





- A promising method for data classifications
- Training and testing
- Training vectors :  $x_i, i = 1, \ldots, l$
- Consider examples with two classes:

$$y_i = \begin{cases} 1 & \text{if } x_i \text{ in class } 1\\ -1 & \text{if } x_i \text{ in class } 2 \end{cases}$$



#### SVM Formulation

- Maximize the margin  $2/||w|| \equiv \text{Minimize } w^T w/2$
- Apply nonlinear mapping  $\phi$  for training data
- Avoid overfitting for training data: allow training error  $\xi$
- A standard problem [Cortes and Vapnik, 1995]:

$$\min_{\substack{w,b,\xi}} \qquad \frac{1}{2}w^T w + C \sum_{i=1}^l \xi_i$$
$$y_i(w^T \phi(x_i) + b) \ge 1 - \xi_i,$$
$$\xi_i \ge 0, \ i = 1, \dots, l$$



#### Large-scale SVM Problems

- Q fully dense, cannot be saved in memory: traditional optimization methods not usable
- Decomposition methods: currently major approach
  - iteratively solve smaller problems by fixing most variables
  - slow convergence for huge problems with many support vectors



- alter the standard SVM formulation
- reduce the size of Q and solve the reduced problem
- For how large problems is reduction better?

Performance not fully studied before

- testing accuracy: compare with standard SVM
- training time: compare with decomposition methods



• RSVM randomly selects a subset R of m samples as support vectors:  $w = \sum_{i \in R} \alpha_i y_i \phi(x_i)$ let  $\bar{\alpha} \equiv \alpha_R$ 

$$\min_{\bar{\alpha},b,\xi} \qquad \frac{1}{2}(\bar{\alpha}^T Q_{RR}\bar{\alpha} + b^2) + C\sum_{i=1}^l \xi_i^2$$
$$Q_{:,R}\bar{\alpha} + by \ge e - \xi$$

• Simplify  $1/2\bar{\alpha}^T Q_{RR}\bar{\alpha}$  to  $1/2\bar{\alpha}^T\bar{\alpha}$ 

• Absorb *b* by 
$$\widetilde{Q} \equiv \begin{bmatrix} Q_{:,R} & y \end{bmatrix}, \widetilde{\alpha} \equiv \begin{bmatrix} \overline{\alpha} \\ b \end{bmatrix}$$

• The formulation of RSVM:

$$\min_{\widetilde{\alpha},\xi} \quad \frac{1}{2}\widetilde{\alpha}^T\widetilde{\alpha} + C\sum_{i=1}^l \xi_i^2$$
$$\widetilde{Q}\widetilde{\alpha} \ge e - \xi$$

We find it similar to radical basis function networks
 – comparisons of RBF networks with SVM was done

## How to Solve RSVM

- Smooth SVM (SSVM) in [Lee and Mangasarian, 2001]
- Transform RSVM to an **unconstrained** problem:

$$\min_{\widetilde{\alpha}} \quad \frac{1}{2} \widetilde{\alpha}^T \widetilde{\alpha} + C \sum_{i=1}^l ((e - \widetilde{Q} \widetilde{\alpha})_i)_+^2$$

- $(.)_+ \equiv max(.,0)$  not differentiable
- Approximate  $(t)_+$  by  $P_{\beta}(t) \equiv t + \beta^{-1} \log(1 + \exp(-\beta t))$ : Differentiable, Newton's method can be used
- Each iteration  $O(lm^2)$  time for Hessian (2nd derivatives)



### Use Least Square SVM

- Proposed in [Suykens and Vandewalle, 1999] – Change  $\widetilde{Q}\widetilde{\alpha} \ge e - \xi$  to equality  $\widetilde{Q}\widetilde{\alpha} = e - \xi$
- $\xi$  is represented by  $\tilde{\alpha}$ :

$$\min_{\widetilde{\alpha}} f(\widetilde{\alpha}) = \frac{1}{2} \widetilde{\alpha}^T \widetilde{\alpha} + C \sum_{i=1}^l (e - \widetilde{Q} \widetilde{\alpha})_i^2$$

• Quadratic unconstrained, equivalent to a linear system:

$$(\widetilde{Q}^T \widetilde{Q} + \frac{I}{2C})\widetilde{\alpha} = \widetilde{Q}^T e$$

• Main cost is  $O(lm^2)$  to calculate  $\widetilde{Q}^T \widetilde{Q}$ 

## Use Decomposition

• The dual form of RSVM:

$$\min_{\alpha} \qquad \frac{1}{2} \alpha^T (\widetilde{Q}\widetilde{Q}^T + \frac{I}{2C})\alpha - e^T \alpha$$
$$0 \le \alpha_i, i = 1, \dots, l$$

