BlinkML: Efficient Maximum Likelihood Estimation with Probabilistic Guarantees

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ABSTRACT
The rising volume of datasets has made training machine learning (ML) models a major computational cost in the enterprise. Given the iterative nature of model and parameter tuning, many analysts use a small sample of their entire data during their initial stage of analysis to make quick decisions (e.g., which features or what hyperparameters to use) and use the entire dataset only in later stages (i.e., when they have converged to specific model). This sampling, however, is performed in an ad-hoc fashion. Most practitioners cannot precisely capture the effect of sampling on the quality of their model, and eventually on their decision-making process during the tuning phase. Moreover, without systematic support for sampling operators, many optimizations and reuse opportunities are lost.

In this paper, we introduce BlinkML, a system for fast, quality-guaranteed ML training. BlinkML allows users to make error-computation tradeoffs: instead of training a model on their full data (i.e., full model), BlinkML can quickly train an approximate model with quality guarantees using a sample. The quality guarantees ensure that, with high probability, the approximate model makes the same predictions as the full model. BlinkML currently supports any ML model that relies on maximum likelihood estimation (MLE), which includes Generalized Linear Models (e.g., linear regression, logistic regression, max entropy classifier, Poisson regression) as well as PPCA (Probabilistic Principal Component Analysis). Our experiments show that BlinkML can speed up the training of large-scale ML tasks by $13.2\times-629\times$ while guaranteeing the same predictions, with 95% probability, as the full model.

ACM Reference Format:

1 INTRODUCTION
While data management systems have been widely successful in supporting traditional OLAP-style analytics, they have not been equally successful in attracting modern machine learning (ML) workloads. To circumvent this, most analytical database vendors have added integration layers for popular ML libraries in Python (e.g., Oracle’s cx_Oracle [4], SQL Server’s pymssql [9], and DB2’s ibm_db [10]) or R (e.g., Oracle’s RODM [11], SQL Server’s RevoScaleR [12], and DB2’s ibmDbR [6]). These interfaces simply allow machine learning algorithms to run on the data in-situ.

However, recent efforts have shown that data management systems have much more to offer. For example, materialization and reuse opportunities [15, 16, 31, 89, 102], cost-based optimization of linear algebraic operators [24, 29, 48], array-based representations [58, 92], avoiding denormalization [63, 64, 86], lazy evaluation [105], declarative interfaces [79, 91, 97], and query planning [62, 80, 90] are all readily available (or at least familiar) database functionalities that can deliver significant speedups for various ML workloads.

One additional but key opportunity that has been largely overlooked is the sampling abstraction offered by nearly every database system. Sampling operators have been mostly used for approximate query processing (AQP) [27, 32, 35, 45, 67, 72, 81, 82]. However, applying the lessons learned in the data management community regarding AQP, we could use a similar sampling abstraction to also speed up an important class of ML workloads.

Our Goal Given that (sub)sampling is already quite common in early stages of ML workloads—such as feature selection and hyper-parameter tuning—we propose a high-level system abstraction for training ML models, with which analysts can explicitly request error-computation trade-offs for several important classes of ML models. This involves systematic support for (i) bounding the deviation of the approximate model’s predictions from those of the full model given a sample size, and (ii) predicting the minimum sample size with which the trained model would meet a given prediction error.
Challenges While estimating sampling error is a well-studied problem for SQL queries [14, 74], it is more involved for ML models. There are two types of approaches here: (i) those that estimate the error before training the model (i.e., \textit{predictive}), and (ii) those that estimate the error after a model is trained (i.e., \textit{descriptive}). A well-known predictive technique is the so-called VC-dimension [73], which upper bounds the generalization error of a model. However, given that VC-dimension bounds are data-independent, they tend to be quite loose in practice [99]. Overestimated error bounds would lead the analysts to use the entire dataset even if similar results could be obtained from a small sample.¹

Common techniques for the descriptive approach include cross-validation [23] and Radamacher complexity [73]. Since these techniques are data-dependent, they provide tighter error estimates. However, they only bound the generalization error. While useful for evaluating the model’s quality on future (i.e., unseen) data, the generalization error provides little help in predicting how much the model quality would differ if the entire dataset were used instead of the current sample. Furthermore, when choosing the minimum sample size needed to achieve a user-specified accuracy, the descriptive approaches can be quite expensive: one would need to train multiple models each on a different sample size until a desirable error tolerance is met. Given that most ML models do not have an incremental training procedure (besides a warm start [28]), training multiple models to find an appropriate sample size might take longer overall than simply training a model on the full dataset (see Section 5.4).

Our Approach BlinkML’s underlying statistical technique offers tight error bounds for approximate models (Section 3), and does so without training multiple approximate models (Section 4).

BlinkML’s statistical techniques are based on the following observation: given a test example $\mathbf{x}$, the model’s prediction is simply a function $m(\mathbf{x}; \theta)$, where $\theta$ is the model parameter learned during the training phase. Therefore, if we could understand how $\theta$ would differ when trained on a sample (instead of the entire dataset), we could also infer its impact on the model’s prediction, i.e., $m(\mathbf{x}; \theta)$.

Specifically, let $\hat{\theta}_N$ be the model parameter obtained if one trains on the entire dataset (say, of size $N$), and $\theta_n$ be the model parameter obtained if one trains on a sample of size $n$. Obtaining $\hat{\theta}_n$ is fast when $n \ll N$; however, $\theta_N$ is unknown unless we use the entire dataset. Our key idea is to exploit the asymptotic distribution of $\hat{\theta}_N - \hat{\theta}_n$ to analytically (thus, efficiently) derive the conditional distribution of $\hat{\theta}_N | \theta_n$, where $\theta_n$ is the random variable for $\theta_n$ and $\hat{\theta}_N$ represents our (limited) probabilistic knowledge of $\theta_N$ (Theorem 1 and Corollary 1). A specific model parameter $\theta_n$ trained on a specific sample (of size $n$) is an instance of $\hat{\theta}_n$.

The asymptotic distribution of $\theta_N - \hat{\theta}_n$ is available for the ML methods relying on maximum likelihood estimation. This indicates that, while we cannot determine the exact value of $\theta_N$ without training the full model, we can use $\hat{\theta}_N | \theta_n$ to probabilistically bound the deviation of $\theta_N$ from $\theta_n$, and consequently, the deviation of $m(\mathbf{x}; \theta_N)$ from $m(\mathbf{x}; \theta_n)$ (Section 3.3). Moreover, we can estimate the deviation of $m(\mathbf{x}; \theta_N)$ from $m(\mathbf{x}; \theta_n)$ for any other sample size, say $n$, using only the model trained on the initial sample of size $n_0$ (Section 4). In other words, without having to perform additional training, we can efficiently search for the minimum sample size $n$, with which the approximate model, $m(\mathbf{x}; \theta_N)$ would be guaranteed, with probability $1 - \delta$, not to deviate from $m(\mathbf{x}; \theta_N)$ by more than $\epsilon$.

To efficiently perform the above process, BlinkML employs sampling-based approximation steps, which can incur small errors; however, BlinkML also reflects these errors by training a slightly more conservative model (Lemma 2).

Difference from Previous Work Existing sampling-based techniques are typically designed for a very specific type of model, such as non-uniform sampling for linear regression [17, 22, 34, 36–38, 41, 47], logistic regression [61, 96], clustering [42, 55], kernel matrices [49, 75], Gaussian mixture models [69], and point processes [66]. In contrast, BlinkML exploits uniform random sampling for training a much wider class of models, i.e., any MLE-based model; thus, no sampling probabilities need to be determined in advance. BlinkML’s contributions also include an efficient accuracy estimation for the approximate model and an accurate minimum sample size estimation for satisfying a user-requested accuracy. (See Sections 6 and 7 for discussions.)

Contributions We make the following contributions:

1. We introduce BlinkML, a system that offers error-computation trade-offs for training any MLE-based ML model, including Generalized Linear Models (e.g., linear regression, logistic regression, max entropy classifier, Poisson regression) and Probabilistic Principal Component Analysis. (Section 2)

2. We formally study the sampling distribution of an approximate model’s parameters, which we use to design an efficient algorithm that computes the probabilistic difference between an approximate model and a full one, without having to train the latter. (Section 3)

3. We develop a technique that can analytically infer the quality of a new approximate model, only using a previous model and without having to train the new one. This ability enables BlinkML to automatically and efficiently

¹This is why VC-dimensions are sometimes used indirectly, as a comparative measure of quality [64].
We empirically validate the statistical correctness and with a typical ML library, the user provides a training set, we formally describe the models supported by BlinkML as depicted in Figure 1 (top), then the traditional ML library outputs a model $D$ is a (multi-)set of $D$ is a (multi-)set of $m$ is called a feature vector and $y$ is called a label. Then, the traditional ML library outputs a model $m$ is trained on the given training set. We call $m$ a full model.

In classification tasks, $m(x)$ predicts a class label for an unseen feature vector $x$. For example, if $x$ encodes a review of a restaurant, a trained logistic regression classifier $m_N(x)$ may predict whether the review is positive or negative.

infer the appropriate sample size for satisfying an error tolerance requested by the user. (Section 4)

4. We empirically validate the statistical correctness and computational benefits of BlinkML through extensive experiments. (Section 5)

2 SYSTEM OVERVIEW

In this section, we provide an overview of BlinkML. We describe BlinkML’s user interface in Section 2.1. In Section 2.2, we formally describe the models supported by BlinkML. We describe BlinkML’s internal workflow in Section 2.3.

