Ensemble methods

- Predict heart disease using ensemble methods
- Use 5-fold cross-validation to estimate test accuracy
- Use a DecisionTree base learner from scikit-learn
- Compare blending, bagging and boosting in terms of mean and standard deviation of accuracy (across the cross-validation folds) and total model training and testing time. Use the same number of base learners (50 for example) to make comparison fair.
  - Use StackingClassifier, RandomForest and AdaBoost from scikit-learn
- Which ensemble method would you use if you had to optimize for memory or speed or performance?

Support Vector Machines

- Implement the linear, polynomial (degree=3) and gaussian kernels
  - Define the parameters according to the scikit-learn default values (https://scikit-learn.org/stable/modules/generated/sklearn.svm.SVC.html)
  - Check your implementations by comparing results with the scikit-learn results (use your implementations as input parameters)
- Use your favorite kernel (your own implementations) with the scikit-learn SVM model to predict heart disease
  - Use 5-fold cross validation (scikit-learn implementation)
  - Try at least 10 C values (input to the scikit-learn model)
  - Print mean training and test accuracies across the cross-validation folds for each C value