A Practical Guide to Support Vector Classification

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Abstract

The support vector machine (SVM) is a popular classification technique. However, beginners who are not familiar with SVM often get unsatisfactory results since they miss some easy but significant steps. In this guide, we propose a simple procedure which usually gives reasonable results.

1 Introduction

SVMs (Support Vector Machines) are a useful technique for data classification. Although SVM is considered easier to use than Neural Networks, users not familiar with it often get unsatisfactory results at first. Here we outline a "cookbook" approach which usually gives reasonable results.

Note that this guide is not for SVM researchers nor do we guarantee you will achieve the highest accuracy. Also, we do not intend to solve challenging or difficult problems. Our purpose is to give SVM novices a recipe for rapidly obtaining acceptable results.

Although users do not need to understand the underlying theory behind SVM, we briefly introduce the basics necessary for explaining our procedure. A classification task usually involves separating data into training and testing sets. Each instance in the training set contains one "target value" (i.e. the class labels) and several "attributes" (i.e. the features or observed variables). The goal of SVM is to produce a model (based on the training data) which predicts the target values of the test data given only the test data attributes.

Given a training set of instance-label pairs $(\mathbf{x}_i, y_i), i = 1, \ldots, l$ where $\mathbf{x}_i \in R^n$ and $\mathbf{y} \in \{1, -1\}^l$, the support vector machines (SVM) (Boser et al., 1992; Cortes and Vapnik, 1995) require the solution of the following optimization problem:

$$\begin{aligned} \min_{\mathbf{w},b,\boldsymbol{\xi}} \quad & \frac{1}{2}\mathbf{w}^T\mathbf{w} + C\sum_{i=1}^{l}\xi_i \\ \text{subject to} \quad & y_i(\mathbf{w}^T\phi(\mathbf{x}_i) + b) \geq 1 - \xi_i, \\ & \xi_i \geq 0. \end{aligned} \tag{1}$$

Table 1: Problem characteristics and performance comparisons.

Applications	#training data	#testing data	#features	#classes	Accuracy by users	Accuracy by our procedure
Astroparticle[1]	3,089	4,000	4	2	75.2%	96.9%
Bioinformatics[2]	391	0[4]	20	3	36%	85.2%
Vehicle[3]	1,243	41	21	2	4.88%	87.8%

Here training vectors $\mathbf{x}_i$ are mapped into a higher (maybe infinite) dimensional space by the function ϕ. SVM finds a linear separating hyperplane with the maximal margin in this higher dimensional space. $C > 0$ is the penalty parameter of the error term. Furthermore, $K(\mathbf{x}_i, \mathbf{x}_j) \equiv \phi(\mathbf{x}_i)^T \phi(\mathbf{x}_j)$ is called the kernel function. Though new kernels are being proposed by researchers, beginners may find in SVM books the following four basic kernels:

- linear: $K(\mathbf{x}_i, \mathbf{x}_j) = \mathbf{x}_i^T \mathbf{x}_j$.
- polynomial: $K(\mathbf{x}_i, \mathbf{x}_j) = (\gamma {\mathbf{x}_i}^T \mathbf{x}_j + r)^d$, $\gamma > 0$.
- radial basis function (RBF): $K(\mathbf{x}_i, \mathbf{x}_j) = \exp(-\gamma \|\mathbf{x}_i - \mathbf{x}_j\|^2)$, $\gamma > 0$.
- sigmoid: $K(\mathbf{x}_i, \mathbf{x}_j) = \tanh(\gamma {\mathbf{x}_i}^T \mathbf{x}_j + r)$.

Here, γ, r, and d are kernel parameters.

1.1 Real-World Examples

Table 1 presents some real-world examples. These data sets are supplied by our users who could not obtain reasonable accuracy in the beginning. Using the procedure illustrated in this guide, we help them to achieve better performance. Details are in Appendix A.

These data sets are at `http://www.csie.ntu.edu.tw/~cjlin/papers/guide/data/`

[1] Courtesy of Jan Conrad from Uppsala University, Sweden.

[2] Courtesy of Cory Spencer from Simon Fraser University, Canada (Gardy et al., 2003).

[3] Courtesy of a user from Germany.

[4] As there are no testing data, cross-validation instead of testing accuracy is presented here. Details of cross-validation are in Section 3.2.

1.2 Proposed Procedure

Many beginners use the following procedure now:

- Transform data to the format of an SVM package
- Randomly try a few kernels and parameters
- Test

We propose that beginners try the following procedure first:

- Transform data to the format of an SVM package
- Conduct simple scaling on the data
- Consider the RBF kernel $K(\mathbf{x}, \mathbf{y}) = e^{-\gamma\|\mathbf{x}-\mathbf{y}\|^2}$
- Use cross-validation to find the best parameter C and γ
- Use the best parameter C and γ to train the whole training set[5]
- Test

We discuss this procedure in detail in the following sections.