2.1 User Interface

In this section, we first describe the interface of a traditional ML library (e.g., scikit-learn [83], Weka [53], MLLib [1]), and then present the difference in BlinkML’s interface. To simplify our presentation, here we focus on classification models; however, our description can be easily generalized to both regression models (e.g., linear regression) and unsupervised learning (e.g., PPCA).

Traditional ML Libraries As depicted in Figure 1 (top), with a typical ML library, the user provides a training set $D \sim D$ and specifies a model class (e.g., linear regression, logistic regression, PPCA) along with model-specific configurations (e.g., regularization coefficients for linear or logistic regression, the number of factors for PPCA). A training set $D$ is a (multi-)set of $N$ training examples, which we denote as $\{(x_1, y_1), \ldots, (x_N, y_N)\}$. The $d$-dimensional vector $x_i$ is called a feature vector, and a real-valued $y_i$ is called a label. Then, the traditional ML library outputs a model $m_N$ trained on the given training set. We call $m_N$ a full model.

In classification tasks, $m(x)$ predicts a class label for an unseen feature vector $x$. For example, if $x$ encodes a review of a restaurant, a trained logistic regression classifier $m_N(x)$ may predict whether the review is positive or negative.

2.2 Supported Models & Abstraction

Here, we formally describe BlinkML’s supported models; then, we describe how BlinkML expresses the supported models in an abstract way.

Formal Description of Supported Models BlinkML supports any model that can be trained by solving the following problem: 

\[
\text{minimize} \quad \mathcal{L}(\theta) \quad \text{subject to} \quad \text{Pr}[y \neq m_N(x)] \leq \epsilon \quad \text{and} \quad \text{Pr}[y \neq m(x)] \leq \epsilon \cdot \delta
\]

where $\mathcal{L}(\theta)$ is the training error, $\epsilon$ is the error bound, and $\delta$ is the probability that the training error exceeds $\epsilon$.

In addition to the inputs required by traditional ML libraries, BlinkML needs one extra input: an approximation contract that consists of an error bound $\epsilon$ and a confidence level $\delta$. Then, BlinkML returns an approximate model $m_\theta$ that makes a different prediction than $m_N$ (for the test set) within $\epsilon$ with probability at least $1 - \delta$. That is, 

\[
\text{Pr}[[m_\theta(x) \neq m_N(x)] \leq \epsilon] \geq 1 - \delta
\]

where $\epsilon = \mathbb{E}_{x \sim D}[\Pr[y \neq m_N(x) \mid m_N(x) \neq y]]$.

We defer the proof to Appendix B. We also empirically confirm this result in Section 5.5.

Table 1: Notations

<table>
<thead>
<tr>
<th>Sym.</th>
<th>Meaning</th>
</tr>
</thead>
<tbody>
<tr>
<td>$N$</td>
<td>the size of dataset</td>
</tr>
<tr>
<td>$n$</td>
<td>the size of a sample</td>
</tr>
<tr>
<td>$D$</td>
<td>the training set (drawn from a distribution $D$)</td>
</tr>
<tr>
<td>$D_n$</td>
<td>a size-$n$ random sample of $D$</td>
</tr>
<tr>
<td>$m_N$</td>
<td>the full model, which is trained on $D$</td>
</tr>
<tr>
<td>$m_n$</td>
<td>an approximate model, which is trained on $D_n$</td>
</tr>
<tr>
<td>$\theta_N$</td>
<td>the parameter of the full model</td>
</tr>
<tr>
<td>$\theta_n$</td>
<td>the parameter of an approximate model</td>
</tr>
<tr>
<td>$v(m_n)$</td>
<td>the probability that $m_n$ makes a different prediction than $m_N$ (for the test set)</td>
</tr>
<tr>
<td>$\epsilon$</td>
<td>the error bound on $v(m_n)$</td>
</tr>
<tr>
<td>$\delta$</td>
<td>the probability of error bound violation</td>
</tr>
<tr>
<td>$n_0$</td>
<td>the size of initial training set (10K by default)</td>
</tr>
<tr>
<td>$D_0$</td>
<td>a size-$n_0$ random sample of $D$</td>
</tr>
<tr>
<td>$m_0$</td>
<td>an initial model trained on $D_0$</td>
</tr>
</tbody>
</table>
convex optimization problem:
\[ \arg \min_{\theta} \ f_n(\theta) \tag{1} \]
where \( f_n(\theta) = \frac{1}{n} \sum_{i=1}^{n} -\log \Pr(x_i, y_i; \theta) + R(\theta) \tag{2} \)

Here, \( \Pr(x_i, y_i; \theta) \) indicates the likelihood of observing the pair \((x_i, y_i)\) given \( \theta \). \( R(\theta) \) is the optional regularization term typically used to prevent overfitting, and \( n \) is the number of training examples used. When \( n=N \), this results in training the full model \( m_N \), and otherwise we have an approximate model \( m_n \). Different ML models use different expressions for \( \Pr(x_i, y_i; \theta) \). We provide specific examples in Appendix A.

The solution \( \theta_n \) to the minimization problem in Equation (1) is a value of \( \theta \) at which the gradient \( g_n(\theta) = \nabla f_n(\theta) \) of the objective function \( f_n(\theta) \) becomes zero.

\[ g_n(\theta_n) = \left[ -\frac{1}{n} \sum_{i=1}^{n} q(\theta_n; x_i, y_i) \right] + r(\theta_n) = 0 \tag{3} \]

where \( q(\theta; x_i, y_i) \) denotes \( -\nabla_{\theta} \log \Pr(x_i, y_i; \theta) \) and \( r(\theta) \) denotes \( \nabla_{\theta} R(\theta) \).

**Examples of Supported Models** BlinkML currently supports the following four model classes: linear regression, logistic regression, max entropy classifier, and PPCA. However, BlinkML’s core technical contributions (Theorems 1 and 2 in Sections 3 and 4) can be generalized to any ML algorithms that rely on maximum likelihood estimation.

**Model Abstraction** A model class specification (MCS) is the abstraction that allows BlinkML’s components to remain generic and not tied to the specific internal logic of the supported ML models. Each MCS must implement the following two methods:

1. \texttt{diff(m1, m2)}: This function computes the prediction difference between two models \( m_1 \) and \( m_2 \), using part of the training set (i.e., holdout set) that was not used during model training.

2. \texttt{gradients}: This function returns a list of \( q(\theta; x_i, y_i) + r(\theta) \) for \( i = 1, \ldots, n \), as defined in Equation (3). Although iterative optimization algorithms typically rely only on the average of this list of values (i.e., the gradient \( \nabla_{\theta} f_n(\theta) \)), the gradients

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2 In this work, we assume \( \theta_n \) has fully converged to the optimal point, satisfying Equation (3). The non-fully converged cases can be handled by simply adding small error terms to the diagonal elements of \( J \) in Theorem 1.

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### 2.3 System Workflow

We describe the workflow between BlinkML’s components depicted in Figure 2. First, Coordinator obtains a size-\( n_0 \) sample \( D_0 \) of the training set \( D \). We call \( D_0 \) the initial training set (10K by default). Coordinator then invokes Model Trainer to train an initial model \( m_0 \) on \( D_0 \), and subsequently invokes Model Accuracy Estimator to estimate the accuracy \( \epsilon_0 \) of \( m_0 \) (with confidence \( 1 - \delta \)). If \( \epsilon_0 \) is smaller than or equal to the user-requested error bound \( \epsilon \), Coordinator simply returns the initial model to the user. Otherwise, Coordinator prepares to train a second model, called the final model \( m_n \). To determine the sample size \( n \) required for the final model to satisfy the error bound, Coordinator consults Sample Size Estimator to estimate the smallest \( n \) with which the model difference between \( m_0 \) and \( m_N \) (i.e., the unknown full model) would not exceed \( \epsilon \) with probability at least \( 1 - \delta \). Note that this operation of Sample Size Estimator does not rely on Model Trainer; that is, no additional (approximate) models are trained for estimating \( n \). Finally, Coordinator invokes Model Trainer (for a second time) to train on a sample of size \( n \) and return \( m_n \) to the user. Therefore, in the worst case, at most two approximate models are trained.

### 3 MODEL ACCURACY ESTIMATOR

Model Accuracy Estimator estimates the accuracy of an approximate model. That is, given an approximate model \( m_n \) and a confidence level \( \delta \), Model Accuracy Estimator computes \( \epsilon \), such that \( v(m_n) \leq \epsilon \) with probability at least \( 1 - \delta \). In Section 3.1, we first overview the process of Model Accuracy Estimator. In Section 3.2, we establish the statistical properties of the models supported by BlinkML. Then, in Section 3.3, we explain how BlinkML exploits these statistical properties to estimate the accuracy of an approximate model.

