models.

3 **Bayesian inference and computation**

The HAPT model is partially conjugate: the conditional posterior for $Q_i \mid Q, \tau, \nu, S_\tau, S_\nu$ is a standard Pólya tree. Though not conjugate, the remaining joint posterior for $Q, \tau, \nu \mid S_\tau, S_\nu$ can be reliably approximated using adaptive quadrature methods. The computational strategies used are described in Section 3.1.

To derive the posterior we use the representation of the Pólya trees $Q$ and $Q_i$ in terms of Beta-distributed random variables $\theta(A)$ and $\theta_i(A)$ for each node $A$ of the tree. With this notation, The second and third lines in (1) can be written in terms of the $\theta$ and $\theta_i$ as in Equation 2:

$$
\begin{align*}
\theta_i(A) & \mid \theta(A) \sim \text{Beta}(\theta(A)\tau(A), (1 - \theta(A))\tau(A)) \\
\theta(A) & \sim \text{Beta}(\theta_0(A)\nu(A), (1 - \theta_0(A))\nu(A)).
\end{align*}
$$
Including the concentration parameters, we can write the posterior for the parameters of a region $A$ in the following form conditional on the state parameters $S_\tau(A), S_\nu(A)$:

$$
\pi(\theta(A), \tau(A), \nu(A) \mid S_\tau(A), S_\nu(A), X) \propto \theta(A)^{\theta_0(A)\nu(A) - 1}(1 - \theta(A))^{(1 - \theta_0(A))\nu(A) - 1} \times [B(\theta(A)\tau(A), (1 - \theta(A))\tau(A))]^{-k} \times \prod_{i=1}^{k} B(\theta(A)\tau(A) + n_i(A_\ell), (1 - \theta(A))\tau(A) + n_i(A_r)) \times 
\pi(\tau(A) \mid S_\tau(A))\pi(\nu(A) \mid S_\nu(A)).
$$

(3)

where $B(\cdot, \cdot)$ is the Beta function. The full posterior is the summation of Equation (3) over the possible states of $S_\tau$ and $S_\nu$, with their respective priors factored in. The derivation of this posterior is given in the supplementary material.

### 3.1 Computation

Posterior computation of the HAPT model requires three distinct computational strategies. We split the model (see Figure 4) into three parts, each of which requires a different approach. Each part of the model is conditioned on all parameters which are further to the right in Figure 4. We describe how to integrate out each of the first two parts, which reduces the problem to evaluating the posterior probabilities of all possible combinations of the state variables $S_\tau, S_\nu$.

1. $\pi(Q_i \mid Q, \tau, \nu, S_\tau, S_\nu, X)$: The individual sample densities $Q_i$, conditional on all other parameters, are a priori distributed according to a standard Pólya tree. The corresponding conditional posterior is therefore also a Pólya tree. This allows us to integrate out the $Q_i$ when computing the posterior. If individual sample densities are of inferential interest their posteriors can easily be reconstructed after the main posterior computation is completed.

2. $\pi(Q, \tau, \nu \mid S_\tau, S_\nu, X)$: The remaining continuous parts of the joint model, namely the common structure $Q$ and the continuous concentration parameters $\tau$ and $\nu$, conditioned on the discrete state parameters $S_\tau$ and $S_\nu$, are not conjugate and must be integrated numerically. Because all parameter dependence across nodes in the Pólya tree topology is restricted to the discrete state parameters, by conditioning on those parameters we are able to compute the posterior of the remaining parameters for each node of the tree independently.

This has two significant implications. First, rather than tackling a very high dimensional integral over the product space of the parameters for all nodes, we have a much more tractable collection of low-dimensional integrals: we need only integrate the three-dimensional joint posterior of $\theta(A), \tau(A), \nu(A)$ for each region $A$ in the Pólya tree. Each of these integrals is tractable using standard quadrature techniques. Second, these integrals can be computed in parallel.
An additional observation allows us to further accelerate the adaptive quadrature. We
note that the joint posterior distribution for $\theta(A), \tau(A), \nu(A)$ conditional on $S_{\tau}(A)$ and
$S_{\nu}(A)$, with the other parameters integrated out, can be factored as

$$\pi(\theta(A), \tau(A), \nu(A) \mid S_{\nu}(A), S_{\tau}(A), X) = g(\theta(A), \tau(A)) \times h(\theta(A), \nu(A)).$$

This allows us to factor the three dimensional integral:

$$\int \int \int \pi(\theta(A), \tau(A), \nu(A) \mid S_{\nu}(A), S_{\tau}(A), x) \ d\tau(A) \ d\nu(A) \ d\theta(A)$$

$$= \int \left[ \int g(\theta(A), \tau(A)) \ d\tau(A) \right] \left[ \int h(\theta(A), \nu(A)) \ d\nu(A) \right] \ d\theta(A),$$

This factorization effectively reduces the dimensionality of the integral: rather than
evaluating the unnormalized posterior at points throughout a 3-dimensional space, we
need only evaluate it on the union of two 2-dimensional spaces.

3. The posterior distribution of the state parameters $S_{\tau}$ and $S_{\nu}$ at first appears to be
the most intimidating part of the model: It is a distribution over the product space
of a large number of discrete parameters, resulting in an enormous number of level
combinations. The naive computation of the joint posterior,

$$P \left( \bigcap_{A \in A} S_{\tau}(A) = i_A, S_{\nu}(A) = j_A \right)$$

is straightforward but needs to be repeated for every possible combination of $S_{\tau}(A)$
and $S_{\nu}(A)$ for every node in the tree, which is computationally prohibitive. Here the
Markov dependency structure comes to our rescue. The shrinkage states constitute a
Hidden Markov Model following the tree topology (Crouse et al., 1998), and we can
factor the joint distribution and calculate the posterior probabilities using a forward-
backward algorithm in a manner analogous to inference strategies for linear Hidden
Markov Models.

