$$
\begin{tikzcd}
 & \mathcal{D}_1 : [\boldsymbol{X}][\boldsymbol{Y}_1] \arrow[r] & h_1 : \mathcal{D}_1 \to \hat{\boldsymbol{Y}}_{\boldsymbol{1}} \\
 & \mathcal{D}_2 : [\boldsymbol{X}][\boldsymbol{Y}_2] \arrow[r] & h_2 : \mathcal{D}_2 \to \hat{\boldsymbol{Y}}_{\boldsymbol{2}} \\
\mathcal{D} : [\boldsymbol{X}][\boldsymbol{Y}] \arrow[ruu, bend left] \arrow[ru, bend left] \arrow[rd, bend right] & \vdots & \\
 & \mathcal{D}_m : [\boldsymbol{X}][\boldsymbol{Y}_m] \arrow[r] & h_m : \mathcal{D}_m \to \hat{\boldsymbol{Y}}_{\boldsymbol{m}}
\end{tikzcd}
$$

SVR Flow Diagram. Firstly, the multi-target dataset is divided into m ST datasets, $\mathcal{D}_1, \mathcal{D}_2, \ldots, \mathcal{D}_m$. Then m models, $h_1, h_2, \ldots, h_m$, are independently trained for each ST dataset.

Multi-Target Support Vector Regression (SVR)

Input: Training dataset $\mathcal{D}$
Output: ST models $h_j, j = 1, \ldots, m$

- **for** $j = 1$ to m **do**
  - $\mathcal{D}_j = \{\boldsymbol{X}, \boldsymbol{Y}_j\}$ ▷ Get ST data
  - $h_j : \boldsymbol{X} \to \mathbb{R}$ ▷ Build ST model for the j^{th} target
- **end for**

Build Chained Model

Input: Training dataset $\mathcal{D}$, random chain $\boldsymbol{C}$
Output: A chained model $h_j, j = \{1, \ldots, m\}$

- $\mathcal{D}_1 = \{\boldsymbol{X}, \boldsymbol{Y}_{\boldsymbol{C}_1}\}$ ▷ Initialize first dataset
- **for** $j = 1$ to m **do** ▷ For each target in chain $\boldsymbol{C}$
  - $h_j : \mathcal{D}_j \to \mathbb{R}$ ▷ Train model on appended dataset
  - **if** $j < m$ **then**
    - $\mathcal{D}_{j+1} = \left\{\mathcal{D}_j, \boldsymbol{Y}_{\boldsymbol{C}_j}\right\}$ ▷ Append new target in chain to dataset
  - **end if**
- **end for**

$$
\begin{aligned}
\min_{\boldsymbol{w}, b, \boldsymbol{\xi}} \ & \frac{1}{2}||\boldsymbol{w}||^2 + C \sum_I \xi_I, \\
\text{s.t. } & Y_I(\langle \boldsymbol{w}, \boldsymbol{x}_{s_I} \rangle + b) \geq 1 - \xi_I, \, \forall I \in \{1, \ldots, n\}, \\
& \xi_I \geq 0, \, \forall I \in \{1, \ldots, n\}, \\
& s_I = \operatorname*{argmax}_{i \in I}(\langle \boldsymbol{w}, \, \boldsymbol{x}_i \rangle + b), \, \forall I \in \{1, \ldots, n\}.
\end{aligned}
$$

$$
\begin{aligned}
\max_{\boldsymbol{\alpha}} \ & \sum_I \alpha_I - \frac{1}{2} \sum_I \sum_{K \in I} \alpha_I \alpha_K Y_I Y_K \mathcal{K}\left(\boldsymbol{x}_{s_I}, \boldsymbol{x}_{s_K}\right) \\
\text{s.t. } & \sum_I \alpha_I Y_I = 0, \\
& 0 \leq \alpha_I \leq C, \, \forall I \in \{1, \ldots, n\}, \\
& s_I = \operatorname*{argmax}_{i \in I}(\boldsymbol{o}_I), \, \forall I \in \{1, \ldots, n\}.
\end{aligned}
$$

$$
\begin{tikzcd}[column sep=small]
 & & \mathcal{D} : [\boldsymbol{X}][\boldsymbol{Y}_1\boldsymbol{Y}_2\boldsymbol{Y}_3] \arrow[dll] \arrow[d] \arrow[drr] & & \\
{[1,2,3]} \arrow[d] & & {[1,3,2]} \arrow[d] & \dots & {[3,2,1]} \arrow[d] \\
h_1 : [\boldsymbol{X}] \to \boldsymbol{\hat{Y}_1} \arrow[d] & & h_1 : [\boldsymbol{X}] \to \boldsymbol{\hat{Y}_1} \arrow[d] & \dots & h_1 : [\boldsymbol{X}] \to \boldsymbol{\hat{Y}_1} \arrow[d] \\
h_2 : [\boldsymbol{X}\boldsymbol{Y_1}] \to \boldsymbol{\hat{Y}_2} \arrow[d] & & h_2 : [\boldsymbol{X}\boldsymbol{Y_1}] \to \boldsymbol{\hat{Y}_3} \arrow[d] & \dots & h_2 : [\boldsymbol{X}\boldsymbol{Y_3}] \to \boldsymbol{\hat{Y}_2} \arrow[d] \\
h_3 : [\boldsymbol{X}\boldsymbol{Y_1}\boldsymbol{Y_2}] \to \boldsymbol{\hat{Y}_3} & & h_3 : [\boldsymbol{X}\boldsymbol{Y_1}\boldsymbol{Y_3}] \to \boldsymbol{\hat{Y}_2} & \dots & h_3 : [\boldsymbol{X}\boldsymbol{Y_3}\boldsymbol{Y_2}] \to \boldsymbol{\hat{Y}_1}
\end{tikzcd}
$$

