

EXERCISE 4

DR. VICTOR UC CETINA

1. SUPPORT VECTOR MACHINES

- (1) Install libSVM from the official site in:

<https://www.csie.ntu.edu.tw/~cjlin/libsvm/>.

There is also a version for python in:

<https://pypi.org/project/libsvm/>.

Or you can use Scikit-Learn.

- (2) Run the experiments with the dataset `heart_scale` that comes with the library. In the readme file it is specified how to test it correctly.

```
matlab> [heart_scale_label, heart_scale_inst] = libsvmread('../heart_scale');
matlab> model = svmtrain(heart_scale_label, heart_scale_inst, '-c 1 -g 0.07');
matlab> [predict_label, accuracy, dec_values] =
svmpredict(heart_scale_label, heart_scale_inst, model); % test the training data
```

Take your time to read the information about how to use the library!

- (3) Apply support vector machines to classify the Chagas parasite images using the feature vectors that you generated in exercise 3. You need to run experiments using the linear, polynomial (degrees $d = 1, 2, 3, 4$), sigmoid and radial basis kernels.
- (4) To run experiments with your data, you need to find the optimal values for **C** and **gamma**. You can download a python program (`grid.py`) for this purpose in:
<https://github.com/cjlin1/libsvm/blob/master/tools/grid.py>.
- (5) Prepare a report containing 1) your final performances with each kernel; 2) how many support vectors were generated with each kernel; 3) descriptions of the features you used; 4) your conclusions.

2. EXERCISE SUBMISSION

- Deadline: June 8th, 2020.