

Solving Non-Linear SVM in Linear Time? A Nyström Approximated SVM with Applications to Image Classification

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May 21, 2013

Outline

- Introduction
- The Nyström Method for Kernel Approximation
- The Nyström Method for Linear SVM Classification
- Experiments and Conclusions

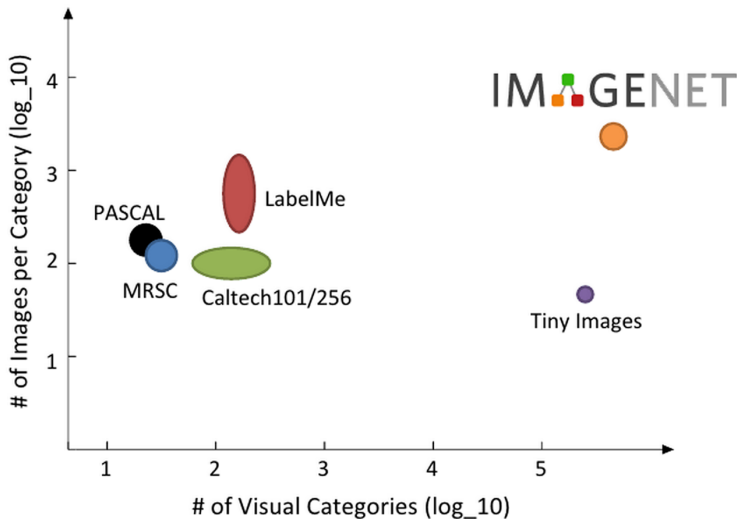
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Visual Classification: Faces, Objects, and Beyond



Example: Some Image Classification Data Sets



We Have Known...

- Non-linear SVM: powerful but slow
- Linear SVM: simple but fast

Paper: “Training Linear SVMs in Linear Time” by Joachims
KDD’06

Software: LIBLINEAR, VW, etc.

We Had Always Wondered...

- But we want something **powerful** and **fast**: train faster than non-linear SVM and generate a more accurate model than linear SVM.

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Yes. Do approximation!

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Definitions and a Brief Review (1/2)

- Input Data: $\{(\mathbf{y}, X)\} = \{(y_i, \mathbf{x}_i)\}_{i=1}^{\ell}$. y_i : label, \mathbf{x}_i : feature vector.
- Dimension of \mathbf{x}_i : d
- Non-linear mapping $\phi(\mathbf{x})$ (e.g. bi-gram features)
- Kernel function: $K(\mathbf{u}, \mathbf{v}) = \phi(\mathbf{u})^T \phi(\mathbf{v})$, usually computed in linear time.
- For ease of representation, for $U = [\mathbf{u}_1, \dots, \mathbf{u}_{\ell}]$ and $V = [\mathbf{v}_1, \dots, \mathbf{v}_{\ell}]$, we define $Q = K(U, V)$, where $Q_{ij} = K(\mathbf{u}_i, \mathbf{v}_j)$

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- Lower bound for data storage and training: $\Omega(\ell d)$.

Definitions and a Brief Review (2/2)

- Primal SVM:

$$\min_{\mathbf{w}, b} \frac{1}{2} \mathbf{w}^T \mathbf{w} + C \sum_{i=1}^{\ell} \max(1 - y_i \mathbf{w}^T \phi(\mathbf{x}_i), 0)$$

- Dual SVM:

$$\begin{aligned} \min_{\alpha} \quad & \frac{1}{2} \alpha^T Q \alpha - \mathbf{e}^T \alpha \\ \text{s.t.} \quad & 0 \leq \alpha_i \leq C \quad \forall i. \end{aligned}$$

- Primal-Dual Correspondence: $\mathbf{w} = \sum_{i=1}^{\ell} y_i \alpha_i \phi(\mathbf{x}_i)$

Kernel in Non-linear SVM

- Dual form:

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- $1M$ images: $1M$ times more computational time than the linear counterpart.

Nyström Method

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- Sample $\tilde{\ell} (\ll \ell)$ feature vectors from X with a basis set $B = \{\mathbf{b}_i\}_{i=1}^{\tilde{\ell}}$.

The low-rank approximated kernel: $Q \sim \tilde{Q} = PW^{-1}P^T$,
 where $P_{ij} = K(\mathbf{x}_i, \mathbf{b}_j)$ and $W_{ij} = K(\mathbf{b}_i, \mathbf{b}_j)$.

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- Set our basis size, $\tilde{\ell}$ to d . The space consumption is optimal.

