

# Streaming Inference for Infinite Feature Models

Rylan Schaeffer<sup>1,2</sup>, Yilun Du<sup>3</sup>, Gabrielle Kaili-May Liu<sup>2</sup>, Ila Rani Fiete<sup>2,4</sup>

<sup>1</sup>Stanford CS, <sup>2</sup>MIT BCS, <sup>3</sup>MIT EECS, <sup>4</sup>McGovern Institute for Brain Research



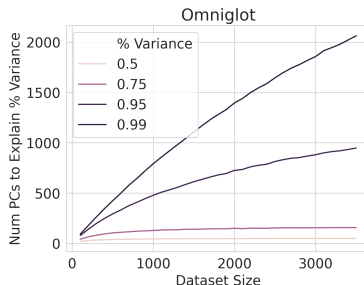
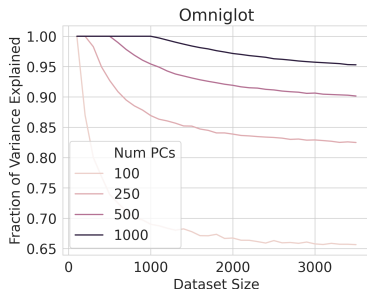
# Introduction

- ▶ Biological intelligence operates in a radically different data regime than (most) artificial intelligence
- ▶ Biological intelligence must contend with data that is (i) unsupervised, (ii) streaming (i.e. online) and (iii) non-stationary
- ▶ In this data regime, how should one approach learning?
- ▶ In this work, we set aside the non-stationary aspect
- ▶ We specifically ask how to use features models (a widely-used family of unsupervised learning algorithms that includes PCA, FA, ICA, NMF) on streaming data

On streaming data, using a preset fixed number of features results in an inability to model the data!

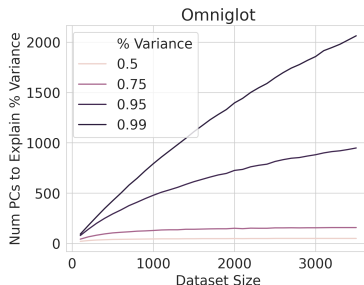
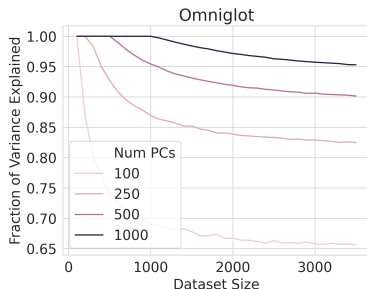
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How can one define a learning algorithm that grows in representational capacity as necessitated by the stream of data?

# Approach: The Recursive Indian Buffet Process

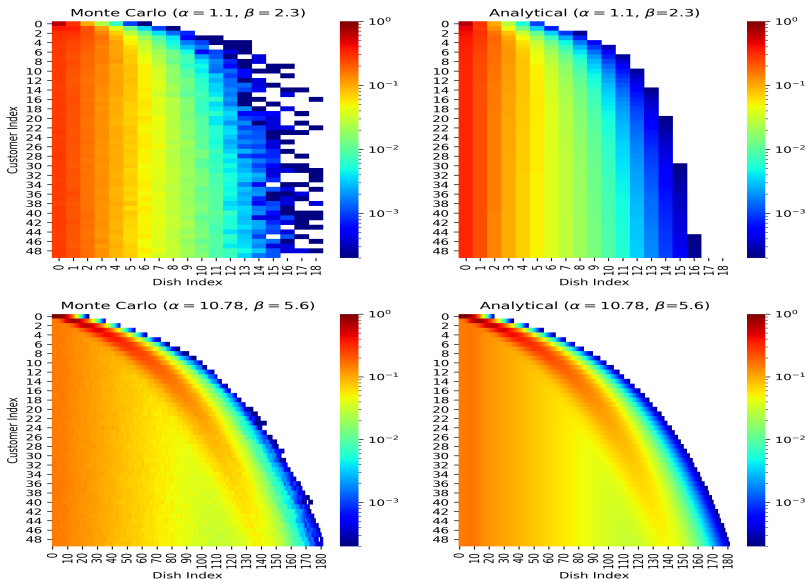
- ▶ Enable any feature model to add features, as necessitated by the data, via Bayesian nonparametrics

