

HIERACHICAL ACTIVE LEARNING BIOINFORMATICS APPLICATION

by

James D. Duin

A THESIS

Presented to the Faculty of

The Graduate College at the University of Nebraska

In Partial Fulfilment of Requirements

For the Degree of Master of Science

Major: Computer Science

Under the Supervision of Professor Stephen Scott

Lincoln, Nebraska

March, 2017

HIERACHICAL ACTIVE LEARNING BIOINFORMATICS APPLICATION

James D. Duin, M.S.

University of Nebraska, 2017

Adviser: Stephen Scott

This study investigates an application of the Support Vector Machine and Logistic Regression machine learning algorithms to a protein dataset labeled according to a proteins location of origin in a cell. The dataset is labeled according to a hierarchical scheme, at the root level the protein is from the mitochondria or not, then the hierarchy breaks down further into specific target compartments at the leaf nodes. Our investigation shows that Leveraging separate fine-grained classifiers for each of the target compartments produces a higher performing classifier at the highest level in the hierarchy according to the Precision-Recall curves area under the curve. Furthermore, new approach in the Active Learning setting termed *active over-labeling* is applied to this dataset. The approach solicits labels at a finer level of granularity than the target concept. We show that purchasing fine-grained labels in each round of active learning produces a higher performing classifier than purchasing coarse labels, and in both cases purchasing labels actively by selecting only the most uncertain labels outperforms purchasing labels passively, i.e. at random. The fine-grained labels also incur a higher cost than coarse-grained labels for this dataset, so multiple cost ratios ran and an optimal Fixed Fine ratio purchasing strategy is determined for each fine cost.

DEDICATION

This thesis is dedicated to my parents Paul and Vicki Duin and fiancée Anna Spady.

ACKNOWLEDGMENTS

I would like to thank my advisor Dr. Stephen Scott for guidance in selecting this research topic, Yugi Mo for his work in developing the HAL methodology, and Dr. Douglas Downey for his work on this topic. I would like to thank Juan Cui, Jiang Shu, Kevin Chiang for assistance accessing and understanding the protein dataset that is the subject of the paper.

Contents

Contents	v
1 Introduction	1
1.1 Machine Learning	1
1.2 Hierarchical Bioinformatics Data Set	2
1.3 Coarse-grained vs Fine-grained Trade Off	4
2 Background and Related Work	6
2.1 Active Learning	6
2.2 Hierarchical Active Learning	7
2.3 Application to Dispatch Dataset	8
3 Experimental Setup	10
3.1 Training and Testing Coarse Grain and Fine Grain Classifiers	10
3.1.1 Varying SVM Scaling Methods	15
3.1.2 Varying SVM Kernels	16
3.1.3 Varying SVM Feature Selection	17
3.1.4 Varying Logistic Regression Scaling	18
3.1.5 Varying Logistic Regression Feature Selection	18
3.1.6 Varying Logistic Regression Postive Class Weight and Cost	19

3.1.7	Varying Logistic Regression Fine Class Weights	21
3.1.7.1	Tune Fine Class 1 Weights	22
3.1.7.2	Tune Fine Class 2 Weights	23
3.1.7.3	Tune Fine Class 3 Weights	23
3.1.7.4	Tune Fine Class 4 Weights	24
3.1.7.5	Tune Fine Class 5 Weights	25
3.1.7.6	Tune Fine Class 6 Weights	26
3.1.7.7	Tune Fine Class 7 Weights	27
3.1.7.8	Tune Fine Class 8 Weights	28
3.1.8	Varying Logistic Regression Tolerance	28
3.1.9	Varying Sample Weight On Test Set and Dropping Intermediate ROC Curve Values	29
3.1.10	Varying Logistic Regression Positive Class Weight For Full Dataset .	30
3.1.11	Varying SVM Gamma	31
3.1.12	Varying SVM Cost	33
4	Results and Analysis	34
4.1	SVM and Logit Classifier Performance	34
4.2	Active vs Passive curves	37
4.2.1	Plots for Logistic Regression Active vs Passive curves	38
4.2.2	Plots for SVM Active vs Passive curves	43
4.3	Plots for Fine Fixed Ratio experiments	45
5	Conclusions and Future Work	53
	Bibliography	54

Chapter 1

Introduction

1.1 Machine Learning

Machine learning (ML) algorithms are defined as computer programs that learn from experience E with respect to some class of tasks T and performance measure P , if their performance at tasks in T , as measured by P , improves with experience E [1]. In the context of this paper, the machine learning algorithms that are used include Support Vector Machines (SVM), and Logistic Regression (Logit). This work uses implementations by the sci-kit learn python library [2] for both algorithms. Our experiment requires a binary classification task, each algorithm takes a protein instance with a list of 449 features as an input and then outputs a 0 or 1 whether or not the protein belongs to a class. A separate classifier is trained for each class in the protein dataset.

Logit is a linear model for classification. The classifier function is shown in *eqn 1.1*. Where x is the vector of features, θ is vector of learned parameters, the function $g(z)$ is the sigmoid function [22].

$$\begin{aligned}
h_{\theta}(x) &= g(\theta \cdot x) \\
g(z) &= \frac{1}{1 + e^{-z}}
\end{aligned} \tag{1.1}$$

The theta parameters are solved for in order to minimize the sum of square errors (L2-norm) in the training set, and also to regularize the theta parameters to prevent them from getting too large and overfitting the dataset [2]. A cost function is used to solve for theta, this function is shown in *eqn 1.2*. The C parameter is the inverse of the regularization strength, a larger value means a stronger regularization [2].

$$\min_{\theta, c} \frac{1}{2} \theta^T \theta + C \sum_{i=1}^n \log(\exp(-y_i(X_i^T \theta + c)) + 1) \tag{1.2}$$

1.2 Hierarchical Bioinformatics Data Set

Bioinformatics is a field using computer science tools and techniques for solving problems in (molecular) biology. The focus of this work is a Bioinformatics dataset developed in order to identify the source of a certain class of mutations causing mitochondrial disease. Mitochondria are present in every cell of the body, with the exception of red blood cells [3]. Mitochondrial diseases may be caused by mutations in the proteins that reside within the mitochondria. These mutations that occur in locally transcribed and translated mitochondrial DNA (mtDNA), or in nuclear DNA (nDNA) whose protein products are imported into the mitochondria. These nDNA have many target locations including the mitochondria's outer and inner membrane, its matrix, and its ribosomes. Identifying the source of the mutation is an important problem in the treatment of a mitochondrial disease. It is an essential classification task to determine whether or not the offending mutation occurs in the mitochondrion or in an imported protein [3]. The positive dataset is composed of 962 human mitochondrial proteins from the Mitoproteome

dataset [4]. The negative dataset is composed of 19,136 experimentally validated human proteins from UniProt [5]. A total of 1099 features were assembled by Kevin Chiang from Dr. Cui's bioinformatics lab at University of Nebraska at Lincoln (UNL), these features are described along with references to their sources in *Table ??*. The features were reduced and combined into a resulting set of 449 dimensions [3]. This bioinformatics dataset is used for experimentation throughout this work.

Table 1.1: Features of the protein dataset along with their respective sources.

Type of Properties	Features (dimension)	Sources
General sequence features	Amino acid composition (20), sequence length (1), di-peptides composition (400)	Calculated by Kevin Chiang at UNL [3]
	Normalized Moreau-Broto, autocorrelation (240), Moran autocorrelation (240), Geary autocorrelation (240), Sequence order (160), Pseudo amino acid composition (50)	Profeat [6]
Physico chemical properties	Hydrophobicity (21), normalized Van der Waals volume (21), polarity (21), polarizability (21), charge (21), secondary structure (21) and solvent accessibility (21)	Computed with three descriptors: composition (C), transition (T), and distribution (D) [7]
	Solubility (1), unfoldability (1), disorder regions (3), global charge (1) and hydrophobicity (1)	PROSO [8], Phobius [9]
Structural properties	Secondary structural content (4), shape (Radius Gyration) (1)	SSCP [10]
Domains and motifs	Signal peptide (1), transmembrane domains (alpha helix and beta barrel) (5), Glycosylation (both N-linked and O-linked) (4), Twin-arginine signal peptides motif (TAT) (1)	SignalP [11], TMB-Hunt [12], NetOgly [13], TatP [14]

The dataset composes a classification problem, each protein is labeled according to where it originates in the cell. At the root is whether or not the protein resides within the mitochondria, then there are the sub level labels if the protein has a separate target compartment specifications. The complete tree along with the number of instances

belonging to the each label is included in *Figure 1.1*.

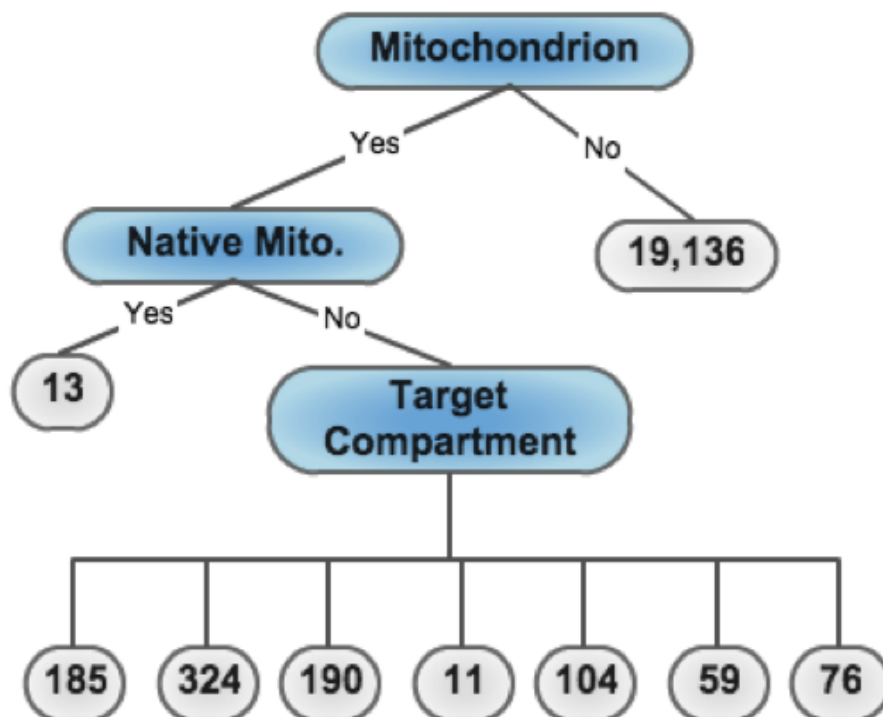


Figure 1.1: The protein dataset hierarchy of labels along with the instance count for each label.

1.3 Coarse-grained vs Fine-grained Trade Off

The classifier that does not take advantage of any of the fine-grained labels works off of the root labels for each instance and does not train separate classifiers for the fine-grained labels. This classifier is referred to as the coarse-grained classifier. The classifier that does use fine-grained labels, and trains a separate classifier for each label, then combines them to generate a root level label is referred to as the fine-grained classifier. It can be demonstrated through a dummy example that for certain datasets, a fine-grained approach to the root level classifier can achieve higher levels of precision for the same

level of recall. Such a dataset is shown in *Figure 1.2*. The classifiers for this dataset can be thought of as a function of axis parallel rectangular boxes. For the coarse grained to have high recall and return all of the positive circle instances, it must encompass the entire dataset and incidentally return all of the negative diamond instances as positive also. A fine-grained approach is preferable for the dummy dataset pictured. It is the intention of this study to demonstrate that the fine-grained classification approach for a root level classifier will achieve higher levels of precision for the same level of recall when applied to the protein dataset.

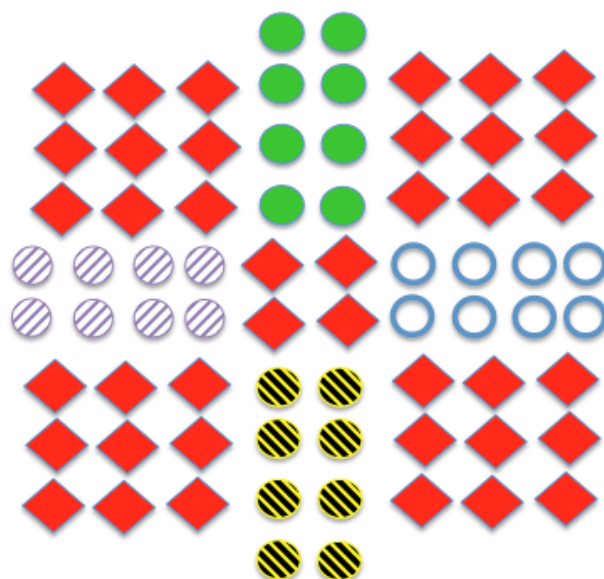


Figure 1.2: Demonstration of a dataset that would benefit from multiple fine-grained learners for each circle type. In order for the coarse-grained learner to have high recall, precision must be sacrificed and a large amount of false positives returned. By combining fine-grained classifiers the same level of recall can be achieved with a higher level of precision because none of the false positive diamonds will be returned

Chapter 2

Background and Related Work

2.1 Active Learning

Active Learning relates to the coarse-grained vs fine-grained tradeoff because it is reasonable to assume that fine-grained labels may not be as readily available as coarse-grained labels, and thus have a higher cost. An active learning approach is used to determine how many fine-grained labels to purchase in order to minimize the total cost to train the algorithm and maximize the precision and recall scores. The following equations for precision, recall, and a weighted F score are shown below in equations 1 through 3.

*Precision*eqn

*Recall*eqn

*F_{0.5}*eqn

The goal in an active learning approach is to maximize the F measure where α equals 0.5 [2]. The F-0.5 measure gives more weight to precision, as opposed to recall, so it gives incentive to purchase enough fine-grained labels to increase the F-0.5 measure. The

coarse-grained labels will cost less than fine-grained labels, but the increase in the F-0.5 measure justifies the increase in cost up to a certain point. The F-0.5 measure is used in the results section of this paper. ... That's why we use PRauc in the results. Describe some of the other papers that Yugi cited.

2.2 Hierarchical Active Learning

The Hierarchical Active Learning algorithm (HAL) is shown diagrammatically in Figure 3. Multiple fine-grained classifiers are trained at each level of the Hierarchy of the dataset. Queries to the oracle are performed purchase the most cost effective labels to add to the training sets of the classifiers. The active learning cycle continues until a cost budget has been reached. The benefit of an active learning approach is to maximize the F-0.5 measure for a given cost budget. It was the goal of this study to apply the HAL algorithm to the protein dataset, however this is not achieved at this time. An existing application of HAL is briefly discussed in the following section.

