Independent finite approximations for Bayesian nonparametric inference

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Abstract: Bayesian nonparametric priors based on completely random measures (CRMs) offer a flexible modeling approach when the number of latent components in a dataset is unknown. However, managing the infinite dimensionality of CRMs typically requires practitioners to derive ad-hoc algorithms, preventing the use of general-purpose inference methods and often leading to long compute times. We propose a general but explicit recipe to construct a simple finite-dimensional approximation that can replace the infinite-dimensional CRMs. Our independent finite approximation (IFA) is a generalization of important cases that are used in practice. The independence of atom weights in our approximation (i) makes the construction well-suited for parallel and distributed computation and (ii) facilitates more convenient inference schemes. We quantify the approximation error between IFAs and the target nonparametric prior. We compare IFAs with an alternative approximation scheme — truncated finite approximations (TFAs), where the atom weights are constructed sequentially. We prove that, for worst-case choices of observation likelihoods, TFAs are a more efficient approximation than IFAs. However, in real-data experiments with image denoising and topic modeling, we find that IFAs perform very similarly to TFAs in terms of task-specific accuracy metrics.

1. Introduction

Many data analysis problems can be seen as discovering a latent set of traits in a population — for example, recovering topics or themes from scientific papers, ancestral populations from genetic data, interest groups from social network data, or unique speakers across audio recordings of many meetings (Palla, Knowles and Ghahramani, 2012; Blei, Griffiths and Jordan, 2010; Fox et al., 2010). In all of these cases, we might reasonably expect the number of latent traits present in a data set to grow with the size of the data. One might choose a prior for different data set sizes, but then model construction potentially becomes inconvenient and unwieldy. A simpler approach is to choose a single prior that naturally yields different expected numbers of traits for different numbers of data points. In theory, Bayesian nonparametric (BNP) priors have exactly this desirable property due to a countable infinity of traits, so that there are always more traits to reveal through the accumulation of more data. However, the infinite-dimensional parameter presents a practical challenge. In what follows, we propose a general but explicit construction of a simple finite-dimensional approximation across a wide range of BNP models. Our approximation generalizes a number of existing special cases that appeared separately in the literature. Furthermore, the proposed approximation is amenable to modern, efficient inference schemes and black-box approximate inference algorithms (Ranganath, Gerrish and Blei, 2014; Kucukelbir et al.,...
2015; Carpenter et al., 2017); fits easily within complex, potentially deep generative models; and admits straightforward parallelization.

The problem. A particular challenge of the infinite-dimensional parameter is that it is impossible to store an infinity of random variables in memory or learn the distribution over an infinite number of variables in finite time. Some authors have developed conjugate priors and likelihoods (Orbanz, 2010) to circumvent the infinite representation; these models allow marginalization of the countable collection of latent traits and thus exact Bayesian posterior inference (James, 2017; Broderick, Wilson and Jordan, 2018). However, these priors and likelihoods are often just a single piece within a more complex generative model, which is no longer fully conjugate and therefore requires an approximate posterior inference scheme such as Markov Chain Monte Carlo (MCMC) or variational inference. Some local steps in, e.g., an MCMC sampler can still take advantage of conditional conjugacy via special marginal forms such the Chinese restaurant process (Teh et al., 2006) or the Indian buffet process (Griffiths and Ghahramani, 2005); see James (2017) and Broderick, Wilson and Jordan (2018) for general treatments. But using these marginal versions of the process rather than a full and explicit representation of the latent variables typically necessitates a Gibbs sampler, which can be slow to mix and may require special-purpose, model-specific sampling moves. An explicit trait representation is generally required to use modern, automated inference schemes — such as black-box variational inference methods (Ranganath, Gerrish and Blei, 2014; Kucukelbir et al., 2015) or MCMC in the Stan language (Carpenter et al., 2017).

An alternative approach that still allows use of these convenient inference methods is to approximate the infinite-dimensional prior with a finite-dimensional prior that essentially replaces the infinite collection of random traits by a finite subset of “likely” traits. Unlike a fixed finite-dimensional prior across all data set sizes, this finite-dimensional prior is seen as an approximation to the BNP prior. Therefore, its cardinality is informed directly by the BNP prior and the data set size one needs to model. Since any moderately complex model will necessitate approximate inference, so long as the approximation error from using the finite-dimensional prior approximation is on the order of the approximation error from, say, using MCMC or variational inference, inferential quality is not affected.

Much of the previous work on finite approximations developed and analyzed truncations of series representations of the random measures underlying the nonparametric prior; we call these truncated finite approximations (TFAs) and refer to Campbell et al. (2019) for a thorough study. TFAs start from a sequential ordering of population traits in a random measure. The TFA retains a finite set of approximating traits; these match the population traits until a finite point and do not include terms beyond that (Doshi-Velez et al., 2009; Paisley, Blei and Jordan, 2012; Roychowdhury and Kulis, 2015; Campbell et al., 2019). Here, we instead develop and analyze a general-purpose finite approximation consisting of independent and identically distributed (i.i.d.) representations of the traits together with their rates within the population; we call these independent finite approximations (IFAs). The IFA approach has the potential to be simpler to incorporate in a complex hierarchical model, to exhibit improved mixing, and to be amenable to parallelizing computation during inference. At the time of writing, we are aware of two concurrent works on generic constructions of finite approximations using i.i.d. random variables, namely Lijoi, Prünster and Rigon (2019) and Lee, Miscouridou and Caron (2019). Lijoi, Prünster and Rigon (2019) design approximations for clustering models, thoroughly characterize posterior predictive distribution, and derive tractable inference schemes. However, without modification, their approximation is not suitable for use in statistical models where the unnormalized atom sizes of the CRM are feature
rates. Lee, Miscouridou and Caron (2019) construct finite approximations through a novel augmentation scheme, which bridges certain types of truncated finite approximations and recovers certain existing i.i.d finite approximations, such as those in Lee, James and Choi (2016). However, Lee, Miscouridou and Caron (2019) lack explicit constructions in other important situations, such as exponential-family rate measures, because the functions involved in the augmentation are only implicitly defined in general. Our construction is more general than these approaches; namely, it is compatible with a larger class of statistical models and admits an explicit construction in more situations.

Our contributions. We propose a general-purpose construction for IFAs. Our construction subsumes a number of special cases that have already been successfully used in applications, with practitioners reporting similar performance to the truncation approach but with faster mixing (Kurihara, Welling and Teh, 2007; Saria, Koller and Penn, 2010; Fox et al., 2010; Johnson and Willsky, 2013). We develop a broad mechanism for our i.i.d. finite approximation and relate our approach to special cases in existing work. As with previous IFA special cases, we observe that our general construction for IFAs benefits from conceptual ease of use, including easier integration with probabilistic programming, over TFAs. We then quantify the error induced by approximating an exact infinite-dimensional prior with an IFA in probabilistic models. Our analysis provides interpretable error bounds with explicit dependence on the size of the approximation and the data cardinality. We examine the worst-case choice of observation likelihoods. Our error bounds reveal that in this worst case, to approximate the target to a desired accuracy, it is necessary to use a large IFA model while a small TFA model would suffice. However, we do not observe a discrepancy in inferential quality in practice, and we confirm through experiments with image denoising and topic modeling that IFAs and TFAs of equal sizes have similar performance on applied problems.

2. Background

Our work will approximate nonparametric priors, so we first review construction of these priors from completely random measures (CRMs). Then we cover existing work on the construction of truncated and independent finite approximations for these CRM priors. Let $\psi_i \in \Psi$ for some space $\Psi$ represent the $i$-th trait of interest, and let $\theta_i > 0$ represent the corresponding rate or frequency of this trait in the population. The total number of traits, $I$, may be finite or, in the nonparametric setting, countably infinite. Collect the pairs of traits and frequencies in a measure $\Theta$ that places non-negative mass $\theta_i$ at location $\psi_i$:

$$\Theta := \sum_{i=1}^{I} \theta_i \delta_{\psi_i},$$

where $\delta_A(\cdot)$ is used to denote a Dirac mass at $A$, i.e. $\delta_A(\cdot) = 1_{\{\cdot \in A\}}$. To perform Bayesian inference, we need to choose a prior distribution on $\Theta$ and a likelihood for the observed data $Y_{1:N} := \{Y_n\}_{n=1}^{N}$ given $\Theta$. Then, applying a disintegration, we can obtain the posterior on $\Theta$ given the observed data.

Completely random measures. Most common BNP priors can be conveniently formulated as completely random measures (or their normalizations). CRMs are constructed from Poisson point processes, which are straightforward to manipulate both analytically and algorithmically (Kingman, 1992). Consider a Poisson point process on $\mathbb{R}_+ := [0, \infty)$

\footnote{For brevity, we do not consider here the possible fixed-location and deterministic components of a CRM (Kingman, 1967). In Bayesian inference, they are purely atomic because we generate parameter tuples. These components can be added and our analysis modified without undue effort.}
with rate measure \( \nu(d\theta) \) such that \( \nu(\mathbb{R}_+) = \infty \) and \( \int \min(1, \theta) \nu(d\theta) < \infty \). Such a process generates a countably infinite set of rates \( \{\theta_i\}_{i=1}^{\infty}, \theta_i \in \mathbb{R}_+ \), having an almost surely finite sum \( \sum_{i=1}^{\infty} \theta_i < \infty \). We assume throughout that \( \psi_i \sim H \) for some diffuse distribution \( H \).

The distribution \( H \), also called the ground measure, serves as a prior on the traits in the space \( \Psi \). For example, in topic modeling, it is typical to assume that each trait \( \psi_i \) represents a latent topic; \( \theta_i \) typically represents the frequency with which the corresponding topic \( \psi_i \) is featured across documents in a corpus. Each topic is modeled as a probability vector in the simplex of vocabulary words. In this case, it is typical to assume that the traits follow a Dirichlet distribution over the simplex of dimension given by the number of words in the vocabulary.

By pairing the jumps of the Poisson process with topics drawn from the ground measure, we obtain a completely random measure (Kingman, 1967). As shorthand, we will write \( \text{CRM}(H, \nu) \) for the completely random measure generated as just described: \( \Theta := \sum_i \theta_i \delta_{\psi_i} \sim \text{CRM}(H, \nu) \). When the total mass \( \Theta(\Psi) \) is strictly positive and finite, the corresponding normalized CRM (NCRM) is \( \Xi := \Theta / \Theta(\Psi) \), which is a discrete probability measure. The set of atom locations of \( \Xi \) is the same as that of \( \Theta \), while the atom sizes are normalized \( \Xi = \sum_i \xi_i \delta_{\psi_i} \), where \( \xi_i = \theta_i / (\sum_j \theta_j) \).

The CRM prior on \( \Theta \) is typically combined with a likelihood that generates trait counts for each data point. Let \( \ell(\cdot | \theta) \) be a proper probability mass function on \( \mathbb{N} \cup \{0\} \) for all \( \theta \) in the support of \( \nu \). The process \( X_n := \sum_i x_{ni} \delta_{\psi_i} \) collects the trait counts, where \( x_{ni} | \Theta \sim \ell(\cdot | \theta_i) \) independently across \( i \) and i.i.d. across \( n \). We denote the distribution of \( X_n \) as \( \text{LP}(\ell, \Theta) \), which we call the likelihood process. Since the trait counts are typically just a latent component in a full generative model specification, we define the observed data to be \( Y_n | X_n \stackrel{\text{iid}}{\sim} f(\cdot | X_n) \) for a probability kernel \( f(dY | X) \). Consider the topic modeling example; if the sequence \( \{\theta_i\}_{i=1}^{\infty} \) represents the topic rates in a document corpus, \( X_n \) might capture how many words in document \( n \) are generated from each topic, and \( Y_n \) might give the observed collection of words for that document.

**Finite approximations.** Since the set \( \{\theta_i\}_{i=1}^{\infty} \) is countably infinite, it may be difficult to simulate or perform posterior inference in the full model. One approximation scheme is to define the finite approximation \( \Theta_K := \sum_{i=1}^{K} \tau_i \delta_{\psi_i} \). The atom sizes \( \{\tau_i\}_{i=1}^{K} \) are designed so that \( \Theta_K \) is a good approximation of \( \Theta \) in a suitable sense. Since it involves a finite number of parameters, \( \Theta_K \) can be used for efficient posterior inference, including black-box MCMC and variational inference algorithms — but some approximation error is introduced by not using the full CRM \( \Theta \).

A truncated finite approximation (TFA; Doshi-Velez et al., 2009; Paisley, Blei and Jordan, 2012; Roychowdhury and Kulis, 2015) requires constructing an ordering on the set of rates from the Poisson process — now, \( \{\theta_i\}_{i=1}^{\infty} \) refers to the sequence of rates. The approximation uses \( \tau_i = \theta_i \) for \( i \) up to some \( K \); i.e. one generates the first \( K \) rates in the sequence and neglects the remaining ones. We also refer to the number of instantiated atoms \( K \) as the approximation level. Campbell et al. (2019) extensively categorizes and analyzes TFAs. TFAs are attractive because of the nestedness of the approximations. At least in expectation, the approximation quality increases with \( K \). To refine existing truncations, it suffices to generate the next terms in the sequence. However, the complex dependencies between the atoms \( \theta_1, \theta_2, \ldots \) potentially make inference more challenging.

We instead develop independent finite approximations (IFAs). Namely, we specify a sequence of probability measures \( \nu_1, \nu_2, \ldots \). The approximation at level \( K \) has \( K \) atoms, and the atom weights are given by \( \tau_1, \ldots, \tau_K \sim \nu_K \). The probability measures are chosen so
that the sequence of approximations converges in distribution to the target CRM: $\Theta_K \xrightarrow{D} \Theta$ as $K \to \infty$. For random measures, convergence in distribution can also be characterized by convergence of integrals under the measures (Kallenberg, 2002, Lemma 12.1 and Theorem 16.16). The advantages and disadvantages of IFAs reverse those of TFAs: the atoms are now i.i.d., potentially making inference easier, but a completely new approximation must be constructed if $K$ changes.

For a normalized measure $\Xi = \sum_i \xi_i \delta_{\psi_i}$, where $\xi_i = \theta_i / (\sum_j \theta_j)$, a finite approximation also involves random measures with finite support. A normalized TFA can be defined in one of two ways. In the first approach, the rates $\{\tau_i\}_{i=1}^{K}$ that target the CRM rates $\{\theta_i\}_{i=1}^{\infty}$ are normalized to form the NCRM approximation i.e. the approximation has atom sizes $\tau_i / \sum_j^{K} \tau_j$ (Campbell et al., 2019). The second approach directly constructs an ordering over the sequence of normalized rates $\xi_i$ (the CRM rates $\{\theta_i\}_{i=1}^{\infty}$ are marginalized out) and truncates this representation. We construct normalized IFAs in a similar manner to the first TFA approach: the NCRM approximation has atom sizes $\tau_i / \sum_j^{K} \tau_j$ where $\{\tau_i\}_{i=1}^{K}$ are the IFA rates.

So far independent finite approximations have been developed only on a case-by-case basis (Paisley and Carin, 2009; Broderick et al., 2015; Acharya, Ghosh and Zhou, 2015; Lee, James and Choi, 2016; Lee, Miscouridou and Caron, 2019). Our goal is to provide a general-purpose mechanism. Lijoi, Prünster and Rigon (2019, Theorem 1) employ infinitely divisible random variables. Since infinitely divisible distributions that are not Dirac measures have unbounded support, the approximate rates $\{\tau_i\}_{i=1}^{K}$ are not naturally compatible with the trait likelihood $\ell(\cdot | \theta)$ if the support of the rate measure $\nu$ is bounded. Therefore, applications of the finite approximations of Lijoi, Prünster and Rigon (2019, Theorem 1) to feature-allocation models require additional work. The construction in Lee, Miscouridou and Caron (2019, Proposition 3.1) yields $\{\tau_i\}_{i=1}^{K}$ that are compatible with $\ell(\cdot | \theta)$ and recovers important cases in the literature. However, outside these special cases, it is unknown if the i.i.d. distributions are tractable because quantities in the definition of the densities $\nu_K$ are not explicitly defined.

Example: the beta process. For concreteness, we consider the (three parameter) beta process (Teh and Görür, 2009; Broderick, Jordan and Pitman, 2012) as a running example of a CRM. The beta process $\text{BP}(\gamma, \alpha, d)$ is defined by a mass parameter $\gamma > 0$, discount parameter $d \in [0, 1)$, and scale parameter $\alpha > -d$. It has rate measure

$$
\nu(d\theta) = \frac{\Gamma(\alpha + 1)}{\Gamma(1 - d)\Gamma(\alpha + d)} \mathbf{1}\{0 \leq \theta \leq 1\} \theta^{-d-1}(1-\theta)^{\alpha+d-1} d\theta.
$$

(1)

The $d = 0$ case yields the standard beta process (Hjort, 1990; Thibaux and Jordan, 2007). The beta process is typically paired with the Bernoulli likelihood process. That is, conditionally on a rate value $\theta$ for a trait $\psi$, we place a unitary mass $x \in \{0, 1\}$ at $\psi$ with probability $\theta$, i.e. $\ell(x | \theta) = \theta x (1-\theta) 1\{x \in \{0, 1\}\}$. The so-called beta–Bernoulli process has been used in factor analysis models (Doshi-Velez et al., 2009; Paisley, Blei and Jordan, 2012) and for dictionary learning (Zhou et al., 2009).

3. Constructing independent finite approximations

In this section we introduce a practical construction of independent finite approximations for a broad class of completely random measures. We highlight a useful special case of our con-
struction for exponential family CRMs (Broderick, Wilson and Jordan, 2018) without power laws. And we extend our general construction to normalized completely random measures. In all of these cases, we prove that as the approximation size increases, the distribution of the approximation converges (in some relevant sense) to that of the exact infinite-dimensional model.

3.1. A general construction for independent finite approximations

Formally, we define IFAs in terms of a fixed, diffuse probability measure $H$ and a sequence of probability measures $\nu_1, \nu_2, \ldots$. The $K$-atom IFA $\Theta_K$ is

$$\Theta_K := \sum_{i=1}^{K} \tau_i \delta_{\psi_i}, \quad \tau_i \sim \nu_K, \quad \psi_i \sim H,$$

which we write as $\Theta_K \sim \text{IFA}_K(H, \nu_K)$. We consider CRM rate measures $\nu$ with densities that, near zero, are (roughly) proportional to $\theta^{-1-d}$, where $d \in [0, 1)$ is the “discount” parameter. We will propose a general construction for IFAs and prove that it converges to the target random measure (Theorem 3.2). We first summarize our assumptions about which CRMs we aim to approximate in Assumption 1. We show in Appendix A that popular BNP priors satisfy Assumption 1; namely, we check the beta, gamma (Ferguson and Klass, 1972; Kingman, 1975; Brix, 1999; Titsias, 2008; James, 2013), beta prime (Broderick et al., 2015), and generalized gamma process (James, 2013).

**Assumption 1.** For $d \in [0, 1)$ and $\eta \in V \subseteq \mathbb{R}^d$, we take $\Theta \sim \text{CRM}(H, \nu(d\cdot; d, \eta))$ for

$$\nu(d\theta; d, \eta) := \gamma \theta^{-1-d} g(\theta) h(\theta; \eta) \frac{\theta^{-d}}{Z(1-d, \eta)} d\theta$$

such that

1. for $\xi > 0$ and $\eta \in V$, $Z(\xi, \eta) := \int \theta^{\xi-1} g(\theta) h(\theta; \eta) d\theta < \infty$;
2. $g$ is continuous, $g(0) = 1$, and there exist constants $0 < c_\eta \leq c^* < \infty$ such that $c_\eta \leq g(\theta)^{-1} \leq c^*(1 + \theta)$;
3. there exists $\epsilon > 0$ such that for all $\eta \in V$, the map $\theta \mapsto h(\theta; \eta)$ is continuous and bounded on $[0, \epsilon]$.

Other than the discount $d$ and mass $\gamma$, the rate measure $\nu$ potentially depends on additional hyperparameters $\eta$. The finiteness of the normalizer $Z$ is necessary in defining finite-dimensional distributions whose densities are similar in form to $\nu$. The conditions on the behaviors of $g(\theta)$ and $h(\theta; \eta)$ ensure that the overall rate measure’s behavior near $\theta = 0$ is dominated by the $\theta^{-1-d}$ term.

Given a CRM satisfying Assumption 1, we can construct a sequence of IFAs that converge in distribution to such a CRM. We will find it useful for our IFA construction to introduce a relaxed version of an indicator function.

**Definition 3.1.** The parameterized function family $\{S_b\}_{b \in \mathbb{R}^+}$ is composed of approximate indicators if, for any $b \in \mathbb{R}^+$, $S_b(\theta)$ is a real, non-decreasing function such that $S_b(\theta) = 0$ for $\theta \leq 0$ and $S_b(\theta) = 1$ for $\theta \geq b$.

Valid examples of approximate indicators are the indicator function $S_b(\theta) = 1\{\theta > 0\}$ and the smoothed indicator function

$$S_b(\theta) = \begin{cases} \exp \left( \frac{-b}{1-(\theta-b)^2/b^2} + 1 \right) & \text{if } \theta \in (0, b) \\ 1\{\theta > 0\} & \text{otherwise.} \end{cases}$$

(2)
Some approximate indicators have a point of discontinuity; e.g., $S_b(\theta) = 1\{\theta > 0\}$. But the smoothed indicator is both continuous and differentiable; see Appendix B.2.

**Theorem 3.2.** Suppose Assumption 1 holds, and let $\{S_b\}_{b \in \mathbb{R}_+}$ be a family of approximate indicators. Fix $a > 0$, and let $(b_K)_{K \in \mathbb{N}}$ be a decreasing sequence such that $b_K \to 0$. For $c := \gamma h(0; \eta)/Z(1-d, \eta)$, let

$$
\nu_K(d\theta) := \theta^{-1+cK^{-1}} - dS_{bK}(\theta-aK^{-1})g(\theta)^cK^{-1} - d h(\theta; \eta)Z_K^{-1}d\theta
$$

be a family of probability densities, where $Z_K$ is chosen such that $\int \nu_K(d\theta) = 1$. If $\Theta_K \sim IFA_K(H, \nu_K)$, then $\Theta_K \overset{D}{\to} \Theta$ as $K \to \infty$.

See Appendix B.1 for a proof of Theorem 3.2. The flexibility in approximate indicator choice is useful in defining differentiable likelihoods, which can then be used in gradient-based black-box inference algorithms. We call the $K$-atom IFA resulting from Theorem 3.2 the automated IFA (AIFA$K$). A particularly convenient default choice is $a = 1$, $b_K = 1/K$, and the smoothed indicators from Eq. (2). We leave to future work to quantify the impact of $S_b$ and $b_K$ on the rate of convergence of the finite approximations to the target model.

Similar in spirit to our Theorem 3.2, Lee, Miscouridou and Caron (2019, Proposition 3.1) verify the validity of a different IFA construction. Their construction requires two functions: (1) a bivariate function $\Lambda(\theta, t)$ such that for any $t > 0$, $\Delta(t) := \int \Lambda(\theta, t)\nu(d\theta) < \infty$, and (2) a univariate function $f(n)$ such that $\Delta(f(n))$ is bounded from both above and below by $n$ as $n \to \infty$. If these functions exist and letting

$$
\bar{\nu}_K(d\theta) := \frac{\Lambda(\theta, f(K))\nu(d\theta)}{\Delta(f(K))},
$$

Lee, Miscouridou and Caron (2019, Proposition 3.1) show that $IFA_K(H, \bar{\nu}_K)$ converges in distribution to $CRM(H, \nu)$ as $K \to \infty$. The usability of Eq. (3) in practice depends on the tractability of $\Lambda$ and $f$. There are typically many tractable $\Lambda(\theta, t)$ (Lee, Miscouridou and Caron, 2019, Section 4). Lee, Miscouridou and Caron (2019, Proposition B.2) list tractable $f$ for the important cases of beta and gamma processes with $d > 0$. However, the choice of $f$ provided in Lee, Miscouridou and Caron (2019, Proposition B.2) for general power-law processes is not tractable because its evaluation requires computing complicated inverses in the asymptotic regime. Furthermore, for processes without power laws, no general recipe for $f$ is known. In contrast, the AIFA construction in Theorem 3.2 always yields densities that can be evaluated up to proportionality constants with the choice of a (universally applicable) family of approximate indicators.

### 3.2. Independent finite approximations for exponential family CRMs

**Exponential family CRMs** with $d = 0$ comprise an important special case of Theorem 3.2. In common BNP models, the relationship between the likelihood $\ell(\cdot | \theta)$ and the CRM prior is closely related to finite-dimensional exponential family conjugacy (Broderick, Wilson and Jordan, 2018, Section 4). In particular, the likelihood has an exponential family form

$$
\ell(x | \theta) := \kappa(x)\theta^{\phi(x)}\exp((\mu(\theta), t(x)) - A(\theta)).
$$

Here $x \in \mathbb{N} \cup \{0\}$, $\kappa(x)$ is the base density, $[\ell(x), \phi(x)]^T$ is the vector of sufficient statistics, $A(\theta)$ is the log partition function, $[\mu(\theta), \ln \theta]^T$ is the vector of natural parameters, and
$\langle \mu(\theta), t(x) \rangle$ is an inner product. The rate measure matches this form and behaves like $\theta^{-1}$ near 0:

$$\nu(d\theta) := \gamma' \theta^{-1} \exp \left\{ \langle \mu(\theta), \lambda^{-A(\theta)} \rangle \right\} 1\{\theta \in U\} d\theta,$$

where $\gamma' > 0$, $\lambda > 0$, and $U \subseteq \mathbb{R}_+$ is the support of $\nu$. Equation (5) leads to the suggestive terminology of exponential family CRMs. The $\theta^{-1}$ dependence near 0 means that these models lack power-law behavior. Models that can be cast in this form include the standard beta process with Bernoulli or negative binomial likelihood (Zhou et al., 2012; Broderick et al., 2015) and the gamma process with Poisson likelihood (Acharya, Ghosh and Zhou, 2015; Roychowdhury and Kulis, 2015). We refer to these models as, respectively, the beta–Bernoulli, beta–negative binomial, and gamma–Poisson processes.

We now state the simple form taken by AIFA$_K$ for exponential family CRMs constructed using Theorem 3.2. For clarity and convenience, we state the result by specializing Assumption 1 to exponential family rate measures.

**Corollary 3.3.** Let $\nu$ be of the form Eq. (5) and assume that

1. For any $\xi > -1$, for any $\eta = [\psi, \lambda]^T$ where $\lambda > 0$, the normalizer defined as

$$Z(\xi, \eta) := \int_U \theta^\xi \exp \left\{ \langle \eta, \left( \frac{\mu(\theta)}{-A(\theta)} \right) \rangle \right\} d\theta$$

is finite, and

2. there exists $\epsilon > 0$ such that, for any $\eta = [\psi, \lambda]^T$ where $\lambda > 0$, the map

$$\varsigma : \theta \mapsto \exp \left\{ \langle \eta, \left( \frac{\mu(\theta)}{-A(\theta)} \right) \rangle \right\} 1\{\theta \in U\}$$

is a continuous and bounded function of $\theta$ on $[0, \epsilon]$.

For $c := \gamma' \varsigma(0)$, let

$$\nu_K(\theta) := \frac{\theta^{c/K-1} \varsigma(\theta)}{Z(c/K - 1, \eta)}. \quad (8)$$

If $\Theta_K \sim$ IFA$_K(H, \nu_K)$, then $\Theta_K \overset{D}{\rightarrow} \Theta$.

Since the discount $d$ is zero, we do not need to set $a, S_0, b_K$, as they do not appear in the density of the atom size distributions. The density in Eq. (8) is almost the same as the rate measure of Eq. (5), except the $\theta^{-1}$ term has become $\theta^{c/K-1}$. As a result, Eq. (8) is a proper exponential-family distribution. Corollary 3.3 is sufficient to recover known IFA results for BP$(\gamma, \alpha, 0)$ (Doshi-Velez et al., 2009; Paisley and Carin, 2009; Griffiths and Ghahramani, 2011).

**Example 3.1** (Beta process). When $d = 0$, the rate measure of the beta process is $\nu(d\theta) = \gamma \alpha \theta^{-1} \exp((\alpha - 1) \ln(1 - \theta)) 1\{0 \leq \theta \leq 1\}$. The normalizer depends only on $\xi$ and $\alpha$:

$$Z_{\text{BP}} = \int_0^1 \theta^\xi (1 - \theta)^{\alpha-1} \exp(0)d\theta = B(\xi + 1, \alpha).$$

The assumptions in Corollary 3.3 are readily verified. $Z_{\text{BP}} < \infty$ for $\xi > -1$ is evident as $B(\xi + 1, \alpha) < \infty$ for $\xi + 1 > 0, \alpha > 0$. The function $\theta \mapsto (1 - \theta)^{\alpha-1}$ is clearly bounded and continuous on the interval $[0, 0.5]$ for any $\alpha > 0$. Therefore $\nu_K = \text{Beta}(\gamma \alpha / K, \alpha)$ yields a valid AIFA for BP$(\gamma, \alpha, 0)$. 
Existing results also use independent finite approximations based on the beta distribution. For example, Doshi-Velez et al. (2009) approximates $\text{BP}(\gamma, 1, 0)$ with $\nu_K = \text{Beta}(\gamma/K, 1)$. For $\text{BP}(\gamma, \alpha, 0)$, Griffiths and Ghahramani (2011) set $\nu_K = \text{Beta}(\gamma\alpha/K, \alpha)$, Paisley and Carin (2009) use $\nu_K = \text{Beta}(\gamma\alpha/K, \alpha(1 - 1/K))$. The difference between $\text{Beta}(\gamma\alpha/K, \alpha)$ and $\text{Beta}(\gamma\alpha/K, \alpha(1 - 1/K))$ is negligible for moderately large $K$. See Appendix A for additional examples of how to construct AIFAs for the beta prime, gamma, and generalized gamma processes using Corollary 3.3.

### 3.3. Normalized independent finite approximations

Given that AIFAs are converging approximations to the corresponding target CRM, it is natural to ask if normalizations of AIFAs converge to the corresponding normalization of the target CRM, i.e., the corresponding NCRM. Our next result shows that normalized AIFAs indeed converge, in the sense of exchangeable partition probability functions, or EPPFs (Pitman, 1995). Given a random sample of size $N$ from an NCRM $\Xi$, the EPPF gives the probability of the induced partition from such sample. In particular, under the model $\Xi \sim \text{NCRM}, X_n \mid \Xi \sim \text{i.i.d.} \Xi$ for $1 \leq n \leq N$ with the effect of $\Xi$ marginalized out, the ties among the $X_n$’s induce a partition over the set $\{1, 2, \ldots, N\}$. Let there be $b \leq N$ distinct values among the $X_n$’s, and let $n_i$ be the number of elements in the $i$-th block of the partition induced by sampling from $\Xi$, so that $n_i \geq 1, \sum_{i=1}^b n_i = N$. The probability of the induced partition is a symmetric function $p(n_1, n_2, \ldots, n_b)$ that depends only on the frequencies $n_i$ of each block. Similarly, we let $p_K(n_1, n_2, \ldots, n_b)$ be the EPPF for the normalized AIFA $K$.

Note that $p_K(n_1, n_2, \ldots, n_b) = 0$ when $K < b$ since the normalized AIFA $K$ at approximation level $K$ generates at most $K$ blocks.

**Theorem 3.4.** Suppose Assumption 1 holds. For any $N$, for any $b \leq N$ and $n_i \geq 1, \sum_{i=1}^b n_i = N$, let $p(n_1, n_2, \ldots, n_b)$ be the EPPF of an NCRM $\Xi$ where $\Xi := \Theta / \Theta(\Psi)$. Let $\Theta_K$ be the AIFA as in Theorem 3.2 and $p_K(n_1, n_2, \ldots, n_b)$ be the EPPF for the corresponding $\Theta_K / \Theta_K(\Psi)$. Then:

$$
\lim_{K \to \infty} p_K(n_1, n_2, \ldots, n_b) = p(n_1, n_2, \ldots, n_b).
$$

The proof can be found in Appendix B.3. Since the EPPF gives the probability of each partition, the point-wise convergence in Theorem 3.4 certifies that the distribution over partitions induced by sampling from the normalized AIFA $K$ converges to that induced by sampling from the target NCRM, for any finite sample size $N$.

### 4. Non-asymptotic error bounds

Theorems 3.2 and 3.4 justify the use of our proposed AIFA construction in the limit $K \to \infty$ but do not provide guidance on how to choose the approximation level $K$ when $N$ observations are available. In Section 4.1, we quantify the error induced by replacing the CRM with the AIFA. In Section 4.2, we quantify the error induced by replacing the Dirichlet process (DP) (Ferguson, 1973; Sethuraman, 1994) with the corresponding normalized AIFA. We derive error bounds that are simple to manipulate and yield recommendations for the appropriate $K$ for a given $N$ and a desired accuracy level.
4.1. Approximating a completely random measure

Recall from Section 2 that the CRM prior $\Theta$ is typically paired with a likelihood process that manifests features $X_n$ and a probability kernel relating active features to observations $Y_n$. The target nonparametric model can be summarized as

$$\Theta \sim \text{CRM}(H, \nu),$$
$$X_n \mid \Theta \overset{i.i.d.}{\sim} \text{LP}(\ell, \Theta), \quad n = 1, 2, \ldots, N,$$
$$Y_n \mid X_n \overset{\text{i.i.d.}}{\sim} f(\cdot \mid X_n), \quad n = 1, 2, \ldots, N.$$  \hfill (9)

The approximating model, with $\nu_K$ as in Theorem 3.2 (or Corollary 3.3), is

$$\Theta_K \sim \text{IFA}_K(H, \nu_K),$$
$$Z_n \mid \Theta_K \overset{i.i.d.}{\sim} \text{LP}(\ell, \Theta_K), \quad n = 1, 2, \ldots, N,$$
$$W_n \mid Z_n \overset{\text{i.i.d.}}{\sim} f(\cdot \mid Z_n), \quad n = 1, 2, \ldots, N.$$ \hfill (10)

Active traits in the approximate model are collected in $Z_n$ and observations are $W_n$. Let $P_{N,\infty}$ be the marginal distribution of the observations $Y_{1:N}$, and $P_{N,K}$ be the marginal distribution of the observations $W_{1:N}$. The approximation error we analyze is the total variation distance $d_{\text{TV}}(P_{N,K}, P_{N,\infty}) := \sup_{0 \leq f \leq 1} \left| \int f \, dP_{N,K} - \int f \, dP_{N,\infty} \right|$ between the two observational processes, one using the CRM and the other one using the approximate AIFA as the prior. Total variation is a standard choice for error of this form (Ishwaran and Zarepour, 2002; Doshi-Velez et al., 2009; Paisley, Blei and Jordan, 2012; Campbell et al., 2019). Small total variation distance implies small differences in expectations of bounded functions.

