

## EXERCISE 4

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### 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/>.

- (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, 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 your final performance results of your classifier with the features you used.

### 2. EXERCISE SUBMISSION

- Deadline: December 3-5, 2019.
- Note: Do not forget to include your names in the report!