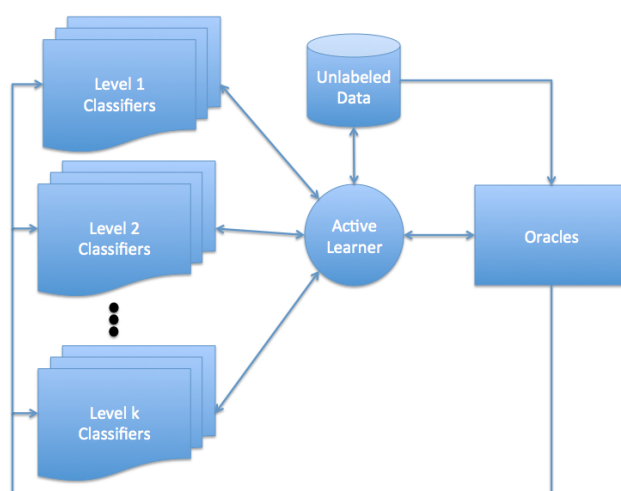


Figure 2.1: Diagram of HAL approach

2.3 Application to Dispatch Dataset

HAL was applied to a Dispatch dataset. This dataset contains 375,026 manually labeled hierarchical names across 1,384 newspaper articles [2]. This is a clear example where fine-grained labels have a higher cost since it is easier for a person to manually determine if the article pertains to an organization or not, rather than if it pertains to a railroad or a zoo, which would be sub labels of the organization root. The first analysis step was to determine that the F-0.5 measure is increased by using fine-grained classifiers. The results are shown in Figure 4. The highest F-0.5 measure for a given iteration of purchases of training instances is obtained by using the active learning approach with all fine-grained labels. The passive learning curves were generated by selecting batches of instances randomly rather than querying the oracle for a specific label type that offers that most gain in classifier accuracy. The active learning curves did take advantage of querying for specific labels in order to maximize gain in classifier accuracy. ... add other data sets.

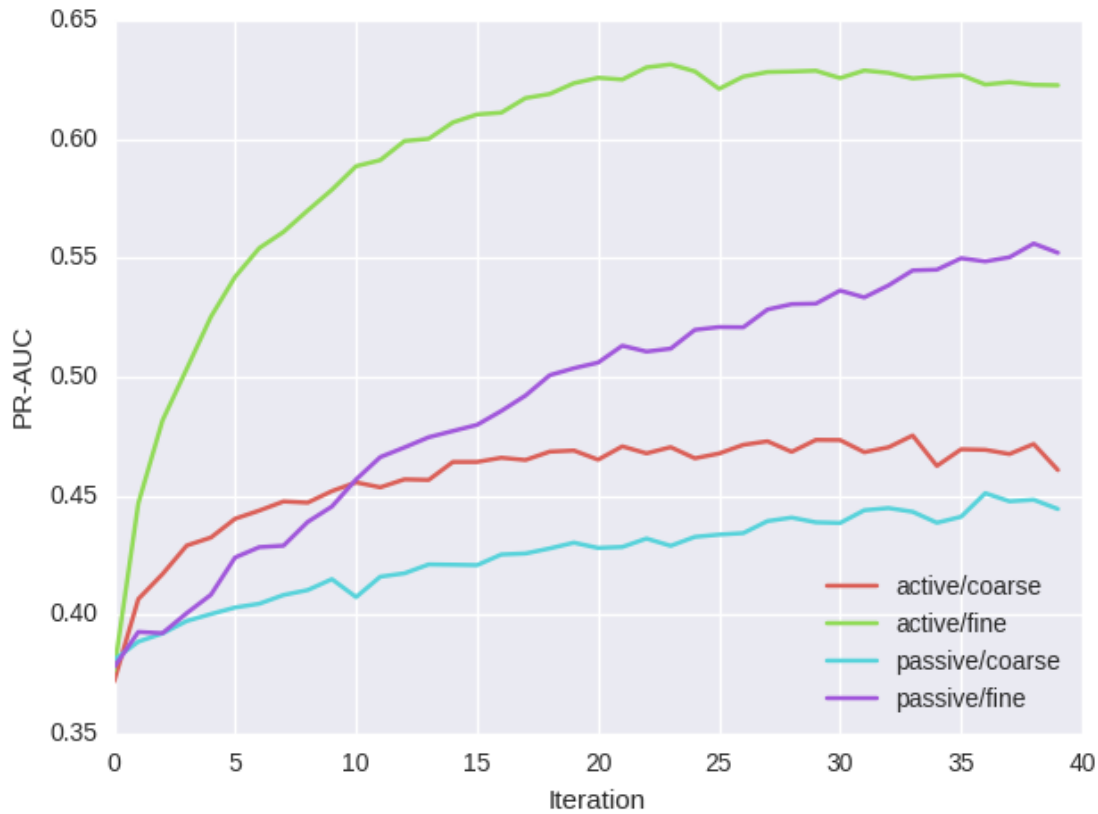


Figure 2.2: Application of HAL demonstrating the benefit of Actively selecting the type of labels to purchase for instances rather than randomly selecting labels to purchase, as in the Passive curves.

The next analysis step is to apply a given ratio of fine-grained vs coarse-grained labels to purchase at each batch request to the oracle. The results of varying the percentage of fine-grained labels purchased are shown in Figure 5. The figure shows that even a small amount of fine-grained labels purchased, that is, 20perc provides a significant increase in the F-0.5 measure for a given iteration. ... pr auc results. Add explanation of Bandit approach and results.

Chapter 3

Experimental Setup

3.1 Training and Testing Coarse Grain and Fine Grain Classifiers

The bioinformatics dataset is composed of 9 classes as shown in *Figure 1.1*. The coarse-level concept is whether or not the protein resides within the mitochondria. The negative case of not residing within the mitochondria is class 0. The positive case of residing within the mitochondria corresponds to any of the 8 target compartment classes, numbered 1 through 8. Since the negative case has no fine-grained labels, the fine-grained classifier is composed of separate classifiers for each of the fine-grained labels. The 8 fine-grained classifiers are trained such that only the instances of the class corresponding to that classifier's target compartment are marked as positive, all the others are treated as negative. The coarse-level classifier treats all fine-grained target compartment instances as members of a single positive class. For all classifiers the non mitochondrial instances are treated as negative or 0 labeled. The totals for each class type is shown in *Table 3.1a*. Throughout this experiment a 10 folds cross validation strategy is used, an example

partitioning is shown in *Table 3.1b*.

Table 3.1: This dataset contains 20098 instances total with 449 features each. An example partitioning is shown, some classes like 1 and 5 contain only 1-2 instances in a given test set. Note there is a heavy class imbalance with approx. 20 negative instances for each positive instance.

Classes	Count											
		Folds	All	0	1	2	3	4	5	6	7	8
0	19136	1	2010	1914	1	19	32	19	1	11	6	7
1	13	2	2010	1914	1	19	32	19	1	11	6	7
2	185	3	2010	1914	1	19	32	19	1	11	5	8
3	324	4	2010	1914	1	19	32	19	1	10	6	8
4	190	5	2010	1914	1	18	33	19	1	10	6	8
5	11	6	2010	1914	1	18	33	19	1	10	6	8
6	104	7	2010	1913	2	18	33	19	1	10	6	8
7	59	8	2010	1913	2	18	33	19	1	10	6	8
8	76	9	2009	1913	2	18	32	19	2	10	6	7
Tot All	20098	10	2009	1913	1	19	32	19	1	11	6	7
Tot Coarse	19136											
Tot Fine	962	Total	20098	19136	13	185	324	190	11	104	59	76
Features	449											

(b) Folds

(a) Classes

Each partition contains a representative portion of each class, the instances are randomly distributed between partitions. The train set is composed of joining 9 of the partitions together holding 1 fold out for the test set. An example of the totals for a Train and Test set is shown on *Table 3.2*.

Table 3.2: Example of totals for the Train and Test corresponding to when the first fold is held out to be the test set.

Train	All	0	1	2	3	4	5	6	7	8
Total	18088	17222	12	166	292	171	10	93	53	69
Test	All	0	1	2	3	4	5	6	7	8
Total	2010	1914	1	19	32	19	1	11	6	7

Because the experiment will involve running multiple rounds iteratively increasing

the number of instances on which the classifiers are trained and tested, a subset was used to tune the parameters of the classifiers. This allowed variations of the classifier parameters to be run rapidly and for the class weight parameter to be tuned for various round sizes. The reduced subset contains a randomly chosen group of approximately 1/5 of the negatives. The class totals and example partitioning for the reduced subset is shown in *Table 3.3*. After tuning parameters on the subset of data, parameter values are held fixed and experiments are re-run on a new partitioning containing the entire dataset.

Table 3.3: The subset of instances used for tuning classifier parameters contains approximately 1/5th and retains all positive instances.

Classes	Count	Folds	All	0	1	2	3	4	5	6	7	8
0	3827											
1	13	1	479	383	1	19	32	19	1	11	6	7
2	185	2	479	383	1	19	32	19	1	11	6	7
3	324	3	479	383	1	19	32	19	1	11	6	7
4	190	4	479	383	1	19	32	19	1	11	5	8
5	11	5	479	383	1	19	32	19	1	10	6	8
6	104	6	479	383	1	18	33	19	1	10	6	8
7	59	7	479	383	1	18	33	19	1	10	6	8
8	76	8	479	382	2	18	33	19	1	10	6	8
Tot All	4789	9	479	382	2	18	33	19	1	10	6	8
Tot Coarse	3827	10	478	382	2	18	32	19	2	10	6	7
Tot Fine	962											
Features	449	Total	4789	3827	13	185	324	190	11	104	59	76

(a) Classes Subset

(b) Folds Subset

Table 3.4: Example totals for the train and test set for the subset of data. The subset of data is used for the majority of the parameter search.

Train	All	0	1	2	3	4	5	6	7	8
Total	4310	3444	12	166	292	171	10	93	53	69
Test	All	0	1	2	3	4	5	6	7	8
Total	479	383	1	19	32	19	1	11	6	7

Throughout this project the python library sci-kit learn is used for the implementation of the classification, preprocessing, and evaluation algorithms [2]. The Support Vector Machine (SVM) supervised learning algorithm is used on the un-scaled subset of the data to obtain the base results shown in *Table 3.5*. The coarse and the fine algorithm performance is shown for each of the 10 folds along with the average performance across the 10 folds. Also the receiver operator characteristic and precision recall curves are calculated with fine instances weighted according to the number of instances in the test set divided by the number of positive instances in the test set which is a value of 4.99 for the data subset.

Table 3.5: SVM default results without parameter selection or preprocessing. Where Precision Recall area under the curve is (pr), Receiver Operator Characteristic area under the curve is (roc), accuracy is (acc), F1-measure is (f1).

coarse-pr	fine-pr	coarse-roc	fine-roc	coarse-acc	fine-acc	coarse-f1	fine-f1
0.807	0.796	0.779	0.768	0.816	0.802	0.214	0.021
0.848	0.822	0.828	0.790	0.825	0.804	0.263	0.041
0.846	0.821	0.810	0.765	0.818	0.802	0.243	0.021
0.860	0.832	0.826	0.775	0.831	0.802	0.319	0.021
0.859	0.829	0.828	0.783	0.833	0.804	0.298	0.041
0.796	0.763	0.748	0.715	0.816	0.806	0.214	0.061
0.838	0.825	0.797	0.792	0.818	0.800	0.243	0.020
0.836	0.816	0.803	0.770	0.823	0.800	0.309	0.020
0.863	0.845	0.833	0.805	0.829	0.797	0.305	0.000
0.844	0.806	0.806	0.758	0.836	0.807	0.339	0.061
avg 0.840	avg 0.815	avg 0.806	avg 0.772	avg 0.825	avg 0.802	avg 0.275	avg 0.031

Table 3.6: SVM default results confusion matrix. Where True Negatives is (tn), False Positives is (fp), False Negatives (fn), True Positives is (tp).

coarse-tn	fine-tn	coarse-fp	fine-fp	coarse-fn	fine-fn	coarse-tp	fine-tp
379	383	4	0	84	95	12	1
380	383	3	0	81	94	15	2
378	383	5	0	82	95	14	1
379	383	4	0	77	95	19	1
382	383	1	0	79	94	17	2
379	383	4	0	84	93	12	3
378	382	5	1	82	95	14	1
375	382	7	0	78	96	19	1
379	382	3	0	79	97	18	0
379	382	3	0	75	92	20	3
avg 378.8	avg 382.6	avg 3.9	avg 0.1	avg 80.1	avg 94.6	avg 16.0	avg 1.5

Table 3.7: SVM default condensed view of summary performance metrics, each value is the average of 10 folds.

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.840	0.806	0.825	0.275	(378.8 / 80.1)	(3.9 / 16.0)
fine	0.815	0.772	0.802	0.031	(382.6 / 94.6)	(0.1 / 1.5)

The primary metric used to make decisions between alternative parameter choices is the PR-AUC and ROC-AUC. The f-measure and accuracy metrics can be shown to be correlated to a chosen point on the ROC or PR curves. As shown in *Figure 4.2* on *page 36*, each point on the ROC curve has an associated chosen accuracy point, both the coarse and fine classifiers have similar sets of accuracy and f-measure points. The chosen threshold used to output the accuracy, f-measure and confusion matrices varies between the coarse and fine classifier, so at a first glance it appears as if fine out performs coarse in these metrics but an alternative threshold could be selected for the coarse classifier to obtain metrics matching the fine output. Alternatively, the PR-AUC and ROC-AUC compare the correctness of the entire ranking of the instances in the test set by the classifier, and thus

eliminate the need to consider the dynamic tuning of the threshold used by the classifier to output a given confusion matrix, accuracy, and f-measure score.

3.1.1 Varying SVM Scaling Methods

Different scaling methods were used to preprocess the data [2]. The standard scaling (std-scaler) strategy centers all features around zero and have variance in the same order, it outputs the features with a mean of zero and a unit variance. The minimum maximum scaling (minmax-scaler) strategy scales features between a minimum and maximum value, which is 0 and 1. The normalization scaling (norm-scaler) strategy scales individual samples to have a unit norm. Each preprocessing strategy is applied on the entire dataset before training and testing is performed. Preprocessing was performed with a radial basis function kernel.

Table 3.8: SVM minmax-scaler results.

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.881	0.855	0.799	0.000	(382.7 / 96.1)	(0.0 / 0.0)
fine	0.840	0.810	0.799	0.000	(382.7 / 96.1)	(0.0 / 0.0)

Table 3.9: SVM norm-scaler results.

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.801	0.791	0.799	0.000	(382.7 / 96.1)	(0.0 / 0.0)
fine	0.636	0.615	0.799	0.000	(382.7 / 96.1)	(0.0 / 0.0)

Table 3.10: SVM std-scaler results. This option is chosen.

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.912	0.882	0.881	0.631	(372.7 / 47.1)	(10.0 / 49.0)
fine	0.879	0.848	0.809	0.094	(382.7 / 91.3)	(0.0 / 4.8)

3.1.2 Varying SVM Kernels

Different kernel functions were used in the SVM classifier including: Radial Basis Function (RBF), Polynomial Degree 3 and 6 (Poly), Linear, and Sigmoid [2]. The chosen preprocessing strategy of std-scaler is used for these results. As parameter selection is elicited the choices from previous sections are used in any sections that follow.

Table 3.11: Linear kernel results.

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.867	0.841	0.853	0.599	(355.5 / 43.4)	(27.2 / 52.7)
fine	0.816	0.789	0.828	0.523	(351.1 / 50.8)	(31.6 / 45.3)

Table 3.12: Poly degree 3 kernel results.

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.816	0.817	0.807	0.169	(376.9 / 86.7)	(5.8 / 9.4)
fine	0.755	0.743	0.801	0.063	(380.3 / 92.9)	(2.3 / 3.2)

Table 3.13: Poly degree 6 kernel results.

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.659	0.637	0.797	0.037	(379.5 / 94.2)	(3.2 / 1.9)
fine	0.624	0.584	0.794	0.020	(379.0 / 95.1)	(3.7 / 1.0)

Table 3.14: Sigmoid kernel results.

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.703	0.693	0.773	0.405	(333.0 / 59.0)	(49.7 / 37.1)
fine	0.653	0.622	0.789	0.127	(370.3 / 88.7)	(12.4 / 7.4)

Table 3.15: RBF kernel results. This option is chosen.