SVRRC Flow Diagram on a dataset with three targets. SVRRC first builds the six random chains of the target's indices (three examples are shown). It then constructs a chained model by proceeding recursively over the chain, building a model, and appending the current target to the input space to predict the next target in the chain.

Multi-Target SVR with Random-Chains (SVRRC)

Input: Training dataset $\mathcal{D}$, c random chains $\mathcal{C}$
Output: An ensemble of chained models $h_{\mathcal{C}}$

for each $\boldsymbol{C} \in \mathcal{C}$ **do** ▷ For each random chain
    $h_{\boldsymbol{C}} \leftarrow$ `buildChainedModel`$(\mathcal{D}, \boldsymbol{C})$ ▷ Build a chained model for chain $\boldsymbol{C}$
end for

$$
\begin{tikzcd}
\mathcal{D} : [\boldsymbol{X}][\boldsymbol{Y}_1\boldsymbol{Y}_2\boldsymbol{Y}_3] \arrow[rr, "\textit{generate maximum correlation chain}", "\frac{\mathbf{E}\left[(Y_i-\mu_i)(Y_j-\mu_j)\right]}{\sqrt{\mathbf{E}[(Y_i-\mu_i)(Y_i-\mu_i)]\mathbf{E}\left[(Y_j-\mu_j)(Y_j-\mu_j)\right]}}"'] & & {[1,2,3]} \arrow[dll, rounded corners] \\
h_1 : [\boldsymbol{X}] \to \boldsymbol{\hat{Y}_1} \arrow[r] & h_2 : [\boldsymbol{X}\boldsymbol{Y_1}] \to \boldsymbol{\hat{Y}_2} \arrow[r] & h_3 : [\boldsymbol{X}\boldsymbol{Y_1}\boldsymbol{Y_2}] \to \boldsymbol{\hat{Y}_3}
\end{tikzcd}
$$

SVRCC Flow Diagram on a sample dataset with three targets. SVRCC first finds the direction of maximum correlation among the targets and uses that order as the only chain. It then constructs the chained model, as done in SVRRC.

Multi-Target SVR with max-Correlation Chain (SVRCC)

$\mathbf{P} = corrcoef(\boldsymbol{Y})$ ▷ Find correlation coefficient matrix for target variables
$\boldsymbol{C} = \sum_{i=1}^{n} \mathbf{P}_{ij}, \forall j = 1, \dots, m$ ▷ Sum rows of the correlation matrix
$\boldsymbol{C} =$ `sort`$(\boldsymbol{C}, \textbf{decreasing})$ ▷ Sort sums in decreasing order
$h_{\boldsymbol{C}} =$ `buildChainedModel`$(\mathcal{D}, \boldsymbol{C})$ ▷ Build a max-correlation chained model

---

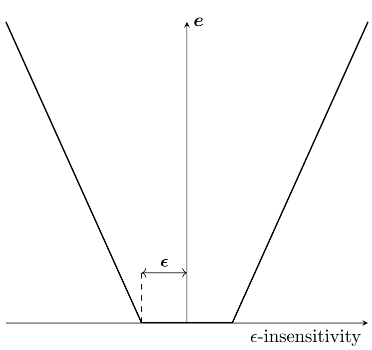


Figure 1: Vapnik's ϵ-insensitivity loss function.

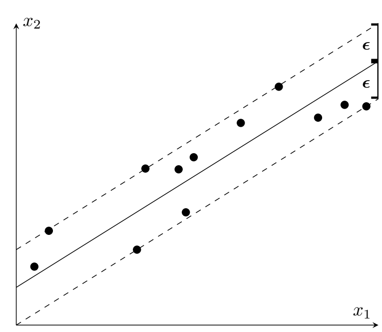


Figure 2: Linear support vector regression example solution on a toy 2D dataset.