**Conditions.** Our analysis guarantees that $d_{\text{TV}}(P_{N,K}, P_{N,\infty})$ is small whenever the AIFA and the exponential family CRM-likelihood pair satisfy certain conditions, which are separate from Assumption 1. In the proof of the error bound, these conditions serve as intermediate results that ultimately lead to small approximation error. Because we can verify the conditions for the common models, we have error bounds in the most prevalent use cases of CRMs. To express these conditions, we use the marginal process representation of the target and the approximate model, i.e., the series of conditional distributions of $X_n \mid X_{1:(n-1)}$ (or $Z_n \mid Z_{1:(n-1)}$) with $\Theta$ (or $\Theta_K$) integrated out.

Broderick, Wilson and Jordan (2018, Corollary 6.2) imply that for each $n \in \mathbb{N}$, $X_n \mid X_{1:(n-1)}$ is a random measure with finite support. Let $\{\zeta_i\}_{i=1}^{K_n-1}$ be the union of atom locations in $X_1, X_2, \ldots, X_{n-1}$. Fix an atom location $\zeta_j$ (the choice of $j$ does not matter). For $1 \leq m \leq n$, let $x_m$ be the atom size of $X_m$ at atom location $\zeta_j$. The distribution of $x_m$ depends only on the conditioning $X_{1:(n-1)}$, which are the atom sizes previous measures $X_m$ put on $\zeta_j$, and are independent of the atom sizes at other atom locations. We denote the p.m.f. of $x_n$ at $x$ to be $h(x \mid x_{1:(n-1)})$. Furthermore, $X_n$ has a finite number of new atoms, which can be grouped together by atom size. Consider any potential atom size $x \in \mathbb{N}$. Define $p_{n,x}$ to be the number of atoms of size $x$. Regardless of atom size, each atom location is a fresh draw from the ground measure $H$ and $p_{n,x}$ is Poisson-distributed with mean $M_{n,x}$ (Broderick, Wilson and Jordan, 2018, Corollary 6.2).

Similarly, in Proposition C.2, we show that $Z_n \mid Z_{1:(n-1)}$ is also a random measure with finite support. We reuse notation and let $\{\zeta_i\}_{i=1}^{K_n-1}$ be the union of atom locations in $Z_1, Z_2, \ldots, Z_{n-1}$. Again fix an atom location $\zeta_j$. For $1 \leq m \leq n$, let $x_m$ be the atom size.
size of $Z_m$ at atom location $\zeta_j$. We write the p.m.f. of $x_n$ at $x$ as $\tilde{h}(x \mid x_{1:(n-1)})$. In addition, $Z_n$ also has a maximum of $K - K_{n-1}$ new atoms with locations disjoint from $\{\zeta_i\}_{i=1}^{K_{n-1}}$, and the distribution of atom sizes is governed by $\tilde{h}(x \mid x_{1:(n-1)} = 0_{n-1})$, where $0_{n-1}$ is the zero vector with $(n-1)$ components.

The functions $h$, $\tilde{h}$, and $M_{n,x}$ are the most relevant aspects of the marginal processes for our analysis. In Appendix C, we describe the marginal processes in more detail, and give formulas for $h$, $\tilde{h}$, and $M_{n,x}$ in terms of the functions that parametrize Eqs. (4) and (5) and the normalizer Eq. (6). For the beta–Bernoulli process with $d = 0$, the functions have particularly simple forms.

**Example 4.1.** For the beta–Bernoulli model with $d = 0$, we have

$$h(x \mid x_{1:(n-1)}) = \frac{\sum_{i=1}^{n-1} x_i}{\alpha - 1 + n} \mathbf{1}\{x = 1\} + \frac{\alpha + \sum_{i=1}^{n-1} (1 - x_i)}{\alpha - 1 + n} \mathbf{1}\{x = 0\}.$$  

$$\tilde{h}(x \mid x_{1:(n-1)}) = \frac{\sum_{i=1}^{n-1} x_i + \gamma \alpha/K}{\alpha - 1 + n + \gamma \alpha/K} \mathbf{1}\{x = 1\} + \frac{\alpha + \sum_{i=1}^{n-1} (1 - x_i)}{\alpha - 1 + n + \gamma \alpha/K} \mathbf{1}\{x = 0\},$$

$$M_{n,1} = \frac{\gamma \alpha}{\alpha - 1 + n}, \quad M_{n,x} = 0 \text{ for } x > 1.$$  

We now formulate conditions on $h$, $\tilde{h}$, and $M_{n,x}$ that will yield small $d_{TV}(P_{N,K}, P_{N,\infty})$.

**Condition 1.** There exist constants $\{C_i\}_{i=1}^5$ such that

1. for all $n \in \mathbb{N}$,

$$\sum_{x=1}^{\infty} M_{n,x} \leq \frac{C_1}{n - 1 + C_1}; \quad (11)$$

2. for all $n \in \mathbb{N}$,

$$\sum_{x=1}^{\infty} \tilde{h}(x \mid x_{1:(n-1)} = 0_{n-1}) \leq \frac{1}{K} \frac{C_1}{n - 1 + C_1}; \quad (12)$$

3. for any $n \in \mathbb{N}$, for any $\{x_i\}_{i=1}^{n-1}$,

$$\sum_{x=0}^{\infty} \left| h(x \mid x_{1:(n-1)}) - \tilde{h}(x \mid x_{1:(n-1)}) \right| \leq \frac{1}{K} \frac{C_1}{n - 1 + C_1}; \quad (13)$$

and

4. for all $n \in \mathbb{N}$, for any $K \geq C_2(\ln n + C_3)$,

$$\sum_{x=1}^{\infty} \left| M_{n,x} - K \tilde{h}(x \mid x_{1:(n-1)} = 0_{n-1}) \right| \leq \frac{1}{K} \frac{C_4 \ln n + C_5}{n - 1 + C_1}. \quad (14)$$

Note that the conditions depend only on the functions governing the CRM-likelihood process, and not on the observation likelihood $f$. Equation (11) constrains the growth rate of the target model since $\sum_{n=1}^{N} \sum_{x=1}^{\infty} M_{n,x}$ is the expected number of components for data cardinality $N$. Because each $\sum_{x=1}^{\infty} M_{n,x}$ is at most $O(1/n)$, the total number of components is $O(\ln N)$. Similarly, Eq. (12) constrains the growth rate of the approximate model. The third condition (Eq. (13)) ensures that $\tilde{h}$ is a good approximation of $h$ in total variation distance, and there is also a reduction in the error as $n$ increases. Finally, Eq. (14) implies
that $K\tilde{h}(x \mid 0_{n-1})$ is an accurate approximation of $M_{n,x}$, and there is also a reduction in the error as $n$ increases. Since $h$, $\tilde{h}$, and $M_{n,x}$ can be expressed with only quantities in Eqs. (4), (5) and (6), the constraints in Condition 1 can be also be articulated using only functions of the exponential family. We conjecture that our assumptions could be almost equivalently restated in terms of the normalizer $Z$ alone.

We show that Condition 1 holds for the most commonly used CRM models; see Example 4.2 for the case of the beta–Bernoulli model and Appendix E for beta–negative binomial and gamma–Poisson model with discount $d = 0$. We give additional comments on why the conditions in Condition 1 are reasonable. Equations (11) and (12) are connected to the typical Bayesian nonparametric growth rate for non-power law models (Griffiths and Ghahramani, 2011). Equations (13) and (14) are likely to hold when the function $h$ is smooth in a suitable sense. For instance, in Example 4.1, the functional form of $\tilde{h}$ is very similar to that of $h$, except that $\tilde{h}$ has the additional $\gamma\alpha/K$ factor. We show in Example 4.2 how that translates into Eq. (13).

Example 4.2 (Beta–Bernoulli with $d = 0$, continued). The growth rate of the target model is

$$\sum_{x=1}^{\infty} M_{n,x} = M_{n,1} = \frac{\gamma\alpha}{n - 1 + \alpha}.$$  

Since $\tilde{h}$ is supported on $\{0, 1\}$, the growth rate of the approximate model is

$$\tilde{h}(1 \mid x_{1:(n-1)} = 0_{n-1}) = \frac{\gamma\alpha/K}{\alpha - 1 + n + \gamma\alpha/K} \leq \frac{1}{K} \frac{\gamma\alpha}{n - 1 + \alpha}.$$  

Since both $h$ and $\tilde{h}$ are supported on $\{0, 1\}$, Eq. (13) becomes

$$\left| h(1 \mid x_{1:(n-1)}) - \tilde{h}(1 \mid x_{1:(n-1)}) \right| = \left| \frac{\sum_{i=1}^{n-1} x_i + \gamma\alpha/K}{\alpha - 1 + n + \gamma\alpha/K} - \frac{\sum_{i=1}^{n-1} x_i}{\alpha - 1 + n} \right| \leq \frac{\gamma\alpha}{K} \frac{1}{n - 1 + \alpha}.$$  

Again, because $M_{n,x} = \tilde{h}(x \mid .) = 0$ for $x > 1$, Eq. (14) becomes

$$\left| M_{n,1} - K\tilde{h}(1 \mid x_{1:(n-1)} = 0_{n-1}) \right| = \left| \frac{\gamma\alpha}{\alpha - 1 + n} - \frac{\gamma\alpha}{\alpha - 1 + n + \gamma\alpha/K} \right| \leq \frac{\gamma^2\alpha}{K} \frac{1}{n - 1 + \alpha}.$$  

Calibrating $\{C_i\}$ based on these inequalities is straightforward.

Upper bound. We now make use of the conditions stated in Condition 1 to derive an upper bound on the approximation error induced by AIFAs.

Theorem 4.1 (Upper bound for exponential family CRMs). If Assumption 1 and Condition 1 hold, then there exist positive constants $C', C''$, $C'''$ depending only on $\{C_i\}_{i=1}^{5}$ such that

$$d_{TV}(P_{N,\infty}, P_{N,K}) \leq \frac{C' + C'' \ln^2 N + C''' \ln N \ln K}{K}.$$  

See Appendix F.1 for the proof. Theorem 4.1 states that the AIFA approximation error grows as $O(\ln^2 N)$ with fixed $K$, and decreases as $O(\ln K/K)$ for fixed $N$. On the one hand, for fixed $K$, it is expected that the error increases as $N$ increases: with more data, the expected number of latent components in the data increases, demanding finite approximations
of increasingly larger sizes. In particular, $O(\ln N)$ is the standard Bayesian nonparametric growth rate for non-power law models (Griffiths and Ghahramani, 2011). It is likely that the $O(\ln^2 N)$ factor can be improved to $O(\ln N)$; more generally, we conjecture that the error directly depends on the expected number of latent components in a model for $N$ observations. On the other hand, for fixed $N$, the error goes to zero at least as fast as $O(\ln K/K)$. We also suspect the $\ln K$ factor in the numerator can be removed.

**Lower bounds.** From the upper bound in Theorem 4.1, we know how to set a sufficient number of atoms for accurate approximations. We now derive lower bounds on the AIFA approximation error to characterize a necessary number of atoms for accurate approximations, by looking at worst-case observational likelihoods $f$. Our lower bounds apply to the beta–Bernoulli process with $d = 0$. Throughout this section, $P_{N,\infty}^{BP}$ refers to the observational process coming from $BP(\gamma, \alpha, 0)$ and $P_{N,K}^{BP}$ refers to the observational process coming from AIFA$_K$ as in Example 3.1 (the observational likelihood will be clear from context). The worst-case observational likelihoods $f$ are pathological. We leave to future work to lower bound the approximation error when more common likelihoods $f$, such as Gaussian or Dirichlet, are used.

We first look at the dependence of the error bound in terms of $\ln N$. For any $N \in \mathbb{N}$, $\alpha > 0$, we define the growth function

$$C(N, \alpha) := \sum_{n=1}^{N} \frac{\alpha}{n - 1 + \alpha},$$

which satisfies $C(N, \alpha) = \Omega(\ln N)$ (see Lemma D.10). Our next result shows that our AIFA construction cannot be accurate if the approximation level is too small compared to the growth function $C(N, \alpha)$.

**Theorem 4.2 (ln $N$ is necessary).** For the beta–Bernoulli model with $d = 0$, there exists an observation likelihood $f$, independent of $K$ and $N$, such that for any $N$, if $K \leq 0.5\gamma C(N, \alpha)$, then

$$d_{TV}(P_{N,\infty}^{BP}, P_{N,K}^{BP}) \geq 1 - \frac{C}{N\gamma^{\alpha/8}},$$

where $C$ is a constant depending only on $\gamma$ and $\alpha$.

See Appendix F.2 for the proof. The intuition is that, with high probability, the number of features that manifest in the target $X_{1:N}$ is greater than $0.5\gamma C(N, \alpha)$. However, the finite model $Z_{1:N}$ has fewer than $0.5\gamma C(N, \alpha)$ components. Hence, there is an event where the target and approximation assign drastically different probability masses. Theorem 4.2 implies that as $N$ grows, if the approximation level $K$ fails to surpass the $0.5\gamma C(N, \alpha) = \Omega(\ln N)$ threshold, then the total variation between the approximate and the target model remains bounded from zero; in fact, the error tends to one.

Now turning to the dependence on $K$ of the upper bound in Theorem 4.1, we discuss a lower bound on the approximation error, which reveals that the $1/K$ factor in the upper bound is tight (up to logarithmic factors).

**Theorem 4.3 (Lower bound of $1/K$).** For the beta–Bernoulli model with $d = 0$, there exists an observation likelihood $f$, independent of $K$ and $N$, such that for any $N$,

$$d_{TV}(P_{N,\infty}^{BP}, P_{N,K}^{BP}) \geq C \frac{1}{(1 + \gamma/K)^2} \frac{1}{K},$$

where $C$ is a constant depending only on $\gamma$. 

See Appendix F.2 for the proof. The intuition is that, under the pathological likelihood \( f \), analyzing the AIFA approximation error is the same as analyzing the binomial–Poisson approximation error (Le Cam, 1960). We then show that \( 1/K \) is a lower bound using the techniques from Barbour and Hall (1984). While Theorem 4.1 implies that an AIFA with \( K = O(\text{poly}(\ln N)/\epsilon) \) atoms suffices in approximating the target model to less than \( \epsilon \) error, Theorem 4.3 implies that an AIFA with \( K = \Omega(1/\epsilon) \) atoms is necessary in the worst case. This dependence on the accuracy level is worse for AIFAs than for TFAs. For example, the Bondesson approximation (Bondesson, 1982; Campbell et al., 2019) of \( \text{BP}(\gamma, \alpha, 0) \) is a TFA with excellent error bounds.

**Example 4.3** (Bondesson approximation (Bondesson, 1982)). Fix \( \alpha \geq 1 \), let \( E_t \overset{\text{i.i.d.}}{\sim} \text{Exp}(1) \), and and let \( \Gamma_k := \sum_{i=1}^{k} E_i \). The \( K \)-atom Bondesson approximation of \( \text{BP}(\gamma, \alpha, 0) \) is a TFA \( \sum_{k=1}^{K} \theta_k \delta_{\psi_k} \), where \( \theta_k := V_k \exp(-\Gamma_k/\gamma \alpha) \), \( V_k \overset{\text{i.i.d.}}{\sim} \text{Beta}(1, \alpha - 1) \), and \( \psi_k \overset{\text{i.i.d.}}{\sim} H \).

The following result gives a bound on the error of the Bondesson approximation:

**Proposition 4.4.** (Campbell et al., 2019, Appendix A.1) For \( \gamma > 0, \alpha \geq 1 \), let \( \Theta_K \) be distributed according to a level-\( K \) Bondesson approximation of \( \text{BP}(\gamma, \alpha, 0) \), \( R_n \mid \Theta_K \overset{\text{i.i.d.}}{\sim} \text{LP}(\ell; \Theta_K) \), \( T_n \mid R_n \overset{\text{d}}{\sim} f(\cdot \mid R_n) \) with \( N \) observations. Let \( Q_{N,K} \) be the distribution of the observations \( T_{1:N} \). Then: \( d_{TV}(P_{N,\infty}^{BP}, Q_{N,K}) \leq N \gamma \left( \frac{\alpha}{1+\gamma \alpha} \right)^K \).

Proposition 4.4 implies that a TFA with \( K = O(\ln\{N/\epsilon\}) \) atoms suffices in approximating the target model to less than \( \epsilon \) error. Up to log factors in \( N \), comparing the necessary \( 1/\epsilon \) level for AIFA and the sufficient \( \ln(1/\epsilon) \) level for TFA, we conclude that the necessary size for AIFA is exponentially larger than the sufficient size for TFA, in the worst-case observational likelihood \( f \).

### 4.2. Approximating a (hierarchical) Dirichlet process

So far we have analyzed AIFA error for CRM-based models. In this section, we analyze the error of using a normalized AIFA as an approximation for an NCRM; here, we focus on a Dirichlet process — i.e., a normalized gamma process without power-law behavior. We first consider a generative model with the same number of layers as in previous sections. But we also consider a more complex generative model, with an additional layer — as is common in, e.g., text analysis. Indeed, one of the strengths of Bayesian modeling is the flexibility facilitated by hierarchical modeling, and a goal of probabilistic programming is to provide fast, automated inference for these more complex models.

**Dirichlet process.** The Dirichlet process is one of the most widely used nonparametric priors. The gamma process CRM is characterized by the rate measure \( \nu(d\theta) = \gamma^{\lambda-d} \theta^{-d-1} e^{-\lambda \theta} d\theta \). We denote its distribution as \( \Gamma P(\gamma, \lambda, d) \). The normalization of \( \Gamma P(\gamma, 1, 0) \) is a Dirichlet process with mass parameter \( \gamma \) (Kingman, 1975; Ferguson, 1973). By Corollary 3.3, \( \text{IFAF}(H, \nu_K) \) with \( \nu_K = \text{Gam}(\gamma/K, 1) \) converges to \( \Gamma P(\gamma, 1, 0) \). Because the normalization of independent gamma random variables is a Dirichlet random variable, the normalization of \( \text{IFAF}(H, \nu_K) \) is equal in distribution to \( \sum_{i=1}^{K} \psi_i \delta_{\psi_i} \), where \( \psi_i \overset{\text{i.i.d.}}{\sim} H \) and \( \{p_i\}_{i=1}^{K} \sim \text{Dir}(\gamma/K, 1_K) \). We call this distribution the finite symmetric Dirichlet (FSD), and denote it as \( \text{FSD}_K(\gamma/K, H) \).

---

3The name “finite symmetric Dirichlet” comes from Kurihara, Welling and Teh (2007). See Ishwaran and James (2001, Section 2.2) for other names this distribution has had in the literature.
In the simplest use case, the Dirichlet process is used as the de Finetti measure for observations $X_n$; i.e., $\Xi \sim \text{DP}, X_n \mid \Xi_{1:n} \sim \Xi$ for $1 \leq n \leq N$. In Appendix G, we state error bounds when FSD$_K$ replaces the Dirichlet process as the mixing measure that are analogous to the results in Section 4.1. The upper bound is similar to Theorem 4.1 in that the error grows as $O(\ln^2 N)$ with fixed $K$, and decreases as $O(\ln K/K)$ for fixed $N$. The lower bounds, which are the analogues of Theorems 4.2 and 4.3, state that $K = \Omega(\ln N)$ is necessary for accurate approximations, and that truncation-based approximations are better than FSD$_K$, in the worst case.

**Hierarchical Dirichlet process.** In modern applications such as text analysis, practitioners use additional hierarchical levels to capture group structure in observed data. In text, we might have $D$ documents with $N$ words in each. More, generally, we might have $D$ groups (each indexed by $d$) with $N$ observations (each indexed by $n$) each. We target the influential model in Wang, Paisley and Blei (2011); Hoffman et al. (2013), which is a variant of the hierarchical Dirichlet process (HDP; Teh et al., 2006). We will refer to the model in Wang, Paisley and Blei (2011); Hoffman et al. (2013) as the modified HDP. In the HDP, $G$ is a population measure with $G \sim \text{DP}(\omega, H)$. The measure for the $d$-th subpopulation is $G_d \mid G \sim \text{DP}(\alpha, G)$; the concentrations $\omega$ and $\alpha$ are potentially different from each other. The modified HDP is defined in terms of the truncated stick-breaking approximation:

**Definition 4.5** (Stick-breaking approximation (Sethuraman, 1994)). For $i = 1, 2, \ldots, K-1$, let $v_i \overset{i.i.d.}{\sim} \text{Beta}(1, \alpha)$. Set $v_K = 1$. Let $\xi_i = v_i \prod_{j=1}^{i-1} (1 - v_j)$. Let $\psi_k \overset{i.i.d.}{\sim} H$, and $\Xi_K = \sum_{k=1}^K \xi_k \delta_{\psi_k}$. We denote the distribution of $\Xi_K$ as TSB$_K(\alpha, H)$.

In the modified HDP, the sub-population measure is distributed as $G_d \mid G \sim \text{TSB}_T(\alpha, G)$. Wang, Paisley and Blei (2011) and Hoffman et al. (2013) set $T$ to be small so that inference in the modified HDP is more efficient than in the HDP, since the number of parameters per group is greatly reduced. From a modeling standpoint, small $T$ is a reasonable assumption since documents typically manifest a small number of topics from the corpus, with the total number depending on the document length and independent of corpus size. For completeness, the generative process of modified HDP is

$$
G \sim \text{DP}(\omega, H),
$$

$$
H_d \mid G \overset{i.i.d.}{\sim} \text{TSB}_T(\alpha, G), \quad \text{across } d,
$$

$$
\beta_{dn} \mid H_d \overset{\text{indep}}{\sim} H_d(\cdot) \quad \text{across } d, n
$$

$$
W_{dn} \mid \beta_{dn} \overset{\text{indep}}{\sim} f(\cdot \mid \beta_{dn}) \quad \text{across } d, n.
$$

$H_d$ contains at most $T$ distinct atom locations, all shared with the base measure $G$.

The finite approximation we consider replaces the population level Dirichlet process with FSD$_K$, keeping the other conditionals intact:

$$
G_K \sim \text{FSD}_K(\omega, H),
$$

$$
F_d \mid G_K \overset{i.i.d.}{\sim} \text{TSB}_T(\alpha, G_K), \quad \text{across } d,
$$

$$
\psi_{dn} \mid F_d \overset{\text{indep}}{\sim} F_d(\cdot) \quad \text{across } d, n,
$$

$$
Z_{dn} \mid \psi_{dn} \overset{\text{indep}}{\sim} f(\cdot \mid \psi_{dn}) \quad \text{across } d, n.
$$

Let $P_{(N,D),\infty}$ be the distribution of the observations $\{W_{dn}\}$. Let $P_{(N,D),K}$ be the distribution of the observations $\{Z_{dn}\}$. We have the following bound on the total variation distance
between $P_{(N,D),\infty}$ and $P_{(N,D),K}$.

**Theorem 4.6 (Upper bound for modified HDP).** For some constants $C_1, C_2, C_3$ that depend only on $\omega$,

$$d_{TV}(P_{(N,D),\infty}, P_{(N,D),K}) \leq \frac{C_1 + C_2 \ln^2(DT)}{K} + C_3 \ln(DT) \ln K.$$  

The proof can be found in Appendix H.1. For fixed $K$, Theorem 4.6 is independent of $N$, the number of observations in each group, but scales with the number of groups $D$ like $O(\text{poly}(\ln D))$. For fixed $D$, the approximation error decreases to zero at rate no slower that $O(\ln(K/K))$. The $O(\ln(DT))$ factor is related to the expected logarithmic growth rate of Dirichlet process mixture models (Arratia, Barbour and Tavaré, 2003, Section 5.2) in the following way. Since there are $D$ groups, each manifesting at most $T$ distinct atom locations from an underlying Dirichlet process prior, the situation is akin to generating $DT$ samples from a common Dirichlet process prior. Hence, the expected number of unique samples is $O(\ln(DT))$. Similar to Theorem 4.1, we speculate that the $O(\ln^2(DT))$ factor can be improved to $O(\ln(DT))$.

5. Conceptual benefits of finite approximations

So far we have explored the approximation properties of independent finite approximations. However, other important factors affect posterior inference in models that use TFAs or AIFAs. For instance, in general a user prefers MCMC or variational inference algorithms that are easy or automatic to derive; not only do simpler or automated derivations save a user time, but they are also less likely to yield errors. In this section we describe some of these less quantitative, more “conceptual” considerations.

**Approximate posterior inference algorithms.** Formally, we are interested in approximating the posterior distribution $P(\tau, \psi, x | y)$ of the finite approximation, where $\tau := (\tau_k)_{k=1}^K$ denotes the collection of atom sizes, $\psi := (\psi_k)_{k=1}^K$ denotes the collection of atom locations, $x := (x_{n,k})_{k=1, n=1}^{K,N}$ denotes the latent trait counts of each observation, and $y := (y_n)_{n=1}^N$ denotes the observed data. Standard tools to explore or approximate the posterior distribution $P(\tau, \psi, x | y)$ require easy-to-simulate Gibbs conditional distributions or tractable expectations. For instance, because of the discreteness of the trait counts $x$, successful Markov chain Monte Carlo (MCMC) algorithms have been based largely on Gibbs sampling (Geman and Geman, 1984) — despite the recent advances in dynamic Hamiltonian Monte Carlo methods (Hoffman and Gelman, 2014). In particular, blocked Gibbs sampling utilizing the natural Markov blanket structure is straightforward to implement when the complete conditionals $P(\tau | x, \psi, y), P(x | \psi, \tau, y)$, and $P(\psi | x, \tau, y)$ are easy to simulate from. As another option, practitioners often use standard mean-field variational inference with coordinate ascent, and the coordinate ascent steps require analytical expectations (Wainwright and Jordan, 2008, Section 6.3). These expectations take the form $E_{\tau \sim q}[\ln \ell(x | \tau)]$, where $q(\tau)$ is the variational distribution over atom sizes. We note that recent black-box variational frameworks (Ranganath, Gerrish and Blei, 2014; Kingma and Welling, 2014; Rezende, Mohamed and Wierstra, 2014; Burda, Grosse and Salakhutdinov, 2016) show promise of moving away from being constrained to simple variational families.
Implementation of truncated versus independent finite approximations. Finite approximations with the same number of atoms $K$ differ only in the prior $\mathbb{P}(\tau)$. So, to compare the ease-of-use between AIFAs and TFAs, it suffices to compare the tractability of $\mathbb{P}(\tau \mid x, \psi, y)$ under different approximations. For exponential family CRMs with $d = 0$, AIFAs are compatible with standard inference schemes, because the Gibbs conditional $\mathbb{P}(\tau \mid x, \psi, y)$ comes from the same exponential family as the prior $\nu_K$.

**Proposition 5.1** (Conditional conjugacy of AIFA). Let $x_{.,k} := (x_{n,k})_{n=1}^{N}$ denote trait counts across observations of the $k$-th trait. Suppose the likelihood is an exponential family (Eq. (4)) and the AIFA prior $\nu_K$ is as in Corollary 3.3. Then the complete conditional of the atom sizes factorizes across atoms:

$$
\mathbb{P}(\tau \mid x, \psi, y) = \prod_{k=1}^{K} \mathbb{P}(\tau_k \mid x_{.,k}).
$$

Furthermore, each $\mathbb{P}(\tau_k \mid x_{.,k})$ is in the same exponential family as the AIFA prior, with density proportional to

$$
1\{\tau \in U\} \tau^{c/K + \sum_{n=1}^{N} \phi(x_{n,k})^{-1}} \exp \left( \langle \psi + \sum_{n=1}^{N} t(x_{n,k}), \mu(\tau) \rangle + (\lambda + N)[-A(\tau)] \right). \tag{18}
$$

The result follows immediately from the results in Appendix C. Consider the derivation of simulation steps in an MCMC scheme or expectation equations for coordinate ascent variational inference for AIFAs of common models such as beta–Bernoulli, gamma–Poisson, and beta–negative binomial. Proposition 5.1 implies that these derivations are straightforward. The complete conditionals over atom sizes are easy-to-simulate because they are well-known exponential families (beta and gamma). Also, the expectations of $\ln \ell(x \mid \tau)$ when $\tau$ has the exponential family distribution (Eq. (18)) are tractable because of the exponential family algebra between log-likelihood and prior (Wainwright and Jordan, 2008, Section 6.3). Finally, a parallelization strategy to utilize the factorization structure across atoms can yield speed-ups in wall-clock time, with the gains being greatest when there are many instantiated atoms.

There are many different types of TFAs, but in general deriving steps for standard inference schemes is substantially more involved than for AIFAs. While the prior $\mathbb{P}(\tau)$ can be reasonably easy to sample from, the incorporation of trait counts leads to intractable conditionals $\mathbb{P}(\tau \mid x)$. We consider two illustrative examples, both for exponential CRMs with $d = 0$. In our first example, the complete conditional of the atom sizes is both hard to sample from and leads to analytically intractable expectations.

**Example 5.1** (Stick-breaking approximation (Broderick, Jordan and Pitman, 2012; Paisley, Carin and Blei, 2011)). The following is a TFA for $\text{BP}(\gamma, \alpha, 0)$:

$$
\Theta_K = \sum_{i=1}^{K} \sum_{j=1}^{C_i} V_{i,j}^{(i)} \prod_{l=1}^{i-1}(1 - V_{i,j}^{(l)}) \delta_{\psi_{i,j}},
$$

where $C_i \overset{i.i.d.}{\sim} \text{Poisson}(\gamma)$, $V_{i,j}^{(l)} \overset{i.i.d.}{\sim} \text{Beta}(1, \alpha)$ and $\psi_{i,j} \overset{i.i.d.}{\sim} \mathcal{H}$. One can sample the atom sizes $V_{i,j}^{(l)} \prod_{l=1}^{i-1}(1 - V_{i,j}^{(l)})$. But there is no tractable way to sample from, or compute expectations with respect to, the conditional distribution $\mathbb{P}(\tau \mid x)$ because of the dependence on $C_i$ as
well as the entangled form of each $\tau$. Strategies to make the model more tractable include introducing auxiliary round indicator variables $r_k$ (Paisley, Carin and Blei, 2011; Broderick, Jordan and Pitman, 2012), marginalizing out the stick-breaking proportions (Broderick, Jordan and Pitman, 2012), and replacing the product $\prod_{i=1}^{l-1}(1 - V_{i,j})$ with a more succinct representation (Paisley, Carin and Blei, 2011). However, the final model in each case will contain at least one Gibbs conditional that is either difficult to sample from (Broderick, Jordan and Pitman, 2012, Equation 37) or lacks tractable expectations (Paisley, Carin and Blei, 2011, Section 3.3).

Other superposition-based approximations, like decoupled Bondesson or power-law (Campbell et al., 2019), present similar challenges due to the number of atoms per round variables $C$ and the dependence among the atom sizes.

In our second example, the complete conditional of the atom sizes can be sampled without auxiliary variables, but important expectations are not analytically tractable.

**Example 5.2** (Bondesson approximation (Doshi-Velez et al., 2009; Teh, Görür and Ghahramani, 2007)). When $\alpha = 1$, the Bondesson approximation in Example 4.3 becomes

$$\Theta_K = \sum_{i=1}^K \tau_i \delta_{\psi_i}, \quad \tau_i = \prod_{j=1}^i p_j, \quad p_j \overset{i.i.d.}{\sim} \text{Beta}(\gamma, 1), \quad \psi_i \overset{i.i.d.}{\sim} H.$$ (19)

The atom sizes are dependent because they jointly depend on $p_1, \ldots, p_K$, but the complete conditional of atom sizes $P(\tau \mid x)$ admits a density proportional to

$$1\{0 \leq \tau_K \leq \tau_{K-1} \leq \ldots \leq \tau_1 \leq 1\} \prod_{j=1}^K \tau_j^{\gamma-1}(1 - \tau_j)^{-\gamma} \frac{1}{\sum_{n=1}^N x_n,j} \sum_{n=1}^N x_n,j.$$  

The conditional distributions $P(\tau_i \mid \tau_{-i}, x)$ are truncated betas, so adaptive rejection sampling (Gilks and Wild, 1992) can be used as a sub-routine to sample each $P(\tau_i \mid \tau_{-i}, x)$, and then sweep over all atom sizes. However, for this exponential family, expectations of the sufficient statistics $\ln \tau_i$ and $\ln(1 - \tau_i)$ are not tractable. For example, the variational inference scheme of Doshi-Velez et al. (2009) requires additional approximations.

Other series-based approximations, like thinning or rejection sampling (Campbell et al., 2019), are characterized by even less tractable dependencies between atom sizes in both the prior and the conditional $P(\tau \mid x)$.

Overall, AIFAs are more compatible with standard approximate inference algorithms than TFAs. In common exponential-family models, the distributions of AIFA atom sizes conditioned on trait counts factorize across the number of atoms $K$, and each distribution is in the same exponential family as the prior. The equivalent TFA distributions do not have the same factorization structure, and in general are too complicated for easy sampling or computing expectations. In the event that black-box approximate inference matures and makes TFAs easier to use, the ability to parallelize computation will still remain an attractive benefit of AIFAs over TFAs.

6. Empirical evaluation

We now report the practical performance of the AIFA construction on a combination of synthetic and real-data examples. Though our theory suggests the performance of TFAs
may be better than AIFAs for worst-case likelihoods, we here find that AIFAs and TFAs perform comparably for common likelihoods and across approximation levels $K$. We find similar results with both a completely random measure (beta–negative binomial process) and normalized completely random measure (modified hierarchical Dirichlet process). We compare the AIFA to another IFA construction; we find that the two perform comparably across approximation levels $K$, and we recall that our construction also works for the non-power-law case — in contrast to the IFA competitor.

In relation to prior studies, existing empirical work has only compared IFAs and TFAs for simpler models and smaller data sets (e.g., Doshi-Velez et al. (2009, Table 1,2) and Kurihara, Welling and Teh (2007, Figure 4)). Our comparison is grounded in models with more levels and analyzes datasets of much larger sizes. For instance, in our topic modeling application, we analyze nearly 1 million documents, while the comparison in Kurihara, Welling and Teh (2007, Figure 4) utilized only 200 synthetic data points.

