HW2: Algorithm Implementation and Basic Model Selection

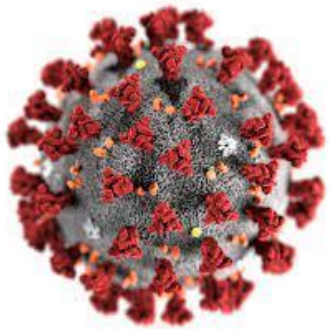
Goal

This assignment is the second of three mini projects that will guide you in your task of stopping the spread of disease around the globe!

In this assignment you will implement Soft-SVM using gradient descent. You will also practice basic hyperparameter tuning (model selection) using three algorithms: k-NN, Decision Trees (with ID3), and Soft-SVM.

Many techniques and ideas from this assignment will greatly help you in Major HW3.

Good Luck!



Instructions

- **Submission**
  - **Submit by:** Tuesday, 27.12.2022, 23:59.

- **Python environments and more**
  - We recommend using jupyter notebooks. Google colab can be very convenient since it does not require installing anything on your local computer. It will also help you to collaborate with your partner online.
  - Initial notebook here.
    - Demonstrates how to upload a dataset to Google colab and how to download files from Google colab.
    - You can save a copy of this notebook to your Google drive.
  - However, you can use any Python IDE you choose. For working locally with an IDE, we recommend first installing conda for package management (with Python 3.6 or 3.8), and then installing an IDE like PyCharm or Spyder.

- **Your code**
  - Should be clearly and briefly documented.
  - Variables/classes/functions should have meaningful names.
  - Will be partially reviewed and graded.

- **Final report**
  - Should be written in a word processor (Office Word, Google docs, etc.).
    - Should not contain the code itself.
    - Do not submit jupyter notebooks as PDFs.
  - Can be in Hebrew, English, or both.
  - **You are primarily assessed based on your written report.**
  - Answer the questions in this instruction file according to their numbering.
  - Add concise explanations, figures (outputs of your code), tables, etc.
  - You are evaluated for your answers but also for clarity, readability, and aesthetics.
  - **Tables** should include feature names and suitable titles.
  - **Plots** should have suitable titles, axis labels, legends, and grid lines (when applicable)
    - We recommend adjusting the default font sizes of matplotlib (see snippet in HW1).

- **Submit a zip file containing** (please use hyphens, not underscores):
  - The report PDF file with all your answers, named *id1-id2.pdf*.
    - Do not include your code in your report.
  - Your code:
    - The following files:
      - *SoftSVM.py* : your completed SVM module (=class).
      - *prepare.py* : your updated data preparation pipeline (including normalization).
    - Also:
      - Working with jupyter: a notebook with your code, *id1-id2.ipynb*.
      - Working with a "traditional" IDE: all relevant python scripts.
  - Do not submit csv files.

- **Failing to follow any of the instructions above may lead to point deduction!**

Preliminary: Data Loading

Task: Follow the procedure below.

a. Start by **loading** the preprocessed data from the previous assignment.
   Note: in Lecture 08 we explain why some preprocess steps (e.g., normalization), should be applied to the validation folds according to statistics computed on the train fold. Here, for simplicity only, you compute these statistics according to the all the training samples (after splitting to train-test, before splitting the training set to additional folds).

b. Make sure the data is **partitioned** correctly to train and test, according to the instructions in the previous assignment.
   The train-test partitions **must** be identical to the ones you used in HW1.

c. Following questions that we received: You shouldn't have deleted features in HW1 other than perhaps `patient_id`, `PCR_date`, and `current_location`, since it was too early for you to decide whether they are useful for classification. If you deleted any other features, that is fine, but now you should bring them back and edit your preprocessing pipeline accordingly (including suitable normalization steps).
   Note: We do not mean that you should restore features that should have been transformed into other features and only then deleted, like the `symptoms` feature.

d. Make sure target variables follow the `{+1,-1}` convention (rather than `{1,0}` or `{True,False}`).

Part 1: Basic model selection with k-Nearest Neighbors

Like in the previous HW, we start with the simple k-NN model and use it to practice some new concepts, like model selection. In this part we will use k-NN on `PCR_01` and `PCR_02` to predict the `spread`, similarly to HW1. You should use sklearn.neighbors.KNeighborsClassifier rather than your custom implementation from the previous HW.