2 Data Preprocessing

2.1 Categorical Feature

SVM requires that each data instance is represented as a vector of real numbers. Hence, if there are categorical attributes, we first have to convert them into numeric data. We recommend using m numbers to represent an m-category attribute. Only one of the m numbers is one, and others are zero. For example, a three-category attribute such as {red, green, blue} can be represented as (0,0,1), (0,1,0), and (1,0,0). Our experience indicates that if the number of values in an attribute is not too large, this coding might be more stable than using a single number.

[5]The best parameter might be affected by the size of data set but in practice the one obtained from cross-validation is already suitable for the whole training set.

2.2 Scaling

Scaling before applying SVM is very important. Part 2 of Sarle's Neural Networks FAQ Sarle (1997) explains the importance of this and most of considerations also apply to SVM. The main advantage of scaling is to avoid attributes in greater numeric ranges dominating those in smaller numeric ranges. Another advantage is to avoid numerical difficulties during the calculation. Because kernel values usually depend on the inner products of feature vectors, e.g. the linear kernel and the polynomial kernel, large attribute values might cause numerical problems. We recommend linearly scaling each attribute to the range $[-1, +1]$ or $[0, 1]$.

Of course we have to use the same method to scale both training and testing data. For example, suppose that we scaled the first attribute of training data from $[-10, +10]$ to $[-1, +1]$. If the first attribute of testing data lies in the range $[-11, +8]$, we must scale the testing data to $[-1.1, +0.8]$. See Appendix B for some real examples.

3 Model Selection

Though there are only four common kernels mentioned in Section 1, we must decide which one to try first. Then the penalty parameter C and kernel parameters are chosen.

3.1 RBF Kernel

In general, the RBF kernel is a reasonable first choice. This kernel nonlinearly maps samples into a higher dimensional space so it, unlike the linear kernel, can handle the case when the relation between class labels and attributes is nonlinear. Furthermore, the linear kernel is a special case of RBF Keerthi and Lin (2003) since the linear kernel with a penalty parameter $\tilde{C}$ has the same performance as the RBF kernel with some parameters (C, γ). In addition, the sigmoid kernel behaves like RBF for certain parameters (Lin and Lin, 2003).

The second reason is the number of hyperparameters which influences the complexity of model selection. The polynomial kernel has more hyperparameters than the RBF kernel.

Finally, the RBF kernel has fewer numerical difficulties. One key point is $0 < K_{ij} \leq 1$ in contrast to polynomial kernels of which kernel values may go to infinity $(\gamma {\mathbf{x}_i}^T \mathbf{x}_j + r > 1)$ or zero $(\gamma {\mathbf{x}_i}^T \mathbf{x}_j + r < 1)$ while the degree is large. Moreover, we must note that the sigmoid kernel is not valid (i.e. not the inner product of two

vectors) under some parameters (Vapnik, 1995).

There are some situations where the RBF kernel is not suitable. In particular, when the number of features is very large, one may just use the linear kernel. We discuss details in Appendix C.

3.2 Cross-validation and Grid-search

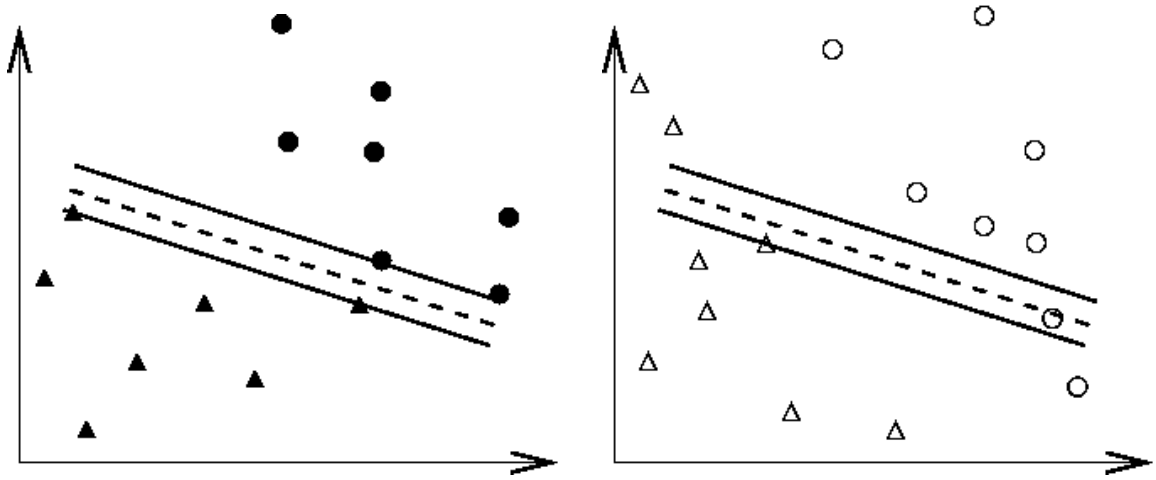
There are two parameters for an RBF kernel: C and γ. It is not known beforehand which C and γ are best for a given problem; consequently some kind of model selection (parameter search) must be done. The goal is to identify good (C, γ) so that the classifier can accurately predict unknown data (i.e. testing data). Note that it may not be useful to achieve high training accuracy (i.e. a classifier which accurately predicts training data whose class labels are indeed known). As discussed above, a common strategy is to separate the data set into two parts, of which one is considered unknown. The prediction accuracy obtained from the "unknown" set more precisely reflects the performance on classifying an independent data set. An improved version of this procedure is known as cross-validation.