– primal RSVM solution  $\tilde{\alpha} = \tilde{Q}^T \alpha$ 

- Each iteration a working set of size q is to be modified
- Main cost is calculating  $Q\Delta \alpha$ : O(lqm) for O(m) kernel
- Speedup for linear kernel and RSVM:  $Q\Delta\alpha = \widetilde{Q}(\widetilde{Q}^T\Delta\alpha)$ O(mq) + O(lm) = O(lm) operations, q times faster
- Used in software  $SVM^{light}$  and BSVM

## Use Lagrangian SVM

- Proposed in [Mangasarian and Musicant, 2001]
- Consider optimality condition of dual RSVM:  $H\alpha - e \ge 0, \alpha \ge 0, (H\alpha - e)^T \alpha = 0$  with  $H \equiv \widetilde{Q}\widetilde{Q}^T + \frac{I}{2C}$
- Equivalent to  $H\alpha e = (H\alpha e \beta\alpha)_+, \forall \beta > 0$ : apply fixed-point iterations (each step O(lm) time)  $\alpha^{k+1} = H^{-1}(e + (H\alpha^k - e - \beta\alpha^k)_+)$
- Can obtain  $H^{-1}$  by SMW identity only for  $m \ll l$ :  $H^{-1} = (\frac{I}{2C} + \widetilde{Q}\widetilde{Q}^T)^{-1} = 2C(I - \widetilde{Q}(\frac{I}{2C} + \widetilde{Q}^T\widetilde{Q})^{-1}\widetilde{Q}^T)$

#### Implementation Issues

- Stopping criteria for iterative methods
  - RSVM form different from SVM
  - we choose as close criteria as possible
- Multi-class problems: we use one-against-one
  - -k(k-1)/2 classifiers for k classes where each one trains data from two classes, when testing they vote
  - suggested in surveys of multi-class SVM, LS-SVM

### Problems for Experiments

Problem	#training data	#testing data	#class	#attribute
dna	2000	1300	3	180
satimage	4435	2000	6	36
letter	15000	5000	26	16
shuttle	43500	14500	7	9
mnist	21000	49000	10	780
ijcnn1	49990	45495	2	22
protein	17766	6621	3	357

#### • Scaling

• Don't use mnist original 60000 training and 10000 testing because too much training time

## Settings

- Decomposition solvers for SVM: libsvm and libsvm-q
- m = 0.1l in most cases
- RBF kernel used, model selection for C and  $\gamma$ 
  - 70%-30% hold-out,  $15\times15$  grid search
- ATLAS to speed up matrix operations
- Caching and shrinking for decomposition methods

#### Table 1: A comparison on RSVM: testing accuracy

	$_{\rm SVM}$				RSVM					
	libsvm		SSVM		LS-SVM		LSVM		Decomposition	
Problem	$C,\gamma$	rate	$C,\gamma$	rate	$C,\gamma$	rate	$C,\gamma$	rate	$C,\gamma$	rate
dna	$2^4, 2^{-6}$	95.447	$2^{12}, 2^{-10}$	92.833	$2^4, 2^{-6}$	92.327	$2^5, 2^{-7}$	93.002	$2^{9}, 2^{-6}$	92.327
satimage	$2^4, 2^0$	91.3	$2^{12}, 2^{-1}$	89.8	$2^{12}, 2^{-3}$	89.9	$2^2, 2^{-1}$	90	$2^{11}, 2^{-1}$	90
letter	$2^4, 2^2$	97.98	$2^{11}, 2^{-1}$	95.9	$2^{12}, 2^{-2}$	95.14	$2^{12}, 2^{-1}$	95.42	$2^{12}, 2^{-1}$	92.76
shuttle	$2^{11}, 2^{3}$	99.924	$2^{12}, 2^4$	99.78	$2^{12}, 2^4$	99.58	$2^{10}, 2^{3}$	99.814	$2^{12}, 2^4$	99.772
mnist	$2^{6}, 2^{-5}$	97.753	$2^{7}, 2^{-6}$	96.833	$2^{9}, 2^{-6}$	96.48	$2^4, 2^{-5}$	96.578	$2^{12}, 2^{-5}$	96.129
ijcnn1	$2^{1}, 2^{1}$	98.76	$2^{12}, 2^{-3}$	95.949	$2^{-2}, 2^{-2}$	91.676	$2^{12}, 2^{-3}$	96.813	$2^{12}, 2^{-1}$	96.11
protein	$2^{1}, 2^{-3}$	69.97	$2^{1}, 2^{-5}$	65.957	$2^{2},2^{-6}$	66.244	$2^{0}, 2^{-5}$	65.957	$2^{11}, 2^{-6}$	66.138
• lil	osvm-(	q ver	y close	to lil	osvm, r	not lis	sted he	ere		