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.912	0.882	0.881	0.630	(372.6 / 47.1)	(10.1 / 49.0)
fine	0.879	0.848	0.809	0.094	(382.7 / 91.3)	(0.0 / 4.8)

3.1.3 Varying SVM Feature Selection

I tried different feature selection percentages. The Select Percentile library was used from sci-kit learn [2]. This is a univariate feature selection strategy that ranks the features usability for classification according to a statistical measure, then keeps a certain percentage of the features. The 100% example is the option chosen in the previous section.

Table 3.16: SVM select percentile, keep 25% of features.

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.907	0.875	0.877	0.623	(370.7 / 47.1)	(12.0 / 49.0)
fine	0.854	0.823	0.806	0.068	(382.7 / 92.7)	(0.0 / 3.4)

Table 3.17: SVM select percentile, keep 50% of features.

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.913	0.885	0.879	0.632	(371.3 / 46.4)	(11.4 / 49.7)
fine	0.874	0.842	0.810	0.097	(382.7 / 91.2)	(0.0 / 4.9)

Table 3.18: SVM select percentile, keep 75% of features. This option is chosen.

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.913	0.883	0.878	0.622	(372.1 / 47.9)	(10.6 / 48.2)
fine	0.880	0.848	0.809	0.089	(382.7 / 91.6)	(0.0 / 4.5)

Note that leveraging the fine-grained labels did not improve classifier performance relative to the coarse classifier. An alternative classifier strategy Logistic Regression (Logit) is investigated.

3.1.4 Varying Logistic Regression Scaling

Tested out the same options for preprocessing scaling, that were varied for SVM.

Table 3.19: Logistic Regression - No scaling.

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.887	0.862	0.867	0.615	(364.1 / 45.0)	(18.6 / 51.1)
fine	0.854	0.837	0.833	0.395	(372.8 / 69.9)	(9.9 / 26.2)

Table 3.20: Logistic Regression standard scaling.

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.864	0.849	0.846	0.583	(353.8 / 44.8)	(28.7 / 51.3)
fine	0.833	0.816	0.831	0.471	(362.0 / 60.2)	(20.5 / 36.0)

Table 3.21: Logistic Regression normalization scaling.

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.790	0.761	0.799	0.000	(382.7 / 96.1)	(0.0 / 0.0)
fine	0.767	0.735	0.799	0.000	(382.7 / 96.1)	(0.0 / 0.0)

Table 3.22: Logistic Regression MinMax scaling. This option is chosen.

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.891	0.867	0.864	0.581	(368.6 / 50.9)	(14.1 / 45.2)
fine	0.888	0.862	0.812	0.130	(382.1 / 89.3)	(0.6 / 6.8)

3.1.5 Varying Logistic Regression Feature Selection

Tested out the same options for feature selection that were varied for SVM.

Table 3.23: Logistic Regression select percentile 25%.

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.872	0.848	0.849	0.497	(370.8 / 60.3)	(11.9 / 35.8)
fine	0.869	0.845	0.804	0.052	(382.2 / 93.5)	(0.5 / 2.6)

Table 3.24: Logistic Regression select percentile 50%.

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.875	0.849	0.849	0.497	(370.8 / 60.3)	(11.9 / 35.8)
fine	0.872	0.846	0.803	0.050	(382.2 / 93.6)	(0.5 / 2.5)

Table 3.25: Logistic Regression select percentile 75%.

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.871	0.847	0.848	0.493	(370.6 / 60.6)	(12.1 / 35.5)
fine	0.869	0.845	0.803	0.048	(382.0 / 93.7)	(0.7 / 2.4)

Table 3.26: Logistic Regression select percentile 100%. This option is chosen.

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.891	0.867	0.864	0.581	(368.6 / 50.9)	(14.1 / 45.2)
fine	0.888	0.862	0.812	0.130	(382.1 / 89.3)	(0.6 / 6.8)

3.1.6 Varying Logistic Regression Postive Class Weight and Cost

Since there is a class imbalance in the dataset, see *Table 3.1a* on *page 11*, class weight and cost parameter pairs are varied. The cost default value is 1.0, and the class weight default value is 1.0. The original value for weighting the fine training instance is the number of instances in the train set divided by the number of postive instances, this is 4.977. The negative instance train weight is always 1.0.

Table 3.27: Logit weight 4.977, cost 1.0

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.886	0.868	0.787	0.606	(298.7 / 17.9)	(84.0 / 78.2)
fine	0.885	0.862	0.857	0.587	(361.7 / 47.3)	(21.0 / 48.8)

Table 3.28: Logit weight 4.977, cost 0.1

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.880	0.861	0.755	0.579	(280.7 / 15.4)	(102.0 / 80.7)
fine	0.880	0.856	0.851	0.483	(374.2 / 62.7)	(8.5 / 33.4)

Table 3.29: Logit weight 4.977, cost 10.0

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.876	0.855	0.793	0.603	(304.6 / 21.1)	(78.1 / 75.0)
fine	0.866	0.842	0.835	0.583	(344.8 / 40.9)	(37.9 / 55.2)

Table 3.30: Logit weight 10.0, cost 1.0

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.883	0.865	0.690	0.536	(245.4 / 10.9)	(137.3 / 85.2)
fine	0.880	0.859	0.822	0.620	(324.2 / 26.7)	(58.5 / 69.4)

Table 3.31: Logit weight 10.0, cost 0.1

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.879	0.863	0.609	0.486	(203.6 / 7.9)	(179.1 / 88.2)
fine	0.881	0.859	0.834	0.621	(334.5 / 31.1)	(48.2 / 65.0)

Table 3.32: Logit weight 10.0, cost 10.0

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.871	0.851	0.723	0.554	(264.1 / 13.9)	(118.6 / 82.2)
fine	0.861	0.837	0.792	0.585	(309.3 / 26.2)	(73.4 / 69.9)

Table 3.33: Logit weight 7.5, cost 1.0

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.884	0.867	0.734	0.566	(268.8 / 13.5)	(113.9 / 82.6)
fine	0.882	0.861	0.846	0.624	(343.4 / 34.6)	(39.3 / 61.5)

Table 3.34: Logit weight 7.5, cost 0.1. This option is chosen due to showing advantage for the fine classifier compared to the coarse classifier.

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.880	0.862	0.668	0.517	(234.8 / 11.1)	(147.9 / 85.0)
fine	0.881	0.858	0.859	0.613	(357.3 / 42.3)	(25.4 / 53.8)

Table 3.35: Logit weight 7.5, cost 10.0

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.873	0.852	0.757	0.578	(283.2 / 16.7)	(99.5 / 79.4)
fine	0.863	0.839	0.810	0.588	(323.3 / 31.4)	(59.4 / 64.7)

3.1.7 Varying Logistic Regression Fine Class Weights

The weight for each of the separate fine classes is tuned by multiplying, the class weight of 7.5, determined in the previous section by a fixed ratio. A weight ratio of 1.0 would output a fine class weight of 7.5. A weight ratio of 0.5 would output a fine class weight of 3.75. Subsections showing the tuning results for each of the 8 fine-grained classes follow. The confusion matrices and output metrics for the individual fine class are shown in order to demonstrate how well the classifier is learning that fine-grained class. These metrics are the average of 10 folds. The coarse classifier output is not shown as it will not vary or be dependent upon the fine class weight tuning.

3.1.7.1 Tune Fine Class 1 Weights

Table 3.36: Logit Class 1 weight ratio 1.0

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
fine	0.881	0.858	0.859	0.613	(357.3 / 42.3)	(25.4 / 53.8)
trainCls-1	0.995	0.999	0.998	0.477	(4297.7 / 7.7)	(0.8 / 4.0)
testCls-1	0.722	0.996	0.997	0.100	(477.4 / 1.2)	(0.1 / 0.1)

Table 3.37: Logit Class 1 weight ratio 0.5

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
fine	0.880	0.856	0.859	0.613	(357.4 / 42.3)	(25.3 / 53.8)
trainCls-1	0.994	0.998	0.997	0.142	(4298.5 / 10.8)	(0.0 / 0.9)
testCls-1	0.696	0.995	0.997	0.000	(477.5 / 1.3)	(0.0 / 0.0)

Table 3.38: Logit Class 1 weight ratio 3.0. This option is chosen.

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
fine	0.882	0.860	0.859	0.617	(357.1 / 41.7)	(25.6 / 54.4)
trainCls-1	0.995	1.000	0.999	0.854	(4295.8 / 1.0)	(2.7 / 10.7)
testCls-1	0.722	0.997	0.998	0.400	(477.1 / 0.7)	(0.4 / 0.6)

Table 3.39: Logit Class 1 weight ratio 5.0

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
fine	0.881	0.859	0.860	0.618	(357.0 / 41.5)	(25.7 / 54.6)
trainCls-1	0.995	1.000	0.999	0.850	(4294.3 / 0.0)	(4.2 / 11.7)
testCls-1	0.722	0.997	0.998	0.513	(476.9 / 0.5)	(0.6 / 0.8)

3.1.7.2 Tune Fine Class 2 Weights

Table 3.40: Logit Class 2 weight ratio 1.0. This option is chosen.

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
fine	0.882	0.860	0.859	0.617	(357.1 / 41.7)	(25.6 / 54.4)
trainCls-2	0.800	0.804	0.952	0.200	(4076.9 / 140.5)	(66.8 / 26.0)
testCls-2	0.655	0.689	0.944	0.081	(450.7 / 17.3)	(9.6 / 1.2)

Table 3.41: Logit Class 2 weight ratio 0.5

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
fine	0.882	0.857	0.862	0.618	(359.1 / 42.5)	(23.6 / 53.6)
trainCls-2	0.785	0.787	0.961	0.052	(4139.4 / 161.9)	(4.3 / 4.6)
testCls-2	0.656	0.694	0.960	0.009	(459.4 / 18.4)	(0.9 / 0.1)

Table 3.42: Logit Class 2 weight ratio 1.5

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
fine	0.877	0.857	0.855	0.620	(352.5 / 39.3)	(30.2 / 56.8)
trainCls-2	0.806	0.814	0.924	0.263	(3924.1 / 108.1)	(219.6 / 58.4)
testCls-2	0.652	0.684	0.914	0.123	(434.8 / 15.6)	(25.5 / 2.9)

3.1.7.3 Tune Fine Class 3 Weights

Table 3.43: Logit Class 3 weight ratio 1.0. This option is chosen.

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
fine	0.882	0.860	0.859	0.617	(357.1 / 41.7)	(25.6 / 54.4)
trainCls-3	0.846	0.852	0.882	0.401	(3628.6 / 120.7)	(390.0 / 170.9)
testCls-3	0.795	0.803	0.873	0.360	(401.2 / 15.4)	(45.2 / 17.0)

Table 3.44: Logit Class 3 weight ratio 0.5

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
fine	0.870	0.852	0.839	0.445	(370.9 / 65.1)	(11.8 / 31.0)
trainCls-3	0.838	0.838	0.929	0.288	(3942.0 / 229.7)	(76.6 / 61.9)
testCls-3	0.792	0.798	0.925	0.246	(437.2 / 26.5)	(9.2 / 5.9)

Table 3.45: Logit Class 3 weight ratio 1.5

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
fine	0.879	0.855	0.832	0.626	(331.2 / 28.9)	(51.5 / 67.2)
trainCls-3	0.849	0.859	0.813	0.351	(3288.4 / 74.5)	(730.2 / 217.1)
testCls-3	0.795	0.805	0.804	0.318	(363.3 / 10.6)	(83.1 / 21.8)

3.1.7.4 Tune Fine Class 4 Weights

Table 3.46: Logit Class 4 weight ratio 1.0

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
fine	0.882	0.860	0.859	0.617	(357.1 / 41.7)	(25.6 / 54.4)
trainCls-4	0.937	0.942	0.960	0.531	(4038.6 / 72.9)	(100.6 / 98.1)
testCls-4	0.882	0.902	0.952	0.433	(447.1 / 10.2)	(12.7 / 8.8)

Table 3.47: Logit Class 4 weight ratio 0.5

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
fine	0.875	0.852	0.855	0.590	(359.2 / 45.9)	(23.5 / 50.2)
trainCls-4	0.928	0.932	0.965	0.397	(4108.1 / 120.9)	(31.1 / 50.1)
testCls-4	0.878	0.898	0.962	0.320	(456.0 / 14.6)	(3.8 / 4.4)

Table 3.48: Logit Class 4 weight ratio 1.5. This option is chosen.

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
fine	0.883	0.861	0.856	0.624	(352.4 / 38.8)	(30.3 / 57.3)
trainCls-4	0.941	0.947	0.936	0.462	(3918.1 / 53.2)	(221.1 / 117.8)
testCls-4	0.886	0.903	0.926	0.382	(432.5 / 8.0)	(27.3 / 11.0)

Table 3.49: Logit Class 4 weight ratio 2.0

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
fine	0.880	0.859	0.853	0.627	(348.9 / 36.7)	(33.8 / 59.4)
trainCls-4	0.943	0.950	0.917	0.429	(3817.7 / 36.5)	(321.5 / 134.5)
testCls-4	0.886	0.903	0.906	0.352	(421.8 / 6.8)	(38.0 / 12.2)

3.1.7.5 Tune Fine Class 5 Weights

Table 3.50: Logit Class 5 weight ratio 1.0

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
fine	0.883	0.861	0.856	0.624	(352.4 / 38.8)	(30.3 / 57.3)
trainCls-5	0.940	0.941	0.998	0.000	(4300.2 / 10.0)	(0.0 / 0.0)
testCls-5	0.393	0.681	0.998	0.000	(477.8 / 1.0)	(0.0 / 0.0)

Table 3.51: Logit Class 5 weight ratio 0.5

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
fine	0.883	0.861	0.856	0.624	(352.4 / 38.8)	(30.3 / 57.3)
trainCls-5	0.911	0.912	0.998	0.000	(4300.2 / 10.0)	(0.0 / 0.0)
testCls-5	0.389	0.672	0.998	0.000	(477.8 / 1.0)	(0.0 / 0.0)

Table 3.52: Logit Class 5 weight ratio 1.5

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
fine	0.883	0.861	0.856	0.624	(352.4 / 38.8)	(30.3 / 57.3)
trainCls-5	0.957	0.958	0.998	0.000	(4300.2 / 10.0)	(0.0 / 0.0)
testCls-5	0.396	0.687	0.998	0.000	(477.8 / 1.0)	(0.0 / 0.0)

Table 3.53: Logit Class 5 weight ratio 5.0

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
fine	0.883	0.861	0.856	0.624	(352.4 / 38.8)	(30.3 / 57.3)
trainCls-5	0.990	0.990	0.998	0.374	(4299.8 / 7.6)	(0.4 / 2.4)
testCls-5	0.401	0.694	0.998	0.000	(477.7 / 1.0)	(0.1 / 0.0)

Table 3.54: Logit Class 5 weight ratio 10.0. This option is chosen.