In v-fold cross-validation, we first divide the training set into v subsets of equal size. Sequentially one subset is tested using the classifier trained on the remaining $v - 1$ subsets. Thus, each instance of the whole training set is predicted once so the cross-validation accuracy is the percentage of data which are correctly classified.

The cross-validation procedure can prevent the overfitting problem. Figure 1 represents a binary classification problem to illustrate this issue. Filled circles and triangles are the training data while hollow circles and triangles are the testing data. The testing accuracy of the classifier in Figures 1a and 1b is not good since it overfits the training data. If we think of the training and testing data in Figure 1a and 1b as the training and validation sets in cross-validation, the accuracy is not good. On the other hand, the classifier in 1c and 1d does not overfit the training data and gives better cross-validation as well as testing accuracy.

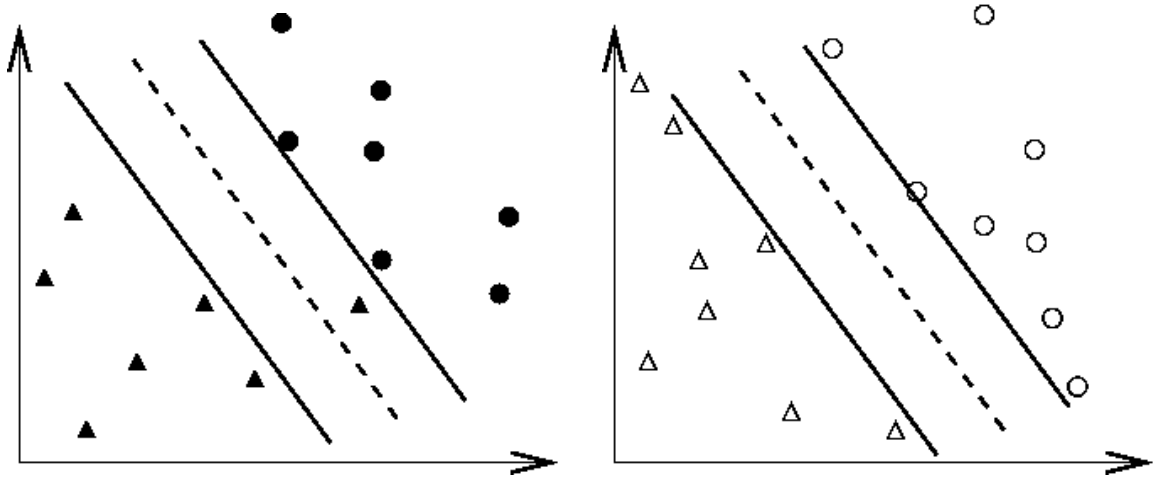
We recommend a "grid-search" on C and γ using cross-validation. Various pairs of (C, γ) values are tried and the one with the best cross-validation accuracy is picked. We found that trying exponentially growing sequences of C and γ is a practical method to identify good parameters (for example, $C = 2^{-5}, 2^{-3}, \ldots, 2^{15}$, $\gamma = 2^{-15}, 2^{-13}, \ldots, 2^{3}$).

The grid-search is straightforward but seems naive. In fact, there are several advanced methods which can save computational cost by, for example, approximating the cross-validation rate. However, there are two motivations why we prefer the simple



(a) Training data and an overfitting classifier

(b) Applying an overfitting classifier on testing data



(c) Training data and a better classifier

(d) Applying a better classifier on testing data

Figure 1: An overfitting classifier and a better classifier (● and ▲: training data; ○ and △: testing data).

grid-search approach.

