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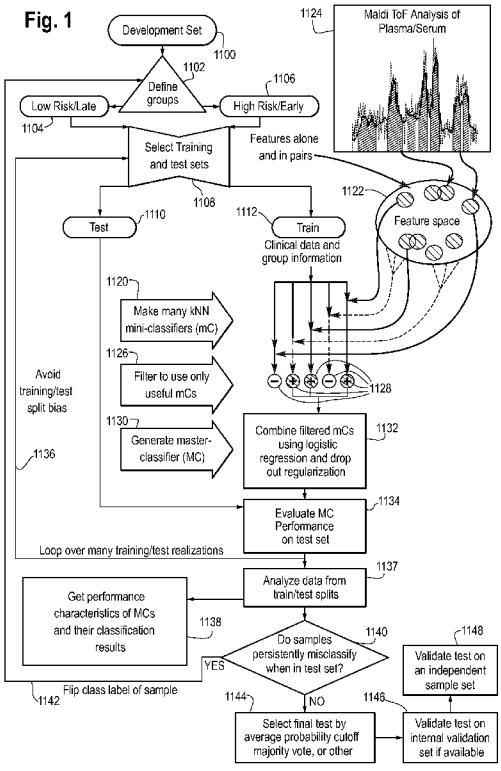
[Continued on next page]

(54) Title: PREDICTIVE TEST FOR AGGRESSIVENESS OR INDOLENCE OF PROSTATE CANCER FROM MASS SPECTROMETRY OF BLOOD-BASED SAMPLE

Fig. 1



(57) Abstract: A programmed computer functioning as a classifier operates on mass spectral data obtained from a blood-based patient sample to predict indolence or aggressiveness of prostate cancer. Methods of generating the classifier and conducting a test on a blood-based sample from a prostate cancer patient using the classifier are described.

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Predictive test for aggressiveness or indolence of prostate cancer from mass spectrometry of blood-based sample

Related Application

This application claims priority benefits to U.S. provisional application serial no. 62/058,792 filed October 2, 2014, the content of which is incorporated by reference herein.

This application is related to U.S. application serial no. 14/486,442 filed September 15, 2014, of H. Röder et al., U.S. patent application publication no. 2015/0102216, assigned to the assignee of the present invention. The content of the '442 application is incorporated by reference herein. The '442 application is not admitted to depict prior art.

Background

Prostate cancer is a cancer that forms in tissues of the prostate, a gland in the male reproductive system. Prostate cancer usually occurs in older men. More than one million prostate biopsies are performed each year in the United States, leading to over 200,000 prostate cancer diagnoses. Managing the care of these patients is challenging, as the tumors can range from quite indolent to highly aggressive.

Current practice is to stratify patients according to risk based on serum prostate specific antigen (PSA) measurements, TNM staging, and Gleason score. High baseline PSA (PSA>20 ng/ml) is taken as a signal of increased risk of aggressive disease and indicates immediate therapeutic intervention. TNM staging of T3a or worse, including metastatic disease, places the patient in the high risk category, whereas a staging of T1 to T2a is required for the patient to be classified as low or very low risk.

In order to have the Gleason score evaluated, a set of biopsies are taken from different regions of the prostate, using hollow needles. When seen through a microscope, the biopsies may exhibit five different patterns (numbered from 1 to 5), according to the distribution/shape/lack of cells and glands. A pathologist decides what the dominant pattern is (Primary Gleason Score) and the next-most frequent pattern (Secondary Gleason Score). The Primary and Secondary scores are then summed up and a Total Gleason Score (TGS) is obtained, ranging from 2 to 10. As the TGS increases the prognosis worsens. Patients with Gleason score of 8 or higher are classified as high risk and are typically scheduled for

immediate treatment, such as radical prostatectomy, radiation therapy and/or systemic androgen therapy. Patients with Gleason score of 7 are placed in an intermediate risk category, while patients with Gleason score of 6 or lower are classified as low or very low risk.

Patients diagnosed with very low, low, and intermediate risk prostate cancer are assigned to watchful waiting, an active surveillance protocol. For these patients, levels of serum PSA are monitored and repeat biopsies maybe ordered every 1-4 years. However, despite low baseline PSA and favorable biopsy results, some patients defined as low risk do experience rapid progression. These patients, especially in the younger age group, would benefit from early intervention. Bill-Axelson, A. et al. *Radical prostatectomy versus watchful waiting in early prostate cancer.* N Engl J Med 364, 1708-17 (2011). Improved identification of prostate cancer patients who in fact have poor prognosis and need to be actively treated is of significant clinical importance.

Investigations into various biomarkers which may help in this indication are ongoing. While measurement of total PSA remains one of the most widely accepted tests for prostate cancer diagnostics, a lot of research is focused on finding additional circulating biomarkers of prognosis of the course of the disease. Several alternative types of PSA measurements, such as percentage of free PSA (% fPSA) and PSA kinetics have been evaluated most extensively. Observed % fPSA seems to be a significant predictor of time to treatment in patients in active surveillance, while PSA velocity and PSA doubling time results are often inconsistent. Trock, B.J. *Circulating biomarkers for discriminating indolent from aggressive disease in prostate cancer active surveillance.* Curr Opin Urol 24, 293-302 (2014); Cary, K.C. & Cooperberg, M.R. *Biomarkers in prostate cancer surveillance and screening: past, present, and future.* Ther Adv Urol 5, 318-29 (2013). Another test based on calculating the Prostate Health Index using measurements of [-2]proPSA (a truncated PSA isoform), fPSA and total PSA, has shown promising results. See the Trock paper, *supra.* Several studies evaluated potential biomarkers in urine, such as prostate cancer antigen3 (PCA3) and fusion gene TMPRSS2-EGR, though the results were contradictory. *Id.* In addition, there are several recent tissue based tests employing gene expression profiles, such as Oncotype DX Prostate Cancer Assay (Genomic health) see Klein, A.E., et al. *A 17-gene Assay to Predict Prostate Cancer Aggressiveness in the Context of Gleason Grade Heterogeneity, Tumor Multifocality, and Biopsy Undersampling,* Euro Urol 66, 550-560 (2014) and the Prolaris assay (Myriad Genetics), see Cooperberg, M.R., et al. *Validation of a Cell-Cycle Progression Gene Panel to*

Improve Risk Stratification in a Contemporary Prostatectomy Cohort, J Clin Oncol 31, 1428-1434 (2013), which are associated with the risk of disease progression (see Sartori, D.A. & Chan, D.W. *Biomarkers in prostate cancer: what's new?* Curr Opin Oncol 26, 259-64 (2014)) however they require an invasive procedure.

