Quasi-Bernoulli Stick-breaking: Infinite Mixture with Cluster Consistency

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Abstract

In mixture modeling and clustering application, the number of components is often not known. The stick-breaking model is an appealing construction that assumes infinitely many components, while shrinking most of the redundant weights to near zero. However, it has been discovered that such a shrinkage is unsatisfactory: even when the component distribution is correctly specified, small and spurious weights will appear and give an inconsistent estimate on the cluster number. In this article, we propose a simple solution that gains stronger control on the redundant weights — when breaking each stick into two pieces, we adjust the length of the second piece by multiplying it to a quasi-Bernoulli random variable, supported at one and a positive constant close to zero. This substantially increases the chance of shrinking all the redundant weights to almost zero, leading to a consistent estimator on the cluster number; at the same time, it avoids the singularity due to assigning an exactly zero weight, and maintains a support in the infinite-dimensional space. As a stick-breaking model, its posterior computation can be carried out efficiently via the classic blocked Gibbs sampler, allowing straightforward extension of using non-Gaussian components. Compared to existing methods, our model demonstrates much superior performances in the simulations and data application, showing a substantial reduction in the number of clusters.

KEY WORDS: Consistent Clustering, Exchangeable Partition Probability Function, Sparse Simplex, Tail bounding.

1 Introduction

Mixture models are extremely popular for analyzing data with unknown group/cluster structure. They give a generative view on the data $y = (y_i)_{i=1}^n$, and uncertainty quantification on the cluster assignment. To review the main idea, consider a generative distribution:

$$\theta_i^* \sim \sum_{k=1}^K w_k \delta_{\theta_k} (\cdot), \quad y_i \sim \mathcal{F} (\theta_i^*),$$

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for \( i = 1, \ldots, n \), where \( F(\theta^*_i) \) is a distribution (with density/mass function \( f \)) parameterized by \( \theta^*_i \), and \( \theta^* = (\theta^*_1)^n \) are discrete random variables supported on values \( (\theta_1, \ldots, \theta_K) \), with corresponding probabilities \( (w_1, \ldots, w_K) \). Using the Bayesian framework, one can easily obtain the posterior estimates on the weights \( (w_1, \ldots, w_K) \) and the parameters \( (\theta_1, \ldots, \theta_K) \), as well as the probability of the component assignment for each data point \( \text{pr}(\theta^*_i = \theta_k | y) \) for \( k = 1, \ldots, K \) [Fraley and Raftery, 2002].

In practice, we usually do not know the number of clusters. The stick-breaking models give an appealing solution, by allowing \( K \rightarrow \infty \), while shrinking some redundant \( w_k \)'s close to zero. A general form of the stick-breaking model on the mixture weights is:

\[
w_1 = v_1, \quad w_k = v_k \prod_{l=1}^{k-1} (1 - v_l), \quad k \geq 2.
\] (1)

The interpretation is that starting from a stick of length 1, each time we break away a proportion of \( v_k \in (0, 1) \) from the remaining stick, and use it as the weight \( w_k \).

There are many proposed parameterizations for the distribution of \( v_k \). Perhaps the most widely used one is when \( v_k \sim \text{Beta}(1, \alpha) \), which is shown to be equivalent to the Dirichlet process with concentration parameter \( \alpha \) [Sethuraman, 1994]. When \( v_k \sim \text{Beta}(1-d, \alpha+kd) \), it leads to the Pitman–Yor process [Pitman and Yor, 1997, Ishwaran and James, 2001]. With an appropriate choice on the hyper-parameters, these models can shrink some of \( w_k \)'s close to zero, leading to a small number of clusters in the posterior.

However, it has been discovered that such a shrinkage is not optimal: as the data sample size increases, more and more spurious small clusters will appear. A long-held belief is that this is a model misspecification problem in the component distribution, which has motivated a large class of models focused on calibrating \( F \): for example, [Kosmidis and Karlis, 2016] uses copulas (modeling cumulative distribution function) to replace standard parametric \( F \); [Miller and Dunson, 2019] replaces \( F \) with a tempered likelihood, giving some tolerance to model misspecification; [Xie and Xu, 2020] regularizes the minimum distance between any two \( \theta_k \)'s away from zero, preventing the creation of new cluster with trivial difference from existing ones. Despite some empirical improvements, it is unknown whether these methods can lead to to an optimal estimate on the cluster number \( \{ \text{although consistency can be achieved on the density estimation [Ghosal et al., 1999], it does not apply on the number of clusters} \} \).

It has been only until recently that, [Miller and Harrison, 2014] showed a striking result: neither of Dirichlet and Pitman–Yor processes could converge to the true number of clusters as \( n \) increases, even when the component distribution \( F \) is correctly specified. Therefore, the real cause of the problem is due to the sub-optimal choice on the distribution of \( v_k \), which failed to yield enough concentration of mass for \( (w_k)_k \) near a finite-dimensional simplex in the infinite-dimensional space.

To fundamentally solve this issue, we propose to gain a more direct control on the shrinkage of \( w_k \). We are inspired by the common heuristic of merging small clusters together after model fitting, as routinely used in the statistical applications [Stephenson et al., 2020]. To achieve a similar effect in a model-based framework, we need a generative mechanism to produce a strict bound on the tail probability for those redundant clusters for \( k > L \),
\[ \sum_{k=L+1}^{\infty} w_k < \epsilon \text{ with } \epsilon \text{ small.} \]

This motivates us to develop a simple tweak to the canonical stick-breaking construction: at each break, we multiply the remaining proportion \((1-v_k)\) with a discrete random variable that takes value either 1 or \(\epsilon\). When the latter happens, we will have a strict \(\epsilon\)-bound as described. We show that if \(\epsilon = o(1/n)\), then the posterior consistency can be obtained on the cluster number. To our best knowledge, one alternative with this property is the mixture of finite mixtures model [Miller and Harrison, 2018], which can be taken as a special case of ours with \(\epsilon = 0\). On the other hand, keeping \(\epsilon > 0\) prevents the singularity at zero weight, allowing the use of the efficient blocked Gibbs sampler [Ishwaran and James, 2001] (instead of the slow-mixing discrete search), and easy extensions for using non-Gaussian mixture components. We will demonstrate improved performances in simulations and a data application of clustering brain networks using a mixture of low-rank matrices.

2 Quasi-Bernoulli Stick-Breaking Process

Starting from the general form of the stick-breaking construction (1), suppose at the \(L\)th stick, we have a breaking proportion \(v_L \approx 1\), then \(w_L\) would take almost all the remaining stick and there is not much left for rest \(w_k \approx 0\) for \(k \geq L + 1\). Based on this intuition, we introduce our specification of the stick-breaking process:

\[
\begin{align*}
\theta_1^* &\sim \sum_{k=1}^{\infty} w_k \delta_{\theta_k} (\cdot), \quad w_1 = v_1, \quad w_k = v_k \prod_{l=1}^{k-1} (1-v_l), \quad k \geq 2, \\
1-v_k &= b_k \beta_k, \\
b_k &\sim p\delta_1(\cdot) + (1-p)\delta_\epsilon(\cdot), \\
\beta_k &\sim \text{Beta}(\alpha, 1),
\end{align*}
\]

where each \(\theta_k \sim G\), a certain base measure. Each \(b_k\) follows a discrete distribution supported at 1 with probability \(p\), and a small \(\epsilon > 0\) with probability \(1-p\). We refer to \(b_k\) as a quasi-Bernoulli random variable, since it resembles the standard Bernoulli supported at \(\{1,0\}\). We refer to (2) as the quasi-Bernoulli stick-breaking process (or, for simplicity, as the “quasi-Bernoulli model”), denoted by \(\theta_1^* \sim \text{QB}_{\epsilon,p}(\alpha, G)\).