#### 3.1 Accuracy Estimation Overview

To compute the probabilistic upper bound \( \epsilon \), Model Accuracy Estimator exploits the fact that both \( m_0 \) and \( m_N \) are essentially the same function (i.e., \( m(x) \)) but with different model parameters (i.e., \( \theta_0 \) and \( \theta_N \)). Although we cannot compute the exact value of \( \theta_N \) without training the full model \( m_N \), we can still estimate its probability distribution (we explain this in Section 3.2). The probability distribution of \( \theta_N \) is then used to estimate the distribution of \( v(m_n) \), which is the quantity we aim to upper bound. The upper bound \( \epsilon \) is determined
we formally present this idea. To account for these differences between models, we can obtain the relationship between \( \hat{\theta}_n - \hat{\theta}_N \), which leads to a larger distance between \( \hat{\theta}_n \) and \( \hat{\theta}_N \). In other words, the approximate model’s parameters; \( \hat{\theta}_n \) is simply one instance of \( \hat{\theta}_N \). We also use \( \hat{\theta}_N \) to represent our (limited) knowledge of \( \theta_N \). Then, our goal is to obtain the distribution of \( \theta_n - \hat{\theta}_N \), and then use this distribution to estimate the prediction difference between \( m(\theta_n) \) and \( m(\hat{\theta}_N) \).

Intuition Since \( \theta_n \) is the value that satisfies Equation (3) for \( n \) training examples (instead of \( N \)), we can obtain the difference \( \alpha J \) between \( g_n(\theta_n) \) and \( g_N(\hat{\theta}_N) \). In addition, we can obtain the relationship \( H \) between \( g_n(\theta_n) - g_N(\hat{\theta}_N) \) and \( \theta_n - \hat{\theta}_N \) using the Taylor expansion of \( g_n(\theta) \). Then, we can finally derive the difference between \( \theta_n \) and \( \hat{\theta}_N \).

Figure 3 depicts this idea intuitively. In the figure, the slope \( H \) captures the surface of the gradient, and \( \alpha J \) captures the variance of the gradient; \( \alpha J \) decreases as \( n \) increases. Thus, if a model is more flexible (e.g., smaller regularization coefficients), the slope becomes more moderate (i.e., smaller elements in \( H \)), which leads to a larger distance between \( \hat{\theta}_N \) and \( \hat{\theta}_N \) given the same \( \alpha J \). In other words, the approximate model will be less accurate given a fixed sample size. Below, we formally present this idea. To account for these differences between models, BlinkML automatically adjusts its sample size \( n \) when it trains an approximate model to satisfy the requested error bound (Section 4).

Parameter Distribution The following theorem provides the distribution of \( \hat{\theta}_n \) \(-\hat{\theta}_N \) (its proof is in Appendix B).

**Theorem 1.** Let \( J \) be the Jacobian of \( g_n(\theta) - r(\theta) \) evaluated at \( \theta_n \), and let \( H \) be the Jacobian of \( g_n(\theta) \) evaluated at \( \hat{\theta}_n \). Then, 
\[
\hat{\theta}_n - \hat{\theta}_N \rightarrow N(0, \alpha H^{-1}JH^{-1}), \quad \alpha = \frac{1}{n} - \frac{1}{N}
\]
as \( n \rightarrow \infty \) and \( N \rightarrow \infty \). \( N \) denotes a normal distribution, which means that \( \hat{\theta}_n - \hat{\theta}_N \) asymptotically follows a multivariate normal distribution with covariance matrix \( \alpha H^{-1}JH^{-1} \).

Directly computing \( H \) and \( J \) requires \( \Omega(d^2) \) space where \( d \) is the number of features. This can be prohibitively expensive when \( d \) is large. To address this, these quantities are indirectly computed (as described in Section 3.4 and Section 4.3), reducing the computational cost to only \( O(d) \). Our empirical study shows that BlinkML can scale up to datasets with a million features (Section 5).

In Theorem 1, \( J \) is essentially the covariance matrix of gradients (computed on individual examples). Since BlinkML uses uniform random sampling, estimating \( J \) is simpler; however, even when non-uniform random sampling is used, \( J \) can still be estimated if we know the sampling probabilities. By assigning those sampling probabilities in a task-specific way, one could obtain higher accuracy, which we leave as future work.

The following corollary provides the conditional distribution of \( \theta_N \) \( \theta_n \) (proof in Appendix B).

**Corollary 1.** Without any a priori knowledge of \( \theta_N \),
\[
\hat{\theta}_N \mid \theta_n \rightarrow N(\theta_n, \alpha H^{-1}JH^{-1}), \quad \alpha = \frac{1}{n} - \frac{1}{N}
\]
as \( n \rightarrow \infty \) and \( N \rightarrow \infty \).

The following section uses the conditional distribution \( \hat{\theta}_N \mid \theta_n \) (in Corollary 1) to obtain an error bound on the approximate model.

**3.3 Error Bound on Approximate Model**

In this section, we describe how Model Accuracy Estimator estimates the accuracy of an approximate model \( m_n \). Specifically, we show how to estimate \( \psi(m_n) \) without training \( m_N \).

Let \( h(\theta_N) \) denote the probability density function of the normal distribution with mean \( \theta_n \) and covariance matrix \( \alpha H^{-1}JH^{-1} \) (obtained in Corollary 1). Then, we aim to find the error bound \( \epsilon \) of an approximate model that holds with probability at least \( 1 - \delta \). That is,
\[
\Pr_{\theta_N}[\psi(m_n) \leq \epsilon] \geq 1 - \delta \quad \text{where}
\]
\[
\Pr_{\theta_N}[\psi(m_n) \leq \epsilon] = \int \mathbb{1}[\psi(m_n; \theta_N) \leq \epsilon] h(\theta_N) \, d\theta_N, \quad \epsilon
\]
where the integration is over the domain of \( \theta_N \) (in \( R^d \)); \( \psi(m_n; \theta_N) \) is the error of \( m_n \) when the full model’s parameter is \( \theta_N \); and \( \mathbb{1}[\cdot] \) is the indicator function that returns 1 if its argument is true and returns 0 otherwise. Since the above expression involves the model’s (blackbox) prediction function \( m(x) \), it cannot be analytically computed in general.
To compute Equation (4), BLINKML’s Model Accuracy Estimator uses the empirical distribution of \( h(\theta_N) \) as follows. Let \( \theta_{N,1}, \ldots, \theta_{N,k} \) be i.i.d. samples drawn from \( h(\theta_N) \). Then,

\[
\int \left[ v(m_n; \theta_N) \right] h(\theta_N) \, d\theta_N \approx \frac{1}{k} \sum_{i=1}^{k} \left[ v(m_n; \theta_{N,i}) \right]
\]

To take into account the approximation error in Equation (5), BLINKML uses conservative estimates on \( \varepsilon \) as formally stated in the following lemma (see Appendix B for proof).

**Lemma 2.** If \( \varepsilon \) satisfies

\[
\frac{1}{k} \sum_{i=1}^{k} \left[ v(m_n; \theta_{N,i}) \right] \leq \varepsilon \quad \text{then} \quad \Pr\left[ v(m_n) \leq \varepsilon \right] \geq 1 - \delta.
\]

The above lemma implies that by using a larger \( k \) (i.e., number of sampled values), we can obtain a tighter \( \varepsilon \). To obtain a large \( k \), an efficient sampling algorithm is necessary. Since \( \hat{\theta}_N \) follows a normal distribution, one can simply use an existing library, such as `numpy.random`. However, BLINKML uses its own fast, custom sampler to avoid directly computing the covariance matrix \( H^{-1} \) (see Section 4.3).

### 3.4 Computing Necessary Statistics

We present three methods—(1) ClosedForm, (2) InverseGradients, and (3) ObservedFisher—for computing \( H \). Given \( H \), computing \( J \) is straightforward since \( J = H - J_r \), where \( J_r \) is the Jacobian of \( r(\theta) \). BLINKML uses ObservedFisher by default since it achieves high memory-efficiency by avoiding the direct computations of \( H \).

**Method 1: ClosedForm**

ClosedForm uses the analytic form of the Jacobian \( H(\theta) \) of \( g_n(\theta) \), and sets \( \hat{\theta} = \theta_n \) by the definition of \( H \). For instance, \( H(\theta) \) of L2-regularized logistic regression is expressed as follows:

\[
H(\theta) = \frac{1}{n} X^T Q X + \beta I
\]

where \( X \) is an \( n \times d \) matrix whose \( i \)-th row is \( x_i \), and \( Q \) is a \( d \times d \) diagonal matrix whose \( i \)-th diagonal entry is \( \sigma(\beta^T x_i)(1 - \sigma(\beta^T x_i)) \), and \( \beta \) is the coefficient of L2 regularization. When \( H(\theta) \) is available, as in the case of logistic regression, ClosedForm is fast and exact.

However, inverting \( H \) is computationally expensive when \( d \) is large. Also, using ClosedForm is less straightforward when obtaining analytic expression of \( H(\theta) \) is non-trivial.