Though the results on a number of biomarkers are promising, most are in early stages of validation and none of them has yet been shown to reliably predict the course of the disease. Thus, there is an unmet need for non-invasive clinical tests that would improve risk discrimination of prostate cancer in order to help select appropriate candidates for watchful waiting and identify men who need an immediate active treatment. The methods and systems of this invention meet that need.

Other prior art of interest includes US patents 8,440,409 and 7,811,772, and U.S. patent application publication 2009/0208921. The assignee of the present invention has several patents disclosing classifiers for predictive tests using mass spectrometry data including, among others, U.S. 7,736,905; 8,718,996 and 7,906,342.

Summary

In a first aspect, a method for predicting the aggressiveness or indolence of prostate cancer in a patient previously diagnosed with prostate cancer is disclosed. The method includes the steps of: obtaining a blood-based sample from the prostate cancer patient; conducting mass spectrometry of the blood-based sample with a mass spectrometer and thereby obtaining mass spectral data including intensity values at a multitude of m/z features in a spectrum produced by the mass spectrometer, and performing pre-processing operations on the mass spectral data, such as for example background subtraction, normalization and alignment. The method continues with a step of classifying the sample with a programmed computer implementing a classifier.

In preferred embodiments the classifier is defined from one or more master classifiers generated as combination of filtered mini-classifiers with regularization. The classifier operates on the intensity values of the spectra obtained from the sample after the pre-processing operations have been performed and a set of stored values of m/z features from a constitutive set of mass spectra.

In this document we use the term "constitutive set of mass spectra" to mean a set of feature values of mass spectral data which are used in the construction and application of a classifier. The final classifier produces a class label for the blood based sample of High, Early, or the equivalent, signifying the patient is at high risk of early progression of the prostate cancer indicating aggressiveness of the prostate cancer, or Low, Late or the equivalent, signifying that the patient is at low risk of early progression of the prostate cancer indicating indolence of the cancer.

In one embodiment, in which the classifier is defined from one or more master classifiers generated as a combination of filtered mini-classifiers with regularization, the mini-classifiers execute a K-nearest neighbor classification (k-NN) algorithm on features selected from a list of features set forth in Example 1 Appendix A, Example 2 Appendix A, or Example 3 Appendix A. The mini-classifiers could alternatively execute another supervised classification algorithm, such as decision tree, support vector machine or other. In one embodiment, the master classifiers are generated by conducting logistic regression with extreme drop-out on mini-classifiers which meet predefined filtering criteria.

In another aspect, a system for prostate cancer aggressiveness or indolence prediction is disclosed. The system includes a computer system including a memory storing a final classifier defined as a majority vote of a plurality of master classifiers, a set of mass spectrometry feature values, subsets of which serve as reference sets for the mini-classifiers, a classification algorithm (e.g., k-NN), and a set of logistic regression weighting coefficients defining one or more master classifiers generated from mini-classifiers with regularization. The computer system includes program code for executing the master classifier on a set of mass spectrometry feature values obtained from mass spectrometry of a blood-based sample of a human with prostate cancer.

In still another example, a laboratory test system for conducting a test on a blood-based sample from a prostate cancer patient to predict aggressiveness or indolence of the prostate cancer is disclosed. The system includes, in combination, a mass spectrometer conducting mass spectrometry of the blood-based sample thereby obtaining mass spectral data including intensity values at a multitude of m/z features in a spectrum produced by the mass spectrometer, and a programmed computer including code for performing pre-processing operations on the mass spectral data and classifying the sample with a final classifier defined by one or more master classifiers generated as a combination of filtered

mini-classifiers with regularization. The final classifier operates on the intensity values of the spectra from a sample after the pre-processing operations have been performed and a set of stored values of m/z features from a constitutive set of mass spectra. The programmed computer produces a class label for the blood-based sample of High, Early or the equivalent, signifying the patient is at high risk of early progression of the prostate cancer indicating aggressiveness of the prostate cancer, or Low, Late or the equivalent, signifying that the patient is at low risk of early progression of the prostate cancer indicating indolence of the cancer.

In yet another aspect, a programmed computer operating as a classifier for predicting prostate cancer aggressiveness or indolence is described. The programmed computer includes a processing unit and a memory storing a final classifier in the form of a set of feature values for a set of mass spectrometry features forming a constitutive set of mass spectra obtained from blood-based samples of prostate cancer patients, and a final classifier defined as a majority vote or average probability cutoff, of a multitude of master classifiers constructed from a combination of mini-classifiers with dropout regularization.

In one possible embodiment, the mass spectrum of the blood-based sample is obtained from at least 100,000 laser shots in MALDI-TOF mass spectrometry, e.g., using the techniques described in the patent application of H. Röder et al., U.S. Serial No. 13/836,436 filed March 15, 2013, the content of which is incorporated by reference herein.

Brief Description of the Drawings

Figure 1 is a flow chart showing a classifier generation process referred to herein as combination of mini-classifiers with drop-out (CMC/D) which was used in generation of the classifiers of Examples 1, 2 and 3.

Figures 2A-2C are plots of the distribution of the performance metrics among the master classifiers (MCs) for Approach 1 of Example 1.

Figures 3A-3C are plots of the distribution of the performance metrics among the MCs for Approach 2 of Example 1.

Figures 4A-4L are plots of the distribution of the performance metrics among the obtained MCs for approach 2 of Example 1 when flipping labels. Each row of plots

corresponds to a sequential iteration of loop 1142 in the classification development process of Figure 1.

Figures 5A-5C are t-Distributed Stochastic Neighbor Embedding (t-SNE) 2D maps of the development sample set labeled according to the initial assignment of group labels for the development sample set in Approach 1 of Example (Figure 5A); an initial assignment for Approach 2 of Example (Figure 5B); and final classification labels after 3 iterations of label flips (Approach 3 of Example 1)(Figure 5C). "1" (triangles) corresponds to "High" and "0" (circles) to "Low" group label assignments.

Figure 6 is a plot of the distribution of the times on study for patients in Example 2 leaving the study early without a progression event.

Figure 7 is a plot of Kaplan-Meier curves for time to progression (TTP) using the modified majority vote (MMV) classification labels obtained by a final classifier in Approach 1 of Example 2.