Note that if \(\epsilon = 1\), we would obtain \(v_k = 1 - \beta_k \sim \text{Beta}(1,\alpha)\), the same as the stick-breaking representation of the Dirichlet process \(\text{DP}(\alpha, G)\); whereas if \(\epsilon = 0\), we would have a random truncation on \((w_1, w_2, \ldots)\). As established later, using \(\epsilon \in (0,1)\) allows us to borrow strengths from both ends, leading to both posterior consistency in clustering and a support for an infinite mixture model, as well as an easy estimation.

For now, to give some intuition, consider the random event \(b_L = \epsilon\). Since \(\beta_L < 1\), we have:

\[ (1-v_L) < \epsilon, \]

hence a bound on the sum of the remaining sticks \(\sum_{k=L+1}^{\infty} w_k \leq (1-v_L) < \epsilon\). Therefore, we refer to (3) as the tail-bounding event at the \(L\)th stick, denoted by \(\mathcal{B}_{L,\epsilon}\).

Now in the generative process (or equivalently, in the prior distribution), the quasi-Bernoulli model has \(\text{pr}(\sum_{k=L+1}^{\infty} w_k \leq \epsilon) \geq \text{pr}(\mathcal{B}_{L,\epsilon}) \geq 1-p\). With a small \(p\), we will have a
large prior \( \text{pr}(B_L, \epsilon) \approx 1 \). As a comparison, the Dirichlet process has prior \( \text{pr}(B_L, \epsilon) = I_\epsilon(\alpha, 1) \), with \( I_\epsilon(q_1, q_2) \) the cumulative distribution function of Beta\((q_1, q_2)\) evaluated at \( \epsilon \) — note that a small \( \alpha \) close to zero can make \( I_\epsilon(\alpha, 1) \approx 1 \) as well, however, this probability quickly drops to zero in the posterior distribution in a small cluster.

To show a major difference in the posterior probability for the quasi-Bernoulli, consider the component assignment \( c_i = k \) representing \( \theta_i^* = \theta_k \), we have the cluster size \( n_k = \sum_{i=1}^{n} 1(c_i = k) \), the posterior distribution for the quasi-Bernoulli model is

\[
\pi\{(\beta_k, b_k)_{k=1}^\infty \mid (c_i)_{i=1}^n\} \propto \prod_{k=1}^{\infty} (1 - \beta_k b_k)^{n_k} (\beta_k b_k)^{m_k} \alpha \beta_k^{\alpha - 1} \{p1(b_k = 1) + (1 - p)1(b_k = \epsilon)\},
\]

where we denote \( m_k = \sum_{l=k+1}^{\infty} n_l \). Marginalizing out \( \beta_k \), we obtain the posterior probability for the tail-bounding event:

\[
\text{pr}(B_L, \epsilon \mid n_L, m_L) = \text{pr}(b_L = \epsilon \mid n_L, m_L) + \text{pr}(b_L = 1 \mid n_L, m_L) \text{pr}(\beta_L < \epsilon \mid n_L, m_L, b_L = 1)
\]

\[
= \frac{(1 - p)e^{-\alpha} + p}{(1 - p)e^{-\alpha} + p/I_\epsilon(m_k + \alpha, n_k + 1)}.
\]

While for the Dirichlet process, we have \( \text{pr}(B_L, \epsilon \mid n_L, m_L) = I_\epsilon(m_L + \alpha, n_L + 1) \).

We illustrate the difference in Figure 1 — consider the case of having \( n_L = 100 \) in the \( L \)th component, we examine the tail-bounding probability over different \( m_L \)'s.

To interpret the results, note that when the tail-bounding event happens for \( m_L \geq 1 \), there is a penalty on such a partition, since its assignment probability will contain a multiplicative term \( \epsilon^{m_L} \) close to zero. On the other hand, this penalty vanishes only when \( \text{pr}(B_L, \epsilon \mid n_L, m_L) \approx 0, \text{ or } m_L = 0 \).

Therefore, by having the tail-bounding probability \( \text{pr}(B_L, \epsilon \mid n_L, m_L) \) slowly decrease over \( m_L > 0 \), the quasi-Bernoulli model effectively penalizes small \( m_L \geq 1 \) (that is, spurious small clusters). In comparison, the Dirichlet process does not have this property, as its tail-bounding probability quickly drops to zero, even at small \( \alpha \approx 0 \) — if we examine \( I_\epsilon(m_L + \alpha, n_L + 1) \), it is not hard to see \( m_L + \alpha \approx m_L \) if \( m_L \geq 1 \), hence the small \( \alpha \) becomes ineffective.
Figure 1: The quasi-Bernoulli stick-breaking model has a slowly decreasing probability over $m_L = \sum_{k \geq L+1} w_k$ for the tail bounding event (which leads to $\sum_{k \geq L+1} w_k \leq \epsilon$), $\text{pr}(1 - v_L < \epsilon | n_L, m_L)$. This creates a penalty on forming new cluster(s) with a small number of data $m_L \geq 1$; whereas the penalty vanishes if $m_L = 0$ or $\text{pr}(1 - v_L < \epsilon | n_L, m_L) \approx 0$ at larger $m_L$. The Dirichlet process does not have this property, as its tail-bounding probability drops to zero rapidly, regardless of the value in the concentration parameter $\alpha$.

3 Theoretic Properties

We now conduct a more theoretic study, by examining the marginal probability on the partition. This can lead to a consistent estimation of the number of clusters with a principled specification on $\epsilon$.

3.1 Exchangeable Random Partitioning

A large class of the stick-breaking models enjoy the exchangeability property — that is, the probability of a partition is invariant to the permutation of the data index. To formalize, letting $[n] = \{1, \ldots, n\}$ be the data index, if there are $t$ unique values in the cluster assignments $c = (c_1, \ldots, c_n)$, then we can form a partition $S = \{S_1, \ldots, S_t\}$ in the following way: (i) add $i = 1$ into $S_1$; (ii) sequentially for $i = 2, \ldots, n$, if $c_i = c_j$ for any existing $j \leq (i - 1)$ and $j \in S_k$, then add $i$ into the same $S_k$; otherwise add $i$ to a new set $S_{k'}$, with $k'$ one index larger than the existing sets.

It is not hard to see that the permutation of $[n]$ is equivalent to the permutation of $\{S_1, \ldots, S_t\}$. Therefore, we marginalize over all permutations to obtain the exchangeable partition probability function.

**Theorem 1** (Exchangeable Partition Probability Function). The probability mass function of random partition on $[n]$, $S = \{S_1, \ldots, S_t\}$ induced by $c$ in the quasi-Bernoulli stick-breaking process is

$$
\text{pr}_{c,n}(S) = \frac{\alpha^t \Gamma(\alpha)}{\Gamma(n + \alpha)} \left\{ \prod_{k=1}^t \Gamma(n_k + 1) \right\} \sum_{\text{all } \sigma} \prod_{k=1}^t \frac{p + (1 - p) I_c(m_{\sigma_k} + \alpha, n_{\sigma_k} + 1}/\epsilon^\alpha}{n_{\sigma_k} + m_{\sigma_k} + \alpha(1 - p)(1 - \epsilon^{n_{\sigma_k} + m_{\sigma_k}})},
$$
where \( \sigma = (\sigma_1, \ldots, \sigma_t) \) is a permutation of \((1, \ldots, t)\), \( n_k = |S_k| \), and \( m_k = \sum_{l=k+1}^t n_l \). \( I_\epsilon(q_1, q_2) \) is the cumulative distribution function of Beta\((q_1, q_2)\) evaluated at \( \epsilon \).