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
fine	0.883	0.861	0.855	0.623	(352.1 / 38.8)	(30.6 / 57.3)
trainCls-5	0.996	0.997	0.998	0.609	(4293.4 / 2.7)	(6.8 / 7.3)
testCls-5	0.402	0.696	0.996	0.000	(476.8 / 1.0)	(1.0 / 0.0)

Table 3.55: LogitCls5-Wt20

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
fine	0.881	0.860	0.854	0.622	(351.6 / 38.7)	(31.1 / 57.4)
trainCls-5	0.998	0.998	0.992	0.355	(4265.8 / 0.5)	(34.4 / 9.5)
testCls-5	0.381	0.616	0.989	0.000	(473.5 / 1.0)	(4.3 / 0.0)

3.1.7.6 Tune Fine Class 6 Weights

Table 3.56: Logit Class 6 weight ratio 1.0

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
fine	0.883	0.861	0.855	0.623	(352.1 / 38.8)	(30.6 / 57.3)
trainCls-6	0.945	0.962	0.976	0.303	(4182.5 / 70.8)	(34.1 / 22.8)
testCls-6	0.892	0.936	0.972	0.191	(463.9 / 8.8)	(4.5 / 1.6)

Table 3.57: Logit Class 6 weight ratio 0.5

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
fine	0.882	0.860	0.855	0.622	(352.1 / 38.9)	(30.6 / 57.2)
trainCls-6	0.938	0.956	0.978	0.006	(4216.5 / 93.3)	(0.1 / 0.3)
testCls-6	0.881	0.928	0.978	0.000	(468.3 / 10.4)	(0.1 / 0.0)

Table 3.58: Logit Class 6 weight ratio 2.0. This option is chosen.

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
fine	0.884	0.861	0.855	0.627	(350.8 / 37.6)	(31.9 / 58.5)
trainCls-6	0.950	0.967	0.949	0.380	(4023.8 / 26.4)	(192.8 / 67.2)
testCls-6	0.897	0.939	0.945	0.292	(447.0 / 5.0)	(21.4 / 5.4)

Table 3.59: Logit Class 6 weight ratio 3.0

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
fine	0.884	0.860	0.850	0.629	(346.6 / 35.5)	(36.1 / 60.6)
trainCls-6	0.952	0.969	0.921	0.335	(3885.8 / 8.3)	(330.8 / 85.3)
testCls-6	0.898	0.940	0.915	0.281	(430.5 / 2.6)	(37.9 / 7.8)

3.1.7.7 Tune Fine Class 7 Weights

Table 3.60: Logit Class 7 weight ratio 1.0

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
fine	0.884	0.862	0.855	0.628	(350.8 / 37.5)	(31.9 / 58.6)
trainCls-7	0.892	0.893	0.988	0.000	(4257.1 / 53.1)	(0.0 / 0.0)
testCls-7	0.648	0.720	0.988	0.000	(472.9 / 5.9)	(0.0 / 0.0)

Table 3.61: Logit Class 7 weight ratio 0.5

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
fine	0.884	0.861	0.855	0.627	(350.8 / 37.6)	(31.9 / 58.5)
trainCls-7	0.859	0.857	0.988	0.000	(4257.1 / 53.1)	(0.0 / 0.0)
testCls-7	0.636	0.708	0.988	0.000	(472.9 / 5.9)	(0.0 / 0.0)

Table 3.62: Logit Class 7 weight ratio 3.0. This option is chosen.

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
fine	0.885	0.863	0.855	0.632	(350.1 / 36.7)	(32.6 / 59.4)
trainCls-7	0.930	0.939	0.986	0.344	(4234.1 / 37.3)	(23.0 / 15.8)
testCls-7	0.667	0.739	0.983	0.105	(470.1 / 5.4)	(2.8 / 0.5)

Table 3.63: Logit Class 7 weight ratio 5.0

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
fine	0.883	0.860	0.847	0.628	(344.0 / 34.4)	(38.7 / 61.7)
trainCls-7	0.941	0.953	0.956	0.265	(4086.0 / 18.9)	(171.1 / 34.2)
testCls-7	0.674	0.744	0.948	0.099	(452.3 / 4.5)	(20.6 / 1.4)

3.1.7.8 Tune Fine Class 8 Weights

Table 3.64: Logit Class 8 weight ratio 1.0. This option is chosen.

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
fine	0.886	0.864	0.855	0.632	(350.1 / 36.6)	(32.6 / 59.5)
trainCls-8	0.967	0.978	0.982	0.453	(4199.8 / 36.1)	(42.0 / 32.3)
testCls-8	0.896	0.952	0.978	0.308	(465.7 / 5.2)	(5.5 / 2.4)

Table 3.65: Logit Class 8 weight ratio 0.5

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
fine	0.885	0.862	0.855	0.630	(350.4 / 37.0)	(32.3 / 59.1)
trainCls-8	0.961	0.972	0.984	0.253	(4229.6 / 56.7)	(12.2 / 11.7)
testCls-8	0.893	0.952	0.982	0.135	(469.5 / 6.8)	(1.7 / 0.8)

Table 3.66: Logit Class 8 weight ratio 1.5

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
fine	0.886	0.864	0.855	0.632	(349.5 / 36.4)	(33.2 / 59.7)
trainCls-8	0.967	0.980	0.978	0.478	(4169.7 / 24.3)	(72.1 / 44.1)
testCls-8	0.892	0.947	0.973	0.376	(462.2 / 3.9)	(9.0 / 3.7)

3.1.8 Varying Logistic Regression Tolerance

There is an additional Logistic parameter for determining a tolerance for the stopping criteria. The default tolerance is 0.0001.

Table 3.67: Logit results after fine tuning, effectively had a tolerance of 0.0001

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.880	0.863	0.668	0.517	(234.8 / 11.1)	(147.9 / 85.0)
fine	0.886	0.864	0.855	0.632	(350.1 / 36.6)	(32.6 / 59.5)

Table 3.68: Logit Tolerance 0.0001, notice that the fine pr and roc decreased by 0.001, and that the coarse roc decreased by 0.001 upon rerunning, there is some statistical variation in these metrics.

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.880	0.862	0.668	0.518	(234.9 / 11.1)	(147.8 / 85.0)
fine	0.885	0.863	0.855	0.632	(350.1 / 36.7)	(32.6 / 59.4)

Table 3.69: Logit Tolerance 0.0001. This option is chosen.

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.880	0.863	0.668	0.517	(234.7 / 11.1)	(148.0 / 85.0)
fine	0.886	0.864	0.855	0.632	(350.1 / 36.6)	(32.6 / 59.5)

Table 3.70: Logit Tolerance 0.000001

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.880	0.862	0.668	0.517	(234.8 / 11.1)	(147.9 / 85.0)
fine	0.885	0.863	0.855	0.632	(350.1 / 36.7)	(32.6 / 59.4)

3.1.9 Varying Sample Weight On Test Set and Dropping Intermediate ROC Curve Values

The sample weight, as stated previously, weights fine instances in the ROC and PR curves by the ratio of total number of instances in the test set divided by the total number of positives in the test set. This weighting is performed identically on the coarse and fine classifier. The ROC curve library has a parameter to determine whether or not to drop some suboptimal thresholds which do not appear on a plotted ROC curve [2]. The default setting is to drop intermediate values True, which has the counterintuitive result of a roc curve having on the order of 150 points even though 497 points are passed to the roc curve library method. If drop intermediate values is set to false then the full 497 points are returned in the calculated roc curve.

Table 3.71: Logit sample weights, drop intermediate values True. The default option is chosen.

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.880	0.862	0.668	0.517	(234.8 / 11.1)	(147.9 / 85.0)
fine	0.885	0.863	0.855	0.632	(350.1 / 36.7)	(32.6 / 59.4)

Table 3.72: Logit no sample weights, drop intermediate values True

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.649	0.862	0.668	0.517	(234.8 / 11.1)	(147.9 / 85.0)
fine	0.663	0.863	0.855	0.632	(350.1 / 36.7)	(32.6 / 59.4)

Table 3.73: Logit sample weights, drop intermediate values False

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.880	0.862	0.668	0.517	(234.8 / 11.1)	(147.9 / 85.0)
fine	0.885	0.863	0.855	0.632	(350.1 / 36.7)	(32.6 / 59.4)

Table 3.74: Logit no sample weights, drop intermediate values False

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.649	0.862	0.668	0.517	(234.8 / 11.1)	(147.9 / 85.0)
fine	0.663	0.863	0.855	0.632	(350.1 / 36.7)	(32.6 / 59.4)

3.1.10 Varying Logistic Regression Positive Class Weight For Full Dataset

The fine class weight for the subset of data is determined be to 7.5, this value should change and be linearly dependent upon the number of instances in the training set. The weight for the fine class is tuned using all of the data, the original value is the total number of instances in the train set divided by the total number of positives in the train

set, which evaluates to 20.887. The previously determined fine class ratios are used in this analysis. The value selected is 23, this value along with 7.5 and the original values of 20.887 and 4.977 for a line with two points that define a function to map a weight original input to a new tuned weight output for all training set sizes.

Table 3.75: Logit entire dataset, weight 20.887

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.867	0.868	0.803	0.280	(1537.6 / 19.2)	(376.0 / 76.9)
fine	0.871	0.868	0.919	0.404	(1792.3 / 41.0)	(121.2 / 55.1)

Table 3.76: Logit entire dataset, weight 23.0. This option is chosen.

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.870	0.871	0.787	0.268	(1503.2 / 17.8)	(410.4 / 78.3)
fine	0.875	0.871	0.913	0.403	(1776.5 / 37.3)	(137.1 / 58.8)

Table 3.77: Logit entire dataset, weight 25.0.

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.867	0.868	0.772	0.256	(1473.0 / 17.3)	(440.6 / 78.8)
fine	0.871	0.868	0.905	0.389	(1758.8 / 35.6)	(154.8 / 60.6)

3.1.11 Varying SVM Gamma

After the Logit classifier is tuned with class weights, the SVM is ran again with the class weights determined by the Logit classifier and a slight advantage for the fine-grained classifier is demonstrated with the SVM as well. The SVM parameters for the Radial Basis Function kernel of Cost and Gamma are varied. The Cost is related to a penalty parameter for the error term and Gamma is the kernel coefficient and determines the relative size of the kernel. The default gamma setting is 0.002967 or $(1/\text{num-features})$

or (1/337). Default cost is actually 1.0, and the default class weight is balanced which weights each class by the number of instances it has in the train set, the same fine class weights used in the LogReg classifier are used in the SVM classifier instead of the SVM's default balanced option.

Table 3.78: SVM Cost 1.0 Gamma 0.0029674

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.901	0.874	0.846	0.651	(336.0 / 27.2)	(46.7 / 68.9)
fine	0.896	0.865	0.871	0.598	(371.1 / 50.1)	(11.6 / 46.0)

Table 3.79: SVM Cost 2.0 Gamma 0.0029674

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.903	0.873	0.866	0.672	(348.9 / 30.4)	(33.8 / 65.7)
fine	0.890	0.857	0.865	0.554	(373.8 / 55.8)	(8.9 / 40.3)

Table 3.80: SVM Cost 0.1 Gamma 0.0029674

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.892	0.869	0.664	0.518	(231.5 / 9.8)	(151.2 / 86.3)
fine	0.899	0.870	0.868	0.623	(363.5 / 43.8)	(19.2 / 52.3)

Table 3.81: SVM Cost 0.05 Gamma 0.0029674

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.883	0.860	0.591	0.474	(194.9 / 8.0)	(187.8 / 88.1)
fine	0.884	0.853	0.858	0.544	(370.1 / 55.5)	(12.6 / 40.6)

Table 3.82: SVM Cost 0.15 Gamma 0.0029674. This cost option is chosen.

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.896	0.873	0.714	0.553	(257.5 / 11.6)	(125.2 / 84.5)
fine	0.902	0.874	0.871	0.640	(362.1 / 41.1)	(20.6 / 55.0)

Table 3.83: SVM Cost 0.2 Gamma 0.0029674.

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.899	0.875	0.755	0.584	(279.6 / 14.0)	(103.1 / 82.1)
fine	0.903	0.875	0.871	0.640	(362.1 / 41.2)	(20.6 / 54.9)

3.1.12 Varying SVM Cost

Table 3.84: SVM Cost 0.15 Gamma 0.002. This option for Cost and Gamma is chosen.

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.894	0.871	0.706	0.545	(253.6 / 11.7)	(129.1 / 84.4)
fine	0.906	0.877	0.869	0.646	(358.3 / 38.5)	(24.4 / 57.6)

Table 3.85: SVM Cost 0.15 Gamma 0.001

title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.883	0.864	0.664	0.516	(232.1 / 10.3)	(150.6 / 85.8)
fine	0.900	0.872	0.868	0.641	(358.5 / 39.2)	(24.2 / 56.9)

Chapter 4

Results and Analysis

4.1 SVM and Logit Classifier Performance

Both the SVM and the Logit classifiers show a slight advantage for the Fine classifier over the Coarse classifier in terms of the PR-AUC metric. The ROC-AUC metric is close to identical between fine and coarse for both classifiers, a slight advantage of 0.002 exists for the Fine classifier in the SVM classifier.

Table 4.1: Logit entire dataset results after parameter tuning

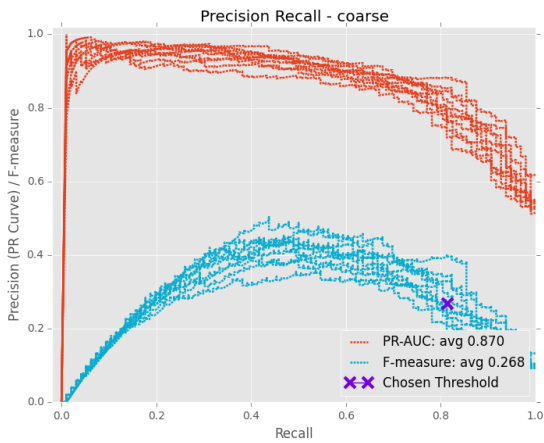
title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.870	0.871	0.787	0.268	(1503.2 / 17.8)	(410.4 / 78.3)
fine	0.875	0.871	0.913	0.403	(1776.5 / 37.3)	(137.1 / 58.8)

Table 4.2: SVM entire dataset results after parameter tuning

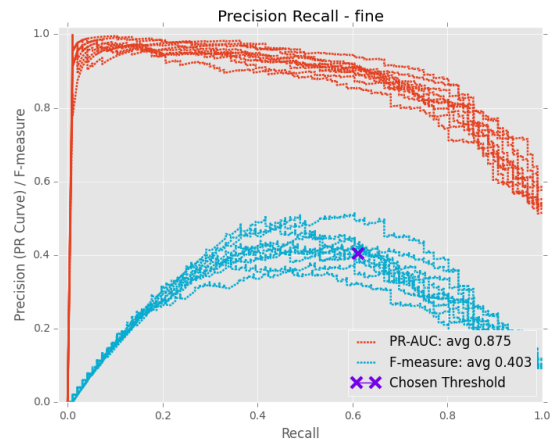
title	pr	roc	acc	f1	conf (tn/fn)	conf (fp/tp)
coarse	0.892	0.880	0.866	0.347	(1669.5 / 24.8)	(244.1 / 71.3)
fine	0.898	0.882	0.942	0.485	(1839.0 / 41.5)	(74.6 / 54.6)

The coarse classifier in both the Logit and SVM classifier has a greater amount of

false positives at the default threshold. A further examination of these values is shown in *Figures 4.1-4.2* and *Figures 4.3-4.4*. The figures plot the PR and the ROC curves for each of the 10 folds. Each point on the PR and ROC curve has a corresponding F-measure or accuracy value, these values are plotted on the graphs as a blue line. The graphs demonstrate that the coarse and fine classifiers have close to equivalent average AUC, on the order of 0.007 max difference between Fine and Coarse. At the default threshold the Fine appears to outperform Coarse for accuracy and F-measure metrics, but inspection of the plots shows that a coarse threshold can be chosen to match the fine output for both accuracy and F-measure. The PR-AUC does show a slight advantage for Fine, which warrants application of the HAL algorithm and Active over labeling approach on this dataset.