Figure 8 is a plot of the Kaplan-Meier curves for TTP for the classifications obtained in Approach 1 of Example 2, including half (46) of the patients who dropped out of the study. For the patients who were used in the test/training splits, the MMV label is taken. For those patients who dropped out of the study the normal Majority Vote of all the 301 MCs is used. Log-rank test p-value = 0.42, log-rank HR = 1.42 with a 95% CI = [0.61 – 3.33].

Figure 9 is a plot of the Kaplan-Meier curves for TTP using the MMV classification labels obtained in Approach 2 of Example 2.

Figure 10 is a plot of the distribution of Cox Hazard Ratios of the individual 301 master classifiers (MCs) created in Approach 2 of Example 2.

Figures 11A-11C are plots of the distribution of the performance metrics among the MCs in Approach 2 of Example 2.

Figure 12 are Kaplan-Meier curves for TTP obtained using the MMV classification labels after each iteration of label flips (using Approach 2 of Example 2 as the starting point) in the classifier development process of Figure 1. The log-rank p-value and the log-rank Hazard Ratio (together with its 95% Confidence Interval) are also shown for each iteration.

Figure 13 are t-Distributed Stochastic Neighbor Embedding (t-SNE) two dimensional maps of the classifier development data set, labeled according to (left) the initial assignment for the group labels in the training set and (right) the final classification labels, for each of three approaches to classifier development used in Example 2.

Figure 14 is a plot of Kaplan-Meier curves for TTP using classification labels obtained in approach 2 of Example 2 and including the patients of the "validation set" cohort. For the patients that were used in the test/training splits the MMV label is taken. For the "validation set" patients, the normal majority vote of all the 301 MCs is used. The log-rank p-value is 0.025 and the log-rank Hazard Ratio 2.95 with a 95% CI of [1.13,5.83]. A table showing the percent progression free for each classified risk group at 3, 4 and 5 years on study is also shown.

Figure 15 are Box and Whisker plots of the distribution of the PSA baseline levels (taken at the beginning of the study) of the two classification groups in Approach 2 of Example 2. For the patients that were used in the test/training splits the MMV label is taken. For the "validation set" patients, the normal majority vote of all the 301 MCs is used. The plot takes into account only the 119 patients (from the development and "validation" sample sets), for whom baseline PSA levels were available.

Figure 16 is a plot of the distribution of the Total Gleason Score (TGS) values of the two classification groups (using Approach 2 of Example 2). For the patients that were used in the test/training splits the MMV label is taken. For the "validation set" patients, the normal majority vote of all the 301 MCs is used. Only the 133 patients (from the development and validation sets) for whom TGSs were available are considered in this plot.

Figure 17 is a box and whisker plot showing normalization scalars for spectra for Relapse and No Relapse patient groups in Example 3.

Figure 18 is a plot of a multitude of mass spectra showing example feature definitions; i.e., m/z ranges over which integrated intensity values are calculated to give feature values for use in classification.

Figure 19 is a box and whisker plot showing normalization scalars found by partial ion current normalization analysis comparison between clinical groups Relapse and No Relapse.

Figures 20A and 20B are Kaplan-Meier plots for time to relapse (TTR) by Early and Late classification groups, showing the performance of the classifiers generated in Example 3. Figure 20A shows the classifier performance for Approach (1) of Example 3, which uses only mass spectral data for classification, whereas Figure 20B shows classifier performance for Approach (2) of Example 3, which uses non-mass spectral information, including patient's age, PSA and % fPSA, in addition to the mass spectral data.

Figure 21 is an illustration of a testing process and system for conducting a test on a blood-based sample of a prostate cancer patient to predict indolence or aggressiveness of the cancer.

Detailed Description

Introduction

A programmed computer is described below which implements a classifier for predicting from mass spectrometry data obtained from a blood-based sample from a prostate cancer patient whether the cancer is aggressive or indolent. The method for development of this classifier will be explained in three separate Examples using three different sets of prostate cancer blood-based samples. The classifier development process, referred to herein as "CMC/D" (combination of mini-classifiers with dropout) incorporates the techniques which are disclosed in US application serial no. 14/486,442 filed September 15, 2014, the content of which is incorporated by reference herein. The pertinent details of the classifier development process are described in this document in conjunction with Figure 1. A testing system, which may be implemented in a laboratory test center including a mass spectrometer and the programmed computer, is also described later on in conjunction with Figure 21.

Example 1: Classifier Development from Oregon Data Set

In this Example, we will describe the generation of a classifier to predict prostate cancer aggressiveness or indolence from a set of prostate cancer patient data in the form of blood-based samples obtained from prostate cancer patients and associated clinical data. This Example will describe the process we used for generating mass spectrometry data, pre-processing steps which were performed on the mass spectra, and the specific steps we used in development of a classifier from the set of data. This set of data is referred to as the "development set" 1100 of Figure 1.

The patients included in this data set all had prostate biopsies and an evaluation of their Gleason Scores made (distributed according to Table 1). 18 of them were classified as low risk, 28 as intermediate risk and 29 as high risk, according to existing guidelines.

Available Samples

Serum samples were available from 79 patients diagnosed with prostate cancer.

Mass Spectral Data Acquisition

A. Sample Preparation

Samples were thawed on ice and spun at 1500g for 5 minutes at 4°C. Each sample was diluted 1:10 with water and then mixed 1:1 with sinapinic acid (25 mg/ml in 50%ACN/0.1% TFA). The samples were spotted in triplicate.

B. Acquisition of mass spectra

Spectra of nominal 2,000 shots were collected on a MALDI-TOF mass spectrometer using acquisition settings we used in the commercially available VeriStrat test of the assignee Biodesix, Inc., see U.S. Patent 7,736,905, the details of which are not particularly important. Spectra could not be acquired from two samples.

C. Spectral Pre-Processing

The data set consists originally of 237 spectra corresponding to 79 patients (3 replicates per patient). The spectra of 4 patients were not used for the study:

- Patient 28 did not have any clinical data available
- Patients 30 and 31 had clinical data available but spectra were not available for them
- Patient N--37—1 had the Total Gleason Score (TGS) available but neither of the Primary or Secondary Scores

In total 75 patients were used in the study, distributed through the following Primary /Secondary Gleason Score combinations:

Table 1: Distribution of the patients included in this analysis according to their primary and secondary Gleason Score combinations

Progression Risk	Primary GS	Secondary GS	Total GS	#Patients
"Low"	3	3	6	18
"Int"	3	4	7	20
	4	3	7	8
"High"	4	4	8	13
	3	5	8	1
	5	3	8	2
	4	5	9	11
	5	4	9	1
	5	5	10	1

D. Averaging of spectra to produce one spectrum per sample

For each of the 3 replicate spectra available for each patient, the background was estimated and then subtracted. Peaks passing a SNR threshold of 6 were identified. The raw spectra (no background subtraction) were aligned using a subset of 15 peaks (Table 2) to correct for slight differences in mass divided by charge (m/z) scale between replicate spectra. The aligned spectra were averaged resulting in a single average spectrum for each patient. With the exception of alignment, no other preprocessing was performed on the spectra prior to averaging.