Using \( \text{pr}_{\epsilon,n}(S) \), we can substantially simplify the stick-breaking process \((\ref{eq:stick-breaking})\) into an equivalent generative process:

\[
S \sim \text{pr}_{\epsilon,n}(S), \\
\theta^*_i = \theta_k, \tag{4}
\]

for \( i \in S_k; \ S_k \in S, \) and \( \theta_k \sim \mathcal{G} \). We now use the above representation to examine the asymptotic behavior of clustering when \( n \to \infty \).

### 3.2 Number of Clusters and Consistency

Note that the number of clusters is effectively \( t = |S| \). We use \( T \) to denote the associated random variable. Using \((\ref{eq:exchangeable})\), we can obtain the marginal posterior of \( T \):

\[
pr(\epsilon)(T = t \mid y) = \frac{\sum_{|S| = t} \pi(y \mid S)pr_{\epsilon,n}(S)}{\sum_S \pi(y \mid S)pr_{\epsilon,n}(S)},
\]

where \( \pi(y \mid S) = \prod_{S \in S} m(y_S) \), in which \( y_S = \{y_i : i \in S\} \) and \( m(y_S) = \int_\theta \prod_{i \in S} f_\theta(y_i) \) \( d\mathcal{G} \) the marginal density of \( y_S \).

Suppose the data are in fact generated from \( t_0 \) clusters, with \( t_0 \) a fixed and finite number. In order to find the theoretic condition needed for \( \text{pr}(\epsilon)(T = t_0 \mid y) \to 1 \) as \( n \to \infty \), we take two steps: 1. first create a finite dimensional model by setting \( \epsilon = 0 \), and establish the posterior consistency; 2. show that the partition function \( \text{pr}_{\epsilon,n}(S) \) converges to \( \text{pr}_{0,n}(S) \) under a suitable choice of \( \epsilon \).

We first focus on the case when \( \epsilon = 0 \), that is, in \((\ref{eq:stick-breaking})\) \( b_k \) is a standard Bernoulli random variable with success rate of \( p \). If the \( K \)th break has \( v_K = 1 \), then \( w_{K+1} = w_{K+2} = \cdots = 0 \). Therefore, \( w \) will have an effectively finite dimension at \( K \), with \( K \) following a geometric distribution \( \pi_K(K) = p^{K-1}(1 - p) \).

\[
K \sim \text{Geometric}(p) \\
v_1, \ldots, v_{K-1} \sim \text{Beta}(1, \alpha), \quad v_K = 1 \\
w_1 = v_1, \quad w_k = v_k \prod_{l=1}^{k-1} (1 - v_l), \quad k \geq 2, \tag{5}
\]

based on which, we can obtain its exchangeable partition probability function.

**Lemma 1.** The probability mass function of random partition on \([n]\), \( S = \{S_1, \ldots, S_t\} \) under \( \text{QB}_{0,p}(\alpha, \mathcal{G}) \) is

\[
pr_{\epsilon=0,n}(S) = \frac{\alpha^t \Gamma(\alpha)}{\Gamma(n + \alpha)} \left\{ \prod_{k=1}^t \Gamma(n_k + 1) \right\} \sum_{\text{all } \sigma} \left[ \prod_{k=1}^{t-1} \frac{\binom{t-1}{k} \binom{p}{n_{\sigma_k} + m_{\sigma_k} + \alpha(1 - p)}}{n_{\sigma_k} + m_{\sigma_k} + \alpha(1 - p)} \right],
\]
where \( \sigma = (\sigma_1, \ldots, \sigma_t) \) is a permutation of \((1, \ldots, t)\).

We now establish the posterior consistency of estimating the effective dimension (the number of non-zero \( w_k \)'s) and the number of non-empty clusters under model (5).

**Theorem 2.** Let \( \Omega = \bigcup_{k=1}^{\infty} \{ k, w_1, \ldots, w_k, \theta_1, \ldots, \theta_k \} \) and \( \Pi_0 \) be the prior on \( \Omega \) from \( QB_{p,0}(\alpha, G) \). Then there is a subset \( \Omega_0 \subset \Omega \) with \( \Pi_0(\Omega_0) = 1 \) such that for true parameter \( \phi = (t_0, w_1^0, \ldots, w_t^0, \theta_1^0, \ldots, \theta_t^0) \in \Omega_0 \), if \( y_1, \ldots, y_n \mid \phi \sim P_\phi \) where \( P_\phi \) has a density \( \pi_\phi = \sum w_0^l f_{\theta_0^l} \), and all of these densities \( \{ \pi_\tilde{\phi} : \tilde{\phi} \in \Omega \} \) are identifiable up to permutation of component index, then as \( n \to \infty \), we have the posterior number of non-zero \( w_k \)'s:

\[
\Pr_{\epsilon=0}(K = t_0 \mid y) \to 1 \quad \text{almost surely } P_\phi.
\]

Further, we have the posterior number of non-empty clusters:

\[
\Pr_{\epsilon=0}(T = t_0 \mid y) \to 1 \quad \text{almost surely } P_\phi.
\]

**Remark 1.** To summarize the proof: the first result is an application of the Doob’s theorem; for the second result, since \( w_k^0 \)'s does not change with \( n \), we can expect that any \( w_k^0 > 0 \) will have at least some data assigned to \( k \)th component, therefore \( K \) and \( T \) would match in the posterior.

Now we consider replacing 0 by \( \epsilon > 0 \) — intuitively, as \( \epsilon \to 0 \), the above results should continue to hold on the number of clusters. Therefore, we let \( \epsilon \) decrease as \( n \) increases. The following theorem formalizes the needed decreasing rate.

**Theorem 3.** The total variation distance between two probability measures on the partition has

\[
\sup_{\mathcal{A}} |\Pr_{\epsilon,n}(\mathcal{A}) - \Pr_{0,n}(\mathcal{A})| \leq \sqrt{\frac{\alpha \epsilon n}{2(\alpha + 1 - \alpha \epsilon n)}},
\]

where \( \Pr_{\epsilon,n}(\mathcal{A}) = \sum_{S \subseteq \mathcal{A}} \Pr_{\epsilon,n}(S) \).

Further, if \( \epsilon = 1/n^u \) with \( u > 1 \), then

\[
\sup_{\mathcal{A}} |\Pr_{\epsilon,n}(\mathcal{A}) - \Pr_{0,n}(\mathcal{A})| \to 0
\]

as \( n \to \infty \).

The interpretation is that, if we let the tail bound to be slightly smaller than \( 1/n \), we have a stick-breaking model supported in the infinite dimensional space: it yields the optimal asymptotic behavior as \( n \to \infty \), whereas at small \( n \), the model is adaptive to having more clusters.