Average Relative Root Mean Square Error (aRRMSE) for MT regressors

Datasets	MORF	ST	MTS	MTSC	RC	ERC	ERCC	SVR	SVRRC	SVRCC
Slump	0.6939	0.6886	0.6690	0.6938	0.7019	0.7022	0.6886	0.5765	**0.5545**	0.5560
Polymer	0.6159	0.5971	0.5778	0.6493	0.6270	0.6544	0.6131	0.5573	0.5253	**0.5116**
Andro	0.5097	0.5979	0.5155	0.5633	0.5924	0.5885	0.5666	0.4856	0.4651	**0.4455**
EDM	0.7337	0.7442	0.7413	0.7446	0.7449	0.7452	0.7443	0.7058	0.7070	**0.6978**
Solar Flare 1	1.3046	1.1357	1.1168	1.0758	0.9951	1.0457	1.0887	0.9917	0.9455	**0.9320**
Jura	0.5969	0.5874	0.5906	0.5892	0.5910	0.5896	0.5880	0.5952	**0.5764**	0.5885
Enb	0.1210	0.1165	0.1231	0.1211	0.1268	0.1250	0.1139	0.0977	0.0910	**0.0899**
Solar Flare 2	1.4167	1.1503	**0.9483**	1.0840	1.0092	1.0522	1.0928	1.0385	1.0253	1.0298
Wisconsin Cancer	0.9413	0.9314	0.9308	0.9336	**0.9305**	0.9313	0.9323	0.9555	0.9483	0.9427
California Housing	0.6611	0.6447	0.6974	0.6630	0.7131	0.6690	0.6146	0.6130	0.5945	**0.5852**
Stock	0.1653	0.1844	0.1787	0.1803	0.1802	0.1789	0.1752	0.1364	**0.1337**	0.1388
SCPF	0.8273	0.8348	0.8436	0.8308	0.8263	0.8105	0.8290	0.8164	0.8037	**0.8013**
Puma8NH	0.7858	0.8142	0.8118	0.8311	0.8199	0.8205	0.8207	**0.7655**	0.7744	0.7676
Friedman	0.9394	0.9214	0.9231	0.9210	0.9231	0.9209	0.9204	0.9218	0.9208	**0.9196**
Puma32H	0.9406	**0.8713**	0.8727	0.8791	0.8752	0.8729	0.8740	0.9364	0.9367	0.9319
Water Quality	**0.8994**	0.9085	0.9109	0.9093	0.9121	0.9097	0.9057	0.9343	0.9310	0.9045
M5SPEC	0.5910	0.5523	0.5974	0.5671	0.5552	0.5542	0.5558	0.2951	0.2935	**0.2925**
MP5SPEC	0.5522	0.5120	0.5683	0.5133	0.5145	0.5143	0.5119	0.2484	**0.2323**	0.2358
MP6SPEC	0.5553	0.5152	0.5686	0.5119	0.5198	0.5187	0.5109	0.2850	0.2669	**0.2623**
ATP7d	0.5563	0.5308	**0.5141**	0.5142	0.5558	0.5397	0.5182	0.5455	0.5371	0.5342
OES97	0.5490	0.5230	0.5229	0.5217	0.5239	0.5237	0.5222	0.4641	**0.4618**	0.4635
Osales	0.7596	0.7471	**0.7086**	0.7268	0.8318	0.7258	0.7101	0.7924	0.7924	0.7811
ATP1d	0.4173	0.3732	0.3733	0.3712	0.3790	**0.3696**	0.3721	0.3773	0.3707	0.3775
OES10	0.4518	0.4174	0.4176	0.4171	0.4178	0.4180	0.4166	0.3570	0.3555	**0.3538**
Average	0.6910	0.6625	0.6551	0.6589	0.6611	0.6575	0.6536	0.6039	0.5935	**0.5893**
Ranks	7.5000	5.7708	5.9375	6.1667	7.4375	6.3750	4.9792	4.7708	3.2708	**2.7917**