Table 2: Calibration points used to align the raw spectra prior to averaging

Calibration point m/z [Da]
4153

6432
6631
8917
9433
9723
12864
13764
13877
14046
15127
15869
18630
21066
28100

Feature Definitions for New Classifier Development

Using a subset of 20 of the averaged spectra, background was subtracted using the same parameters as in the previous step. They were then normalized using Partial Ion Current (PIC) normalization and the normalization windows shown in Table 3. A total of 84 features were identified by overlaying the spectral sample averages and assessing the spread of the band from the overlay to define the left and right boundaries. When identified, oxidation states were combined into single features. The feature definitions are given in Example 1, Appendix A at the end of this document.

Table 3: Windows used in the initial PIC normalization, before feature definition

Min m/z	Max m/z
3000	4138
4205	11320
12010	15010
16320	23000

Normalization of the averaged spectra

Using all pre-processed, averaged spectra, a set of features, stable across patient spectra, was determined that was suitable for a refined Partial Ion Current (PIC) normalization. These features are listed in Table 4.

Table 4: Features used in the final PIC normalization. For further details on the feature ranges see Example 1 Appendix A.

Feature (m/z position)
3330
5071
5109
5293
6591
6653
6797
6860
6891
6836
6947

13706

13758

13798

13877

13970

Using this optimized PIC normalization, a new feature table, containing all feature values for all samples, was constructed for all the patients and used during the subsequent classifier development steps of Figure 1.

CMC/D Process for New Classifier Development

The new classifier development process using the method of combination of mini-classifiers (mCs) with dropout (CMC/D) is shown schematically in Figure 1. The steps in this process are explained in detail below. The methodology, and its various advantages are explained in great detail in US patent application serial no. 14/486,442 filed September 15, 2014. See U.S. patent application publication no. 2015/0102216, H. Roder et al. inventors, which is incorporated by reference herein.

Division of Samples into Development and Validation Sets

Given the low number of patients (75), all of them were used as a development set 1100 (Figure 1) for classifier development and no separate validation set was available.

Step 1102 Definition of Initial Groups

The only available clinical data for each patient was the Primary, Secondary and Total Gleason Scores. Generally, the higher the Total Gleason Score (TGS) the poorer is the prognosis for the patient (although the same TGS, obtained from two different combinations of Primary and Secondary Gleason Scores might be considered of different risk). Because there is no well-defined boundary between High and Low risk based in this grading system and because the evaluation of a score is somewhat subjective, we considered two different arrangements of the patients in terms of group labels:

Approach 1. The patients were arranged according to the prognostic risk depicted in Table 1. The "Low" (18 patients) and "High" (29 patients) were used to construct a binary CMC/D classifier (considering as "positive" outcome the "High" group). The patients with intermediate cancer risk (labeled as "Int") were left aside and later evaluated with the resulting CMC/D classifier.

Approach 2. In this approach, the "Low" training/test group 1104 consisted of the patients with both low and intermediate prognostic risks, comprising a total of 46 patients. The "High" group 1106 was the same as in Approach 1, comprising the 29 patients with high prognostic risk in Table 1. Thus, in this approach all the samples were used in the test/training splits when creating the CMC/D classifiers.

Step 1108 Select training and test sets

Once the initial definition of the class groupings has been established and assignment of group labels to the members of the development set is made, the development set 1100 is split in step 1108 into test and training sets, shown in Figure 1 as 1110 and 1112. The training set group 1112 was then subject to the CMC/D classifier development process shown in steps 1120, 1126 and 1130 and the master classifier generated at step 1130 was evaluated by classifying those samples which were assigned to the test set group 1110 and comparing the resulting labels with the initial ones.

Step 1120 Creation of Mini-Classifiers

Many k-nearest neighbor (kNN) mini-classifiers (mCs) that use the training set as their reference set are constructed using single features or pairs of features from the 84 mass spectral features identified (1124), and listed in Example 1 Appendix A. Basically, as explained in this example, samples are spotted in triplicate on a MALDI-TOF sample plate and a 2,000 shot spectrum is acquired from each spot. The three replicate spectra are aligned and averaged to yield one average spectrum per sample. Features for use in classification are defined as mass/charge (m/z) regions in MALDI spectra (shown as the distinct regions in the inset of 1124) and feature values are the integrated area under the curve for these regions (integrated intensity values). For 84 features, this amounts to considering 3,570 possible mCs. The parameters used to traverse the space of mCs for this project are listed in Table 5.

Table 5: Parameters used to create mCs

kNN parameters: k = 5

mC traversal parameters: Max number of features = 2

Each mini-classifier is created using the known k-NN algorithm and either a single feature or a pair of features from feature space 1122.

Step 1126 Filtering of mini-classifiers

To target a final classifier that has optimal performance characteristics, these mCs were filtered. Each mC was applied to its training set and performance metrics were calculated from the resulting classifications. Only mCs that satisfied thresholds on these performance metrics (shown as + in step 1128) passed filtering to be used further in the process. For this project filtering was based on classification accuracy, overall and within each reference class ("High" and "Low") separately.

Step 1130 and 1132 Generation of Master Classifier (MC) by combination of mini-classifiers using logistic regression with dropout (CMC/D)

Once the filtering of the mCs is complete, a master classifier (MC) is generated in step 1130. In this step, the mCs are combined in one master classifier (MC) using a logistic regression trained using the training set labels as indicated at 1132. To help avoid over-fitting, the regression is regularized using extreme drop out. A total of 5 randomly selected mCs are included in each logistic regression iteration and the weights for the mCs averaged over 6,000 dropout iterations.

While similar in spirit to standard classifier combination methods (see e.g. S. Tulyakov et al, Review of Classifier Combination Methods, Studies in Computational Intelligence, Volume 90, 2008, pp. 361-386), we have the particular problem (with many more mCs than instances (samples in training set) that some "mini-classifiers" could be artificially perfect just by random chance, and hence would dominate the combinations. To avoid this overfitting to particular dominating "mini-classifiers", we generate many logistic training steps by randomly selecting only a small fraction of the "mini-classifiers" for each of these logistic training steps. This is a regularization of the problem in the spirit of dropout as used in deep learning theory. In this case, where we have many mini-classifiers and a small training set we use extreme dropout, where in excess of 99% of pre-filtered mini-classifiers are dropped out in each iteration.