Visualization and basic analysis

Task: Create a temporary `DataFrame` containing only `PCR_01` and `PCR_02`.

Reminder: Use the preprocessed (normalized) training set.

(Q1) Attach a `jointplot` of `PCR_01`, `PCR_02` (use the `spread` class as the `hue` argument).

(Q2) Train a k-NN model using $k = 1$ on your training set and use the `visualize_clf` method (given in this HW) to visualize the resulted decision regions. Make sure to have appropriate title and labels.

Model selection

Most ML models are characterized by a set of parameters that control the learning process and are not optimized during training (e.g., `k` in k-NN or `max_depth` in decision trees). As we learned, these hyperparameters can change the learning outcome dramatically. Hyperparameters are often tuned using k-fold-cross-validation, where we split the training data into k_v folds and train k_v models – each trained on $k_v - 1$ folds and use the last fold for validation (i.e., performance evaluation). This procedure estimates the model's performance on unseen data; thus, we can find the (estimated) optimal hyperparameters.

Remember: DO NOT use the test set for hyperparameter tuning.

(Q3) Use sklearn.model_selection.cross_validate to find the best k (neighbors) value in `list(range(1, 20, 2)) + list(range(20, 871, 85))` for predicting the `spread` class using `PCR_01` and `02`. Read the API carefully to understand how to extract train scores. Use the (default) accuracy metric and 8-folds to perform cross-validation.

Using the outputs of `cross_validate`, plot a *validation curve*, i.e., the (mean) training and validation accuracies (y-axis) as functions of the k values (x-axis). Make the x-axis logarithmic (using `plt.semilogx`) and attach the plot (with the 2 curves) to your report.

Answer: Which k value is the best? What are its mean training and validation accuracies (computed during the cross validation)? Also explain which k values cause overfitting and underfitting (and why is that).

(Q4) Use the optimal k value you found and retrain a k-NN model on all the training samples. In your report: plot the decision regions of this final model (using `visualize_clf`) and write its test accuracy (computed on the separate test split) of this model.

(Q5) Using all training samples, train two additional models with $k = \{1, 501\}$. Visualize their decision regions as well.

Compare the boundaries of these two k-values to the ones of the optimal one you found earlier; and discuss the results and the exhibited behaviors (2-3 sentences).

(Q6) Repeat (Q3) using all the features in the training dataset (instead of only `PCR_01` & `02`). Add the validation curve (train and validation) to your report.

Discuss in detail the differences between the results here to those of (Q3) and try to explain them considering the mechanism of k-NN models.

Part 2: Decision trees

In this part we will focus on predicting the `risk` class using decision trees. Rather than implementing the models by yourself, you will use sklearn's DecisionTreeClassifier with entropy as a splitting criterion (ID3) and focus on hyperparameter tuning and visualization.

Visualization

(Q7) Train a model with ID3 and `max_depth=4` (not including the root level; use the entire training set, i.e., all the features after preprocessing from all the training samples). What is the training accuracy?

Visualize the trained tree using `plot_tree` (provide feature and class names; use `filled=True`) and attach the plot to your report. The plot should be readable!

Model selection

It is time to search for the best tree to fight covid! Using the DecisionTreeClassifier documentation, understand how the `min_samples_leaf` argument can mitigate overfitting.

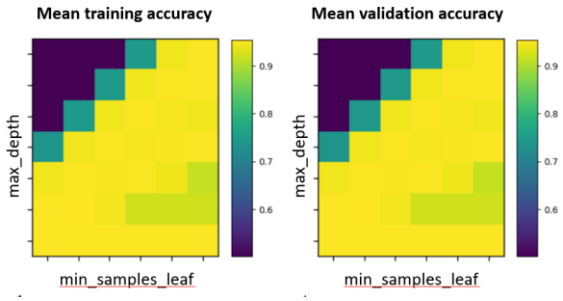
You will now tune two hyperparameters simultaneously – both `min_samples_leaf` and `max_depth`. You need to look for the combination of these two hyperparameters that lead to the best validation performance. There are many approaches for tuning multiple hyperparameters, and here we take the grid search approach (shortly explained here).