One is that, psychologically, we may not feel safe to use methods which avoid doing an exhaustive parameter search by approximations or heuristics. The other reason is that the computational time required to find good parameters by grid-search is not much more than that by advanced methods since there are only two parameters. Furthermore, the grid-search can be easily parallelized because each (C, γ) is independent. Many of advanced methods are iterative processes, e.g. walking along a path, which can be hard to parallelize.

Since doing a complete grid-search may still be time-consuming, we recommend

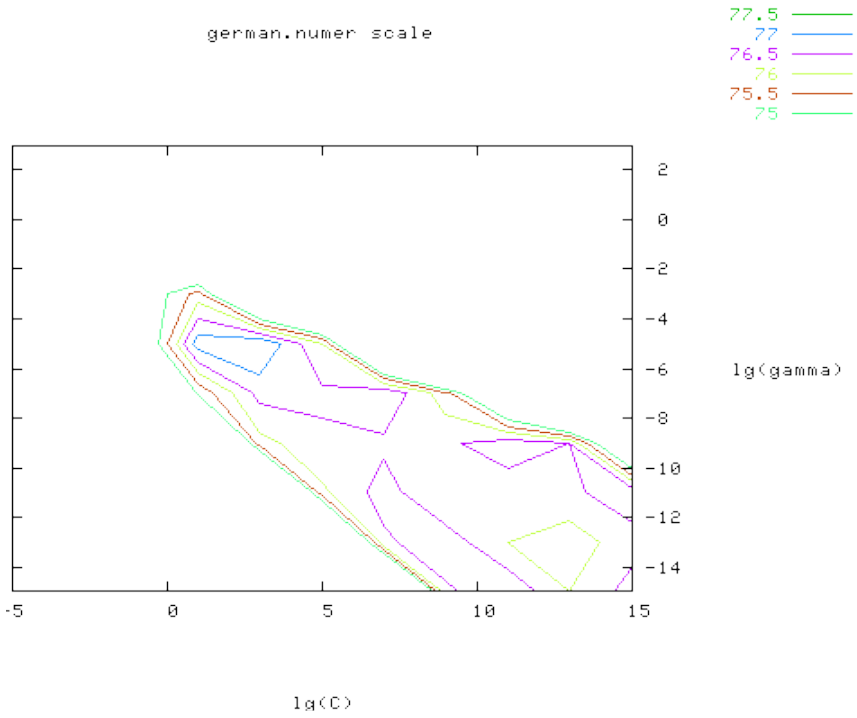


Figure 2: Loose grid search on $C = 2^{-5}, 2^{-3}, \ldots, 2^{15}$ and $\gamma = 2^{-15}, 2^{-13}, \ldots, 2^{3}$.

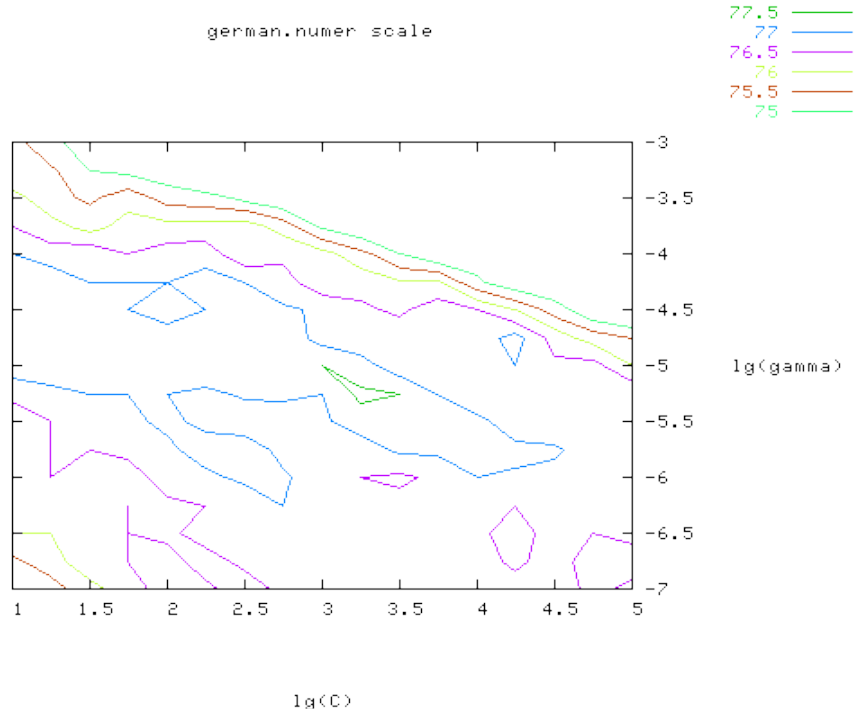


Figure 3: Fine grid-search on $C = 2^{1}, 2^{1.25}, \ldots, 2^{5}$ and $\gamma = 2^{-7}, 2^{-6.75}, \ldots, 2^{-3}$.