**Method 2: InverseGradients**

InverseGradients numerically computes \( H \) by relying on the Taylor expansion of \( g_n(\hat{\theta}) \): \( g_n(\theta_n + d\theta) \approx g_n(\theta_n) + H d\theta \). Since \( g_n(\theta_n) = 0 \), the Taylor expansion simplifies to:

\[
g_n(\theta_n + d\theta) \approx H d\theta
\]

The values of \( g_n(\theta_n + d\theta) \) and \( g_n(\theta_n) \) are computed using the \texttt{grads} function provided by the \texttt{MCS}. The remaining question is what values of \( d\theta \) to use for computing \( H \). Since \( H \) is a \( d \times d \) matrix, BLINKML uses \( d \) number of linearly independent \( d\theta \) to fully construct \( H \). That is, let \( P = eI \), where \( e \) is a small real number (10^{-6} by default). Also, let \( R \) be the \( d \times d \) matrix whose \( i \)-th column is \( g_n(\theta_n + P_{:,i}) \), where \( P_{:,i} \) is the \( i \)-th column of \( P \). Then, \( \varepsilon \approx \Pr\left[ v(m_n) \leq \varepsilon \right] \geq 1 - \delta \).

Since InverseGradients only relies on the \texttt{grads} function, it is applicable to all supported models. Although InverseGradients is accurate, it is still computationally inefficient for high-dimensional data, since the \texttt{grads} function must be called \( d \) times. We study its runtime overhead in Section 5.6.

**Method 3: ObservedFisher**

ObservedFisher numerically computes \( H \) by relying on the information matrix equality [76].\(^3\) According to the information matrix equality, the covariance matrix \( C \) of \( q(\theta_n; x_i, y_i) \), for \( i = 1, \ldots, n \), is asymptotically identical to \( J_r(\theta_n) \). In addition, given \( J \), we can simply obtain \( H = C + J_r \). Our empirical study in Section 5.6 shows that ObservedFisher is highly accurate for \( n \geq 5K \).

Instead of computing the \( d \times d \) matrix \( C \) directly, ObservedFisher takes a slightly different approach. That is, ObservedFisher computes factors \( U \) and \( \Sigma \) such that \( C = U \Sigma^2 U^T \), where \( U \) is a \( d \times d \) matrix, and \( \Sigma \) is an \( n \times n \) diagonal matrix. As described below, this factor-based approach is significantly more efficient when \( d \) is large, hence allowing BLINKML to scale up to high-dimensional data.

Specifically, let \( Q \) be the \( n \times d \) matrix whose \( i \)-th row is \( q(\theta_n; x_i, y_i) \). Then, ObservedFisher performs the singular value decomposition of \( Q^T \) to obtain \( U \), \( \Sigma \), and \( V \) such that \( Q^T = U \Sigma V^T \). Then, the following relationship holds:

\[
C = Q^T Q = U \Sigma^2 U^T
\]

As stated above, ObservedFisher never computes \( C \); it only stores \( U \) and \( \Sigma \), which are used directly for obtaining samples from \( N(0, H^{-1} J H^{-1}) \) (see Section 4.3). The cost of singular value decomposition is \( O(\min(n^2 d, nd^2)) \). When \( d \geq n \), this time complexity becomes \( O(n^2 d) = O(d) \) for a fixed sample size \( (n_0 = 10K) \) by default. Moreover, ObservedFisher requires only a single call of the \texttt{grads} function. Section 5.6 empirically studies the relationship between \( n \) and ObservedFisher’s runtime.

### 4 SAMPLE SIZE ESTIMATOR

Sample Size Estimator estimates the minimum sample size \( n \) such that \( E(m_n(x) \neq m_N(x)) \) is not larger than the requested error bound \( \varepsilon \) with probability at least \( 1 - \delta \). In this process,

\(^3\)ObservedFisher is also inspired by Hessian-free optimizations [68, 71].
Sample Size Estimator does not train any additional approximate models; it only relies on the initial model \( m_0 \) given to this component.

### 4.1 Quality Estimation sans Training

This section explains how Sample Size Estimator computes the probability of \( E_x(m_n(x) \neq m_N(x)) \leq \epsilon \) given the initial model \( m_0 \). Since both models—\( m_n(x) = m(x; \hat{\theta}_n) \) and \( m_N(x) = m(x; \hat{\theta}_N) \)—are uncertain, Sample Size Estimator uses the joint probability distributions of \( \hat{\theta}_n \) and \( \hat{\theta}_N \) to compute the probability. To make it clear that both models involve uncertain parameters, we use the following notation:

\[
v(m_n, m_N; \theta_n, \theta_N) = E_x \cdot D(1 \mid m(x; \theta_n) \neq m(x; \theta_N))
\]

The computed probability, i.e., \( \Pr(v(m_n, m_N; \theta_n, \theta_N) \leq \epsilon) \) is then used in the following section for finding \( n \) that makes the probability at least \( 1 - \delta \).

Like Model Accuracy Estimator, Sample Size Estimator computes the probability using the i.i.d. samples from the joint distribution \( h(\theta_n, \theta_N) \) of \( (\theta_n, \theta_N) \) as follows:

\[
\Pr(v(m_n, m_N; \theta_n, \theta_N) \leq \epsilon) = \int \int 1 \cdot [v(m_n, m_N; \theta_n, \theta_N) \leq \epsilon] \cdot h(\theta_n, \theta_N) \, d\theta_n \, d\theta_N
\]

\[
= \frac{1}{k} \sum_{i=1}^{k} 1 \cdot [v(m_n, m_N; \theta_n, \theta_N) \leq \epsilon]
\]

where the integration is over the domain of \( \theta_n \) and the domain of \( \theta_N \), both of which are \( \mathbb{R}^d \). To offset the approximation error in Equation (8), BlinkML makes conservative estimates using Lemma 2.

To obtain i.i.d. samples, \( (\theta_n, i, \theta_N, i) \) for \( i = 1, \ldots, k \), from \( h(\theta_n', \theta_N') \), Sample Size Estimator follows the following:

\[
\Pr(\theta_n, \theta_N \mid \theta_0) = \Pr(\theta_N \mid \theta_0) \Pr(\theta_n \mid \theta_0)
\]

where the conditional distributions, \( \theta_N \mid \theta_n \) and \( \theta_n \mid \theta_0 \), are obtained using Corollary 1. That is, Model Accuracy Estimator uses the following two-stage sampling procedure. It first samples \( \theta_n \) from \( N(\theta_0, \alpha_1 H^{-1} J H^{-1}) \) where \( \alpha_1 = \frac{1}{n_0 - 1/n} \); then, samples \( \theta_N \) from \( N(\theta_n, \alpha_2 H^{-1} J H^{-1}) \) where \( \alpha_2 = \frac{1}{n_0 - 1/n} \). This process is repeated for every \( i = 1, \ldots, k \) to obtain \( k \) pairs of \( (\theta_n, i, \theta_N, i) \). Figure 4 depicts this process.

### 4.2 Sample Size Searching

To find the minimum \( n \) such that \( \Pr(v(m_n, m_N; \theta_n, \theta_N) \leq \epsilon) \geq 1 - \delta \), Sample Size Estimator uses binary search, exploiting that the probability tends to be an increasing function of \( n \). We first provide an intuitive explanation; next, we present a formal argument.

Observe that \( \Pr(v(m_n, m_N; \theta_n, \theta_N) \leq \epsilon) \) relies on the two model parameters \( \theta_n \) and \( \theta_N \). If \( \theta_n = \theta_N \), the probability is trivially equal to 1. According to Theorem 1, the difference between those two parameters, i.e., \( \hat{\theta}_n - \hat{\theta}_N \), follows a normal distribution whose covariance matrix shrinks by a factor of \( 1/n - 1/N \). Therefore, those parameter values become closer as \( n \to N \), which implies that the probability must increase toward 1 as \( n \to N \). The following theorem formally shows that \( \Pr(v(m_n, m_N; \theta_n, \theta_N) \leq \epsilon) \) is guaranteed to be an increasing function for a large class of cases (its proof is in Appendix B).

**Theorem 2.** Let \( h(\theta; \gamma C) \) be the probability density function of a normal distribution with mean \( \theta_N \) and covariance matrix \( \gamma C \), where \( \gamma \) is a real number, and \( C \) is an arbitrary positive semidefinite matrix. Also, let \( B \) be the box area of \( \theta \) such that \( v(m_n, m_N; \theta_n, \theta_N) \leq \epsilon \). Then, the following function \( p_v(\gamma) \)

\[
p_v(\gamma) = \int_B h(\theta; \gamma C) \, d\theta
\]

is a decreasing function of \( \gamma \).

Since binary search is used, Sample Size Estimator needs to compute \( \frac{1}{k} \sum_{i=1}^{k} 1 \cdot [v(m_n, m_N; \theta_n, \theta_N) \leq \epsilon] \) (in Equation (8)) for different values of \( n \); in total, \( O(\log_2(N - n_0)) \) times. Thus, a fast mechanism for producing i.i.d. samples is desirable. The following section describes BlinkML’s optimizations.

### 4.3 Optimizations for Fast Sampling

This section describes how to quickly generate i.i.d. samples from the normal distribution with covariance matrix \( (1/n - 1/N) H^{-1} J H^{-1} \). A basic approach would be to use off-the-shelf functions, such as the one shipped in the numpy random module, for every different \( n \). Albeit simple, this basic approach involves many redundant operations that could be avoided. We describe two orthogonal approaches to reduce the redundancy.