## 4 Posterior Sampling Algorithm

Since the quasi-Bernoulli model takes a small modification to classic stick-breaking construction, we can use the efficient Gibbs sampling algorithm to estimate posterior distribution. Following Ishwaran and James [2001], we first take a truncation approximation \( k = 1, \ldots, M \) with a finite and large \( M \). The Gibbs sampler then iterates in the following steps:
For $i = 1, \ldots, n$: sample $c_i \in \{1, \ldots, M\}$ from categorical distribution

$$\text{pr}\{c_i = k \mid (\theta_i)_{i=1}^M, (w_i)_{i=1}^M\} = \frac{w_k f(y_i \mid \theta_k)}{\sum_{i=1}^M w_i f(y_i \mid \theta_i)} \quad (k = 1, \ldots, M).$$

Update $n_k = \sum_i 1(c_i = k)$, and $m_k = \sum_i 1(c_i > k)$.

- For $k = 1, \ldots, M$:
  - Sample $b_k \in \{\epsilon, 1\}$ from quasi-Bernoulli distribution
    $$\text{pr}(b_k = \epsilon \mid n_k, m_k) = \frac{(1 - p)\epsilon^{-\alpha} I(1) (m_k + \alpha, n_k + 1)}{p + (1 - p)\epsilon^{-\alpha} I(1) (m_k + \alpha, n_k + 1)},$$
    and $\text{pr}(b_k = 1 \mid c) = 1 - \text{pr}(b_k = \epsilon \mid c)$.
  - Sample $\beta_k \mid b_k, n_k, m_k$ from
    
    $$\beta_k \mid b_k = 1, n_k, m_k \sim \text{Beta}(m_k + \alpha, n_k + 1),$$
    $$\beta_k \mid b_k = \epsilon, n_k, m_k \sim \frac{1}{\epsilon} \text{Beta}(0, \epsilon) (m_k + \alpha, n_k + 1),$$

    where $\text{Beta}(0, \epsilon)$ denotes a Beta distribution with truncated upper bound at $\epsilon$.
  - Update $w_k \mid b_k, \beta_k$ using [2] afterwards.

In the second step above, we first sample the distribution marginalized over $\beta_k$, then sample $\beta_k \mid b_k$. This is equivalent to a blocked sampling step $\pi(b_k, \beta_k \mid n_k, m_k) = \pi(\beta_k \mid b_k, n_k, m_k) \pi(b_k \mid n_k, m_k)$ for $k = 1, \ldots, M$ at the same time.

Due to the tail-bounding event, in the high posterior probability region, the first few components before the first $b_k = \epsilon$ will have $\beta_k$ corresponding to large clusters with large $n_k$, while the components after the first $b_k = \epsilon$ should have small or zero $n_k$. Therefore, to accelerate the convergence and take advantage of the exchangeability in partition index, we propose a new Metropolis-Hastings step that permutes the components according to the size of the clusters.

Specifically, we consider the proposal based on reordering the component indices $n_{\sigma_1} \geq n_{\sigma_2} \geq \ldots \geq n_{\sigma_K}$. Sample $u \sim \text{Unif}(0, 1)$ and accept the proposal if

$$u \leq \frac{\pi\{y; (\sigma_1, \ldots, \sigma_K)\} \pi\{(\sigma_1, \ldots, \sigma_K)\}}{\pi\{y; (1, \ldots, K)\} \pi\{(1, \ldots, K)\}} = \frac{\pi\{(\sigma_1, \ldots, \sigma_K)\}}{\pi\{(1, \ldots, K)\}},$$

where $\pi\{(\sigma_1, \ldots, \sigma_K)\} = \prod_{k=1}^K \alpha B(m_{\sigma_k} + \alpha, n_{\sigma_k} + 1) \{p + (1-p)\epsilon^{-\alpha} I(1) (m_{\sigma_k} + \alpha, n_{\sigma_k} + 1)\}$, and the Jacobian determinant is 1 since it is a permutation. The likelihood $\pi\{y; (\sigma_1, \ldots, \sigma_K)\}$ is canceled because it is invariant to the index permutation. If the proposal is accepted, we update $b_k, \beta_k$ and $w_k$ immediately afterwards for all $k$.

**Remark 2.** Empirically, we found that the above Metropolis-Hastings step significantly improves the mixing of the Markov chains, and is applicable to all stick-breaking constructions with an exchangeability in $[n]$, hence may be of independent interest.
5 Simulations

We now use simulations to illustrate the strengths of the quasi-Bernoulli model. We compare with three popular alternatives, the Dirichlet process, the Pitman-Yor process, and the mixture of finite mixtures model.

We demonstrate the consistency of quasi-Bernoulli model for estimating the number of clusters $t$, when the component distribution is known and correctly specified. In the meantime, we compare the blocked Gibbs sampling algorithm for our model and the split-merge algorithm [Jain and Neal, 2007] for the mixture of finite mixtures model.

For the quasi-Bernoulli probability $p$ in (2), we choose $p = 0.9$ as a weakly information choice that favors more clusters. Alternatively, one could assign another Beta hyper-prior on $p$. We use $\epsilon = 1/n^{1.1}$. To have a fair comparison, we choose the concentration parameter $\alpha = 1$ for both quasi-Bernoulli stick-breaking process and Dirichlet process. For mixture of finite mixtures, we set a prior on number of components $\Pi_K(k) = p^{k-1}(1-p)$ where $p = 0.9$ as well, and a prior on weights $(w_1, \ldots, w_K) \sim \text{Dir}_K(\alpha, \ldots, \alpha)$ where $\alpha = 1$. For the Pitman-Yor process $\text{PY}(\alpha, d)$, we use $\alpha = -0.2$ and $d = 0.35$ as parameterized in [Ishwaran and James, 2001].

5.1 Estimating Gaussian mixture

For the mixture of finite mixtures model, the only available implementation for the split-merge algorithm is based on the Gaussian mixture. Therefore, to show comparable performance on the consistency, as well as much improved mixing via the simple Gibbs sampler, we first focus on using Gaussian distribution $\text{No}((\mu, \Sigma))$ as the mixture component.

We first generate data with sample sizes $n = 50, 200, 500, 1000$ and 2500 from a 3-component Gaussian mixture distribution in one-dimensional $\mathbb{R}$: $0.3 \text{No}(-4, 1^2) + 0.3 \text{No}(0, 1^2) + 0.4 \text{No}(5, 1^2)$. We follow Richardson and Green [1997] and using an empirical prior (base measure $G$) on $(\mu, \Sigma)$: $\mu \sim \text{No}(m_\mu, \sigma^2_\mu)$ and $\Sigma \sim \text{Ga}^{-1}(2, \gamma)$ \{ where $\text{Ga}^{-1}(a, b)$ has density $f(x) \propto x^{-a-1} \exp(-b/x)$ \}, with a hyper-prior $\text{Ga}(g, h)$ on $\gamma$, where $m_\mu = \frac{\max\{y\} + \min\{y\}}{2}$, $\sigma_\mu = \max\{y\} - \min\{y\}$, $g = 0.2$, and $h = 10/\max\{y\} - \min\{y\}^2$.

In all settings, we run the Markov chain for 20,000 iterations and discard the first 10,000 as burn-ins, and we use thinning at every 25th iteration. We repeat each experiment by five times and report the point-wise mean on the posterior distribution of $T$, as well as the 95% credible interval.

Figure 2 plots the posterior distribution on the number of clusters $T$ at each $n$. For both small and large $n$, our model correctly recovers the truth at the posterior mode $t = 3$. As $n$ becomes larger, the posterior distribution on $T$ converges to a point mass at 3.