using a coarse grid first. After identifying a "better" region on the grid, a finer grid search on that region can be conducted. To illustrate this, we do an experiment on the problem `german` from the Statlog collection (Michie et al., 1994). After scaling this set, we first use a coarse grid (Figure 2) and find that the best (C, γ) is $(2^3, 2^{-5})$ with the cross-validation rate 77.5%. Next we conduct a finer grid search on the neighborhood of $(2^3, 2^{-5})$ (Figure 3) and obtain a better cross-validation rate 77.6% at $(2^{3.25}, 2^{-5.25})$. After the best (C, γ) is found, the whole training set is trained again to generate the final classifier.

The above approach works well for problems with thousands or more data points. For very large data sets a feasible approach is to randomly choose a subset of the data set, conduct grid-search on them, and then do a better-region-only grid-search on the complete data set.

4 Discussion

In some situations the above proposed procedure is not good enough, so other techniques such as feature selection may be needed. These issues are beyond the scope of this guide. Our experience indicates that the procedure works well for data which do not have many features. If there are thousands of attributes, there may be a need to choose a subset of them before giving the data to SVM.

Acknowledgments

We thank all users of our SVM software LIBSVM and BSVM, who helped us to identify possible difficulties encountered by beginners. We also thank some users (in particular, Robert Campbell) for proofreading the paper.

A Examples of the Proposed Procedure

In this appendix we compare accuracy by the proposed procedure with that often used by general beginners. Experiments are on the three problems mentioned in Table 1 by using the software LIBSVM (Chang and Lin, 2011). For each problem, we first list the accuracy by direct training and testing. Secondly, we show the difference in accuracy with and without scaling. From what has been discussed in Section 2.2, the range of training set attributes must be saved so that we are able to restore them while scaling the testing set. Thirdly, the accuracy by the proposed procedure

(scaling and then model selection) is presented. Finally, we demonstrate the use of a tool in LIBSVM which does the whole procedure automatically. Note that a similar parameter selection tool like the `grid.py` presented below is available in the R-LIBSVM interface (see the function `tune`). We also provide an example in Jupyter Notebook, please see Appendix A.4.

A.1 Astroparticle Physics

- Original sets with default parameters

```
$ ./svm-train svmguide1
$ ./svm-predict svmguide1.t svmguide1.model svmguide1.t.predict
 → Accuracy = 66.925%
```

- Scaled sets with default parameters

```
$ ./svm-scale -l -1 -u 1 -s range1 svmguide1 > svmguide1.scale
$ ./svm-scale -r range1 svmguide1.t > svmguide1.t.scale
$ ./svm-train svmguide1.scale
$ ./svm-predict svmguide1.t.scale svmguide1.scale.model svmguide1.t.predict
 → Accuracy = 96.15%
```

- Scaled sets with parameter selection (change to the directory `tools`, which contains `grid.py`)

```
$ python grid.py svmguide1.scale
...
2.0 2.0 96.8922
```

(Best C=2.0, γ=2.0 with five-fold cross-validation rate=96.8922%)

```
$ ./svm-train -c 2 -g 2 svmguide1.scale
$ ./svm-predict svmguide1.t.scale svmguide1.scale.model svmguide1.t.predict
 → Accuracy = 96.875%
```

- Using an automatic script

```
$ python easy.py svmguide1 svmguide1.t
Scaling training data...
Cross validation...
Best c=2.0, g=2.0
Training...
Scaling testing data...
Testing...
Accuracy = 96.875% (3875/4000) (classification)
```

A.2 Bioinformatics

- Original sets with default parameters

```
$ ./svm-train -v 5 svmguide2
 → Cross Validation Accuracy = 56.5217%
```

- Scaled sets with default parameters

```
$ ./svm-scale -l -1 -u 1 svmguide2 > svmguide2.scale
$ ./svm-train -v 5 svmguide2.scale
 → Cross Validation Accuracy = 78.5166%
```

- Scaled sets with parameter selection

```
$ python grid.py svmguide2.scale
...
2.0 0.5 85.1662
 → Cross Validation Accuracy = 85.1662%
```

(Best C=2.0, γ=0.5 with five fold cross-validation rate=85.1662%)