During the forward-backward algorithm we can compute expectations of any function
that can be expressed in the form

$$f(\cdot) = \prod_A f^*(\theta(A), \tau(A), \nu(A)),$$

where $f^*(\cdot)$ is an arbitrary function in $L_1$. This includes the marginal likelihood, the
expected value of the estimated common density $q(\cdot)$ or any individual sample density
$q_i(\cdot)$ at any given point, expectations of random variables $Y \sim Q$ or $Y_i \sim Q_i$, and a
wide variety of other functions, such as the variance function described in Section 5.1.

This computation is recursive, and we give a brief example of how it is carried out
for the marginal likelihood. The previous two computational strategies give us the
ability to calculate (up to quadrature approximation) the marginal likelihood, within
a given node, of all remaining parameters conditional on $S_{\tau}$ and $S_{\nu}$. Combining
this with the prior transition parameters specified in $\Gamma$ we are able to calculate the posterior probabilities for $S_\tau(A)$ and $S_\nu(A)$, and the overall marginal likelihood of the distribution on $A$, by considering the recursively-calculated marginal likelihoods of the child regions of $A$ under each possible state.

Obviously this recursion requires a stopping point. The simplest method is to truncate the tree at a predetermined depth. [Hanson (2006)] offers some guidance on how to choose the depth of a truncated Pólya tree based on sample size and other considerations. We recommend using as large a tree as is computationally feasible in order to minimize approximation errors due to truncation. If the data deviate very strongly from the prior distribution—as is common, for example, in high-dimensional settings—a more sophisticated approach may be required, such as truncating a branch of the tree when it reaches a depth where the node contains only a few data points.

4 Theoretical results

We describe several desirable theoretical properties of the HAPT model. Proofs are given in the supplementary material.

**Theorem 1** (Absolute Continuity) Let $Q, Q_1, \ldots, Q_k$ be random measures distributed according to a HAPT model with base measure $Q_0$. If the SIS priors on $\tau$ and $\nu$ each include a complete shrinkage state that absorbs all possible chains in a finite number of steps with probability 1, then $Q, Q_1, \ldots, Q_k \ll Q_0$ with probability 1.

**Remark 1** A sufficient condition for the complete shrinkage state to absorb all chains in a finite number of steps with probability 1 is that the transition probability from every other state to the complete shrinkage state is bounded away from zero, which is satisfied by our choice of $\Gamma$.

**Theorem 2** (Prior support) Let $f, f_1, \ldots, f_k$ be the probability density functions corresponding to arbitrary absolutely continuous distributions on $\Omega$. Let $q, q_1, \ldots, q_k$ be corresponding densities from a HAPT model satisfying

1. $Q_0$ and $\mu$ are equivalent measures, that is $Q_0 \ll \mu$ and $\mu \ll Q_0$;

2. $I_\tau, I_\nu \geq 2$, i.e. there are at least two shrinkage states, including the complete shrinkage state, at each level.

Then $f, f_1, \ldots, f_k$ are in the $L_1$ prior support.

Our final result gives posterior consistency in the case where the groups have equal sample sizes:

**Theorem 3** (Posterior consistency) Let $D_n = \{X_1, \ldots, X_k\}$ be observed data consisting of $k$ independent samples, each of size $n$, from absolutely continuous distributions $P_1, \ldots, P_k$. Let $\pi(\cdot)$ be a Hierarchical Adaptive Pólya tree model on the $k$ densities with overall prior
mean $Q_0^*$, and let $\pi(\cdot \mid D_n)$ be the corresponding posterior. If $P_i \ll Q_0^*$ for all $i$ then we have posterior consistency under the weak topology. That is,

$$\pi(U \mid D_n) \to 1 \text{ as } n \to \infty$$

for any weak neighborhood $U$ of the product measure $P_1 \times \cdots \times P_k$.

5 Methodological applications of the HAPT

We present two ways in which the HAPT model can be applied to infer structure that existing models have not been able to capture. The first application is the ability of HAPT to model the "dispersion function" (defined below) on the sample space; we show how to calculate the posterior dispersion function from the $\tau$ parameter. According to our knowledge, at the time of the writing, no existing model permits inference on the variation between sample densities in this manner. The second application is clustering samples based on their distributions, while allowing for within-cluster variation. While the Nested Dirichlet process clusters distributions, it allows no variation (beyond sampling variation) within clusters. The importance of allowing for variation within clusters was first pointed out by MacEachern (2008), who described a dependent Dirichlet process which would incorporate within-cluster variation.

5.1 Inferring the between-sample dispersion function

The primary target of inference in problems with multiple samples is often the variation between samples. It is this inference, for example, which lends ANOVA its name, though the model is typically presented in terms of the overall and sample means.

In the HAPT model, variation between samples is captured by $\tau$, an infinite-dimensional parameter which estimates variation at different locations and scales. Rather than trying to provide guidance on how to interpret the multiscale structure in $\tau$, we show how to recast it into an estimate of the variation between samples at any given point in the sample space, giving us a posterior dispersion function analogous to the posterior mean function.

Let $q_\star$ be the posterior predictive density for a new sample, with corresponding Beta-distributed random variables $\theta_\star(A)$ for each region $A$ in the recursive partition. Since $q_\star$ is random, we can estimate the variance function $v : \Omega \to \mathbb{R}^+$ which gives, for any point $x$ in the sample space, the variance of $q_\star(x)$ conditional on the density of the common structure, $q(\cdot)$. This is analogous to the variance between treatments in traditional ANOVA. We have

$$q_\star(x) = q_0(x) \prod_{A \ni x} \left( \frac{\theta_\star(A)}{||A||} \right)^{1(x \in A)} \left( \frac{1 - \theta_\star(A)}{||A||} \right)^{1(x \in \bar{A})},$$

where $q_0(\cdot)$ is the density corresponding to the prior mean distribution $Q_0$. We note that

$$\theta_\star(A) \theta(A), \tau(A) \sim \text{Beta}(\theta(A) \tau(A), (1 - \theta(A)) \tau(A)).$$

