Stacked Density Estimation

Padhraic Smyth*
Information and Computer Science
University of California, Irvine
CA 92697-3425
smyth@ics.uci.edu

David Wolpert
IBM Almaden Research,
650 Harry Road, San Jose, CA 95120
dhw@almaden.ibm.com

AREA: ALGORITHMS AND ARCHITECTURES

Abstract

In this paper, the technique of stacking, previously only used for supervised learning, is applied to unsupervised learning. Specifically, it is used for non-parametric multivariate density estimation, to combine finite mixture model and kernel density estimators. Experimental results on both simulated data and real world data sets clearly demonstrates that stacked density estimation outperforms other strategies such as choosing the single best model based on cross-validation, combining with uniform weights, and even the single best model chosen by "cheating" by looking at the data used for independent testing.

1 Introduction

As argued by Draper (1996), model uncertainty can contribute significantly to predictive error in machine learning. While usually considered in the context of supervised learning, model uncertainty is also important in unsupervised learning applications such as density estimation. Even when the model class under consideration contains the true density, if we are only given a finite data set, then there is always a chance of selecting the wrong model. Moreover, even if the correct model is selected, there will typically be estimation error in the parameters of that model. These difficulties are summarized by writing

$$P(f \mid D) = \sum_M \int d\theta_M P(\theta_M \mid D, M) \times P(M \mid D) \times f_{M,\theta_M}, \tag{1}$$

where f is a density, D is the data set, M is a model, and θ_M is a set of values for the parameters for model M. The posterior probability $P(M \mid D)$ reflects model

*Corresponding Author. Also with the Jet Propulsion Laboratory 525-3660, California Institute of Technology, Pasadena, CA 91109.

uncertainty, and the posterior $P(\theta_M \mid D, M)$ reflects uncertainty in setting the parameters even once one knows the model. Note that if one is privy to $P(M, \theta_M)$, then Bayes' theorem allows us to write out both of our posteriors explicitly, so that we explicitly have $P(f \mid D)$ (and therefore the Bayes-optimal density) given by a weighted average of the f_{M,θ_M}. (See also Escobar and West (1995)). However even when we know $P(M, \theta_M)$, calculating the combining weights can be difficult. Thus, various approximations and sampling techniques are often used, a process that necessarily introduces extra error (Chickering and Heckerman 1997).

More generally, consider the case of mis-specified models where the model class does not include the true model, so our presumption for $P(M, \theta_M)$ is erroneous. In this case often one should again average. In particular, prediction using the single model which is closest to the true density (in the sense of Kullback-Leibler or cross-entropy distance) can be shown to be inferior to prediction based on averaging over multiple models (Madigan and Raftery, 1994).

Thus, a natural approach to improving density estimators is to consider empirically-driven combinations of multiple density models. There are several ways to do this, especially if one exploits previous combining work in supervised learning. For example, Ormontreit and Tresp (1996) have shown that "bagging" (uniformly weighting different parametrizations of the same model trained on different bootstrap samples), originally introduced for supervised learning (Breiman 1996a), can improve accuracy for mixtures of Gaussians with a fixed number of components.

Another supervised learning technique for combining different types of models is "stacking" (Wolpert 1992), which has been found to be very effective for both regression and classification (e.g., Breiman (1996b), Leblanc and Tibshirani (1993)). This paper applies stacking to density estimation, in particular to combinations involving kernel density estimators together with finite mixture model estimators. In Section 2 we give some background on those density estimators and present stacked density estimators. Then in Section 3 we present experimental results demonstrating the utility of stacked density estimation. Sections 4 and 5 contain a brief discussion of links to related prior work, future directions, and conclusions.

2 Stacked Density Estimation

2.1 Background on Density Estimation with Mixtures and Kernels

Consider a set of d real-valued random variables $\underline{X} = \{X^1, \ldots, X^d\}$ Upper case symbols denote variable names (such as X^j) and lower-case symbols a particular value of a variable (such as x^j). $\underline{x}$ is a realization of the vector variable $\underline{X}$. $f(\underline{x})$ is shorthand for $f(\underline{X} = \underline{x})$ and represents the joint probability distribution of $\underline{X}$. $D = \{\underline{x}_1, \ldots, \underline{x}_N\}$ is a training data set where each sample $\underline{x}_i, 1 \leq i \leq N$ is an independently drawn sample from the underlying density function $f(\underline{x})$.