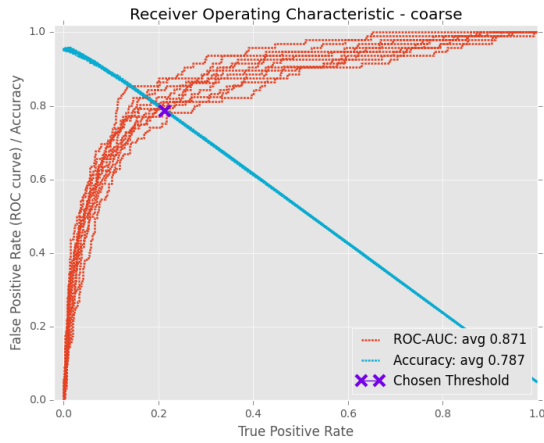


(a) Log Reg Pr Curves - Coarse

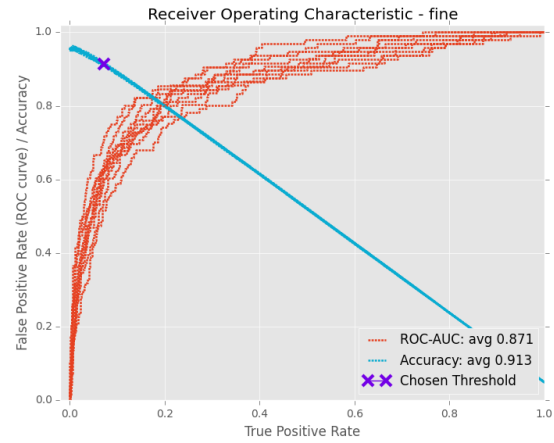


(b) Log Reg Pr Curves - Fine

Figure 4.1: The Fine default threshold occurs at a point on the PR curve associated with a higher F-measure score compared to the Coarse curves.

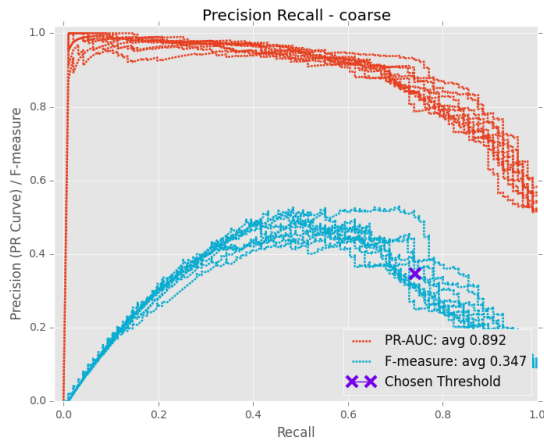


(a) Log Reg ROC Curves - coarse

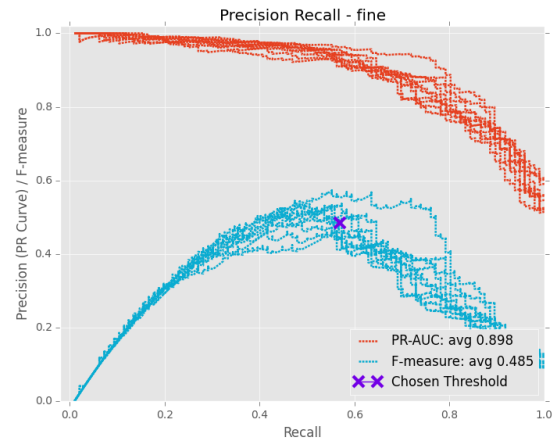


(b) Log Reg ROC Curves - fine

Figure 4.2: Fine has a higher accuracy than coarse at the default threshold for the Logit classifier.

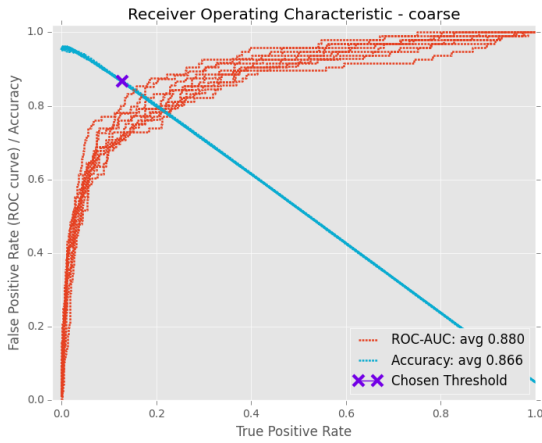


(a) SVM Pr Curves - Coarse

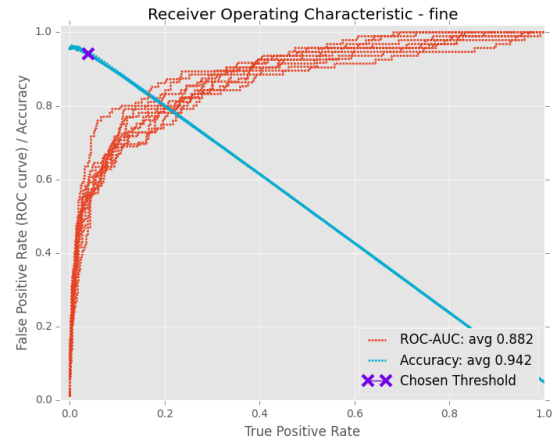


(b) SVM Pr Curves - Fine

Figure 4.3: SVM results for PR curves and F-measure have Coarse and Fine picking different parts of the curves for their respective thresholds. This results in a slight advantage for Fine at the default threshold, similar to the results for the Logit classifier.



(a) SVM ROC Curves - Coarse



(b) SVM ROC Curves - Fine

Figure 4.4: SVM accuracy results are similar between Coarse and Fine.

4.2 Active vs Passive curves

The plots in *Figures 4.5-4.9* were obtained with a round batch size of 100 and a starter set of 1040 instances out of the total 20098 instances. The plots are the average of 10 folds, for each fold a test set of 2010 instances is used. The test set remains constant throughout the rounds and contains a representative proportion of each of the classes. The starter set is chosen out of the remaining 18088 and it also contains representatives from each class in proportion to that class's prominence in the dataset. The 17048 non-test set, non-starter set instances are added to the training set in batches of 100. This results in total of 171 rounds, 170 batch selecting rounds and 1 starter set round. The Passive approach selects 100 random instances and adds them to the train set. The Active approach runs the classifier on the eligible instances, orders them by their uncertainty and adds the 100 most uncertain instances to the train set. Coarse and fine classifiers share the same starter set. During each round, Coarse and Fine classifiers are trained on their corresponding sets, which are independent of one another, metrics are outputted on the held out test set which is the same for both Coarse and Fine.

4.2.1 Plots for Logistic Regression Active vs Passive curves

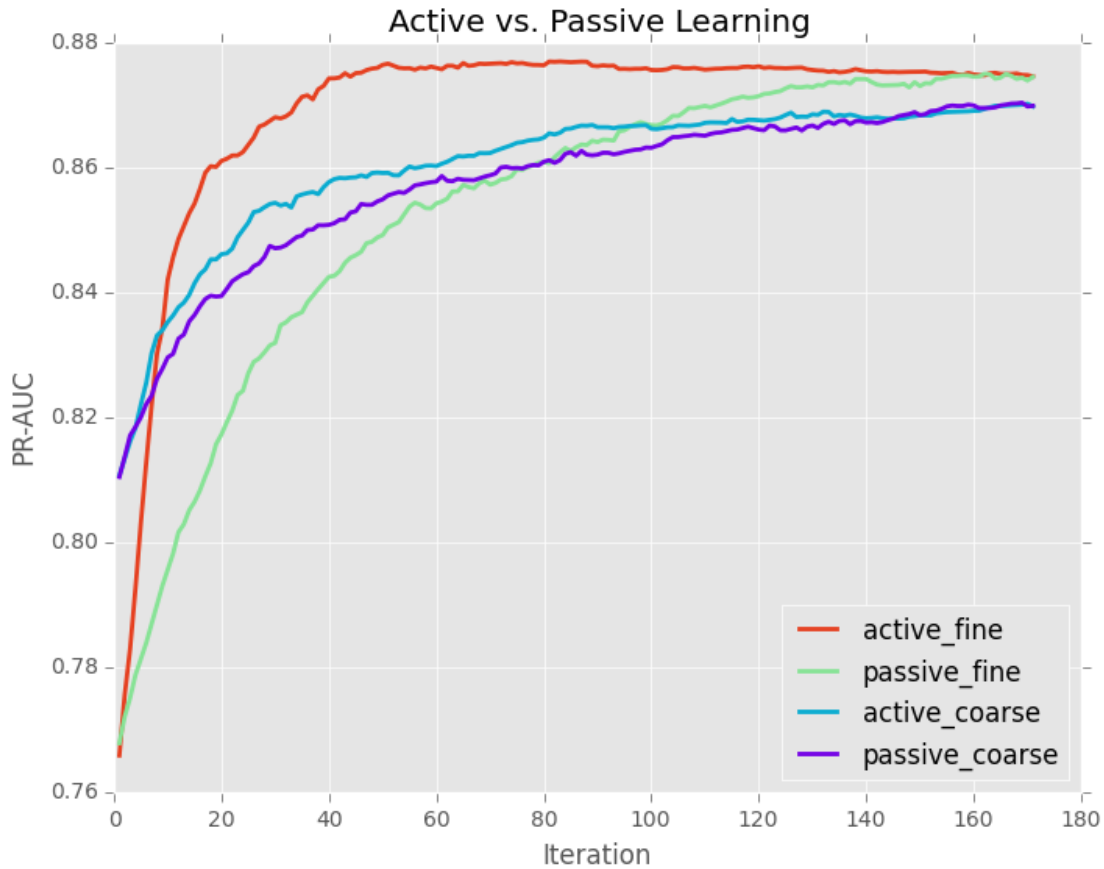


Figure 4.5: The PR-AUC curves for rounds with the Logistic Regression classifier conforms to expectations, with Active Fine having the highest performance, and Active outperforming Passive for both Coarse and Fine classifier types.

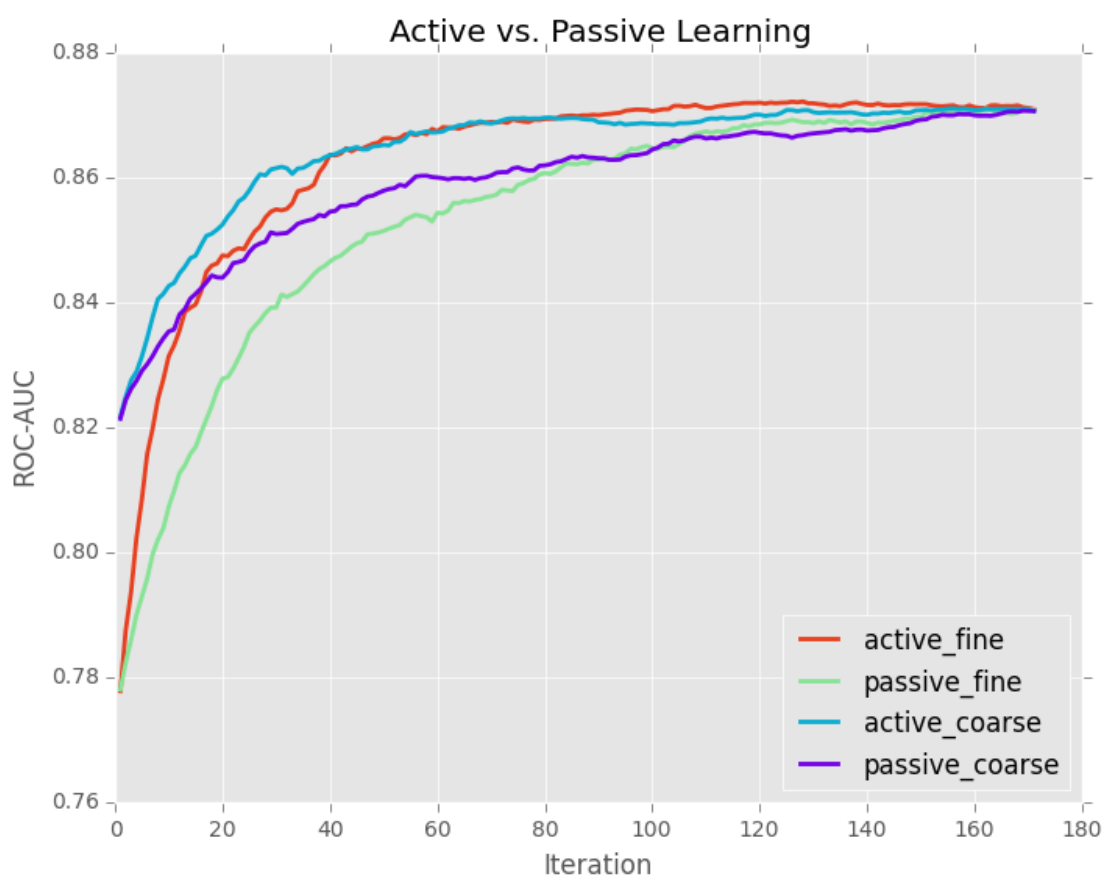
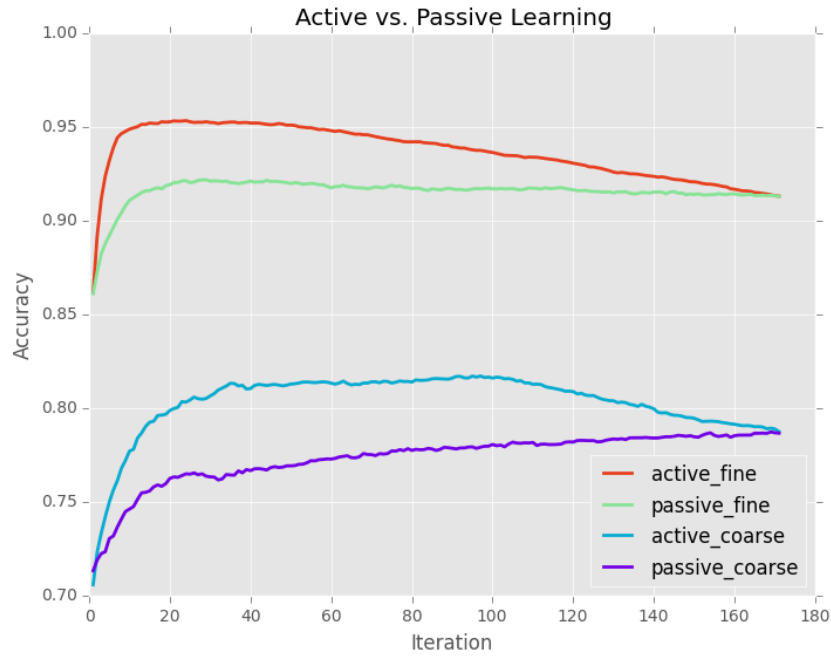
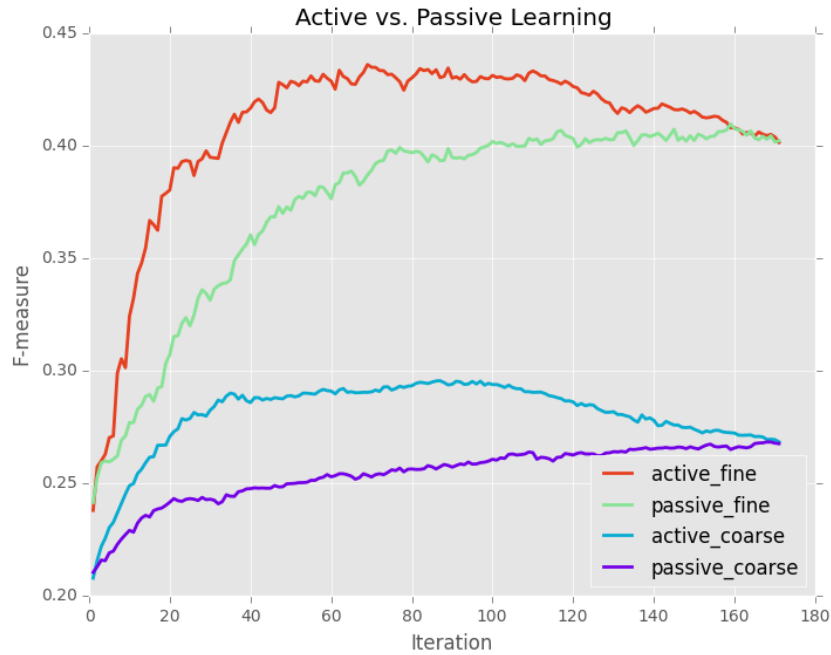


Figure 4.6: The ROC-AUC curves for rounds with the Logistic Regression classifier. The active curves beat out the passive curves for both Coarse and Fine. Note that Active Fine ROC curve doesn't converge to the Active Coarse ROC curve until round 40. This is contrasted to a dominance of the Active Fine PR curve after round 10.



