Interactive Clustering with a High-Performance ML Toolkit

Biye Jiang
Computer Science Division
UC Berkeley
Berkeley, CA 94720
bjiang@cs.berkeley.edu

John Canny
Computer Science Division
UC Berkeley
Berkeley, CA 94720
jfc@cs.berkeley.edu

ABSTRACT

Clustering is a class of machine learning algorithms which has important applications in many different fields. Users often use clustering to find hidden structures from data for those domain specific problems. However, evaluating clustering results is always a hard problem. In many and perhaps most of these applications, users need to trade off competing goals and encode prior knowledge into the model to define what is the best result. The learning algorithm however has evolved around the optimization of a single, usually narrowly-defined criterion, which may not obtain satisfactory results. In most cases, an expert makes trade-offs between different criteria which requires high-level (human) intelligence. This motivates us to provide *interactive customization and optimization* so that the expert can incorporate secondary criteria into the model-generation process in an interactive way.

In this demo paper we will demonstrate the techniques we developed to do customized and interactive model optimization for clustering algorithms. The keys to the approach are (i) high-performance training so that non-trivial models can be trained in real-time (using roofline design and GPU hardware), (ii) a machine learning architecture which is modular, and supports primary and secondary loss functions, and (iii) highly-interactive visualization tools that support dynamic creation of visualizations and controls to match the bespoke criteria being optimized.

Keywords

Interactive, Machine learning, Clustering, GPU

1. INTRODUCTION

Machine Learning is now at the center of data analysis in many fields across the sciences, business, health care and other realms. Among those ML algorithms, clustering is a class of unsupervised learning algorithms which is often used to find hidden structures of the data. In contrast to supervised learning which always uses accuracy to measure model quality, in general it is hard to evaluate clustering results. In practice users often need to trade off competing goals. Latent variable models such as K-Means clustering, or LDA[3] or NMF[18] find latent factors which maximize the likelihood of the observed data, but which may have secondary desiderata such as uniform cluster size, independence of factors, or coherence of topics.

The learning algorithms have evolved around the optimization of a single, usually narrowly-defined criterion, but users often find it hard to represent their criteria as a single objective function. The lack of evaluation methods also make it hard for analyzing algorithm behavior as well as debugging. In many cases, using clustering algorithms requires high-level (human) intelligence to make trade-offs between these criteria and examine the results manually.

Because ML models today are not flexible enough to incorporate all these criteria, secondary constraints are often applied *after* model training (by overriding the model's choices) in a way that is inevitably sub-optimal. Furthermore, the effects of downstream interventions require live testing to quantify. By contrast, *interactive customization and optimization* allows the analysts to incorporate secondary constraints into the model-generation process in an interactive way. There are several benefits to this:

- Models can be fully optimized given a suitable mixture of the criteria.
- Families of models can be trained to deal with variability in the application context.
- Analysts can explore the effects of particular trade-offs instantly, without waiting for a live test.
- Through this exploration, an analyst can gain intuition for the effects of various criteria, and make better trade-offs in the long run.

In this paper we develop the techniques to do customized and interactive model optimization, and demonstrate the approach on several examples. The keys to the approach are (i) high-performance training so that non-trivial models can be trained in real-time (using roofline design and GPU hardware), (ii) a machine learning architecture which is modular, and support primary and secondary loss functions, and (iii) highly-interactive visualization tools that support dynamic creation of visualizations and controls to match the bespoke criteria being optimized.

KDD 2015 Workshop on Interactive Data Exploration and Analytics (IDEA'15) August 10th, 2015, Sydney, Australia.

2. RELATED WORK

2.1 Interactive clustering

Interactive clustering is an active area. Since clustering is widely-used to simplify the interpretation of large datasets, and since the natural metrics for a new domain may be difficult to articulate, interactive exploration [8, 24, 29] is a natural and powerful approach. In [8, 24] authors used visualization to rapidly explore the results of a clustering algorithm, and these approaches have become important tools in computational biology [8]. AverageExplorer [29] allow users to explore and summarize large collection of images by interactively posing constraints.

Recently, there has been much interest in using visualization to support the refinement of topic models [26, 12, 7]. Since the latent topics extracted by the algorithm are not always semantically meaningful [22, 6], different constrained topic models [20, 2, 21] have been developed. Systems like [26, 12] also allow users to iteratively refine the model based on their preference. However, those models always require solving a complicated optimization problem with some very specific constraint. And few systems have demonstrated real-time interaction with large scale dataset.

2.2 Interactive model refinement

In the context of supervised learning, one early influential paper on interactive machine learning was Fail and Olsen's paper [9], which describes partially-supervised learning with a user supplying some (sparse) labelled data to help an ML algorithm label the rest. A number of other works have followed this route, by focusing on manipulation of the training data rather than internals of a particular algorithm. Other work focused on human-assisted feature selection (rather than algorithm training) [23]. Amershi et al. [1] provides a detailed summary of the work in this area. Much of these works attempt to improve only the accuracy of a machine learning problem by adding a human in the loop, which is quite different from our work. Perhaps the closest to ours is [13] which integrates a human-assisted optimization strategy with the design of multi-class classifiers. But in this paper we focus on clustering and the optimization algorithms are different.

2.3 Large scale machine learning system

There has been a great deal of work recently on tools for Big Data. But much of these works emphasize scalability on clusters [14, 25, 10] without applying single-node acceleration (CPU and GPU-specific acceleration libraries). Those systems are typically optimized for scalability rather than latency, which is more important for interactive modeling.

3. SYSTEM DESIGN

3.1 BIDMach: high-performance, customized machine learning

The first key to interactive, customized machine learning is an architecture which supports it. BIDMach [5] is a new machine learning toolkit which has demonstrated extremely high performance with modest hardware (single computers with GPUs), and which has the modular design shown in Fig 1. BIDMach use minibatch updates, typically many per second, so that models are being updated continuously. This is a good match to interactive modeling, since the effects of analysts actions will be seen quickly. Rather than a single model class, models comprise first a primary model (which typically outputs the model loss on a minibatch and a derivative or other update for it). Next an optimizer is responsible for updating the model given gradients. Several are available including simple SGD, ADAGRAD, and Preconditioned CG. Finally, mixins represent secondary constraints or likelihoods. Gradient-based primary models and mixins are combined with a weighted sum. In our interactive context, these weights are set interactively.