(Q8) Using 8-fold cross-validation, tune the two hyperparameters by performing a grid search (see GridSearchCV). Find the combination yielding the best validation error for predicting the `risk` class. You should:

a. Choose appropriate ranges for both hyperparameters. This may require a few attempts. To make things quicker when trying to find appropriate hyperparameter ranges, you can start by using only 2 folds.

b. Since we tune two hyperparameters, instead of a validation curve, plot two heatmaps (seaborn / pyplot), one for the cross-validated training accuracy and one for the cross-validated validation accuracy.

These heatmaps should roughly have the following style / structure:



Make sure to plot the appropriate "ticks" on both axes and use annotations (`annot=True`) to explicitly write the accuracies inside the heatmap cells.

Important: The plots should be readable and informative!

c. Add the 2 plots to your report and specify which hyperparameter combination is optimal.

d. Write a hyperparameter-combination that causes underfitting.

e. Write a hyperparameter-combination that causes overfitting.

f. Add a short discussion regarding why each specific hyperparameter-combination from sub-questions 'd' and 'e' resulted in under/over-fitting.

(Q9) Use the optimal hyperparameter combination you found and retrain a decision tree on all the training samples. In your report write the test accuracy of this model.

Part 3: Linear SVM and the Polynomial kernel

In this part we will implement a Soft-SVM classifier to better understand this model. We will be predicting the `spread`, using only `PCR_01` and `PCR_02`. We will use gradient-based optimization to find the optimal parameter. Recall that using the whole dataset to perform one step update is costly. To mitigate this problem, we will implement the Stochastic Gradient Descent (SGD) algorithm.

Implementation of the loss and its gradient

Recall the Soft-SVM formulation:

$$\underset{\boldsymbol{w}\in\mathbb{R}^d, b\in\mathbb{R}}{\operatorname{argmin}} \underbrace{\|\boldsymbol{w}\|_2^2 + C\sum_{i=1}^{m}\max\{0, 1-y_i(\boldsymbol{w}^\top \boldsymbol{x}_i + b)\}}_{\triangleq p_C(\boldsymbol{w},b)}$$

Following is the **analytic** sub-gradient of the objective function above

$$\nabla_w p_C(\boldsymbol{w}, b) = 2\boldsymbol{w} + C\sum_{i=1}^{m} f\big(y_i(\boldsymbol{w}^\top \boldsymbol{x}_i + b)\big) y_i \boldsymbol{x}_i \text{ , where } f(z) = \begin{cases} -1, & z < 1 \\ 0, & z \geq 1 \end{cases}$$

$$\frac{\partial}{\partial b} p_C(\boldsymbol{w}, b) = C\sum_{i=1}^{m} f\big(y_i(\boldsymbol{w}^\top \boldsymbol{x}_i + b)\big) y_i$$

Task: Copy the `SoftSVM` module from the given *`SoftSVM.py`* into your notebook / project.

Task: Complete the (static) `SoftSVM.loss` method in the module, so that it computes the objective loss $p_C(w, b)$ on a given dataset.

Remember: `w` is a vector and `b` is a scalar.

Tip: When possible, prefer vector operations (e.g., `np.sum`, `np.sign`, `np.maximum`). Avoid using `for` loops.

Task: Complete the (static) `SoftSVM.subgradient` method in the module, so that it computes the analytic sub-gradients $\nabla_w p_C(w, b)$ and $\frac{\partial}{\partial b} p_C(w, b)$ described above.

Tip: When possible, prefer vector operations (e.g., `np.sum`, `np.sign`, `np.maximum`). Avoid using `for` loops.