- Using an automatic script

```
$ python easy.py svmguide2
Scaling training data...
Cross validation...
Best c=2.0, g=0.5
Training...
```

A.3 Vehicle

- Original sets with default parameters

```
$ ./svm-train svmguide3
$ ./svm-predict svmguide3.t svmguide3.model svmguide3.t.predict
 → Accuracy = 2.43902%
```

- Scaled sets with default parameters

```
$ ./svm-scale -l -1 -u 1 -s range3 svmguide3 > svmguide3.scale
$ ./svm-scale -r range3 svmguide3.t > svmguide3.t.scale
$ ./svm-train svmguide3.scale
$ ./svm-predict svmguide3.t.scale svmguide3.scale.model svmguide3.t.predict
 → Accuracy = 12.1951%
```

- Scaled sets with parameter selection

```
$ python grid.py svmguide3.scale
...
128.0 0.125 84.8753
```

(Best C=128.0, γ=0.125 with five-fold cross-validation rate=84.8753%)

```
$ ./svm-train -c 128 -g 0.125 svmguide3.scale
$ ./svm-predict svmguide3.t.scale svmguide3.scale.model svmguide3.t.predict
 → Accuracy = 87.8049%
```

- Using an automatic script

```
$ python easy.py svmguide3 svmguide3.t
Scaling training data...
Cross validation...
Best c=128.0, g=0.125
Training...
Scaling testing data...
Testing...
Accuracy = 87.8049% (36/41) (classification)
```

A.4 A Jupyter Notebook Example for Appendix A.1

To make the discussion easier, we show only the example from Appendix A.1 here. For examples with other data sets, please see this link.

A.4.1 Package Installation

```
%%capture
%pip install -U libsvm-official
%pip install numpy
%pip install scipy
```

```
from libsvm.svmutil import *
import numpy as np

import io
import urllib.request
```

A.4.2 Astroparticle Physics

- Load data

  You can find data sets at LIBSVM Data Sets.

```
def load_url_libsvm(url, return_scipy=True):
    with io.TextIOWrapper(urllib.request.urlopen(url)) as r:
        return svm_read_problem(r, return_scipy=return_scipy)

svmguide1_train_url = 'https://www.csie.ntu.edu.tw/~cjlin/\
libsvmtools/datasets/binary/svmguide1'
svmguide1_test_url = 'https://www.csie.ntu.edu.tw/~cjlin/\
libsvmtools/datasets/binary/svmguide1.t'
y_train, x_train = load_url_libsvm(svmguide1_train_url)
y_test, x_test = load_url_libsvm(svmguide1_test_url)
```

- Original sets with default parameters

```
m = svm_train(y_train, x_train, "-q")
pred_labels, pred_metrics, pred_values = svm_predict(
    y_test, x_test, m
    )
```

```
Accuracy = 66.925% (2677/4000) (classification)
```

- Scaled sets with default parameters

```
%%capture
scale_param = csr_find_scale_param(x_train, lower=-1, upper=1)
x_train_scaled = csr_scale(x_train, scale_param)
x_test_scaled = csr_scale(x_test, scale_param)
```

```
m_scaled = svm_train(y_train, x_train_scaled, "-q")
pred_labels, pred_metrics, pred_values = svm_predict(
    y_test, x_test_scaled, m_scaled
    )
```

```
Accuracy = 96.15% (3846/4000) (classification)
```