Other methods for performing the regularized combination of the mini-classifiers that could be used include:

- Logistic regression with a penalty function like ridge regression (based on Tikhonov regularization, Tikhonov, Andrey Nikolayevich (1943). "Об устойчивости обратных задач" [*On the stability of inverse problems*]. Doklady Akademii Nauk SSSR 39 (5): 195–198.)

- The Lasso method (Tibshirani, R. (1996). *Regression shrinkage and selection via the lasso*. J. Royal. Statist. Soc B., Vol. 58, No. 1, page1138s 267-288).

- Neural networks regularized by drop-out (Nitish Shrivastava, "*Improving Neural Networks with Dropout*", Master's Thesis, Graduate Department of Computer Science, University of Toronto; available at online from the Computer Science department of the University of Toronto).

- General regularized neural networks (Girosi F. et al, Neural computation, (7), 219 (1995)). The above-cited publications are incorporated by reference herein.

In more detail, in step 1132, the result of each mini-classifier is one of two values, either "Low" or "High". We can then use logistic regression to combine the results of the mini-classifiers in the spirit of a logistic regression by defining the probability of obtaining a "Low" via standard logistic regression (see e.g. http://en.wikipedia.org/wiki/Logistic_regression)

Eq. (1)

$$P(\text{"Low"}|\textit{feature for a spectrum}) = \frac{\exp\left(\sum_{\textit{mini classifiers}} w_{mc}\, I(mc(\textit{feature values}))\right)}{\textit{Normalization}}$$

where $I(mc(\textit{feature values})) = 1$, if the mini-classifier mc applied to the feature values of a sample returns "Low", and 0 if the mini-classifier returns "High". The weights w_{mc} are unknown and need to be determined from a regression fit of the above formula for all samples in the training set using 1 for the left hand side of the formula for the Low-labeled samples in the training set, and 0 for the High-labeled samples, respectively. As we have many more mini-classifiers, and therefore weights, than samples, typically thousands of mini-classifiers and only tens of samples, such a fit will always lead to nearly perfect

classification, and can easily be dominated by a mini-classifier that, possibly by random chance, fits the particular problem very well. We do not want our final test to be dominated by a single special mini-classifier which only performs well on this particular set and is unable to generalize well. Hence we designed a method to regularize such behavior: Instead of one overall regression to fit all the weights for all mini-classifiers to the training data at the same time, we use only a few of the mini-classifiers for a regression, but repeat this process many times. For example we randomly pick three of the mini-classifiers, perform a regression for their three weights, pick another set of three mini-classifiers, and determine their weights, and repeat this process many times, generating many random picks, i.e. realizations of three mini-classifiers. The final weights defining the CMC/D master classifier are then the averages of the weights over all such realizations. The number of realizations should be large enough that each mini-classifier is very likely to be picked at least once during the entire process. This approach is similar in spirit to "drop-out" regularization, a method used in the deep learning community to add noise to neural network training to avoid being trapped in local minima of the objective function.

Step 1134 Evaluate Master Classifier performance

At step 1134, the MC created at step 1130 is then evaluated by performing classification on the test set 1110 and evaluating the results. Methods of evaluating classifier performance are described in US Serial no. 14/486,442 filed September 15, 2014 and include, among others, the distribution of Hazard Ratios, overall accuracy, sensitivity and specificity.

Step 1136 Loop over many Training/Test set splits

At step 1136, the process loops back to step 1108 and a new separation of the development set 1100 into training and test sets is performed and the steps 1120, 1126, 1130 and 1132 are performed on a new random realization of the training set and test set split. The use of multiple training/test splits avoids selection of a single, particularly advantageous or difficult, training set for classifier creation and avoids bias in performance assessment from testing on a test set that could be especially easy or difficult to classify.

We tried two different approaches to splitting over the sample set into training and test sets and repetition of the classifier development steps, depending on the approach used to define the initial groups.

Approach 1. In this approach, the training/test sets split is performed 301 times. A total of 10 samples of each group are randomly assigned, in each realization, to the training set while the remaining samples are used in the test set (8 for the "Low" group and 19 for the "High" group). Each training/test split produces a MC which is applied to the split test set to assess performance.

Approach 2. In this approach, the training/test splits are performed randomly 301 times. A total of 15 samples of each group are assigned, in each realization, to the training set while the remaining samples are used in the test set (31 for the "Low" group and 19 for the "High" group). The performance of each MC is evaluated considering the classification output of the test set.

Step 1137 analyze data from the training/test set splits

At step 1137, the MC performance over all the training and test set splits is performed. This can be done by obtaining performance characteristics of the MCs and their classification results, for example as indicated in block 1138.

Step 1140 Redefine training labels

One other advantage of these multiple training/test splits (and reiteration of steps 1120, 1126 and 1130 many times) is that it allows for the refinement of the initial assignment for the "High"/"Low" groups, particularly for those samples which are persistently misclassified. For the training/test splits where a particular sample from the reference group is in the test set, the resulting classifications for the sample can be obtained by the majority vote of the MCs (or by a Modified Majority Vote, MMV, explained below). If the sample persistently misclassifies relative to the initial guess as to the risk group, the sample can be moved from the "High" into the "Low" group, or vice versa, as indicated in loop 1142. Carrying out this procedure for all samples in the development set produces a new, refined version of the risk groups (1102) which is the starting point for a second iteration of the CMC/D classifier development process as indicated by the loop 1142. This refinement process can be iterated so that the risk groups are determined at the same time as a classifier is constructed, in an iterative way.

Approach 3. We performed three successive iterations of the loop 1142:

Iteration 1: The labels of the patients for which the classification MMV Label (from approach 2) was mismatching the initial classification group assignment (for 9 patients from the "High" group and 18 patients from the "Low" group) were flipped and a new CMC/D iteration was run. After label flipping, 37 patients were defined as belonging to the "Low" group and 38 to the "High" group. The 301 test/training splits took randomly 15 patients from each group and assigned them to the training set, while leaving the remaining patients in the test set.