Run Time (seconds) for MT regressors

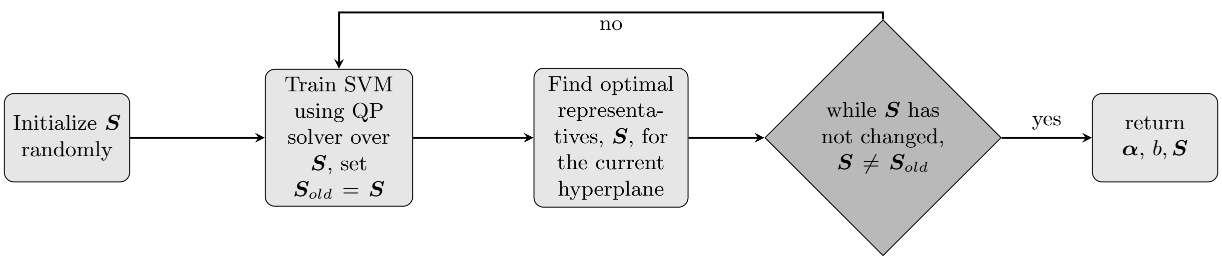
Datasets	MORF	ST	MTS	MTSC	RC	ERC	ERCC	SVR	SVRRC	SVRCC
Slump	38.1	2.6	9.9	15.9	1.8	11.1	50.5	**0.6**	1.9	0.7
Polymer	7.6	2.7	9.1	15.5	1.9	14.9	80.5	**0.5**	2.6	**0.5**
Andro	25.7	4.4	15.0	34.2	3.4	33.2	197.9	**1.1**	6.2	**1.1**
EDM	24.8	2.8	9.4	18.1	2.1	5.8	19.0	**0.9**	1.0	**0.9**
Solar Flare 1	34.1	3.5	13.6	26.7	2.7	17.7	86.9	**2.3**	9.3	2.6
Jura	64.3	7.9	31.8	74.3	6.4	43.5	254.2	**4.7**	18.7	5.3
Enb	71.4	6.6	26.1	63.6	**5.4**	15.6	69.6	11.3	17.7	15.9
Solar Flare 2	55.4	7.4	30.7	68.0	**6.3**	42.9	241.5	9.4	53.5	15.6
Wisconsin Cancer	51.4	6.1	21.9	53.7	4.9	14.8	61.6	**2.0**	2.4	**2.0**
California Housing	93.0	9.7	34.8	75.9	**8.2**	21.3	102.0	15.8	25.2	23.6
Stock	93.7	11.7	46.8	96.7	**11.0**	75.4	427.3	18.5	90.5	26.3
SCPF	66.3	19.3	65.9	176.3	**15.0**	104.2	734.2	32.8	162.8	48.8
Puma8NH	130.4	29.7	106.7	288.6	**27.9**	201.6	1227.7	94.1	516.6	177.1
Friedman	79.5	27.0	81.2	258.3	25.0	273.7	2871.6	**12.3**	322.3	18.8
Puma32H	93.9	68.1	181.0	635.0	87.7	667.9	6087.0	**32.2**	1018.7	53.1
Water Quality	108.4	**93.1**	262.1	912.3	127.2	925.4	10993.3	110.2	2567.9	189.5
M5SPEC	89.8	68.9	166.3	604.6	73.7	262.3	3132.1	**39.2**	546.7	45.1
MP5SPEC	84.5	94.6	221.2	888.3	91.5	557.0	6864.1	**49.3**	1132.1	58.4
MP6SPEC	90.3	93.4	212.6	871.0	89.1	557.6	6761.3	**47.2**	1227.1	58.5
ATP7d	**70.5**	262.6	452.1	2319.8	242.1	1779.2	24373.8	80.0	1897.4	136.5
OES97	**83.4**	485.3	1146.6	4928.9	499.8	5315.0	58072.1	148.2	3759.1	342.6
Osales	**92.0**	1094.8	2340.7	8322.2	986.5	11361.2	122265.3	437.0	4830.1	843.6
ATP1d	**70.7**	272.9	476.5	2568.9	261.9	2138.9	26768.9	95.0	2127.8	174.4
OES10	**90.0**	738.9	1633.6	6682.9	688.5	7150.8	83533.1	229.1	5419.4	577.1
Average	71.2	142.2	316.5	1250.0	136.2	1316.3	14803.2	**61.4**	1073.2	117.4
Ranks	5.5	3.71	6.0	8.29	3.0	7.08	9.92	**1.88**	6.71	2.92

$$\min_{(\boldsymbol{w},b)\in\mathcal{H}_o\times\mathbb{R}} R \;=\; \frac{1}{2}||\boldsymbol{w}||^2 + C\sum_{i=1}^{n} L(y_i,\, o_{(w,b)}(\boldsymbol{x}_i)) \tag{1}$$

$$L(y_i,\, o_{(w,b)}(\boldsymbol{x}_i)) = \max\left\{0, 1 - y_i o_{(w,b)}(\boldsymbol{x}_i)\right\} \tag{2}$$

$$\min_{(\boldsymbol{w},b)\in\mathcal{H}_o\times\mathbb{R}} R \;=\; \frac{1}{2}||\boldsymbol{w}||^2 + C\sum_{i=1}^{n}(|y_i - o_{(w,b)}(\boldsymbol{x_i})|_\epsilon) \tag{3}$$

$$L(y_i,\, o_{(w,b)}(\boldsymbol{x}_i)) = \begin{cases} 0 & if|y_i - o_{(w,b)}(\boldsymbol{x_i})| \le \epsilon \\ |y_i - o_{(w,b)}(\boldsymbol{x_i})| - \epsilon & \text{otherwise.} \end{cases} \tag{4}$$

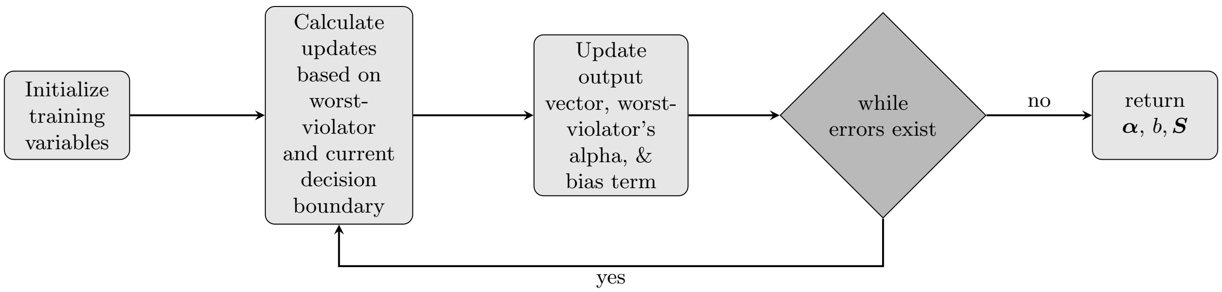


A summary of the steps performed by MIRSVM. The representatives are first randomly initialized and continuously updated according to the current hyperplane. Upon completion, the model is returned along with the optimal bag-representatives.