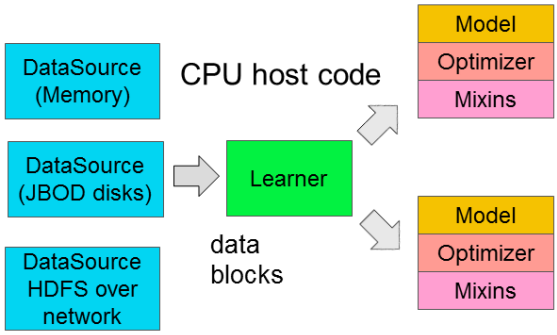


Figure 1: BIDMach's Architecture

Beyond the architecture of Fig 1, BIDMach has two layers. A general-purpose matrix layer called BIDMat, and BIDMach which includes the machine learning classes from figure 1. This organization shortens development time by providing high-level primitives for writing learning algorithms, and also allows us to leverage recent gains in the performance of GPU hardware. BIDMat is completely agnostic about matrix type: both CPU and GPU matrices (and sparse or dense and single or double precision) can be used and code is written generically.

BIDMach contrasts with most high-performance machine learning systems [14, 25, 10] in its emphasis on optimizing single-machine performance first, and then scale-up if needed. BIDMach uses *roofline design* to optimize computational kernels toward hardware limits. On a large collection of benchmarks it has proved to be typically two orders of magnitude faster than other single-machine toolkits (when BIDMach is used with a GPU), and one to two orders of magnitude faster than cluster toolkits running on 10-100 nodes. Part of the difference is due to BIDMach's complete suite of GPU primitives. Almost all computation is done on the GPU, CPU/GPU transfers are minimized, and custom kernels give close to theoretically optimal GPU performance. GPUs typically achieve an order-of-magnitude speedup in dense matrix operations vs. mid-range CPUs. Less well know is their advantage in main memory speed, which (at 300 GB/s) is nearly an order-of-magnitude faster than recent quad-channel CPUs (at around 40 GB/s). This memory speed gap also gives GPUs a similar advantage for *sparse* matrix operations which are central to most real-world ML applications. These differences explain one order of magnitude of the performance gap that we observe with BIDMach. The balance is due to the fact that most other systems are not close to their (CPU) rooflines. Because of this BIDMach

has a significant performance edge for most ML algorithms even when run on one CPU.

High performance is very important for interactivity. BIDMach has reduced the running time of many non-trivial ML tasks from hours to minutes. And even for models that take minutes to train fully, the effects of parameter changes are typically visible in seconds. We will see this in the examples later.

3.2 Client-server architecture

We use a client-server architecture with 3 components as shown in Fig 2: a computing (BIDMach) engine, a web server, and a web based front end. BIDMach is implemented in the Scala language which supports concurrency with high level "actor" primitives. Another thread runs in the same Scala runtime, communicating with the web server. This thread receives parameter updates from the web server, and updates the corresponding model training parameters. As the model is trained, primary and mixin cost functions are evaluated on minibatches, providing regular updates which are passed to the web server.

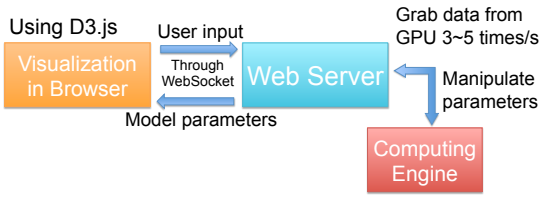


Figure 2: Visualization Architecture

In the client side, we implement a web based interface which uses D3.js[4] for data visualization. D3 is widely used, has very powerful graphics elements, and good support for animation. As a browser-based system, it runs transparently with a local or remote server. We will discuss the interface design in detail in the next section.

The communication between client and server is bi-directional, with both client and server initiating transfers. We therefore use WebSockets instead of e.g. a one-way RESTful web service. For simplicity and extensibility, we use JSON as the over-the-wire exchange format.

3.3 Secondary criteria as Mixins

Model customization is useful for both supervised and unsupervised problems. Unsupervised learning involves a certain amount of arbitrariness in the criteria for the "best" latent state. Therefore regularization is widely used as a secondary constraint on the primary objective [20, 2, 21, 26].

In a bit more detail, clustering algorithms like KMeans usually use the measure of model/centroid similarity, and may or may not use intra-model coherence measures or inter-cluster distance. Indeed, unsupervised learning models are often *evaluated* using a variety of criteria that are much more complex than the criteria used to derive the learning algorithms [22, 6]. The same holds true for topic models such as LDA, NMF and Word2Vec, and for collaborative filtering.

This is a paradox. Clearly one should get better scores for these criteria if they were directly optimized as part of training. Beyond these standard criteria, there are many others that are commonly used in the applications of machine learning. Historically it has probably been too difficult to optimize these criteria (the criteria may be expensive to evaluate, or non-locally computable).

On the other hand computing power is abundantly available now, especially in graphics processors. The bottleneck is often *moving* data rather than computing on it. Thus it is often practical to evaluate multiple, relatively complex criteria as part of optimization.

Combining these approaches, we can deal with a variety of secondary or "mixin" criteria as part of the learning process. In our present implementation, we use a linear combination of cost functions for primary and secondary criteria:

$$arg\min_x f(x,d) + \sum_i \lambda_i * g_i(x)$$

Where x is the model parameters, d is data, f is the primary cost function and g_i are the user-defined *Mixin* functions. The weights λ_i are "controls" that are dynamically adjusted by the analyst as part of training. For the primary criterion f and each secondary criteria g_i there should be at least one dynamic graphic that captures changes in that criterion in an intuitive way. The analyst watches these as each of the controls are adjusted to monitor the tradeoff between them.

4. INTERFACE DESIGN

In this section, we will describe the visual interface of our interactive machine learning system.

4.1 Visual dashboard

We use a dashboard approach where user can customize their own visualizations. As shown in Fig 3, the left side of the interface contains the menus and control sliders. From the menus, a user can select the metrics and controls for the modeling task. A corresponding control or metric visualization is then added to the dashboard, which can then be dragged, dropped and resized. There is at least one corresponding performance indictor for each control parameter, and more than one can be added to the dashboard. The details of each visualization component will be described next.