Iteration 2: The labels of the patients for which the classification MMV Label was mismatching the classification from Iteration 1 (3 patients from the "High" group and 4 patients from the "Low" group) were flipped and a new CMC/D iteration was run. After label flipping, 36 patients were defined as belonging to the "Low" group and 39 to the "High" group. The 301 test/training splits took randomly 15 patients from each group and assigned them to the training set, while leaving the remaining patients in the test set.

Iteration 3: The labels of the patients for which the classification MMV Label was mismatching the classification from Iteration 2 (1 patient from the "High" group and 2 patients from the "Low" group) were flipped and a new CMC/D iteration was run. After label flipping, 35 patients were defined as belonging to the "Low" group and 40 to the "High" group. The 301 test/training splits took randomly 15 patients from each group and assigned them to the training set, while leaving the remaining patients in the test set.

Step 1144 Define final test/classifier

At step 1144, a final classifier is defined from one or more of the master classifiers (MCs) generated in the previous iterations of the process. There are several possibilities for defining the final classifier, including by selection of one master classifier which has typical performance, by majority vote of all master classifier from each realization of the sample set into training and test sets, by modified majority vote, or other. In this example, the final classifier is created from 301 MCs (301 different realizations of the training/test set split) by taking a majority vote over the MCs.

Modified Majority Vote (MMV)

Within the CMC/D process, each training/test split realization produces one master classifier (MC) generated from the combination of mini-classifiers (mCs) through logistic regression with dropout regularization. The output of this logistic regression is, in the first instance, not a binary label but a continuous probability taking values between 0 and 1. Applying a cutoff (e.g. 0.5, but any choice is possible) to these MC probabilities, we can turn them from a continuous variable into a binary label. So, each MC produces a classification label for a given sample. However, this step is not essential, and one can choose not to apply a cutoff here, but instead to retain the information in the continuous probability variable.

Having obtained the outputs from the MCs (either in terms of binary labels via use of a cutoff or in terms of probabilities), these need to be combined ("bagged" in learning theory language) across the MCs to produce a single binary classification for a particular sample. The way the CMC/D process is implemented means that when a sample is used in the training set of the MC for a realization, the sample almost always classifies correctly (in terms of binary labels after implementation of a cutoff or in terms of probabilities close to target of 0 for one class and 1 for the other class). Hence, use of a simple majority vote over all MCs can produce an artificially good assessment of classifier performance for samples that are used in the training set for some of the MCs. To avoid this, we can use a modified majority vote (MMV) to obtain a classification for samples used directly in the development of the classifier. This procedure is a majority vote over the MC outputs only when the sample is not included in the training set of the MC. (For samples never used in training the MCs, the majority vote and MMV are the same.) This MMV can be used after implementation of a cutoff by taking a majority vote of the classifications produced by all MCs for which the sample is not included in the training set. If, instead, we want to avoid the use of a cutoff at this point and work with the MC probability outputs, the average of the probabilities across the MCs for which the sample is not included in the training set can be calculated. Taking the latter approach, the MMV produces another, averaged, continuous variable that can take values between 0 and 1, an average probability of being in a particular class. This can be converted into a binary classification label via implementation of a cutoff after averaging over MCs.

Direct averaging of the probabilities provides some advantages. If we obtain an average probability for each sample, it is possible to assess simultaneously the performance of the whole family of classifiers that can be produced by imposing different cutoffs on the average probability. This can be done by using the standard receiver operating characteristic

(ROC) curve approach, a well-known method. For a particular choice of cutoff on the average probabilities, classification labels are generated for all samples and these labels can be compared with the known or initially defined class labels to calculate the sensitivity and specificity of the classifier defined by this cutoff. This can be carried out for many values of the cutoff and the results plotted in terms of sensitivity versus 1-specificity (the ROC curve). Overall performance of the family of classifiers can be characterized by the area under the curve (AUC). The ROC curve can be inspected and a particular cutoff selected that best suits the target performance desired for the classifier, in terms of sensitivity and specificity.

Results for Example 1

Approach 1 (no label flips). The resulting CMC/D classifier obtained using the group definitions of this approach achieves a performance described by the following metrics, obtained by comparing the classification label with the defined label only when a given sample is in the test set (Modified Majority Vote, MMV).

Accuracy	Sensitivity (Positive = "High")	Specificity (Negative = "Low)
0.65	0.69	0.61

The distribution of each of these metrics across the 301 MCs created is shown in Figure 2. All the metrics are centered between 60 and 70 %, indicating some performance of the classifiers and some hint that, with better MALDI spectra or a new sample set incorporating more detailed clinical data, a reasonable test might be created.

Regarding the patients assigned to the "Int" group, 10 of them (36 %) are classified as belonging to the "High" group and 18 of them (64 %) to group "Low". This shows a tendency for the intermediate risk patients to be classified as low risk, which justifies the reference set arrangement chosen in approach 2.

Approach 2 (no label flips). The resulting CMC/D classifier obtained achieves a performance described by the following metrics, obtained through MMV.

Accuracy	Sensitivity (Positive = "High")	Specificity (Negative = "Low)

0.64	0.68	0.61

The distributions of each of these metrics across the created 301 MCs are shown in Figure 3. The average performance is similar to that of approach 1 although the accuracy and specificity distributions seem to be narrower. One hypothesis for this behavior might be the larger training sets (15 patients for each group instead of 10).

Approach 3 (with label flips). The resulting CMC/D classifiers, created in each iteration of the labels flips are described by the following average metrics (obtained through MMV):

Iteration	Accuracy	Sensitivity (Positive = "High")	Specificity (Negative = "Low")
0	0.64	0.68	0.61
1	0.91	0.92	0.89
2	0.96	0.97	0.94
3	0.99	0.98	1

It should be noted that the metrics, after iteration 0, do not correspond to accuracy relative to the initial group definitions, due to the label flips. The distributions of these metrics for all the 301 MCs are shown in Figure 4.

After 3 iterations of labels flips, we tried to correlate the final classification labels with the only available clinical data: the Gleason Score. Table 6 summarizes the distribution of the final labels among the different Primary + Secondary Gleason Scores combinations and Table 7 shows the frequency distributions of the final labels versus the initial guess based on TGS. The individual MMV classification labels, obtained after 3 iterations, are shown in the table of Example 1 Appendix C for all the patients.