6.1. Image denoising with the beta–Bernoulli process

We first compare the quality of the AIFA construction to that of a standard TFA for a CRM-based target model. We use MCMC for image denoising through dictionary learning because it is an application where finite approximations of BNP models — in particular beta–Bernoulli with $d = 0$ — have proven useful (Zhou et al., 2009). The observational likelihood in this dictionary learning model is not one of the worst cases in Section 4.1. We find that the performance of AIFAs and TFAs is comparable across $K$, and the posterior modes across TFA and AIFA models are similar to each other.

The goal of image denoising is to recover the original, noiseless image (Fig. 1a) from a corrupted one (Fig. 1b). To do so, the input image is decomposed into small contiguous patches. The model assumes that each patch is a combination of a set of latent basis elements. By estimating the coefficients expressing the combination, one can denoise the individual patches and ultimately the overall image. The beta–Bernoulli process allows simultaneous estimation of both basis elements and basis assignments. Because the number of extracted patches depends on both the patch size and the input image size, even on the same input image, the analysis might process a varying number of “observations.” The nonparametric nature of the beta–Bernoulli process sidesteps the cumbersome problem of calibrating the number of basis elements for these different data set sizes, which can be large even for a relatively small image (for a 256 $\times$ 256 image like Fig. 1b, the number of extracted patches, $N$, is about 60,000). We quantify denoising quality by computing the peak signal-to-noise ratio (PNSR) between the original and the denoised image (Hore and Ziou, 2010). The higher the PNSR, the more similar the images.

We use Gibbs sampling to approximate the posterior distributions. To ensure stability and accuracy of the sampler, patches (i.e., observations) are gradually introduced in epochs, and the sampler modifies only the latent variables of the current epoch’s observations. See Appendix I.1 for more details about the finite approximations, the hyperparameter settings, and the inference algorithm.

Figures 1c and 1d visually summarize the results of posterior inference for a particular image. We report experiments with other images in Appendix J. Our results across all images indicate that the AIFA and TFA perform similarly. Figure 2 quantitatively confirms these qualitative findings. Figure 2a shows how PNSR changes as a function of the approximation level $K$. We find that the quality of denoised images improves with increasing $K$. Furthermore, the quality is very similar across the two types of approximation. Both
approximations perform much better than the baseline (i.e., the noisy input image). The improvement with $K$ is largest for small $K$, and plateaus for larger values of $K$. For a given approximation level, the quality of TFA denoising and that of the AIFA are almost the same. Each TFA denoised image is more similar to the AIFA denoised image than to the original image, indicated by the large gap in PSNR.

Figure 2b uses the output of inference with the AIFA as an initial value for inference with the TFA; similarly Fig. 2c uses the output with the TFA to initialize inference with the AIFA. For both approximations, $K = 60$. Rather than randomly initializing the latent variables at the beginning of the Gibbs sampler of one model (i.e., cold start), we use the last configuration of latent variables visited in the other model as the initial state of the Gibbs sampler (i.e., warm start). Because at the end of training, all latent variables for all patches have been assigned, for this experiment, instead of gradually introducing patches, we make all patches available from the start. For both approximations, the Gibbs sampler initialized at the warm start visits candidate images that essentially have the same PSNR as the starting configuration; the PSNR values never deviate from the initial PSNR by more than 1%. The early iterates of the cold-start Gibbs sampler are noticeably lower in quality compared to the warm-start iterates, and the quality at the plateau is still lower than that of the warm start. Each trace of PSNR of cold-start Gibbs corresponds to a random seed in initialization and simulation of the conditionals, while each trace of warm-start PSNR corresponds to a different final state of the alternative model’s training. The variation across warm starts is small; the variation across cold starts is larger but still quite small. In all, the modes of TFA posterior are good initializations for inference with the AIFA model, and vice-versa.

6.2. Topic modelling with the modified hierarchical Dirichlet process

We next compare the performance of normalized AIFAs (namely, FSD$_K$) and TFAs (namely, TSB$_K$) in a DP-based model with additional hierarchy: the modified HDP from Section 4.2. As in Section 6.1, we find that the approximations perform similarly.

Fig 1: AIFA and TFA denoised images have comparable quality. (a) shows the noiseless image. (b) shows the corrupted image. (c,d) are sample denoised images from finite models with $K = 60$. We report PSNR (in dB) with respect to the noiseless image.
Fig 2: (a) Peak signal-to-noise ratio (PSNR) as a function of approximation level $K$. The error bars reflect randomness in both initialization and simulation of the conditionals across 5 trials. AIFA denoising quality improves as $K$ increases, and the performance is similar to TFA across approximation levels. Moreover, the TFA- and AIFA-denoised images are very similar: the PSNR $\approx 50$ for TFA versus AIFA, whereas PSNR $< 35$ for TFA or AIFA versus the original image. (b,c) Show how PSNR evolves during inference. The “warm-start” lines in indicate that the AIFA-inferred (respectively, TFA-inferred) parameters are excellent initializations for TFA (respectively, AIFA) inference.

Specifically, we use the modified HDP for topic modeling. We use stochastic variational inference with mean-field factorization (Hoffman et al., 2013) to approximate the posterior over the latent topics based on training documents. The training corpus consists of nearly one million documents from Wikipedia. We measure the quality of inferred topics via predictive log-likelihood on a set of 10,000 held-out documents. See Appendix I.2 for complete experimental details.

Figure 3a shows that, as expected, the quality of the inferred topics improves as the approximation level grows. For a given approximation level, the quality of the topics learned using the TFA and the normalized AIFA are almost the same.

Rather than randomly initializing the variational parameters at the start of variational inference of one model (i.e., cold start), we can use the variational parameters at the end of the other model’s training as the initialization (i.e., warm start). Figure 3b uses the outputs of inference with the normalized AIFA approximation as initial values for inference with the normalized TFA; similarly Fig. 3c uses the TFA to initialize inference with the AIFA. We fix the number of topics to $K = 300$. For both kinds of approximation, the test log-likelihood basically stays the same for warm-start training iterates; the test log-likelihood for the iterates never deviate more than 0.5% from the initial value. The early iterates after the cold start are noticeably lower in quality compared to the warm iterates; however at the end of training, the test log-likelihoods are nearly the same. Each trace of cold start corresponds to a different initialization and ordering of data batches processed. Each trace of warm start corresponds to a different output of the other model’s training and a different ordering of data batches processed. The variation across either cold starts or warm starts is small. So, in sum, the modes of the TFA posterior are good initializations for inference with the AIFA model, and vice-versa.
Fig 3: (a) Test log-likelihood (testLL) as a function of approximation level $K$. The error bars reflect randomness in both initialization and data mini-batches across 5 trials. AIFA topic quality improves as $K$ increases, and the performance is similar to TFA across approximation levels. (b,c) show how testLL evolves during inference. The “warm-start” lines in (b,c) indicate that the AIFA-inferred (respectively, TFA-inferred) parameters are excellent initializations for TFA (respectively, AIFA) inference.

### 6.3. Comparing independent finite approximations

Having established that the AIFA is competitive with TFAs, we finally turn to comparing the AIFA construction with other IFAs. We consider a linear–Gaussian factor analysis model with the power-law beta–Bernoulli process (Griffiths and Ghahramani, 2011). We compare to the BFRY IFA construction of Lee, James and Choi (2016). For the beta–Bernoulli target, both the AIFA and BFRY IFA can be used as is. We omit a comparison to Lijoi, Prünster and Rigon (2019, Theorem 1) since using this latter IFA would require additional development; in the beta–Bernoulli process, the atom sizes potentially fall outside the support of the Bernoulli likelihood, and therefore the existing approximation cannot be used directly.

We generate 2,000 data points from the full CRM model with a discount of $d = 0.6$. We use 1,500 for training and report predictive log-likelihood on the 500 held-out data points. To compare predictive performance, we use automatic differentiation variational inference as implemented in Pyro (Bingham et al., 2018). To isolate the effect of the approximation type, we use “ideal” initialization conditions: we initialize the variational parameters using the latent features, assignments, and variances that generated the training set. See Appendix I.3 for more details about the model, BFRY, and the approximate inference scheme. Figure 4 shows that across approximation levels $K$, the predictive performances of the AIFA and BFRY are similar. A benefit of the AIFA is that it is well-defined in the limit of $d \to 0$, but the limit $d \to 0$ of BFRY is not established.

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In Fig. 4, we used the default settings of $a, S_b, b_K$ discussed following Theorem 3.2. In Appendix J, we show how the AIFA performance is not sensitive to $a$ and $b_K$ by reporting test likelihoods for $a \in \{0.1, 1\}$ and $b_K = 1/\sqrt{K}$ or $b_K = 1/K$.

---

5 The approach of Lee, James and Choi (2016) to construct IFAs for the beta process with $d > 0$ was later generalized to other CRMs by Lee, Missouridou and Caron (2019).
Fig 4: AIFA (blue) and BFRY (orange) provide similar predictive performance in a linear-Gaussian factor analysis model using a beta–Bernoulli process. (a) Average predictive log-likelihood, across 5 trials with different random seeds for the stochastic optimizer. (b) Highest predictive log-likelihood attained across the same 5 trials.

7. Discussion

We have provided a general construction of automated independent finite approximations (AIFAs) for completely random measures and their normalizations. For processes without power-law behavior, we provide approximation error bounds; our bounds show that we can ensure accurate approximation by setting the number of atoms $K$ to be (1) logarithmic in the number of observations $N$ and (2) inverse to the error tolerance $\epsilon$. We have discussed how the independence and automatic construction of AIFA atom sizes lead to convenient inference schemes. A natural competitor for AIFAs is a truncated finite approximation (TFA). We show that, for the worst case choice of observational likelihood and the same $K$, AIFAs can incur larger error than the corresponding TFAs. However, in our experiments, we find that the two methods have essentially the same performance in practice. Meanwhile, AIFAs are overall easier to work with than TFAs, whose coupled atoms complicate the development of inference schemes. Future work might extend our error bound analysis to conjugate family CRMs with power-law behavior. Another direction is to tighten the error upper bound by focusing on specific, commonly-used observational likelihoods — in contrast to the worst-case analysis we provide here. Finally, more work is required to directly compare the size of error in the finite approximation to the size of error due to approximate inference algorithms such as Markov chain Monte Carlo or variational inference.

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Appendix A: Additional examples of AIFA construction

Let \( B(\alpha, \beta) = \frac{\Gamma(\alpha)\Gamma(\beta)}{\Gamma(\alpha+\beta)} \) denote the beta function.

**Example A.1** (Beta process). Taking \( V = \mathbb{R}_+ \), \( g(\theta) = 1 \), \( h(\theta; \eta) = (1-\theta)^{\eta-1}1[\theta \leq 1] \), and \( Z(\xi, \eta) = B(\xi, \eta) \) in Theorem 3.2 yields the three-parameter beta process BP(\( \gamma, \eta - d, d \)) (Teh and Görür, 2009; Broderick, Jordan and Pitman, 2012), which has rate measure

\[
\nu(d\theta) = \gamma \frac{1[\theta \leq 1]}{B(\eta, 1-d)} \theta^{-d}(1 - \theta)^{\eta-1} d\theta.
\]

Since \( h \) is continuous and bounded on \([0, 1/2]\), Assumption 1 holds.

**Example A.2** (Beta prime process). Taking \( V = \mathbb{R}_+ \), \( g(\theta) = (1+\theta)^{-1} \), \( h(\theta; \eta) = (1+\theta)^{-\eta} \), and \( Z(\xi, \eta) = B(\xi, \eta) \) in Theorem 3.2 yields the beta prime process of Broderick et al. (2015), which has rate measure

\[
\nu(d\theta) = \frac{\gamma}{B(\eta, 1-d)} (1+\theta)^{-d-\eta} d\theta.
\]

Since \( g \) is continuous, \( g(0) = 1, 1 \leq g(\theta) \leq 1 + \theta \), and \( h(\theta; \eta) \) is continuous and bounded on \([0, 1]\), Assumption 1 holds.

In the case of \( d = 0 \), the corresponding exponential family distribution is beta prime. With two placeholder parameters \( \alpha \) and \( \beta \), the beta prime density at \( \theta > 0 \) is

\[
\text{Beta}'(\theta; \alpha, \beta) = \theta^{\alpha-1}(1+\theta)^{-\alpha-\beta}.
\]

To construct AIFA using Corollary 3.3, we set \( c = \gamma \eta \) and

\[
\nu_K(\theta) = \text{Beta}'(\theta; \gamma \eta / K, \eta)
\]

**Example A.3** (Gamma process). Taking \( V = \mathbb{R}_+ \), \( g(\theta) = 1 \), \( h(\theta; \lambda) = e^{-\lambda \theta} \), and \( Z(\xi, \lambda) = \Gamma(\xi/\lambda) \) in Theorem 3.2 yields the gamma process, with rate measure

\[
\nu(d\theta) = \lambda e^{-\lambda \theta} \Gamma(1-d) \theta^{-d-1} d\theta.
\]

Since \( h(\theta; \eta) \) is continuous and bounded on \([0, 1]\), Assumption 1 holds.

In the case of \( d = 0 \), the corresponding exponential family distribution is gamma. To construct AIFA using Corollary 3.3, we set \( c = \gamma \lambda \) and

\[
\nu_K(\theta) = \text{Gamma}(\theta; \gamma \lambda / K, \lambda).
\]

**Example A.4** (Generalized gamma process). Taking \( V = \mathbb{R}_+^2 \), \( g(\theta) = 1 \), \( h(\theta; \eta) = e^{-(\eta_1 \theta)^\eta_2} \), and \( Z(\xi, \eta) = \Gamma(\xi/\eta_2) (\eta_1 \eta_2)^{-\xi} \) in Theorem 3.2 yields the generalized gamma process whose rate measure is

\[
\nu(d\theta) = \frac{\gamma (\eta_1 \eta_2)^{1-d}}{\Gamma((1-d)/\eta_2)} (1 + (\eta_1 \theta)^\eta_2)^{-d} e^{-(\eta_1 \theta)^\eta_2} d\theta.
\]

Since \( h(\theta; \eta) \) is continuous and bounded on \([0, 1]\), Assumption 1 holds.
In the case of \( d = 0 \), the corresponding exponential family distribution is generalized gamma. With three placeholder parameters \( \xi', \eta'_1, \) and \( \eta'_2 \), the generalized gamma density at \( \theta > 0 \) is

\[
\text{GenGamma}(\theta; \xi', \eta'_1, \eta'_2) = \left( \frac{\eta'_2}{\eta'_1} \right) \theta^{\eta'_1 - 1} e^{-(\theta/\xi')}^{\eta'_2} \\
\Gamma(\eta'_1, / \eta'_2)
\]

To construct AIFA using Corollary 3.3, we set \( c = \gamma \eta_1 \eta_2 \) and

\[
\nu_K(\theta) = \text{GenGamma} \left( \theta; \frac{1}{\eta_1} \gamma \eta_1 \eta_2, \frac{1}{K \Gamma(\eta_2)} \right).
\]

Appendix B: Proofs of AIFA convergence

In this appendix, to highlight the fact that the i.i.d. distributions are different across \( K \), we use \( \tau_{K,i} \) to denote the \( i \)-th atom size in the approximation of level \( K \) i.e. the \( K \)-atom AIFA is

\[
\Theta_K := \sum_{i=1}^{K} \tau_{K,i} \delta_{\psi_{K,i}}, \quad \tau_{K,i} \sim \nu_K, \quad \psi_{K,i} \sim H.
\]

B.1. AIFA converges to CRM in distribution

In order to prove our main result, we require a few auxiliary results.

**Lemma B.1** (Kallenberg (2002, Lemma 12.1, Lemma 12.2 and Theorem 16.16)). Let \( \Theta \) be a random measure and \( \Theta_1, \Theta_2, \ldots \) a sequence of random measures. If for all measurable sets \( A \) and \( t > 0 \),

\[
\lim_{K \to \infty} \mathbb{E}[e^{-t \Theta_K(A)}] = \mathbb{E}[e^{-t \Theta(A)}],
\]

then \( \Theta_K \xrightarrow{D} \Theta \).

For a density \( f \), let \( \mu(t, f) : \theta \mapsto (1 - e^{-t \theta})f(\theta) \). In results that follow we assume all measures on \( \mathbb{R}_+ \) have densities with respect to Lebesgue measure. We abuse notation and use the same symbol to denote the measure and the density.

**Proposition B.2.** Let \( \Theta \sim \text{CRM}(H, \nu) \) and for \( K = 1, 2, \ldots \), let \( \Theta_K \sim \text{IFA}_K(H, \nu_K) \) where \( \nu \) is a measure and \( \nu_1, \nu_2, \ldots \) are probability measures on \( \mathbb{R}_+ \), all absolutely continuous with respect to Lebesgue measure. If \( \|\mu(1, t \nu_K) - \mu(1, \nu)\|_1 \to 0 \), then \( \Theta_K \xrightarrow{D} \Theta \).

**Proof.** Let \( t > 0 \) and \( A \) a measurable set. First, recall that the Laplace functional of the CRM \( \Theta \) is

\[
\mathbb{E}[e^{-t \Theta(A)}] = \exp \left\{ -H(A) \int_0^\infty \mu(t, \nu)(\theta) \, d\theta \right\}.
\]

We have

\[
\mathbb{E}[e^{-t \tau_{K,1} \mathbb{1}(\psi_{K,1} \in A)}] = \mathbb{P}(\psi_{K,1} \in A) \mathbb{E}[e^{-t \tau_{K,1} \mathbb{1}}} + \mathbb{P}(\psi_{K,1} \notin A)
\]

\[
= H(A) \mathbb{E}[e^{-t \tau_{K,1} \mathbb{1}}} + 1 - H(A)
\]

\[
= 1 - H(A)(1 - \mathbb{E}[e^{-t \tau_{K,1} \mathbb{1}}])
\]

\[
= 1 - \frac{H(A)}{K} \int_0^\infty \mu(t, K \nu_K)(\theta) \, d\theta.
\]
Since $\left| \frac{1-e^{-\theta t}}{1-e^{-\pi t}} \right| \leq \max(1, t)$, it follows by hypothesis that $\|\mu(t, K \nu_K) - \mu(t, \nu)\|_1 \to 0$. Thus, by dominated convergence and the standard exponential limit,

$$
\lim_{K \to \infty} \mathbb{E}[e^{-t\tau_{K,1}(\psi_K,1 \in A)}]^K = \lim_{K \to \infty} \left( 1 - \frac{H(A)}{K} \int_0^\infty \mu(t, K \nu_K)(\theta) \, d\theta \right)^K
= \exp \left\{ - \lim_{K \to \infty} H(A) \int_0^\infty \mu(t, K \nu_K)(\theta) \, d\theta \right\}
= \exp \left\{ -H(A) \int_0^\infty \mu(t, \nu)(\theta) \, d\theta \right\}.
$$

Finally, by the independence of the random variables $\{\theta_{K,i}\}_{i=1}^K$ and $\{\psi_{K,i}\}_{i=1}^K$, we have

$$
\lim_{K \to \infty} \mathbb{E}[e^{-t\theta_{K,A}(\nu)}] = \lim_{K \to \infty} \mathbb{E}[e^{-t\tau_{K,1}(\psi_K,1 \in A)}]^K,
$$

so the result follows from Lemma B.1.

\begin{lemma}
If there exist measures $\pi(\theta) \, d\theta$ and $\pi'(\theta) \, d\theta$ on $\mathbb{R}_+$ such that for some $\kappa > 0$ and $c, c'$,

1. the measures $\mu, \mu_1, \mu_2, \ldots$ have densities $f, f_1, f_2, \ldots$ with respect to $\pi$ and densities $f', f'_1, f'_2, \ldots$ with respect to $\pi'$,
2. $\int_0^\kappa |f'(\theta) - f'_K(\theta)| \, d\theta \xrightarrow{K \to \infty} 0$,
3. $\sup_{\theta \in [0, \kappa]} |f(\theta) - f_K(\theta)| \xrightarrow{K \to \infty} 0$,
4. $\sup_{\theta \in [0, \kappa]} \pi'(\theta) \leq c' < \infty$, and
5. $\int_\kappa \pi(\theta) \, d\theta \leq c < \infty$,

then

$$
\|\mu - \mu_K\|_1 \xrightarrow{K \to \infty} 0.
$$

\begin{proof}
We have, using the assumptions and Hölder’s inequality,

$$
\|\mu - \mu_K\|_1 = \int_0^\kappa |f'(\theta) - f'_K(\theta)| \pi'(d\theta) + \int_\kappa^\infty |f(\theta) - f_K(\theta)| \pi(d\theta)
\leq \left( \sup_{\theta \in [0, \kappa]} \pi'(\theta) \right) \int_0^\kappa |f'(\theta) - f'_K(\theta)| \, d\theta
+ \left( \sup_{\theta \in [\kappa, \infty)} |f(\theta) - f_K(\theta)| \right) \int_\kappa^\infty \pi(d\theta)
\leq c' \int_0^\kappa |f'(\theta) - f'_K(\theta)| \, d\theta + c \sup_{\theta \in [\kappa, \infty)} |f(\theta) - f_K(\theta)|.
$$

The conclusion follows by the assumptions.
\end{proof}

\begin{proof}[Proof of Theorem 3.2]
Note that since $h$ is continuous and bounded on $[0, \epsilon]$, $c$ as given in the theorem statement is finite. We will apply Lemma B.3 with $\kappa = \min(1, \epsilon)$, $\mu = (1, \nu)$, $\mu_K = \mu(1, n\nu_K)$,

$$
\pi(\theta) = \frac{\theta^{-d} g(\theta)^{1-d} h(\theta; \eta)}{Z(1-d, \eta)},
$$

where

$$
Z(d, \eta) = \frac{\theta_{d, \eta}^{1-d} (1-\theta_{d, \eta})^d}{\Gamma(1-d, \eta) + \Gamma(d, \eta)}.
$$

\end{proof}
and \( \pi'(\theta) := (\theta g(\theta))^d \pi(\theta) \). Thus, \( f(\theta) = \gamma (1 - e^{-\theta})(\theta g(\theta))^{-1} \),
\[
f_K(\theta) = nZ_K^{-1} (1 - e^{-\theta}) \theta^{-1+cK^{-1}+d-dS_{bK} (\theta-aK^{-1})} g(\theta)^{-1+cK^{-1}},
\]
and \( f'(\theta) = (\theta g(\theta))^{-d} f(\theta) \), and \( f'_K(\theta) = (\theta g(\theta))^{-d} f_K(\theta) \).

We now note a few useful properties that we will use repeatedly in the proof. Observe that \((a/K)^{cK^{-1}} = 1 + o(1)\). The assumption that \( h \) is bounded and continuous implies that on \( [0, a/K], h(\theta; \eta) = h(0; \eta) + o(1) \). Similarly, for any \( \delta > 0 \), \( g(\theta) \) is bounded and continuous for \( \theta \in [0, \delta] \) and therefore, together with the fact that \( g(0) = 1 \), we can conclude that on \([0, a/K], g(\theta) = 1 + o(1)\).

For the remainder of the proof we will consider \( K \) large enough that \( aK^{-1} + 2bK \) and \( cK^{-1} \) are less than \( \kappa \). The normalizing constant \( Z_K \) can be written as
\[
Z_K = \int_0^{a/K} (\theta g(\theta))^{-1+cK^{-1}} \pi'(d\theta) + \int_{a/K}^\kappa \theta^{-1+cK^{-1}+d-dS_{bK} (\theta-aK^{-1})} g(\theta)^{-1+cK^{-1}} \pi'(d\theta) + \int_\kappa^\infty (\theta g(\theta))^{-1+cK^{-1}+d} \pi'(d\theta).
\]

We rewrite each term in turn. For the first term,
\[
\int_0^{a/K} \theta^{-1+cK^{-1}} g(\theta)^{-1+cK^{-1}} \pi'(d\theta) = (c/\gamma + o(1)) \int_0^{a/K} \theta^{-1+cK^{-1}} d\theta = (c/\gamma + o(1)) \frac{K}{c} \left( \frac{a}{K} \right)^{cK^{-1}} = \frac{K}{\gamma} + o(K).
\]

Since \( \kappa \leq 1 \) and \( S_{bK} \in [0, 1] \), for \( \theta \in [a/K, \kappa] \), \( \theta^{-dS_{bK} (\theta-aK^{-1})} \leq \theta^{-d} \). Since \( g(0) = 1 \), \( c_* \leq 1 \) and therefore \( g(\theta)^{-1+cK^{-1}} \leq c_*^{-1+c} \). Hence the second term is upper bounded by
\[
c_*^{-1+c} \int_{a/K}^\kappa \theta^{-1+cK^{-1}-d} \pi'(d\theta) \leq c_*^{-1} (c/\gamma + O(1)) \frac{K^d}{a^d} \frac{K}{c} \left( \kappa^{cK^{-1}} - (a/K)^{cK^{-1}} \right) = O(K^d) \times O(\ln K) = o(K).
\]

For the third term,
\[
\int_\kappa^\infty (\theta g(\theta))^{-1+cK^{-1}+d} \pi'(d\theta) = \int_\kappa^\infty (\theta g(\theta))^{-1+cK^{-1}} \pi(d\theta) \leq (\kappa c_*)^{-1+1+cK^{-1}} \int_\kappa^\infty \pi(d\theta) \leq (\kappa c_*)^{-1}.
\]

Hence, \( Z_K = \frac{K}{\gamma} + o(K) \) and \( KZ_K^{-1} = \gamma (1 + e_K) \), where \( e_K = o(1) \).
Next, we have
\[
\sup_{\theta \in [\kappa, \infty]} |f(\theta) - f_K(\theta)| = \sup_{\theta \in [\kappa, \infty]} (1 - e^{-\theta})(\theta g(\theta))^{-1}\left|\gamma - KZ_{-1}^{2}(\theta g(\theta))^{cK-1}\right|
\]
\[
\leq \sup_{\theta \in [\kappa, \infty]} \gamma(\theta g(\theta))^{-1}\left|1 - (1 + cK)(\theta g(\theta))^{cK-1}\right|
\]
\[
\leq \gamma \sup_{\theta \in [\kappa, \infty]} (\theta g(\theta))^{-1}\left|1 - (\theta g(\theta))^{cK-1}\right|
\]
\[
+ \gamma e_K \sup_{\theta \in [\kappa, \infty]} (\theta g(\theta))^{-1+cK-1}.
\] (B.1)

To bound the two terms we will use the fact that if $\theta \geq \kappa$, then
\[
\theta g(\theta) \geq \frac{\theta}{c^*(1+\theta)} \geq \frac{\kappa}{c^*(1+\kappa)} =: \tilde{\kappa}
\]
and if $\theta \leq 1$ then $\theta g(\theta) \leq c_* \leq 1$. Hence, letting $\psi := g(\theta)$, for the first term in Eq. (B.1) we have
\[
\gamma \sup_{\theta \in [\kappa, \infty]} (\theta g(\theta))^{-1}\left|1 - (\theta g(\theta))^{cK-1}\right|
\]
\[
\leq \gamma \sup_{\psi \in [\tilde{\kappa}, \infty]} \psi^{-1}\left|1 - \psi^{cK-1}\right|
\]
\[
\leq \gamma \sup_{\psi \in [\tilde{\kappa}, 1]} \psi^{-1}\left|1 - \psi^{cK-1}\right| + \gamma \sup_{\psi \in [1, \infty)} \psi^{-1}\left|1 - \psi^{cK-1}\right|
\]
\[
\leq \gamma \tilde{\kappa}^{-1} \sup_{\psi \in [\tilde{\kappa}, 1]} \left|1 - \psi^{cK-1}\right| + \gamma \left(\frac{K - c}{K}\right)^{K^{-1}} \left|1 - \frac{K}{K - c}\right|
\]
\[
\leq \gamma \tilde{\kappa}^{-1} (1 - \tilde{\kappa}^{cK-1}) + O(1) \times \frac{c}{K - c}
\]
\[
= \gamma \tilde{\kappa}^{-1} \times o(1) + O(K^{-1})
\]
\[
\to 0.
\]

Similarly, for the second term in Eq. (B.1) we have
\[
\gamma e_K \sup_{\theta \in [\kappa, \infty]} (\theta g(\theta))^{-1+cK-1} \leq \gamma e_K \sup_{\psi \in [\tilde{\kappa}, \infty)} \psi^{-1+cK-1}
\]
\[
\leq \gamma \tilde{\kappa}^{-1} e_K
\]
\[
\to 0.
\]

Since $g(\theta)$ is bounded on $[0, \kappa]$, $g(\theta)^{cK-1} = 1 + o(1)$ and therefore $(1 + e_K)g(\theta)^{cK-1} = 1 + e'_K$, where $e'_K = o(1)$. Using this observation together with the bound $(1 - e^{-\theta})\theta^{-1} \leq 1$, we have
\[
\int_0^\kappa |f'(\theta) - f'_K(\theta)|d\theta = \int_0^\kappa (\theta g(\theta))^{-d}|f(\theta) - f_K(\theta)|d\theta
\]
\[
= \int_0^\kappa (1 - e^{-\theta})(\theta g(\theta))^{-1-d}|\gamma - KZ_{-1}^{2}(\theta g(\theta))^{cK-1}|d\theta
\]

We bound the first integral in Eq. (B.2) in four parts: from 0 to \(aK^{-1}\), from \(aK^{-1}\) to \(aK^{-1} + b_K\), from \(aK^{-1} + b_K\) to \(\kappa - b_K\), and from \(\kappa - b_K\) to \(\kappa\). The first part is equal to
\[
\int_0^{aK^{-1}} \theta^{-d}|1 - \theta^{d+cK^{-1}}|d\theta \leq \int_0^{aK^{-1}} \theta^{-d} + \theta^{cK^{-1}}d\theta 
\]
\[
= \frac{\theta^{1-d}}{1-d} + \frac{K}{c+K} \theta^{1+cK^{-1}} \bigg|_0^{aK^{-1}} 
\]
\[
= \frac{1}{1-d} (aK^{-1})^{1-d} + \frac{K}{c+K} (aK^{-1})^{1+cK^{-1}} 
\]
\[
\to 0. 
\]

The second part is equal to
\[
\int_{aK^{-1}}^{aK^{-1}+b_K} \theta^{-d}|1 - \theta^{d+cK^{-1}}|d\theta \leq \int_{aK^{-1}}^{aK^{-1}+b_K} \theta^{-d} + \theta^{cK^{-1}-d}d\theta
\]
\[
\leq 2 \int_{aK^{-1}}^{aK^{-1}+b_K} \theta^{-d}d\theta 
\]
\[
= \frac{2}{1-d} \theta^{1-d} \bigg|_{aK^{-1}}^{aK^{-1}+b_K} 
\]
\[
= \frac{2}{1-d} ((aK^{-1} + b_K)^{1-d} - (aK^{-1})^{1-d}) 
\]
\[
\to 0. 
\]

The third part is equal to
\[
\int_{aK^{-1}+b_K}^{\kappa-b_K} \theta^{-d}|1 - \theta^{d+cK^{-1}}|d\theta = \int_{aK^{-1}+b_K}^{\kappa-b_K} \theta^{-d} - \theta^{cK^{-1}-d}d\theta 
\]
\[
= \frac{1}{1-d} \theta^{1-d} - \frac{K}{c+K(1-d)} \theta^{1-d+cK^{-1}} \bigg|_{aK^{-1}+b_K}^{\kappa-b_K} 
\]
\[
= \frac{(\kappa - b_K)^{1-d}}{1-d} - \frac{K}{c+K(1-d)} (\kappa - b_K)^{1-d+cK^{-1}} 
\]
\[
- \frac{(aK^{-1} + b_K)^{1-d}}{1-d} + \frac{K}{c+K} (aK^{-1} + b_K)^{1-d+cK^{-1}} 
\]
\[
\to 0. 
\]

The fourth part is equal to
\[
\int_{\kappa-b_K}^{\kappa} \theta^{-d}|1 - \theta^{d+cK^{-1}}|d\theta \leq \int_{\kappa-b_K}^{\kappa} \theta^{-d} + \theta^{cK^{-1}-d}d\theta 
\]
\[
\to 0. 
\]
using the same argument as the second part. The second integral in Eq. (B.2) is upper bounded by
\[ \gamma c' K \int_0^K \theta^{-d} d \theta = \gamma c' \frac{K^{1-d}}{1-d} = \alpha(K). \]
Since \( \sup_{\theta \in [0, K]} \pi'(\theta) < \infty \) by the boundedness of \( g \) and \( h \) and \( \pi \) is a probability density by construction, conclude using Lemma B.3 that \( \| \mu - \mu_K \|_1 \to 0 \). It then follows from Lemma B.1 that \( \Theta_K \xrightarrow{\mathcal{D}} \Theta \).

\[ \text{B.2. Differentiability of smoothed indicator} \]

We show that
\[ S_b(\theta) = \begin{cases} \exp \left( \frac{1}{1-(\theta-b)^2/b^2} + 1 \right) & \text{if } \theta \in (0, b) \\ 1/\theta > 0 & \text{otherwise.} \end{cases} \]
is differentiable over the whole real line. Since on the separate domains \((-\infty, 0), (0, b), \) and \((b, \infty), \) the derivative exists and is continuous, we only need to show that the values of the derivative at \( \theta = 0 \) and \( \theta = b \) from either side match.

To start, we show that \( S_b(\theta) \) is continuous at \( \theta = 0 \) and \( \theta = b \).

\[ \lim_{\theta \to b^-} S_b(\theta) = \exp \left( \frac{1}{1-0} + 1 \right) = 1, \]
\[ \lim_{\theta \to 0^+} S_b(\theta) = \exp \left( \frac{1}{1/\infty} \right) = 0. \]

For \( \theta = b, \) the derivative from the right \( (\theta \to b^+) \) is 0 since constant function. The derivative on the interval \((0, b)\) equals
\[ \frac{dS_b}{d\theta} = S_b(\theta) \left[ \left( \frac{-1}{(\theta-b)^2/b^2} \right) - \frac{2(\theta-b)}{b^2} \right]. \quad (B.3) \]
The limit as we approach \( b \) from the left is 0 since \( \lim_{\theta \to b^-} S_b(\theta) = 1 \) and the term \((\theta-b)\) vanishes. So the one-sided derivative is continuous at \( \theta = b \).

For \( \theta = 0, \) the derivative from the left \( (\theta \to 0^-) \) is 0 since also constant function. The limit of Equation (B.3) as we approach 0 from the right is also 0. It suffices to show
\[ \lim_{\theta \to 0^+} S_b(\theta) \left[ \left( \frac{-1}{(\theta-b)^2/b^2} \right) - \frac{2(\theta-b)}{b^2} \right] = 0. \]
Reparametrizing \( x = \frac{1}{1-(\theta-b)^2/b^2}, \) we have that \( x \to \infty \) and \( \theta \to 0^+. \) The last limit becomes
\[ \lim_{x \to \infty} \frac{\exp(-x)}{x^2} = 0, \]
which is true because the decay of the exponential function is faster than any polynomial.