We will need the facts that

$$\mathbb{E}(\theta_\star(A) \mid \theta(A), \tau(A)) = \theta(A)$$
and

$$\text{Var}(\theta_*(A) \mid \theta(A), \tau(A)) = \text{Var}(1 - \theta_*(A) \mid \theta(A), \tau(A)) = \frac{\theta(A)(1 - \theta(A))}{\tau(A) + 1},$$

which together imply

$$\mathbb{E}(\theta_*(A)^2 \mid \theta(A), \tau(A)) = \frac{\theta(A)(1 - \theta(A))}{\tau(A) + 1} + \theta(A)^2$$

$$= \frac{\theta(A)(\theta(A)\tau(A) + 1)}{\tau(A) + 1}$$

$$\mathbb{E}((1 - \theta_*(A))^2 \mid \theta(A), \tau(A)) = \frac{\theta(A)(1 - \theta(A))}{\tau(A) + 1} + (1 - \theta(A))^2$$

$$= \frac{(1 - \theta(A))(1 - \theta(A))\tau(A) + 1}{\tau(A) + 1}.$$

Let \( \theta(x) = \{\theta(A) : A \ni x\} \). It is clear that \( \theta(x) \) contains exactly the information about \( q \) which is relevant to \( q_*(x) \); that is, the distribution of \( q_*(x) \mid \theta(x) \) is identical to the distribution of \( q_*(x) \mid q \). With the above, we can calculate

$$\text{Var}(q_*(x) \mid q) = \mathbb{E}_{\theta(x), \tau} \left[ \text{Var}(q_*(x) \mid q, \tau, S_\tau) \mid q \right] + \text{Var}_{\theta(x), \tau} \left[ \mathbb{E}(q_*(x) \mid q, \tau, S_\tau) \mid q \right] =$$

$$q_0(x)^2 \mathbb{E}_{\theta(x), \tau} \left[ \text{Var} \left( \prod_{A \ni x} \left( \frac{\theta_*(A)}{||A_\ell||} \right)^{1(x \in A_\ell)} \left( \frac{1 - \theta_*(A)}{||A_\ell||} \right)^{1(x \in A_r)} \right) \mid \theta(x), \tau, S_\tau \right] +$$

$$q_0(x)^2 \text{Var}_{\theta(x), \tau} \left[ \mathbb{E} \left( \prod_{A \ni x} \left( \frac{\theta_*(A)}{||A_\ell||} \right)^{1(x \in A_\ell)} \left( \frac{1 - \theta_*(A)}{||A_\ell||} \right)^{1(x \in A_r)} \right) \mid \theta(x), \tau, S_\tau \right] \mid \theta(x) \right].$$

We note that the expectation in the second term can be factored into a product of expectations, none of which depend on \( \tau \) or \( S_\tau \). The variance of this product is thus zero. We rewrite the remaining line using the identity \( \text{Var}(X) = \mathbb{E}(X^2) - \mathbb{E}(X)^2 \):

$$\text{Var}(q_*(x) \mid q) = q_0(x)^2 \times$$

$$\mathbb{E}_{\theta(x)} \left[ \mathbb{E} \left( \prod_{A \ni x} \left( \frac{\theta_*(A)}{||A_\ell||} \right)^{1(x \in A_\ell)} \left( \frac{1 - \theta_*(A)}{||A_\ell||} \right)^{1(x \in A_r)} \right)^2 \mid \theta(x), \tau, S_\tau \right] -$$

$$\left( \mathbb{E} \left( \prod_{A \ni x} \left( \frac{\theta_*(A)}{||A_\ell||} \right)^{1(x \in A_\ell)} \left( \frac{1 - \theta_*(A)}{||A_\ell||} \right)^{1(x \in A_r)} \right) \mid \theta(x), \tau, S_\tau \right)^2 \mid \theta(x) \right].$$

Conditional on \( \theta(x) \) and \( S_\tau \), the terms in both products are mutually independent, both \( a \)
We call this expectation the variance function \( \text{Var}(q_*(x) \mid q) = q_0(x)^2 \times \)

\[
\mathbb{E}_{S_r, \tau} \left[ \prod_{A \ni x} \mathbb{E} \left( \left( \frac{\|A\|}{\|A_r\|} \right)^{1(x \in A_r)} \left( \frac{1 - \theta_*(A)}{\|A_r\|} \right)^{1(x \in A_r)} \right)^2 \theta(A), \tau(A), S_r(A) \right] - \]

\[\prod_{A \ni x} \mathbb{E} \left( \left( \frac{\|A\|}{\|A_r\|} \right)^{1(x \in A_r)} \left( \frac{1 - \theta_*(A)}{\|A_r\|} \right)^{1(x \in A_r)} \right)^2 \theta(A), \tau(A), S_r(A) \right] \frac{1}{\|A_r\|^2} \left( \frac{1 - \theta(A)}{\|A_r\|} \right)^{1(x \in A_r)} \frac{1}{\|A_r\|^2} \left( \frac{1 - \theta(A)}{\|A_r\|} \right)^{1(x \in A_r)} \right] \cdot \]

Since \( q \) is itself unknown, we take the expectation with respect to it:

\[
\mathbb{E}_q \left[ \mathbb{E}_{S_r, \tau} \left[ \prod_{A \ni x} \mathbb{E} \left( \left( \frac{\|A\|}{\|A_r\|} \right)^{1(x \in A_r)} \left( \frac{1 - \theta_*(A)}{\|A_r\|} \right)^{1(x \in A_r)} \right)^2 \theta(A), \tau(A), S_r(A) \right] - \right]

\[\prod_{A \ni x} \mathbb{E} \left( \left( \frac{\|A\|}{\|A_r\|} \right)^{1(x \in A_r)} \left( \frac{1 - \theta_*(A)}{\|A_r\|} \right)^{1(x \in A_r)} \right)^2 \theta(A), \tau(A), S_r(A) \right] \frac{1}{\|A_r\|^2} \left( \frac{1 - \theta(A)}{\|A_r\|} \right)^{1(x \in A_r)} \frac{1}{\|A_r\|^2} \left( \frac{1 - \theta(A)}{\|A_r\|} \right)^{1(x \in A_r)} \right] \cdot \]

