The dataset used for this assignment was retrieved from <https://archive.ics.uci.edu/ml/datasets/Breast+Cancer+Wisconsin+%28Original%29>. The data reflects samples from clinical cases of breast cancer with 699 datapoints collected. The column headers are: Sample code number (id number), Clump Thickness (1 – 10), Uniformity of Cell Size (1 – 10), Uniformity of Cell Shape (1 – 10), Marginal Adhesion (1 – 10), Single Epithelial Cell Size (1 – 10), Bare Nuclei (1 – 10), Bland Chromatin (1 – 10), Normal Nucleoli (1 – 10), Mitoses (1 – 10), and Class (2 for benign, 4 for malignant). After the missing entries were removed from the dataset, we are left with a 683x11 shape. My SVM had a success rate of accuracy of 96.5% +/- 1.9% which satisfies the requirements. The most obvious choice for the feature with the highest importance would be column class, since we were calculating the prediction of whether a mass will be benign or malignant.