A commonly used model for density estimation is the *finite mixture model* with k components, defined as:

$$f^k(\underline{x}) = \sum_{j=1}^{k} \alpha_j g_j(\underline{x}), \tag{2}$$

where $\sum_{j=1}^{k} \alpha_j = 1$. The component g_j's are usually relatively simple unimodal densities such as Gaussians. Density estimation with mixtures involves finding the locations, shapes, and weights of the component densities from the data (using for example the Expectation-Maximization (EM) procedure). *Kernel density estimation* can be viewed as a special case of mixture modeling where a component is centered at each data point, given a weight of $1/N$, and a common covariance structure (kernel shape) is estimated from the data.

The quality of a particular probabilistic model can be evaluated by an appropriate scoring rule on independent out-of-sample data, such as the test set log-likelihood (also referred to as the log-scoring rule in the Bayesian literature). Given a test data set D^{test}, the test log likelihood is defined as

$$\log f(D^{test}|f^k(\underline{x})) = \sum_{D^{test}} \log f^k(\underline{x}_i) \quad (3)$$

This quantity can play the role played by classification error in classification or squared error in regression. For example, cross-validated estimates of it can be used to find the best number of clusters to fit to a given data set (Smyth, 1996).

2.2 Background on Stacking

Stacking can be used either to combine algorithms or to improve a single algorithm. In the former guise it proceeds as follows. First, subsamples of the training set are formed. Next the algorithms are all trained on one subsample and resultant joint predictive behavior on another subsample is observed, together with information concerning the optimal predictions on the elements in that other subsample. This is repeated for other pairs of subsamples of the training set. Then an additional ("stacked") algorithm is trained to learn, from the subsample-based observations, the relationship between the observed joint predictive behavior of the algorithms and the optimal predictions. Finally, this learned relationship is used in conjunction with the predictions of the individual algorithms being combined (now trained on the entire data set) to determine the full system's predictions.

2.3 Applying Stacking to Density Estimation

Consider a set of M different density models, $f_m(\underline{x}), 1 \leq m \leq M$. In this paper each of these models will be either a finite mixture with a fixed number of component densities or a kernel density estimate with a fixed kernel and a single fixed global bandwidth in each dimension. (In general though no such restrictions are needed.) The procedure for stacking the M density models is as follows:

1. Partition the training data set D v times, exactly as in v-fold cross validation (we use $v = 10$ throughout this paper), and for each fold:
   (a) Fit each of the M models to the training portion of the partition of D.
   (b) Evaluate the likelihood of each data point in the test partition of D, for each of the M fitted models.
2. After doing this one has M density estimates for each of N data points, and therefore a matrix of size $N \times M$, where each entry is $f_m(\underline{x}_i)$, the out-of-sample likelihood of the mth model on the ith data point.
3. Use that matrix to estimate the combination coefficients $\{\alpha_1, \ldots, \alpha_M\}$ that maximize the log-likelihood at the points $\underline{x}_i$ of a stacked density model of the form:

   $$f_{\text{stacked}}(\underline{x}) = \sum_{m=1}^{M} \alpha_m f_m(\underline{x}).$$

   Since this is itself a mixture model, but where the $f_m(\underline{x}_i)$ are fixed, the EM algorithm can be used to (easily) estimate the α_m.

4. Finally, re-estimate the parameters of each of the m component density models using *all* of the training data D. The stacked density model is then the linear combination of those density models, with combining coefficients given by the α_m.