We call this expectation the variance function. Finally, we note that conditional on \( S_r, \theta(A), \tau(A) \) are independent of \( \theta(A'), \tau(A') \) for any two distinct regions \( A \) and \( A' \). This allows
us to rearrange our expectation to obtain

\[ \mathbb{E}_q [\text{Var}(q_\star(x) \mid q)] = q_0(x)^2 \times \]

\[ \mathbb{E}_{S, \tau} \left[ \prod_{A \ni x} ||A||^2 \mathbb{E}_{\theta(A), \tau(A)} \left( \frac{\theta(A)(\theta(A)\tau(A) + 1)}{||A||^2(\tau(A) + 1)} \right) S_\tau(A) \right]^{1(x \in A_\ell)} \]

\[ \mathbb{E}_{\theta(A), \tau(A)} \left( \frac{(1 - \theta(A))((1 - \theta(A))\tau(A) + 1)}{||A_\ell||^2(\tau(A) + 1)} \right) S_\tau(A) \right]^{1(x \in A_r)} \]

\[ \prod_{A \ni x} ||A||^2 \mathbb{E}_{\theta(A), \tau(A)} \left( \frac{\theta(A)^2}{||A_r||^2} \right) S_\tau(A) \right]^{1(x \in A_r)} \]

\[ \mathbb{E}_{\theta(A), \tau(A)} \left( \frac{(1 - \theta(A))^2}{||A_r||^2} \right) S_\tau(A) \right]^{1(x \in A_r)} \].

The expectations with respect to \(\theta(A)\) and \(\tau(A)\) can be estimated during the same quadrature routines used to compute the posterior distributions of \(\theta(A)\), described in Section 3.1. The expectation with respect to \(S_\tau\) can then be calculated during the forward-backward routine used to calculate the posterior distribution of \(S_\tau\), as described in the same section.

We naturally expect more absolute variation between samples in areas where the densities of all the samples are higher, so we prefer a standardized dispersion function measuring the coefficient of variation. The posterior mean coefficient of variation of \(q_\star\) at any given point is not analytically tractable; we can obtain an estimate by taking the square root of the variance function and dividing by the mean density function. We illustrate the application of the dispersion functions in Section 6.1.

### 5.2 Dirichlet Process Mixture of HAPT

In many applications we may not believe that the samples collected all share a single common structure. A more appropriate model may be that the samples are drawn from several latent populations, with samples being drawn from the same population having structure in common. In this case we may reconstruct the latent structure by clustering the samples. To learn the clustering of samples without fixing the number of clusters in advance, we add a Dirichlet process component to the model. We can write the model as follows:

\[ X_{ij} \mid Q_i \overset{i.i.d.}{\sim} Q_i \]

\[ Q_i \mid Q_i^*, \tau_i^* \overset{i.i.d.}{\sim} \text{PT}(Q_i^*, \tau_i^*) \]

\[ (Q_i^*, \nu_i^*, \tau_i^*) \mid G \overset{i.i.d.}{\sim} G \]

\[ G \sim \text{DP}(\alpha H(Q^*, \nu^*, \tau^*)) \]

where the base measure can be factored as

\[ H(Q^*, \nu^*, \tau^*) = [\pi(Q^* \mid \nu^*) \times \pi(\nu^*)] \times \pi(\tau^*) \]

\[ = [\text{PT}(Q_0, \nu^*) \times \text{SIS}(\Gamma^*)] \times \text{SIS}(\Gamma^*) \].

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The Dirichlet process introduces clustering among the samples, so that some set of $Q_i$, belonging to the same cluster, share a corresponding $Q^*_i$, $\tau^*_i$, and $\nu^*_i$. Conditional on the clustering structure, the model reduces to a collection of independent HAPT models.

We call this model a Dirichlet Process Mixture of Hierarchical Adaptive Pólya Trees, or DPM-HAPT. It is comparable to the Nested Dirichlet process in the way it induces clustering among the samples, but is considerably more flexible. While the NDP requires that all samples in a cluster have identical distributions (MacEachern, 2008), DPM-HAPT allows the distributions within each cluster to vary according to the HAPT model. In addition, the advantages of the HAPT model discussed earlier, such as flexible modeling of variation in different parts of the sample space, still apply.

Posterior computation for HAPT-DPM consists of a combination of standard Dirichlet Process methods and the HAPT posterior calculations described in Section 3.1. As noted above, conditional on the clustering structure, the model consists of a number of independent HAPT models. Although the HAPT model is not fully conjugate, our posterior computation strategy allows us to calculate the marginal likelihood to arbitrary precision. This allows the use of a Dirichlet process algorithm designed for conjugate mixture models. We use the Chinese Restaurant Process representation to sample the clustering structure, using marginal likelihoods calculated from the HAPT model.

This algorithm requires the computation of

1. marginal likelihoods under the HAPT model for clusters including a single sample, and
2. marginal posterior predictive likelihoods under the HAPT model of one sample conditional on one or more other samples making up a cluster.

The first item is straightforward. The second is easily achieved by fitting the HAPT model twice, and calculating

$$f(X_i \mid X_{j_1}, \ldots, X_{j_k}) = \frac{f(X_i, X_{j_1}, \ldots, X_{j_k})}{f(X_{j_1}, \ldots, X_{j_k})}.$$

6 Simulation results

6.1 Estimation of the dispersion function

In order to obtain data with dispersion that varies across the sample space, we simulate from a mixture of three Beta distributions, such that the variation between sample densities is low in the middle of the space and much higher near zero and one. Details of the simulation setting are described in the supplementary material. One hundred sample densities are plotted in Figure 5(a). The variation in the dispersion of the sample densities can be seen clearly.

Figure 5(b) shows the estimated centroid and sample densities from fitting the HAPT model. The dispersion function, or estimated coefficient of variation is plotted in Figure 5(c). The dispersion function clearly shows how the variation between samples is low near the center of the space and high on either end.
6.2 DPM-HAPT Simulations

We simulate a simple 1-dimensional example to demonstrate the clustering behavior of the DPM-HAPT model. The simulation contains 30 samples belonging to three true clusters, with 15, 10, and 5 samples respectively. Each sample is drawn from a mixture of a Uniform(0,1) distribution and a Beta distribution, with the parameters of the Beta varying by cluster: Beta(1,5) for the first cluster, Beta(3,3) for the second cluster, and Beta(5,1) for the third cluster. The weights of the two components are randomized in each sample. The weight of one component is drawn from a Beta(10,10) distribution, which creates weights varying approximately between 0.3 and 0.7, with the actual observed proportions in realized samples varying more widely due to the additional Binomial variation. Sample densities are plotted in Figure 6(a). Each sample contains \( n = 300 \) points.