Table 6: Distribution of the classification labels, obtained after 3 iterations of label flips, according to the different Primary + Secondary Gleason Scores combinations

Risk	Primary + Secondary GS	Total GS	#Patients	#HighClassifications	#LowClassifications
Low	3+3	6	18	8	10

Int	3+4	7	20	8	12
	4+3	7	8	4	4
High	3+5	8	1	1	0
	4+4	8	13	10	3
	5+3	8	2	1	1
	4+5	9	11	7	4
	5+4	9	1	0	1
	5+5	10	1	0	1
		Totals	75	39	36

Table 7: Contingency table showing the frequency distribution according to the initial assignment and the final classification labels achieved after 3 iterations of label flipping.

		Final Label	
		High	Low
Initial group definition	High	19	10
	Low/Int	20	26

By applying a Fisher's exact statistical test to the numbers of Table 7, we get a 9.6 % probability of getting these results or results with stronger correlation between classification labels and those based on TGS assuming that the final classification labels "High" and "Low" are not correlated with TGS risk groups. This p-value is small enough to believe that the final labels may be meaningful and still are somehow related to the TGS distribution and our initial guess for the indolence or aggressiveness (Low, High) labels.

t-SNE visualization

t-Distributed Stochastic Neighbor Embedding (t-SNE) is a tool that allows the visualization of high-dimensional data in a 2D or 3D-map, capturing much of the local structure of the data while also revealing global structure (e.g., the presence of clusters at several scales). The method converts high-dimensional Euclidean distances between data points into Gaussian similarities. In the low-dimensional (2D or 3D) space, the same process is applied using a Student-t distribution instead of a Gaussian distribution to compute the similarity between pairs of points. Then, iteratively, the method searches for a low-dimensional representation of the original data set that minimizes the mismatch between the similarities computed in the high- and low-dimensional spaces. In this way, a 2D or a 3D point map is constructed that allows the visualization and identification of structure in a given dataset and may possibly guide research. The method is introduced by the paper of L.J.P. van

der Maaten and G.E. Hinton, *Visualizing High-Dimensional Data Using t-SNE,* Journal of Machine Learning Research 9 (Nov): 2579-2605 (2008), the content of which is incorporated by reference herein.

In Figure 5A-5C, the 2D maps of the data obtained through t-SNE are shown for 3 different situations: the initial group definitions for approaches 1 and 2 (no label flips), and the final classification labels after 3 iterations of label flips (approach 2 with label flips). Each point is represented with a marker that identifies to which risk label it was assigned ("1" corresponds to "High" and "0" to "Low"). In Figure 5A-5C, the data points are labeled according to the initial group assignments based on TGS for approach 1 (Figure 5A); initial assignment for approach 2 (Figure 5B); final classification labels after 3 iterations of label flips (approach 3) (Figure 5C). "1" (triangles) corresponds to "High" and "0" (circles) to "Low".

Example 1 conclusions

By using MALDI-TOF mass spectra obtained from serum samples from 75 patients for whom Gleason Scores were available, it was possible to create CMC/D binary classifiers that assigned a "High" or a "Low" risk label to each patient and were described by accuracies, sensitivities and specificities of 60-70%, when using Modified Majority Votes taken from 301 Master Classifiers. Two different approaches, differing in the initial group definitions were tried achieving very similar performances. The distributions of the performance metrics of the 301 Master Classifiers are, for both approaches, peaked at the previously mentioned averages, not showing unreasonable shapes. Although the accuracies do not seem to be great, the only available clinical variable (the TGS) is also not a perfect method of risk assessment, and it might be that a study including more clinical data that allows the assessment of outcomes might reveal better performances. Better quality mass spectra, from which more features may be extracted, would also represent a good addition to any new data set.

Starting with the output of approach 2, we have also tried to iteratively flip the initial classification group assignment in order to achieve better performance based on the accuracy metrics (>95 %). The final labels seem to be statistically significantly correlated with risk as assessed by Gleason score (at the 10 % confidence level), deserving further investigation, in which additional clinical data would help. Hence, we obtained a second set of data (Arizona

data set) and applied the process of generating a classifier to this new data set which will be described below in Example 2.

Note that in the procedure of Figure 1 there is step 1146 of validation of the test defined at step 1144 on an internal validation set if available, and a step 1148 of validation of the test on an independent sample set. In the work described in Example 1 we had no internal validation set since the sample size was small and step 1146 was not performed. We could have used the samples described below in Example 2 as a validation set to perform step 1148, however they were plasma and not serum samples, and it was not known whether the classifier would transfer across sample type. So, instead we decided in Example 2 to repeat the classifier generation process of Figure 1.

Example 2: Arizona Data Set

This example involves the analysis of MALDI-TOF mass spectra obtained from plasma samples from patients diagnosed with prostate cancer. All the patients that comprise the data set had their Total Gleason Score (TGS) evaluated as being lower than 8. This range of TGS is considered to be associated with low progression risk and thus these patients are not treated immediately, but instead put in watchful waiting.

The aim of the work described in this Example was to develop a classifier capable of evaluating the aggressiveness or indolence of the prostate cancer of a patient put in watchful waiting (TGS<8). During the clinical study the patients had periodic physician visits (quarterly), having blood samples drawn and their disease status assessed. Evidence of progression could be based on the rate of rise in PSA, Chromogramin A or alkaline phosphatase. Progression could also be detected based on a degradation of patient's symptoms. In case of progression, the patient followed a treatment plan and was dropped from the study. A classifier that could be run at the moment of the cancer diagnosis and could give a good prognostic indication would be a valuable addition to the monitoring of PSA level or other biomarkers as an aid to more refined treatment guidance for this group of patients following diagnosis.

Although the clinical data does not include a precise record of the Time to Progression (TTP) of the patients, we have records of the dates when the patients had their physician visits and their PSA levels assessed. This allows us to make a crude estimation of

the TTP by considering it to be the time difference between the last recorded patient visit and the date of entry into the study.

Available Samples

The dataset used in this classifier feasibility assessment was obtained from another study that investigated the ability of Selenium (Se) to delay the progression of prostate cancer after diagnosis. Patients were randomized into three groups which received placebo or two different doses of Se supplementation. It turned out that Se did not show a protective effect, and thus we assume that the dataset can be used without taking into consideration the supplementation doses given to each patient.

A total of 441 mass spectra acquired from plasma samples of prostate cancer patients were available, corresponding to 147 patients (3 replicates per patient). The spectra of 10 patients (Patient IDs: WW000059, WW000062, WW000068, WW000070, WW000073, WW000074, WW000076, WW000079, WW001835 and WW040568) were not used in the study because there was no clinical/outcome data available for them.

The remaining 137 patients, with valid data for the study, were distributed according to the progression outcome and TGS presented in Table 8.