#### Table 2: A comparison on RSVM: number of support vectors

$\mathbf{S}$	VM	RSVM					
libsvm	libsvm-q	SSVM	LS-SVM	LSVM	Decomposition		
#SV			#SV (all same)				
973	1130		372				
1611	1822		1826				
8931	8055		13928				
285	652		4982				
8333	8364		12874				
4555	9766		200				
14770	16192		596				
	S libsvm # 973 1611 8931 285 8333 4555 14770	SVM         libsvm       libsvm-q         #SV         973       1130         1611       1822         8931       8055         285       652         8333       8364         4555       9766         14770       16192	SVM       SVM         libsvm       SSVM         #SV       973         973       1130         1611       1822         8931       8055         285       652         8333       8364         4555       9766         14770       16192	SVM       SVM         libsvm       SSVM       LS-SVM         #SV       #SV         973       1130       372         1611       1822       1826         8931       8055       13928         285       652       4982         8333       8364       12874         4555       9766       200         14770       16192       596	SVMRSVMlibsvmSSVMLS-SVM $\#SV$ $\#SV$ $\#SV$ 9731130372161118221826893180551392828565249828333836412874455597662001477016192596		

# Table 3: A comparison on RSVM: training time and testing time (in seconds)

		SV	M		RSVM					
	libs	vm	libsv	m-q	SSVM	LS-SVM	LSVM	Decomp	osition	
Problem	training	testing	training	testing	training	training	training	training	testing	
dna	7.09	4.65	8.5	5.39	5.04	2.69	23.4	7.59	1.52	
satimage	16.21	9.04	19.04	10.21	23.77	11.59	141.17	43.75	11.4	
letter	230	89.53	140.14	75.24	193.39	71.06	1846.12	446.04	149.77	
shuttle	113	2.11	221.04	3.96	576.1	150.59	3080.56	562.62	74.82	
mnist	1265.67	4475.54	1273.29	4470.95	1464.63	939.76	4346.28	1913.86	7836.99	
ijcnn1	492.53	264.58	2791.5	572.58	57.87	19.42	436.46	16152.54	6.36	
protein	1875.9	687.9	9862.25	808.68	84.21	64.6	129.47	833.35	35	

## Observations

- Accuracy: all RSVM implementations lower than SVM
- LS-SVM a little lower among RSVM implementations
- Optimal models for RSVM have much larger  ${\cal C}$
- For median-sized problems RSVM not much faster
- RSVM is much faster for ijcnn1 and protein
  - larger problem or many support vectors for SVM
  - -m is set small
  - LS-SVM fastest

#### Incomplete Cholesky Factorization

- Find lower triangular  $V: VV^T$  approximates a matrix
- Primarily used for conjugate gradient methods
- Used for SVM in [Fine and Scheinberg, 2001]
  - motivation: to solve SVM by interior point method, low-rank representation  $Q \sim VV^T$  needed
  - factorize Q
    - \* large dense, entries calculated when needed
    - \* only some ICF algorithms are suitable

## ICF Algorithms

• Based on a columnwize Cholesky factorization method:

$$\begin{bmatrix} \alpha & v^T \\ v & B \end{bmatrix} = \begin{bmatrix} \sqrt{\alpha} & 0 \\ \frac{v}{\sqrt{\alpha}} & I \end{bmatrix} \begin{bmatrix} 1 & 0 \\ 0 & B - \frac{vv^T}{\alpha} \end{bmatrix} \begin{bmatrix} \sqrt{\alpha} & \frac{v^T}{\sqrt{\alpha}} \\ 0 & I \end{bmatrix}$$

- 1st ICF algorithm in [Lin and Saigal, 2000]
  - stores largest m values in each column of V
  - may fail: add  $\beta \mathbf{I}$  and restart
- 2nd ICF algorithm in [Fine and Scheinberg, 2001]
  - early stop, fewer columns of Cholesky factorization
  - also uses symmetric pivoting





- Solving primal (SSVM,LS-SVM) versus solving dual (LSVM, decomposition)
- ICFSVM in dual form: use decomposition to implement
- Should we solve the corresponding primal?