**Sampling by Scaling** We can avoid invoking a sampling function multiple times for different \( n \) by exploiting the structural similarity of the covariance matrices associated with different \( n \). Let \( \hat{\theta}_n \sim N(0, (1/n - 1/N) H^{-1} J H^{-1}) \), and let
\( \hat{\theta}_n \sim N(0, H^{-1}JH^{-1}) \). Then, there exists the following relationship:

\[
\hat{\theta}_n = \sqrt{1/n - 1/N} \hat{\theta}_0.
\]

This indicates that we can first draw i.i.d. samples from the unscaled distribution \( N(0, H^{-1}JH^{-1}) \); then, we can scale those sampled values by \( \sqrt{1/n - 1/N} \) whenever the i.i.d. samples from \( N(0, (1/n - 1/N)H^{-1}JH^{-1}) \) are needed.

**Avoiding Direct Covariance Computation** When \( r(\theta) = \beta \theta \) in Equation (3) (i.e., no regularization or L2 regularization), Sample Size Estimator avoids the direct computations of \( H^{-1}JH^{-1} \). Instead, it simply draws samples from the standard normal distribution and applies an appropriate linear transformation \( L \) to the sampled values (\( L \) is obtained shortly). This approach is used in conjunction with ObservedFisher, which is BlinkML’s default strategy for computing its necessary statistics (Section 3.4).

Avoiding the direct computation of the covariances has two benefits. First, we can completely avoid the \( O(d^2) \) cost of computing/storing \( H^{-1}JH^{-1} \). Second, sampling from the standard normal distribution is much faster because no dependencies need to be enforced among sampled values.

We use the following relationship:

\[
z \sim N(0, I) \Rightarrow Lz \sim N(0, LL^T).
\]

That is, if there exists \( L \) such that \( LL^T = H^{-1}JH^{-1} \), we can obtain the samples of \( \hat{\theta}_0 \) by multiplying \( L \) to the samples drawn from the standard normal distribution.

Specifically, Sample Size Estimator performs the following for obtaining \( L \). Observe from Equation (6) that \( J = U \Sigma^2 U^T \). Since \( H = J + \beta, H = U (\Sigma^2 + \beta I) U^T \). Thus,

\[
H^{-1}JH^{-1} = U (\Sigma^2 + \beta I)^{-1} U^T U \Sigma^2 U^T U (\Sigma^2 + \beta I)^{-1} U^T \Rightarrow H^{-1}JH^{-1} = (UA) (UA)^T = LL^T
\]

where \( \Lambda \) is a diagonal matrix whose \( i \)-th diagonal entry is \( s_i/(s_i^2 + \beta) \), where \( s_i \) is the \( i \)-th singular value of \( J \) contained in \( \Sigma \). Note that both \( U \) and \( \Sigma \) are already available as part of computing the necessary statistics in Section 3.4. Thus, computing \( L \) only involves a simple matrix multiplication.

## 5 EXPERIMENTS

Our experimental results show the following:

1. **BlinkML** is highly effective and accurate even for high-dimensional data, and its runtime overhead is much smaller than the time needed for training a full model. (Section 5.5)
2. **BlinkML**’s default statistics computation method, ObservedFisher, is both accurate and efficient. (Section 5.6)
3. **BlinkML** offers significant benefits in hyperparameter optimization compared to full model training (Section 5.7); BlinkML’s sample size estimation is adaptive to the properties of models (Section 5.8).

### 5.1 Experiment Setup

Here, we present our computational environment as well as the different models and datasets used in our experiments.

**Models** We tested BlinkML with four different ML models:

1. **Linear Regression (Lin).** Lin is the standard linear regression model with L2-regularization coefficient \( \beta \) set as 0.001. Different values of \( \beta \) are tested in Section 5.8.
2. **Logistic Regression (LR).** LR is the standard logistic regression (binary) classifier with L2-regularization coefficient \( \beta \) set as 0.001.
3. **Max Entropy Classifier (ME).** ME is the standard max entropy (multiclass) classifier with L2-regularization coefficient \( \beta \) set as 0.001.
4. **PPCA.** PPCA is the standard probabilistic principal component analysis model [95], with the number of factors \( q \) set as 10.

**Datasets** We used six real-world datasets. The key characteristics of these datasets are summarized in Table 2.

#### 1. Linear Regression:

- **Gas:** This dataset contains chemical sensor readings exposed to gas mixtures at varying concentration levels [44]. We use the sensor reading as a target variable and gas concentration levels as independent variables.
- **Power:** This dataset contains power consumption measurements [7]. We use the household power consumption...
as a target variable and global power consumptions as independent variables.

Logistic Regression:
3. Criteo: This is a click-through rates dataset made publicly available by Criteo Labs [5]. The label of each example indicates if an ad was clicked or not.
4. Higgs: This is a Higgs bosons simulation dataset [18]. Each example is a pair of physical properties of an environment and a binary indicator of Higgs bosons production.

Max Entropy Classifier:
5. MNIST: This is a hand-written digits image dataset (a.k.a. infinite MNIST [8]). Each example is a pair of an image (intensity value per pixel) and the actual digit in the image.
6. Yelp: This is a collection of publicly available Yelp reviews [13]. Each example is a pair of an English review and a rating (between 0 and 5).

Probabilistic Principal Component Analysis:
7. MNIST: We use the features of MNIST for PPCA.
8. Higgs: We use the features of Higgs for PPCA.
For each dataset, we used 80% for training and 20% for testing.

Environment All our experiments were conducted on an EC2 cluster with one m5.4xlarge node as a master and five m5.2xlarge nodes as workers. We used Python 3.6 shipped with Conda [3] and Apache Spark 2.2 shipped with Cloudera Manager 5.11.

5.2 Training Time Savings
This section measures the time savings by BlinkML, compared to training the full model. We used eight model and dataset combinations: (Lin, Gas), (Lin, Power), (LR, Criteo), (LR, Higgs), (ME, MNIST), (ME, Yelp), (PPCA, MNIST), and (PPCA, Higgs). For Lin, LR and ME, we varied the requested accuracy \((1−ε)×100\%) from 80% to 99%. For PPCA, we varied the requested accuracy \((1−ε)×100\%) from 90% to 99.99%. We fixed \(δ\) at 0.05. For each case, we repeated BlinkML’s training 20 times.

Figure 5 shows BlinkML’s speedups and training time savings in comparison to full model training. The full model training times were 345 seconds for (Lin, Gas), 876 seconds for (Lin, Power), 5,727 seconds for (LR, Criteo), 530 seconds for (LR, Higgs), 35,361 seconds for (ME, MNIST), 3,048 seconds for (ME, Yelp), 35 seconds for (PPCA, MNIST), and 2 seconds for (PPCA, Higgs).

Two patterns were observed. First, as expected, BlinkML took relatively longer for training a more accurate approximate model. This is because BlinkML’s Sample Size Estimator correctly estimated that a larger sample was needed to satisfy the requested accuracy. Second, the relative training times were longer for complex models (ME took longer than LR). This is because multi-class classification (by ME) involved more possible class labels; thus, even a small error in parameter values could lead to misclassification. Thus, a larger sample was needed to sufficiently upper bound the chances of a misclassification. Nevertheless, training 95% accurate ME models on MNIST still took only 1.53% of the time needed for training a full model. In other words, even
As stated in Equation (8) in Section 4, the actual accuracy in this case, we observed a 65.27× speedup, or equivalently, 98.47% savings in training time. In all cases, BlinkML’s ability to automatically infer appropriate sample sizes and train approximate models on those samples led to significant training time savings. In the subsequent section, we analyze the actual accuracies of those approximate models.

5.3 Accuracy Guarantees

As stated in Equation (8) in Section 4, the actual accuracy of BlinkML’s approximate model is guaranteed to never be less than the requested accuracy, with probability at least $1 - \delta$. In this section, we also empirically validate BlinkML’s accuracy guarantees. Specifically, we ran an experiment to compare the requested accuracies and the actual accuracies of the approximate models returned by BlinkML.

We varied the requested accuracy from 80% to 99% and requested a confidence level of 95%, i.e., $\delta = 0.05$. The results are shown in Figure 6 for the same combinations of models and datasets used in the previous section.

In each case, 5th percentile of the actual accuracies was higher than the requested accuracy. In other words, in 95% of the cases, the delivered accuracy was higher than the requested one, confirming that BlinkML’s probabilistic accuracy guarantees were satisfied.

Notice that, in some cases, e.g., (LR, Criteo), (ME, MNIST), the actual accuracies remained identical even though the requested accuracies were different. This was due to BlinkML’s design. Recall that BlinkML first trains an initial model $m_0$ and then trains a subsequent model only when the estimated model difference $e_k$ of $m_k$ is higher than the requested error $\epsilon$. In the aforementioned cases, the initial models were already accurate enough; therefore, no additional models needed to be trained. Consequently, the actual accuracies did not vary in those cases. In other words, the actual accuracies of those initial models were higher than the requested accuracies.

5.4 Sample Size Estimation

Sample Size Estimator (SSE) is responsible for estimating the minimum sample size, which is a crucial operation in BlinkML. Too large a sample eliminates the training time savings; likewise, too small a sample can violate the accuracy guarantees. In this section, we examine SSE’s operations in BlinkML. We analyze both the accuracy and the efficiency of SSS.