An MCMC sampler is run using the Chinese Restaurant Process to sample the clustering structure. We summarize the results by looking at how often each of the 30 samples is clustered together with each other sample. These results are plotted in Figure 6(b). We can see in the figure that the DPM-HAPT model clearly identified the three clusters.

We now consider an example in which the variation between samples differs across the sample space. Samples with heterogeneous variation are drawn from mixtures of four Beta distributions, with varying parameters for each cluster. The parameter are chosen so that each cluster has much higher variation between sample densities on the right half of the space than on the left half. The data generating process is described in the supplementary material. We consider 30 samples belonging to three true clusters, as above. Figure 7(a) shows one hundred draws from each of three clusters used in this simulation, to illustrate the variability between and within clusters and the heterogeneity across the sample space.

As in the previous example, we simulate three clusters with 15, 10 and 5 groups respectively. We draw 150 observations from each group, and apply DPM-HAPT to cluster the resulting samples. We run the MCMC for 1,000 draws after burnin; estimated coclustering probabilities are plotted in Figure 7(b). The three true clusters are clearly identified even in the presence of substantial heterogeneity.
Figure 6: (a) Sample densities for the clustering simulation, and (b) probability of two samples clustering together based on the DPM-HAPT model, which clearly identifies the three clusters that exist in this simulation, despite significant variation between samples within clusters.

Figure 7: (a) One hundred draws from each of three clusters in the heterogeneous variation clustering example; (b) Probability of two samples clustering together based on 1,000 MCMC draws for the heterogeneous variance example. Despite the variation in the dispersion of the densities, HAPT-DPM clearly identifies the three true clusters.
7 Applications

7.1 DNase-seq profile clustering

DNase sequencing (DNase-seq) is a method used to identify regulatory regions of the genome ([Song and Crawford, 2010]). DNA is treated with Deoxyribonuclease (DNase) I, an enzyme that cuts the DNA strand. The cut strands are then sequenced and the locations of the cuts are identified and tallied. The vulnerability of the DNA strand to DNase varies by location, resulting in a distribution of cut counts which is nonuniform. The density of this distribution is related to various biological factors of interest: for example, it tends to be high near potential binding sites for transcription factors, since these proteins require access to the DNA strand in much the same way as DNase I, but will be low if a transcription factor already bound at that site blocks access to the DNA strand.

We consider the problem of clustering DNase-seq profiles near potential transcription binding sites, identified by a specific genetic motif. Each sample consists of observed counts in a range of 100 base pairs on either side of one occurrence of the motif. A single motif, consisting of 10–20 base pairs, may appear tens of thousands of time in the genome, with each occurrence presenting one sample for analysis. Many samples, however, have very few cuts observed. For analysis we restrict ourselves to samples which meet a minimum sample size threshold.

Different locations where the transcription factor motif of interest appears may be expected to show different DNase behavior in the region around the motif for a variety of reasons. This makes clustering a more appropriate approach to the problem than treating all the samples as having a single common structure. Identifying clusters of locations which have similar DNase-seq profiles may reveal previously unrecognized factors. We also expect within-cluster variation above and beyond sampling variation, which makes the Nested Dirichlet process unsuitable.

Here we present data from the ENCODE project ([ENCODE Project Consortium, 2012] for locations surrounding a motif associated with the RE1-silencing transcription factor (REST). REST suppresses neuronal genes in non-neuronal cells ([Chong et al., 1995]). The data includes 48,549 locations where the REST motif appears in the genome. The motif consists of 21 base pairs, and the data includes an additional 100 base pairs on each side, for a total of 221 base pairs. In all, 922,704 cuts were tallied, an average of 19 per location. 468 locations have zero cuts observed. The number of cuts per location is heavily right skewed, with a median of 13 observations, first and third quartiles of 7 and 21 respectively, and a maximum of 2,099 cuts observed in a single sample.

For this analysis we restrict ourselves to locations which have at least 200 observations, a total of 265 samples. These samples include a total of 70,225 observations, an average of 330 observations per sample. The distribution is still quite skewed, with a minimum of 201 observations and a maximum of 2099. The median is 279 and the first and third quartiles are 232 and 366 observations. Histograms of 30 of the 265 locations are shown in the supplementary material.

We fit the DPM-HAPT clustering model to this data, using 100 post-burnin draws for inference. The model estimates 7 clusters with high probability (see Figure 8(a)), of which there are three large clusters and four singleton locations, each of which consists of a single
Figure 8: (a) Posterior distribution of the number of clusters from the DPM-HAPT in the DNase-seq application; (b) the model shows clear clustering of the samples.

large spike. One of the singleton locations occasionally joins one of the larger clusters, resulting in 6 clusters. A heatmap of the clustering structure is shown in Figure 8(b). The clusters are clearly differentiated and vary in size, with the largest cluster containing about 130 locations, though the cluster sizes vary from iteration to iteration due to uncertainty in the cluster assignment.

The estimated mean densities of the three largest clusters are plotted in Figure 9. One of these clusters includes locations with cuts which are roughly symmetric around the transcription factor binding site with a dip in the middle. The central dip indicates that a transcription factor may be bound at that location, blocking access for the DNase I molecule. The other two largest clusters include locations which have cuts heaped up on one side or another of the binding site, suggestive of larger-scale patterns in the DNase I sensitivity due to factors like the folded structure of the DNA. The four singleton clusters show other densities which do not conform to the general patterns of the three largest clusters. The plots show substantial variation around the cluster centroid, much more than can be explained by sampling variation alone. The estimated dispersion functions are quite noisy; this is not surprising given that they are between-sample dispersions estimated with relatively few degrees of freedom.