Multi-Instance Representative SVM (MIRSVM)

Input: Training dataset $\mathcal{D}$, SVM Parameters C and σ
Output: SVM model parameters $\boldsymbol{\alpha}$ and b, Bag Representative IDs $\boldsymbol{S}$

for $I \in \{1, \ldots, n\}$ **do**
  $\boldsymbol{S}_I \leftarrow$ rand $(|\mathcal{B}_I|, 1, 1)$ ▷ Assign each bag a random instance
end for
while $\boldsymbol{S} \neq \boldsymbol{S}_{old}$ **do**
  $\boldsymbol{S}_{old} \leftarrow \boldsymbol{S}$
  $\boldsymbol{X}_S \leftarrow \boldsymbol{X}(\boldsymbol{S})$, $\boldsymbol{Y}_S \leftarrow \boldsymbol{Y}(\boldsymbol{S})$ ▷ Initialize the representative dataset
  $\boldsymbol{G} \leftarrow (\boldsymbol{Y}_S \times \boldsymbol{Y}_S) \cdot \mathcal{K}(\boldsymbol{X}_S,\, \boldsymbol{X}_S,\, \sigma)$ ▷ Build Gram matrix
  $\boldsymbol{\alpha} \leftarrow$ quadprog $(\boldsymbol{G}, \boldsymbol{-1}^n, \boldsymbol{Y}_S, \boldsymbol{0}^n, \boldsymbol{0}^n, \boldsymbol{C}^n)$ ▷ Solve QP Problem
  $\boldsymbol{sv} \leftarrow$ find $(0 < \boldsymbol{\alpha} \le C)$ ▷ Get the support vector indices
  $n_{\boldsymbol{sv}} \leftarrow$ count $(0 < \boldsymbol{\alpha} \le C)$ ▷ Get the number of support vectors
  $b \leftarrow \frac{1}{n_{\boldsymbol{sv}}}\sum_{i=1}^{n_{\boldsymbol{sv}}}(\boldsymbol{Y_{sv}} - \boldsymbol{G_{sv}} * (\boldsymbol{\alpha_{sv}} \cdot \boldsymbol{Y_{sv}}))$ ▷ Calculate the bias term
  for $I \in \{1, \ldots, n\}$ **do**
    $\boldsymbol{G}_I \leftarrow (Y_I \times \boldsymbol{Y}_S) \cdot \mathcal{K}(\mathcal{B}_I,\, \boldsymbol{X}_S,\, \sigma)$
    $\boldsymbol{S}_I \leftarrow \mathrm{argmax}_{i\in I}(\boldsymbol{G}_I * \boldsymbol{\alpha} + b)$ ▷ Select optimal bag-representatives
  end for
end while



Summary of the steps performed by OLLAWV. The model parameters ($\boldsymbol{\alpha}$, b, $\boldsymbol{S}$) and the algorithm variables ($\boldsymbol{o}$, t, wv, and yo) are first initialized. The worst-violator with respect to the current hyperplane is then found and the model parameters are updated. Once no violating samples are found, the model is returned.

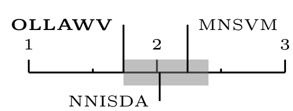
OnLine Learning Algorithm using Worst-Violators (OLLAWV)

Input: $\mathcal{D}$, C, γ, β, M
Output: $\boldsymbol{\alpha}$, b, $\boldsymbol{S}$

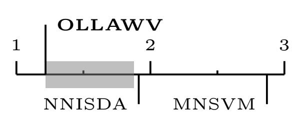
$\boldsymbol{\alpha} \leftarrow \mathbf{0}$, $b \leftarrow 0, \boldsymbol{S} \leftarrow \mathbf{0}$ ▷ Initialize OLLAWV model parameters
$\boldsymbol{o} \leftarrow \mathbf{0}$, $t \leftarrow 0$ ▷ Initialize the output vector and iteration counter
$wv \leftarrow 0$, $yo \leftarrow y_{wv} * \boldsymbol{o}_{wv}$ ▷ Initialize hinge loss error and worst-violator index
while $yo < M$ **do**
  $t \leftarrow t + 1$
  $\eta \leftarrow 2/\sqrt{t}$ ▷ Learning rate
  $\Lambda \leftarrow \eta * C * y_{wv}$ ▷ Calculate hinge loss update
  $B \leftarrow (\Lambda * \beta)/n$ ▷ Calculate bias update
  $\boldsymbol{o} \leftarrow \boldsymbol{o} + \Lambda * \mathcal{K}(\boldsymbol{x}_{\neg \boldsymbol{S}}, \boldsymbol{x}_{wv}, \gamma) + B$ ▷ Update output vector
  $\boldsymbol{\alpha}_{wv} \leftarrow \boldsymbol{\alpha}_{wv} + \Lambda$ ▷ Update worst-violator's alpha value
  $b \leftarrow b + B$ ▷ Update bias term
  $\boldsymbol{S}_t \leftarrow wv$ ▷ Save index of worst-violator
  $[yo, wv] \leftarrow \min_{wv \in \{\neg \boldsymbol{S}\}} \{y_{wv} \cdot o_{wv}\}$ ▷ Find the worst-violator
end while