3 Experimental Results

In our stacking experiments $M = 6$: three triangular kernels with bandwidths of $0.1, 0.4$, and 1.5 of the standard deviation (of the full data set) in each dimension, and three Gaussian mixture models with $k = 2, 4$, and 8 components. This set of models was chosen to provide a reasonably diverse representational basis for stacking. We follow roughly the same experimental procedure as described in Breiman (1996b) for stacked regression:

- Each data set is randomly split into training and test partitions 50 times, where the test partition is chosen to be large enough to provide reasonable estimates of out-of-sample log-likelihood.
- The following techniques are run on each training partition:
  1. **Stacking:** The stacked combination of the six constituent models.
  2. **Cross-Validation:** The single best model as indicated by the maximum likelihood score of the $M = 6$ single models in the $N \times M$ cross-validated table of likelihood scores.
  3. **Uniform Weighting:** A uniform average of the six models.
  4. **"Cheating:"** The best single model, i.e., the model having the largest likelihood on the *test* data partition,
  5. **Truth:** The true model structure, if the true model is one of the six generating the data (only valid for simulated data).
- The log-likelihoods of the models resulting from these techniques are calculated on the test data partition. The log-likelihood of a single Gaussian model (parameters determined on the training data) is subtracted from each model's log-likelihood to provide some normalization of scale.

Four data sets were chosen for experimental evaluation. The diabetes data set consists of 145 data points used in Gaussian clustering studies by Banfield and Raftery (1991) and others. Fisher's iris data set is a classic data set in 4 dimensions with 150 data points. Both of these data sets are thought to consist roughly of 3 clusters which can be reasonably approximated by 3 Gaussians. The Barney and Peterson vowel data (2 dimensions, 639 data points) contains 10 distinct vowel sounds and so is thought to be highly multi-modal. The star-galaxy data (7 dimensions, 499 data points) contains fairly non-Gaussian looking structure in various 2d projections.

Table 1 summarizes the results. In all cases stacking had the highest average log-likelihood, even out-performing "cheating" (the single best model chosen from the test data). (Breiman (1996b) also found for regression that stacking outperformed the "cheating" method.) We considered two null hypotheses: stacking has the same predictive accuracy as cross-validation, and it has the same accuracy as uniform weighting. (Testing the difference between stacking and cheating seems meaningless). Each hypothesis can each be rejected with a chance of less than 0.01% of being incorrect, according to the Wilcoxon signed-rank test i.e., the observed differences in performance are extremely strong.

On the vowel data set uniform weighting performs much worse than the other methods: it is closer in performance to stacking on the other 3 data sets. On three

Table 1: Relative performance of stacking multiple mixture models, for various data sets, measured (relative to the performance of a single Gaussian model) by mean log-likelihood on test data partitions. The maximum for each data set is underlined.

Data Set	Gaussian	Cross-Validation	"Cheating"	Uniform	Stacking
Diabetes	-352.9	27.8	30.4	29.2	<u>31.8</u>
Fisher's Iris	-52.6	18.3	21.2	18.3	<u>22.5</u>
Vowel	128.9	53.5	54.6	40.2	<u>55.8</u>
Star-Galaxy	-257.0	678.9	721.6	789.1	<u>888.9</u>

Table 2: Average across 20 runs of the stacked weights found for each constituent model. The columns with $h = \ldots$ are for the triangular kernels and the columns with $k = \ldots$ are for the Gaussian mixtures.

Data Set	h=0.1	h=0.4	h=1.5	$k = 2$	$k = 4$	$k = 8$
Diabetes	0.01	0.09	0.03	0.13	0.41	0.32
Fisher's Iris	0.02	0.16	0.00	0.26	0.40	0.16
Vowel	0.00	0.25	0.00	0.02	0.20	0.53
Star-Galaxy	0.00	0.04	0.03	0.03	0.27	0.62

of the data sets, using cross-validation to select a single model is the worst method. "Cheating" is second-best to stacking except on the star-galaxy data, where it is worse than uniform weighting also: this may be because the star-galaxy data probably induces the greatest degree of mis-specification relative to this 6-model class (based on visual inspection).

Table 2 shows the averages of the stacked weight vectors for each data set. The mixture components generally got higher weight than the triangular kernels. The vowel and star-galaxy data sets have more structure than can be represented by any of the component models and this is reflected in the fact that for each most weight is placed on the most complex mixture model with $k = 8$.