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An Equivalent Representation (1/2)

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- $Q = \tilde{X}^T \tilde{X}$ by Cholesky decomposition. (This is valid because Q is PSD by definition.)
- Investigate the columns of $\tilde{X} = [\tilde{\mathbf{x}}_1 \dots \tilde{\mathbf{x}}_\ell]$. We have $\tilde{\mathbf{x}}_i^T \tilde{\mathbf{x}}_j = Q_{ij} = \phi(\mathbf{x}_i)^T \phi(\mathbf{x}_j) = K(\mathbf{x}_i, \mathbf{x}_j)$.

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- We represent the kernelized linear products as regular linear products. Let's call \tilde{X} a compact representation.

An Equivalent Representation (2/2)

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- Issue: computing $\tilde{\mathbf{x}}_i$ requires the computation of the ℓ^2 -sized kernel.

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- Needs a linear feature selection method!

Brief Recap

- Nyström approximation

$$Q = P W^{-1} P^T$$

- Nyström approximation for linear representation

$$X = P R$$

Another View of Basis Selection (1/2)

- Recall that: $P_i = [K(\mathbf{x}_i, \mathbf{b}_1), \dots, K(\mathbf{x}_i, \mathbf{b}_{\tilde{\ell}})]$
- Can we view PR as input data and do feature selection?

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- Can we view PR as input data and do feature selection?
- No! R introduces dependency between dimensions.
- We remove R ! Each dimension is then independent of other basis vector.
- L1-regularized linear SVM which runs linear time in data size is used in the work.

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- $R^{T-1} \mathbf{w}$ separates $R^T \mathbf{p}_+$ and $R^T \mathbf{p}_-$.
- When doing the linear transformation by R , we preserve separability.

The Algorithm Workflow

- 1 Input data: (\mathbf{y}, X) , a kernel K .
- 2 Run basis selection on $K(X, B)$.
- 3 Compute the new data $\tilde{X} = RK(X, B)$, where $R^T R = K(B, B)^{-1}$.
- 4 Train on (\mathbf{y}, \tilde{X})

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Time: $O(\ell \tilde{\ell} d)$ overall.

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Experimental Settings

- We conduct experiments on two benchmark datasets: USPS and MNIST.
- We randomly split 70% of the data for training and the remaining 30% for testing. (Repeat 5 times)
- We perform a five-fold cross validation to select the parameters γ and C .

Table: Dataset descriptions (with the number ℓ of instances and the dimension d of the data). The sizes for storing the data ℓd and the associated kernel matrices ℓ^2 are also listed.

	ℓ	d	kernel size ℓ^2	data size ℓd
USPS	7291	256	53M	2M
MNIST	60000	780	3.6G	47M

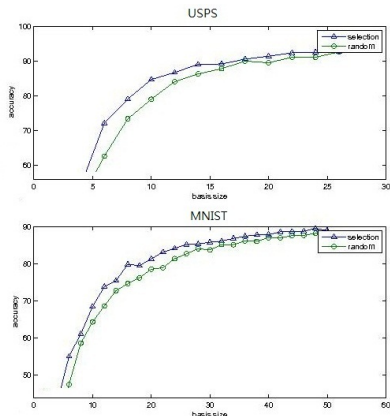
Compare Accuracy between Different Types of Methods

- Our method achieved improved accuracy than linear SVMs
- The time for training and testing using our proposed model is comparable to that of linear SVMs
- The standard nonlinear SVM utilizes the full kernel matrix whose time complexity is quadratically scaled-up with ℓ .

USPS	Accuracy	Training Time	Testing Time
Nyström primal SVM	97.057 ± 0.402	3.764	0.320
nonlinear SVM	98.007 ± 0.198	14.507	4.129
linear SVM	95.009 ± 0.275	2.274	0.079
MNIST	Accuracy	Training Time	Testing Time
Nyström primal SVM	93.833 ± 0.115	24.6092	2.006
nonlinear SVM	98.547 ± 0.066	3650.334	524.487
linear SVM	91.917 ± 0.077	14.510	0.381

Comparisons to Random Basis Selection

- Compare basis matrix determined by our method to
- the random sampling basis selection strategy



Conclusion

- Primal low-rank representation of Nyström-approximated dual SVM.

Training: linearly in time and space.

Accuracy: almost as good as non-linear SVM.

Prediction: nearly as fast as linear SVM. (e.g. Realtime robot vision applications.)

- Connect feature selection with basis selection in Nyström method.

A basis selection method that preserves separability.

- Applications: Large-Scale Image Retrieval, Realtime Machine Vision (training/test should be nearly as fast as feature extraction,) etc.

Thank You

The most update-to-date code and slides are at
<https://github.com/scan33scan33>.
Feel free to drop me questions and discussions.