Verifying your implementation: Numerical vs. analytical gradients

Recall from your calculus course, the definition of the derivative of a function $f: \mathbb{R} \to \mathbb{R}$ is:

$$f'(x_0) = \frac{f(x_0 + \delta) - f(x_0)}{\delta}$$

Thus, we can deduce a method to compute the **numerical** partial derivative w.r.t. w_i by approximating the limit expression with a finite δ:

$$\forall i = 1, \dots, d: \ \frac{\partial p_C}{\partial w_i} \approx \frac{p_C(\boldsymbol{w} + \delta \boldsymbol{e}_i, b) - p_C(\boldsymbol{w}, b)}{\delta} \triangleq u_i, \ \text{ where } \boldsymbol{e}_i = [0, \dots, 0, \underbrace{1}_{i-th}, 0, \dots, 0]$$

Denote the **numerical** sub-gradient by $\boldsymbol{u}_\delta(\boldsymbol{w}, b) = \begin{bmatrix} u_1 \\ \vdots \\ u_d \end{bmatrix}$.

Using the numerical sub-gradient, we will now verify the correctness of your implementation for the loss and its analytic sub-gradient.

We will plot the residuals $\| \underbrace{\nabla_{\boldsymbol{w}} p_C(\boldsymbol{w}, b)}_{\text{analytic}} - \underbrace{\boldsymbol{u}_\delta(\boldsymbol{w}, b)}_{\text{numeric}} \|_2$ over many repeats as a function of δ.

Task: Copy the functions from the given `verify_gradients.py` into your notebook / project. Read and understand these functions but do not edit them.

For the rest of the assignment, we will use again only `PCR_01`, `PCR_02` to predict the `spread`.

(Q10) Using `PCR_01`, `PCR_02`, generate a plot that compares the numerical gradients to the analytic gradients. Do this by running the following command:

```
compare_gradients(X_train, y_train, deltas=np.logspace(-9, -1, 12))
```

Attach the plot to your report. Briefly discuss and justify the demonstrated behavior.

Solving Soft SVM problems using Stochastic Gradient Descent (SGD)

Task: Complete the given `SoftSVM.predict` method according to the decision rule of linear classifiers (return the predicted labels using the `{+1,-1}` convention).

Tip: prefer vector operations (e.g., `np.dot` and `np.sign`) when possible.

Avoid using `for` loops.

Task: Read and understand the given `SoftSVM.fit_with_logs` method.

Complete the code inside the loop to perform a gradient step (compute `g_w` and `g_b` and use them to update `w` and `b`).

SGD is an iterative learning algorithm. A common method to analyze such algorithms is to plot a *learning curve*, i.e., plot the accuracy and/or loss of the model over time (i.e., steps).

Task: First, we wish to understand the effect of the learning rate (step size) and make sure that our models converge.

The following snippet trains a `SoftSVM` model and plots the learning curves. Plot the graphs for the learning rates in `np.logspace(-3, 0, 4)` without changing the `C` value given below. You may use the following snippet to help you (add suitable labels and titles):

```
clf = SoftSVM(C=0.1, lr=lr)
losses, accuracies = clf.fit_with_logs(X_train, y_train, max_iter=3000)

plt.figure(figsize=(13, 6))
plt.subplot(121), plt.grid(alpha=0.5), plt.title ("TODO")
plt.semilogy(losses), plt.xlabel("TODO"), plt.ylabel("TODO")
plt.subplot(122), plt.grid(alpha=0.5), plt.title ("TODO")
plt.plot(accuracies), plt.xlabel("TODO"), plt.ylabel("TODO")
```

(Q11) Add the plot(s) to your report.

a. Given the plots, which learning rate would you choose?

b. Train this linear model with the chosen learning rate and plot its decision regions (at the end of training).

c. For the chosen learning rate, what is the maximal training accuracy and the minimal training loss achieved by your model (during training, according to your plots)? Are they attained at the same step? If so – must it be so? If not – how is it possible?

Submit: Copy your completed `SoftSVM` module into a separate file called *`SoftSVM.py`*.

Submit this file at the end of your work.

Using a feature mapping

We now want to understand the polynomial feature mapping and its corresponding kernel. To make our following explanation clearer, assume we want to use a 2nd-degree polynomial feature mapping on a 2-dimensional data (i.e., having two raw features).