- Scaled sets with parameter selection

```
def compute_acc(y_true, y_pred):
    return np.mean(y_true==y_pred)

evaluations = {
    "ACC": compute_acc
}

def grid_serach(y, x, n_folds=5,
                c_exp_space=[-10, 10, 5], g_exp_space=[-10, 10, 5],
                metric="ACC"):
    c_seq = np.linspace(*c_exp_space)
    g_seq = np.linspace(*g_exp_space)
    grid_space = [(c, g) for c in c_seq for g in g_seq]
```

```
    l = len(y)

    y_pred = np.zeros(l)

    permutation = np.random.permutation(l)
    index_per_fold = [
        permutation[int(i * l / n_folds):int((i+1) * l / n_folds)]
        for i in range(n_folds)
    ]

    best_score = 0
    best_params = best_params_info = ""

    for params in grid_space:
        for i in range(n_folds):
            valid_index = index_per_fold[i]
            train_index = np.concatenate(
                index_per_fold[:i] + index_per_fold[i+1:]
                )

            options = f"-c {2**params[0]} -g {2**params[1]} -q"
            m = svm_train(y[train_index], x[train_index], options)

            pred_labels, _, _ = svm_predict(
                y[valid_index], x[valid_index], m, "-q"
                )
            y_pred[valid_index] = np.array(pred_labels)

        cv_score = evaluations[metric](y, y_pred) * 100
        if cv_score > best_score:
            best_score = cv_score
            best_params = params
            best_params_info = \
                "(best c={0}, g={1}, rate={2:.4f})".format(
                    2**best_params[0], 2**best_params[1], best_score
                    )
```

```
        print("{0:>5} {1:>5} {2:.4f} {3}".format(
            *params, cv_score, best_params_info
        ))

    print("{0:>5} {1:>5} {2:.4f}".format(
        *best_params, best_score
    ))
    return best_params

best_params = grid_serach(y_train, x_train_scaled)
```

```
-10.0 -10.0 64.7459 (best c=0.0009765625, g=0.0009765625, rate=64.7459)
-10.0  -5.0 64.7459 (best c=0.0009765625, g=0.0009765625, rate=64.7459)
-10.0   0.0 64.7459 (best c=0.0009765625, g=0.0009765625, rate=64.7459)
-10.0   5.0 64.7459 (best c=0.0009765625, g=0.0009765625, rate=64.7459)
-10.0  10.0 64.7459 (best c=0.0009765625, g=0.0009765625, rate=64.7459)
 -5.0 -10.0 64.7459 (best c=0.0009765625, g=0.0009765625, rate=64.7459)
 -5.0  -5.0 64.9077 (best c=0.03125, g=0.03125, rate=64.9077)
 -5.0   0.0 93.2988 (best c=0.03125, g=1.0, rate=93.2988)
 -5.0   5.0 86.9861 (best c=0.03125, g=1.0, rate=93.2988)
 -5.0  10.0 64.7459 (best c=0.03125, g=1.0, rate=93.2988)
  0.0 -10.0 65.0049 (best c=0.03125, g=1.0, rate=93.2988)
  0.0  -5.0 93.6225 (best c=1.0, g=0.03125, rate=93.6225)
  0.0   0.0 96.6656 (best c=1.0, g=1.0, rate=96.6656)
  0.0   5.0 95.8886 (best c=1.0, g=1.0, rate=96.6656)
  0.0  10.0 73.7132 (best c=1.0, g=1.0, rate=96.6656)
  5.0 -10.0 93.2988 (best c=1.0, g=1.0, rate=96.6656)
  5.0  -5.0 95.8886 (best c=1.0, g=1.0, rate=96.6656)
  5.0   0.0 96.8598 (best c=32.0, g=1.0, rate=96.8598)
  5.0   5.0 94.8203 (best c=32.0, g=1.0, rate=96.8598)
  5.0  10.0 76.0764 (best c=32.0, g=1.0, rate=96.8598)
 10.0 -10.0 95.4678 (best c=32.0, g=1.0, rate=96.8598)
 10.0  -5.0 96.4713 (best c=32.0, g=1.0, rate=96.8598)
 10.0   0.0 96.6008 (best c=32.0, g=1.0, rate=96.8598)
 10.0   5.0 94.5290 (best c=32.0, g=1.0, rate=96.8598)
 10.0  10.0 76.0764 (best c=32.0, g=1.0, rate=96.8598)
```

```
  5.0   0.0 96.8598
```

- Use the best parameters C and γ to train on the entire training set and evaluate the model on the test set.

```
options = f"-c {2**best_params[0]} -g {2**best_params[1]} -q"
m_scaled = svm_train(y_train, x_train_scaled, options)
pred_labels, pred_metrics, pred_values = svm_predict(
    y_test, x_test_scaled, m_scaled
    )
```

```
Accuracy = 96.85% (3874/4000) (classification)
```

B Common Mistakes in Scaling Training and Testing Data

Section 2.2 stresses the importance of using the same scaling factors for training and testing sets. We give a real example on classifying traffic light signals (courtesy of an anonymous user) It is available at LIBSVM Data Sets.

If training and testing sets are separately scaled to $[0, 1]$, the resulting accuracy is lower than 70%.

```
$ ../svm-scale -l 0 svmguide4 > svmguide4.scale
$ ../svm-scale -l 0 svmguide4.t > svmguide4.t.scale
$ python easy.py svmguide4.scale svmguide4.t.scale
Accuracy = 69.2308% (216/312) (classification)
```

Using the same scaling factors for training and testing sets, we obtain much better accuracy.

```
$ ../svm-scale -l 0 -s range4 svmguide4 > svmguide4.scale
$ ../svm-scale -r range4 svmguide4.t > svmguide4.t.scale
$ python easy.py svmguide4.scale svmguide4.t.scale
Accuracy = 89.4231% (279/312) (classification)
```

With the correct setting, the 10 features in `svmguide4.t.scale` have the following maximal values:

0.7402, 0.4421, 0.6291, 0.8583, 0.5385, 0.7407, 0.3982, 1.0000, 0.8218, 0.9874

Clearly, the earlier way to scale the testing set to $[0, 1]$ generates an erroneous set.