Accuracy To analyze the accuracy of SSS, we implemented three other baselines: FixedRatio, RelativeRatio, IncEstimator. FixedRatio always used $1\%$ samples for training approximate models. RelativeRatio used $(1 - \epsilon) \times 10\%$ samples for training approximate models (e.g., 9.5% sample for 95% requested accuracy). IncEstimator gradually increased the sample size until the approximate model trained on that sample satisfied the requested accuracy; the sample size at $k$-th iteration was $1000 \cdot k^2$. We tested these three baselines and BlinkML on both (Lin, Power) and (LR, Criteo).

Figure 7a shows the results. Since FixedRatio and RelativeRatio set the sample sizes regardless of the model, they either failed to satisfy the requested accuracies or were overly costly. In contrast, IncEstimator and BlinkML adjusted their
sample sizes according to the models and the requested accuracies; hence, they were able to satisfy the requested accuracies. However, IncEstimator was much more expensive than BlinkML, as described next.

**Efficiency** To measure the efficiency, we measured the training times of BlinkML and all three baselines. To show the overhead of SSS, we also measured BlinkML’s training time excluding the time spent by SSS (referred to as “BlinkML’s pure training time”). Figure 7b shows the results. In this figure, the runtimes of IncEstimator were significantly larger than those of BlinkML. For instance, IncEstimator took 5,704 seconds for a 99% accurate model of (LR, Criteo) while BlinkML took only 228 seconds (i.e., 25× faster than IncEstimator). Moreover, the runtime overhead of SSS was small enough to keep BlinkML’s entire approximate training fast enough. We also study this overhead more systematically, as reported in the following section.

### 5.5 Impact of Data Dimension

In this section, we analyze the impact of data dimension (i.e., the number of features) on BlinkML’s runtime overhead, generalization error, and number of optimization iterations.

**Runtime Overhead** To analyze BlinkML’s runtime overhead, we separately measured (1) the time taken for training an initial model (using a sample of size $n_0$), (2) the time taken by ObservedFisher for computing statistics, (3) the time taken for sample size estimation, and (4) the time taken for training a final model. Figure 8a shows the results for (LR, Criteo). As expected, the times for statistics computations and sample size estimation increased as the number of features increased. However, the overall training time was still significantly smaller than training the full model (e.g., 0.8% for 100K features).

**Generalization Error** Figure 8b compares the generalization error (or equivalently, test error) of full models and BlinkML’s approximate models. Since BlinkML probabilistically guarantees that its approximate models produce the same predictions as the full models (for the same number of features), the generalization errors of BlinkML’s approximate models were highly similar to those of the full models. Moreover, the full model’s generalization errors were within the predicted bounds for more than 95% of the test cases (as stated in Lemma 1).

**Number of Iterations** Lastly, to better understand the reason behind BlinkML’s training time savings, we measured the number of iterations taken by an optimization algorithm (i.e., L-BFGS). Figure 8c shows the results. In general, the number of iterations for BlinkML were comparable to those for full model training. The number of iterations were similar...
To compare the accuracy, we first estimated the accuracy where (i.e., the ratio approached 1.0); further, the accuracy of ObservedFisher. Then, we computed the variances of the parameters using each of ClosedForm, InverseGradients, and ObservedFisher. To measure the accuracy, we calculated the average Frobenius norm, i.e., $(1/d^2) \| C_f - C_e \|_F$, where $C_e$ was the true covariance matrix and $C_f$ was the estimated covariance matrix.

This analysis serves as an empirical justification for why ObservedFisher is BlinkML’s default choice.

**Accuracy** To compare the accuracy, we first estimated the variances of the parameters using each of ClosedForm, InverseGradients, and ObservedFisher. Then, we computed the ratio between those estimated variances and the actual variances. Thus, an ratio close to 1 would indicate high accuracy. Figure 9 shows the result for (Lin, Power). In general, for small samples ($n \leq 1000$), ObservedFisher was relatively inaccurate in comparison to other methods. However, as the sample size increased, the accuracy of all methods improved (i.e., the ratio approached 1.0); further, the accuracy of ObservedFisher was comparable to other methods. Recall that ClosedForm is applicable to certain types of models (e.g., Lin and LR) while InverseGradients and ObservedFisher are applicable to all MLE-based models. Overall, the estimated variances of the parameters were larger than the actual variances, showing that BlinkML’s probabilistic guarantees were met. Below, we compare the runtime overhead of InverseGradients and ObservedFisher.

**Efficiency** For an in-depth comparison of InverseGradients and ObservedFisher, we used two more combinations (LR, Higgs) and (ME, MNIST). Recall from Table 2 that Higgs is a low-dimensional dataset ($d = 28$) while MNIST is high-dimensional ($d = 784$). We used each method to compute the covariance matrix $H^{-1} J H^{-1}$, which determines the parameter distribution in Theorem 1 (Section 3). We measured the runtime of each method and calculated the accuracy of its estimated covariance matrix. To measure the accuracy, we calculated the average Frobenius norm, i.e., $(1/d^2) \| C_f - C_e \|_F$, where $C_e$ was the true covariance matrix and $C_f$ was the estimated covariance matrix.

### 5.6 Statistics Computation

In this section, we compare ClosedForm, InverseGradients, and ObservedFisher in terms of both accuracy and efficiency. This analysis serves as an empirical justification for why ObservedFisher is BlinkML’s default choice.

![Figure 9: A study of statistics computation methods: (left) a comparison of estimated parameter variances to the actual parameter variances, and (right) a comparison of two statistics computation methods.](image)

Figure 9b summarizes the results of this experiment. For the low-dimensional data (Higgs), the runtimes and the accuracies of the two methods were comparable. While their accuracies remained comparable for the high-dimensional data (MNIST), their performance differed. Since InverseGradients had to invoke the $\text{grads}$ function repeatedly (i.e., $d$ times), its runtime increased drastically. In contrast, ObservedFisher had to call the $\text{grads}$ function only once.

### 5.7 Hyperparameter Optimization

This section studies BlinkML’s overall benefit for performing hyperparameter optimization. Specifically, we compared BlinkML to a traditional approach (i.e., full model training) in searching for an optimal combination of a feature set and a hyperparameter. As performed by the Random Search hyperparameter optimization method [21], we first generated a sequence of (pairs of) a randomly chosen feature set and a regularization coefficient. Then, we let BlinkML train a series of 95% accurate models using the feature set and the regularization coefficient in the sequence. Similarly, we let the traditional approach train a series of exact models using the same combination of the feature set and the regularization coefficient.

Figure 10 shows the result, where each dot represents a model. Within half an hour, BlinkML trained 961 models while the traditional approach was able to train only 3. Both BlinkML and the traditional approach found the second-best model (with test accuracy 74%) at the second iteration (since they used the same sequence); however, BlinkML took only 1.03 seconds while the traditional approach took 817 seconds. After 387 seconds (about 6 mins), BlinkML found...
We also study the impact of model complexity (i.e., regularization) on the estimated sample size. Typically, the sampling is optimized for a specific type of model, such as linear regression [17, 22, 30, 34, 36–38, 41, 47], logistic regression [61, 96], clustering [42, 55], Kernel matrices [49, 75], point processes [66], Gaussian mixture model [69]. Woodruf [98] overviews sketching techniques for least squares and low-rank approximation. Zombie [16] employs a clustering-based active learning technique for training approximate models, but does not offer any error guarantees. In contrast, BlinkML offers probabilistic error guarantees for any MLE-based model. Cohen [30] studies uniform sampling for ML but for only linear regression. Bottou [25] and Shalev-Shwartz [88] study the optimization errors.

5.8 Impact of Model Complexity on Estimated Sample Sizes

We also study the impact of model complexity (i.e., regularization coefficients and the number of parameters) on BlinkML’s estimated sample size. Intuitively, if a model is more complex (i.e., smaller regularization coefficients or more parameters), a larger sample would be needed to satisfy a user-requested error bound.

Figure 11 shows the results. The left subfigure (Figure 11a) shows that as the regularization coefficient increased, the estimated sample size decreased. The right subfigure (Figure 11b) shows that as the model had a larger number of parameters, the estimated sample size increased. Both observations are consistent with our intuition (Section 3).

6 RELATED WORK

In this section, we first discuss three types of work closely related to BlinkML: Sampling for ML, Hyperparameter Optimization, and Feature Selection. We summarize their key contributions in Table 3.

Next, we overview the techniques inspired by familiar database techniques (DBMS-Inspired Optimization) and the recent advances in statistical optimization methods (Faster Optimization Algorithms)

Sampling for ML

Sampling for ML has been extensively studied in the literature. Typically, the sampling is optimized for a specific type of model, such as linear regression [17, 22, 30, 34, 36–38, 41, 47], logistic regression [61, 96], clustering [42, 55], Kernel matrices [49, 75], point processes [66], Gaussian mixture model [69]. Woodruf [98] overviews sketching techniques for least squares and low-rank approximation. Zombie [16] employs a clustering-based active learning technique for training approximate models, but does not offer any error guarantees. In contrast, BlinkML offers probabilistic error guarantees for any MLE-based model. Cohen [30] studies uniform sampling for ML but for only linear regression. Bottou [25] and Shalev-Shwartz [88] study the optimization errors.