Recap: solving SVMs with feature mappings

We have two ways to use this feature mapping (we present Hard-SVM for simplicity):

1. *Explicitly apply the feature mapping* $\phi(x) = \left[1, \sqrt{2}x_1, \sqrt{2}x_2, \sqrt{2}x_1x_2, x_1^2, x_2^2\right]$ *and solve the primal problem in the new 6-dimensional space:*

$$\underset{\boldsymbol{w}\in\mathbb{R}^6}{\operatorname{argmin}} \|\boldsymbol{w}\|_2^2 \quad \text{s.t.} \quad y_i \cdot \boldsymbol{w}^\top \phi(\boldsymbol{x}_i) \geq 1, \ \ \forall i \in [m]$$

2. *Use an appropriate kernel function, i.e.,* $K(\boldsymbol{u}, \boldsymbol{v}) = \phi(\boldsymbol{u})^\top \phi(\boldsymbol{v}) = (\boldsymbol{u}^\top \boldsymbol{v} + 1)^2$*, and solve the dual problem in an* m*-dimensional space (without explicitly computing the feature mappings):*

$$\max_{\boldsymbol{\alpha}\in\mathbb{R}_+^m} \sum_{i=1}^m \alpha_i - \frac{1}{2}\sum_{i,j=1}^m y_i y_j \alpha_i \alpha_j \underbrace{\phi(\boldsymbol{x}_i)^\top \phi(\boldsymbol{x}_j)}_{=K(\boldsymbol{x}_i, \boldsymbol{x}_j)}$$

We will now use the polynomial feature mapping to predict the `spread` using `PCR_01` and `02`. Since you only implemented the primal (Soft-)SVM problem, we will use the **first** way and explicitly transform the 2 features with a 2nd and 3rd degree polynomial mappings

We now wish to create a single model that: (1) transforms the 2 features with a p-degree polynomial mapping; and then (2) normalizes the transformed data; and (3) trains your custom `SoftSVM` module on the data. To do so, we will use a Pipeline.

The following code snippet creates such a pipeline:

```
C = 1e13
from sklearn.preprocessing import StandardScaler
svm_clf = Pipeline([('feature_mapping', TODO),
                    ('scaler', StandardScaler()),
                    ('SVM', SoftSVM(C=C, lr=(1/(C*5e2))))])
```

We wish to set the SVM's `max_iter` to 10,000. Since you work with a pipeline, use the following way to specify an argument of an inner model inside the pipeline:

```
svm_clf.fit(X_train, y_train, SVM__max_iter=10000)
```

where "SVM" is the name of the final step of your pipeline.

Task: Complete the first step in the pipeline above to make it apply a 2nd-degree PolynomialFeatures transformation, keep the `C` and `lr` values that we defined.
Train the model.
Repeat the process for a 3rd degree transformation.

(Q12) In your report:

(a) Write the respective train and test accuracies of both models (2nd and 3rd degree).

(b) Add a plot of the decision boundaries for each classifier.

(c) Briefly discuss and explain the difference in decision regions between the two models.

(Q13) Train the 3rd degree polynomial mapping SVM 5 times (on all the training samples), using the hyperparameters written in the snippet above.
In your report:

(a) Write the 5 resulting train accuracies, their mean, and their standard deviation.

(b) Plot the 5 resulting decision regions (use `visualize_clf` on the training set). Remember that you are evaluated on the aesthetics of your report as well.

(c) Answer: what is (are) the source(s) of the variability in the resulting models? Your answer should refer also to the convexity of the problem.

Part 4: The RBF kernel

Before we start: what is the Radial Basis Function kernel?

In Lectures 04 and 05 we presented the RBF kernel (also called the Gaussian kernel). This kernel is often defined as $K(\boldsymbol{u},\boldsymbol{v}) = \exp\left\{-\frac{1}{2\sigma^2}\|\boldsymbol{u}-\boldsymbol{v}\|_2^2\right\}$ *or* $\exp\{-\gamma\|\boldsymbol{u}-\boldsymbol{v}\|_2^2\}$*, which can be decomposed using an infinite-dimensional feature mapping (see the lecture).*

Note: If you wish, you can already practice this mapping by solving Q4 in Exam A from Winter 2021-22.