Classification Datasets

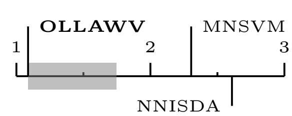
Dataset	# Samples	# Attributes	# Classes
small datasets			
iris	150	4	3
teach	151	5	3
wine	178	13	3
cancer	198	32	2
sonar	208	60	2
glass	214	9	6
vote	232	16	2
heart	270	13	2
dermatology	366	33	6
prokaryotic	997	20	3
eukaryotic	2,427	20	4
medium datasets			
optdigits	5,620	64	10
satimage	6,435	36	6
usps	9,298	256	10
pendigits	10,992	16	10
reuters	11,069	8,315	2
letter	20,000	16	26
large datasets			
adult	48,842	123	2
w3a	49,749	300	2
shuttle	58,000	7	7
web (w8a)	64,700	300	2
ijcnn1	141,691	22	2
intrusion	5,209,460	127	2



Bonferroni-Dunn test for Accuracy



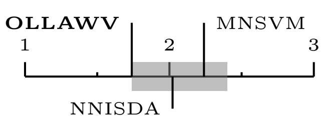
Bonferroni-Dunn test for Run Time



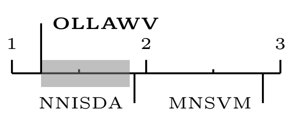
Bonferroni-Dunn test for % Support Vectors

Comparison of OLLAWV vs. NNISDA and MNSVM

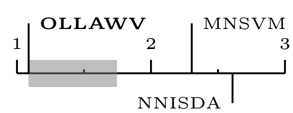
Dataset	Accuracy (%)			Run Time (s)			Support Vectors (%)		
	OLLAWV	NNISDA	MNSVM	OLLAWV	NNISDA	MNSVM	OLLAWV	NNISDA	MNSVM
small datasets									
iris	**97.33**	94.00	96.67	**0.05**	0.27	3.57	**13.50**	40.20	29.80
teach	52.32	52.31	**52.95**	**0.12**	0.44	8.85	**69.19**	99.80	87.40
wine	**98.87**	96.60	96.60	**0.28**	0.43	4.84	**15.02**	44.40	48.60
cancer	80.36	**81.86**	81.38	**0.49**	0.85	4.46	**42.79**	83.80	89.60
sonar	**92.32**	89.48	87.57	**0.59**	0.98	3.03	**31.26**	73.00	66.00
glass	**72.41**	67.81	69.30	**0.46**	1.01	11.94	**62.84**	90.80	87.60
vote	**96.54**	96.11	93.99	**0.26**	0.46	1.49	**13.36**	33.20	34.00
heart	82.22	**83.33**	**83.33**	**0.50**	0.91	6.45	**37.69**	73.00	82.00
dermatology	97.82	**98.36**	**98.36**	**1.62**	2.47	11.68	**36.94**	59.00	59.80
prokaryotic	88.96	88.86	**88.97**	**6.09**	10.64	50.86	**29.01**	51.20	49.00
eukaryotic	77.38	79.56	**81.21**	61.95	**49.16**	342.76	**54.11**	76.40	72.60
medium datasets									
optdigits	99.11	99.29	**99.31**	**411**	528	787	**28.64**	31.60	30.60
satimage	91.66	**92.39**	92.35	1,334	**687**	1,094	**20.72**	45.00	44.80
usps	97.49	98.05	**98.24**	10,214	**5,245**	7,777	**11.22**	29.40	28.00
pendigits	99.56	**99.62**	99.61	**723**	909	1,500	**10.27**	17.60	16.60
reuters	98.03	**98.08**	97.99	**954**	1,368	1,657	**8.770**	18.20	18.60
letter	96.99	99.11	**99.13**	**5,259**	12,009	26,551	**43.56**	57.60	56.60
large datasets									
adult	84.75	85.07	**85.13**	**21,025**	72,552	123,067	**34.66**	56.00	56.60
w3a	**98.86**	98.82	98.82	**6,532**	15,951	24,562	**3.270**	14.60	12.40
shuttle	99.77	99.83	**99.87**	**2,833**	7,420	45,062	**2.010**	6.00	16.40
web	98.94	**99.00**	99.00	**12,067**	30,583	38,040	**4.320**	13.20	10.80
ijcnn1	98.31	99.34	**99.41**	**162,587**	296,917	370,144	16.36	11.00	**7.600**
intrusion	**99.77**	99.67	99.66	**2,402,804**	4,646,810	3,772,113	**0.780**	2.000	1.700
Average	**91.29**	91.15	91.25	**114,209**	221,350	191,861	**25.66**	44.65	43.79
Ranks	**1.739**	2.022	2.239	**1.217**	1.913	2.869	**1.087**	2.609	2.304