Hyperparameter Optimization

Automatic hyperparameter optimization (i.e., AutoML) has been pursued by AutoWeka [93], auto-sklearn [43], and Google’s Cloud AutoML [2]. These techniques have typically taken a Bayesian approach to hyperparameter optimization [87]. The ML community has also studied how to optimize deep neural networks [20, 21, 70]. What BlinkML offers is orthogonal to these hyperparameter optimization methods since BlinkML speeds up the individual model training via approximation, while hyperparameter optimization methods focus on finding an optimal sequence of hyperparameters to test.

Feature Selection

Choosing a relevant set of features is an important task in ML [26, 51]. Feature selection can either be performed before training a final model [56] or during model training relying on sparsity-inducing models [77, 100]. One approach to accelerate feature selection is preprocessing the data in advance [102]. BlinkML can be used in conjunction with these methods.

DBMS-Inspired Optimization

A salient feature of database systems is their declarative interface (SQL) and the resulting optimization opportunities. These ideas have been applied to speed up ML workloads. SystemML [24, 40, 48] ScalOps [97], Pig Latin [79], KeystoneML [91] propose high-level ML languages for automatic parallelization and materialization, as well as easier programming. Hamlet [64] and others [63, 86] avoid expensive denormalizations. Hemingway [80], MLBase [60], and TuPAQ [90] automatically choose an optimal plan for a given ML workload. SciDB [58, 92], MADLib [29, 54], and RIOT [105] exploit in-database computing. Kumar et al. [62] uses a model selection management system to unify feature engineering [15], algorithm selection, and parameter tuning. NoScope [57] and tKDC [46] speed up the prediction at the cost of more preprocessing.

Faster Optimization Algorithms

Advances in optimization algorithms are largely orthogonal to ML systems; however, understanding their benefits is necessary for developing faster ML systems. Recent advances can be categorized into software- and hardware-based approaches.

Software-based methods are mostly focused on improving gradient descent variants (e.g., SGD), where a key question is how to adjust the step size in order to accelerate the convergence rate towards the optimal solution. Recent advances...
Table 3: Previous work on Sampling for ML / Hyperparameter Optimization / Feature Selection

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<thead>
<tr>
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<td>Coreset (LR) [17, 41, 47]</td>
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<td>Cohen [30]</td>
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<td>Derezinski [34]</td>
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<td>SafeScreening [78]</td>
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<td><strong>BLINKML (ours)</strong></td>
<td>Develops efficient algorithms for training MLE models with error guarantees</td>
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| Hyperparameter Optimization | |
| Bergstra [21], Bergstra [20] | Optimizes hyperparameter optimization for deep neural network |
| Maclaurin [70] | Proposes gradient-based hyperparameter optimization |
| Shahriari [87] | Reviews Bayesian approach to hyperparameter optimization |
| Bardenet [19] | Proposes a collaborative hyperparameter tuning among similar tasks |
| TuPAQ [90] | Provides a systematic support for hyperparameter optimization |

| Feature Selection | |
| Guyon [51], Boyce [26], John [56] | Introduces concepts related to feature selection |
| Ng [77], Yang [100] | Performs feature selection via sparse models |
| AutoWeka [93] | See the description of AutoWeka in Hyperparameter Optimization |
| Columnbus [102] | Optimizes feature selection by materialization |

include adaptive rules for accelerating this rate, e.g., Ada-grad [39], Adadelta [101], RMSprop [94], and Adam [59]. Hogwild! [84] and related techniques [50, 52, 104] disable locks to speed up SGD via asynchronous updates. There is also recent work on rediscovering the benefits of quasi-Newton optimization methods, e.g., showing that minibatch variants of quasi-Newton methods (such as L-BFGS or CG) can be superior to SGD due to their higher parallelism [65].

Hardware-based techniques speed up training by relaxing strict precision requirements, e.g., DimmWitted [103] and BuckWild! [33].

7 CONCLUSION

In this work, we have developed BLINKML, an approximate machine learning system with probabilistic guarantees for MLE-based models. BLINKML uses sampling to dramatically reduce time and computational costs, which is particularly beneficial in the early stages of model tuning. Through an extensive set of experiments on several large-scale, real-world datasets, we showed that BLINKML produced 95% accurate models of linear regression, logistic regression, max entropy classifier, and Probabilistic Principal Component Analysis, while using only 0.16%–7.57% of the time needed for training the full model. Our future plan is to extend beyond the maximum likelihood estimation models, such as decision trees, Gaussian Process regression, Naïve Bayes classifiers, and Deep Boltzmann Machines [85]. We also plan to open-source BLINKML, with wrappers for various popular ML libraries, including scikit-learn (Python), glm (R), and MLlib. Finally, given that BLINKML’s underlying techniques are extensible to non-uniform sampling, we plan to further explore task- and model-specific non-uniform sampling strategies.

REFERENCES

BlinkML: Efficient Maximum Likelihood Estimation

SIGMOD 2019, June 2019, Amsterdam, The Netherlands
A MODEL ABSTRACTION EXAMPLES

This section shows that BlinksML-supported ML models can be cast into the abstract form in Equation (2). For illustration, we use logistic regression and PPCA.

Logistic Regression

The objective function of logistic regression captures the difference between true class labels and the predichative class labels. An optional regularization term may be placed to prevent a model to be overfitted to a training set. For instance, the objective function of L2-regularized logistic regression is expressed as follows:

\[ f_{\text{logistic}}(\theta) = -\frac{1}{n} \sum_{i=1}^{n} \log (\sigma(\theta^T x_i)) + (1 - t_i) \log (1 - \sigma(\theta^T x_i)) + \frac{\beta}{2} \| \theta \|^2 \]

where \( \sigma(y) = 1/(1 + \exp(y)) \) is a sigmoid function, and \( \beta \) is the coefficient that controls the strength of the regularization penalty. The observed class labels, i.e., \( t_i \) for \( i = 1, \ldots, n \), are either 0 or 1. The above expression is minimized when \( \theta \) is set to the value at which the gradient \( \nabla f_{\text{logistic}}(\theta) \) of \( f_{\text{logistic}}(\theta) \) becomes a zero vector; that is,

\[ \nabla f_{\text{logistic}}(\theta) = - \frac{1}{n} \sum_{i=1}^{n} (\sigma(\theta^T x_i) - t_i) x_i + \beta \theta = 0 \]

It is straightforward to cast the above expression into Equation (3). That is, \( q(\theta; x_i, t_i) = (\sigma(\theta^T x_i) - t_i) x_i \) and \( r(\theta) = \beta \theta \).

PPCA

The objective function of PPCA captures the difference between the covariance matrix \( \mathbf{S} \) of the training set and the covariance matrix \( \mathbf{C} = \mathbf{\Theta} \mathbf{\Theta}^\top + \sigma^2 I \) reconstructed from the \( q \) number of extracted factors \( \Theta \), as follows:

\[ f_{\text{PPCA}}(\Theta) = \frac{1}{2} (d \log 2\pi + \log |C| + \text{tr}(C^{-1} S)) \]

where \( d \) is the dimension of feature vectors. \( \Theta \) is \( d \times q \) matrix in which each column represents a factor, and \( \sigma \) is a real-valued scalar that represents the noise in data not explained by those factors. The optimal value for \( \sigma \) can be obtained once the values for \( \Theta \) are determined. The value of \( q \), or the number of the factors to extract, is a user parameter. The above expression \( f_{\text{PPCA}}(\Theta) \) is minimized when its gradient \( \nabla f_{\text{PPCA}}(\Theta) \) becomes a zero vector; that is,

\[ \nabla f_{\text{PPCA}}(\Theta) = C^{-1} (\Theta - S C^{-1} \Theta) = 0 \]

The above expression can be cast into the form in Equation (3) by observing \( S = (1/n) \sum_{i=1}^{n} x_i x_i^\top \). That is, \( q(\Theta; x_i) = C^{-1} (\Theta - S C^{-1} \Theta - x_i x_i^\top) C^{-1} \Theta \) and \( r(\Theta) = 0 \). \( t_i \) is omitted on purpose since

\[ \text{This sample covariance expression assumes that the training set is zero-centered.} \]
PPCA does not need observations (e.g., class labels). Although we used a matrix form Θ in the above expression for simplicity, BlinkML internally uses a vector θ when passing parameters among components. The vector is simply flattened and unflattened as needed.

B DEFERRED PROOFS

B.1 Generalization Error

Proof of Lemma 1. Note that the reason why BlinkML’s error guarantee, i.e., ν(mₙ) ≤ ε, is probabilistic is because the uniform random sample of the dataset D, which is independent of the distribution of (x, y) ~ D. This property is used shortly.

\[ E_{(x,y) \sim D}(1 \mid m_N(x) \neq y) = \int 1 \mid m_N(x) \neq y \mid p(x) \, dx \]

\[ = \int (m_n(x) \neq y \land m_n(x) = m_N(x)) \lor (m_n(x) = y \land m_n(x) \neq m_N(x)) \, p(x) \, dx \]

\[ \leq \int (m_n(x) \neq y) \lor (m_n(x) = y \land m_n(x) \neq m_N(x)) \, p(x) \, dx \]

\[ \leq \int (m_n(x) \neq y) \, p(x) \, dx \]

\[ \lor \int (m_n(x) = y \land m_n(x) \neq m_N(x)) \, p(x) \, dx \]

By definition, \( \int (m_n(x) \neq y) \, p(x) \, dx = \epsilon_g \). Based on the independence described above and \( \Pr(E_x(m_n(x) \neq m_N(x)) \leq \epsilon) \geq 1 - \delta \),

\[ \int (m_n(x) = y \land m_n(x) \neq m_N(x)) \, p(x) \, dx \leq (1 - \epsilon_g) \cdot \epsilon \]

with probability at least 1 - δ. Thus,

\[ E_{(x,y) \sim D}(1 \mid m_N(x) \neq y) \leq \epsilon_g + \epsilon - \epsilon_g \cdot \epsilon \]

with probability at least 1 - δ. □

B.2 Model Parameter Distribution

Proof of Theorem 1. We first derive the distribution of \( \hat{\theta}_n - \theta_N \), which will then be used to derive the distribution of \( \theta_n - \hat{\theta}_N \). Our derivation is the generalization of the result in [76]. The generalization is required since the original result does not include \( \hat{\theta} \).