Both our model (blue) and the mixture of finite mixtures model (green) yields the consistency results. Their posterior distributions of $T$ become very close especially at large $n$. This is coherent with our theory [5], as the mixture of finite mixtures model is close to a special case of quasi-Bernoulli with $\epsilon = 0$. As expected, the Dirichlet process mixture model fails to recover the truth on the number of clusters.

We found similar results in multivariate settings. We generate data from $0.3 \text{No}\{(-4, 1), I_2\} + 0.3 \text{No}\{(0, 2), I_2\} + 0.4 \text{No}\{(5, 3), I_2\}$, and we use the empirical prior $\mu \sim \text{No}(m, C)$ and
Figure 2: Posterior distribution on number of clusters for data generated from a 3-component Gaussian mixture in $\mathbb{R}$. Quasi-Bernoulli stick-breaking process mixture model correctly recovers 3 clusters as the ground truth.

$$\Sigma \sim \text{Wishart}_2^{-1}(C^{-1}/2, 2),$$ where $m$ is the sample mean and $C$ is the sample covariance. We provide the result in the appendix.
Figure 3: Compared to the mixture of finite mixtures model, the quasi-Bernoulli stick breaking model shows much better mixing in the Markov chains. There is a major difference in the computing performance. As shown in Figure 3, the mixture of finite mixtures suffers from slow mixing with high auto-correlation (effective sample size 8.0% in one dimension, and 6.3% in two dimensions); whereas the quasi-Bernoulli model has a much faster drop in the auto-correlation within a few lags (effective sample size 16.0% in one dimension, and 91.4% in two dimensions), thanks to the blocked Gibbs sampler.

5.2 Estimating Non-Gaussian Mixture

The quasi-Bernoulli model can be easily extended to the general mixture model with non-Gaussian components. To demonstrate that the consistency result still holds, we illustrate using data generated from Laplace mixture (for conciseness, we omit the similar results in the mixture of $t$-distribution, and the mixture of skewed normal).
Figure 4: Quasi-Bernoulli stick-breaking process mixture model correctly recovers 3 clusters as the ground truth, when each component is from a Laplace distribution; whereas the Dirichlet process and Pitman–Yor process over-estimate the cluster number, due to the spurious small clusters.

We generate data from a 3-component Laplace mixture: 0.35 Laplace($-10, 1$) + 0.3 Laplace($0, 1.5$) + 0.35 Laplace($10, 0.5$), where Laplace($\mu, \lambda$) denotes a Laplace distribution with mean $\mu$ and scale $\lambda$. We use an empirical prior (base measure $\mathcal{G}$) on $(\mu, \lambda)$: $\mu \sim \text{Normal}(m_\mu, \sigma_\mu^2)$ and $\lambda \sim \text{Gamma}^{-1}(2, 1)$, where $m_\mu = \frac{\max\{y\} + \min\{y\}}{2}$ and $\sigma_\mu = \max\{y\} - \min\{y\}$. Figure 4 shows that the quasi-Bernoulli stick-breaking process successfully recovers the true number of components, while Dirichlet process (red) and Pitman–Yor process (yellow) fail to do so.

6 Data Application: Clustering Brain Networks

To demonstrate the ease of using our model in an advanced data analysis, we cluster the brain network data, using a Bernoulli mixture model based on latent low-rank matrices.

We use the data from the human connectome project [Marcus et al., 2011]: for each experiment subject, the resting-state functional magnetic resonance imaging time series signals were collected from $V = 50$ regions on brain, indexed by $i = 1, \ldots, 50$. These 50 regions were obtained using group independent component analysis based on a high resolution raw data. There are $n = 812$ connectivity graphs indexed by $s = 1, \ldots, 812$, and each graph is recorded in a binary adjacency matrix $A^{(s)} \in \{0, 1\}^{50 \times 50}$, with matrix symmetry $A^{(s)} = A^{(s)^T}$.

To handle the high dimensionality, we use a probit-Bernoulli model, with the latent structure parameterized as low-rank and following a group structure. Since we do not know
how many groups there are, it is natural to use an infinite mixture model:
\[
A_{i,j}^{(s)} \sim \text{Bernoulli}\{\Phi(B_{i,j}^{(s)} + D_{i,j})\}, \text{ for } j < i
\]
\[
B^{(s)} \sim \sum_{k=1}^{\infty} w_k \delta_{M_k}(\cdot),
\]
\[
M_k = Q_k \Lambda_k Q_k^T.
\]

We use \(D\) as a symmetric and unstructured matrix, shared by all subjects \(s\). This is a nuisance parameter used to effectively induce a low rank in \(B\). We assign a normal prior on \(D_{i,j} \sim \text{No}(0, 10^2)\).

To parameterize a low-rank structure, we follow [Hoff 2009] and set \(Q_k\) on a Stiefel manifold \(\mathcal{V}_{d,V} = \{Q \in \mathbb{R}^{V \times d} : Q^T Q = I_d\}\), and \(\Lambda_k = \text{diag}(\lambda_{k,1}, \ldots, \lambda_{k,d})\), where \(\lambda_{k,l} > 0\) for \(l = 1, \ldots, d\). We set \(d = 10\) and assign a uniform form prior on \(Q_k \in \mathcal{V}_{d,V}\), a truncated normal prior on \(\lambda_{k,l} \sim \text{No}(0, 10^2)1(\lambda_{k,l} > 0)\).

Figure 5: The quasi-Bernoulli model produces 5 clusters when clustering 812 brain connectivity networks, which is substantially fewer compared to the Dirichlet process (11 clusters at its mode).

![Figure 5: The quasi-Bernoulli model produces 5 clusters when clustering 812 brain connectivity networks, which is substantially fewer compared to the Dirichlet process (11 clusters at its mode).](image)

Figure 6: The edge connectivity probabilities \(\Pr(A_{i,j} = 1)\) over the 5 groups (the edges with probability smaller than 0.05 are hidden for better visualization).

![Figure 6: The edge connectivity probabilities \(\Pr(A_{i,j} = 1)\) over the 5 groups (the edges with probability smaller than 0.05 are hidden for better visualization).](image)

(a) Group 1 (43.2% of the subjects) (b) Group 2 (22.4% of the subjects) (c) Group 3 (16.4% of the subjects) (d) Group 4 (9.8% of the subjects) (e) Group 5 (8.3% of the subjects)

For the quasi-Bernoulli stick-breaking process, we use \(p = 0.1\) and \(\epsilon = 1/n^{1.1}\). We run the blocked Gibbs sampler for 5,000 iterations and discard the first 1,000 as burn-ins.
The subjects are clustered into 5 groups, and we plot the posterior means of the connectivity probability $\text{pr}(A_{i,j} = 1)$ in Figure 6. In the result, we have three groups of subjects that have very sparse connectivity (that account for 82% of the subjects), compared to the rest of two groups. As a comparison, we also use a Dirichlet process mixture, and it produces 11 clusters (Figure 5) in its posterior distribution mode. Clearly, the result from the quasi-Bernoulli model is more interpretable.

7 Discussion

In this article, we propose a modification to the canonical stick-breaking construction, which leads to an infinite mixture model that enjoys consistency in the number of clusters. There are several extensions worth further pursuing.