4.2 Visualizing the model

Directly visualizing the model provides a nice summarization for the dataset and users can gain a general understanding about the behavior of the algorithms. It can also help identify obvious errors and verify assumptions or intuitions. While there are different types of data and algorithm, the visualizations are necessarily model-specific, and should provide a natural interpretation of the model directly. For image data, the cluster centers can usually be visualized as in Fig 4a. For dictionary learning algorithms like NMF[18], the learned image dictionary can also be directly visualized as in Fig 4b, which is a much sparser representation. For more general matrix data, a simple direct visualization of element weights can work well. This was the approach taken

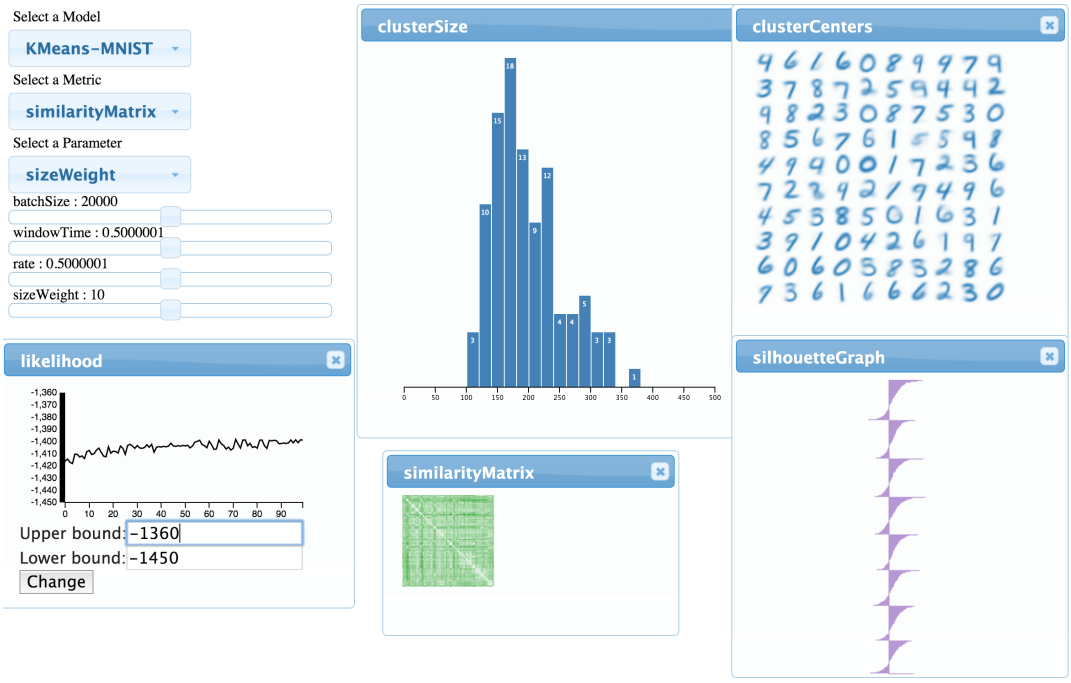
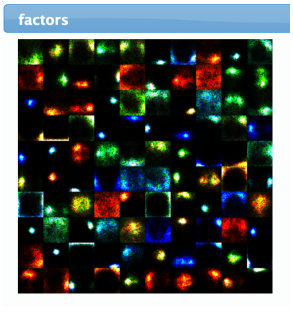


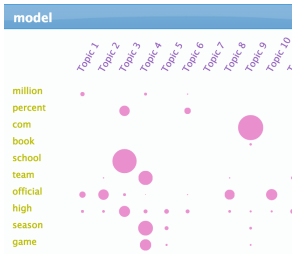
Figure 3: Dashboard for KMeans using MNIST dataset

in the "termite" system [7] and we use it also for our topic model visualization.

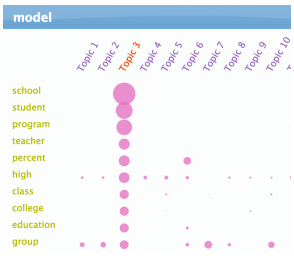
(a) MNIST clustering centers



(b) Dictionary learned by NMF on CIFAR dataset



(c) Ranking by global frequency



(d) Ranking within a topic

Figure 4: Model visualization

The topic model visualization follows the design from [7], as shown in Fig 4c and 4d. The radius of each pink circle in row i and column j encodes the weight for word i in topic j. We also display the word itself on the left side of each row to help people interpret the numbers. One common challenge for visualizing topic model comes from the huge size of the model. Typically hundreds or thousands of topics and even tens of thousands of different words. Limited screen size and limited human perception power require us to filter out information according to some saliency metric[7]. The metric will provide an ordering for words and topics and only the most important words and topics are displayed. Also, such an approach will significantly reduce the the amount of data that need to be transferred from the server to the client.

As we are displaying in real-time an evolving model, it is important to have a smooth and consistent word order after each update. We therefore only use the original topic weight to get the order of the words. In order to support a detailed zoom in for each topic, we also support ranking within a topic. This feature will be triggered when user mouse over the topic title, as shown in Fig 4d.

4.3 Continuous visualization of model quality

As described in 3.3, we are optimizing an additive function which consists of a main loss term as well as several *Mixin* terms. The value of the cost function can reflect how the model behaves under each criteria. As the engine keeps computing the update, we visualize those metrics as streaming data, as shown in Fig 5. Visualizing the main loss function is very important when we change the control parameters. It will reflect how algorithm responses to the user control and whether the tradeoff for *Mixin* functions may affect the general model performance.

As discussed earlier, the main loss function is computed on each minibatch, and is a single scalar. We use a simple, dynamic curve plot to display its state. This style of plot is easy to read and understand. With the parameters fixed, one normally sees a rapid initial increase in likelihood, followed by a slow increase on a plateau as in fig 5.