The derivative defined over disjoint intervals are continuous at the boundary points, so the overall approximate indicator is differentiable.
B.3. Normalized AIFA EPPF converges to NCRM EPPF

Proof of Theorem 3.4. First, we show that the total mass of AIFA converges in distribution to the total mass of CRM. It suffices to consider $K \geq b$ so that the AIFA EPPF is non-zero since we only care about the asymptotic behavior of $p_K(n_1, n_2, \ldots, n_b)$. Through Appendix B.1, we have shown that for all measurable sets $A$ and $t > 0$, the Laplace functionals converge:

$$\lim_{K \to \infty} E[e^{-t\Theta_K(A)}] = E[e^{-t\Theta(A)}],$$

By choosing $A = \Psi$ i.e. the ground space, we have that $\Theta_K(\Psi)$ is the total mass of AIFA and $\Theta(\Psi)$ is the total mass of CRM

$$\Theta_K(\Psi) = \sum_{i=1}^{K} \tau_{K,i}, \quad \Theta(\Psi) = \sum_{i=1}^{\infty} \theta_i.$$

Since for any $t > 0$, the Laplace transform of $\Theta_K(\Psi)$ converges to that of $\Theta(\Psi)$, we conclude that $\Theta_K(\Psi)$ converges to $\Theta(\Psi)$ in distribution (Kallenberg, 2002, Theorem 5.3):

$$\sum_{i=1}^{K} \tau_{K,i} \xrightarrow{D} \Theta(\Psi). \quad \text{(B.4)}$$

Second, we show that the decreasing order statistics of AIFA atom sizes converges (in finite-dimensional distributions i.e., in f.d.d) to the decreasing order statistics of CRM atom sizes. For each $K$, the decreasing order statistics of AIFA atoms is denoted by $\{\tau_{K,(i)}\}_{i=1}^{K}$:

$$\tau_{K,(1)} \geq \tau_{K,(2)} \geq \cdots \geq \tau_{K,(K)}.$$

We will leverage Loève (1956, Theorem 4 and page 191) to find the limiting distribution $\{\tau_{K,(i)}\}_{i=1}^{K}$ as $K \to \infty$. It is easy to verify the conditions to use the theorem: because the sums $\sum_{i=1}^{K} \tau_{K,i}$ converge in distribution to a limit, we know that all the $\tau_{K,i}$’s are uniformly asymptotically negligible (Kallenberg, 2002, Lemma 15.13). Now, we discuss what the limits are. It is well-known that $\Theta(\Psi)$ is an infinitely divisible positive random variable with no drift component and Levy measure exactly $\nu(d\theta)$ (Perman, Pitman and Yor, 1992). In the terminology of Loève (1956, Equation 2), the characteristics of $\Theta(\Psi)$ are $a = b = 0$ (no drift or Gaussian parts), $L(x) = 0$, and

$$M(x) = -\nu([x, \infty)).$$

Let $I$ be a counting process in reverse over $(0, \infty)$ defined based on the Poisson point process $\{\theta_i\}_{i=1}^{\infty}$ in the following way. For any $x$, $I(x)$ is the number of points $\theta_i$ exceeding the threshold $x$:

$$I(x) := |\{i : \theta_i \geq x\}|.$$

We augment $I(0) = \infty$ and $I(\infty) = 0$. As a stochastic process, $I$ has independent increments, in that for all $0 = t_0 < t_1 < \cdots < t_k$, the increments $I(t_i) - I(t_{i-1})$ are independent, furthermore the law of the increments is $I(t_{i-1}) - I(t_i) \sim \text{Poisson}(M(t_i) - M(t_{i-1}))$. These properties are simple consequences of the counting measure induced by the Poisson point
process. According to Loeve (1956, Page 191), the limiting distribution of \( \{ \tau_{K,i} \}_{i=1}^K \) is governed by \( I \), in the sense that for any fixed \( t \in \mathbb{N} \), for any \( x_1, x_2, \ldots, x_t \in [0, \infty) \):

\[
\lim_{K \to \infty} \mathbb{P}(\tau_{K,1} < x_1, \tau_{K,2} < x_2, \ldots, \tau_{K,t} < x_t) = \mathbb{P}(I(x_1) < 1, I(x_2) < 2, \ldots, I(x_t) < t).
\]  

(B.5)

Because the \( \theta_i \)'s induce \( I \), we can relate the left hand side to the order statistics of the Poisson point process. We denote the decreasing order statistic of the \( \{ \theta_i \}_{i=1}^\infty \) as:

\[
\theta(1) \geq \theta(2) \geq \cdots \geq \theta(n) \geq \cdots
\]

Clearly, for any \( t \in \mathbb{N} \), the event that \( I(x) \) exceeds \( t \) is the same as the top \( t \) jumps among the \( \{ \theta_i \}_{i=1}^\infty \) exceed \( x \): \( I(x) \geq t \iff \theta(t) \geq x \). Therefore Eq. (B.5) can be rewritten as, for any fixed \( t \in \mathbb{N} \), for any \( x_1, x_2, \ldots, x_t \in [0, \infty) \):

\[
\lim_{K \to \infty} \mathbb{P}(\tau_{K,1} < x_1, \tau_{K,2} < x_2, \ldots, \tau_{K,t} < x_t) = \mathbb{P}(\theta(1) < x_1, \theta(2) < x_2, \ldots, \theta(t) < x_t).
\]  

(B.6)

It is well-known that convergence of the distribution function imply weak convergence — for instance, see Pollard (2012, Chapter III, Problem 1). Actually, from Loeve (1956, Theorem 5 and page 194), for any fixed \( t \in \mathbb{N} \), the convergence in distribution of \( \{ \tau_{K,i} \}_{i=1}^K \) to \( \{ \theta_i \}_{i=1}^\infty \) holds jointly with the convergence of \( \sum_{i=1}^K \tau_{K,i} \) to \( \sum_{i=1}^\infty \theta_i \): the two conditions of the theorem, which are continuity of the distribution function of each \( \tau_{K,i} \) and \( M(0) = -\infty^6 \), are easily verified. Therefore, by the continuous mapping theorem, if we define the normalized atom sizes:

\[
p_{K,s} := \frac{\tau_{K,s}}{\sum_{i=1}^K \tau_{K,i}}, \quad p(s) := \frac{\theta(s)}{\sum_{i=1}^\infty \theta_i},
\]

we also have that the normalized decreasing order statistics converge:

\[
(p_{K,i})_{i=1}^K \xrightarrow{f.d.d.} (p_{K,i})_{i=1}^\infty.
\]  

Finally we show that the EPPFs converge. In addition, if we define the \textit{size-biased permutation} (in the sense of Gnedenin (1998, Section 2)) of the normalized atom sizes:

\[
\{ \tilde{p}_{K,i} \} \sim \text{SBP}(p_{K,s}), \quad \{ \tilde{p}_i \} \sim \text{SBP}(p(s)),
\]

then by Gnedenin (1998, Theorem 1), the finite-dimensional distributions of the size-biased permutation also converges:

\[
(\tilde{p}_{K,i})_{i=1}^K \xrightarrow{f.d.d.} (\tilde{p}_i)_{i=1}^\infty.
\]  

(B.7)

Pitman (1996, Equation 45) gives the EPPF of \( \Xi = \Theta/\Theta(\Psi) \):

\[
p(n_1, n_2, \ldots, n_b) = \mathbb{E} \left( \prod_{i=1}^b \tilde{p}_{n_i}^{n_i-1} \prod_{i=1}^{b-1} \left( 1 - \sum_{j=1}^i \tilde{p}_{j} \right)^i \right),
\]

Likewise, the EPPF of \( \Xi_K = \Theta_K/\Theta_K(\Psi) \) is:

\[
p_K(n_1, n_2, \ldots, n_t) = \mathbb{E} \left( \prod_{i=1}^b \tilde{p}_{K,i}^{n_i-1} \prod_{i=1}^{b-1} \left( 1 - \sum_{j=1}^i \tilde{p}_{K,j} \right)^i \right).
\]

---

\textsuperscript{6}There is a typo in Loeve (1956).
Since $b$ is fixed, and each $p_j$ is $[0,1]$ valued, the mapping from the $b$-dimensional vector $p$ to the product $\prod_{i=1}^{b} p_i^{n_i - 1} \prod_{i=1}^{b-1} \left(1 - \sum_{j=1}^{i} p_j\right)$ is continuous and bounded. The choice of $N$, $b$, $n_i$ have been fixed but arbitrary. Hence, the convergence in finite-dimensional distributions of in Eq. (B.7) imply that the EPPFs converge. 

\[ \square \]

**Appendix C: Marginal processes of exponential CRMs**

The marginal process characterization describes the probabilistic model not through the two-stage sampling $\Theta \sim \text{CRM}(H, \nu)$ and $X_n \mid \Theta \sim \text{LP}(\ell; \Theta)$, but through the conditional distributions $X_n \mid X_{n-1}, X_{n-2}, \ldots, X_1$ i.e. the underlying $\Theta$ has been marginalized out. This perspective removes the need to infer a countably infinite set of target variables. In addition, the exchangeability between $X_1, X_2, \ldots, X_N$ i.e. the joint distribution’s invariance with respect to ordering of observations (Aldous, 1985), often enables the development of inference algorithms, namely Gibbs samplers.

Broderick, Wilson and Jordan (2018, Corollary 6.2) derive the conditional distributions $X_n \mid X_{n-1}, X_{n-2}, \ldots, X_1$ for general exponential family CRMs Eqs. (4) and (5).

**Proposition C.1** (Target’s marginal process (Broderick, Wilson and Jordan, 2018, Corollary 6.2)). For any $n$, $X_n \mid X_{n-1}, \ldots, X_1$ is a random measure with finite support.

1. Let $\{\zeta_i\}_{i=1}^{K_n-1}$ be the union of atom locations in $X_1, X_2, \ldots, X_{n-1}$. For $1 \leq m \leq n-1$, let $x_{m,i}$ be the atom size of $X_m$ at atom location $\zeta_i$. Denote $x_{n,i}$ to be the atom size of $X_n$ at atom location $\zeta_i$. The $x_{n,i}$’s are independent across $i$ and the p.m.f. of $x_{n,i}$ at $x$ is

\[
 h(x \mid x_{1:(n-1)}) = \frac{1 + \sum_{m=1}^{n-1} \phi(x_{m,i}) + \phi(x), \eta + \left(\sum_{m=1}^{n-1} t(x_{m,i}) + t(x)\right)}{Z \left(1 + \sum_{m=1}^{n-1} \phi(x_{m,i}), \eta + \left(\sum_{m=1}^{n-1} t(x_{m,i})\right)\right)},
\]

2. For each $x \in \mathbb{N}$, $X_n$ has $p_{n,x}$ atoms whose atom size is exactly $x$. The locations of each atom are iid $H$: as $H$ is diffuse, they are disjoint from the existing union of atoms $\{\zeta_i\}_{i=1}^{K_n-1}$. $p_{n,x}$ is Poisson-distributed, independently across $x$, with mean:

\[
 M_{n,x} = \frac{\gamma'(0)^{n-1} \kappa(x) Z \left(-1 + (n-1) \phi(0) + \phi(x), \eta + \left((n-1)t(0) + t(x)\right)\right)}{Z \left(1 + \sum_{m=1}^{n-1} \phi(x_{m,i}), \eta + \left(\sum_{m=1}^{n-1} t(x_{m,i})\right)\right)}.
\]

In Proposition C.2, we state a similar characterization of $Z_n \mid Z_{n-1}, Z_{n-2}, \ldots, Z_1$ for the finite-dimensional model in Eq. (10) and give the proof.

**Proposition C.2** (Approximation’s marginal process). For any $n$, $Z_n \mid Z_{n-1}, \ldots, Z_1$ is a random measure with finite support.

1. Let $\{\zeta_i\}_{i=1}^{K_n-1}$ be the union of atom locations in $Z_1, Z_2, \ldots, Z_{n-1}$. For $1 \leq m \leq n-1$, let $z_{m,j}$ be the atom size of $Z_m$ at atom location $\zeta_j$. Denote $z_{n,i}$ to be the atom size of $Z_n$.
at atom location $\zeta_i$, $z_{n,i}$'s are independently across $i$ and the p.m.f. of $z_{n,i}$ at $x$ is:

$$
\tilde{h}(x \mid z_{1:(n-1)}) = \frac{Z}{\kappa(x)} \left( \frac{c/K - 1 + \sum_{m=1}^{n-1} \phi(z_{m,i}) + \phi(x), \eta + \left( \frac{\sum_{m=1}^{n-1} t(z_{m,i}) + t(x)}{n} \right)}{Z \left( c/K - 1 + \sum_{m=1}^{n-1} \phi(z_{m,i}), \eta + \left( \frac{\sum_{m=1}^{n-1} t(z_{m,i})}{n-1} \right) \right)} \right).
$$

2. $K - K_{n-1}$ atom locations are generated iid from $H$. $Z_n$ has $p_{n,x}$ atoms whose size is exactly $x$ (for $x \in \mathbb{N} \cup \{0\}$) over these $K - K_{n-1}$ atom locations (the $p_{n,0}$ atoms whose atom size is 0 can be interpreted as not present in $Z_n$). The joint distribution of $p_{n,x}$ is a multinomial with $K - K_{n-1}$ trials, with success of type $x$ having probability:

$$
\tilde{h}(x \mid z_{1:(n-1)} = 0_{n-1}) = \frac{Z}{\kappa(x)} \left( \frac{c/K - 1 + (n-1)\phi(0) + \phi(x), \eta + \left( \frac{(n-1)t(0) + t(x)}{n-1} \right)}{Z \left( c/K - 1 + (n-1)\phi(0), \eta + \left( \frac{(n-1)t(0)}{n-1} \right) \right)} \right).
$$

Proof of Proposition C.2. We only need to prove the conditional distributions for the atom sizes; that the $K$ distinct atom locations are generated iid from the base measure is clear.

First we consider $n = 1$. By construction in Corollary 3.3, a priori, the trait frequencies $\{\tau_i\}_{i=1}^K$ are independent, each following the distribution:

$$
\mathbb{P}(\tau_i \in d\theta) = \frac{1\{\theta \in U\}}{Z(c/K - 1, \eta)} \theta^{c/K - 1} \exp \left( - \eta \left( \frac{\mu(\theta)}{A(\theta)} \right) \right).
$$

Conditioned on $\{\tau_i\}_{i=1}^K$, the atom sizes $z_{1,i}$ that $Z_1$ puts on the $i$-th atom location are independent across $i$ and each is distributed as:

$$
\mathbb{P}(z_{1,i} = x \mid \tau_i) = \kappa(x) \phi(x) \exp \left( (\mu(\tau_i), t(x)) - A(\tau_i) \right).
$$

Integrating out $\tau_i$, the marginal distribution for $z_{1,i}$ is:

$$
\mathbb{P}(z_{1,i} = x) = \int \mathbb{P}(z_{1,i} = x \mid \tau_i = \theta) \mathbb{P}(\tau_i \in d\theta) = \frac{\kappa(x)}{Z(c/K - 1, \eta)} \int_U \theta^{c/K - 1 + \phi(x)} \exp \left( - \eta \left( \frac{t(x)}{1} + \left( \frac{\mu(\theta)}{A(\theta)} \right) \right) \right) d\theta
$$

$$
= \frac{\kappa(x)}{Z(c/K - 1, \eta)} \left( c/K - 1 + \phi(x), \eta + \left( \frac{t(x)}{1} \right) \right).
$$

by definition of $Z$ as the normalizer Eq. (6).

Now we consider $n \geq 2$. The distribution of $z_{n,\cdot}$ only depends on the distribution of $z_{n-1,\cdot}$, $z_{n-2,\cdot}, \ldots, z_{1,\cdot}$, since the atom sizes across different atoms are independent of each other both a priori and a posteriori. The predictive distribution is an integral:

$$
\mathbb{P}(z_{n,i} = x \mid z_{1:(n-1),i}) = \int \mathbb{P}(z_{n,i} = x \mid \tau_i) \mathbb{P}(\tau_i \in d\theta \mid z_{1:(n-1),i}).
$$
Because the prior over \( \tau_i \) is conjugate for the likelihood \( z_{i,j} \mid \tau_i \), and the observations \( z_{i,j} \) are conditionally independent given \( \tau_i \), the posterior \( \mathbb{P}(\tau_i \in d\theta \mid z_{1:(n-1),i}) \) is in the same exponential family but with different natural parameters:

\[
\theta^{c/K - 1 + \sum_{m=1}^{n-1} \phi(z_{m,i})} \exp \left( \eta + \left( \sum_{m=1}^{n-1} \frac{t(z_{m,i})}{n} \right) \left( \begin{bmatrix} \mu(\theta) \\ -A(\theta) \end{bmatrix} \right) \right) \frac{1}{Z(c/K - 1 + \sum_{m=1}^{n-1} \phi(z_{m,i}), \eta + \left( \sum_{m=1}^{n-1} \frac{t(z_{m,i})}{n} \right))} d\theta.
\]

This means that the predictive distribution \( \mathbb{P}(z_{n,i} = x \mid z_{1:(n-1),i}) \) equals:

\[
\int_U \theta^{c/K - 1 + \sum_{m=1}^{n-1} \phi(z_{m,i}) + \phi(x)} \exp \left( \eta + \left( \sum_{m=1}^{n-1} \frac{t(z_{m,i}) + t(x)}{n} \right) \left( \begin{bmatrix} \mu(\theta) \\ -A(\theta) \end{bmatrix} \right) \right) \frac{1}{Z(c/K - 1 + \sum_{m=1}^{n-1} \phi(z_{m,i}), \eta + \left( \sum_{m=1}^{n-1} \frac{t(z_{m,i}) + t(x)}{n} \right))} d\theta
\]

\[
= \kappa(x) \frac{Z(c/K - 1 + \sum_{m=1}^{n-1} \phi(z_{m,i}) + \phi(x), \eta + \left( \sum_{m=1}^{n-1} \frac{t(z_{m,i}) + t(x)}{n} \right))}{Z(c/K - 1 + \sum_{m=1}^{n-1} \phi(z_{m,i}), \eta + \left( \sum_{m=1}^{n-1} \frac{t(z_{m,i})}{n} \right))}.
\]

The predictive distribution \( \mathbb{P}(z_{n,i} = x \mid z_{1:(n-1),i}) \) govern both the distribution of atom sizes for known atom locations and new atom locations. \( \square \)

Appendix D: Technical lemmas

D.1. Concentration

**Lemma D.1** (Modified upper tail Chernoff bound). Let \( X = \sum_{i=1}^{n} X_i \), where \( X_i = 1 \) with probability \( p_i \) and \( X_i = 0 \) with probability \( 1 - p_i \), and all \( X_i \) are independent. Let \( \mu \) be an upper bound on \( E(X) = \sum_{i=1}^{n} p_i \). Then for all \( \delta > 0 \):

\[
\mathbb{P}(X \geq (1 + \delta)\mu) \leq \exp \left( -\frac{\delta^2}{2 + \delta} \mu \right).
\]

**Proof of Lemma D.1.** The proof relies on the regular upper tail Chernoff bound (Doerr and Neumann, 2019, Theorem 1.10.1) and an argument using stochastic domination. We pad the first \( n \) Poisson trials that define \( X \) with additional trials \( X_{n+1}, X_{n+2}, \ldots, X_{n+m} \). \( m \) is the smallest natural number such that \( \frac{\mu - E[X]}{m} \leq 1 \). Each \( X_{n+i} \) is a Bernoulli with probability \( \frac{\mu - E[X]}{m} \), and the trials are independent. Then \( Y = X + \sum_{j=1}^{m} X_{n+j} \) is itself the sum of Poisson trials with mean exactly \( \mu \), so the regular Chernoff bound applies:

\[
\mathbb{P}(Y \geq (1 + \delta)\mu) \leq \exp \left( -\frac{\delta^2}{2 + \delta} \mu \right),
\]

where we used (Doerr and Neumann, 2019, Equation 1.10.13) and the simple observation that \( 2/3\delta < \delta \). By construction, \( X \) is stochastically dominated by \( Y \), so the tail probabilities of \( X \) are upper bounded by the tail probabilities of \( Y \). \( \square \)
Lemma D.2 (Lower tail Chernoff bound (Doerr and Neumann, 2019, Theorem 1.10.5)). Let $X = \sum_{i=1}^{n} X_i$, where $X_i = 1$ with probability $p_i$ and $X_i = 0$ with probability $1 - p_i$, and all $X_i$ are independent. Let $\mu := E(X) = \sum_{i=1}^{n} p_i$. Then for all $\delta \in (0, 1)$:

$$ P(X \leq (1 - \delta)\mu) \leq \exp\left(-\mu\delta^2/2\right). $$

Lemma D.3 (Tail bounds for Poisson distribution). If $X \sim \text{Poisson}(\lambda)$ then for any $x > 0$:

$$ P(X \geq \lambda + x) \leq \exp\left(-\frac{x^2}{2(\lambda + x)} \psi\left(\frac{x}{\lambda}\right)\right), $$

and for any $0 < x < \lambda$:

$$ P(X \leq \lambda - x) \leq \exp\left(-\frac{x^2}{2\lambda}\right). $$

Proof of Lemma D.3. For $x \geq -1$, let $\psi(x) := 2((1 + x) \ln(1 + x) - x)/x^2$.

We first inspect the upper tail bound. If $X \sim \text{Poisson}(\lambda)$, for any $x > 0$, Pollard (2001, Exercise 3 p.272) implies that:

$$ P(X \geq \lambda + x) \leq \exp\left(-\frac{x^2}{2\lambda \psi\left(\frac{x}{\lambda}\right)}\right). $$

To show the upper tail bound, it suffices to prove that $\frac{x^2}{2\lambda \psi\left(\frac{x}{\lambda}\right)}$ is greater than $\frac{x^2}{2(\lambda + x)}$. In general, we show that for $u \geq 0$:

$$(u + 1)\psi(u) - 1 \geq 0. \quad (D.1)$$

The denominator of $(u + 1)\psi(u) - 1$ is clearly positive. Consider the numerator of $(u + 1)\psi(u) - 1$, which is $g(u) := 2((u + 1)^2 \ln(u + 1) - u(u + 1) - u^2$. Its 1st and 2nd derivatives are:

$$ g'(u) = 4(u + 1) \ln(u + 1) - 2u + 1, $$

$$ g''(u) = 4 \ln(u + 1) + 2. $$

Since $g''(u) \geq 0$, $g'(u)$ is monotone increasing. Since $g'(0) = 1$, $g'(u) > 0$ for $u \geq 0$, hence $g(u)$ is monotone increasing. Because $g(0) = 0$, we conclude that $g(u) \geq 0$ for $u > 0$ and Eq. (D.1) holds. Plugging in $u = x/\lambda$:

$$ \psi\left(\frac{x}{\lambda}\right) \geq \frac{1}{1 + \frac{x}{\lambda}} = \frac{\lambda}{x + \lambda}, $$

which shows $\frac{x^2}{2\lambda} \psi\left(\frac{x}{\lambda}\right) \geq \frac{x^2}{2(\lambda + x)}$.

Now we inspect the lower tail bound. We follow the proof of Canonne, Theorem 1. We first argue that:

$$ P(X \leq \lambda - x) \leq \exp\left(-\frac{x^2}{2\lambda \psi\left(-\frac{x}{\lambda}\right)}\right). \quad (D.2) $$

For any $\theta$, the moment generating function $E[\exp(\theta X)]$ is well-defined and well-known:

$$ E[\exp(\theta X)] := \exp(\lambda(\exp(\theta) - 1)). $$
Therefore:
\[
\mathbb{P}(X \leq \lambda - x) \leq P(\exp(\theta X) \leq \exp(\theta(\lambda - x))) \leq \mathbb{P}(\exp(\theta(\lambda - x - X)) \geq 1) \\
\leq \exp(\theta(\lambda - x))\mathbb{E}[\exp(-\theta X)],
\]
where we have used Markov’s inequality. We now aim to minimize \(\exp(\theta(\lambda - x))\mathbb{E}[\exp(-\theta X)]\) as a function of \(\theta\). Its logarithm is:
\[
\lambda(\exp(-\theta) - 1) + \theta(\lambda - x).
\]
This is a convex function, whose derivative vanishes at \(\theta = -\ln \left(1 - \frac{x}{\lambda}\right)\). Overall this means the best upper bound on \(P(X \leq \lambda - x)\) is:
\[
\exp \left( -\lambda \left( \frac{x}{\lambda} + (1 - \frac{x}{\lambda}) \ln(1 - \frac{x}{\lambda}) \right) \right),
\]
which is exactly the right hand side of Eq. (D.2). Hence to demonstrate the lower tail bound, it suffices to show that:
\[
\psi \left( -\frac{x}{\lambda} \right) \geq 1.
\]
More generally, we show that for \(-1 \leq u \leq 0\), \(\psi(u) - 1 \geq 0\). Consider the numerator of \(\psi(u) - 1\), which is \(h(u) := 2((1 + u) \ln(1 + u) - u) - u^2\). The first two derivatives are:
\[
h'(u) = 2(1 + \ln(1 + u)) - 2u \\
h''(u) = \frac{2}{1 + u} - 2
\]
Since \(h''(u) \geq 0\), \(h(u)\) is convex on \([-1, 0]\). Note that \(h(0) = 0\). Also, by simple continuity argument, \(h(-1) = 2\). Therefore, \(h\) is non-negative on \([0, 1]\), meaning that \(\psi(u) \geq 1\).  

**Lemma D.4** (Multinomial-Poisson approximation). Let \(\{p_i\}_{i=1}^{\infty}, p_i \geq 0, \sum_{i=1}^{\infty} p_i < 1\). Suppose there are \(n\) independent trials: in each trial, success of type \(i\) has probability \(p_i\). Let \(X = \{X_i\}_{i=1}^{\infty}\) be the number of type \(i\) successes after \(n\) trials. Let \(Y = \{Y_i\}_{i=1}^{\infty}\) be independent Poisson random variables, where \(Y_i\) has mean \(np_i\). Then, there exists a coupling \((\hat{X}, \hat{Y})\) of \(P_X\) and \(P_Y\) such that
\[
\mathbb{P}(\hat{X} \neq \hat{Y}) \leq n \left( \sum_{i=1}^{\infty} p_i \right)^2.
\]
Furthermore, the joint distribution \((\hat{X}, \hat{Y})\) naturally disintegrates i.e. the conditional distribution \(X | \hat{Y}\) exists.

**Proof of Lemma D.4.** First, we recognize that both \(X\) and \(Y\) can be sampled in two steps.

- Regarding \(X\), first sample \(N_1 \sim \text{Binom}(n, \sum_{i=1}^{\infty} p_i)\). Then, for each \(1 \leq k \neq N_1\), independently sample \(Z_k\) where \(P(Z_k = i) = \frac{p_i}{\sum_{j=1}^{\infty} p_j}\). Then, \(X_i = \sum_{k=1}^{N_1} 1\{Z_k = i\}\) for each \(i\).

- Regarding \(Y\), first sample \(N_2 \sim \text{Poisson}(n \sum_{i=1}^{\infty} p_i)\). Then, for each \(1 \leq k \leq N_2\), independently sample \(T_k\) where \(P(T_k = i) = \frac{p_i}{\sum_{j=1}^{\infty} p_j}\). Then, \(Y_i = \sum_{k=1}^{N_2} 1\{T_k = i\}\) for each \(i\).
The two-step sampling perspective for $X$ comes from rejection sampling: to generate a success of type $k$, we first generate some type of success, and then re-calibrate to get the right proportion for type $k$. The two-step perspective for $Y$ comes from the thinning property of Poisson distribution (Last and Penrose, 2017, Exercise 1.5). The thinning property implies that for any finite index set $K$, all $\{Y_i\}$ for $i \in K$ are mutually independent and marginally, $Y_i \sim \text{Poisson}(np_i)$. Hence the whole collection $\{Y_i\}_{i=1}^{\infty}$ are independent Poissons and the mean of $Y_1$ is $np_1$.

Observing that the conditional $X \mid N_1 = n$ is the same as $Y \mid N_2 = n$, we propose the coupling that essentially proves propagation rule Lemma D.8. The proposed coupling $(\hat{X}, \hat{Y})$ is that

- Sample $(\hat{N}_1, \hat{N}_2)$ from the maximal coupling that attains $d_{TV}$ between $\text{Binom}(n, \sum_{i=1}^{\infty} p_i)$ and Poisson $(n \sum_{i=1}^{\infty} p_i)$.
- If $\hat{N}_1 = \hat{N}_2$, let the common value be $n$, sample $\hat{X} \mid \hat{N}_1 = n$ and set $\hat{Y} = \hat{X}$. Else $\hat{N}_1 \neq \hat{N}_2$, independently sample $\hat{X} \mid \hat{N}_1$ and $\hat{Y} \mid \hat{N}_2$.

From the classic binomial-Poisson approximation (Le Cam, 1960), we know that

$$\mathbb{P}(\hat{N}_1 \neq \hat{N}_2) = d_{TV}(P_{N_1}, P_{N_2}) \leq n \left( \sum_{i=1}^{\infty} p_i \right)^2,$$

which guarantees that

$$\mathbb{P}(\hat{X} \neq \hat{Y}) \leq n \left( \sum_{i=1}^{\infty} p_i \right)^2.$$

Alternatively, we can sample from the conditional $\hat{X} \mid \hat{Y}$ in the following way. From $\hat{Y}$, compute $\hat{N}_2$, which is just $\sum_{x=1}^{\infty} \hat{Y}_i$. Sample $\hat{N}_1$ from the conditional distribution $\hat{N}_1 \mid \hat{N}_2$ of the maximal coupling that attains the binomial-Poisson total variation. If $\hat{N}_1 = \hat{N}_2$, set $\hat{X} = \hat{Y}$. Else sample $\hat{X}$ from the conditional $\hat{X} \mid \hat{N}_1$. It is straightforward to verify that this is the conditional $\hat{X} \mid \hat{Y}$ of the joint $(\hat{X}, \hat{Y})$ described above.

\[ \square \]

**Lemma D.5** (Total variation between Poissons (Adell and Lekuona, 2005, Corollary 3.1)). Let $P_1$ be the Poisson distribution with mean $s$, $P_2$ the Poisson distribution with mean $t$. Then:

$$d_{TV}(P_1, P_2) \leq 1 - \exp(-|s - t|) \leq |s - t|.$$

### D.2. Total variation

We will frequently use the following relationship between total variation and coupling. For two distributions $P_X$ and $P_Y$ over the same measurable space, it is well-known that the total variation distance between $P_X$ and $P_Y$ is at most the infimum over joint distributions $(\hat{X}, \hat{Y})$ which are couplings of $P_X$ and $P_Y$:

$$d_{TV}(P_X, P_Y) \leq \inf_{\hat{X}, \hat{Y} \text{ coupling of } P_X, P_Y} \mathbb{P}(\hat{X} \neq \hat{Y}).$$

When $P_X$ and $P_Y$ are discrete distributions, the inequality is actual equality, and there exists couplings that attain the equality (Levin and Peres, 2017, Proposition 4.7).

We first state the chain rule, which will be applied to compare joint distributions that admit densities.
Lemma D.6 (Chain rule). Suppose $P_{X_1,Y_1}$ and $P_{X_2,Y_2}$ are two distributions that have densities with respect to a common measure over the ground space $\mathcal{A} \times \mathcal{B}$. Then:

$$d_{TV}(P_{X_1,Y_1}, P_{X_2,Y_2}) \leq d_{TV}(P_{X_1}, P_{X_2}) + \sup_{a \in \mathcal{A}} d_{TV}(P_{Y_1|X_1=a}, P_{Y_2|X_2=a}).$$

Proof of Lemma D.6. Because both $P_{X_1,Y_1}$ and $P_{X_2,Y_2}$ have densities, total variation distance is half of $L_1$ distance between the densities:

$$d_{TV}(P_{X_1,Y_1}, P_{X_2,Y_2}) = \frac{1}{2} \int_{\mathcal{A} \times \mathcal{B}} |P_{X_1,Y_1}(a,b) - P_{X_2,Y_2}(a,b)|\,dadb$$

$$= \frac{1}{2} \int_{\mathcal{A} \times \mathcal{B}} |P_{X_1,Y_1}(a,b) - P_{X_2,a}(a)P_{Y_1|X_1=b}(a) + P_{X_2,a}P_{Y_1|X_1=a} - P_{X_2,Y_2}(a,b)|\,dadb$$

$$\leq \frac{1}{2} \int_{\mathcal{A} \times \mathcal{B}} (P_{Y_1|X_1=b}(a) - P_{X_2,a}(a) | + P_{X_2,a} | P_{Y_1|X_1=a} - P_{X_2,a}X_2(b|a))\,dadb$$

$$= \frac{1}{2} \int_{\mathcal{A} \times \mathcal{B}} P_{Y_1|X_1=b}(a) | P_{X_1,a} - P_{X_2,a} | dadb + \frac{1}{2} \int_{\mathcal{A} \times \mathcal{B}} P_{X_2,a} | P_{Y_1|X_1=a} - P_{X_2,a}X_2(b|a)|dadb,$$

where we have used triangle inequality. Regarding the first term, using Fubini:

$$\frac{1}{2} \int_{\mathcal{A} \times \mathcal{B}} P_{Y_1|X_1=b}(a) | P_{X_1,a} - P_{X_2,a} | dadb$$

$$= \frac{1}{2} \int_{\mathcal{A}} \left( \int_{\mathcal{B}} P_{Y_1|X_1=b}(a) \, db \right) | P_{X_1,a} - P_{X_2,a} | \, da$$

$$= \frac{1}{2} \int_{\mathcal{A}} | P_{X_1,a} - P_{X_2,a} | \, da$$

$$= d_{TV}(P_{X_1}, P_{X_2}).$$

Regarding the second term:

$$\frac{1}{2} \int_{\mathcal{A} \times \mathcal{B}} P_{X_2,a} | P_{Y_1|X_1=a} - P_{Y_2|X_2=a} | dadb$$

$$= \int_{\mathcal{A}} \frac{1}{2} \int_{\mathcal{B}} | P_{Y_1|X_1=a} - P_{Y_2|X_2=a} | \, db \, P_{X_2,a} \, da$$

$$\leq \left( \sup_{a \in \mathcal{A}} d_{TV}(P_{Y_1|X_1=a}, P_{Y_2|X_2=a}) \right) \int_{\mathcal{A}} P_{X_2,a} \, da$$

$$= \sup_{a \in \mathcal{A}} d_{TV}(P_{Y_1|X_1=a}, P_{Y_2|X_2=a}).$$

The sum between the first and second upper bound gives the total variation chain rule. □

An important consequence of Lemma D.6 is when the distributions being compared have natural independence structures.