8 Discussion

The HAPT model offers a compelling alternative to existing nonparametric models that share information across multiple samples. The Pólya tree’s ability to directly model the density of an absolutely continuous distribution frees us from the necessity of using mixture models to obtain densities, while the computational tractability of the posterior avoids the need to run MCMC chains for posterior inference. The addition of the SIS prior allows
us not only to more accurately model the densities of interest, but also to estimate a fully nonparametric dispersion function over the sample space. The model extends easily—both conceptually and computationally—to the setting where we do not believe all our samples have the same common structure, where DPM-HAPT allows us to learn both clustering structure and the distributional structure within each cluster.

Although we have presented HAPT in a one-dimensional space for the sake of clarity, adoption of the randomized recursive partitioning scheme first introduced in [Wong and Ma (2010)] allows the extension of HAPT to model densities in multidimensional spaces. Variables other than simple continuous ones can also be handled naturally—all that is needed is the definition of an appropriate recursive partition. This allows inclusion of categorical and ordinal-valued variables, as well as more exotic possibilities: a continuous variable that lives on the surface of a torus, a partially ordered categorical variable, or a zero-inflated variable with a point mass at zero and a continuous component on the positive halfline.

The Pólya tree’s decomposition of the density space into orthogonal Beta-distributed random variables, which extends to HAPT, is central to HAPT’s computational efficiency. It also allows the performance of quick online updates in the HAPT model: when a new data point arrives we only need to update the nodes of the Pólya tree which contain the new data point, rather than recomputing the entire posterior. In a HAPT truncated at a depth of $L$ levels, this means we need to reevaluate the posteriors of only $L$ nodes, rather than $2^L$. 
HAPT may thus be used in streaming data settings where fast online updates are essential. This is one of our current developments.

The DPM-HAPT model may also be easily extended by replacing the Dirichlet process by any clustering-inducing process which admits inference given the marginal likelihoods and conditional probabilities of the clusters. This includes, for example, the Pitman-Yor process. This allows the properties of the clustering process to be adapted if the clustering assumptions implicit in the Dirichlet process are not appropriate.

Software

An R package, HAPT-package, which implements the HAPT model is available at https://github.com/MaStatLab/HAPT-package.

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Supplementary material

S1: Posterior derivation

We use the following notation in this section:

- $A$ is a set in the recursive partition of $\Omega$ implicit in the Pólya tree.
- $A_\ell$ and $A_r$ indicate the left and right children of $A$, respectively; these are also sets in the recursive partition of $\Omega$.
- $n(A)$ is the number of data points across all samples that are contained in $A$; $n_i(A)$ is the number of datapoints in sample $i$ that are contained in $A$. Thus $n(A) = \sum_i n_i(A)$.

We ignore for the time being the priors on $\tau$ and $\nu$, as they are not important for this derivation and can be reinserted at the end.

The density of the distribution generated from the HAPT model at an observation $x_{ij}$ consists of three factors:

1. The baseline density $q_0(x_{ij})$

2. A term indicating how the common structure modifies the density:
   \[
   \prod_{A: x_{ij} \in A_\ell} \theta(A) \frac{Q_0(A)}{Q_0(A_\ell)} \prod_{A: x_{ij} \in A_r} (1 - \theta(A)) \frac{Q_0(A)}{Q_0(A_r)}
   \]
   Note that under the canonical representation, $\frac{Q_0(A)}{Q_0(A_\ell)} \equiv 2$

3. A term indicating how the idiosyncratic structure of the particular sample containing $x$ modifies the density:
   \[
   \prod_{A: x_{ij} \in A_\ell} \theta_i(A) \frac{Q(A)}{Q(A_\ell)} \prod_{A: x_{ij} \in A_r} (1 - \theta_i(A)) \frac{Q(A)}{Q(A_r)}
   \]
   Note that by definition, $\frac{Q(A)}{Q(A_\ell)} = 1/\theta(A)$ and $\frac{Q(A)}{Q(A_r)} = 1/(1 - \theta)$.

Altogether this gives us the following likelihood:

\[
f(X \mid \theta, \theta_i) = \prod_{x_{ij}} \left[ q_0(x_{ij}) \prod_{A: x_{ij} \in A_\ell} \left[ \theta(A) \frac{Q_0(A)}{Q_0(A_\ell)} \right] \prod_{A: x_{ij} \in A_r} \left[ (1 - \theta(A)) \frac{Q_0(A)}{Q_0(A_r)} \right] \right] \prod_{A: x_{ij} \in A_\ell} \left[ \theta_i(A) \frac{Q(A)}{Q(A_\ell)} \right] \prod_{A: x_{ij} \in A_r} \left[ (1 - \theta_i(A)) \frac{Q(A)}{Q(A_r)} \right]
\]

\[
= \prod_{x_{ij}} \left[ q_0(x_{ij}) \prod_{A: x_{ij} \in A_\ell} \left[ \theta_i(A) \frac{Q_0(A)}{Q_0(A_\ell)} \right] \prod_{A: x_{ij} \in A_r} \left[ (1 - \theta_i(A)) \frac{Q_0(A)}{Q_0(A_r)} \right] \right].
\]
Rearranging terms, the likelihood can be written as follows:

\[
f(X \mid \theta_i, \theta) = \prod_{x_{ij}} q_0(x_{ij}) \times \prod_A \left[ \prod_{i=1}^k \left[ \frac{\theta_i(A) Q_0(A)}{Q_0(A_i)} \right]^{n_i(A_i)} \left[ (1 - \theta_i(A)) \frac{Q_0(A)}{Q_0(A_r)} \right]^{n_i(A_r)} \right],
\]

which gives the following form for the posterior of \( \theta(A), \theta_i(A) \) for a particular \( A \):

\[
\pi(\theta(A), \theta_i(A) \mid \tau(A), \nu(A), x) \propto \theta(A)^{\theta_0(A)\nu(A)-1} (1 - \theta(A))^{(1-\theta_0(A))\nu(A)-1} \times \\
\left[ \frac{\Gamma(\tau(A))}{\Gamma(\theta(A)\tau(A))\Gamma((1 - \theta(A))\tau(A))} \right]^k \times \\
\prod_{i=1}^k \frac{\Gamma(\theta(A)\tau(A) + n_i(A_i)) \Gamma((1 - \theta(A))\tau(A) + n_i(A_r))}{\Gamma(\tau(A) + n_i(A))}.
\]