(a) Logit accuracy



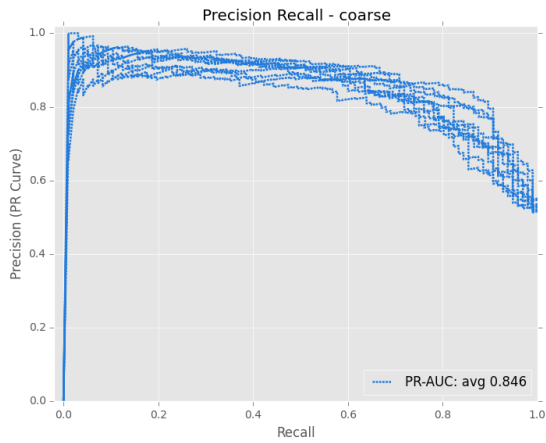
(b) Logit F-measure

Figure 4.7: The accuracy of the classifiers stays at roughly the same rate throughout the rounds; this is due to an effective weighting scheme. Both curves show a dominance of Fine over Coarse and Active over Passive.

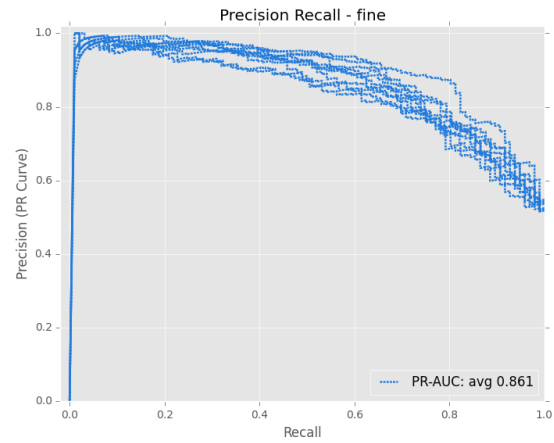
Note that the Active Fine PR-AUC curve surpasses Active Coarse after round 10 while the Active Fine ROC-AUC curve is still well below the Active Coarse at that round. These curves are shown in *Figures 4.8- 4.9*. This is counter-intuitive, because according to a proof in Davis [15] “For a fixed number of positive and negative examples, one curve dominates a second curve in ROC space if and only if the first dominates the second in Precision-Recall space”. The theorem uses the following definition of dominance: that every value in the first curve is above the corollary value in second curve. The correlation between PR and ROC curves is that Recall in the PR curve is equivalent to the True Positive Rate in the ROC curve. The average PR-AUC concept is different than that of a plot of PR curves for a round, but if all of the PR curves for Fine dominate the curves for Coarse then we would expect all of the ROC curves for Fine to dominate the ROC curves for coarse and both the ROC-AUC and PR-AUC averages for Fine to be greater than that for Coarse. However it is shown in *Figure 4.8* that the PR curves for Fine do not completely dominate the PR curves for coarse, and similarly for the ROC curves in *Figure 4.9*. Active Fine PR-AUC curve does not satisfy the theorem’s definition of dominance, since each individual ROC and PR curve contains intersection points between Coarse and Fine. Thus given that the average PR-AUC for Fine is great at round 20 than average Coarse PR-AUC, this relationship is not expected to hold between the average ROC-AUC curves.

According to Davis [15], a large change in the number of false positives can still yield only a small change in the number of false positives and thus not affect ROC curve performance. However, Davis states, “Precision, on the other hand, by comparing false positives to true positives rather than true negatives, captures the effect of the large number (incorrectly classified) of negative examples on the algorithm’s performance” [15]. Since our dataset demonstrates a heavy class imbalance with a roughly 1:20 ratio of Positive to Negative instances, the algorithm’s ability to classify negative instances

should be taken into account when considering overall classifier performance. The PR curve's ability to capture and have a greater sensitivity to the increased number of False Positives, reveals the advantage that the Fine classifier has over the Coarse classifier. This justifies purchasing Fine grained labels over Coarse grained labels to improve classifier performance.

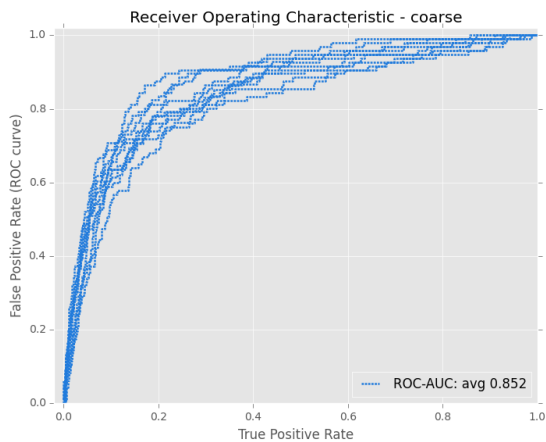


(a) Coarse PR curves at Round 20

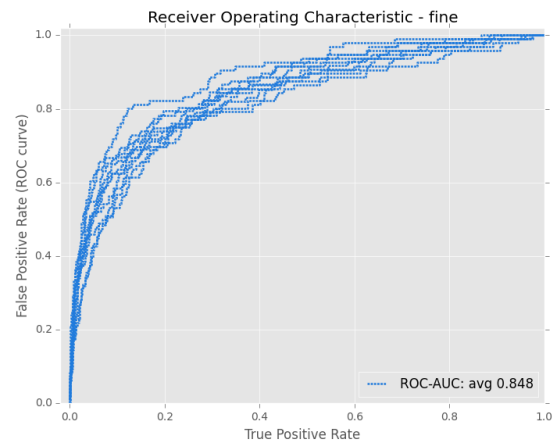


(b) Fine PR curves at Round 20

Figure 4.8: PR curves for each fold at Round 20



(a) Coarse ROC curves at Round 20



(b) Fine ROC curves at Round 20

Figure 4.9: ROC curves for each fold at Round 20

4.2.2 Plots for SVM Active vs Passive curves

The SVM Active vs Passive experiment is performed with the same methodology as the previous section detailed with the exception that a SVM classifier is substituted for the Logit classifier. Due to the greater advantage of average PR-AUC in the Logit classifier, the SVM is not used in the Fixed Fine ratio experiments in section 4.3 Plots for Fine Fixed Ratio experiments.

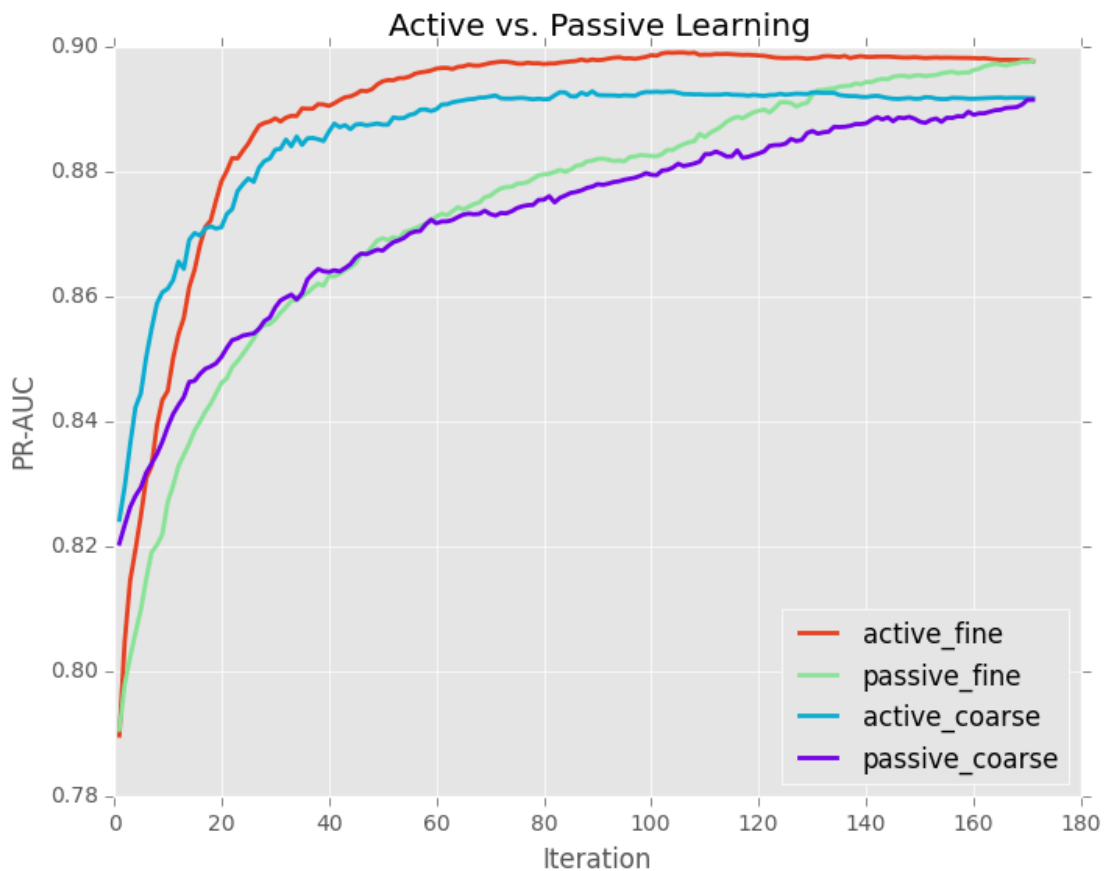


Figure 4.10: The PR AUC curves for SVM show a slight advantage for Active Fine, similar to the Logit results.

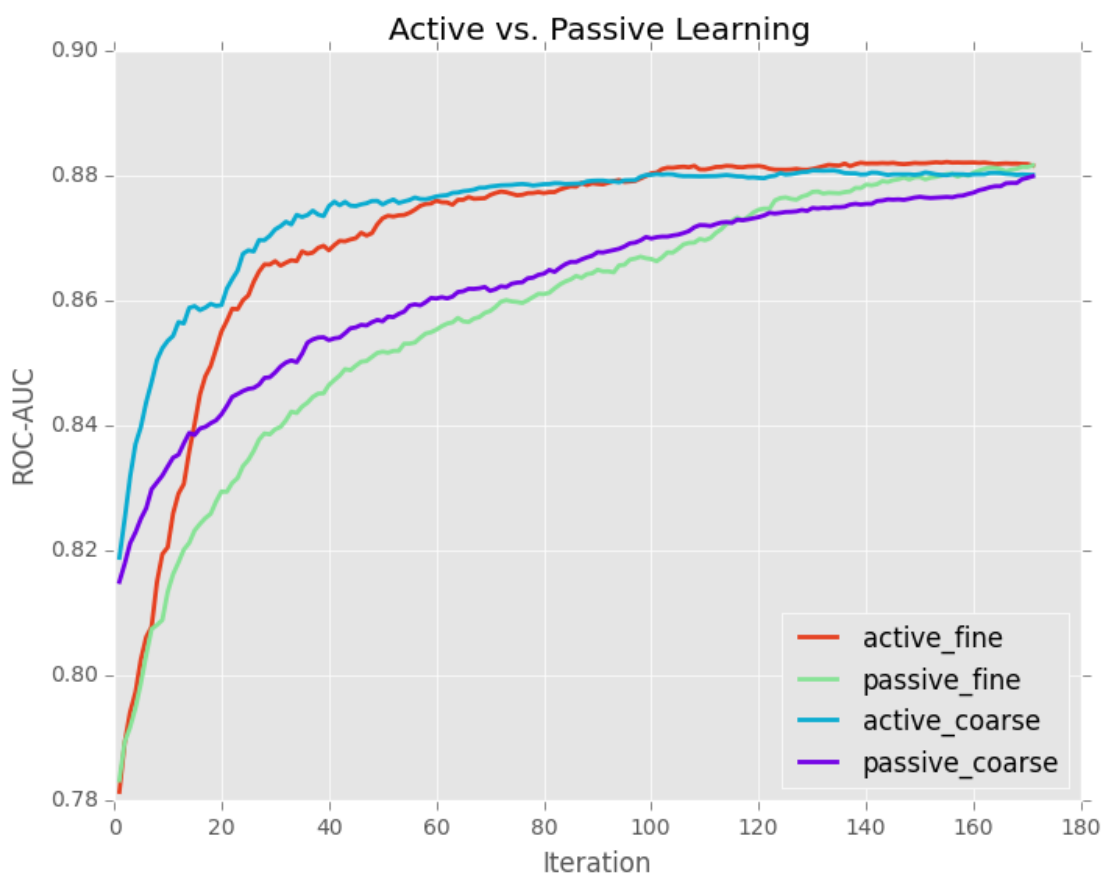


Figure 4.11: The ROC AUC curves for SVM match the Logit results, the convergence of Active Fine to Active Coarse takes slightly longer, round 60 compared to round 40.

4.3 Plots for Fine Fixed Ratio experiments

The strategy is changed from purchasing a set number of instances per round to having a set budget per round and spending a portion of that budget on fine and coarse grained labels. The Fine Fixed Ratio (FFR), ranges from 0.0 to 1.0 in increments of 0.1. Note that the FFR 0.0 should roughly correlate to the Active Coarse curve shown in *Figure 4.5*. Likewise the Active Fine curve should roughly correlate to the FFR 1.0 curve. However, the correlation is not exact since the FFR experiments use a combination classifier, it trains Fine and Coarse classifiers on a starter set of the same size and proportion as used in the Logit Active vs Passive experiment, then uses the confidence of both of those classifiers and the end prediction is the max of the two classifiers. Thus even for the FFR 0.0 and FFR 1.0 the starter set trained Fine or Coarse classifier still contributes to the PR-AUC curve even at the final round 180. The results are an average of 10 folds.