Lemma D.7 (Product rule). Let $P_{X_1,Y_1}$ and $P_{X_2,Y_2}$ be discrete distributions. In addition, suppose $P_{X_1,Y_1}$ factorizes into $P_{X_1}P_{Y_1}$ and similarly $P_{X_2,Y_2} = P_{X_2}P_{Y_2}$. Then:

$$d_{TV}(P_{X_1,Y_1}, P_{X_2,Y_2}) \leq d_{TV}(P_{X_1}, P_{X_2}) + d_{TV}(P_{Y_1}, P_{Y_2}).$$
Proof of Lemma D.7. Since $P_{X_1,Y_1}$ and $P_{X_2,Y_2}$ are discrete distributions, we can apply Lemma D.6 (the common measure is the counting measure). Because each joint distribution $P_{X_1,Y_1}$ factorizes into $P_X, P_Y$, for any $a \in \mathcal{A}$, the right most term in the inequality of Lemma D.6 simplifies into

$$\sup_{a \in \mathcal{A}} d_{TV}(P_{Y_1 \mid X_1 = a}, P_{Y_2 \mid X_2 = a}) = d_{TV}(P_{Y_1}, P_{Y_2}),$$

since $P_{Y_1} = P_{Y_1 \mid X_1 = a}$ and $P_{Y_2} = P_{Y_2 \mid X_2 = a}$ for any $a$. \hfill \square

We call the next lemma the propagation rule, which applies even if distributions do not have densities.

**Lemma D.8** (Propagation rule). Suppose $P_{X_1,Y_1}$ and $P_{X_2,Y_2}$ are two distributions over the same measurable space. Suppose that the conditional $Y_2 \mid X_2 = a$ is the same as the conditional $Y_1 \mid X_1 = a$, which we just denote as $Y \mid X = a$. Then:

$$d_{TV}(P_{Y_1}, P_{Y_2}) \leq \inf_{\tilde{X}_1, \tilde{X}_2 \text{ coupling of } P_{X_1, P_{X_2}}} \mathbb{P}(\tilde{X}_1 \neq \tilde{X}_2).$$

If $P_{X_1}$ and $P_{X_2}$ are discrete distributions, we also have:

$$d_{TV}(P_{Y_1}, P_{Y_2}) \leq d_{TV}(P_{X_1}, P_{X_2}).$$

Proof of Lemma D.8. Let $(\tilde{X}_1, \tilde{X}_2)$ be any coupling of $P_{X_1}$ and $P_{X_2}$. The following two-step process generates a coupling of $P_{Y_1}$ and $P_{Y_2}$:

- Sample $(\tilde{X}_1, \tilde{X}_2)$.
- If $\tilde{X}_1 = \tilde{X}_2$, let the common value be $x$. Sample $\tilde{Y}_1$ from the conditional distribution $Y \mid X = x$, and set $\tilde{Y}_2 = \tilde{Y}_1$. Else if $\tilde{X}_1 \neq \tilde{X}_2$, independently sample $\tilde{Y}_1$ from $Y \mid X = \tilde{X}_1$ and $\tilde{Y}_2$ from $Y \mid X = \tilde{X}_2$.

It is easy to verify that the tuple $(\tilde{Y}_1, \tilde{Y}_2)$ is a coupling of $P_{Y_1}$ and $P_{Y_2}$. In addition, $(\tilde{Y}_1, \tilde{Y}_2)$ has the property that

$$\mathbb{P}(\tilde{Y}_1 \neq \tilde{Y}_2, \tilde{X}_1 = \tilde{X}_2) = 0,$$

since conditioned on $\tilde{X}_1 = \tilde{X}_2$, the values of $\tilde{Y}_1$ and $\tilde{Y}_2$ always agree. Therefore:

$$\mathbb{P}(\tilde{Y}_1 \neq \tilde{Y}_2) = \mathbb{P}(\tilde{Y}_1 \neq \tilde{Y}_2, \tilde{X}_1 \neq \tilde{X}_2) \leq \mathbb{P}(\tilde{X}_1 \neq \tilde{X}_2).$$

This means that $d_{TV}(P_{Y_1}, P_{Y_2})$ is small:

$$d_{TV}(P_{Y_1}, P_{Y_2}) \leq \mathbb{P}(\tilde{X}_1 \neq \tilde{X}_2).$$

So far $(\tilde{X}_1, \tilde{X}_2)$ has been an arbitrary coupling between $P_{X_1}$ and $P_{X_2}$. The final step is taking the infimum on the right hand side over couplings. When $P_{X_1}$ and $P_{X_2}$ are discrete distributions, the infimum over couplings is equal to the total variation distance. \hfill \square

The final lemma is the reduction rule, which says that the a larger collection of random variables, in general, has larger total variation distance than a smaller one.

**Lemma D.9** (Reduction rule). Suppose $P_{X_1,Y_1}$ and $P_{X_2,Y_2}$ are two distributions over the same measurable space $\mathcal{A} \times \mathcal{B}$. Then:

$$d_{TV}(P_{X_1,Y_1}, P_{X_2,Y_2}) \geq d_{TV}(P_{X_1}, P_{X_2}).$$
Proof of Lemma D.9. By definition,
\[ d_{TV}(P_X, P_Y) = \sup_{\text{measurable } A} |P_X(A) - P_Y(A)|. \]

For any measurable \( A \), the product \( A \times B \) is also measurable. In addition:
\[ P_X(A) - P_Y(A) = P_{X,Y}(A,B) - P_{X',Y'}(A,B). \]

Therefore, for any \( A \),
\[ |P_X(A) - P_Y(A)| \leq d_{TV}(P_{X,Y}, P_{X',Y'}), \]

since \( P_{X,Y}(A,B) - P_{X',Y'}(A,B) \) is the difference in probability mass for one measurable event. The final step is taking supremum of the left hand side. \( \square \)

D.3. Miscellaneous

Lemma D.10 (Order of growth of harmonic-like sums).
\[ \sum_{n=1}^{N} \frac{\alpha}{n - 1 + \alpha} \geq \alpha(\ln N - \psi(\alpha) - 1). \]

where \( \psi \) is the digamma function.

Proof of Lemma D.10. Because of the digamma function identity \( \psi(z + 1) = \psi(z) + 1/z \) for \( z > 0 \), we have:
\[ \sum_{n=1}^{N} \frac{\alpha}{n - 1 + \alpha} = \alpha[\psi(\alpha + N) - \psi(\alpha)]. \]

Gordon (1994, Theorem 5) says that
\[ \psi(\alpha + N) \geq \ln(\alpha + N) - \frac{1}{2(\alpha + N)} - \frac{1}{12(\alpha + N)^2} \geq \ln N - 1. \]

\( \square \)

We list a collection of technical lemmas that are used when verifying Condition 1 for the recurring examples.

The first set assists in the beta–Bernoulli model.

• For \( \alpha > 0 \) and \( i = 1, 2, 3, \ldots \):
\[ \frac{1}{i + \alpha - 1} \leq 2 \left( \frac{1}{2 \alpha} \mathbf{1}\{i = 1\} + \frac{1}{i} \mathbf{1}\{i > 1\} \right). \] (D.3)

• For \( m, x, y > 0, m \leq y \):
\[ \frac{m + x - m}{y + x - y} \leq \frac{x}{y}. \] (D.4)

Proof of Eq. (D.3). If \( i = 1 \), \( \frac{1}{i + \alpha - 1} = \frac{1}{\alpha} \). If \( i \geq 1 \), \( \frac{1}{i + \alpha - 1} \leq \frac{1}{i - 1} \leq \frac{2}{i}. \) \( \square \)
Proof of Eq. (D.4).

\[
\begin{align*}
|m+x|^{\frac{m}{y}} |y+x|^{-m} &= \left| \frac{(m+x)y-m(y+x)}{y(y+x)} \right| = \left| \frac{x(y-m)}{y(y+x)} \right| \leq \frac{x}{y}.
\end{align*}
\]

The second set aid in the gamma–Poisson model.

- For \( x \in [0,1) \):
  
  \[(1-x) \ln(1-x) + x \geq 0. \tag{D.5}\]

- For \( x \in (0,1) \), for \( p \geq 0 \):
  
  \[(1-x)^p + p \frac{x}{1-x} \geq 1. \tag{D.6}\]

- For \( \lambda > 0 \), for \( m > 0, t > 1, x > 0 \):
  
  \[
d_{TV}(\text{NB}(m,t^{-1}),\text{NB}(m+x,t^{-1})) \leq x \frac{1/t}{1-1/t}, \tag{D.7}\]

  where \( \text{NB}(r, \theta) \) is the negative binomial distribution.

- For \( y \in \mathbb{N}, K > m > 0 \):
  
  \[
  \left| \frac{m}{y} - K \Gamma(m/K + y) \frac{1}{\Gamma(m/K)y!} \right| \leq e \frac{m^2}{K}. \tag{D.8}\]

  where \( e \) is the Euler constant and \( \Gamma(y) \) is the gamma function.

Proof of Eq. (D.5). Set \( g(x) \) to \((1-x) \ln(1-x) + x \). Then its derivative is \( g'(x) = -\ln(1-x) \geq 0 \), meaning the function is monotone increasing. Since \( g(0) = 0 \), it’s true that \( g(x) \geq 0 \) over \([0,1)\).

Proof of Eq. (D.6). Let \( f(p) = (1-x)^p + p \frac{x}{1-x} - 1 \). Then \( f'(p) = \ln(1-x)(1-x)^p + \frac{x}{1-x} \). Also \( f''(p) = (\ln(1-x))^2(1-x)^p > 0 \). So \( f'(p) \) is monotone increasing. At \( p = 0 \), \( f'(0) = \ln(1-x) + \frac{x}{1-x} \geq 0 \). Therefore \( f'(p) \geq 0 \) for all \( p \). So \( f(p) \) is increasing. Since \( f(0) = 0 \), it’s true that \( f(p) \geq 0 \) for all \( p \).

Proof of Eq. (D.7). It is known that \( \text{NB}(r, \theta) \) is a Poisson stopped sum distribution (Johnson, Kemp and Kotz, 2005, Equation 5.15):

- \( N \sim \text{Poisson}(-r \ln(1-\theta)). \)
- \( Y_i \sim \text{Log}(\theta) \) where the Log(\theta) distribution’s pmf at \( k \) equals \( \frac{-\theta^k}{k \ln(1-\theta)} \).
- \( \sum_{i=1}^N Y_i \sim \text{NB}(r, \theta). \)

Therefore, by the propagation rule Lemma D.8, to compare \( \text{NB}(m,t^{-1}) \) with \( \text{NB}(m+x,t^{-1}) \), it suffices to compare the two generating Poissons.

\[
d_{TV}(\text{NB}(m,t^{-1}),\text{NB}(m+x,t^{-1})) \\
\leq d_{TV}(\text{Poisson}(-m \ln(1-t^{-1}),\text{Poisson}(-(m+x) \ln(1-t^{-1}))) \\
\leq -\ln(1-t^{-1})x \leq x \frac{t^{-1}}{1-t^{-1}}.
\]

We have used the fact that total variation distance between Poissons is dominated by their different in means Lemma D.5 and Eq. (D.5).
Proof of Eq. (D.8). Since $\Gamma\left(\frac{m}{K} + y\right) = \left(\prod_{j=0}^{y-1}\left(\frac{m}{K} + j\right)\right) \Gamma\left(\frac{m}{K}\right) = \Gamma\left(\frac{m}{K}\right) \prod_{j=1}^{y-1}\frac{m}{K} + j$, we have:

$$\left|\frac{m}{y} - K \frac{\Gamma(m/K + y)}{\Gamma(m/K) y!}\right| = \frac{m}{y} \left(\prod_{j=1}^{y-1} \frac{m/K + j}{j} - 1\right).$$

We inspect the product in more detail.

$$\prod_{j=1}^{y-1} \frac{m/K + j}{j} = \prod_{j=1}^{y-1} \left(1 + \frac{m/K}{j}\right) \leq \prod_{j=1}^{y-1} \exp\left(\frac{m/K}{j}\right)$$

$$= \exp\left(\frac{m}{K} \sum_{j=1}^{y-1} \frac{1}{j}\right) \leq \exp\left(\frac{m}{K} (\ln y + 1)\right) = (ey)^{m/K}.$$

where the $(y-1)$-th Harmonic sum is bounded by $\ln y + 1$. Therefore

$$\left|\frac{m}{y} - K \frac{\Gamma(m/K + y)}{\Gamma(m/K) y!}\right| \leq \frac{m}{y} \left((ey)^{m/K} - 1\right).$$

We quickly prove that for any $u \geq 1, 0 < a < 1$, we have

$$u^a - 1 \leq a(u - 1).$$

Truly, consider the function $g(u) = a(u - 1) - u^a + 1$. The derivative is $g'(u) = a - au^{a-1} = a(1 - u^{a-1})$. Since $a \in (0, 1)$ and $u \geq 1$, $g'(u) > 0$. Therefore $g(u)$ is monotone increasing. Since $g(1) = 0$, we have reached the conclusion. Applying to our situation:

$$(ey)^{m/K} - 1 \leq \frac{m}{K} (ey - 1).$$

In all:

$$\left|\frac{m}{y} - K \frac{\Gamma(m/K + y)}{\Gamma(m/K) y!}\right| \leq \frac{m^2}{K}.$$

The third set aid in the beta–negative binomial model.

- For $x > 0, z \geq y > 1$:

$$B(x, y) - B(x, z) \leq (z - y)B(x + 1, y - 0.5) \leq (z - y)B(x + 1, y - 1). \quad (D.9)$$

- For any $r > 0, b \geq 1$:

$$\sum_{y=1}^{\infty} \frac{\Gamma(y + r)}{y! \Gamma(r)} B(y, b + r) \leq \frac{r}{b - 0.5}. \quad (D.10)$$

- For $b \geq 1$, for any $c > 0$, for any $K \geq c$:

$$\left|1 - \frac{\Gamma(b)}{\Gamma(b + c/K)}\right| \leq \frac{c}{K} (2 + \ln b). \quad (D.11)$$
• For $b > 1, c > 0, K \geq 2c(\ln b + 2)$:

$$
|c - \frac{K}{B(c/K, b)}| \leq \frac{c}{K}(3\ln b + 8).
$$

(D.12)

Proof of Eq. (D.9). First we prove that for any $x \in [0, 1)$:

$$
\sqrt{1-x}\ln(1-x) + x \geq 0.
$$

Truly, let $g(x)$ be the function on the left hand side. Then its derivative is

$$
g'(x) = \frac{2\sqrt{1-x} - \ln(1-x) - 2}{2\sqrt{1-x}}.
$$

Denote the numerator function by $h(x)$. Its derivative is

$$
h'(x) = \frac{1}{1-x} - \frac{1}{\sqrt{1-x}} \geq 0,
$$

since $x \in [0, 1]$ meaning $h$ is monotone increasing. Since $h(0) = 0$, it means $h(x) \geq 0$. This means $g'(x) \geq 0$ i.e. $g$ itself is monotone increasing. Since $g(0) = 0$ it’s true that $g(x) \geq 0$ for all $x \in [0, 1)$.

Second we prove that for all $x \in [0, 1]$, for all $p \geq 0$:

$$
(1-x)^p + p\frac{x}{\sqrt{1-x}} - 1 \geq 0.
$$

(D.13)

Truly, let $f(p) = (1-x)^p + p\frac{x}{\sqrt{1-x}} - 1$. Then $f'(p) = \ln(1-x)(1-x)^p + \frac{x}{\sqrt{1-x}}$. Also $f''(p) = (\ln(1-x))^2(1-x)^p > 0$. So $f'(p)$ is monotone increasing. At $p = 0$, $f'(0) = \ln(1-x) + \frac{x}{\sqrt{1-x}} > 0$. Therefore $f'(p) \geq 0$ for all $p$. So $f(p)$ is increasing. Since $f(0) = 0$, it’s true that $f(p) \geq 0$ for all $p$.

We finally prove the inequality about beta functions.

$$
B(x, y) - B(x, z) = \int_0^1 \theta^{x-1}(1-\theta)^{y-1}(1-(1-\theta)^{z-y})d\theta
\leq \int_0^1 \theta^{x-1}(1-\theta)^{y-1}(z-y)\theta(1-\theta)^{-0.5}d\theta
= (z-y)\int_0^1 \theta^x(1-\theta)^{y-1.5}d\theta = (z-y)B(x+1, y-0.5).
$$

where we have use $1-(1-\theta)^{z-y} \leq (z-y)\theta(1-\theta)^{-1/2}$ from Eq. (D.13). As for $B(x+1, y-0.5) \leq B(x+1, y-1)$, it is because of the monotonicity of the beta function.

Proof of Eq. (D.10):

$$
\sum_{y=1}^{\infty} \frac{\Gamma(y+r)}{y!\Gamma(r)} B(y, b+r) = \int_0^1 \sum_{y=1}^{\infty} \frac{\Gamma(y+r)}{y!\Gamma(r)} \theta^{y-1}(1-\theta)^{b+r-1}d\theta
= \int_0^1 \theta^{-1} \left( \sum_{y=1}^{\infty} \frac{\Gamma(y+r)}{y!\Gamma(r)} \theta^y \right) (1-\theta)^{b+r-1}d\theta
$$
\[
\int_0^1 \left( \theta^{-1} \left( \frac{1}{(1-\theta)^r} - 1 \right) \right) (1-\theta)^{b+r-1} d\theta
\]
\[
= \int_0^1 \left( \theta^{-1} (1-\theta)^r \right) (1-\theta)^{b-1} d\theta
\]
\[
\leq \int_0^1 \theta^{-1} r \frac{\theta}{\sqrt{1-\theta}} (1-\theta)^{b-1} d\theta
\]
\[
= r \int_0^1 (1-\theta)^{b-1.5} d\theta = \frac{r b}{b-0.5},
\]
where the identity \( \sum_{y=1}^{\infty} \frac{\Gamma(y+r)}{y! \Gamma(y)} \theta^y = \frac{1}{(1-\theta)^r} - 1 \) is due to the normalization constant for negative binomial distributions, and we also used Eq. (D.13) on \( 1-(1-\theta)^r \).

**Proof of Eq. (D.11).** First we prove that:

\[
1 - \frac{\Gamma(b)}{\Gamma(b+c/K)} \leq \frac{c}{K}(2 + \ln b).
\]

The recursion defining \( \Gamma(b) \) allows us to write:

\[
1 - \frac{\Gamma(b)}{\Gamma(b+c/K)} = 1 - \left( \prod_{i=1}^{b-1} \frac{b-i}{b+c/K-i} \right) \frac{\Gamma(b-|b|+1)}{\Gamma(b+c/K-|b|+1)}.
\]

The argument proceeds in one of two ways. If \( \frac{\Gamma(b-|b|+1)}{\Gamma(b+c/K-|b|+1)} \geq 1 \), then we have:

\[
1 - \frac{\Gamma(b)}{\Gamma(b+c/K)} \leq 1 - \prod_{i=1}^{b-1} \frac{b-i}{b+c/K-i}
\]
\[
= \left( 1 - \frac{b-1}{b+c/K-1} \right) + \frac{b-1}{b+c/K-1} - \left( \prod_{i=1}^{b-1} \frac{b-i}{b+c/K-i} \right)
\]
\[
= \frac{c}{K} \frac{1}{b+c/K-1} + \frac{b-1}{b+c/K-1} \left( 1 - \prod_{i=2}^{b-1} \frac{b-i}{b+c/K-i} \right)
\]
\[
\leq \frac{c}{K} \frac{1}{b-1} + \frac{1}{b+c/K-1} \left( 1 - \prod_{i=2}^{b-1} \frac{b-i}{b+c/K-i} \right)
\]
\[
\leq ... \leq \frac{c}{K} \sum_{i=1}^{b-1} \frac{1}{b-i} \leq \frac{c}{K} (\ln b + 1).
\]

Else, \( \frac{\Gamma(b-|b|+1)}{\Gamma(b+c/K-|b|+1)} < 1 \) and we write:

\[
1 - \frac{\Gamma(b)}{\Gamma(b+c/K)}
\]
\[
= 1 - \frac{\Gamma(b-|b|+1)}{\Gamma(b+c/K-|b|+1)} + \frac{\Gamma(b-|b|+1)}{\Gamma(b+c/K-|b|+1)} \left( 1 - \prod_{i=1}^{b-1} \frac{b-i}{b+c/K-i} \right)
\]
\[
\leq \left(1 - \frac{\Gamma(b - |b| + 1)}{\Gamma(b + c/K - |b| + 1)}\right) + \frac{c}{K}(\ln b + 1).
\]

We now argue that for all \(x \in [1, 2)\), for all \(K \geq c\), \(1 - \frac{\Gamma'(x)}{\Gamma(x + c/K)} \leq \frac{c}{K}\). By convexity of \(\Gamma(x)\), we know that \(\Gamma(x) \geq \Gamma(x + c/K) - \frac{c}{K} \Gamma'(x + c/K)\). Hence \(\frac{\Gamma(x)}{\Gamma(x + c/K)} \geq 1 - \frac{c}{K} \frac{\Gamma'(x + c/K)}{\Gamma(x + c/K)}\). Since \(x + c/K \in [1, 3)\) and \(\psi(y) = \frac{\Gamma'(y)}{\Gamma(y)}\), the digamma function, is a monotone increasing function (it is the derivative of a \(\ln \Gamma(x)\), which is also convex), \(\left|\frac{\Gamma'(x + c/K)}{\Gamma(x + c/K)}\right| \leq \left|\frac{\Gamma'(3)}{\Gamma(3)}\right| \leq 1\). Applying this to \(x = b - |b| + 1\), we conclude that:

\[
1 - \frac{\Gamma(b)}{\Gamma(b + c/K)} \leq \frac{c}{K}(2 + \ln b).
\]

We now show that:

\[
\frac{\Gamma(b)}{\Gamma(b + c/K)} - 1 \geq -\frac{c}{K}(\ln b + \ln 2).
\]

Convexity of \(\Gamma(y)\) means that:

\[
\Gamma(b) \geq \Gamma(b + c/K) - \frac{c}{K} \Gamma'(b + c/K) \rightarrow \frac{\Gamma(b)}{\Gamma(b + c/K)} - 1 \geq -\frac{c}{K} \frac{\Gamma'(b + c/K)}{\Gamma(b + c/K)}.
\]

From Alzer (1997, Equation 2.2), we know that \(\psi(x) \leq \ln(x)\) for positive \(x\). Therefore:

\[
-\frac{c}{K} \frac{\Gamma'(b + c/K)}{\Gamma(b + c/K)} \geq -\frac{c}{K} \ln(b + c/K) \geq -\frac{c}{K}(\ln b + \ln 2)
\]

since \(b + \frac{c}{K} \leq 2b\).

We combine two sides of the inequality to conclude that the absolute value is at most \(\frac{c}{K}(2 + \ln b)\).

\(\square\)

**Proof of Eq. (D.12).**

\[
\left|c - \frac{K}{B(c/K, b)}\right| = c \left|\frac{K/c}{\Gamma(c/K)} - 1\right|
\]

\[
= c \left|\frac{K/c}{\Gamma(c/K)} \left(\frac{\Gamma(c/K + b)}{\Gamma(b)} - 1\right) + \left(\frac{K/c}{\Gamma(c/K)} - 1\right)\right|
\]

\[
\leq c \left(\frac{K/c}{\Gamma(c/K)} \left|\frac{\Gamma(c/K + b)}{\Gamma(b)} - 1\right| + \left|\frac{K/c}{\Gamma(c/K)} - 1\right|\right).
\]

On the one hand:

\[
\frac{K/c}{\Gamma(c/K)} = \frac{\Gamma(1)}{\Gamma(1 + c/K)}.
\]

From Eq. (D.11), we know:

\[
\left|\frac{\Gamma(1)}{\Gamma(1 + c/K)} - 1\right| \leq \frac{2c}{K}.
\]

On the other hand, let \(y = \Gamma(b)/\Gamma(c/K + b)\). Then:

\[
\left|\frac{\Gamma(c/K + b)}{\Gamma(b)} - 1\right| = \left|\frac{1}{y} - 1\right| = \left|1 - y\right|/y.
\]
Again using Eq. (D.11), \(|1 - y| \leq \frac{c}{K}(2 + \ln b)|. Since \(K \geq 2c(ln b + 2)\), \(\frac{c}{K}(2 + \ln b)\) is at most 0.5, meaning \(|1 - y| \leq 0.5\) and \(y \geq 0.5\). Therefore

\[
\left| \frac{\Gamma(c/K + b)}{\Gamma(b)} - 1 \right| \leq \frac{2c}{K}(2 + \ln b).
\]

In all:

\[
\left| c - \frac{K}{B(c/K, b)} \right| \leq c \left( \left( 1 + \frac{2c}{K} \right) \frac{c}{K}(2 + \ln b) + \frac{2c}{K} \right)
\]

\[
\leq \frac{c}{K}(3\ln b + 8).
\]

\[\square\]

**Appendix E: Verification of upper bound's assumptions for additional examples**

Recall the definitions of \(h\), \(\tilde{h}\), and \(M_{n,x}\) for exponential family CRM-likelihood in Appendix C.

**E.1. Gamma–Poisson with zero discount**

First we write down the functions in Condition 1 for non-power-law gamma–Poisson. This requires expressing the rate measure and likelihood in exponential-family form:

\[
\ell(x | \theta) = \frac{1}{x!} \theta^x \exp(-\theta), \quad \nu(d\theta) = \gamma \lambda \theta^{-1} \exp(-\lambda \theta),
\]

which means that \(\kappa(x) = 1/x!, \phi(x) = x, \mu(\theta) = 0, A(\theta) = \theta\). This leads to the normalizer

\[
Z = \int_0^{\infty} \theta^x \exp(-\lambda \theta) d\theta = \Gamma(\xi + 1)\lambda^{-(\xi + 1)}.
\]

Therefore, \(h\) is

\[
h(x_n = x | x_{1:(n-1)}) = \frac{1}{x!} \frac{\Gamma\left(-1 + \sum_{i=1}^{n-1} x_i + x + 1\right)(\lambda + n)^{-1} + \sum_{i=1}^{n-1} x_i + x + 1}{\Gamma\left(-1 + \sum_{i=1}^{n-1} x_i + 1\right)(\lambda + n - 1)^{-1} + \sum_{i=1}^{n-1} x_i + 1}
\]

\[
= \frac{1}{x!} \frac{\Gamma\left(\sum_{i=1}^{n-1} x_i + x\right)}{\Gamma\left(\sum_{i=1}^{n-1} x_i\right)} \left(\frac{1}{\lambda + n}\right)^x \left(1 - \frac{1}{\lambda + n}\right)^{\sum_{i=1}^{n-1} x_i},
\]

and similarly \(\tilde{h}\) is

\[
\tilde{h}(x_n = x | x_{1:(n-1)}) = \frac{1}{x!} \frac{\Gamma\left(-1 + \sum_{i=1}^{n-1} x_i + x + 1 + \gamma \lambda / K\right)(\lambda + n)^{-1} + \sum_{i=1}^{n-1} x_i + x + 1 + \gamma \lambda / K}{\Gamma\left(-1 + \sum_{i=1}^{n-1} x_i + 1 + \gamma \lambda / K\right)(\lambda + n - 1)^{-1} + \sum_{i=1}^{n-1} x_i + 1 + \gamma \lambda / K}
\]

\[
= \frac{1}{x!} \frac{\Gamma\left(\sum_{i=1}^{n-1} x_i + x + \gamma \lambda / K\right)}{\Gamma\left(\sum_{i=1}^{n-1} x_i + \gamma \lambda / K\right)} \left(\frac{1}{\lambda + n}\right)^x \left(1 - \frac{1}{\lambda + n}\right)^{\sum_{i=1}^{n-1} x_i + \gamma \lambda / K},
\]
and $M_{n,x}$ is
\[ M_{n,x} = \gamma \lambda \frac{1}{x!} \Gamma(x)(\lambda + n)^{-x} = \frac{\gamma \lambda}{x(\lambda + n)^{x}}. \]

Now, we state the constants so that gamma–Poisson satisfies Condition 1, and give the proof.

**Proposition E.1** (Gamma–Poisson satisfies Condition 1). The following hold for arbitrary $\gamma, \lambda > 0$. For any $n$:
\[ \sum_{x=1}^{\infty} M_{n,x} \leq \frac{n - 1 + \lambda}{\gamma \lambda}. \]
\[ \sum_{x=1}^{\infty} \tilde{h}(x \mid x_{1:(n-1)} = 0_{n-1}) \leq \frac{n - 1 + \lambda}{\gamma \lambda}. \]

For any $K$:
\[ \sum_{x=1}^{\infty} \left| h(x \mid x_{1:(n-1)}) - \tilde{h}(x \mid x_{1:(n-1)}) \right| \leq \frac{2 \gamma \lambda}{K} \frac{1}{n - 1 + \lambda}. \]

For any $K \geq \gamma \lambda$:
\[ \sum_{x=1}^{\infty} M_{n,x} - K \tilde{h}(x \mid x_{1:(n-1)} = 0_{n-1}) \leq \frac{2 \gamma \lambda + e \gamma^2 \lambda^2}{K} \frac{1}{n - 1 + \lambda}. \]

**Proof of Proposition E.1.** The growth rate condition of the target model is simple:
\[ \sum_{x=1}^{\infty} M_{n,x} = \gamma \lambda \sum_{x=1}^{\infty} \frac{1}{x(\lambda + n)^{x}} \leq \gamma \lambda \sum_{x=1}^{\infty} \frac{1}{(\lambda + n)^{x}} = \frac{\gamma \lambda}{n - 1 + \lambda}. \]

The growth rate condition of the approximate model is also simple:
\[ \sum_{x=1}^{\infty} \tilde{h}(x \mid x_{1:(n-1)} = 0_{n-1}) = 1 - \tilde{h}(0 \mid x_{1:(n-1)} = 0_{n-1}) = 1 - \left( 1 - \frac{1}{\lambda + n} \right)^{\gamma \lambda / K} \leq \frac{\gamma \lambda}{K} \frac{(\lambda + n)^{-1}}{1 - (\lambda + n)^{-1}} = \frac{\gamma \lambda}{K} \frac{1}{n - 1 + \lambda}, \]
where we have used Eq. (D.6) with $p = \frac{\gamma \lambda}{K}, x = (\lambda + n)^{-1}$.

For the total variation between $h$ and $\tilde{h}$ condition, observe that $h$ and $\tilde{h}$ are p.m.f’s of negative binomial distributions, namely:
\[ h(x \mid x_{1:(n-1)}) = NB \left( x \mid \sum_{i=1}^{n-1} x_i, (\lambda + n)^{-1} \right), \]
\[ \tilde{h}(x \mid x_{1:(n-1)}) = NB \left( x \mid \sum_{i=1}^{n-1} x_i + \gamma \lambda / K, (\lambda + n)^{-1} \right). \]

The two negative binomial distributions have the same success probability and only differ in the number of trials. Hence using Eq. (D.7), we have:
\[ \sum_{x=0}^{\infty} \left| h(x \mid x_{1:(n-1)}) - \tilde{h}(x \mid x_{1:(n-1)}) \right| \leq \frac{2 \gamma \lambda}{K} \frac{(\lambda + n)^{-1}}{1 - (\lambda + n)^{-1}} = \frac{2 \gamma \lambda}{K} \frac{1}{n - 1 + \lambda}. \]
where the factor 2 reflects how total variation distance is $1/2$ the $L_1$ distance between p.m.f’s.

For the total variation between $M_{n,.}$ and $K\tilde{h}(\cdot \mid 0)$ condition,

\[
\sum_{x=1}^{\infty} \left| M_{n,x} - K\tilde{h}(x \mid x_{1:(n-1)} = 0_{n-1}) \right|
= \sum_{x=1}^{\infty} \frac{1}{(\lambda + n)^x} \left| \frac{\gamma \lambda}{x} - K \frac{\Gamma(\gamma \lambda/K + x)}{\Gamma(\gamma \lambda/K)!} \left(1 - \frac{1}{\lambda + n}\right)^{\gamma \lambda/K} \right|
\leq \sum_{x=1}^{\infty} \frac{1}{(\lambda + n)^x} \left(\left| \frac{\gamma \lambda}{x} \right| \left| 1 - \left(1 - \frac{1}{\lambda + n}\right)^{\gamma \lambda/K} \right| + \left| \frac{\gamma \lambda}{x} - K \frac{\Gamma(\gamma \lambda/K + x)}{\Gamma(\gamma \lambda/K)!} \right| \right).
\]

Using Eq. (D.7) we can upper bound:

\[
1 - \left(1 - \frac{1}{\lambda + n}\right)^{\gamma \lambda/K} \leq \frac{\gamma \lambda}{K} \frac{1}{\lambda + n - 1},
\]

while Eq. (D.8) gives the upper bound:

\[
\left| \frac{\gamma \lambda}{x} - K \frac{\Gamma(\gamma \lambda/K + x)}{\Gamma(\gamma \lambda/K)!} \right| \leq e^{\gamma^2 \lambda^2 / K}.
\]

This means:

\[
\sum_{x=1}^{\infty} \left| M_{n,x} - K\tilde{h}(x \mid x_{1:(n-1)} = 0_{n-1}) \right|
\leq \sum_{x=1}^{\infty} \frac{1}{(\lambda + n)^x} \frac{\gamma \lambda}{x} \frac{1}{K} \frac{1}{\lambda + n - 1} + \sum_{x=1}^{\infty} \frac{1}{(\lambda + n)^x} \frac{e^{\gamma^2 \lambda^2}}{K}
\leq \frac{\gamma^2 \lambda^2}{K} \frac{1}{(\lambda + n - 1)^2} + \frac{e^{\gamma^2 \lambda^2} \frac{1}{K}}{\lambda + n - 1}
\leq \frac{\gamma^2 \lambda + e^{\gamma^2 \lambda^2}}{K} \frac{1}{n - 1 + \lambda}.
\]

\[\square\]

\section*{E.2. Beta–negative binomial with zero discount}

First we write down the functions in Condition 1 for non-power-law beta–negative binomial. This requires expressing the rate measure and likelihood in exponential-family form:

\[
\ell(x \mid \theta) = \frac{\Gamma(x + r)}{x! \Gamma(r)} \theta^x \exp(r \ln(1 - \theta)),
\]

\[
\nu(d\theta) = \gamma \alpha \theta^{-1} \exp(\ln(1 - \theta)(\alpha - 1))1\{\theta \leq 1\},
\]

which means that $\kappa(x) = \Gamma(x + r)/\Gamma(r)x!, \phi(x) = x, \mu(\theta) = 0, A(\theta) = -r \ln(1 - \theta)$. This leads to the normalizer:

\[
Z = \int_0^1 \theta^\xi (1 - \theta)^\gamma d\theta = B(\xi + 1, r \lambda + 1).
\]
To match the parametrizations, we need to set \( \lambda = \frac{\alpha - 1}{r} \) i.e. \( r\lambda = \alpha - 1 \). Therefore, \( h \) is

\[
h(x_n = x \mid x_{1:(n-1)}) = \frac{\Gamma(x + r)}{x!\Gamma(r)} \frac{B(\sum_{i=1}^{n-1} x_i + x, \alpha + \alpha)}{B(\sum_{i=1}^{n-1} x_i, r(n-1) + \alpha)}
\]

and \( \tilde{h} \) is

\[
\tilde{h}(x_n = x \mid x_{1:(n-1)}) = \frac{\Gamma(x + r)}{x!\Gamma(r)} \frac{B(\gamma\alpha/K + \sum_{i=1}^{n-1} x_i + x, \alpha + \alpha)}{B(\gamma\alpha/K + \sum_{i=1}^{n-1} x_i, r(n-1) + \alpha)}
\]

and \( M_{n,x} \) is

\[
M_{n,x} = \gamma\alpha \frac{\Gamma(x + r)}{x!\Gamma(r)} B(x, \alpha + \alpha).
\]

Now, we state the constants so that beta–negative binomial satisfies Condition 1, and give the proof.