Conditional on \( \theta(A) \) and \( \tau(A) \) the \( \theta_i(A) \) are Beta distributed, and we can integrate them out analytically:

\[
\pi(\theta(A) \mid \tau(A), \nu(A), x) \propto \theta(A)^{\theta_0(A)\nu(A)-1} (1 - \theta(A))^{(1-\theta_0(A))\nu(A)-1} \times \\
\left[ \frac{\Gamma(\tau(A))}{\Gamma(\theta(A)\tau(A))\Gamma((1 - \theta(A))\tau(A))} \right]^k \times \\
\prod_{i=1}^k \frac{\Gamma(\theta(A)\tau(A) + n_i(A_i)) \Gamma((1 - \theta(A))\tau(A) + n_i(A_r))}{\Gamma(\tau(A) + n_i(A))}.
\]

We can then simply multiply by the priors on \( \tau(A) \) and \( \nu(A) \) to obtain

\[
\pi(\theta(A), \tau(A), \nu(A) \mid S_\tau(A), S_\nu(A), x) \propto \theta(A)^{\theta_0(A)\nu(A)-1} (1 - \theta(A))^{(1-\theta_0(A))\nu(A)-1} \times \\
\left[ \frac{\Gamma(\tau(A))}{\Gamma(\theta(A)\tau(A))\Gamma((1 - \theta(A))\tau(A))} \right]^k \times \\
\prod_{i=1}^k \frac{\Gamma(\theta(A)\tau(A) + n_i(A_i)) \Gamma((1 - \theta(A))\tau(A) + n_i(A_r))}{\Gamma(\tau(A) + n_i(A))} \times \\
\pi(\tau(A))\pi(\nu(A)).
\]

**S2: Proofs of theoretical results**

**Proof of Theorem 1: Absolute continuity.** The result follows directly from repeated application of Theorem 3 in [Ma (2017)](#). From one application of that theorem we have that \( Q \ll Q_0 \) with probability 1; by a second application we have that \( Q_i \ll Q \) for each \( Q_i \) with probability 1. Thus \( Q_i \ll Q_0 \) with probability 1.

**Proof of Theorem 2: Large L1 Support.** The upper level of the hierarchy \( (q) \) follows immediately from Theorem 4 in [Ma (2017)](#), since its prior coverage is not altered by
the addition of the hierarchy. For the second level of the hierarchy, note that by Theorem 4 in [Ma (2017)] we have

$$\forall q \ll \mu, \ P(\int |q_i(x) - f_i(x)|d\mu < \tau_i | q) > 0.$$  

Further, by definition of conditional expectation,

$$P\left(\int |q_i(x) - f_i(x)|d\mu < \tau_i | q\right) = E\left(1 \left[\int |q_i(x) - f_i(x)|d\mu < \tau_i \right] | q\right)$$

is measurable with respect to $Q$. Thus

$$P\left(\int |q_i(x) - f_i(x)|d\mu < \tau_i \right) = \int P\left(\int |q_i(x) - f_i(x)|d\mu < \tau_i | q\right) dQ > 0,$$

as the integrand is positive with probability 1.

**Proof of Theorem 3: Weak Consistency.** By Schwartz’s theorem, it is sufficient to show that $P_1, \ldots, P_k$ jointly lie in the Kullback-Leibler support of the prior. The proof proceeds as follows: We consider the product space of all $k$ distributions so that we can show joint convergence. We restrict ourselves to a compact set with mass $1 - \epsilon'$, and define a set $\bar{D}_\epsilon$, which depends on $p_0$. We show that $\bar{D}_\epsilon$ has positive prior mass. We then show that by choosing $\epsilon$ and $\epsilon'$ appropriately, we can make $\bar{D}_\epsilon$ lie within an arbitrarily small K-L ball around $p_0$. This shows that $P_1, \ldots, P_k$ are jointly in the support of the prior, and concludes the proof. We follow closely the proof of Theorem 5 in [Ma (2017)].

Let $P_0$ be the product measure $P_0 = P_1 \otimes \cdots \otimes P_k$ on $\Omega^k$, and let $p_0 = dP_0/d\mu$ be the corresponding density. Let $Q_0 = Q_0^1 \otimes \cdots \otimes Q_0^k$, and let $q_0 = dQ_0/d\mu$. Define additionally the densities $\tilde{p}_0 = dP_0/dQ_0$ and $\tilde{q} = dQ/dQ_0$ for any $Q \ll Q_0$. Let $M$ be a finite upper bound on $\tilde{p}_0$. The Kullback-Leibler distance between $p_0$ and $q$ is given by

$$\text{KL}_{\mu}(p_0, q) = \int p_0 \log(p_0/q) d\mu = \int \tilde{p}_0 \log(\tilde{p}_0/\tilde{q}) dQ_0 = \text{KL}_{Q_0}(\tilde{p}_0, \tilde{q}).$$

By Lusin’s theorem, for any $\epsilon' > 0$ there exists a compact set $E \subset \Omega$ with $Q_0(E^c) < \epsilon'$, such that $\tilde{p}_0$ is continuous (and so uniformly continuous) on $E$. For any $\epsilon > 0$ there exists a partition $\Omega = \bigcup_i A_i$ with all $A_i \in \mathcal{A}(k)$ for some $k$, such that the diameter of each $A_i \cap E$ is less than $\epsilon$. We define

$$\delta_E(\epsilon) = \sup_{x,y \in E: |x-y|< \epsilon} |\tilde{p}_0(x) - \tilde{p}_0(y)|$$

and

$$d_i = \max_{A_i \cap E} \left(\sup_{A_i \cap E} \tilde{p}_0(x) + \delta_E(\epsilon), \epsilon\right).$$

Note that because $p_0$ is uniformly continuous on $E$, $\delta_E(\epsilon) \to 0$ as $\epsilon \to 0$.