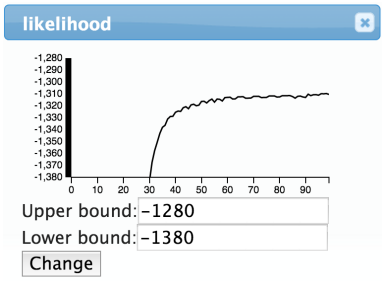


Figure 5: Continuous visualization of the likelihood function

4.4 Visualizing other performance indictors for Clustering

As mentioned above, the evaluation of unsupervised clustering algorithm is hard in general. Therefore showing multiple aspects of the clustering results at the same time would help users better interpret the model.

4.4.1 *Cluster size distribution*

To examine the cluster size balance, we are interested in the *distribution* of cluster sizes. The natural visualization for this kind of data is a histogram or kernel density plot. Fig 6a shows the size distribution for the clusters of digits on the MNIST dataset.

4.4.2 *Silhouette graph*

Another useful metric is the widely used silhouette graph (Fig 6b) for evaluating clustering results. The silhouette score is calculated for each data point x_j as:

$$s_j = \frac{b_j - a_j}{max(a_j, b_j)}$$

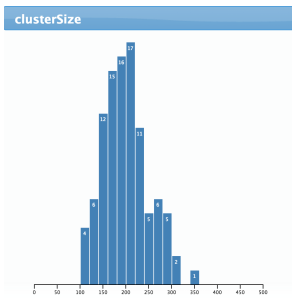
Where a_j is the average distance between x_j and all other data points in the same cluster, b_j is the lowest average distance of x_j to any other cluster. It could be seen that $-1 \leq s_j \leq 1$ and larger value indicates better clustering results.

4.4.3 *Recovered images from NMF*

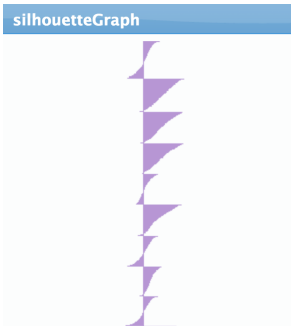
For the Non-negative Matrix Factorization algorithm[18], it is easy to recover the approximated matrix by multiplying the two factorized matrixes. Although the quality of the recovered matrix can be measured using L2-distance between the original matrix and the approximated one, directly showing the recovered result for image data (Fig 6c) can provide more details about what kind of information is being lost or preserved.

4.5 Slider controls

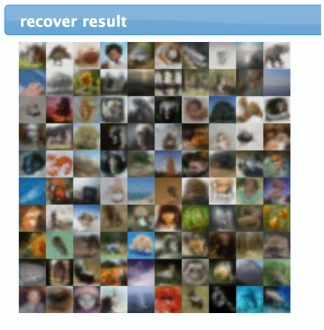
Along with the visual interface, we also provide several kinds of control including weights for *Mixin*, learning rate, etc. We also provide temperature control by changing the sample variance of the Gibbs sampler using SAME sampling[27]. So far these are all continuous scalars, and are all implemented as slider widgets. When the user select one of the controls from the menu, a labeled slider widget is created on the dashboard. The user drags and resizes this widget in an appropriate area of their dashboard. The selection of controls is currently independent of the selection of related



(a) Distribution of Cluster Size



(b) Silhouette graph



(c) Recovered images from NMF on CIFAR dataset

Figure 6: Performance indictors for clustering

metrics, and they are placed separately as well. In future we will explore intuitive ways of linking them (e.g. highlighting related metrics when a control is selected and vice-versa, or moving them as a group).

5. USE CASES

In this section, we will demonstrate several representative use cases for our system.