To determine the number of instances to purchase each round the FFR is multiplied by the round budget of 100, then the round budget for the coarse labels are purchased at a cost of 1.0. The cost of the fine labels will vary and if a decimal occurs it is resolved by randomly purchasing an extra fine label with the probability of the decimal value. For example, if the fine cost is 16 and FFR is 0.5, 50 instances are bought for coarse and 3.125 instances are bought for fine. The remainder 0.125 is then turned into a 0.125 chance for any round to purchase an extra fine label. The round size for the FFR 1.0 curve is very small, with only 7 labels purchased per iteration.

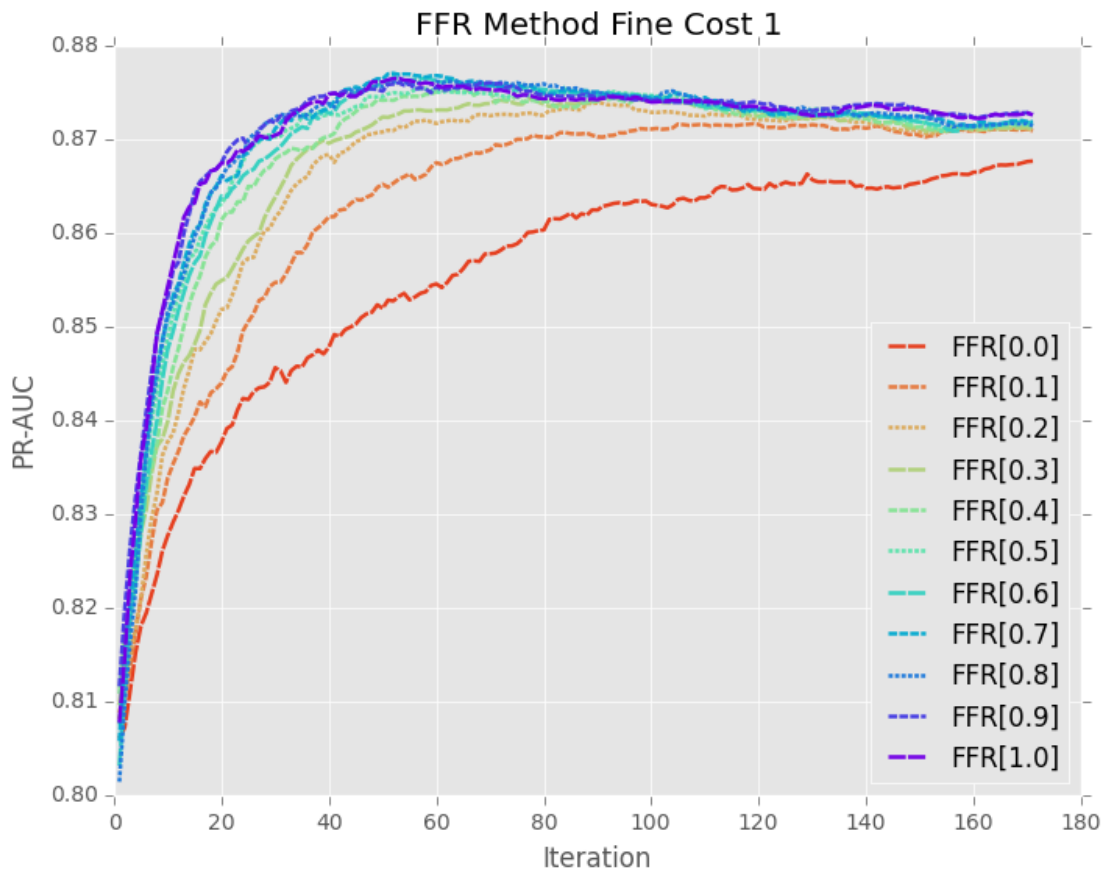


Figure 4.12: For this curve the fine and coarse grain labels both have a cost of 1. The purple 1.0 curve shows that if only fine-grained labels are purchased, the highest performing PR-AUC can be obtained. All FFR ratios end at the same round since the cost of the Fine and Coarse instances is the same the budget

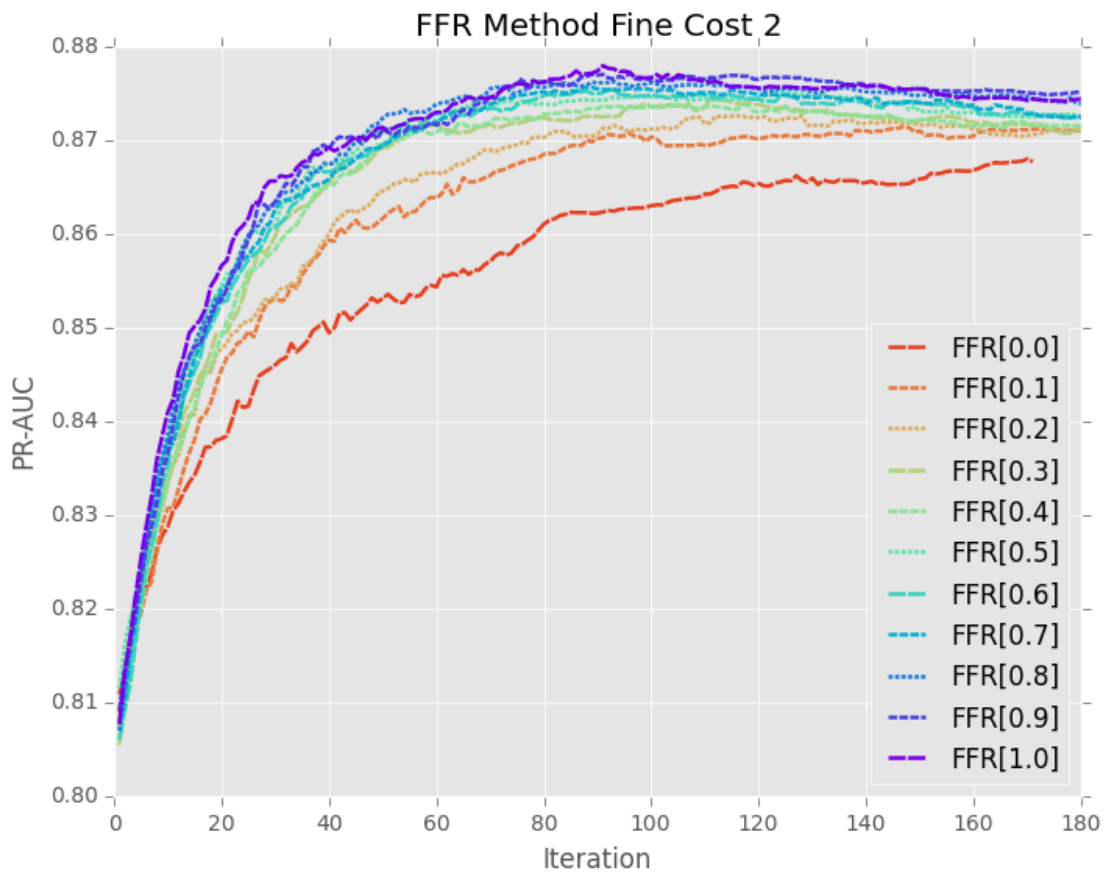


Figure 4.13: At fine cost 2, advantage of the higher FFR values decreases but the ordering of the curves remains unchanged.

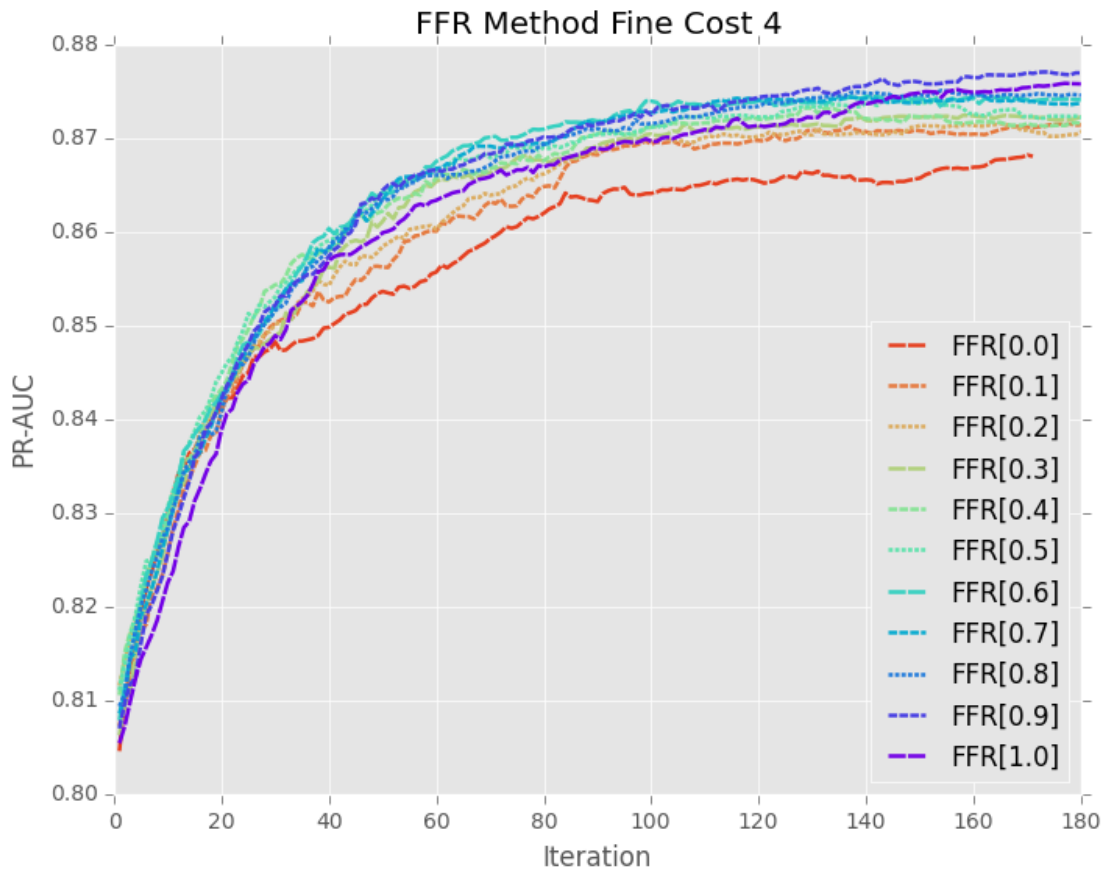


Figure 4.14: At fine cost 4, the highest FFR 1.0 is no longer preferred, the cost is too high for Fine instances PR-AUC utility to overcome the PR-AUC increase gained by purchasing more Coarse instances.

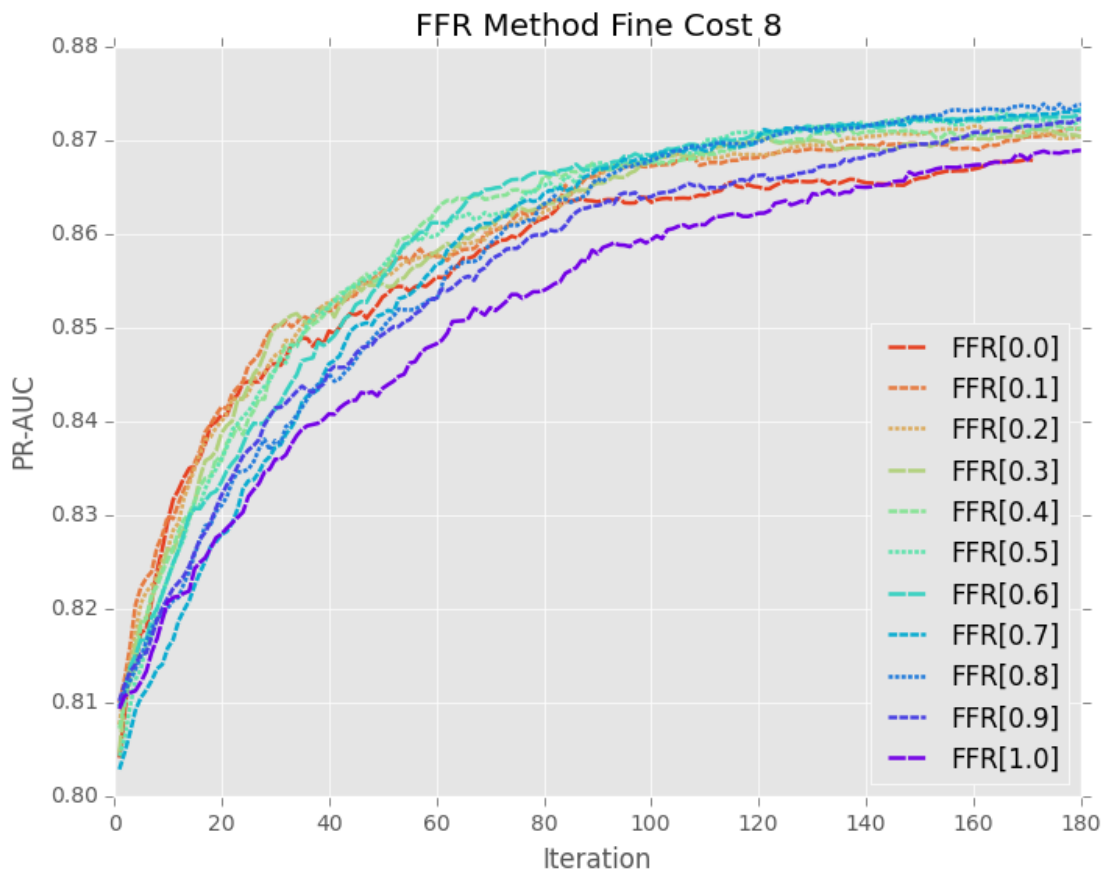


Figure 4.15: At fine cost 8 the middle FFR values outperform the extreme values for rounds 0 to 180.

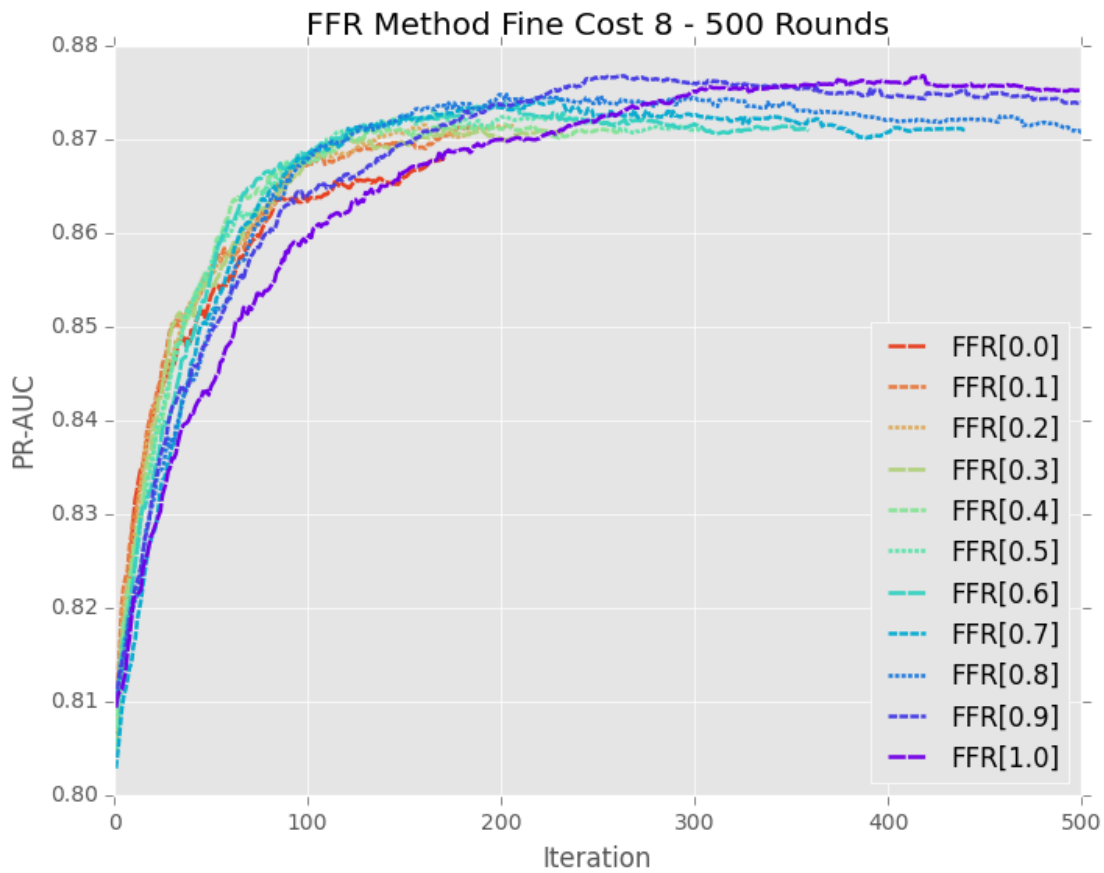


Figure 4.16: This shows the iterations continuing through round 500, the curves with the higher fine rates eventually settle to the same end point that the curves with the high rates of coarse labels purchased achieved at previous iterations.