3.1 Results on Simulated Data with no Model Mis-Specification

We simulated data from a 2-dimensional 4 Gaussian mixture model with a reasonable degree of overlap (this is the data set used in Ripley (1994) with the class labels removed) and compared the same models and combining/selection schemes as before, except that this time we also could include "truth", i.e., the scheme which always selects the model structure with $k = 4$ Gaussians. The training sample size was varied from 30 to 200 and the test results were determined on an independent sample of size 800.

Note that here we are assured of having the true model in the set of models being considered, something that is presumably never exactly the case in the real world (and presumably was not the case for the experiments recounted in Table 1.) Nonetheless, as indicated in (Figure 1), stacking performed about as well as the "cheating" method and significantly outperformed the other methods, including "truth." (Results where some of the methods had log-likelihoods *lower* than the single Gaussian are not shown for clarity).

The fact that "truth" performed poorly on the smaller sample sizes is due to the fact

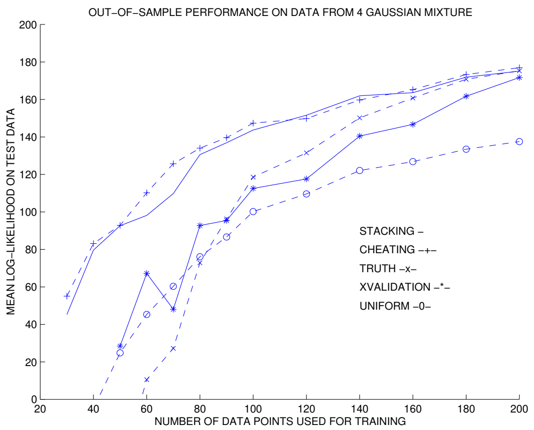

Figure 1: Plot of mean log-likelihood (relative to a single Gaussian model) for various density estimation schemes on data simulated from a 4-component Gaussian mixture.

that with smaller sample sizes it was often better to fit a simpler model with reliable parameter estimates (which is what "cheating" typically would do) than a more complex model which may overfit (even when it is the true model structure). As the sample size increases, both "truth" and cross-validation approach the performance of "cheating" and stacking: uniform weighting is universally poorer as one would expect when the true model is within the model class. The stacked weights at the different sample sizes (not shown) start out with significant weight on the triangular kernel model and gradually shift to the $k = 2$ Gaussian mixture model and finally to the (true) $k = 4$ Gaussian model as sample size grows. Thus, stacking is seen to incur no penalty when the true model is within the model class being fit. In fact the opposite is true; for small sample sizes stacking outperforms other density estimation techniques which place full weight on a single (but poorly parametrized) model.

4 Discussion and Future Work

Selecting a global bandwidth for kernel density estimation is still a topic of debate among statisticians. Stacking allows the possibility of side-stepping the issue of a single bandwidth by combining kernels with different bandwidths and different kernel shapes. A stacked combination of such kernel estimators is equivalent to using a single composite kernel that is a convex combination of the underlying kernels. So for example kernel estimators based on finite support kernels can be regularized in a data-driven manner by combining them with infinite support kernels. The key point is that the shape and width of the resulting "effective" kernel is driven by the data.

It is also worth noting that by combining Gaussian mixture models with different k values one gets a hierarchical "mixture of mixtures" model. This hierarchical model can provide a natural multi-scale representation of the data, which is clearly similar in spirit to wavelet density estimators, although the functional forms and estimation methodologies for each technique can be quite different. There is also a representational similarity to Jordan and Jacob's (1994) "mixture of experts" model where the weights are allowed to depend directly on the inputs. Exploiting that similarity, one direction for further work is to investigate adaptive weight parametrizations in the stacked density estimation context.

5 Conclusion

In this paper stacked density estimation was introduced and proposed as a practical method for generating better density estimators. For mis-specified models (i.e., most real-world data sets) the method was shown empirically to provide clearly better density estimates than a single model chosen by cross-validation, uniform weighting of models, or even the single best model chosen by looking at the test data set. For well-specified models (simulated data, where the true model is within the model class being considered), stacking was seen to provide a regularization effect for small sample sizes and outperformed even the single true model.

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