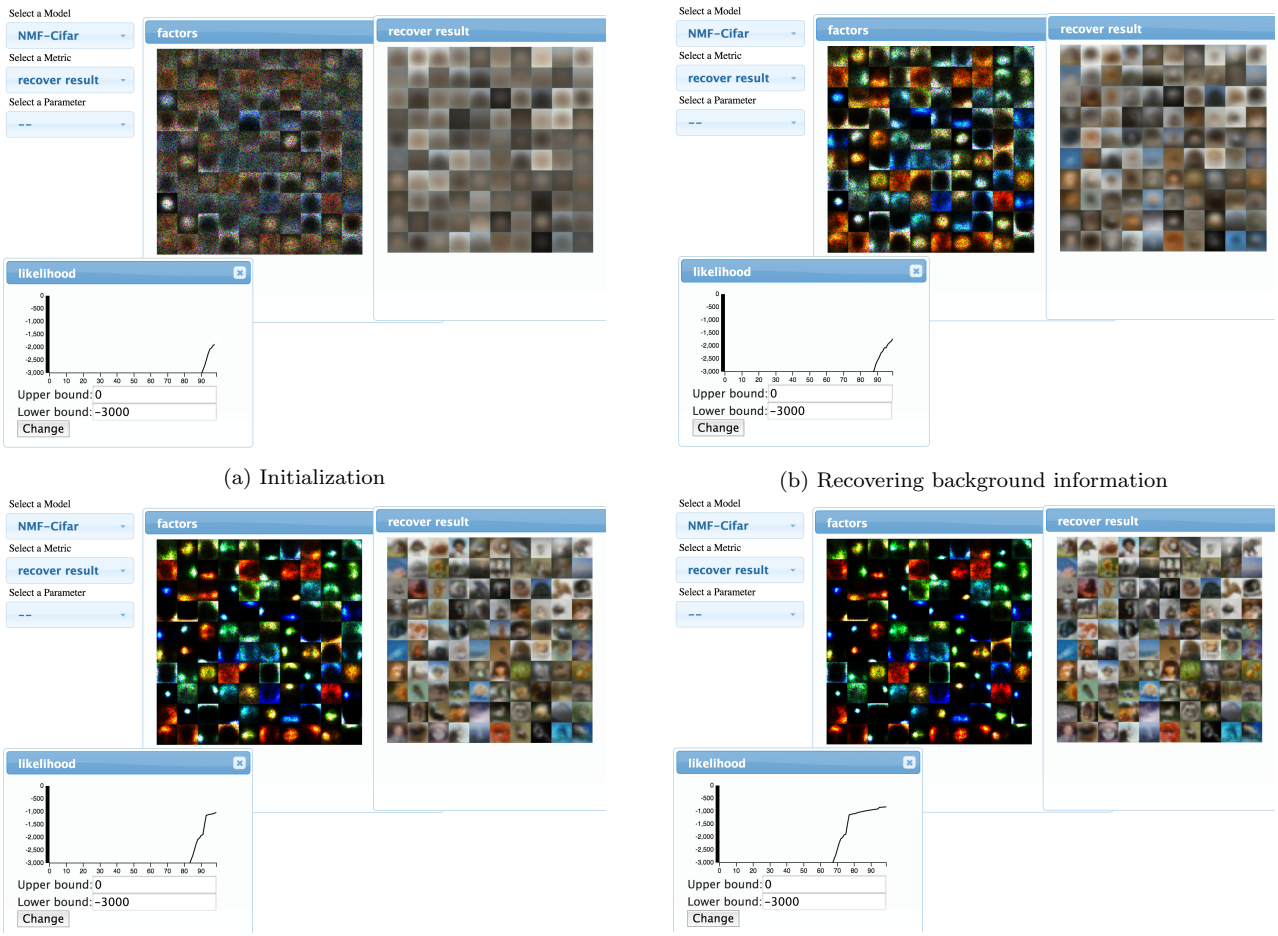
5.1 Non-negative Matrix Factorization

Our first demo is to monitor model update of the NMF algorithm in real-time. Although in this demo we don't have interactive control to the algorithm, we will still demonstrate how we can gain insight by viewing the learning process.

The NMF algorithm is trying to find low rank representation of the data matrix V by factorizing it into a product of two matrixes W, H with lower dimension. This is done by solving the optimization problem using multiplicative updates described in[18]:

$$arg \min_{W,H} ||V - WH||_2$$

This technique is very powerful in practice and can be used to find clusters of local patches for image data, or topics for text data. In our demo, we apply the NMF algorithm on the CIFAR-100 dataset[15]. The CIFAR dataset contains 50000 32*32 tiny RGB images which is stored in a 3072*50000 matrix. As we set the number of factors to be 256, the data matrix will be factorized into a 3072*256 matrix which is the dictionary for images and a 256*50000 matrix which contains the weights for each original image. Therefore each



(a) Initialization

(b) Recovering background information

(c) Recovering texture and edge

(d) Details become clearer

Figure 7: Online update for NMF

original image can be approximated as a linear combination of the 256 template images.

We train the model using a NVIDIA GTX-690 GPU with 2GB graphics memory, which costs less than a second for one iteration on the entire dataset, achieving around 150 GFlops. Such speed allows us to monitor real-time update as the model converges. We visualize the first 100 template images as well as the first 100 recovered images to help interpret what information is being extracted from the dataset. We also visualize the L2-loss $||V - WH||_2$ as a quantitative measurement.

The four representative stages of the training procedure is shown in Fig 7. Initially, the weight matrix are set to all one. Therefore a reasonable local optimal is to find some averaging images as the dictionary, and the recovered results all look similar, as shown in Fig 7a. Later in the procedure, the algorithm begins to recover background information as shown in Fig 7b. The sparseness of NMF model can also be seen since most pixels in the dictionary are black. This is consistent with [17] that the NMF algorithm always learns parts of the images. More texture and edge information will then be learned in the third stage, shown in Fig 7c. Some of the recovered images gradually become recognizable. Also, the template images clearly fall into two categories. One captures background information and the other represents tiny local patterns. Finally, in the last stage (Fig 7d), more details are being recovered and the L2-loss is about to converge. User now can trade off the model quality and training time based on their requirement.

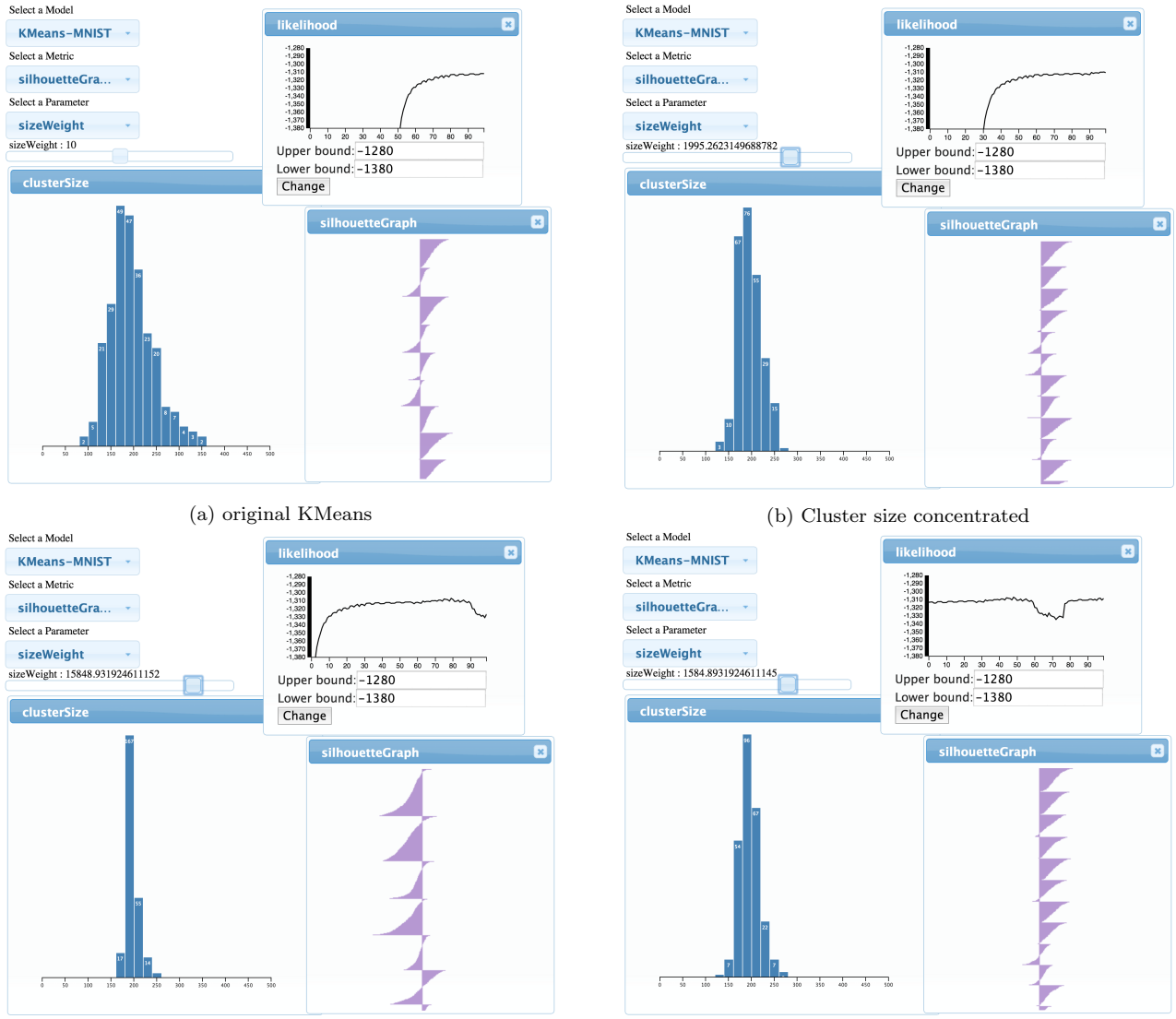
Comparing to the L2-loss metric, directly visualizing the model provides much more information than a single scalar. Users can gain more insight about the algorithm behavior by viewing the whole training process, which could help them make better decisions in the future.