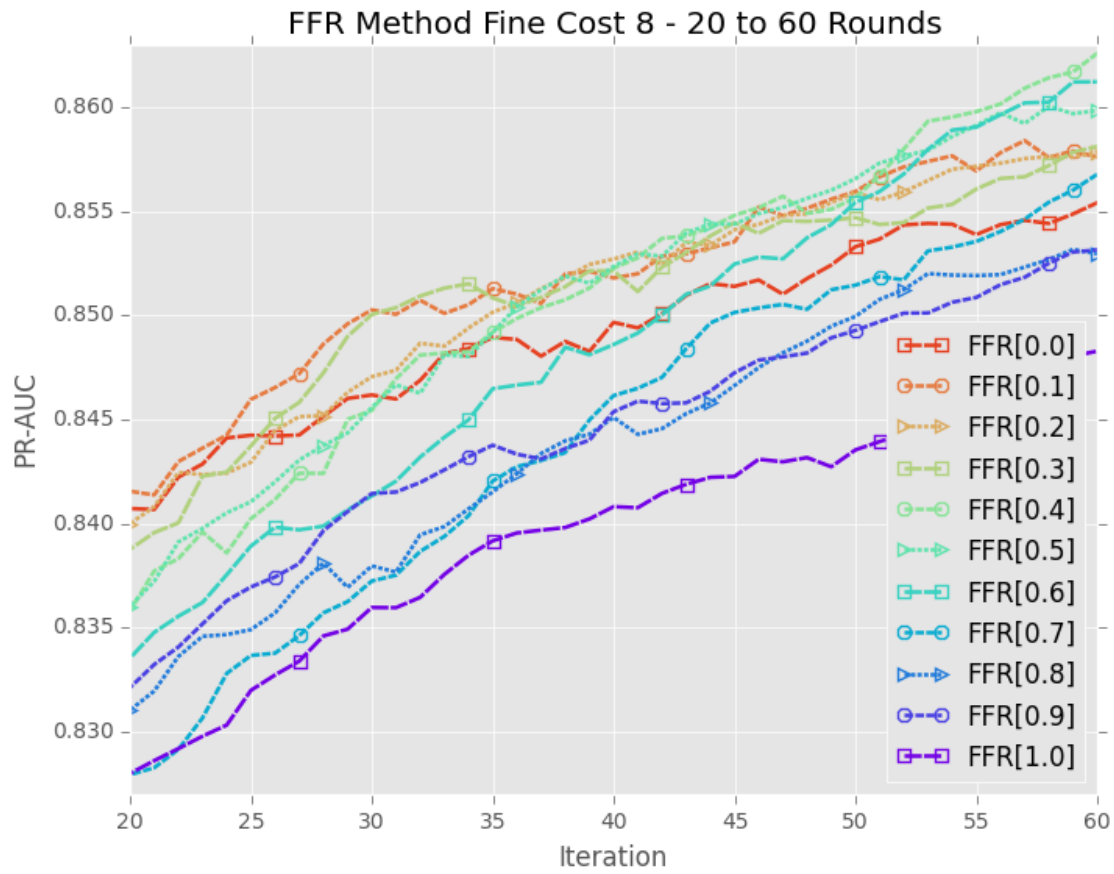


Figure 4.17: The fine cost 8 curves shown expanding the rounds 20-60. If a round budget of 40 occurs than the recommended Fine Fixed Ratio would be 0.2

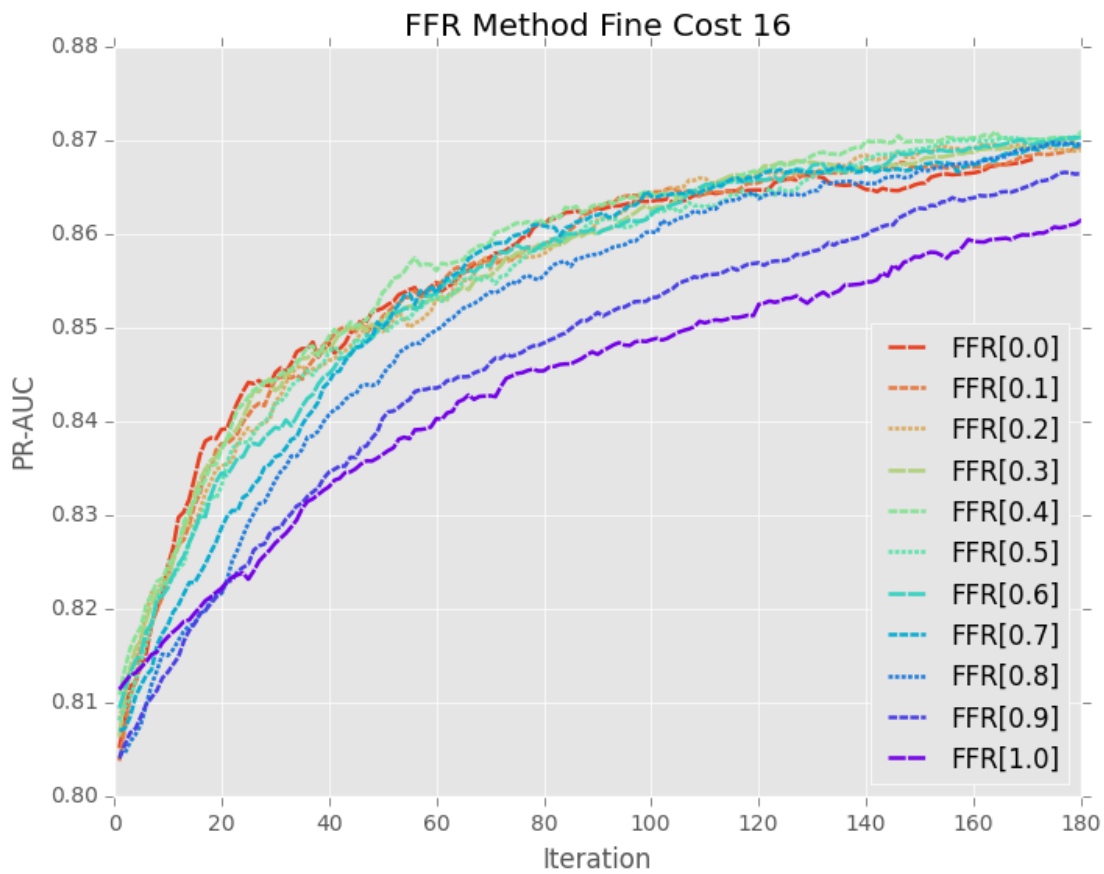


Figure 4.18: The fine cost is increased to 16. The cost is too high for the fine label advantage to offset the decreased number of instances purchased.

Chapter 5

Conclusions and Future Work

I should probably do the Bandit experiments.

Bibliography

- [1] T. M. Mitchell, *Machine Learning*, 1st ed. New York, NY, USA: McGraw-Hill, Inc., 1997. 1.1
- [2] F. Pedregosa, G. Varoquaux, A. Gramfort, V. Michel, B. Thirion, O. Grisel, M. Blondel, P. Prettenhofer, R. Weiss, V. Dubourg, J. Vanderplas, A. Passos, D. Cournapeau, M. Brucher, M. Perrot, and E. Duchesnay, "Scikit-learn: Machine learning in Python," *Journal of Machine Learning Research*, vol. 12, pp. 2825–2830, 2011. 1.1, 1.1, 3.1, 3.1.1, 3.1.2, 3.1.3, 3.1.9
- [3] J. Z. Kevin Chiang, Juan Cui, "Prediction of nuclear and locally encoded mitochondrion." Lincoln, NE: Nebraska Gateway to Nutrigenomics 6th Annual Retreat, June 9 2014. [Online]. Available: <http://cehs.unl.edu/nutrigenomics/nebraska-gateway-nutrigenomics-6th-annual-retreat/> 1.2, 1.1
- [4] D. Cotter, P. Guda, E. Fahy, and S. Subramaniam, "Mitoproteome: mitochondrial protein sequence database and annotation system," *Nucleic Acids Research*, vol. 32, no. suppl1, p. D463, 2004. [Online]. Available: <http://dx.doi.org/10.1093/nar/gkho48> 1.2
- [5] "Activities at the universal protein resource (uniprot)," *Nucleic Acids Research*, vol. 42, no. D1, p. D191, 2014. [Online]. Available: <http://dx.doi.org/10.1093/nar/gkt1140> 1.2

- [6] Z. R. Li, H. H. Lin, L. Y. Han, L. Jiang, X. Chen, and Y. Z. Chen, "Profeat: a web server for computing structural and physicochemical features of proteins and peptides from amino acid sequence," *Nucleic Acids Research*, vol. 34, no. Web Server issue, pp. W32–W37, 07 2006. [Online]. Available: <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC1538821/> 1.1
- [7] J. Cui, L. Y. Han, H. Li, C. Y. Ung, Z. Q. Tang, C. J. Zheng, Z. W. Cao, and Y. Z. Chen, "Computer prediction of allergen proteins from sequence-derived protein structural and physicochemical properties," *Molecular Immunology*, vol. 44, no. 4, pp. 514 – 520, 2007. [Online]. Available: <http://www.sciencedirect.com/science/article/pii/S0161589006000368> 1.1
- [8] J. M. Brown and A. J. Giaccia, "The unique physiology of solid tumors: Opportunities (and problems) for cancer therapy," *Cancer Research*, vol. 58, no. 7, pp. 1408–1416, 1998. [Online]. Available: <http://cancerres.aacrjournals.org/content/58/7/1408> 1.1
- [9] L. Kll, A. Krogh, and E. L. L. Sonnhammer, "An hmm posterior decoder for sequence feature prediction that includes homology information," *Bioinformatics*, vol. 21, no. suppl-1, p. i251, 2005. [Online]. Available: [+http://dx.doi.org/10.1093/bioinformatics/bti1014](http://dx.doi.org/10.1093/bioinformatics/bti1014) 1.1
- [10] F. Eisenhaber, C. Frmmel, and P. Argos, "Prediction of secondary structural content of proteins from their amino acid composition alone. ii. the paradox with secondary structural class," *Proteins: Structure, Function, and Bioinformatics*, vol. 25, no. 2, pp. 169–179, 1996. [Online]. Available: [http://dx.doi.org/10.1002/\(SICI\)1097-0134\(199606\)25:2<169::AID-PROT3>3.0.CO;2-D](http://dx.doi.org/10.1002/(SICI)1097-0134(199606)25:2<169::AID-PROT3>3.0.CO;2-D) 1.1
- [11] J. D. Bendtsen, H. Nielsen, G. von Heijne, and S. Brunak, "Improved prediction of signal peptides: Signalp 3.0," *Journal of Molecular Biology*, vol. 340, no. 4, pp. 783 –

- 795, 2004. [Online]. Available: <http://www.sciencedirect.com/science/article/pii/S0022283604005972> 1.1
- [12] A. G. Garrow, A. Agnew, and D. R. Westhead, "Tmb-hunt: a web server to screen sequence sets for transmembrane -barrel proteins," *Nucleic Acids Research*, vol. 33, no. suppl2, p. W188, 2005. [Online]. Available: <http://dx.doi.org/10.1093/nar/gki384> 1.1
- [13] K. Julenius, A. Mlgaard, R. Gupta, and S. Brunak, "Prediction, conservation analysis, and structural characterization of mammalian mucin-type o-glycosylation sites," *Glycobiology*, vol. 15, no. 2, p. 153, 2005. [Online]. Available: <http://dx.doi.org/10.1093/glycob/cwh151> 1.1
- [14] J. D. Bendtsen, H. Nielsen, D. Widdick, T. Palmer, and S. Brunak, "Prediction of twin-arginine signal peptides," *BMC bioinformatics*, vol. 6, no. 1, p. 167, 2005. 1.1
- [15] J. Davis and M. Goadrich, "The relationship between precision-recall and roc curves," in *Proceedings of the 23rd International Conference on Machine Learning*, ser. ICML '06. New York, NY, USA: ACM, 2006, pp. 233–240. [Online]. Available: <http://doi.acm.org/10.1145/1143844.1143874> 4.2.1
- [16] W. Luo, A. Schwing, and R. Urtasun, "Latent structured active learning," in *Advances in Neural Information Processing Systems (NIPS)*, 2013.
- [17] S. Dasgupta and D. Hsu, "Hierarchical sampling for active learning," *Proceedings of the 25th international conference on Machine learning - ICML '08*, pp. 208–215, 2008. [Online]. Available: <http://portal.acm.org/citation.cfm?doid=1390156.1390183>
- [18] A. Merialdo, "Improving Collaborative Filtering For New-Users By Smart Object Selection," In *Proceedings of International Conference on Media Features (ICMF)*,

- May 2001. [Online]. Available: <http://www.eurecom.fr/publication/670https://www.eurecom.fr/fr/publication/670/download/mm-kohrar-010508.pdf>
- [19] X. Ling and D. Weld, "Fine-grained entity recognition," *Proceedings of the 26th Conference on Artificial Intelligence*, 2012. [Online]. Available: <http://www.cs.washington.edu/ai/pubs/ling-aaai12.pdfhttp://www.aaai.org/ocs/index.php/AAAI/AAAI12/paper/download/5152/5124>
- [20] L. Buitinck, G. Louppe, M. Blondel, F. Pedregosa, A. Mueller, O. Grisel, V. Niculae, P. Prettenhofer, A. Gramfort, J. Grobler, R. Layton, J. VanderPlas, A. Joly, B. Holt, and G. Varoquaux, "API design for machine learning software: experiences from the scikit-learn project," in *ECML PKDD Workshop: Languages for Data Mining and Machine Learning*, 2013, pp. 108–122.
- [21] E. Alpaydin, *Introduction to Machine Learning (Adaptive Computation and Machine Learning series)*, 2nd ed. Cambridge, Massachusetts: The MIT Press, 2009. [Online]. Available: <https://amzn.com/026201243X>
- [22] A. Ng, "Machine Learning by Stanford University," <https://www.coursera.org/learn/machine-learning/home/welcome>, 2016, accessed: 2016-12-5.