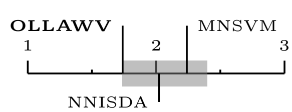
Bonferroni-Dunn test for Accuracy



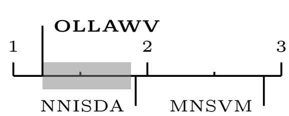
Bonferroni-Dunn test for Run Time



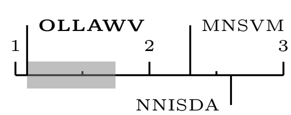
Bonferroni-Dunn test for % Support Vectors



Accuracy (%)



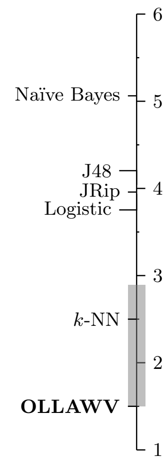
Run Time (s)

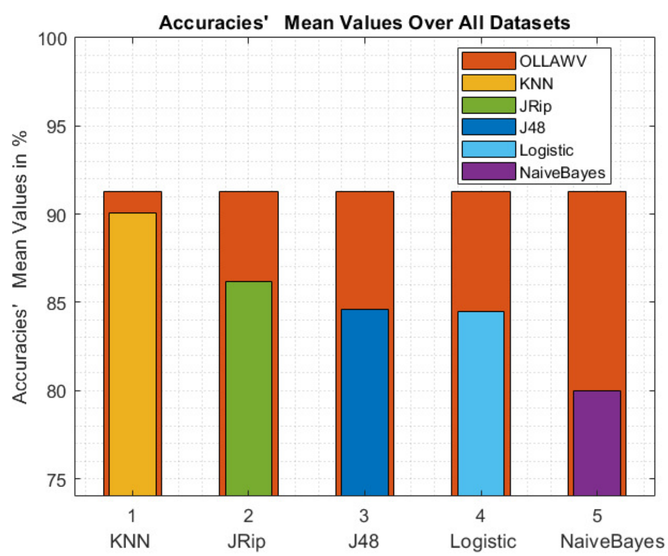


Support Vectors (%)

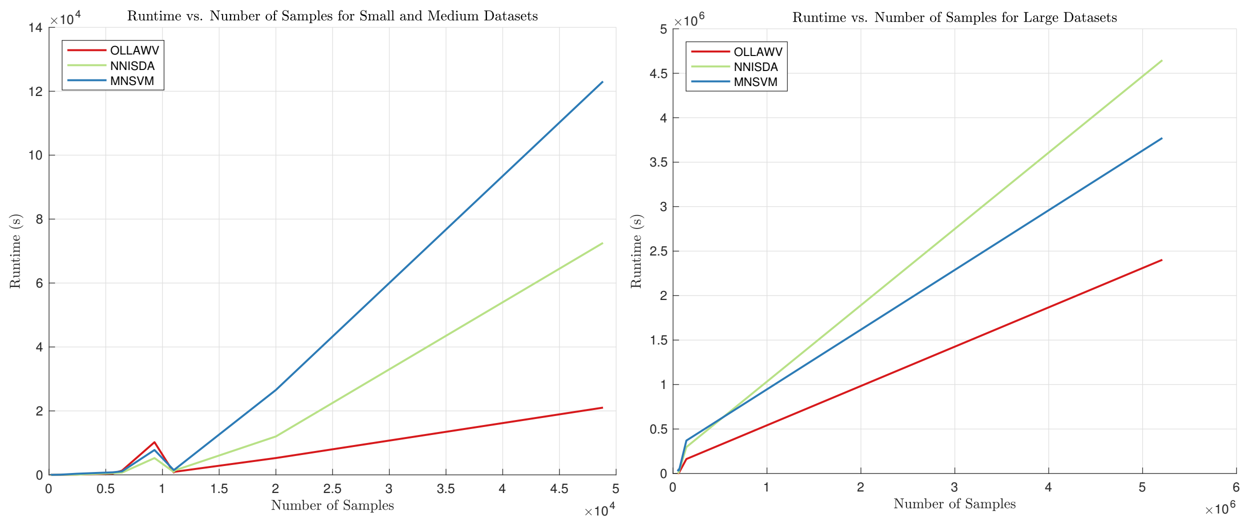
Accuracy (%) for Non-SVM Methods vs. OLLAWV