**Proposition E.2** (Beta–negative binomial satisfies Condition 1). The following hold for any \( \gamma > 0 \) and \( \alpha > 1 \). For any \( n \):

\[
\sum_{x=1}^{\infty} M_{n,x} \leq \frac{\gamma\alpha}{n - 1 + (\alpha - 0.5)/r}.
\]

For any \( n \), any \( K \):

\[
\sum_{x=1}^{\infty} \tilde{h}(x \mid x_{1:(n-1)} = 0_{n-1}) \leq \frac{1}{K} \frac{4\gamma\alpha}{n - 1 + (\alpha - 0.5)/r}.
\]

For any \( K \):

\[
\sum_{x=0}^{\infty} \left| h(x \mid x_{1:(n-1)}) - \tilde{h}(x \mid x_{1:(n-1)}) \right| \leq 2\frac{\gamma\alpha}{K} \frac{1}{n - 1 + \alpha/r}.
\]

For any \( n \), for \( K \geq \gamma\alpha(3\ln(r(n-1) + \alpha) + 8) \):

\[
\sum_{x=1}^{\infty} \left| M_{n,x} - K\tilde{h}(x \mid x_{1:(n-1)} = 0_{n-1}) \right| \leq \frac{\gamma\alpha}{K} \frac{(4\gamma\alpha + 3)\ln(rn + \alpha + 1) + (10 + 2r)\gamma\alpha + 24}{n - 1 + (\alpha - 0.5)/r}.
\]

**Proof of Proposition E.2.** The growth rate condition for the target model is easy to verify:

\[
\sum_{x=1}^{\infty} M_{n,x} = \gamma\alpha \sum_{x=1}^{\infty} \frac{\Gamma(x + r)}{\Gamma(r)x!} B(x, \alpha + \alpha) \leq \gamma\alpha \frac{r}{r(n-1) + \alpha - 0.5},
\]

where we have used Eq. (D.10) with \( b = r(n-1) + \alpha \).

As for the growth rate condition of the approximate model,

\[
\sum_{x=1}^{\infty} \tilde{h}(x \mid x_{1:(n-1)} = 0_{n-1}) = 1 - \tilde{h}(0 \mid x_{1:(n-1)} = 0_{n-1}) = 1 - \frac{B(\gamma\alpha/K, \alpha + \alpha)}{B(\gamma\alpha/K, r(n-1) + \alpha)} = \frac{B(\gamma\alpha/K, r(n-1) + \alpha) - B(\gamma\alpha/K, \alpha + \alpha)}{B(\gamma\alpha/K, r(n-1) + \alpha)}.
\]
The numerator is small because of Eq. (D.9) where \( x = \gamma_0/K, y = r(n-1) + \alpha, z = r\alpha + \alpha \):

\[
B(\gamma_0/K, r(n-1) + \alpha) - B(\gamma_0/K, r\alpha + \alpha) \leq rB(\gamma_0/K + 1, r(n-1) + \alpha - 0.5) \\
\leq rB(1, r(n-1) + \alpha - 0.5)
\]

\[
= \frac{1}{n-1+(\alpha-0.5)/r}.
\]

The denominator is large because Equation (D.12) with Equation (D.12) with \( c = \gamma, b = r(n-1) + \alpha \):

\[
\frac{1}{B(\gamma_0/K, r(n-1) + \alpha)} \leq \frac{4\gamma}{K}.
\]

Combining the two gives yields

\[
\sum_{x=1}^{\infty} \tilde{h}(x | x_{1:n-1} = 0_{n-1}) \leq \frac{1}{K} \frac{4\gamma}{n-1+(\alpha-0.5)/r}.
\]

For the total variation between \( h \) and \( \tilde{h} \) condition, we first discuss how each function can be expressed a p.m.f. of so-called beta negative binomial i.e., BNB (Johnson, Kemp and Kotz, 2005, Section 6.2.3) distribution. Let \( A = \sum_{i=1}^{n-1} x_i \). Observe that:

\[
\frac{\Gamma(x+r) \ B(A+x, r\alpha+\alpha)}{\Gamma(r) x! \ B(A, r(n-1)+\alpha)} = \frac{\Gamma(A+r) \ B(r+x, A+r(n-1)+\alpha)}{\Gamma(A) x! \ B(r, r(n-1)+\alpha)}.
\]

(E.1)

The random variable \( V_1 \) whose p.m.f at \( x \) appears on the right-hand side of Eq. (E.1) is the result of a two-step sampling procedure:

\[
P \sim \text{Beta}(r, r(n-1)+\alpha), \quad V_1 \mid P \sim \text{NB}(A; P).
\]

We denote such a distribution as \( V_1 \sim \text{BNB}(A; r, r(n-1)+\alpha) \). An analogous argument applies to \( \tilde{h} \):

\[
P \sim \text{Beta}(r, r(n-1)+\alpha), \quad V_2 \mid P \sim \text{NB} \left( A + \frac{\gamma_0}{K}; P \right).
\]

Therefore:

\[
h(x | x_{1:n-1}) = \text{BNB}(x | A; r, r(n-1)+\alpha) \\
\tilde{h}(x | x_{1:n-1}) = \text{BNB}(x | A + \frac{\gamma_0}{K}; r, r(n-1)+\alpha).
\]

We now bound the total variation between the BNB distributions. Because they have a common mixing distribution, we can upper bound the distance with an integral using simple triangle inequalities:

\[
d_{TV}(h, \tilde{h}) = \frac{1}{2} \sum_{x=0}^{\infty} |\mathbb{P}(V_1 = x) - \mathbb{P}(V_2 = x)|
\]

\[
= \frac{1}{2} \sum_{x=0}^{\infty} \int_0^1 |\mathbb{P}(V_1 = x | P = p) - \mathbb{P}(V_2 = x | P = p)| \mathbb{P}(P \in dp) \mid
\]

\[
\leq \int_0^1 \left( \frac{1}{2} \sum_{x=0}^{\infty} |\mathbb{P}(V_1 = x | P = p) - \mathbb{P}(V_2 = x | P = p)| \right) \mathbb{P}(P \in dp)
\]

\[
= \int_0^1 d_{TV}(\text{NB}(A, p), \text{NB}(A + \gamma_0/K, p)) \mathbb{P}(P \in dp).
\]
For any $p$, we use Eq. (D.7) to upper bound the total variation distance between negative binomial distributions. Therefore:

$$d_{TV} \left( h, \tilde{h} \right) \leq \int_0^1 \frac{\gamma_\alpha}{K} \frac{p}{1-p} \Pr(P \in dp)$$

$$= \frac{\gamma_\alpha}{K} \frac{1}{B(r, r(n-1) + \alpha)} \int_0^1 p^{r-1} (1-p)^{r(n-1)+\alpha-2} dp$$

$$= \frac{\gamma_\alpha}{K} \frac{B(r+1, r(n-1)+\alpha-1)}{B(r, r(n-1)+\alpha)} = \frac{\gamma_\alpha}{K} \frac{1}{n-1 + \alpha/r}.$$ 

Finally, we verify the condition between $K\tilde{h}$ and $M_n$, which is showing that the following sum is small:

$$\sum_{x=1}^\infty \frac{\gamma_\alpha B(x, rn + \alpha)}{x! \Gamma(r)} \left| \gamma_\alpha B(x, rn + \alpha) - K \frac{B(\gamma_\alpha/K, x, rn + \alpha)}{B(\gamma_\alpha/K, r(n-1) + \alpha)} \right|.$$ 

We look at the numerator of the right hand side in Eq. (E.3):

$$\frac{\Gamma(r+1)}{\Gamma(r)} \left| \gamma_\alpha B(1, rn + \alpha) - K \frac{B(1 + \gamma_\alpha/K, rn + \alpha)}{B(\gamma_\alpha/K, r(n-1) + \alpha)} \right| \leq \frac{4r^2\alpha^2}{K} \frac{2 + \ln(rn + \alpha + 1)}{rn + \alpha}. \quad (E.2)$$

Expanding gives:

$$\left| \gamma_\alpha B(1, rn + \alpha) - K \frac{B(1 + \gamma_\alpha/K, rn + \alpha)}{B(\gamma_\alpha/K, r(n-1) + \alpha)} \right| = \frac{\left| \gamma_\alpha B(1, rn + \alpha)B(\gamma_\alpha/K, r(n-1) + \alpha) - KB(1 + \gamma_\alpha/K, rn + \alpha) \right|}{B(\gamma_\alpha/K, r(n-1) + \alpha)}. \quad (E.3)$$

We look at the numerator of the right hand side in Eq. (E.3):

$$\left| \gamma_\alpha B(1, rn + \alpha) \frac{\Gamma(\gamma_\alpha/K) \Gamma(r(n-1) + \alpha)}{\Gamma(\gamma_\alpha/K + r(n-1) + \alpha)} - K \frac{\Gamma(1 + \gamma_\alpha/K) \Gamma(rn + \alpha)}{\Gamma(1 + \gamma_\alpha/K + rn + \alpha)} \right|$$

$$= \frac{\gamma_\alpha \Gamma(\gamma_\alpha/K)}{rn + \alpha} \left| \frac{1}{rn + \alpha} \frac{\Gamma(r(n-1) + \alpha)}{\Gamma(\gamma_\alpha/K + r(n-1) + \alpha)} - \frac{\Gamma(rn + \alpha)}{\Gamma(\gamma_\alpha/K + \gamma_\alpha/K + rn + \alpha)} \right|$$

$$= \frac{\gamma_\alpha \Gamma(\gamma_\alpha/K)}{rn + \alpha} \left| \frac{\Gamma(r(n-1) + \alpha)}{\Gamma(\gamma_\alpha/K + r(n-1) + \alpha)} - \frac{\Gamma(rn + \alpha)}{\Gamma(\gamma_\alpha/K + \gamma_\alpha/K + rn + \alpha)} \right|$$

$$\leq \frac{\gamma_\alpha \Gamma(\gamma_\alpha/K)}{rn + \alpha} \left( \left| \frac{\Gamma(r(n-1) + \alpha)}{\Gamma(\gamma_\alpha/K + r(n-1) + \alpha)} - 1 \right| + \left| \frac{\Gamma(rn + \alpha)}{\Gamma(\gamma_\alpha/K + \gamma_\alpha/K + rn + \alpha)} - 1 \right| \right)$$

$$\leq \frac{\gamma_\alpha \Gamma(\gamma_\alpha/K)}{rn + \alpha} \frac{2\gamma_\alpha}{K} (2 + \ln(rn + \alpha + 1)), $$

where we have used Eq. (D.11) with $c = \gamma_\alpha$ and $b = r(n-1) + \alpha$ or $b = rn + \alpha + 1$. In all,
Eq. (E.3) is upper bounded by:

\[
\frac{2\gamma^2 \alpha^2}{r n + \alpha} \frac{2 + \ln(r n + \alpha + 1)}{\Gamma(r n + \alpha)} \frac{2 + \ln(r n + \alpha + 1)}{\Gamma(r n + \alpha)} \frac{\Gamma(\gamma \alpha / K)}{\Gamma(n(n + 1) + 1)} \frac{B(\gamma \alpha / K, r(n - 1) + \alpha)}{B(\gamma \alpha / K, r(n - 1) + \alpha)} = \frac{2\gamma^2 \alpha^2}{r n + \alpha} \frac{2 + \ln(r n + \alpha + 1)}{\Gamma(r n + \alpha)} \frac{\Gamma(\gamma \alpha / K)}{\Gamma(n(n + 1) + 1)} \frac{B(\gamma \alpha / K, r(n - 1) + \alpha)}{B(\gamma \alpha / K, r(n - 1) + \alpha)} \leq \frac{4\gamma^2 \alpha^2}{r n + \alpha} \frac{2 + \ln(r n + \alpha + 1)}{\Gamma(r n + \alpha)} \frac{\Gamma(\gamma \alpha / K)}{\Gamma(n(n + 1) + 1)},
\]

since \(\frac{\Gamma(r(n-1)+\alpha)}{r(n-1)+\alpha+\gamma \alpha / K} \geq 1 - \frac{\gamma \alpha}{K} (2 + \ln(r(n-1)+\alpha)) \geq 0.5 \) with \(K \geq 2\gamma \alpha (2 + \ln(r(n-1)+\alpha)).\)

Combining with \(\Gamma(r + 1)/\Gamma(r) = r\), this is the proof of Eq. (E.2).

We now move onto the summands from \(x = 2\) to \(\infty\). By triangle inequality:

\[
\left| \gamma \alpha B(x, rn + \alpha) - K B(\gamma \alpha / K + x, rn + \alpha) / B(\gamma \alpha / K, r(n - 1) + \alpha) \right| \leq T_1(x) + T_2(x),
\]

where:

\[
T_1(x) := B(x, rn + \alpha) \left| \gamma - \frac{K}{B(\gamma \alpha / K, r(n - 1) + \alpha)} \right|,
\]

\[
T_2(x) := K \left| B(x, rn + \alpha) - B(\gamma \alpha / K, r + \alpha) / B(\gamma \alpha / K, r(n - 1) + \alpha) \right|.
\]

The helper inequalities we have proven once again are useful:

\[
\left| \frac{\gamma \alpha - K}{B(\gamma \alpha / K, r(n - 1) + \alpha)} \right| \leq \frac{\gamma \alpha}{K} (3 \ln(r(n - 1) + 1) + 8)
\]

\[
\left| \frac{K}{B(\gamma \alpha / K, r(n - 1) + \alpha)} \right| \leq \gamma \alpha + \frac{\gamma \alpha}{K} (3 \ln(r(n - 1) + 1) + 8) \leq 2\gamma \alpha,
\]

\[
\left| B(x, rn + \alpha) - B(\gamma \alpha / K + x, rn + \alpha) / B(\gamma \alpha / K, r(n - 1) + \alpha) \right| \leq \frac{\gamma \alpha}{K} B(x - 1, rn + 1 + \alpha)
\]

since \(K \geq \gamma \alpha (3 \ln(r(n - 1) + 1) + 8),\) we have applied Eq. (D.12) in the first and second inequality and Eq. (D.9) in the third one. So for each \(x \geq 2,\) each summand is at most:

\[
\frac{\Gamma(x + r)}{x! \Gamma(r)} \left| \varepsilon B(x, rn + \alpha) - K B(\gamma \alpha / K + x, rn + \alpha) / B(\gamma \alpha / K, r(n - 1) + \alpha) \right| \leq \frac{\gamma \alpha (3 \ln(r(n - 1) + 1) + 8) \Gamma(x + r)}{K} B(x, rn + \alpha) + \frac{2\gamma^2 \alpha^2 \Gamma(x + r)}{x! \Gamma(r)} B(x - 1, rn + 1 + \alpha).
\]

To upper bound the summation from \(x = 2\) to \(\infty,\) it suffices to bound:

\[
\sum_{x=2}^{\infty} \frac{\Gamma(x + r)}{\Gamma(x)!} B(x, rn + \alpha) \leq \sum_{x=1}^{\infty} \frac{\Gamma(x + r)}{\Gamma(x)!} B(x, rn + \alpha) \leq \frac{r}{r(n - 1) + \alpha - 0.5},
\]
and:
\[
\sum_{x=2}^{\infty} \frac{\Gamma(x + r)}{\Gamma(r) x!} B(x - 1, rn + \alpha + 1) \leq r \sum_{x=2}^{\infty} \frac{\Gamma(x - 1 + r + 1)}{\Gamma(r + 1)(x - 1)!} B(x - 1, rn + \alpha + 1)
\]
\[
\leq r \sum_{z=1}^{\infty} \frac{\Gamma(z + r + 1)}{\Gamma(r + 1) z!} B(z, rn + \alpha + 1)
\]
\[
\leq \frac{r(r + 1)}{r(n - 1) + \alpha - 0.5},
\]
where we have used Eq. (D.10) in each upper bound. So the summation from \(x = 2\) to \(\infty\) is upper bounded by:
\[
\frac{\gamma \alpha (3 \ln(n - 1) + \alpha) + 8}{K} \frac{r}{r(n - 1) + \alpha - 0.5} + \frac{2 \gamma^2 \alpha^2}{K} \frac{r(r + 1)}{r(n - 1) + \alpha - 0.5}
\]
(E.4)

Eqs. (E.2) and (E.4) combine to give:
\[
\sum_{x=1}^{\infty} \left| M_{n,x} - K \tilde{h}(x \mid x_{1:(n-1)} = 0_{n-1}) \right|
\]
\[
\leq \frac{\gamma \alpha (4 \gamma \alpha + 3) \ln(rn + \alpha + 1) + (10 + 2r) \gamma \alpha + 24}{K} \frac{n - 1 + (\alpha - 0.5)/r}{n - 1 + (\alpha - 0.5)/r}.
\]

Appendix F: Proofs of CRM bounds

F.1. Upper bound

Proof of Theorem 4.1. Let \(\beta\) be the smallest positive constant where \(\beta^2/(1 + \beta) \geq 2/C_1\). Such constant exists because \(\beta^2/(1 + \beta)\) is an increasing function. We will focus on the case where the approximation level \(K\) is \(\Omega(\ln N)\):
\[
K \geq \max \{ ((\beta + 1) \max(C(K, C_1), C(N, C_1)), C_2(\ln N + C_3) \}, \quad (F.1)
\]
where \(C(N, \alpha)\) is the growth function from Eq. (15). To see why it is sufficient, observe that the upper bound in Theorem 4.1 naturally holds for \(K\) smaller than \(\ln N\). Total variation distance is always upper bounded by 1; if \(K = o(\ln N)\), then by selecting small constants \(C', C'', C'''\), we can make the right hand side at least 1, and satisfy the inequality. In the sequel, we will only consider the situation in Eq. (F.1).

First, we argue that it suffices to bound the total variation distance between the feature-allocation matrices coming from the target model and the approximate model. Given the latent measures \(X_1, X_2, \ldots, X_N\) from the target model, we can read off the feature-allocation matrix \(F\), which has \(N\) rows and as many columns as there are unique atom locations among the \(X_i\)’s:
1. The \(i\)-th row of \(F\) records the atom sizes of \(X_i\).
2. Each column corresponds to an atom location: the locations are sorted first according to the index of the first measure \(X_i\) to manifest it (counting from 1, 2, \ldots), and then its atom size in \(X_i\).
For illustration, suppose $X_1 = 3\delta_{\psi_1} + 4\delta_{\psi_2} + 4\delta_{\psi_3}$, $X_2 = 2\delta_{\psi_1} + \delta_{\psi_3} + 2\delta_{\psi_4}$, and $X_3 = 6\delta_{\psi_2} + 2\delta_{\psi_3} + \delta_{\psi_5} + 2\delta_{\psi_6} + 3\delta_{\psi_7}$. Then the associate feature allocation matrix has 3 rows and 7 columns and has entries equal to

\[
\begin{bmatrix}
3 & 4 & 4 & 0 & 0 & 0 & 0 \\
2 & 0 & 1 & 1 & 2 & 0 & 0 \\
0 & 6 & 2 & 0 & 1 & 2 & 3 \\
\end{bmatrix}.
\] (F.2)

The marginal process that described the atom sizes of $X_n|X_{n-1},X_{n-2},\ldots,X_1$ in Proposition C.1 is also the description of how the rows of $F$ are generated. The joint distribution $X_1,X_2,\ldots,X_n$ can be two-step sampled. First, the feature-allocation matrix $F$ is sampled. Then, the atom locations are drawn iid from the base measure $\mathcal{H}$; each column of $F$ is assigned an atom location, and the latent measure $F_{i,j}$ on the $j$th atom location. A similar two-step sampling generates $Z_1,Z_2,\ldots,Z_n$, the latent measures under the approximate model: the distribution over the feature-allocation matrix $F$ is sampled.

In other words, this implies that the conditional distributions $Y_{1:N}|F$ and $W_{1:N}|F'$ when $F = F'$ are the same, since both models have the same the observational likelihood $f$ given the latent measures 1 through $N$. Denote $P_F$ to be the distribution of the feature-allocation matrix under the target model, and $P_{F'}$ the distribution of the feature-allocation matrix under the approximate model. Lemma D.8 implies that

\[
d_{TV}(P_{N,\infty},P_{N,K}) \leq \inf_{F,F' \text{ coupling of } P_F,P_{F'}} \mathbb{P}(F \neq F').
\] (F.3)

Next, we parametrize the feature-allocation matrices in a way that is convenient for the analysis of total variation distance. Let $J$ be the number of columns of $F$. Our parametrization involves $d_{n,x}$, for $n \in [N]$ and $x \in \mathbb{N}$, and $s_j$, for $j \in [J]$:

1. For $n = 1,2,\ldots,N$:
   (a) If $n = 1$, for each $x \in \mathbb{N}$, $d_{1,x}$ counts the number of columns $j$ where $F_{1,j} = x$.
   (b) For $n \geq 2$, for each $x \in \mathbb{N}$, let $J_n = \{j: \forall i < n, F_{i,j} = 0\}$ i.e. no observation before $n$ manifests the atom locations indexed by columns in $J_n$. For each $x \in \mathbb{N}$, $d_{n,x}$ counts the number of columns $j \in J_n$ where $F_{n,j} = x$.

2. For $j = 1,2,\ldots,J$, let $I_j = \min\{i: F_{i,j} > 0\}$ i.e. the first row to manifest the $j$-th atom location. Let $s_j = F_{I_j,N,j}$ i.e. the history of the $j$-th atom location.

In words, $d_{n,x}$ is the number of atom locations that is first instantiated by the individual $n$ and each atom has size $x$, while $s_j$ is the history of the $j$-th atom location. $\sum_{n=1}^{N} \sum_{x=1}^{\infty} d_{n,x}$ is exactly $J$, the number of columns. For the example in Eq. (F.2):

1. For $n = 1,2,\ldots,3$:
   (a) For $n = 1$, $d_{1,1} = d_{1,2} = d_{1,3} = 0$ for $j > 4$, $d_{1,3} = 1$, $d_{1,4} = 2$.
   (b) For $n = 2$, $d_{2,1} = 1$, $d_{2,2} = 1$, $d_{2,3} = 0$ for $j > 2$.
   (c) For $n = 3$, $d_{3,1} = 0$, $d_{3,2} = 1$, $d_{3,3} = 1$, $d_{3,4} = 0$ for $j > 3$.

2. For $j = 1,2,\ldots,7$, $s_1 = [3,2,0]$, $s_2 = [4,0,6]$, $s_3 = [4,1,2]$, $s_4 = [1,0]$, $s_5 = [2,1]$, $s_6 = [2]$, $s_7 = [3]$.
We use the short-hand $d$ to refer to the collection of $d_{n,x}$ and $s$ the collection of $s_i$. There is a one-to-one mapping between $(d,s)$ and the feature allocation matrix $f$, since we can read-off $(d,s)$ from $f$ and use $(d,s)$ to reconstruct $f$. Let $(D,S)$ be the distribution of $d$ and $s$ under the target model, while $(D',S')$ is the distribution under the approximate model. We have that

$$d_{TV}(P_{N,\infty}, P_{N,K}) \leq \inf_{(D,S),(D',S')} \mathbb{P}((D,S) \neq (D',S')).$$

To find an upper bound on $d_{TV}(P_{N,\infty}, P_{N,K})$, we will demonstrate a joint distribution such that $\mathbb{P}((D,S) \neq (D',S'))$ is small. The rest of the proof is dedicated to that end. To start, we only assume that $(D, S, D', S')$ is a proper coupling, in that marginally $(D, S) \sim P_{D,S}$ and $(D', S') \sim P_{D', S'}$. As we progress, gradually more structure is added to the joint distribution $(D, S, D', S')$ to control $\mathbb{P}((D, S) \neq (D', S'))$.

We first decompose $\mathbb{P}((D, S) \neq (D', S'))$ into other probabilistic quantities which can be analyzed using Condition 1. Define the typical set:

$$\mathcal{D}^* = \left\{ d : \sum_{n=1}^{N} \sum_{x=1}^{\infty} d_{n,x} \leq (\beta + 1) \max(C(K,C_1), C(N,C_1)) \right\}.$$

$d \in \mathcal{D}^*$ means that the feature-allocation matrix $f$ has a small number of columns. The claim is that:

$$\mathbb{P}((D, S) \neq (D', S')) \leq \mathbb{P}(D \neq D') + \mathbb{P}(S \neq S' \mid D = D', D \in \mathcal{D}^*) + \mathbb{P}(D \in \mathcal{D}^*).$$

This is true from basic properties of probabilities and conditional probabilities:

$$\mathbb{P}((D, S) \neq (D', S')) = \mathbb{P}(D \neq D') + \mathbb{P}(S \neq S' \mid D = D')$$
$$= \mathbb{P}(D \neq D') + \mathbb{P}(S \neq S' \mid D = D', D \in \mathcal{D}^*) + \mathbb{P}(S \neq S' \mid D = D', D \notin \mathcal{D}^*)$$
$$\leq \mathbb{P}(D \neq D') + \mathbb{P}(S \neq S' \mid D = D', D \in \mathcal{D}^*) + \mathbb{P}(D \notin \mathcal{D}^*).$$

The three ideas behind this upper bound are the following. First, because of the growth condition, we can analyze the atypical set probability $\mathbb{P}(D \notin \mathcal{D}^*)$. Second, because of the total variation between $h$ and $\tilde{h}$, we can analyze $\mathbb{P}(S \neq S' \mid D = D', D \in \mathcal{D}^*)$. Finally, we can analyze $\mathbb{P}(D \neq D')$ because of the total variation between $K h$ and $M_{n,\ldots}$. In what follows we carry out the program.

**Atypical set probability.** The $\mathbb{P}(D \notin \mathcal{D}^*)$ term in Eq. (F.4) is easiest to control. Under the target model Proposition C.1, the $D_{i,x}$’s are independent Poissons with mean $M_{i,x}$, so the sum $\sum_{i=1}^{N} \sum_{x=1}^{\infty} D_{i,x}$ is itself a Poisson with mean $M = \sum_{i=1}^{N} \sum_{x=1}^{\infty} M_{i,x}$. Because of Lemma D.3, for any $x > 0$:

$$\mathbb{P} \left( \sum_{i=1}^{N} \sum_{x=1}^{\infty} D_{i,x} > M + x \right) \leq \exp \left( -\frac{x^2}{2(M+x)} \right).$$

For the event $\mathbb{P}(D \notin \mathcal{D}^*)$, $M + x = (\beta + 1) \max(C(K,C_1), C(N,C_1))$, $M \leq C(N,C_1)$ due to Eq. (11), so that $x \geq \beta \max(C(K,C_1), C(N,C_1))$. Therefore:

$$\mathbb{P}(D \notin \mathcal{D}^*) \leq \exp \left( -\frac{\beta^2}{2(\beta + 1)} \max(C(K,C_1), C(N,C_1)) \right).$$

(F.5)
**Difference between histories.** To minimize the difference probability between the histories of atom sizes i.e. the $\mathbb{P}(S \neq S' \mid D = D', D \in \mathcal{D}^*)$ term in Eq. (F.4), we will use Eq. (13). The claim is, there exists a coupling of $S' \mid D'$ and $S \mid D$ such that:

$$
\mathbb{P}(S \neq S' \mid D = D', D \in \mathcal{D}^*) \leq \frac{(\beta + 1) \max(C(K, C_1), C(N, C_1))}{K} C(N, C_1). \quad (F.6)
$$

Fix some $d \in \mathcal{D}^*$ — since we are in the typical set, the number of columns in the feature-allocation matrix is at most $(\beta + 1) \max(C(K, C_1), C(N, C_1))$. Conditioned on $D = d$, there is a finite number of history variables $S$, one for each atom location; similar for conditioning of $S'$ on $D' = d$. For both the target and the approximate model, the density of the joint distribution factorizes:

$$
\mathbb{P}(S = s \mid D = d) = \prod_{j=1}^{J} \mathbb{P}(S_j = s_j \mid D = d)
$$

$$
\mathbb{P}(S' = s \mid D' = d) = \prod_{j=1}^{J} \mathbb{P}(S'_j = s_j \mid D' = d),
$$

since in both marginal processes, the atom sizes for different atom locations are independent of each other. Each $S_j$ (or $S'_j$) only takes values from a countable set. Therefore, by Lemma D.7,

$$
d_{TV}(P_S \mid D = d, P_{S'} \mid D' = d) \leq \sum_{j=1}^{J} d_{TV}(P_{S_j} \mid D = d, P_{S'_j} \mid D' = d).
$$

We inspect each $d_{TV}(P_{S_j} \mid D = d, P_{S'_j} \mid D' = d)$. Fixing $d$ also fixes $I_j$, the first row to manifest the $j$-th atom location. The history $s_j$ is then a $N - I_j + 1$ dimensional integer vector, whose $t$-th entry is the atom size over the $t$-the atom location of the $t + I_j - 1$ row. Because of Eq. (13), we know that conditioned on the same partial history $S_j(1 : (t - 1)) = S'_j(1 : (t - 1)) = s$, the distributions $S_j(t)$ and $S'_j(t)$ are very similar. The conditional distribution $S_j(t) \mid D = d, S_j(1 : (t - 1)) = s$ is governed by $h$ Proposition C.1 while $S'_j(t) \mid D' = d, S'_j(1 : (t - 1)) = s$ is governed by $\tilde{h}$ Proposition C.2. Hence:

$$
d_{TV} \left( P_{S_j(t)} \mid D = d, S_j(1 : (t - 1)) = s, P_{S'_j(t)} \mid D' = d, S'_j(1 : (t - 1)) = s \right) \leq 2 \frac{1}{K} \frac{C_1}{t + I_j - 2 + C_1},
$$

for any partial history $s$. To use this conditional bound, we repeatedly use Lemma D.6 to compare the joint $S_j = (S_j(1), S_j(2), \ldots, S_j(N - I_j + 1))$ with the joint $S'_j = (S'_j(1), S'_j(2), \ldots, S'_j(N - I_j + 1))$, peeling off one layer of random variables (indexed by $t$) at a time.

$$
d_{TV}(P_{S_j} \mid D = d, P_{S'_j} \mid D' = d)
\leq \sum_{t=1}^{N - I_j + 1} \max_s d_{TV} \left( P_{S_j(t)} \mid D = d, S_j(1 : (t - 1)) = s, P_{S'_j(t)} \mid D' = d, S'_j(1 : (t - 1)) = s \right)
\leq \sum_{t=1}^{N - I_j + 1} 2 \frac{1}{K} \frac{C_1}{t + I_j - 2 + C_1}
\leq 2 \frac{C(N, C_1)}{K}.
$$
Multiplying the right hand side by $(\beta + 1) \max(C(K, C_1), C(N, C_1))$, the upper bound on $J$, we arrive at the same upper bound for the total variation between $P_{S | D = d}$ and $P_{S' | D' = d}$ in Eq. (F.6). Furthermore, our analysis of the total variation can be back-tracked to construct the coupling between the conditional distributions $S | D = d$ and $S' | D' = d$ which attains that small probability of difference because all the distributions being analyzed are discrete. Since the choice of conditioning $d \in D^*$ was arbitrary, we have actually shown Eq. (F.6).