Let \( \theta_N \) be the parameter values at which \( g_n(\theta)_N \) becomes zero. Since the size of the training set is only \( N \), \( \theta_N \) exists only conceptually. Since \( \theta_n \) is the optimal parameter values, it satisfies \( g_n(\theta_n) = 0 \). According to the mean-value theorem, there exists \( \hat{\theta} \) between \( \theta_n \) and \( \theta_N \) that satisfies:

\[ H(\hat{\theta})(\theta_n - \theta_N) = g_n(\theta_n) - g_n(\theta_N) = -g_n(\theta_N) \]

where \( H(\hat{\theta}) \) is the Jacobian of \( g_n(\hat{\theta}) \) evaluated at \( \hat{\theta} \). Note that \( g_n(\theta_N) \) is zero since \( \theta_N \) is obtained by finding the parameter at which \( g_n(\theta) \) becomes zero.

Applying the multidimensional central limit theorem to the above equation produces the following:

\[ \sqrt{n}(\hat{\theta}_n - \theta_N) = -H(\hat{\theta})^{-1} \sqrt{n} g_n(\theta_N) \]

\[ = -H(\hat{\theta})^{-1} \frac{1}{\sqrt{n}} \sum_{i=1}^{n} (q(\theta_N; x_i, y_i) + r(\theta_N)) \]

\[ n \rightarrow \infty \mathcal{N}(0, H^{-1}JH^{-1}) \]

where \( H \) is a shorthand notation of \( H(\hat{\theta}) \). To make a transition from Equation (9) to Equation (10), an important relationship called the information matrix equality is used. According to the information matrix equality, the covariance of \( q(\theta; x_i, y_i) \) is equal to the Hessian of the negative log-likelihood expression, which is equal to \( J \).

Now, we derive the distribution of \( \hat{\theta}_n - \theta_N \). We use the fact that \( \theta_N \) is the optimal parameter for \( D_N \) which is a union of \( D_n \) and \( D_N - D_n \), where \( \hat{\theta}_N \) is the optimal parameter for \( D_n \). To separately capture the randomness stemming from \( D_n \) and \( D_N - D_n \), we introduce two random variables \( X_1, X_2 \) that independently follow \( \mathcal{N}(0, H^{-1}JH^{-1}) \). From Equation (10),

\[ \hat{\theta}_n - \theta_N \rightarrow (1/\sqrt{n})X_1. \]

Also, let \( q_i = q(\theta_N; x_i, y_i) \) for simplicity; then,

\[ \sqrt{n}(\hat{\theta}_n - \theta_N) \rightarrow -H(\hat{\theta})^{-1} \frac{1}{\sqrt{n}} \sum_{i=1}^{n} q_i + \frac{1}{\sqrt{n}} \sum_{i=1}^{n} \sum_{i=1}^{N-n} q_i \]

\[ n \rightarrow \infty \rightarrow \mathcal{N}(0, H^{-1}JH^{-1}) \]

Since \( \hat{\theta}_n - \theta_N = (\hat{\theta}_n - \theta_N) - (\hat{\theta}_N - \theta_N) \), and the limit of each of \( (\hat{\theta}_n - \theta_N) \) and \( (\hat{\theta}_N - \theta_N) \) exists,

\[ \hat{\theta}_n - \hat{\theta}_N \rightarrow \frac{1}{\sqrt{N}}X_1 - \frac{\sqrt{n}}{N}X_1 - \frac{\sqrt{N-n}}{N}X_2 \]

\[ = \left( \frac{1}{\sqrt{N}} - \frac{\sqrt{n}}{N} \right)X_1 - \frac{\sqrt{N-n}}{N}X_2 \]

Note that \( \hat{\theta}_n - \hat{\theta}_N \) asymptotically follows a normal distribution since it is a linear combination of two random variables.
Thus, using Bayes' theorem, it suffices to show that independently follow normal distributions. Thus, 

$$\hat{\theta}_n - \hat{\theta}_N \xrightarrow{\text{as } n \to \infty} \mathcal{N} \left( 0, \left( \frac{1}{\sqrt{n}} - \frac{\sqrt{N}}{N} \right)^2 \right)$$

$$= \mathcal{N} \left( 0, \left( \frac{1}{n - 1} - \frac{1}{N} \right) \right)$$

Proof of Corollary 1. Observe that $$\hat{\theta}_n - \hat{\theta}_N$$ and $$\hat{\theta}_N - \theta_\infty$$ are independent because they are jointly normally distributed and the covariance between them is zero as shown below:

$$\text{Cov}(\hat{\theta}_n - \hat{\theta}_N, \hat{\theta}_N - \theta_\infty)$$

$$= \frac{1}{2} \text{Var}(\hat{\theta}_n - \hat{\theta}_N + \hat{\theta}_N - \theta_\infty) - \text{Var}(\hat{\theta}_n - \hat{\theta}_N) - \text{Var}(\hat{\theta}_N - \theta_\infty)$$

$$= \frac{1}{2} \left( \frac{1}{n} - \frac{1}{n - 1} - \frac{1}{N} \right) H^{-1} J H^{-1} = 0$$

Thus, $$\text{Var}(\hat{\theta}_n - \hat{\theta}_N) = \text{Var}(\hat{\theta}_n - \hat{\theta}_N | \theta_\infty) = \alpha H^{-1} J H^{-1}$$, which implies

$$\hat{\theta}_n \sim \mathcal{N}(\theta_\infty, \alpha H^{-1} J H^{-1})$$

(11)

Proof of Lemma 2. We first define three events $$A$$, $$B$$, and $$C$$ as follows:

$$A : v(m_n) \leq \varepsilon$$

$$B : \int 1 \{ v(m_n) \leq \varepsilon \} h(\theta_N) \ d\theta_N \geq 1 - \frac{\delta}{0.95}$$

$$C : \frac{1}{k} \sum_{i=1}^{k} 1 \{ v(m_n; \theta_{N,i}) \leq \varepsilon \} = 1 - \delta$$

It suffices to show that $$P(A | C) \geq 1 - \delta$$, for which we use the relationship $$P(A | C) = P(A | B) P(B | C)$$. First, by the basic relationship between the probability and the indicator function, $$P(A | B) = (1 - \delta)/0.95$$. Second, by the Hoeffding’s inequality,

$$\Pr \left[ a \geq b - \sqrt{\frac{\log 0.95}{-2k}} \right] \geq 0.95$$

where $$a = \int 1 \{ v(m_n; \theta_N) \leq \varepsilon \} h(\theta_N) \ d\theta_N$$

$$b = \frac{1}{k} \sum_{i=1}^{k} 1 \{ v(m_n; \theta_{N,i}) \leq \varepsilon \}$$

since $$b$$ is the degree-$$k$$ U-statistics of $$a$$. Thus, $$P(B | C) \geq 0.95$$. Therefore, $$P(A | C) = P(A | B) P(B | C) \geq (1 - \delta)/0.95 \times 0.95 = 1 - \delta.$$ □

B.3 Sample Size Estimation

Proof of Theorem 2. Without loss of generality, we prove Theorem 2 for the case where the dimension of training examples, $$d$$, is 2. It is straightforward to generalize our proof for the case with an arbitrary $$d$$. Also, without loss of generality, we assume $$B$$ is the box area bounded by $$(-1, -1)$$ and $$(1, 1)$$. Then, $$p_v(y)$$ is expressed as

$$\int_{-1}^{1} \frac{1}{\sqrt{2\pi}} \exp \left( -\theta^T (y_C)^{-1} \theta \right) d\theta$$

To prove the theorem, it suffices to show that $$y_1 < y_2 \Rightarrow p_v(y_1) > p_v(y_2)$$ for arbitrary $$y_1$$ and $$y_2$$. By definition,

$$p_v(y_1) = \int_{-1}^{1} \frac{1}{\sqrt{2\pi}} \exp \left( -\theta^T (y_1 C)^{-1} \theta \right) d\theta$$

By substituting $$\sqrt{y_1/y_2} \theta$$ for $$\theta$$,

$$p_v(y_1) = \int_{-1}^{1} \frac{1}{\sqrt{2\pi}} \exp \left( -\theta^T (y_2 C)^{-1} \theta \right) d\theta$$

$$> \int_{-1}^{1} \frac{1}{\sqrt{2\pi}} \exp \left( -\theta^T (y_2 C)^{-1} \theta \right) d\theta = p_v(y_2)$$

because the integration range for $$p_v(y_1)$$ is larger. □