Dataset	OLLAWV	k-NN	J48	JRip	Naïve Bayes	Logistic
small datasets						
iris	**97.33 ± 1.49**	96.00 ± 3.65	94.00 ± 2.79	90.67 ± 4.35	96.00 ± 2.79	97.33 ± 2.79
teach	52.32 ± 3.46	**59.64 ± 2.89**	49.72 ± 7.58	56.75 ± 9.60	53.75 ± 6.46	51.77 ± 6.68
wine	**98.87 ± 1.54**	97.73 ± 3.72	90.43 ± 5.83	93.24 ± 3.27	96.60 ± 3.14	96.05 ± 2.58
cancer	**80.36 ± 5.80**	77.32 ± 6.93	73.81 ± 8.57	73.78 ± 5.81	67.73 ± 5.07	77.32 ± 7.78
sonar	**92.32 ± 3.11**	88.99 ± 4.59	76.16 ± 10.6	75.18 ± 6.77	73.69 ± 7.65	75.18 ± 7.31
glass	**72.41 ± 2.28**	67.73 ± 5.91	65.06 ± 5.51	65.59 ± 9.66	49.46 ± 5.19	62.04 ± 5.75
vote	**96.54 ± 1.87**	92.26 ± 3.19	95.70 ± 2.12	96.54 ± 2.45	92.24 ± 3.24	93.54 ± 2.59
heart	82.22 ± 2.93	79.63 ± 5.71	78.52 ± 2.81	80.74 ± 4.06	**84.44 ± 4.46**	83.33 ± 3.93
dermatology	**97.82 ± 0.05**	96.18 ± 1.78	94.52 ± 2.21	91.27 ± 5.08	97.28 ± 1.64	96.98 ± 2.28
prokaryotic	**88.96 ± 2.14**	87.96 ± 3.01	78.54 ± 1.62	79.13 ± 2.78	62.38 ± 3.54	87.57 ± 2.56
eukaryotic	77.38 ± 1.96	**81.42 ± 2.06**	65.27 ± 2.92	66.42 ± 3.47	39.27 ± 3.43	69.55 ± 1.34
medium datasets						
optdigits	**99.11 ± 0.38**	98.74 ± 0.39	90.87 ± 1.09	91.28 ± 0.40	92.42 ± 0.75	95.05 ± 0.91
satimage	**91.66 ± 0.80**	90.38 ± 0.72	85.64 ± 1.21	85.33 ± 0.77	85.41 ± 0.92	88.14 ± 1.11
usps	**97.49 ± 0.22**	97.04 ± 0.47	88.73 ± 0.46	89.20 ± 1.00	79.45 ± 0.59	91.88 ± 0.65
pendigits	**99.56 ± 0.12**	99.33 ± 0.17	96.24 ± 0.31	96.34 ± 0.41	88.34 ± 0.65	95.59 ± 0.18
reuters	**98.03 ± 0.22**	97.15 ± 0.43	96.90 ± 0.32	97.18 ± 0.44	93.52 ± 0.02	69.54 ± 0.28
letter	**96.99 ± 0.21**	95.71 ± 0.19	87.34 ± 0.68	87.02 ± 0.66	74.12 ± 0.97	77.45 ± 0.16
large datasets						
adult	**84.75 ± 0.26**	83.85 ± 0.28	84.38 ± 0.28	83.73 ± 0.17	80.57 ± 0.09	82.46 ± 0.14
w3a	**98.86 ± 0.04**	98.60 ± 0.06	98.71 ± 0.05	98.41 ± 0.10	96.71 ± 0.20	98.61 ± 0.12
shuttle	99.77 ± 0.03	99.93 ± 0.03	**99.97 ± 0.02**	99.96 ± 0.02	98.57 ± 0.24	96.83 ± 0.12
web	**98.94 ± 0.05**	98.89 ± 0.06	98.79 ± 0.09	98.50 ± 0.13	96.71 ± 0.21	98.70 ± 0.08
ijcnn1	98.31 ± 0.07	**98.48 ± 0.04**	98.40 ± 0.09	98.11 ± 0.10	90.69 ± 0.26	92.29 ± 0.16
intrusion	**99.77 ± 0.02**	88.20 ± 1.06	58.01 ± 26.6	87.66 ± 3.79	49.75 ± 30.7	65.15 ± 15.7
Average	**91.29 ± 1.26**	90.05 ± 2.06	84.60 ± 3.64	86.18 ± 2.84	79.96 ± 3.58	84.45 ± 2.83
Ranks	**1.500**	2.500	4.041	3.958	5.063	3.938





Mean accuracy over all datasets for OLLAWV
and the 5 non-SVM competing methods.



Run time in seconds versus the number of samples, divided into two groups: small & medium (left) versus large (right). Note OLLAWV's gradual increase in run time as the number of samples increases compared to NNISDA and MNSVM's steeper change. In almost all cases, OLLAWV displays superior run time over state-of-the-art. Run time depends upon many characteristics: dimensionality, class-overlapping, complexity of the separation boundary, number of classes, as well as the number of support vectors, which partly explains the tiny bump in the left figure.