**Difference between new atom sizes.** Finally, to control the difference probability for the distribution over new atom sizes i.e. the $P(D \neq D')$ term in Eq. (F.4), we will utilize Eqs. (12) and (14). For each $n$, define the short-hand $d_{1:n}$ to refer to the collection $d_{i,x}$ for $i \in [n]$, $x \in \mathbb{N}$, and the typical sets:

$$D^*_n = \left\{ d_{1:n} : \sum_{i=1}^{n} \infty d_{i,x} \leq (\beta + 1) \max(C(K, C_1), C(N, C_1)) \right\}. $$

The type of expansion performed in Eq. (F.4) can be done once here to see that:

$$P(D \neq D') = P(D_{1:(N-1), D_N} \neq (D'_{1:(N-1), D'_N})) \leq P(D_{1:(N-1)} \neq D'_{1:(N-1)})$$

$$+ P(D_{N} \neq D'_N | D_{1:(N-1)} = D'_{1:(N-1)}, D_{1:(N-1)} \in D^*_n_{\infty})$$

$$+ P(D_{1:(N-1)} \notin D^*_n_{\infty}).$$

Apply the expansion once more to $P(D_{1:(N-1)} \neq D'_{1:(N-1)})$, then to $P(D_{1:(N-2)} \neq D'_{1:(N-2)}).$

If we define:

$$B_j = P(D_j \neq D'_j | D_{1:(j-1)} = D'_{1:(j-1)}, D_{1:(j-1)} \in D^*_j_{\infty}),$$

with the special case $B_1$ simply being $P(D_{1} \neq D'_{1})$, then:

$$P(D \neq D') \leq \sum_{j=1}^{N} B_j + \sum_{j=2}^{N} P(D_{1:(j-1)} \notin D^*_j_{\infty}). \tag{F.7}$$

The second summation in Eq. (F.7), comprising of only atypical probabilities, is easier to control. For any $j$, since $\sum_{i=1}^{j-1} \sum_{x=1}^{\infty} D_{i,x} \leq \sum_{i=1}^{N} \sum_{x=1}^{\infty} D_{i,x}$, $P(D_{1:(j-1)} \notin D^*_j_{\infty}) \leq P(D \notin D^*)$, so a generous upper bound for the contribution of all the atypical probabilities including the first one from Eq. (F.5) is

$$P(D \notin D^*) + \sum_{j=2}^{N} P(D_{1:(j-1)} \notin D^*_j_{\infty}) \leq \exp\left(-\left(\frac{\beta^2}{2(\beta + 1)} \max(C(K, C_1), C(N, C_1)) - \ln N\right)\right).$$

By Lemma D.10, $\max(C(K, C_1), C(N, C_1)) \geq C_1(\max(\ln N, \ln K) - C_1(\psi(C_1) + 1)).$ Since we have set $\beta$ so that $\frac{\beta^2}{\beta + 1} C_1 = 2$, we have

$$\frac{\beta^2}{2(\beta + 1)} \max(C(K, C_1), C(N, C_1)) - \ln N \geq \ln K - \text{constant.}$$
meaning the overall atypical probabilities is at most
\[
\mathbb{P}(D \notin D^*) + \sum_{j=2}^{N} \mathbb{P}(D_{1:(j-1)} \notin D_{j-1}^*) \leq \frac{\text{constant}}{K}. \tag{F.8}
\]

As for the first summation in Eq. (F.7), we look at the individual $B_j$'s. For any fixed $d_{1:(j-1)} \in D_{j-1}^*$, we claim that there exists a coupling between the conditionals $D_j \mid D_{1:(j-1)} = d_{1:(j-1)}$ and $D_j' \mid D_{1:(j-1)} = d_{1:(j-1)}$ such that
\[
\mathbb{P}(D_j \neq D_j' \mid D_{1:(j-1)} = d_{1:(j-1)}) \leq \frac{\text{constant}}{K} \frac{1}{(j-1 + C_1)^2} + \frac{\text{constant}}{K} \frac{(\ln N + \ln K)}{j-1} \leq \frac{1}{j-1 + C_1}. \tag{F.9}
\]
Because the upper bound holds for arbitrary values $d_{1:(j-1)}$, the coupling actually ensures that, as long as $D_{1:(j-1)} = D_{1:(j-1)}'$ for some value in $D_{j-1}^*$, the probability of difference between $D_j$ and $D_j'$ is small i.e. $B_j$ is at most the right hand side.

We demonstrate the existence of a distribution $U = \{U_x\}_{x=1}^{\infty}$ of independent Poisson random variables, such that both the total variation between $P_{D_j} \mid D_{1:(j-1)} = d_{1:(j-1)}$ and $P_U$ and the total variation between $P_{D_j'} \mid D_{1:(j-1)} = d_{1:(j-1)}$ and $P_U$ are small. Here, each $U_x$ has mean:
\[
\mathbb{E}(U_x) = \left( K - \sum_{i=1}^{j-1} \sum_{y=1}^{\infty} d_{i,y} \right) \tilde{h}(x \mid x_{1:(j-1)} = 0).
\]
On the one hand, conditioned on $D_{1:(j-1)}' = d_{1:(j-1)}$, $D_j' = \{D_{j,x}'\}_{x=1}^{\infty}$ is the joint distribution of types of successes of type $x$, where there are $K - \sum_{i=1}^{j-1} \sum_{y=1}^{\infty} d_{i,y}$ independent trials and types $x$ success has probability $\tilde{h}(x \mid x_{1:(j-1)} = 0)$ by Proposition C.2. Because of Lemma D.4 and Eq. (12):
\[
\mathbb{P}(D_{j} \neq U' \mid D_{1:(j-1)} = d_{1:(j-1)}) \leq \left( K - \sum_{i=1}^{j-1} \sum_{y=1}^{\infty} d_{i,y} \right)^2 \left( \sum_{x=1}^{\infty} \tilde{h}(x \mid x_{1:(j-1)} = 0) \right)^2 \leq K \left( \frac{1}{j-1 + C_1} \right) \leq K \left( \frac{C_1^2}{(j-1 + C_1)^2} \right). \tag{F.10}
\]
On the other hand, conditioned on $D_{1:(j-1)}$, $D_j = \{D_{j,x}\}_{x=1}^{\infty}$ consists of independent Poissons, where the mean of $D_{j,x}$ is $M_{j,x}$ by Proposition C.1. We show that there exists a coupling of $P_U$ and $P_{D_j}$ such that
\[
\mathbb{P}(U \neq D_j) \leq \sum_{x=1}^{\infty} d_{\text{TV}}(P_{U_x}, P_{D_{j,x}}). \tag{F.11}
\]
For each $x \geq 1$, let $O_x$ be the maximal coupling distribution between $P_{U_x}$ and $P_{D_{j,x}}$, i.e. for $(A, B) \sim O_x$, $\mathbb{P}(A \neq B) = d_{\text{TV}}(P_{U_x}, P_{D_{j,x}})$. Such $O_x$ exists because both $P_{U_x}$ and $P_{D_{j,x}}$ are Poisson (hence discrete) distributions. Furthermore, since $O_x$ is itself a discrete distribution, the conditional distributions $D_{j,x} \mid U_x$ exists. Denote the natural zig-zag bijection from $\{N \cup \}$.  

on the second term is:

\[ \sum \]

The first term is upper bounded by Eq. (14). Regarding the second term, since we are in the

If \( U \) we know \( U \)

Since the coupling (\( D_j \)) is different from \( D_i \) is independent of each other because we use i.i.d uniform r.v’s. Alternatively, the

conditional distribution of \( D_j \) implied by this joint distribution is as follows:

- For \( x \geq 1 \), sample \( U_x | D_j, x \) from the conditional distribution implied by the maximal
coupling \( O_x \).

If \( U \) is different from \( D_j \), it must be that for at least one \( x, U_x \neq D_j, x \). Therefore

\[ \mathbb{P}(U \neq D_j) \leq \sum_{x=1}^{\infty} \mathbb{P}(U_x \neq D_j, x) . \]

Since the coupling \((U_x, D_j, x)\) attains the \( d_{TV}(P_{U_x}, P_{D_j, x}) \), we are done. From Lemma D.5, we know

\[ \sum_{x=1}^{\infty} d_{TV}(P_{U_x}, P_{D_j, x}) \]

\[ \leq \sum_{x=1}^{\infty} \left| M_{j, x} - \left( K - \sum_{i=1}^{j-1} \sum_{y=1}^{\infty} d_{i, y} \right) \tilde{h}(x | x_{1:(j-1)} = 0) \right| \]

\[ \leq \sum_{x=1}^{\infty} \left( |M_{j, x} - K\tilde{h}(x | x_{1:(j-1)} = 0)| + \sum_{i=1}^{j-1} \sum_{y=1}^{\infty} d_{i, y} \tilde{h}(x | x_{1:(j-1)} = 0) \right) \]

\[ \leq \sum_{x=1}^{\infty} |M_{j, x} - K\tilde{h}(x | x_{1:(j-1)} = 0)| + \left( \sum_{i=1}^{j-1} \sum_{y=1}^{\infty} d_{i, y} \right) \left( \sum_{x=1}^{\infty} \tilde{h}(x | x_{1:(j-1)} = 0) \right) . \]  \( \text{(F.12)} \)

The first term is upper bounded by Eq. (14). Regarding the second term, since we are in the
typical set, \( \sum_{i=1}^{j-1} \sum_{y=1}^{\infty} d_{i, y} \) is small and we also use Eq. (12). Therefore the overall bound
on the second term is:

\[ (\beta + 1) \max(C(K, C_1), C(N, C_1)) \frac{1}{K \bar{j} - 1 + C_1} . \]

Combining the two bounds and Eq. (F.11) give the following bound on \( \mathbb{P}(U \neq D_j) \):

\[ \mathbb{P}(U \neq D_j) \leq \frac{C_4 \ln j + C_5}{K \bar{j} - 1 + C_1} + (\beta + 1) \max(C(K, C_1), C(N, C_1)) \frac{1}{K \bar{j} - 1 + C_1} \]

\[ \leq \text{constant} \frac{(\ln N + \ln K)}{K} \frac{1}{\bar{j} - 1 + C_1} . \]  \( \text{(F.13)} \)

We now show how the combination of Eqs. (F.10) and (F.13) imply Eq. (F.9). From
Eq. (F.13), there exists a coupling of \( P_{U} \) and \( P_{D_j} \) such that the difference probability is

\( L(0, 0) = 1, L(0, 1) = 2, L(1, 0) = 3, L(2, 0) = 4, L(1, 1) = 5, L(0, 2) = 6 \) and so on.
small. From Eq. (F.10), there exists a coupling of $P_U$ and $P_{D_j'|D_{1:(j-1)}}$ such that the difference probability is small. In both cases, we can sample from the conditional distribution based on $U$. $D_j|U$ exists because of the discussion after Eq. (F.11), while $D_j'|D_{1:(j-1)} = d_{1:(j-1)}, U$ exists because of Lemma D.4. Therefore, we can glue the two couplings together, by first sampling $U$, and then sample from the appropriate conditional distributions. By taking expectations of the simple triangle inequality for the discrete metric i.e.

$$1\{D_j \neq D_j'\} \leq 1\{D_j \neq U\} + 1\{D_j' \neq U\},$$

we reach Eq. (F.9).

The summation of the right hand side of Eq. (F.9) across $j$ leads to:

$$\sum_{j=1}^N B_j \leq \frac{\text{constant}}{K} + \text{constant} \frac{(\ln N + \ln K) \ln N}{K}. \quad (F.14)$$

In all, because of Eqs. (F.8) and (F.14), we can couple $D$ and $D'$ such that $P(D \neq D')$ is at most:

$$\frac{\text{constant}}{K} + \text{constant} \frac{(\ln N + \ln K) \ln N}{K}. \quad (F.15)$$

Aggregating the results from Eqs. (F.5), (F.6) and (F.15) (replacing the upper bound in Eq. (F.5) with the type of upper bound in Eq. (F.8)), we are done.

In applications, the observational likelihood $f$ and the ground measure $H$ might be random rather than fixed quantities. For instance, in linear–Gaussian beta–Bernoulli processes without good prior information, probabilistic models put priors on the variances of the Gaussian features as well as the noise in observed data. In such cases, the AIFAs remain the same as the in Theorem 3.2 (or Corollary 3.3) since the rate measure $\nu$ is still fixed. The above proof of Theorem 4.1 can be easily extended to the case where $f$ and $H$ are random, because the argument leading to Eq. (F.3) retains validity when $f$ and $H$ have the same distribution under the target and the approximate model. For completeness, we state the error bound in such cases where hyper-priors are used.

**Corollary F.1** (Upper bound for hyper-priors). Let $\mathcal{H}$ be a prior distribution for ground measures $H$ and $\mathcal{F}$ be a prior distribution for observational likelihoods $f$. Suppose the target model is

$$H \sim \mathcal{H}(.),$$

$$f \sim \mathcal{F}(.),$$

$$\Theta | H \sim \text{CRM}(H, \nu),$$

$$X_n | \Theta \overset{i.i.d.}{\sim} \text{LP}(\ell, \Theta), \quad n = 1, 2, \ldots, N,$$

$$Y_n | f, X_n \overset{\text{dep}}{\sim} f(\cdot | X_n), \quad n = 1, 2, \ldots, N.$$
The approximate model, with \( \nu_K \) as in Theorem 3.2 (or Corollary 3.3), is

\[
\begin{align*}
H & \sim \mathcal{H}(.), \\
f & \sim \mathcal{F}(.), \\
\Theta_K | H & \sim \text{IFA}_K(H, \nu_K), \\
Z_n | \Theta_K & \overset{i.i.d.}{\sim} \text{LP}(\ell, \Theta_K), \quad n = 1, 2, \ldots, N, \\
W_n | f, Z_n & \overset{\text{indep}}{\sim} f(\cdot | Z_n), \quad n = 1, 2, \ldots, N.
\end{align*}
\]

If Assumption 1 and Condition 1 hold, then there exist positive constants \( C', C'', C''' \) depending only on \( \{ C_i \}_{i=1}^5 \) such that

\[
d_{TV}(P_{Y_{1:N}}, P_{W_{1:N}}) \leq C' + C'' \ln 2 N + C''' \ln N \ln K.
\]

The upper bound in Corollary F.1 is visually identical to Theorem 4.1, and has no dependence on the hyper-priors \( \mathcal{H} \) or \( \mathcal{F} \).

F.2. Lower bound

Proof of Theorem 4.2. First we mention which probability kernel \( f \) results in the large total variation distance: the pathological \( f \) is the Dirac measure i.e., \( f(\cdot | X) := \delta_X(\cdot) \). With this conditional likelihood \( X_n = Y_n \) and \( Z_n = W_n \), meaning:

\[
d_{TV}(P_{BP_{N,\infty}}, P_{BP_{N,K}}) = d_{TV}(P_{X_{1:N}}, P_{Z_{1:N}}).
\]

Now we discuss why the total variation is lower bounded by the function of \( N \). Let \( A \) be the event that there are at least \( \frac{1}{2} \gamma C(N, \alpha) \) unique atom locations in among the latent states:

\[
A := \left\{ x_{1:N} : \# \text{unique atom locations} \geq \frac{1}{2} \gamma C(N, \alpha) \right\}.
\]

The probabilities assigned to this event by the approximate and the target models are very different from each other. On the one hand, since \( K < \frac{\gamma C(N, \alpha)}{2} \), under AIFA\(_K\), \( A \) has measure zero:

\[
P_{Z_{1:N}}(A) = 0. \tag{F.16}
\]

On the other hand, under beta–Bernoulli, the number of unique atom locations drawn is a Poisson random variable with mean exactly \( \gamma C(N, \alpha) \) — see Proposition C.1 and Proposition C.2. The complement of \( A \) is a lower tail event. By Lemma D.3 with \( \lambda = \gamma C(N, \alpha) \) and \( x = \frac{1}{2} \gamma C(N, \alpha) \):

\[
P_{X_{1:N}}(A) \geq 1 - \exp \left( -\frac{\gamma C(N, \alpha)}{8} \right). \tag{F.17}
\]

Because of Lemma D.10, we can lower bound \( C(N, \alpha) \) by a multiple of \( \ln N \):

\[
\exp \left( -\frac{\gamma C(N, \alpha)}{8} \right) \leq \exp \left( -\frac{\gamma \alpha \ln N}{8} + \frac{\alpha \gamma (\psi(\alpha) + 1)}{8} \right) = \frac{\text{constant}}{N^{\gamma \alpha / 8}}.
\]

We now combine Eqs. (F.16) and (F.17) and recall that total variation is the maximum over discrepancy in probabilistic masses. \qed
The proof of Theorem 4.3 relies on the ability to compute a lower bound on the total variation distance between a binomial distribution and a Poisson distribution.

**Proposition F.2** (Lower bound on total variation between binomial and Poisson). For all $K$, it is true that

$$d_{TV}\left(\text{Poisson} \left(\gamma\right), \text{Binom}\left(K, \frac{\gamma}{K+1}\right)\right) \geq C(\gamma)K\left(\frac{\gamma}{K+1}\right)^2,$$

where

$$C(\gamma) = \frac{1}{8} \frac{1}{\gamma + \exp(-1)(\gamma + 1)\max(12\gamma^2, 48\gamma, 28)}.$$

**Proof of Proposition F.2.** We adapt the proof of (Barbour and Hall, 1984, Theorem 2) to our setting. The Poisson($\gamma$) distribution satisfies the functional equality:

$$E[y(Z + 1) - Zy(Z)] = 0,$$

where $y$ is any real-valued function and $Z \sim \text{Poisson}(\gamma)$.

Denote $\gamma_K = \frac{\gamma}{K+1}$. For $m \in \mathbb{N}$, let

$$x(m) = m \exp\left(-\frac{m^2}{\gamma_K \theta}\right),$$

where $\theta$ is a constant which will be specified later. $x(m)$ serves as a test function to lower bound the total variation distance between $\text{Poisson}(\gamma)$ and $\text{Binom}(K, \gamma_K / K)$. Let $X_i \sim \text{Ber}(\frac{\gamma_K}{K})$, independently across $i$ from 1 to $K$, and $W = \sum_{i=1}^{K} X_i$. Then $W \sim \text{Binomial}(K, \gamma_K / K)$.

The following identity is adapted from (Barbour and Hall, 1984, Equation 2.1):

$$E[\gamma_K x(W + 1) - Wx(W)] = \left(\frac{\gamma_K}{K}\right)^2 \sum_{i=1}^{K} E[x(W_i + 2) - x(W_i + 1)],$$

where $W_i = W - X_i$.

We first argue that the right hand side is not too small i.e. for any $i$,

$$E[x(W_i + 2) - x(W_i + 1)] \geq 1 - \frac{3\gamma_K^2 + 12\gamma_K + 7}{\theta \gamma_K}.$$  (F.20)

Consider the derivative of $x(m)$:

$$\frac{d}{dm} x(m) = \exp\left(-\frac{m^2}{\gamma_K \theta}\right)\left(1 - \frac{2m^2}{\gamma_K \theta}\right) \geq 1 - \frac{3m^2}{\theta \gamma_K},$$

because of the easy-to-verify inequality $e^{-x}(1 - 2x) \geq 1 - 3x$ for $x \geq 0$. This means that

$$x(W_i + 2) - x(W_i + 1) \geq \int_{W_i + 1}^{W_i + 2} \left(1 - \frac{3m^2}{\theta \gamma_K}\right) dm = 1 - \frac{1}{\theta \gamma_K}(3W_i^2 + 9W_i + 7).$$

Taking expectations, noting that $E(W_i) \leq \gamma_K$ and $E(W_i^2) = \text{Var}(W_i) + [E(W_i)]^2 \leq \sum_{j=1}^{K} \frac{\gamma_K}{K} + (\gamma_K)^2 = \gamma_K^2 + \gamma_K$ we have proven Eq. (F.20).
Now, because of positivity of $x$, and that $\gamma \geq \gamma_K$, we trivially have
\[
\mathbb{E}[\gamma(x(W + 1) - Wx(W))] \geq \mathbb{E}[\gamma_K x(W + 1) - Wx(W)].
\] (F.21)

Combining Eq. (F.19), Eq. (F.20) and Eq. (F.21) we have that
\[
\mathbb{E}[\gamma x(W + 1) - Wx(W)] \geq K \left( \frac{\gamma_K}{K} \right)^2 \left( 1 - \frac{3\gamma_K^2 + 12\gamma_K + 7}{\theta\gamma_K} \right).
\]

Recalling Eq. (F.18), for any coupling $(W, Z)$ such that $W \sim \text{Binom} \left( K, \frac{\gamma/K}{\gamma/K + 1} \right)$ and $Z \sim \text{Poisson}(\gamma)$:
\[
\mathbb{E}[\gamma(x(W + 1) - x(Z + 1)) + Zx(Z) - Wx(W)] \geq \frac{\gamma^2_K}{K} \left( 1 - \frac{3\gamma_K^2 + 12\gamma_K + 7}{\theta\gamma_K} \right).
\]

Suppose $(W, Z)$ is the maximal coupling attaining the total variation distance between $P_W$ and $P_Z$ i.e. $\mathbb{P}(W \neq Z) = d_{TV}(P_Y, P_Z)$. Clearly,
\[
\begin{align*}
\gamma(x(W + 1) - x(Z + 1)) + Zx(Z) - Wx(W) \\
\leq & \ 1 \{W \neq Z\} \sup_{m_1, m_2} \left| (\gamma x(m_1 + 1) - m_1 x(m_1)) - (\gamma x(m_2 + 1) - m_2 x(m_2)) \right| \\
\leq & \ 21 \{W \neq Z\} \sup_m \left| \gamma x(m + 1) - mx(m) \right|.
\end{align*}
\]

Taking expectations on both sides, we conclude that
\[
2d_{TV}(P_W, P_Z) \times \sup_m \left| \gamma x(m + 1) - mx(m) \right| \geq \frac{\gamma^2_K}{K} \left( 1 - \frac{3\gamma_K^2 + 12\gamma_K + 7}{\theta\gamma_K} \right). \tag{F.22}
\]

It remains to upper bound $\sup_m \left| \gamma x(m + 1) - mx(m) \right|$. Recall that the derivative of $x$ is $\exp \left( -\frac{m^2}{\gamma_K \theta} \right) \left( 1 - \frac{2m^2}{\gamma_K \theta} \right)$, taking values in $[-2e^{-3/2}, 1]$. This means for any $m$, $-2e^{-3/2} \leq x(m + 1) - x(m) \leq 1$. Hence:
\[
\left| \gamma x(m + 1) - mx(m) \right| = |\gamma (x(m + 1) - x(m)) + (\gamma - m)x(m)|
\leq \gamma + (m + \gamma - m)x(m)
\leq \gamma + (m + \gamma) m \exp \left( -\frac{m^2}{\gamma_K \theta} \right)
\leq \gamma + (m + \gamma) m \exp \left( -\frac{m^2}{\gamma_K \theta} \right)
\leq \gamma + \gamma K \theta (\gamma + 1) \exp(-1). \tag{F.23}
\]

where the last inequality owes to the easy-to-verify $x \exp(-x) \leq \exp(-1)$. Combining Eq. (F.23) and Eq. (F.22) we have that
\[
d_{TV} \left( \text{Binom} \left( K, \frac{\gamma/K}{\gamma/K + 1} \right), \text{Poisson}(\gamma) \right) \geq \frac{1}{2} \frac{1 - \frac{3\gamma_K^2 + 12\gamma_K + 7}{\theta\gamma_K} \exp(-1)}{K} \frac{\gamma_K}{K}.
\]

Finally, we calibrate $\theta$. By selecting $\theta = \max \left( 12\gamma_K, \frac{28}{\gamma_K}, 48 \right)$ we have that the numerator of the unwieldy fraction is at least $\frac{1}{2}$ and its denominator is at most $\gamma + \exp(-1)(\gamma + 1) \max(12\gamma^2, 48\gamma, 28)$, because $\gamma_K < \gamma$. This completes the proof. \qed
Proof of Theorem 4.3. The constant \( C \) in the theorem statement is
\[
C := \gamma^2 / \left( \gamma + \exp(-1)(\gamma + 1) \max(12\gamma^2, 48\gamma, 28) \right),
\]
which is equal to \( \gamma^2 C(\gamma) \), with \( C(\gamma) \) from Proposition F.2.

First we mention which probability kernel \( f \) results in the large total variation distance. For any discrete measure \( \sum_{i=1}^M \delta_{\psi_i} \), \( f \) is the Dirac measure sitting on \( M \), the number of atoms.
\[
f(. | \sum_{i=1}^M \delta_{\psi_i}) := \delta_M(.).
\]
(F.24)

Now we show that under such \( f \), the total variation distance is lower bounded. From Lemma D.9, we know that
\[
d_{TV}(P_{Y_1}, P_{W_1}) \geq d_{TV}(P_{Y_1}, P_{W_1}).
\]
Hence it suffices to show:
\[
d_{TV}(P_{Y_1}, P_{W_1}) \geq C(\gamma) \frac{\gamma^2}{K} \frac{1}{(1 + \gamma/K)^2}.
\]

Recall the generative process defining \( P_{Y_1} \) and \( P_{W_1} \). \( Y_1 \) is an observation from the target beta–Bernoulli model, and the functions \( h, \bar{h}, \) and \( M_{n,x} \) are given in Example 4.1. By Proposition C.1,
\[
N_T \sim \text{Poisson}(\gamma), \quad \psi_k \overset{i.i.d.}{\sim} H, \quad X_1 = \sum_{i=1}^{N_T} \delta_{\psi_k}, \quad Y_1 \sim f(. | X_1).
\]
\( W_1 \) is an observation from the approximate model, so by Proposition C.2,
\[
N_A \sim \text{Binom} \left( K, \frac{\gamma/K}{1 + \gamma/K} \right), \quad \phi_k \overset{i.i.d.}{\sim} H, \quad Z_1 = \sum_{i=1}^{N_A} \delta_{\phi_k}, \quad W_1 \sim f(. | Z_1).
\]
Because of the choice of \( f \), \( Y_1 = N_T \) and \( W_1 = N_A \). Hence, by Proposition F.2,
\[
d_{TV}(P_{Y_1}, P_{W_1}) = d_{TV}(P_{N_T}, P_{N_A}) \geq C(\gamma) \frac{\gamma^2}{K} \frac{1}{(1 + \gamma/K)^2}.
\]
\( \Box \)

Appendix G: DPMM results

We consider Dirichlet process mixture models (Antoniak, 1974)
\[
\Theta \sim \text{DP}(\alpha, H), \quad X_n | \Theta \overset{i.i.d.}{\sim} \Theta, \quad n = 1, 2, \ldots, N, \quad (G.1)
\]
\[
Y_n | X_n \overset{\text{indep}}{\sim} f(\cdot | X_n), \quad n = 1, 2, \ldots, N.
\]
with corresponding approximation

\[ \Theta_K \sim \text{FSD}_K(\alpha, H), \]
\[ Z_n \mid \Theta_K \overset{i.i.d.}{\sim} \Theta_K, \quad n = 1, 2, \ldots, N, \quad (G.2) \]
\[ W_n \mid Z_n \overset{\text{indep}}{\sim} f(\cdot \mid Z_n), \quad n = 1, 2, \ldots, N. \]

Let \( P_{N,\infty} \) be the distribution of the observations \( Y_{1:N} \). Let \( P_{N,K} \) be the distribution of the observations \( W_{1:N} \).

**G.1. Upper bound**

Upper bounds on the error made by \( \text{FSD}_K \) can be used to determine the sufficient \( K \) to approximate the target process for a given \( N \) and accuracy level. We upper bound \( d_{TV}(P_{N,\infty}, P_{N,K}) \) in Theorem G.1.

**Theorem G.1** (Upper bound for DP mixture model). For some constants \( C_1, C_2, C_3 \) that only depend on \( \alpha \),

\[ d_{TV}(P_{N,\infty}, P_{N,K}) \leq \frac{C_1 + C_2 \ln^2 N + C_3 \ln N \ln K}{K}. \]

The proof is given in Appendix H.1. Theorem G.1 is similar to Theorem 4.1. The \( O(\ln^2 N) \) growth of the bound for fixed \( N \) can likely be reduced to \( O(\ln N) \), the inherent growth rate of DP mixture models (Arratia, Barbour and Tavaré, 2003, Section 5.2). The \( O(\ln K/K) \) rate of decrease to zero is tight because of a \( 1/K \) lower bound on the approximation error. Theorem G.1 is an improvement over the existing theory for \( \text{FSD}_K \), in the sense that Ishwaran and Zarepour (2002, Theorem 4) provide an upper bound on \( d_{TV}(P_{N,\infty}, P_{N,K}) \) that lacks an explicit dependence on \( K \) or \( N \) — that bound cannot be inverted to determine the sufficient \( K \) to approximate the target to a given accuracy, while it is simple to determine using Theorem G.1.

**G.2. Lower bounds**

As Theorem G.1 is only an upper bound, we now investigate the tightness of the inequality in terms of \( N \) and \( K \). We first look at the dependence of the error bound in terms of \( \ln N \). Theorem G.2 shows that finite approximations cannot be accurate if the approximation level is too small compared to the growth rate \( \ln N \).

**Theorem G.2** (\( \ln N \) is necessary). There exists a probability kernel \( f(\cdot) \), independent of \( K, N \), such that for any \( N \geq 2 \), if \( K \leq \frac{1}{2} C(N, \alpha) \), then

\[ d_{TV}(P_{N,\infty}, P_{N,K}) \geq 1 - \frac{C_3}{N^{\alpha/8}} \]

where \( C_3 \) is a constant only dependent on \( \alpha \).

The proof is given in Appendix H.2. Theorem G.2 implies that as \( N \) grows, if the approximation level \( K \) fails to surpass the \( C(N, \alpha)/2 \) threshold, then the total variation between the approximate and the target model remains bounded from zero — in fact, the error tends
to one. Recall that $C(N, \alpha) = \Omega(\ln N)$, so the necessary approximation level is $\Omega(\ln N)$.

Theorem G.2 is the analog of Theorem 4.2.

We also investigate the tightness of Theorem G.1 in terms of $K$. In Theorem G.3, our lower bound indicates that the $1/K$ factor in Theorem G.1 is tight (up to log factors).

**Theorem G.3** ($1/K$ lower bound). There exists a probability kernel $f(\cdot)$, independent of $K, N$, such that for any $N \geq 2$,

$$d_{TV}(P_{N,\infty}, P_{N,K}) \geq \frac{\alpha}{1 + \alpha K}.$$  

The proof is given in Appendix H.2. While Theorem G.1 implies that the normalized AIFA with $K = O\left(\text{poly}(\ln N)/\epsilon\right)$ atoms suffices in approximating the DP mixture model to less than $\epsilon$ error, Theorem G.3 implies that a normalized AIFA with $K = \Omega\left(1/\epsilon\right)$ atoms is necessary in the worst case. This worst-case behavior is analogous to Theorem 4.3 for DP-based models.

The $1/\epsilon$ dependence means that AIFAs are worse than TFAs in theory. It is known that small TFA models are already excellent approximations of the DP. Definition 4.5 is a very well-known finite approximation whose error is upper bounded in Proposition G.4.

**Proposition G.4.** (Ishwaran and James, 2001, Theorem 2) Let $\Xi_K \sim \text{TSB}_K(\alpha, H)$, $R_n \mid \Xi_K \sim \Xi_K$, $T_n \mid R_n \xrightarrow{unif} f(\cdot \mid R_n)$ with $N$ observations. Let $Q_{N,K}$ be the distribution of the observations $T_1:N$. Then:

$$d_{TV}(P_{N,\infty}, Q_{N,K}) \leq 2N \exp\left(-\frac{K - 1}{\alpha}\right).$$

Proposition G.4 implies that a TFA with $K = O\left(\ln \left(N/\epsilon\right)\right)$ atoms suffices in approximating the DP mixture model to less than $\epsilon$ error. Modulo log factors, comparing the necessary $1/\epsilon$ level for AIFA and the sufficient $\ln (1/\epsilon)$ level for TFA, we conclude that the necessary size for normalized IFA is exponentially larger than the sufficient size for TFA, in the worst case.

**Appendix H: Proofs of DP bounds**

Our technique to analyze the error made by FSD$_K$ follows a similar vein to the technique in Appendix F. We compare the joint distribution of the latents $X_{1:N}$ and $Z_{1:N}$ (with the underlying $\Theta$ or $\Theta_K$ marginalized out) using the conditional distributions $X_n \mid X_{1:(n-1)}$ and $Z_n \mid Z_{1:(n-1)}$. Before going into the proofs, we give the form of the conditionals.

The conditional $X_{1:N} \mid X_{1:(n-1)}$ is the well-known Blackwell-MacQueen prediction rule.

**Proposition H.1.** Blackwell and MacQueen (1973) For $n = 1$, $X_1 \sim H$. For $n \geq 2$,

$$X_n \mid X_{n-1}, X_{n-2}, \ldots, X_1 \sim \frac{\alpha}{n - 1 + \alpha} H + \sum_{j} \frac{n_j}{n - 1 + \alpha} \delta_{\psi_j},$$

where $\{\psi_j\}$ is the set of unique values among $X_{n-1}, X_{n-2}, \ldots, X_1$ and $n_j$ is the cardinality of the set $\{i : 1 \leq i \leq n - 1, X_i = \psi_j\}$.

The conditionals $Z_n \mid Z_{1:(n-1)}$ are related to the Blackwell-MacQueen prediction rule.

**Proposition H.2.** Pitman (1996) For $n = 1$, $Z_1 \sim H$. For $n \geq 2$, let $\{\psi_j\}_{j=1}^{n}$ be the set of unique values among $Z_{n-1}, Z_{n-2}, \ldots, Z_1$ and $n_j$ is the cardinality of the set $\{i : 1 \leq i \leq n - 1, Z_i = \psi_j\}$.
The case where \( n = \psi_1 \). If \( J_n < K \):

\[
Z_n \mid Z_{n-1}, Z_{n-2}, \ldots, Z_1 \sim (K - J_n)\alpha/K \quad n - 1 + \alpha \quad H + \sum_{j=1}^{J_n} n_j + \alpha/K \delta_{\psi_j},
\]

Otherwise, if \( J_n = K \), there is zero probability of drawing a fresh component from \( H \) i.e. \( Z_n \) comes only from \( \{\psi_j\}_{j=1}^{J_n} \):

\[
Z_n \mid Z_{n-1}, Z_{n-2}, \ldots, Z_1 \sim \sum_{j=1}^{J_n} n_j + \alpha/K \delta_{\psi_j}.
\]

\( J_n \leq K \) is an invariant of these of prediction rules: once \( J_n = K \), all subsequent \( J_m \) for \( m \geq n \) is also equal to \( K \).

### H.1. Upper bounds

**Proof of Theorem G.1.** To begin, observe that the conditional distributions of the observations given the latent variables are the same across target and approximate models: \( P_{X_{1:N} \mid Z_{1:N}} \) is the same as \( P_{Z_{1:N} \mid Z_{1:N}} \) if \( X_{1:N} = Z_{1:N} \). Therefore, using Lemma D.8, we want to show that there exists a coupling of \( P_{X_{1:N}} \) and \( P_{Z_{1:N}} \) that has small difference probability.

First, we construct a coupling of \( P_{X_{1:N}} \) and \( P_{Z_{1:N}} \) such that, for any \( n \geq 1 \), for any \( x_{1:(n-1)} \) such that \( J_n \) is the number of unique atom locations among \( x_{1:(n-1)} \) is at most \( K \),

\[
\mathbb{P}(X_n \neq Z_n \mid X_{1:(n-1)} = Z_{1:(n-1)} = x_{1:(n-1)}) \leq \frac{\alpha J_n}{K n - 1 + \alpha}.
\] (H.1)

The case where \( n = 1 \) reads that \( \mathbb{P}(X_1 \neq Z_1) = 0 \). Such a coupling exists because the total variation distance between the prediction rules \( X_n \mid X_{1:(n-1)} \) and \( Z_n \mid Z_{1:(n-1)} \) is small. Let \( \{\psi_j\}_{j=1}^{J_n} \) be the unique atom locations in \( x_{1:(n-1)} \) and \( n_j \) be the number of latents \( x_i \) that manifest atom location \( \psi_j \). The distribution \( X_n \mid X_{1:(n-1)} \) can be sampled from in two steps:

- Sample \( I_1 \) from the categorical distribution over \( J_n + 1 \) elements where, for \( 1 \leq j \leq J_n \), \( \mathbb{P}(I_1 = j) = n_j/(n - 1 + \alpha) \) and \( \mathbb{P}(I_1 = J_n + 1) = \alpha/(n - 1 + \alpha) \).
- If \( I_1 = j \) for \( 1 \leq j \leq J_n \), set \( X_n = \delta_{\psi_j} \). If \( I_1 = J_n + 1 \), draw a fresh atom from \( H \), label \( \psi_{J_n + 1} \) and set \( X_n = \delta_{\psi_{J_n + 1}} \).