# Approach: The Recursive Indian Buffet Process

- ▶ Enable any feature model to add features, as necessitated by the data, via Bayesian nonparametrics
- ▶ Specifically, we derive a novel recursive form of the Indian Buffet Process designed specifically for streaming data:

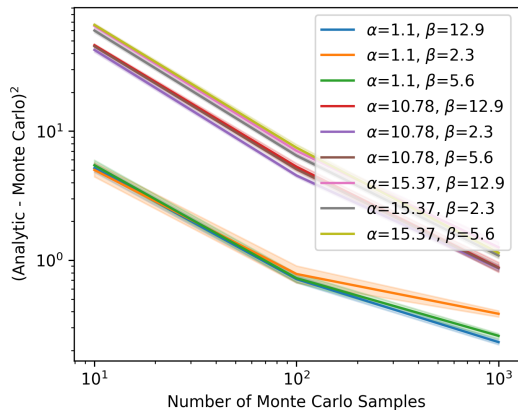
$$\underbrace{p(z_{nk} = 1)}_{\text{P}(n \text{ obs contains } k\text{th feature})} = \underbrace{\frac{1}{\beta + n - 1} \sum_{n' < n} p(z_{n'k} = 1)}_{\text{How probable is } k\text{th feature}} + \underbrace{p(\Lambda_{n-1} \leq k - 1) - p(\Lambda_{n-1} + \lambda_n \leq k - 1)}_{\text{Pressure to create new features as } n \rightarrow \infty}$$

# Monte Carlo Estimate vs. Analytical Expression





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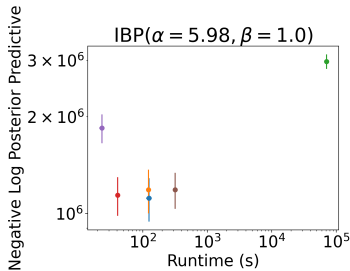
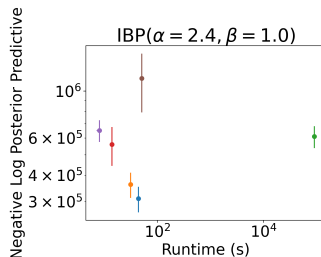
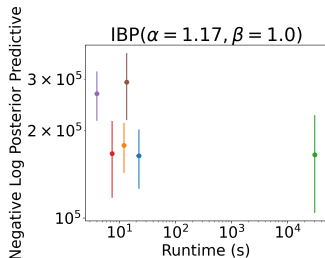
As the number of Monte Carlo samples increase, the average difference between the analytical R-IBP and the numerical estimate falls as an approximate power law for all combinations of  $\alpha, \beta$ .

# Intuition: Analytical Results

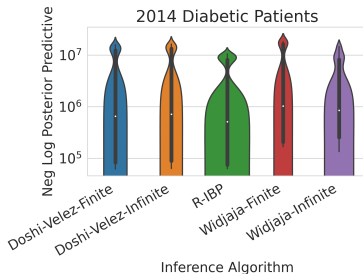
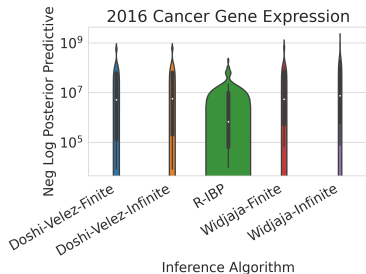
- The Recursive IBP follows a simple objective function: learn features  $A$  and indicators  $Z$  that maximize the likelihood while penalizing the number of used features  $\Lambda_N$

$$\arg \min_{A, Z, \Lambda_N} \quad \text{Tr} \left[ (O - ZA)^T (O - ZA) \right] + \gamma^2 \Lambda_N$$

# Synthetic Data: Faster & Equal/Better Performance



# Tabular Data: Faster & Equal/Better Performance



On cancer gene expression (left) and diabetic patient (right) data, R-IBP matches or outperforms baseline algorithms across hyperparameter configurations.

# Conjecture

The Recursive IBP outperforms non-streaming offline baselines because its graphical structure avoids chain multiplying inferred variables, instead adding inferred variables to running sums.