5.2 KMeans

Our second demo is KMeans. This time we will have some direct control to the model which can demonstrate the full power of interactive clustering.

5.2.1 Evaluation and implementation for KMeans

For KMeans, the primary loss function is inertia: the sum of squared distances from points to their centroid. And the algorithm is straightforward: iteratively assigns data points to clusters and updates the cluster centroids using the mean of data.



(a) original KMeans

(b) Cluster size concentrated

(c) Begin to loss performance

(d) Recover the model

Figure 8: Interactive tuning for KMeans

However, as mentioned previously, the evaluation and tuning of the KMeans algorithm turn out to be hard. We therefore use multiple criteria to examine different aspects of the clustering results. Aside from the main loss, we use silhouette graph to measure how tight it is for each cluster. A low silhouette score typically indicates small clusters at the periphery of larger ones.

Besides, we also use cluster size balance as a criteria, which could be naturally visualized with a histogram. This criteria can also be optimized within the KMeans algorithm by adding size as a secondary loss. The overall minimization problem then becomes:

$$id(x) = arg\min_i ||cluster_i - x||_2^2 + \lambda * size_i \qquad (1)$$

$id(x)$ is used to assign a cluster id for each data point x. Where $size_i$ represents how many data points have already been assigned to the i-th cluster, $cluster_i$ is the center of the i-th cluster.

The loss term $\lambda * size_i$ penalizes clusters with a larger size. The algorithm would prefer to assign new data points to a smaller cluster, which will tend to balance cluster sizes over time. Size homogeneity matches most users' intuition about clustering, and it may also be important for accurate estimation of cluster statistics. The λ also becomes a parameter that we can interactively tune.

5.2.2 *Incremental update*

In order to take the advantage of mini-batch processing which can return early feedback during the training, we follow a similar approach to [28] for incremental KMeans updating. And we also need an averaging update for $size_i$ to maintain its scale and make the visualization consistent. For

each batch $\{x_j\}$, we compute the update as:

$$average_i = \frac{\sum_j x_j * \mathbb{1}(id(x_j) = i)}{\sum_j \mathbb{1}(id(x_j) = i)}$$

$$cluster_i = cluster_i + \eta * average_i$$

$$size_i = size_i + \alpha * \sum_j \mathbb{1}(id(x_j) = i)$$

Normally η and α are set to $0.1 \sim 0.2$.

5.2.3 Experiment on MNIST dataset

We ran an experiment on the MNIST dataset [16], which contains 8 million 28×28 images of hand written digits. We train the model using NVIDIA GTX-690 GPU, which could process roughly 500MB raw data (16.7k images) per second. As we set the batch size to be 50000, every second the system could perform 3 batch updates, which is enough for real-time visualization.

In our dashboard, we choose to visualize the main loss, cluster size distribution, as well as the silhouette graph. The main loss is the averaging distance between the data points and their assigned cluster centers (not taking into account size).

The parameter that we choose to tune is the size weight λ in eq(1), which we refer as $sizeWeight$ in the interface. Initially, we set the number of clusters K as 250 and we assigned a small value to $sizeWeight$, so that the algorithm will behave as the original KMeans algorithm. As shown in Fig 8a, the likelihood is gradually improving and it quickly converges to local minimal. The cluster size distribution is quite diverse. We then increase the $sizeWeight$ slightly, which gives us a more concentrated cluster size distribution, while the main loss and silhouette score are not affected, as shown in Fig 8b. This implies that the algorithm now moves to another local optimal by assigning some data points to a suboptimal but smaller cluster. Notice that this has almost no effect on the primary likelihood.

However, as we continue to increase $sizeWeight$, the loss will start to increase, and the silhouette graph also shows more defects (more negative area) (Fig 8c). From here, we decrease the $sizeWeight$. Since the KMeans algorithm is incremental, this change brings us back close to the likelihood before the last increase, as shown in Fig 8d. This example illustrates the tradeoffs that can be made, and the speed of recognizing poor parameter choices.

5.3 L1-regularized Topic Model

Our last demo is applying our system to Latent dirichlet allocation(LDA) topic modeling [3], one of the most widely used topic models.

5.3.1 Implementation

LDA is a generative process to model the documents. For each document d, it proceeds as follows (K is the number of latent factors):

- Draw a topic distribution for the document d as $\theta_d \sim Dirichlet(\alpha)$, a K-dimensional Dirichlet.
- For each word position i (across all docs), draw a topic index $z_{d,i} \in \{1, ..., K\}$ from $z_{d,i} \sim \theta_d$
- Draw the word $w_{d,i}$ from the multinomial distribution $w_{d,i} \sim \varphi_{z_{d,i}}$, which also has a prior: $\varphi_{z_{d,i}} \sim Dirichlet(\beta)$

α, and β are hyper-parameters specifying the Dirichlet prior. The other two parameters of the model are θ, which can be represented as a document-topic matrix, and φ, the word-topic matrix. The algorithm therefore is to use Gibbs sampler to draw samples for hidden states z_i:

$$P_X(z_{d,i} = k | z_{-d,i}, \alpha, \beta, x_{d,i} = w) \sim \theta_{d,k} * \varphi_{k,w} \qquad (2)$$

After drawing the samples, θ and φ can be updated via Maximum Likelihood Estimation. In order to apply annealing to the optimization procedure, we further use SAME sampling [27] to draw m independent samples instead of just one from Z each time. This results in a cooled Gibbs sampler and the parameter m can be used to control the temperature. A low value of m gives a higher-variance random-walk while increasing m can cause parameters converge to a nearby optimum. By default m is set to 100, and it can be tuned during the training. We refer m as $nsamps$ in the interface.