After solving the appropriate 2 optimization problem, we get a dual solution $\boldsymbol{\alpha} \in \mathbb{R}_+^m$*. Like we saw in the lecture, given a new datapoint* $\boldsymbol{x} \in \mathbb{R}^d$ *for prediction, the model predicts* $h(\boldsymbol{x}) = \text{sign}(\sum_{i=1}^m \alpha_i y_i K(\boldsymbol{x},\boldsymbol{x}_i)) = \text{sign}\left(\sum_{i\in[m],\alpha_i>0} \alpha_i y_i K(\boldsymbol{x},\boldsymbol{x}_i)\right)$.

This rule acts similarly to a weighted nearest-neighbor algorithm (on the training set), where "neighborhoods" of datapoints are computed using the kernel function.

For instance, consider a 1-dimensional training dataset: $\{\underbrace{(0,-1)}_{(x_1,y_1)}, \underbrace{(2,+1)}_{(x_2,y_2)}, \underbrace{(-1,+1)}_{(x_2,y_2)}\}$.

Assume the dual SVM solution is $\boldsymbol{\alpha} = (1,1,2)$.

When $\sigma = 1$*, we get the (weighted) Gaussians on Figure (a) below.*

Given a new datapoint $x = 0.5$*, the model predicts:*

$$h(\boldsymbol{x}) = \text{sign}\sum_i \alpha_i y_i K(\boldsymbol{x},\boldsymbol{x}_i) = \text{sign}\big(1\cdot(-1)\cdot K(0.5,0) + 1\cdot 1\cdot K(0.5,2) + 2\cdot 1\cdot K(0.5,-1)\big)$$

$$= \text{sign}\left(-\exp\left\{-\frac{\|0.5-0\|_2^2}{2}\right\} + \exp\left\{-\frac{\|0.5-2\|_2^2}{2}\right\} + 2\exp\left\{-\frac{\|0.5-(-1)\|_2^2}{2}\right\}\right)$$

$$= \text{sign}\left(-\exp\left\{-\frac{0.25}{2}\right\} + \exp\left\{-\frac{2.25}{2}\right\} + 2\exp\left\{-\frac{2.25}{2}\right\}\right) \approx \text{sign}(-0.88 + 0.32 + 0.65) = +1$$

In fact, we can create an even clearer visualization by drawing the weighted sum of positive points' Gaussians (blue) and the one of negative ones (red) in Figure (b).

Finally, Figure (c) shows the case resulted Gaussians when $\sigma = \frac{1}{10}$*. Notice how each training point influences only a small environment around it. We explain this below.*

Figure (a)

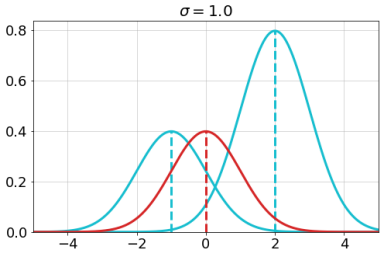
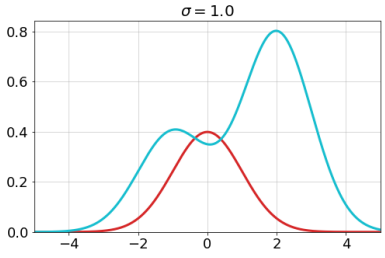
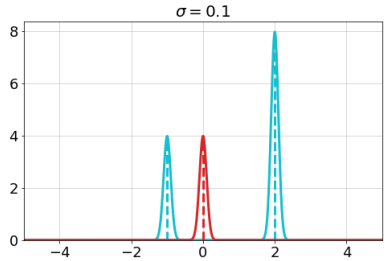


Figure (b)



Only very closely to $x = 0$*, the model predicts* $y = -1$.

Figure (c)



Each points effects only a small environment around it

As another example, consider a (finite) solution vector $\boldsymbol{\alpha} \in \mathbb{R}_{+}^{m}$ in the extreme case where $\sigma^2 \to 0$ and $\gamma \to \infty$, it can be easily shown that we should get a similar behavior (perhaps up to edge cases) to the 1-nearest-neighbor algorithm on the support vectors, i.e., the vectors with corresponding nonzero α weights:

$$h(\boldsymbol{x}) = \operatorname{sign}\left(\sum_{i\in[m],\alpha_i>0} \alpha_i y_i K(\boldsymbol{x},\boldsymbol{x}_i)\right) = \lim_{\gamma\to\infty} \operatorname{sign}\left(\sum_{i\in[m],\alpha_i>0} \alpha_i y_i \exp\{-\gamma\|\boldsymbol{x}-\boldsymbol{x}_i\|_2^2\}\right)$$
$$= \cdots = y_{i^*}, \text{ where } i^* = \operatorname{argmin}_{i\in[m],\alpha_i>0}\|\boldsymbol{x}-\boldsymbol{x}_i\|_2^2$$