Let $D_\epsilon(\tilde{p}_0)$ be the collection of step functions $g(x) = \sum_i g_i 1_{A_i}(x)$ with $d_i \leq g_i < d_i + \delta_E(\epsilon)$. For every $g \in D_\epsilon(\tilde{p}_0)$, let $\tilde{g} = g/\int g dQ_0$ be the normalized version of $g$, and let $\bar{D}_\epsilon(\tilde{p}_0)$ be the collection of the $\tilde{g}$.

Let $I$ be the number of sets $A_i$ in the partition $\Omega = \bigcup_i A_i$. We can consider each step function $g$ as a point in $I$-dimensional space, where the $i$th dimension corresponds to the value
of the step function on the set $A_i$. Note that $D_r(\tilde{p}_0) = [d_1, d_1 + \delta_E(\epsilon)] \times \cdots \times [d_I, d_I + \delta_E(\epsilon)]$ is a convex set in this $I$-dimensional space, and we can find an open ball in this $I$-dimensional space which is a subset of $D_r(\tilde{p}_0)$. The normalized version $\tilde{D}_r(\tilde{p}_0)$ is in turn a convex set in the $(I - 1)$-simplex, which also contains an open ball in the $(I - 1)$-simplex.

The HAPT model places positive probability on normalized step functions taking unique values precisely on the sets $A_i$, i.e. the same $(I - 1)$-simplex noted above. Because each of the mass assignment parameters in HAPT has a Beta prior, HAPT has positive prior density everywhere in the $(I - 1)$-simplex. Because $\tilde{D}_r(\tilde{p}_0)$ contains an open ball, it follows that it has positive prior mass.

It now remains to show that we can bound $\tilde{D}_r(\tilde{p}_0)$ within an arbitrarily small ball about $p_0$. The remainder of the proof follows exactly as Ma (2016). For every $\tilde{g} \in \tilde{D}_r(\tilde{p}_0)$, we have

$$0 \leq \text{KL}_{Q_0}(\tilde{p}_0, \tilde{g}) = \int \tilde{p}_0 \log(\tilde{p}_0 / \tilde{g}) \, dQ_0$$

$$= \int \tilde{p}_0 \log(\tilde{p}_0 / g) \, dQ_0 + \log \left( \int g \, dQ_0 \right)$$

$$= \int_E \tilde{p}_0 \log(\tilde{p}_0 / g) \, dQ_0 + \int_{E^c} \tilde{p}_0 \log(\tilde{p}_0 / g) \, dQ_0 + \log \left( \int g \, dQ_0 \right).$$

Because $g \geq p_0$ everywhere in $E$, the first integral is not greater than 0. The second integral is bounded by $M \log(M/e')e'$, which goes to zero as $e' \to 0$. To bound the third term, we note that

$$\log \left( \int g \, dQ_0 \right) = \log \left( 1 + \int (g - \tilde{p}_0) \, dQ_0 \right) \leq \int (g - \tilde{p}_0) \, dQ_0,$$

We can bound this last integral by

$$\int (g - \tilde{p}_0) \, dQ_0 \leq \int_E (g - \tilde{p}_0) \, dQ_0 + \int_{E^c} |g - \tilde{p}_0| \, dQ_0.$$

On the set $E$, we have $g_0 - \tilde{p}_0 \leq 3\delta_E(\epsilon) + e'$, and on $E^c$ we have $g_0 - \tilde{p}_0 \leq 3M + e'$. Thus

$$\int (g - \tilde{p}_0) \, dQ_0 \leq 3\delta_E(\epsilon) + e' + (3M + e')e' \to 0$$

as $\epsilon, e' \to 0$.

This shows that by picking $\epsilon, e'$ appropriately, $\tilde{D}_r(\tilde{p}_0)$ is contained within an arbitrarily small KL ball about $\tilde{p}_0$, and so $p_0$ is in the KL support of the HAPT model.

**S3: Description of simulation settings**

**Heterogenous dispersion I**

This section describes the generative model used in the simulation showing the ability of HAPT to model dispersion between samples that varies across the sample space.

Each sample is a mixture of three components: Beta(2,2), Beta(1,12), and Beta(12,1). The corresponding weights $w_1, w_2, w_3$ of the three components are drawn according to the following scheme. First we draw $w_1 \sim \text{Beta}(80,20)$. Then we draw $v \sim \text{Beta}(1,1)$ and set $w_2 = v(1 - w_1)$ and $w_3 = (1 - v)(1 - w_1)$. This results in the central part of the sample space having a small amount of variation between samples, while the edges on either side have much more variation. Sample densities are illustrated in Figure 5.
Heterogenous dispersion II

This section describes the generative model used in the DPM-HAPT simulation with heterogenous dispersion. The previous heterogenous dispersion model lacks degrees of freedom to create differentiated clusters with heterogenous dispersion, so here we add a fourth mixture component.

Each sample is a mixture of four components, shown in Figure 10: Beta(1,6), Beta(2,5), Beta(5,2), and Beta(6,1). The corresponding weights \( w_1, w_2, w_3, \) and \( w_4 \) of the mixture components are drawn according to the following scheme. Let \( v_1, v_2, v_3 \) be Beta random variables whose parameters that differ by cluster, with \( v_3 \) having a much larger variance than \( v_1 \) and \( v_2 \). Then we calculate the weights as follows:

\[
\begin{align*}
    w_1 &= v_1 v_2 \\
    w_2 &= v_1 (1 - v_2) \\
    w_3 &= (1 - v_1)v_3 \\
    w_4 &= (1 - v_1)(1 - v_3).
\end{align*}
\]

Because \( v_3 \) has a much larger variance than \( v_1 \) and \( v_2 \), we end up with much more variation between densities on the right half of the space than on the left half.

For this simulation study we use

\[
\begin{align*}
    v_1 &\sim \text{Beta}(1000,1000) \\
    v_2 &\sim \text{Beta}(200,200) \\
    v_3 &\sim \text{Beta}(1,1).
\end{align*}
\]

S4: Sample histograms for DNase-seq data
Figure 10: The four mixture components used in the simulation in Sections 6.1.
Figure 11: Histograms of 30 locations from the DNase-seq data analyzed in Section 7.