Similar to KMeans, we also use incremental update for LDA as described in [11]. A L1-regularization is also added into the model to enforce sparsity. As describe in 3.3, the implementation is very straightforward. For each batch, after computing the model update φ', we also compute the subgradient update for the L1-regularization:

$$g(\varphi_{k,w}) = -\lambda * sign(\varphi_{k,w})$$

We then add those two terms φ' and $g(\varphi)$ into the model using the weighted averaging approach we discussed above. We refer the weight λ as $L1 - reg$ in the interface.

5.3.2 Experiment on NYTimes dataset

We run an experiment on the NYTimes dataset [19], which contains about 300K documents, 102K different words and totally 100M tokens. Again, we train our model using GTX 690 GPU.

We first set topic number K as 1024 and the model converged in about two minutes. As shown in Fig 9, the resulting topic matrix is very sparse even without adding the L1-regularization. This is due to that we set a large K and many independent topics are generated.

We then set K to be 32. Without any regularization, the algorithm's behavior is shown in Fig 10. The likelihood quickly converges to a local optimal, but the topic results are still very noisy, and the topics are overlapping. We then adjust the $L1 - reg$ slider away from zero. However, tuning $L1 - reg$ will not always give good results on complex likelihood functions due to local optima. Since SAME sampling is used in our LDA implementation, we can decrease $nsamps$ to increase the variance of the random-walk, which makes it easier to jump between possible solutions.

After we increase the temperature, as shown in Fig 11, the likelihood drops significantly but we get a very sparse model.

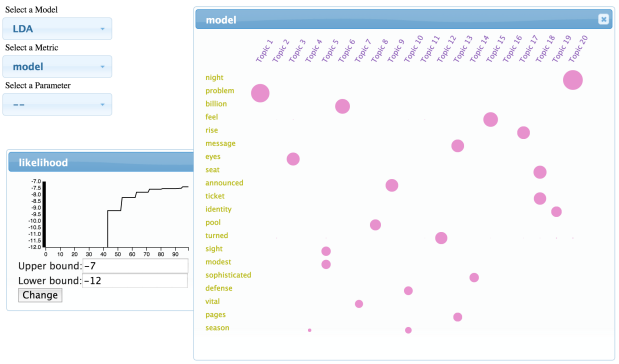


Figure 9: Converged sparse model, K=1024

Afterward, we set the $L1-reg$ back to a small value and use a large *nsamps* (cold state) which prevents large changes in model state. This is equivalent to only allowing the model to make very small movement around that local optimal. From Fig 12, we can see that the likelihood returns to a normal value while the sparsity is maintained.

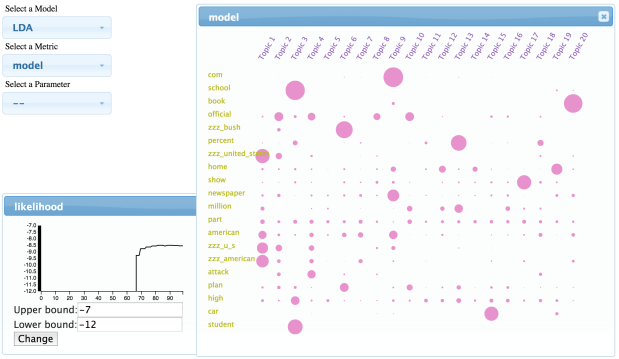


Figure 10: Overlapping topics, K=32

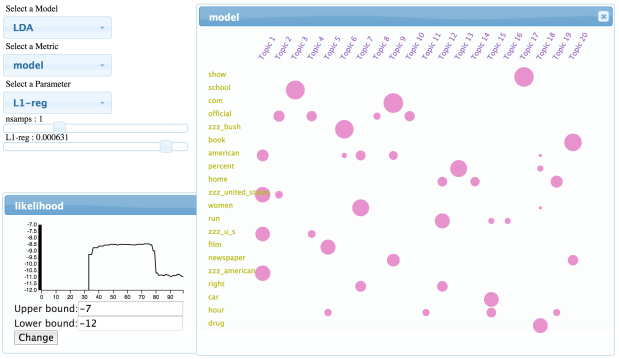


Figure 11: High temperature with high L1-reg

6. CONCLUSION & FUTURE WORK

We have demonstrated how to perform interactive optimization on customized models using our system. The *Mixin* function is a convenient and useful way to capture user's intuition and create customized model. The dashboard also enable users to easily monitor several performance indicators at the same time, which help users to evaluate the model

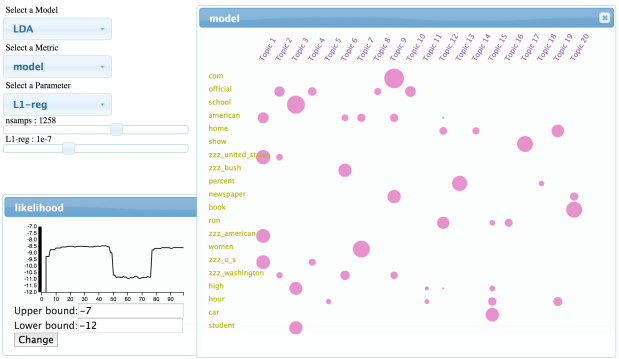


Figure 12: Likelihood back to normal, sparsity preserved

from different perspectives. By summarizing this information, the trade-off decisions become straightforward. Also, the GPU accelerated toolkit makes it possible to get real-time feedback. This ensures that users can understand cause and effect of the algorithm behavior in an iterative refinement procedure.