$$\min_{\widetilde{w},\xi} \qquad \frac{1}{2}\widetilde{w}^T\widetilde{w} + C(\sum_{i=1}^l \xi_i)$$
  
subject to  $V\widetilde{w} \ge e - \xi, \xi \ge 0$ 

• V not meaningful in primal: solution cannot be used

## **Experimental Results**

• m = 0.1l in most cases, same way with RSVM

#### Table 4: A comparison on ICFSVM: testing accuracy

	SVM RSVM		ICFSVM(decomposition implementation)								
	libsvm Decomp		Decompo	osition 1st		CF	2nd ICF		2nd ICF+retrain		
Problem	$C,\gamma$	rate	$C,\gamma$	rate	$C,\gamma$	rate	$C,\gamma$	rate	$C,\gamma$	rate	
dna	$2^4, 2^{-6}$	95.447	$2^9, 2^{-6}$	92.327	$2^{-1}, 2^{-4}$	66.273	$2^0, 2^{-9}$	92.917	$2^2, 2^{-4}$	87.436	
satimage	$2^4, 2^0$	91.3	$2^{11}, 2^{-1}$	90	$2^{-1}, 2^{1}$	87.2	$2^{6}, 2^{-5}$	89.2	$2^1, 2^1$	72.65	
letter	$2^4, 2^2$	97.98	$2^{12}, 2^{-1}$	92.76	$2^2, 2^2$	96.66	$2^5, 2^{-2}$	96.16	$2^0, 2^2$	94.06	
shuttle	$2^{11}, 2^3$	99.924	$2^{12}, 2^4$	99.772	$2^{-1}, 2^4$	94.4	$2^9, 2^4$	99.862	$2^0, 2^{-1}$	94.331	
mnist	$2^6, 2^{-5}$	97.753	$2^{12}, 2^{-5}$	96.129	N/A	N/A	$2^1, 2^{-7}$	96.045	$2^1, 2^{-5}$	95.259	
ijcnn1	$2^1, 2^1$	98.76	$2^{12}, 2^{-1}$	96.11	$2^{-2}, 2^{-10}$	90.185	$2^9, 2^{-5}$	92.274	$2^{-2}, 2^{0}$	91.711	
protein	$2^1, 2^{-3}$	69.97	$2^{11}, 2^{-6}$	66.138	N/A	N/A	$2^{-1}, 2^{-6}$	65.398	$2^{-2}, 2^{-5}$	65.926	
	N/A: training time too large to apply the model selection										

Table 5: A comparison on ICFSVM: number of support vectors

	SVM RSVM		ICFSVM						
	libsvm	Decomposition	1st ICF	2nd ICF	2nd ICF+retrain				
Problem			#SV	#SV					
dna	973	372	1688	1389	1588				
satimage	1611	1826	4022	1187	1507				
letter	8931	13928	12844	5390	8953				
shuttle	285	4982	43026	308	3714				
mnist	8333	12874	N/A	5295	5938				
ijcnn1	4555	200	49485	4507	8731				
protein	14770	596	N/A	15049	15512				

N/A: training time too large to apply the model selection

# Table 6: A comparison on ICFSVM: training time and ICF time (in seconds)

	SVM	RSVM			VM			
	libsvm	Decomposition	$1 { m st}$	ICF	2nd	ICF	2nd ICF-	+retrain
Problem	training	training	training	ICF	training	ICF	training	ICF
dna	7.09	7.59	440.41	427.18	9.62	5.45	33.77	5.52
satimage	16.21	43.75	558.23	467.48	48.49	28.37	61.59	28.32
letter	230	446.04	3565.31	2857.95	484.59	222.4	635.41	221.93
shuttle	113	562.62	70207.76	13948.14	1251.17	1184.63	1811.6	1265.51
mnist	1265.67	1913.86	N/A	N/A	2585.13	2021.64	2565.08	1866.9
ijcnn1	492.53	16152.54	21059.3	4680.63	5463.8	103.97	1579.73	102.52
protein	1875.9	833.35	N/A	N/A	217.53	92.52	3462.57	110.54

N/A: training time too large to apply the model selection



- ICFSVM accuracy like RSVM, lower than SVM Used if decomposition for SVM cannot afford
- ICFSVM optimal models have smaller C than RSVM
- Support vectors of ICFSVM as sparse as SVM
- ICFSVM not faster than RSVM: ICF time too much
- Retrain SV from ICFSVM by SVM: not good
- First algorithm strange: ICF may not close