C When to Use Linear but not RBF Kernel

If the number of features is large, one may not need to map data to a higher dimensional space. That is, the nonlinear mapping does not improve the performance. Using the linear kernel is good enough, and one only searches for the parameter C. While Section 3.1 describes that RBF is at least as good as linear, the statement is true only after searching the (C, γ) space.

Next, we split our discussion to three parts:

C.1 Number of instances $\ll$ number of features

Many microarray data in bioinformatics are of this type. We consider the Leukemia data from the LIBSVM data sets (`http://www.csie.ntu.edu.tw/~cjlin/libsvmtools/datasets`). The training and testing sets have 38 and 34 instances, respectively. The number of features is 7,129, much larger than the number of instances. We merge the two files and compare the cross validation accuracy of using the RBF and the linear kernels:

- RBF kernel with parameter selection

  ```
  $ cat leu leu.t > leu.combined
  $ python grid.py leu.combined
  ...
  8.0 3.0517578125e-05 97.2222
  ```

  (Best C=8.0, $\gamma = 0.000030518$ with five-fold cross-validation rate=97.2222%)

- Linear kernel with parameter selection

  ```
  $ python grid.py -log2c -1,2,1 -log2g 1,1,1 -t 0 leu.combined
   ...
  0.5 2.0 98.6111
  ```

  (Best C=0.5 with five-fold cross-validation rate=98.61111%)

  Though `grid.py` was designed for the RBF kernel, the above way checks various C using the linear kernel (`-log2g 1,1,1` sets a dummy γ).

The cross-validation accuracy of using the linear kernel is comparable to that of using the RBF kernel. Apparently, when the number of features is very large, one may not need to map the data.

In addition to LIBSVM, the LIBLINEAR software mentioned below is also effective for data in this case.

C.2 Both numbers of instances and features are large

Such data often occur in document classification. LIBSVM is not particularly good for this type of problems. Fortunately, we have another software LIBLINEAR (Fan et al., 2008), which is very suitable for such data. We illustrate the difference between LIBSVM and LIBLINEAR using a document problem `rcv1_train.binary` from the LIBSVM data sets. The numbers of instances and features are 20,242 and 47,236, respectively.

```
$ time libsvm-3.32/svm-train -c 4 -t 0 -e 0.1 -m 800 -v 5 rcv1_train.binary
Cross Validation Accuracy = 96.8136%
202.448s
$ time liblinear-2.47/train -c 4 -e 0.1 -v 5 rcv1_train.binary
Cross Validation Accuracy = 96.858%
0.651s
```

For five-fold cross validation, LIBSVM takes around 350 seconds, but LIBLINEAR uses only 3. Moreover, LIBSVM consumes more memory as we allocate some spaces to store recently used kernel elements (see `-m 800`). Clearly, LIBLINEAR is much faster than LIBSVM to obtain a model with comparable accuracy.

LIBLINEAR is efficient for large-scale document classification. Let us consider a large set `rcv1_test.binary` with 677,399 instances.

```
$ time liblinear-2.47/train -c 0.25 -v 5 rcv1_test.binary
Cross Validation Accuracy = 97.7859%
19.901s
```

Note that reading the data takes most of the time. The training of each training/validation split is *less than four seconds*.

C.3 Number of instances $\gg$ number of features

As the number of features is small, one often maps data to *higher dimensional spaces* (i.e., using nonlinear kernels). However, if you really would like to use the linear kernel, you may use LIBLINEAR with the option `-s 2`. When the number of features is small, it is often faster than the default `-s 1`. Consider the data

http://www.csie.ntu.edu.tw/~cjlin/libsvmtools/datasets/binary/covtype.libsvm.binary.scale.bz2. The number of instances 581,012 is much larger than the number of features 54. We run LIBLINEAR with `-s 1` (default) and `-s 2`.

```
$ time liblinear-2.47/train -c 4 -v 5 -s 2 covtype.libsvm.binary.scale
Cross Validation Accuracy = 75.6683%
25.148s
$ time liblinear-2.47/train -c 4 -v 5 -s 1 covtype.libsvm.binary.scale
Cross Validation Accuracy = 75.6728%
134.857s
```

Clearly, using `-s 2` leads to shorter training time.

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