More *Mixin* functions like measuring independence of factors, or coherence of topics could be implemented in the future. Also, our framework is not limited to the unsupervised learning algorithms. Some concrete examples of competing goals in supervised learning include computational marketing where the primary goal is maximize revenue, but where secondary goals include user satisfaction, advertiser satisfaction, and budget constraints. Recommender systems seek to recommended the highest-rated items, but may also need to cover the available item inventory, favor more or less expensive items, or favor items which encourage future purchases. Those are all potential extensions that could be explored in the future.

7. REFERENCES

[1] S. Amershi, M. Cakmak, W. B. Knox, and T. Kulesza. Power to the people: The role of humans in interactive machine learning. *AI Magazine*, 35(4):105–120, 2014.

[2] D. Andrzejewski, X. Zhu, M. Craven, and B. Recht. A framework for incorporating general domain knowledge into latent dirichlet allocation using first-order logic. In *IJCAI Proceedings-International Joint Conference on Artificial Intelligence*, volume 22, page 1171, 2011.

[3] D. M. Blei, A. Y. Ng, and M. I. Jordan. Latent dirichlet allocation. *the Journal of machine Learning research*, 3:993–1022, 2003.

[4] M. Bostock, V. Ogievetsky, and J. Heer. D^3 data-driven documents. *Visualization and Computer Graphics, IEEE Transactions on*, 17(12):2301–2309, 2011.

[5] J. Canny and H. Zhao. Big data analytics with small footprint: Squaring the cloud. In *Proceedings of the 19th ACM SIGKDD international conference on Knowledge discovery and data mining*, pages 95–103. ACM, 2013.

[6] J. Chang, S. Gerrish, C. Wang, J. L. Boyd-graber, and D. M. Blei. Reading tea leaves: How humans interpret topic models. In *Advances in neural information*

processing systems, pages 288–296, 2009.

[7] J. Chuang, C. D. Manning, and J. Heer. Termite: Visualization techniques for assessing textual topic models. In *Proceedings of the International Working Conference on Advanced Visual Interfaces*, pages 74–77. ACM, 2012.

[8] M. B. Eisen, P. T. Spellman, P. O. Brown, and D. Botstein. Cluster analysis and display of genome-wide expression patterns. *Proceedings of the National Academy of Sciences*, 95(25):14863–14868, 1998.

[9] J. A. Fails and D. R. Olsen Jr. Interactive machine learning. In *Proceedings of the 8th international conference on Intelligent user interfaces*, pages 39–45. ACM, 2003.

[10] J. E. Gonzalez, Y. Low, H. Gu, D. Bickson, and C. Guestrin. Powergraph: Distributed graph-parallel computation on natural graphs. In *OSDI*, volume 12, page 2, 2012.

[11] M. Hoffman, F. R. Bach, and D. M. Blei. Online learning for latent dirichlet allocation. In *advances in neural information processing systems*, pages 856–864, 2010.

[12] Y. Hu, J. Boyd-Graber, and B. Satinoff. Interactive topic modeling. In *Association for Computational Linguistics*, 2011.

[13] A. Kapoor, B. Lee, D. S. Tan, and E. Horvitz. Performance and preferences: Interactive refinement of machine learning procedures. In *AAAI*. Citeseer, 2012.

[14] T. Kraska, A. Talwalkar, J. C. Duchi, R. Griffith, M. J. Franklin, and M. I. Jordan. Mlbase: A distributed machine-learning system. In *CIDR*, 2013.

[15] A. Krizhevsky and G. Hinton. Learning multiple layers of features from tiny images. *Computer Science Department, University of Toronto, Tech. Rep*, 1(4):7, 2009.

[16] Y. LeCun, L. Bottou, Y. Bengio, and P. Haffner. Gradient-based learning applied to document recognition. *Proceedings of the IEEE*, 86(11):2278–2324, 1998.

[17] D. D. Lee and H. S. Seung. Learning the parts of objects by non-negative matrix factorization. *Nature*, 401(6755):788–791, 1999.

[18] D. D. Lee and H. S. Seung. Algorithms for non-negative matrix factorization. In *Advances in neural information processing systems*, pages 556–562, 2001.

[19] M. Lichman. UCI machine learning repository, 2013.

[20] Q. Mei, D. Cai, D. Zhang, and C. Zhai. Topic modeling with network regularization. In *Proceedings of the 17th international conference on World Wide Web*, pages 101–110. ACM, 2008.

[21] D. Newman, E. V. Bonilla, and W. Buntine. Improving topic coherence with regularized topic models. In *Advances in neural information processing systems*, pages 496–504, 2011.

[22] D. Newman, J. H. Lau, K. Grieser, and T. Baldwin. Automatic evaluation of topic coherence. In *Human Language Technologies: The 2010 Annual Conference of the North American Chapter of the Association for Computational Linguistics*, pages 100–108. Association for Computational Linguistics, 2010.

[23] H. Raghavan, O. Madani, and R. Jones. Interactive feature selection. In *IJCAI*, volume 5, pages 841–846, 2005.

[24] J. Seo and B. Shneiderman. Interactively exploring hierarchical clustering results [gene identification]. *Computer*, 35(7):80–86, 2002.

[25] E. R. Sparks, A. Talwalkar, V. Smith, J. Kottalam, X. Pan, J. Gonzalez, M. J. Franklin, M. I. Jordan, and T. Kraska. Mli: An api for distributed machine learning. In *Data Mining (ICDM), 2013 IEEE 13th International Conference on*, pages 1187–1192. IEEE, 2013.

[26] Y. Yang, S. Pan, Y. Song, J. Lu, and M. Topkara. User-directed non-disruptive topic model update for effective exploration of dynamic content. In *Proceedings of the 20th International Conference on Intelligent User Interfaces*, pages 158–168. ACM, 2015.

[27] H. Zhao, B. Jiang, and J. F. Canny. SAME but different: Fast and high-quality gibbs parameter estimation. *CoRR*, abs/1409.5402, 2014.

[28] S. Zhong. Efficient online spherical k-means clustering. In *Neural Networks, 2005. IJCNN'05. Proceedings. 2005 IEEE International Joint Conference on*, volume 5, pages 3180–3185. IEEE, 2005.

[29] J.-Y. Zhu, Y. J. Lee, and A. A. Efros. Averageexplorer: Interactive exploration and alignment of visual data collections. *ACM Transactions on Graphics (TOG)*, 33(4):160, 2014.