First, the recovery of the true cluster number under a misspecified model is still an open problem. In a recent preprint by Cai et al. (2020, arXiv 2007.04470), it is theoretically shown that the component misspecification will result in an over-estimated number of clusters in the overfitted finite mixture models. Intuitively, this suggests that besides controlling the spurious mixture weight, it is equally important to ensure that the mixture component is flexibly parameterized to minimize the chance of model misspecification. Second, it is interesting to explore whether the combination of the quasi-Bernoulli infinite mixture framework and distance clustering approaches, such as the Laplacian-based approach Rohe et al. [2011], can lead to a consistency result on the cluster number.

APPENDIX

Proof of Theorem 1

Proof. We denote $g_k = n_k + m_k$. The conditional probability mass function of assignment variables is

$$\text{pr}(c \mid (b_k)_{k=1}^{\infty}, (\beta_k)_{k=1}^{\infty}) = \prod_{k=1}^{\infty} (1 - \beta_k b_k)^{n_k} (\beta_k b_k)^{g_k+1},$$
where $n_k = \sum_{i=1}^{n} 1(c_i = k)$ and $g_k = \sum_{i=1}^{n} 1(c_i \geq k)$. Let $M(c) = \max\{c_1, \ldots, c_n\}$. Then

$$
pr(c) = \prod_{k=1}^{\infty} \int_0^{\infty} \left\{ p(1 - \beta_k)^{n_k} (\beta_k)^{g_k} + (1 - p)(1 - \epsilon \beta_k)^{n_k} (\epsilon \beta_k)^{g_k + 1} \right\} \alpha^\beta \, d\beta_k
$$

$$
= \prod_{k=1}^{\infty} \left\{ p \alpha B(n_k + 1, g_k + 1 + \alpha) + (1 - p) \frac{\alpha}{c^\alpha} B(n_k + 1, g_k + 1 + \alpha) \right\} \mathcal{I}_\epsilon(g_k + 1 + \alpha, n_k + 1)
$$

$$
= \prod_{k=1}^{\infty} \left\{ p \alpha \Gamma(n_k + 1) \Gamma(g_k + 1 + \alpha) \right\} \mathcal{I}_\epsilon(g_k + 1 + \alpha, n_k + 1)
$$

$$
= \prod_{k=1}^{\infty} \frac{\alpha \Gamma(n_k + 1) \Gamma(g_k + 1 + \alpha)}{\Gamma(n_k + g_k + 1 + \alpha + 1)} \mathcal{I}_\epsilon(g_k + 1 + \alpha, n_k + 1)
$$

$$
= \prod_{k=1}^{M(c)} \frac{\Gamma(n_k + 1) \Gamma(g_k + 1 + \alpha)}{\Gamma(g_k + \alpha + 1)} \prod_{k=1}^{M(c)} \alpha \mathcal{I}_\epsilon(g_k + 1 + \alpha, n_k + 1)
$$

$$
= \frac{\Gamma(\alpha)}{\Gamma(n + \alpha)} \left\{ \prod_{k=1}^{M(c)} \Gamma(n_k + 1) \right\} \prod_{k=1}^{M(c)} \frac{\alpha Q_k}{g_k + \alpha}
$$

where (a) is using $B(1, \alpha) = 1/\alpha$ and $\mathcal{I}_\epsilon(\alpha, 1) = e^\alpha$ when $n_k = 0$ and $g_k + 1 = 0$, and $Q_k = p + (1 - p)\mathcal{I}_\epsilon(g_k + 1 + \alpha, n_k + 1)/e^\alpha$.

Let $S_c$ be the partition on $[n]$ formed from $c$. For fixed $S = \{S_1, \ldots, S_t\}$, when $S_c = S$, there are exactly $t$ unique values among $c_1, \ldots, c_n$. Let $k_1 < k_2 < \cdots < k_t$ denote these unique values, and set $k_0 = 0$.

For $k_{i-1} < k < k_i$, we have $n_k = 0$ and $g_k = g_k$, leading to $Q_k = p + (1 - p)e^{g_k}$, while for $k = k_i$, we have $n_k = n_{k_i}$ and $g_k = g_{k + 1}$, which leads to $Q_k = p + (1 - p)\mathcal{I}_\epsilon(g_k + 1 + \alpha, n_k + 1)/e^\alpha$. Hence for $c$ satisfying $S_c = S$, we have $pr(c) = \Gamma(\alpha) / \Gamma(n + \alpha) \left\{ \prod_{i=1}^{t} \Gamma(n_k + 1) \right\} \prod_{i=1}^{t} A_i(c)$, where

$$
A_i(c) = \left\{ \frac{\alpha p}{g_k + \alpha} + \frac{\alpha (1 - p) \mathcal{I}_\epsilon(g_k + 1 + \alpha, n_k + 1)}{e^\alpha(g_k + \alpha)} \right\} \left\{ \frac{\alpha p + \alpha (1 - p) e^{g_k}}{g_k + \alpha} \right\}^{d_i}
$$

where $d_i = k_i - k_{i-1} - 1 (i = 1, \ldots, t)$.

Since there is a unique permutation $\sigma = (\sigma_1, \ldots, \sigma_t)$ of $[t]$ such that $S_{\sigma_i} = \{j : c_j = k_i\}$, it is clear that the mapping between $\{c : S_c = S\}$ and $\{\sigma, d_1, \ldots, d_t : \sigma\}$ is a permutation of $[t], d_i \in \mathbb{N}$ is a bijection. Letting $n_k^* = |S_k|$ and $g_k^* = \sum_{i=1}^{t} n_{\sigma_i}$, we have

$$
pr_{e,n}(S) = \sum_{S_c = S} pr(c) = \frac{\Gamma(\alpha)}{\Gamma(n + \alpha)} \prod_{k=1}^{t} \Gamma(n_k^* + 1) \sum_{\sigma} \sum_{d_i = 0}^{\infty} \sum_{d_i = 0}^{\infty} \prod_{i=1}^{t} A_i(c).
$$
By changing the order of summations and multiplication, we have

\[
\sum_{d_1=0}^{\infty} \cdots \sum_{d_t=0}^{\infty} \prod_{i=1}^{t} A_i(c) = \prod_{k=1}^{t} \left\{ \frac{\alpha p}{g_{\sigma_k}^* + \alpha} + \frac{\alpha (1-p)I_t(g_{\sigma_k+1}^* + \alpha, n_{\sigma_k}^* + 1)}{\epsilon^\alpha (g_{\sigma_k}^* + \alpha)} \right\} \sum_{d_k=0}^{\infty} \left\{ \frac{\alpha p + \alpha (1-p)\epsilon^{g_{\sigma_k}^*}}{g_{\sigma_k}^* + \alpha} \right\}^{d_k}
\]
\[
= \prod_{k=1}^{t} \left\{ \frac{\alpha p}{g_{\sigma_k}^* + \alpha} + \frac{\alpha (1-p)I_t(g_{\sigma_k+1}^* + \alpha, n_{\sigma_k}^* + 1)}{\epsilon^\alpha (g_{\sigma_k}^* + \alpha)} \right\} \left\{ 1 - \frac{\alpha p + \alpha (1-p)\epsilon^{g_{\sigma_k}^*}}{g_{\sigma_k}^* + \alpha} \right\}^{-1}
\]
\[
= \alpha^t \prod_{k=1}^{t} \frac{p (1 - \beta_k)^n (\beta_k b_k)^{g_{k+1}} + (1 - p)1(g_{k+1} = 0)}{\epsilon^\alpha (g_{\sigma_k}^* + \alpha)}
\]

This proves the result. \(\square\)