To complete our explanations, read this blogpost and then watch this short video. While doing this, keep in mind the prediction rule $h(\boldsymbol{x}) = \operatorname{sign}\left(\sum_{i\in[m],\alpha_i>0} \alpha_i y_i K(\boldsymbol{x},\boldsymbol{x}_i)\right)$.

(Q14) Complete the derivation above to prove the behavior of RBF on the extreme of $\gamma \to \infty$. That is, prove that:

$\lim_{\gamma\to\infty} \operatorname{sign}\left(\sum_{i\in[m],\alpha_i>0} \alpha_i y_i \exp\{-\gamma\|\boldsymbol{x}-\boldsymbol{x}_i\|_2^2\}\right) = y_{i^*}$, *where* $i^* = \operatorname{argmin}_{i\in[m],\alpha_i>0}\|\boldsymbol{x}-\boldsymbol{x}_i\|_2^2$.

Simplification: you can assume that no two samples $i \neq j$ hold $\|\boldsymbol{x}-\boldsymbol{x}_i\| = \|\boldsymbol{x}-\boldsymbol{x}_j\|$.

Hint: $\forall t \in \mathbb{R}, \alpha \in \mathbb{R}_{>0}$: $\operatorname{sign}(t) = \operatorname{sign}(t/\alpha)$.

Finally, let us use a Kernel SVM with an RBF kernel to predict the `spread` using `PCR_01,02`. Since the corresponding feature mapping is of an infinite dimensionality, we will have to use the kernel trick and solve the dual problem, like we explained 2. Our custom SoftSVM class is not suitable for solving dual formulations, hence we will use sklearn's implementation.

Task: Use sklearn.svm.SVC to train an SVM with an RBF kernel on the two features and the `spread` variable. We first wish to visualize the regularizing effect of γ, so you should begin by fixing `C=1e4` and train 10 different models (on the entire training set, i.e., all training samples, narrowed down to the two features) with all γ values in `np.logspace(-5, 4, 10)`.

Notice that we don't adjust the learning rate by ourselves, since sklearn does its own fancy optimization process for us.

(Q15) Use our visualization method to visualize the ten models' decision regions (use the `marker_size` argument to adjust the plots for small decision regions).

Attach the ten plots to your report (resize them to fit in a single page of your report). Remember that all plots should have suitable titles. You are evaluated on the aesthetics of your report as well.

We recommend that you try to understand the exhibited behaviors in these ten plots in light of the explanations at the beginning of this part. You are not required to explain these behaviors in your report.

(Q16) Compare the decision regions of the k-NN model with $k = 1$ from (Q2) to those of the RBF model with $\gamma = 10^4$ from the previous question. We expected the two models to be very similar, but we should still see significant differences. Try to explain the differences (try to give several reasons, there isn't a single correct answer).

(Q17) Now, given the problem at hand (predicting the `spread` using an SVM with the RBF kernel on `PCR_01` and `02`), we wish to find an optimal γ given `C=1e4`. To this end, perform 8-fold cross validation on γ.

Remember: when looking for appropriate value intervals for γ, you may start by using only two folds. Once the ranges are set, increase the folds' number to 8 and sample many values throughout the interval. We recommend sampling the hyperparameter values at logarithmic intervals for good results.

Attach here the required plots and explanations, as in (Q8).

(Q18) Use the optimal hyperparameter you found and retrain an RBF model on the all the training samples. In your report: plot the decision regions of this final model and write its test accuracy. Compare these results to those from (Q4) in 3-4 sentences.

Based on the test accuracy, which model is better for the task of predicting the `spread`?

Submitting the files

Return to the instructions on Pages 2-3 and make sure you submit **all** required files.