Similarly, we can generate \( Z_n \mid Z_{1:(n-1)} \) in two steps:

- Sample \( I_2 \) from the categorical distribution over \( J_n + 1 \) elements where, for \( 1 \leq j \leq J_n \), \( \mathbb{P}(I_2 = j) = n_j + \alpha/K/(n - 1 + \alpha) \) and \( \mathbb{P}(I_2 = J_n + 1) = \alpha(1 - J_n/K)/(n - 1 + \alpha) \).
- If \( I_2 = j \) for \( 1 \leq j \leq J_n \), set \( Z_n = \delta_{\psi_j} \). If \( I_2 = J_n + 1 \), draw a fresh atom from \( H \), label \( \psi_{J_n + 1} \) and set \( Z_n = \delta_{\psi_{J_n + 1}} \).

Still conditioning on \( X_{1:(n-1)} \) and \( Z_{1:(n-1)} \), we observe that the distribution of \( X_n \mid I_1 \) is the same as \( Z_n \mid I_1 \). Hence, using the propagation argument from Lemma D.8, it suffices to couple \( I_1 \) and \( I_2 \) so that

\[
\mathbb{P}(I_1 \neq I_2 \mid X_{1:(n-1)} = Z_{1:(n-1)} = x_{1:(n-1)})
\]
is small. Since $J_1$ and $J_2$ are categorical distributions, the minimum of the difference probability is the total variation distance between the two distributions, which equals $1/2$ the $L_1$ distance between marginals

$$
\sum_{j=1}^{J_n} \left| \frac{n_j + \alpha/K}{n - 1 + \alpha} - \frac{n_j}{n - 1 + \alpha} \right| + \left| \frac{\alpha}{n - 1 + \alpha} - \frac{\alpha(1 - J_n/K)}{n - 1 + \alpha} \right| = \frac{2}{K} \frac{\alpha J_n}{n - 1 + \alpha}.
$$

Dividing the last equation by $2$ gives Eq. (H.1). The joint coupling of $P_{X_1:N}$ and $P_{Z_1:N}$ is the natural gluing of the couplings $P_{X_n | x_{1:(n-1)}}$ and $P_{Z_n | z_{1:(n-1)}}$.

We now show that for the coupling satisfying Eq. (H.1), the overall probability of difference $P(X_{1:N} \neq Z_{1:N})$ is small. Recall the growth function from Eq. (15). We will use the notation of a typical set in the rest of the proof:

$$
D_n := \{ x_{1:(n-1)} : J_n \leq (1 + \delta) \max (C(N - 1, \alpha), C(K, \alpha)) \}.
$$

In other words, the number of unique values among the $x_{1:(n-1)}$ is small. The definition of a typical set depends on the relative deviation $\delta$, which we calibrate at the end of the proof.

The following decomposition is used to investigate the difference probability on the typical set:

$$
P(X_{1:N} \neq Z_{1:N}) = P((X_{1:(N-1)}, X_N) \neq (Z_{1:(N-1)}, Z_N))
= P(X_{1:(N-1)} \neq Z_{1:(N-1)}) + P(X_N \neq Z_N, X_{1:(N-1)} = Z_{1:(N-1)}).
$$

(H.2)

The second term can be further expanded:

$$
P(X_N \neq Z_N, X_{1:(N-1)} = Z_{1:(N-1)}, X_{1:(N-1)} \in D_N)
+ P(X_N \neq Z_N, X_{1:(N-1)} = Z_{1:(N-1)}, X_{1:(N-1)} \notin D_N).
$$

The former term is at most

$$
P(X_N \neq Z_N | X_{1:(N-1)} = Z_{1:(N-1)}, X_{1:(N-1)} \in D_N),
$$

while the latter term is at most

$$
P(X_{1:(N-1)} \notin D_N).
$$

To recap, we can bound $P(X_{1:N} \neq Z_{1:N})$ by bounding three quantities:

1. The difference probability of a shorter process $P(X_{1:(N-1)} \neq Z_{1:(N-1)})$.
2. The difference probability of the prediction rule on typical sets $P(X_N \neq Z_N | X_{1:(N-1)} = Z_{1:(N-1)}, X_{1:(N-1)} \in D_N)$.
3. The probability of the atypical set $P(X_{1:(N-1)} \notin D_N)$.

By recursively applying the expansion initiated in Eq. (H.2) to $P(X_{1:(N-1)} \neq Z_{1:(N-1)})$, we actually only need to bound difference probability of the different prediction rules on typical sets and the atypical set probabilities.

Regarding difference probability of the different prediction rules, being in the typical set allows us to control $J_n$ in Eq. (H.1). Summation across $n = 1$ through $N$ gives the overall bound of

$$
2 \frac{\alpha}{K} (1 + \delta) \max (C(N - 1, \alpha), C(K, \alpha)) C(N, \alpha) \leq \text{constant} \frac{\ln N (\ln N + \ln K)}{K}.
$$

(H.3)
Regarding the atypical set probabilities, because \( J_{n-1} \) is stochastically dominated by \( J_n \), i.e., the number of unique values at time \( n \) is at least the number at time \( n-1 \), all the atypical set probabilities are upper bounded by the last one i.e. \( \mathbb{P}(X_{1:(N-1)} \notin D_N) \). \( J_{N-1} \) is the sum of independent Poisson trials, with an overall mean equaling exactly \( C(N-1, \alpha) \). 
Therefore, the atypical event has small probability because of Lemma D.1:

\[
\mathbb{P}(J_{N-1} > (1 + \delta) \max(C(N-1, \alpha), C(K, \alpha)) \leq \exp \left(-\frac{\delta^2}{2 + \delta} \max(C(N-1, \alpha), C(K, \alpha)) \right).
\]

Even accounting for all \( N \) atypical events, the total probability is small:

\[
\exp \left(-\left(\frac{\delta^2}{2 + \delta} \max(C(N-1, \alpha), C(K-1, \alpha) - \ln(N-1)\right)\right).
\]

By Lemma D.10, \( \max(C(N-1, \alpha), C(K-1, \alpha) \geq \alpha \max(\ln(N-1), \ln K - \alpha(\psi(\alpha) + 1)) \).
Therefore, if we set \( \delta \) such that \( \frac{\delta^2}{2 + \delta} = 2 \), we have

\[
\frac{\delta^2}{2 + \delta} \max(C(N-1, \alpha), C(K-1, \alpha) - \ln(N-1) \geq \ln K - \text{constant},
\]

meaning the overall atypical probabilities is at most

\[
\frac{\text{constant}}{K}.
\] (H.4)

The overall total variation bound combines Eqs. (H.3) and (H.4).

**Proof of Theorem 4.6.** The main idea is reducing to the Dirichlet process mixture model. We do this in two steps.

First, the conditional distribution of the observations \( W \mid H_{1:D} \) of the target model is the same as the conditional distribution \( Z \mid F_{1:D} \) of the approximate model if \( H_{1:D} = F_{1:D} \). Second, there exists latent variables \( \Lambda \) and \( \Phi \) such that the conditional distribution of \( H_{1:D} \mid \Lambda \) and the conditional \( F_{1:D} \mid \Phi \) are the same when \( \Lambda = \Phi \). Recall the construction of the \( F_d \) in terms of atom locations \( \phi_{d,j} \) and stick-breaking weights \( \gamma_{d,j} \):

\[
G_K \sim \text{FSD}_K(\omega, H),
\]

\[
\phi_{d,j} \mid G_K \sim \text{G}(.), \quad \text{across } d, j,
\]

\[
\gamma_{d,j} \sim \text{Beta}(1, \alpha), \quad \text{across } d, j \text{ (except } \gamma_{dT} = 1),
\]

\[
F_d \mid \phi_{d,.}, \gamma_{d,.} = \sum_{i=1}^{T} \left(\gamma_{di} \prod_{j<i} (1-\gamma_{dj})\right) \delta_{\phi_{d,i}}.
\]

Similarly \( H_d \) is also constructed in terms of atom locations \( \lambda_{d,j} \) and stick-breaking weights \( \eta_{d,j} \):

\[
G \sim \text{DP}(\omega, H),
\]

\[
\lambda_{d,j} \mid G \sim \text{G}(.), \quad \text{across } d, j,
\]

\[
\eta_{d,j} \sim \text{Beta}(1, \alpha), \quad \text{across } d, j \text{ (except } \eta_{dT} = 1),
\]

\[
H_d \mid \lambda_{d,.}, \eta_{d,.} = \sum_{i=1}^{T} \left(\eta_{di} \prod_{j<i} (1-\eta_{dj})\right) \delta_{\lambda_{d,i}}.
\]
Therefore, if we set \( \Lambda = \{\lambda_{d,j}\}_{d,j} \) and \( \Phi = \{\phi_{d,j}\}_{d,j} \), then \( H_1: D \mid \Lambda \) is the same as the conditional \( F_1: D \mid \Phi \) if \( \Lambda = \Phi \).

Overall, this means that \( W \mid \Lambda \) is the same as \( Z \mid \Phi \). Again by Lemma D.8, we only need to demonstrate a coupling between \( P_\Lambda \) and \( P_\Phi \) such that the difference probability is small.

From the proof of Theorem 4.1 in Appendix H.1, we already know how to couple \( P_\Lambda \) and \( P_\Phi \). On the one hand, since \( \lambda_{d,j} \) are conditionally iid given \( G \) across \( d,j \), the joint distribution of \( \lambda_{d,j} \) is from a DPMM (probability kernel \( f \) being Dirac \( f(x|\lambda) = \delta_x(\cdot) \)) where the underlying DP has concentration \( \omega \). On the other hand, since \( \phi_{d,j} \) are conditionally iid given \( G \) across \( d,j \), the joint distribution \( \phi_{d,j} \) comes from the finite mixture with FSD \( K \).

Each observational process has cardinality \( DT \). Therefore, we can couple \( P_\Lambda \) and \( P_\Phi \) such that

\[
P(\Lambda \neq \Phi) \leq \frac{C_1 + C_2 \ln^2(DT) + C_3 \ln(DT) \ln K}{K},
\]

where the constants \( C_i \) only depend on \( \omega \). \( \square \)

**H.2. Lower bounds**

**Proof of Theorem G.2.** First we mention which probability kernel \( f \) results in the large total variation distance: the pathological \( f \) is the Dirac measure i.e., \( f(\cdot | x) = \delta_x(\cdot) \). With this conditional likelihood \( X_n = Y_n \) and \( Z_n = W_n \), meaning:

\[
d_{TV}(P_{\infty}, P_{K}) = d_{TV}(P_{X_1:N}, P_{Z_1:N}).
\]

Now we discuss why the total variation is lower bounded by the function of \( N \). Let \( A \) be the event that there are at least \( \frac{1}{2} C(N, \alpha) \) unique components in among the latent states:

\[
A := \left\{ x_{1:N} : \text{#unique values} \geq \frac{1}{2} C(N, \alpha) \right\}.
\]

The probabilities assigned to this event by the approximate and the target models are very different from each other. On the one hand, since \( K < \frac{C(N, \alpha)}{2} \), under FSD \( K \), \( A \) has measure zero:

\[
P_{Z_1:N}(A) = 0. \tag{H.5}
\]

On the other hand, under DP, the number of unique atoms drawn is the sum of Poisson trials with expectation exactly \( C(N, \alpha) \). The complement of \( A \) is a lower tail event. Hence by Lemma D.2 with \( \delta = 1/2, \mu = C(N, \alpha) \), we have:

\[
P_{X_1:N}(A) \geq 1 - \exp \left(-\frac{C(N, \alpha)}{8}\right) \tag{H.6}
\]

Because of Lemma D.10, we can lower bound \( C(N, \alpha) \) by a multiple of \( \ln N \):

\[
\exp \left(-\frac{C(N, \alpha)}{8}\right) \leq \exp \left(-\frac{\alpha \ln N}{8} + \frac{\alpha(\psi(\alpha) + 1)}{8}\right) = \frac{\text{constant}}{N^{\alpha/8}}.
\]

We now combine Equations (H.5) and (H.6) and recall that total variation is the maximum over probability discrepancies. \( \square \)
Proof of Theorem G.3. First we mention which probability kernel \( f \) results in the large total variation distance: the pathological \( f \) is the Dirac measure i.e., \( f(\cdot | x) = \delta_x(\cdot) \).

Now we show that under such \( f \), the total variation distance is lower bounded. Observe that it suffices to understand the total variation between \( P_{Y_1,Y_2} \) and \( P_{W_1,W_2} \), because Lemma D.9 already implies

\[
d_{TV}(P_{N,\infty},P_{N,K}) \geq d_{TV}(P_{Y_1,Y_2},P_{W_1,W_2}).
\]

Since \( f \) is Dirac, \( X_n = Y_n \) and \( Z_n = W_n \) and we have:

\[
d_{TV}(P_{Y_1,Y_2},P_{W_1,W_2}) = d_{TV}(P_{X_1,X_2},P_{Z_1,Z_2}).
\]

Consider the event that the two latent states are equal. Under the target model,

\[
\mathbb{P}(X_2 = X_1) = \frac{1}{1 + \alpha},
\]

while under the approximate one,

\[
\mathbb{P}(Z_2 = Z_1) = \frac{1 + \alpha/K}{1 + \alpha}.
\]

They are simple consequences of the prediction rules in Propositions H.1 and H.2. Therefore, there exists a measurable event where the probability mass assigned by the target and approximate models differ by

\[
\frac{1 + \alpha/K}{1 + \alpha} - \frac{1}{1 + \alpha} = \frac{\alpha}{1 + \alpha} \frac{1}{K} \quad \text{(H.7)}
\]

meaning

\[
d_{TV}(P_{X_1,X_2},P_{Z_1,Z_2}) \geq \frac{\alpha}{1 + \alpha} \frac{1}{K}.
\]

Appendix I: Experimental setup

In this section, the notation for atom sizes, atom locations, latent trait counts and observed data follow that of Section 5 i.e. \((\tau_k)_{k=1}^K\) denotes the collection of atom sizes, \((\psi_k)_{k=1}^K\) denotes the collection of atom locations, \((x_{n,k})_{k=1,n=1}^{K,N}\) denotes the latent trait counts of each observation, and \((y_n)_{n=1}^N\) denotes the observed data.

I.1. Image denoising using the beta–Bernoulli process

Data. We obtain the “clean” house image from http://sipi.usc.edu/database/. We downscale the original 512 \times 512 image to 256 \times 256 and convert colors to gray scale. We add iid Gaussian noise to the pixels of the clean image, resulting in the noisy input image. We follow Zhou et al. (2009) in extracting the patches. We use patches of size 8 \times 8, and flatten each observed patch \( y_i \) into a vector in \( \mathbb{R}^{64} \).
Finite approximations. We use finite approximations that target the beta–Bernoulli process with \( BP(1, 0) \) i.e. \( \gamma = 1, \alpha = 1, d = 0 \). Zhou et al. (2009) remark that the denoising performance is not sensitive to the choice of \( \gamma \) and \( \alpha \). Therefore, we pick \( \gamma = \alpha = 1 \) for computational convenience, since the beta process with \( \alpha = 1 \) has the simple TFA in Example 5.2. To be explicit, the TFA for the given beta–Bernoulli process is

\[
v_j \sim \text{Beta}(1, 1), \quad i = 1, 2, \ldots, K,
\]

\[
\tau_i = \prod_{j=1}^{i} v_j, \quad i = 1, 2, \ldots, K,
\]

\[
x_{n,i} \mid \tau_i \sim \text{Ber}(\tau_i), \quad \text{across } n, i.
\]

while the corresponding AIFA is

\[
\tau_i \sim \text{Beta} \left( \frac{1}{K}, 1 \right), \quad i = 1, 2, \ldots, K,
\]

\[
x_{n,i} \mid \tau_i \sim \text{Ber}(\tau_i), \quad \text{across } n, i.
\]

We report the performance for \( K \)'s between 10 and 100 with spacing 10.

Ground measure and observational likelihood. Following Zhou et al. (2009), we fix the ground measure but put a hyper-prior (in the sense of Corollary F.1) on the observational likelihood. The ground measure is a fixed Gaussian distribution:

\[
\psi_i \sim \mathcal{N} \left( 0, \frac{1}{64} I_{64} \right), \quad i = 1, 2, \ldots, K.
\]

The observational likelihood involves two Gaussian distributions with random variances:

\[
\begin{align*}
\gamma_w &\sim \text{Gamma}(10^{-6}, 10^{-6}), \\
\gamma_e &\sim \text{Gamma}(10^{-6}, 10^{-6}), \\
w_{n,i} \mid \gamma_w &\sim \mathcal{N}(0, \gamma_w^{-1}), \quad \text{across } i, n, \\
y_n \mid x_n, w_n, \psi, \gamma_e &\sim \text{Indep} \left( \sum_{i=1}^{K} x_{n,i} w_{n,i} \psi_i, \gamma_e^{-1} I_{64} \right), \quad \text{across } n.
\end{align*}
\]

We use the (shape,rate) parametrization of the gamma distribution. The weights \( w_{n,i} \) enable an observation to manifest a non-integer (and potentially negative) scaled version of the \( i \)-th basis element. The precision \( \gamma_w \) determines the scale of these weights. The precision \( \gamma_e \) determines the noise variance of the observations. We are uninformative about the precisions by choosing the Gamma\((10^{-6}, 10^{-6})\) priors.

In sum, the full finite models combine either Eqs. (I.2), (I.3) and (I.4) (for AIFA) or Eqs. (I.1), (I.3) and (I.4) (for TFA).

Approximate inference. We use Gibbs sampling to traverse the posterior over all the latent variables — the ones that are most important for denoising are \( x, w, \psi \). The chosen ground measure and observational likelihood have the right conditional conjugacies so that blocked Gibbs sampling is conceptually simple for most of the latent variables. The only
difference between AIFA and TFA is the step to sample the feature proportions \( \tau \): TFA updates are much more involved compared to AIFA (see Section 5). The order in which Gibbs sampler scans through the blocks of variables does not affect the denoising quality. To generate the PSNR in Fig. 2a, after finishing the gradual introduction of all patches, we run 150 Gibbs sweeps. We use the final state of the latent variables at the end of these Gibbs sweep as the warm-start configurations in Figs. 2b and 2c.

**Evaluation metric.** We discuss how iterates from Gibbs sampling define output images. Each configuration of \( x, w, \psi \) defines each patch’s “noiseless” value:

\[
\bar{y}_n = \sum_{i=1}^{K} x_{n,i} w_{n,i} \psi_i.
\]

Each pixel in the overall image is covered by a small number of patches. The “noiseless” value of each pixel is the average of the pixel value suggested by the various patches that cover that pixel. We aggregate the output images across Gibbs sweeps by a simple weighted averaging mechanism. We report the PSNR of the output image with the original image following the formulas from Hore and Ziou (2010).

**I.2. Topic modelling with the modified HDP**

**Data.** We download and pre-process into bags-of-words about one million random Wikipedia documents, following Hoffman, Bach and Blei (2010).

**Finite models.** We fix the ground measure to be a Dirichlet distribution and the observational likelihood to be a categorical distribution i.e. no hyper-priors. The AIFA is

\[
G_0 \sim \text{FSD}_K(\omega, \text{Dir}(\eta 1_V)),
\]

\[
G_d \mid G_0 \sim \text{TSB}_T(\alpha, G_0),
\]

\[
\beta_{dn} \mid G_d \sim \text{G}(\cdot),
\]

\[
w_{dn} \mid \beta_{dn} \sim \text{Categorical}(\beta_{dn}),
\]

while the TFA is

\[
G_0 \sim \text{TSB}_K(\omega, \text{Dir}(\eta 1_V)),
\]

\[
G_d \mid G_0 \sim \text{TSB}_T(\alpha, G_0),
\]

\[
\beta_{dn} \mid G_d \sim \text{G}(\cdot),
\]

\[
w_{dn} \mid \beta_{dn} \sim \text{Categorical}(\beta_{dn}),
\]

We set the hyper-parameters \( \eta, \alpha, \omega, \) and \( T \) following Wang, Paisley and Blei (2011), in that \( \eta = 0.01, \alpha = 1.0, \omega = 1.0, T = 20 \). We report the performance for \( K \)’s between 20 and 300 with spacing 40.

**Approximate inference.** We approximate the posterior in each model using stochastic variational inference (Hoffman et al., 2013). Both models have conditional conjugacies that enable the use of exponential family variational distributions and closed-form expectation
equations for all update types. The batch size is 500. We use the learning rate parametrized by $\rho_t = (t + \tau)^{-\kappa}$, where $t$ is the number of data mini-batches. For cold-start experiments, we set $\tau = 1.0$ and $\kappa = 0.9$. To generate the results of Fig. 3a, we process 4000 mini-batches of documents. We obtain the warm-start initializations in Figs. 3b and 3c by processing 512 mini-batches of documents. When training from warm-start initialization, to reflect the fact that the initial topics are the results of a training period, we change $\tau = 512$, but use the same $\kappa$ as cold start.

Evaluation metrics. We compute held-out log-likelihood following Hoffman et al. (2013). Each test document $d'$ is separated into two parts $w_{\text{ho}}$ and $w_{\text{obs}}$, with no common words between the two. In our experiments, we set 75% of words to be observed, the remaining 25% unseen. The predictive distribution of each word $w_{\text{new}}$ in the $w_{\text{ho}}$ is exactly equal to:

$$p(w_{\text{new}} | D, w_{\text{obs}}) = \int_{\theta_d', \beta} p(w_{\text{new}} | \theta_d', \beta)p(\theta_d', \beta | D, w_{\text{obs}}) d\theta_d' d\beta.$$ 

This is an intractable computation as the posterior $p(\theta_d', \beta | D, w_{\text{obs}})$ is not analytical. We approximate it with a factorized distribution:

$$p(\theta_d', \beta | D, w_{\text{obs}}) \approx q(\beta | D)q(\theta_d'),$$

where $q(\beta | D)$ is fixed to be the variational approximation found during training and $q(\theta_d')$ minimizes the KL between the variational distribution and the posterior. Operationally, we do an E-step for the document $d'$ based on the variational distribution of $\beta$ and the observed words $w_{\text{obs}}$, and discard the distribution over $z_{d', i}$, the per-word topic assignments because of the mean-field assumption. Using those approximations, the predictive approximation is approximately:

$$p(w_{\text{new}} | D, w_{\text{obs}}) \approx \bar{p}(w_{\text{new}} | D, w_{\text{obs}}) = \sum_{k=1}^{K} \mathbb{E}_{q(\theta_d'(k))} \mathbb{E}_{q(\beta_k(w_{\text{new}}))},$$

and the final number we report for document $d'$ is:

$$\frac{1}{|w_{\text{ho}}|} \sum_{w \in w_{\text{ho}}} \ln \bar{p}(w | D, w_{\text{obs}}).$$

I.3. Comparing IFAs

Data. We generate synthetic data $\{y_n\}_{n=1}^{2000}$ from a power-law beta–Bernoulli process $BP(2, 0, 0.6)$.

$$\sum_{i=1}^{\infty} \theta_i \psi_i \sim BP(2, 0, 0.6; N(0, 5I_5)), \quad x_{n,i} | \theta_i \sim \text{Ber}(\theta_i), \quad \text{across } n, i,$$

$$y_n | x_{n, \cdot}, \psi \sim \text{Ber}(\sum_{i} x_{n,i} \psi_i, I_5), \quad \text{across } n.$$

Footnote: How each document is separated into these two parts can have an impact on the range of test log-likelihood values encountered. For instance, if the first (in order of appearance in the document) $x\%$ of words were the observed words and the last $(100 - x)\%$ words were unseen, then the test log-likelihood is low, presumably since predicting future words using only past words and without any filtering is challenging. Randomly assigning words to be observed and unseen gives better test log-likelihood.
We marginalize out the feature proportions $\theta_i$ and sample the assignment matrix $X = \{x_{n,i}\}$ from the power-law Indian buffet process (Teh and Görür, 2009). The feature means are Gaussian distributed, with prior mean 0 and prior covariance $5I_5$. Conditioned on the feature combination, the observations are Gaussian with noise variance $I_5$. For $N = 2000$ observations and the chosen random seed, there are over 200 latent features, but half of these features only appear once in the dataset. Since the data is exchangeable, without loss of generality, we use $y_{1:1500}$ for training and $y_{1501:2000}$ for evaluation.

**Finite approximations.** We use finite approximations that target the beta–Bernoulli process with $\text{BP}(2,0.0.6)$ i.e. $\gamma = 2, \alpha = 0, d = 0.6$. The $K$-atom AIFA prior over atom sizes uses the smoothed indicators from Eq. (2) and sets $a = 1$ and $b_K = 1/K$. In other words, the densities are

$$\nu_K(d\theta) := \frac{1\{0 \leq \theta \leq 1\}}{Z_K} \theta^{-1+c/K-dS(\theta-1/K)}(1-\theta)^{a+d-1}d\theta, \quad (I.5)$$

where $c := \frac{\gamma}{\alpha + d, 1-d}$ and $S(\theta) = \begin{cases} \exp \left( \frac{1}{\theta-1/K} - 1 \right) + 1 & \text{if } \theta \in (0, 1/K) \\ 1 & \text{otherwise.} \end{cases}$

The suitable normalization constant. The atom size distribution in $BFRY_K$ requires the two-parameter ($c, \alpha$) $BFRY$ random variable (Lee, James and Choi, 2016, Equation 8). The density of this random variable at $s$ equals

$$g(s) := \frac{c}{\Gamma(1-\alpha)} s^{-\alpha-1} \left( 1 - \exp\left(-\frac{\alpha}{c}s\right) \right).$$

Lee, James and Choi (2016, Equation 15) state that the iid atom weights that approximate beta process with mass $\gamma$, discount $d$, concentration $\alpha = 0$ are $J_k$ where $J_k := S_k/(S_k + 1)$ with

$$S_k \sim BFRY(\gamma/K,d). \quad (I.6)$$

In all, the approximation to the beta–Bernoulli part of the generative process is

$$\tau_i \overset{i.i.d.}{\sim} \tilde{\nu}(\cdot) \quad \text{for } i \in [K],$$

$$x_{n,i} | \tau_i \overset{\text{iid}}{\sim} \text{Ber}(\tau_i) \quad \text{across } n, i. \quad (I.7)$$

where $\tilde{\nu}$ is either for Eq. (I.5) for AIFA or the right hand side of Eq. (I.6) for BFRY. We report the performance for $K \in \{2, 4, 6, 8, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100\}$.

**Ground measure and observational likelihood.** We use hyper-priors in the sense of Corollary F.1. The ground measure is random because we do not fix the variance of the feature means.

$$\sigma_g \sim \text{Gamma}(5,5),$$

$$\psi_i \overset{i.i.d.}{\sim} \mathcal{N}(0, \sigma^2_g I_5) \text{ for } i \in [K]. \quad (I.8)$$

The observational likelihood is also random because we do not fix the noise variance of the observed data.

$$\sigma_c \sim \text{Gamma}(5,5),$$

$$y_n | x_{n,,}, \psi, \sigma_c \overset{\text{iid}}{\sim} \mathcal{N}\left( \sum_i x_{n,i} \psi_i, \sigma^2_c I_5 \right). \quad (I.9)$$

---

3We set the concentration $\alpha$ of the target beta process to be zero, because the competitor IFA only approximates beta processes with $\alpha = 0$. 
In Eqs. (I.8) and (I.9), we use the (shape, rate) parametrization of the gamma distribution. The full finite models are described by Eqs. (I.7), (I.8) and (I.9).

**Approximate inference.** We use mean-field variational inference to approximate the posterior. We pick the variational distribution 

\[ q(\sigma_c, \sigma_g, \tau, \psi, x) \]

with the following factorization:

\[ q(\sigma_c)q(\sigma_g)\prod_i q(\tau_i)\prod_i q(\psi_i)\prod_{i,n} q(x_{n,i}). \]

Each variation distribution is the natural exponential family:

\[ q(\sigma_c) = \text{Gamma}(\nu_c(0), \nu_c(1)), \]
\[ q(\sigma_g) = \text{Gamma}(\nu_g(0), \nu_g(1)), \]
\[ q(\psi_i) = \mathcal{N}(\tau_i, \zeta_i), \]
\[ q(\tau_i) = \text{Beta}(\kappa_i(0), \kappa_i(1)), \]
\[ q(x_{n,i}) = \text{Ber}(\phi_{n,i}). \]

We set the initial variational parameters using using the latent features, feature assignment matrix, and the variances of the features prior and the observations around the feature combination. We use the ADAM optimizer in Pyro (learning rate 0.01, \(\beta_1 = 0.9\), clipping gradients if their norms exceed 40) to minimize the KL divergence between the approximation and exact posterior. We sub-sample 50 data points at a time to form the objective for stochastic variational inference. We terminate training after processing 1,500 mini-batches of data.

**Evaluation metrics.** We use the following definition of predictive likelihood:

\[
\sum_{i=1}^{m} \ln \mathbb{P}(y_{n+i} \mid y_{1:n}),
\]

where \(y_{1:n}\) are the training data and \(\{y_{n+i}\}_{i=1}^{m}\) are the held-out data points.

We estimate \(\mathbb{P}(y_{n+i} \mid y_{1:n})\) using Monte Carlo samples, since the predictive likelihood is an integral of the posterior over training data:

\[
\mathbb{P}(y_{n+i} \mid y_{1:n}) = \int x_{n+i, \sigma, \psi, \tau} \mathbb{P}(y_{n+i} \mid x_{n+i, \psi, \sigma})\mathbb{P}(x_{n+i, \psi, \sigma, \tau} \mid y_{1:n}),
\]

where \(x_{n+i}\) is the assignment vector of the \(n+i\) test point. Let \(\{x_{(n+1):m+m}, \tau^s, \psi^s, \sigma^s\}_{s=1}^{S}\) be the \(S\) Monte Carlo samples of the variational approximation to the posterior. We jointly estimate \(\mathbb{P}(y_{n+i} \mid y_{1:n})\) across test points \(y_{n+i}\) using the \(S\) Monte Carlo samples:

\[
\mathbb{P}(y_{n+i} \mid y_{1:n}) \approx \frac{1}{S} \sum_{s=1}^{S} \mathbb{P}(y_{n+i} \mid x_{n+i}^s; \psi^s, \sigma^s).
\]

We use \(S = 1,000\) samples from the (approximate) posterior to estimate the average log test-likelihood in Equation (I.10).

**Appendix J: Additional experiments**

**J.1. Denoising plane image**

Similar to the house image, the clean plane image was obtained from [http://sipi.usc.edu/database/](http://sipi.usc.edu/database/). The clean, the corrupted, and the example denoised images from AIFA/TFA for plane images are given in Fig. J.1. In Figs. J.2b and J.2c, the approximation level is \(K = 60\).

\[10\] During inference, we add a small tolerance of \(10^{-3}\) to the standard deviations \(\sigma_c, \sigma_g, \zeta_i\) in the model to avoid singular covariance matrices, although this is not strictly necessary if we clip gradients.
Fig J.1: Sample AIFA and TFA denoised images have comparable quality. (a) shows the noiseless image. (b) shows the corrupted image. (c,d) are sample denoised images from finite models with $K = 60$. PSNR (in dB) is computed with respect to the noiseless image.

Fig J.2: (a) Peak signal-to-noise ratio (PNSR) as a function of approximation level $K$. The error bars reflect randomness in both initialization and simulation of the conditionals across 5 trials. AIFA denoising quality improves as $K$ increases, and the performance is similar to TFA across approximation levels. Moreover, the TFA- and AIFA-denoised images are very similar: the PSNR $\approx 50$ for TFA versus AIFA, whereas PSNR $< 35$ for TFA or AIFA versus the original image. (b,c) Show how PSNR evolves during inference. The “warm-start” lines in indicate that the AIFA-inferred (respectively, TFA-inferred) parameters are excellent initializations for TFA (respectively, AIFA) inference.

J.2. Denoising truck image

Similar to the house image, the clean truck image was obtained from http://sipi.usc.edu/database/. The clean, the corrupted, and the example denoised images from AIFA/TFA for truck images are given in Fig. J.3. In Figs. J.4b and J.4c, the approximation level is $K = 60$. 

(a) Original  (b) Input, 24.69 dB  (c) AIFA, 30.06 dB  (d) TFA, 30.24 dB

Fig J.3: Sample AIFA and TFA denoised images have comparable quality. (a) shows the noiseless image. (b) shows the corrupted image. (c,d) are sample denoised images from finite models with $K = 60$. PSNR (in dB) is computed with respect to the noiseless image.

Fig J.4: (a) Peak signal-to-noise ratio (PSNR) as a function of approximation level $K$. The error bars reflect randomness in both initialization and simulation of the conditionals across 5 trials. AIFA denoising quality improves as $K$ increases, and the performance is similar to TFA across approximation levels. Moreover, the TFA- and AIFA-denoised images are very similar: the PSNR $\approx 47$ for TFA versus AIFA, whereas PSNR $< 31$ for TFA or AIFA versus the original image. (b,c) Show how PSNR evolves during inference. The “warm-start” lines in indicate that the AIFA-inferred (respectively, TFA-inferred) parameters are excellent initializations for TFA (respectively, AIFA) inference.

J.3. Effect of $a$ and $b_K$ on AIFA

The setting of $a$ and $b_K$ do not have a big impact on the performance of AIFA in Fig. J.5. We report results for a combination of $a \in \{0.1, 1\}$ and $b_K = 1/\sqrt{K}$ or $b_K = 1/K$. 
Fig J.5: The predictive log-likelihood of AIFA is not sensitive to different settings of \( a \) and \( b_K \). Each color corresponds to a combination of \( a \) and \( b_K \). (a) is the average across 5 trials with different random seeds for the stochastic optimizer, while (b) is the best across the same trials.