**Proof of Lemma 1**

**Proof.** The conditional probability mass function of assignment variables is

\[
\text{pr}(c \mid (b_k)_{k=1}^{\infty}, (\beta_k)_{k=1}^{\infty}) = \prod_{k=1}^{\infty} (1 - \beta_k b_k)^{n_k} (\beta_k b_k)^{g_{k+1}},
\]

where \(n_k = \sum_{i=1}^{n} 1(c_i = k)\) and \(g_k = \sum_{i=1}^{n} 1(c_i \geq k)\). Let \(M(c) = \max\{c_1, \ldots, c_n\}\). Then

\[
\begin{align*}
\text{pr}(c) &= \prod_{k=1}^{\infty} \int_{0}^{1} \{p(1 - \beta_k)^n (\beta_k b_k)^{g_{k+1}} + (1 - p)1(g_{k+1} = 0)\} \alpha^\beta \beta^{-1} d\beta_k \\
&= \prod_{k=1}^{M(c)} \{p\alpha \Gamma(n_k + 1, g_{k+1} + \alpha) + (1 - p)1(g_{k+1} = 0)\} \\
&= \prod_{k=1}^{M(c)} \frac{p\alpha \Gamma(n_k + 1) \Gamma(g_{k+1} + \alpha)}{\Gamma(n_k + g_{k+1} + \alpha + 1)} \times \{p\alpha \Gamma(n_{M(c)} + 1, \alpha) + 1 - p\} \\
&= \prod_{k=1}^{M(c)-1} \Gamma(n_k + 1) \prod_{k=1}^{M(c)} \frac{p\alpha \Gamma(g_{k+1} + \alpha)}{\Gamma(g_k + \alpha + 1)} \times \{p\alpha \Gamma(n_{M(c)} + 1, \alpha) + 1 - p\} \\
&= \frac{\Gamma(\alpha)}{\Gamma(n + \alpha)} \left\{ \prod_{i=1}^{M(c)} \Gamma(n_i + 1) \right\} \prod_{k=1}^{M(c)-1} \frac{p\alpha}{g_k + \alpha} \times \frac{p\alpha + (1 - p)B(n_{M(c)} + 1, \alpha)}{n_{M(c)} + \alpha}
\end{align*}
\]

where (a) is using \(B(1, \alpha) = 1/\alpha\) when \(n_k = 0\) and \(g_{k+1} = 0\).

Let \(S_c\) be the partition on \([n]\) formed from \(c\). For fixed \(S = \{S_1, \ldots, S_t\}\), when \(S_c = S\), there are exactly \(t\) unique values among \(c_1, \ldots, c_n\). Let \(k_1 < k_2 < \cdots < k_t\) denote these unique values, and set \(k_0 = 0\).

For \(k_{i-1} < k \leq k_i\), we have \(g_k = g_{k_i}\). Hence for \(c\) satisfying \(S_c = S\), we have \(\text{pr}(c) = \Gamma(\alpha)/\Gamma(n + \alpha) \{\prod_{i=1}^{t} \Gamma(n_i + 1)\} \prod_{i=1}^{t} A_i(c)\), where \(A_i(c) = \{p\alpha/(g_{k_i} + \alpha)\}^{d_i}\) and

\[
A_i(c) = \frac{p\alpha + (1 - p)B(n_i + 1, \alpha)}{n_i + \alpha} \times \left( \frac{\alpha p}{g_{k_i} + \alpha} \right)^{d_i - 1}
\]
where \( d_i = k_i - k_{i-1} \) (\( i = 1, \ldots, t \)).

Since there is a unique permutation \( \sigma = (\sigma_1, \ldots, \sigma_t) \) of \([t]\) such that \( S_{\sigma_i} = \{ j : c_j = k_i \} \), it is clear that the mapping between \( \{ c : S_c = S \} \) and \( \{ (\sigma, d_1, \ldots, d_t) : \sigma \text{ is a permutation of } [t], d_i \in \mathbb{N} \} \) is a bijection. Letting \( n_k^* = |S_k| \) and \( g^*_{\sigma_k} = \sum_i n_{\sigma_i}^* \), we have

\[
pr_{0,n}(S) = \sum_{S_c=S} \Pr(c) = \frac{\Gamma(n)\prod_{k=1}^t \Gamma(n_k^* + 1)}{\Gamma(n + \alpha)} \sum_{\sigma} \prod_{k=1}^t \sum_{d=0}^\infty \sum_{i=1}^\infty \prod_{l=0}^d A_i(c).
\]

By changing the order of summations and multiplication, we have

\[
\sum_{d_1=0}^{\infty} \cdots \sum_{d_t=0}^{\infty} \prod_{i=1}^t A_i(c) = \frac{p \alpha + (1 - p)/B(n_t^* + 1, \alpha)}{n_t^* + \alpha} \prod_{k=1}^{t-1} \sum_{d_{k-1}=1}^{\infty} \left( \frac{\alpha p}{g^*_{\sigma_k} + \alpha} \right)^{d_{k-1}} \prod_{k=1}^{t-1} \left( \frac{\alpha p}{g^*_{\sigma_k} + \alpha} \right)^{-1} \left( 1 - \frac{\alpha p}{\alpha p + g^*_{\sigma_k} \alpha} \right)^{-1} \left( \alpha p / (1 - p) \right) \prod_{k=1}^t \frac{p}{g^*_{\sigma_k} + \alpha (1 - p)}.
\]

This proves the result.

**Proof of Theorem 2**

Proof. By Doob’s theorem, there is a subspace \( \Omega_0 \subset \Omega \) with \( \Pi_0(\Omega_0) = 1 \) such that for true parameter \( \phi \in \Omega_0 \), if \( y_1, \ldots, y_n \mid \phi \sim P_\phi \), then for all measurable \( A \in \Omega \), as \( n \to \infty \), we have \( pr_{\epsilon=0}(A \mid y) \to 1(\phi \in A) \). The first result is proved by letting \( A \) be \( \{ k \} \times \Delta^{k-1} \times \Theta^k \).

For the second result, as \( n \to \infty \), since in (5) \( w_k \) does not change with \( n \), we can expect that any \( w_k > 0 \) will have at least some data assigned to \( k \)th component, therefore \( K \) and \( T \) would match in the posterior.

We firstly prove that \( pr_{\epsilon=0}(T = k \mid K = k) \to 1 (k \geq 1) \) as \( n \to \infty \). We fix \( K = K \), which is equivalent to \( v_K = 1 \). Let random variables \( A_k = \sum_{i=1}^n 1(c_i = k) \) (\( k = 1, \ldots, K \)) be the number of \( k \) in \( c \). Then

\[
pr_{\epsilon=0}(A_k = 0 \mid K, v_1, \ldots, v_{K-1}) = pr_{\epsilon=0}[\cap_{i=1}^n \{ c_i \neq k \} \mid K, v_1, \ldots, v_{K-1}] = [pr_{\epsilon=0}(c_1 \neq k \mid K, v_1, \ldots, v_{K-1})]^n = (1 - w_k)^n.
\]
Hence the probability of having $K$ clusters from $n$ assignments

$$\text{pr}_{\epsilon=0}(T = K \mid K)$$

$$= \int_0^1 \cdots \int_0^1 \text{pr}_{\epsilon=0}(T = K \mid K, v_1, \ldots, v_{K-1}) \pi_{\epsilon=0}(v_1, \ldots, v_{K-1} \mid K) \, dv_1 \cdots dv_{K-1}$$

$$= \int_0^1 \cdots \int_0^1 \text{pr}_{\epsilon=0}(A_1 > 0, A_2 > 0, \ldots, A_K > 0 \mid K, v) \prod_{k=1}^{K-1} \alpha(1 - v_k)^{\alpha-1} \, dv_1 \cdots dv_{K-1}$$

$$= \int_0^1 \cdots \int_0^1 [1 - \text{pr}_{\epsilon=0}(\bigcup_{k=1}^K \{ A_k = 0 \} \mid K, v)] \prod_{k=1}^{K-1} \alpha(1 - v_k)^{\alpha-1} \, dv_1 \cdots dv_{K-1}$$

$$\geq \int_0^1 \cdots \int_0^1 [1 - \sum_{k=1}^K (1 - w_k)^n] \prod_{k=1}^{K-1} \alpha(1 - v_k)^{\alpha-1} \, dv_1 \cdots dv_{K-1}$$

$$= 1 - \sum_{k=1}^K \int_0^1 \cdots \int_0^1 (1 - w_k)^n \prod_{k=1}^{K-1} \alpha(1 - v_k)^{\alpha-1} \, dv_1 \cdots dv_{K-1}$$

converges to 1 when $n \to \infty$ since the integrands converge to 0, which leads to $\text{pr}_{\epsilon=0}(T < k \mid K = k) \to 0$, so we have for any $k > t$,

$$\frac{\text{pr}_{\epsilon=0}(T = t \mid K = k)}{\text{pr}_{\epsilon=0}(T = t \mid K = t)} \to 0$$

as $n \to \infty$, which leads to

$$\frac{\sum_{k=t+1}^{\infty} \text{pr}_{\epsilon=0}(T = t \mid K = k) \pi_{\epsilon=0}(K = k)}{\text{pr}_{\epsilon=0}(T = t \mid K = t) \pi_{\epsilon=0}(K = t)} \to 0$$

as $n \to \infty$ for any given $t$ by discrete version dominated convergence theorem. Hence we have

$$\text{pr}_{\epsilon=0}(K = k \mid T = t) = \frac{\text{pr}_{\epsilon=0}(T = t \mid K = k) \pi_{\epsilon=0}(K = k)}{\sum_{k=t}^{\infty} \text{pr}_{\epsilon=0}(T = t \mid K = k) \pi_{\epsilon=0}(K = k)} \to 1(k = t)$$

as $n \to \infty$ for $t \leq k$. Finally, the result

$$\text{pr}_{\epsilon=0}(K = k \mid y) = \sum_{t=1}^k \text{pr}_{\epsilon=0}(K = k \mid T = t, y) \text{pr}_{\epsilon=0}(T = t \mid y)$$

$$= \sum_{t=1}^k \text{pr}_{\epsilon=0}(K = k \mid T = t) \text{pr}_{\epsilon=0}(T = t \mid y)$$

proves the theorem. 

\[\square\]
Proof of Theorem 3

*Proof.** Denote the term in \( \text{pr}_{\epsilon,n}(S) \) and \( \text{pr}_{0,n}(S) \) as

\[
A_k(\sigma) = \frac{p}{g_{\sigma_k} + \alpha(1-p)} \quad \text{for } k = 1, \ldots, t - 1, \quad A_t(\sigma) = \frac{p + (1 - p)/\{\alpha B(\alpha, n_{\sigma_t}, 1)\}}{g_{\sigma_t} + \alpha(1-p)},
\]

and

\[
B_k(\sigma) = \frac{p + (1 - p)I_\epsilon(g_{\sigma_{k+1}} + \alpha, n_{\sigma_k} + 1)/\epsilon^\alpha}{g_{\sigma_k} + \alpha(1-p)(1 - \epsilon^{g_{\sigma_k}})} \quad \text{for } k = 1, \ldots, t.
\]

When \( k < t \), we have \( A_k(\sigma) \leq B_k(\sigma) \) since \( (1 - p)I_\epsilon(g_{\sigma_{k+1}} + \alpha, n_{\sigma_k} + 1)/\epsilon^\alpha > 0 \) and \( g_{\sigma_k} + \alpha(1-p) > g_{\sigma_k} + \alpha(1-p)(1 - \epsilon^{g_{\sigma_k}}) > 0 \).

For the case \( k = t \), we have

\[
\frac{A_t(\sigma)}{B_t(\sigma)} \leq \frac{(a) p + (1 - p)/\{\alpha B(\alpha, n_{\sigma_t}, 1)\}}{p + (1 - p)I_\epsilon(\alpha, n_{\sigma_t} + 1)/\epsilon^\alpha} = \frac{(b) \alpha B(\alpha, n_{\sigma_t} + 1) + 1 - p}{\alpha B(\alpha, n_{\sigma_t} + 1) + (1 - p)\{1 - \alpha e n_{\sigma_t}/(\alpha + 1)\}} = 1 + \frac{(c) \alpha e}{\alpha + 1 - \alpha e n_{\sigma_t}},
\]

where \( (a) \) uses \( g_{\sigma_k} + \alpha(1-p) > g_{\sigma_k} + \alpha(1-p)(1 - \epsilon^{g_{\sigma_k}}) > 0 \), \( (b) \) uses

\[
\frac{\alpha B(\alpha, n_{\sigma_t} + 1)I_\epsilon(\alpha, n_{\sigma_t} + 1)}{\epsilon^\alpha} = \frac{\alpha}{\epsilon^\alpha} \int_0^\epsilon x^{\alpha-1}(1 - x)^{n_{\sigma_t}} \, dx \geq \frac{\alpha}{\epsilon^\alpha} \int_0^\epsilon x^{\alpha-1}(1 - n_{\sigma_t}x) \, dx = 1 - \frac{\alpha e n_{\sigma_t}}{\alpha + 1},
\]

and \( (c) \) uses \( \alpha e B(\alpha, n_{\sigma_t} + 1) > 0 \) and \( n_{\sigma_t} \leq n \).

The ratio of two probability mass functions

\[
\frac{\text{pr}_{0,n}(S)}{\text{pr}_{\epsilon,n}(S)} = \sum_{\sigma} \prod_{k=1}^t \left\{ \frac{A_k(\sigma)/B_k(\sigma)}{\max_{\sigma} \prod_{k=1}^t B_k(\sigma)} \right\} \leq 1 + \frac{\alpha e}{\alpha + 1 - \alpha e n},
\]

where \( (a) \) uses \( \prod_{k=1}^t \{A_k(\sigma)/B_k(\sigma)\} \leq \max_{\sigma} \prod_{k=1}^t \{A_k(\sigma)/B_k(\sigma)\} \), so the Kullback–Leibler divergence

\[
D_{KL}(\text{pr}_{0,n}||\text{pr}_{\epsilon,n}) = \sum_S \text{pr}_{0,n}(S) \log \frac{\text{pr}_{0,n}(S)}{\text{pr}_{\epsilon,n}(S)} \leq \sum_S \text{pr}_{0,n}(S) \frac{\alpha e}{\alpha + 1 - \alpha e n} = \frac{\alpha e}{\alpha + 1 - \alpha e n},
\]

where the summation is for all partitions of \([n]\) and the inequality uses \( \log(x) \leq x - 1 \). The result follows by Pinsker’s inequality. □

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Additional simulation result

Figure 7: Posterior distribution on number of clusters for data generated from a 3-component Gaussian mixture in \(\mathbb{R}^2\). Quasi-Bernoulli stick-breaking process mixture model correctly recovers 3 clusters as the ground truth.

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