Table 8: Distribution of the patients according to their outcome and TGS

Outcome	TGS	#Patients	Sub totals
Left the study after randomization (code = 8)	Unknown	2	
	3	2	
	4	3	
	5	14	
	6	58	
	7	13	92
Completed the study (5 years) without progressing (code = 90)	Unknown	0	
	3	0	
	4	5	
	5	5	
	6	12	
	7	0	22
Progressed (code = 99)	Unknown	1	
	3	2	
	4	0	
	5	1	23

	6	17	
	7	2	
		Total	137

Note: Patients WW001545, WW001636 and WW040733 did not have their TGS available, but were still included in study, because the construction of the classifier is based on the progression outcome data and not on TGS.

Spectral Acquisition

Sample Preparation

Samples were thawed on ice and spun at 1500g for 5 minutes at 4°C. Each sample was diluted 1:10 with water and then mixed 1:1 with sinapinic acid (25 mg/ml in 50%ACN/0.1% TFA). The samples were spotted in triplicate.

Acquisition of mass spectra

Spectra of nominal 2,000 shots were collected on a MALDI-TOF mass spectrometer.

Spectral Pre-Processing

Averaging of spectra to produce one spectrum per sample

For each of the 3 replicate spectra available for each patient, the background was estimated and subtracted. Peaks passing a SNR threshold of 6 were identified. The raw spectra (no background subtraction) were aligned using a subset of 15 peaks (Table 2 above) to correct for slight differences in m/z scale between replicate spectra. The aligned spectra were averaged resulting in a single average spectrum for each patient. With the exception of alignment, no other preprocessing was performed on the spectra prior to averaging.

Feature Definitions for New Classifier Development using all valid samples

The averaged spectra from the patients that either progressed during the study or completed the study without progression were background subtracted using the same parameters as in the previous step. They were then initially normalized using PIC with the normalization windows shown in Table 3. Such windows were defined to avoid the peaks due to the known contaminant at m/z ~ 4138 – 4205 Da, the hemoglobin peaks, the peaks used in applicants' VeriStrat test noted in US patent 7,736,905, and everything with poor

reproducibility above m/z = 23000 Da. A total of 104 features were identified by overlaying the spectral sample averages and assessing the spread of the band from the overlay to define the left and right boundaries. Oxidation states were combined into single features when seen. The feature definitions are given in Example 2 Appendix A. Further details on partial ion current normalization of mass spectral data are known in the art and therefore omitted for the sake of brevity, see U.S. patent 7,736,905 for further details.

Normalization of the averaged spectra

Using these specified feature definitions, a feature table for non-normalized spectra (just background subtracted) was constructed for all the 137 patients. The feature values were normalized using partial ion current (PIC) based on the ranges of the features listed in Table 9.

Table 9: Features used in the final PIC normalization. For further details on the feature ranges see Example 2 Appendix A.

Feature
6838
6859
6882
6941
13795
13840
13878
13915
13979
14157

Using this optimized PIC normalization, a new feature table was constructed for all the patients and used downstream in the classifier development process (Figure 1).

Classifier development process

Basically, the classifier development process of Figure 1 and described in detail above was used for generation of a new CMC/D classifier using the Arizona data set.

Division of Samples into Development and Validation Sets

After randomization, patients could leave the study by withdrawal of consent. In addition, Se levels in the blood were monitored regularly during the study and, if three (not necessarily consecutive) Se blood levels above 1,000 ng/ml were measured for a given patient, he was dropped from the study. Although dropped from the study without progression, these patients give us additional information, as we do know that they did not progress while on the study. The distribution of the time on study of this subset of patients is shown in Figure 6. We split this set of samples (from patients leaving the study without progression) into two halves, one of which was added to the other samples (from patients completing the study or progressing during the study) to make the development set (1100, Figure 1) and the second half was used as a partial "validation set" (step 1146 of Figure 1). Note that this "validation" set does not contain any patients with progression during the study, so it will be of limited utility in classifier validation. The splitting of these patients leaving the study without progression into two subsets was made randomly, but stratified to ensure a nearly balanced number of patients with similar TGS and time on study in both sets.

Definition of Initial Classifier Reference Set Groups (step 1102)

We tried to develop a classifier for assessing the aggressiveness or indolence of a patient's cancer and used the inferred progression outcome data for its performance assessment. With this in mind we tried a few different approaches. For each approach, a plot of the 2D mapped space, obtained using t-SNE, is shown in Figure 13 together with the labels shown for the initial development set assignments and for the final classification labels.

Approach 1. We used the samples from patients completing the study without progression (22 patients) and the samples from patients progressing during the study (23 patients) to construct a final (binary) CMC/D classifier that would distinguish between "High" and "Low" risk of cancer progression within 5 years. Patients without progression during the 5 years of the trial were assigned to the "Low" risk reference group and patients who progressed on the study to the "High" risk. The patients who dropped out of the study without progression were left aside and later evaluated with the CMC/D classifier resulting from this approach. This arrangement would presumably give the clearest separation in terms

of progression risk, because we leave aside the patients that dropped out of the study (and for whom we do not really know what happened).

Approach 2. We included half of the patients who dropped out of the study without progression in the test/training splits, by considering the label assigned by the classifier developed in Approach 1 as the initial guess for their risk group.

Approach 3. We tried an iterative label flip process (loop 1142), starting with the group definitions of Approach 2 in order to verify if such method would lead to improved discrimination in terms of outcome data (i.e., better Hazard Ratio for time to progression between High and Low risk groups).

Once the initial definition of the groups for the mini-classifiers has been established, the development set 1100 is split into training (1112) and test sets (1110).

Creation and Filtering of Mini-Classifiers (steps 1120 and 1126)

Many k-nearest neighbor (kNN) mini-classifiers (mCs) that use the training set as their reference set are constructed using single features or pairs of features from the 104 mass spectral features identified. This corresponds to a total of 5,460 possible mCs. The parameters used to traverse the space of mCs for this project are listed in Table 12.

Table 12: Parameters used to create mCs

kNN parameters	
k	5
mC traversal parameters	
Max number of features	2

To target a final classifier that has optimal performance characteristics, these mCs were filtered. Each mC was applied to its training set and the Hazard Ratio (HR) was calculated using the resulting classifications. Only mCs that satisfied thresholds in terms of HR (Table 11) passed filtering and were used further in the process.

Table 11: Summary of mC filtering options used

Filtering Criteria	Filtering Parameters
Hazard Ratio	$3.0 < HR < 10.0$

Generation of MC by combination of mini-classifiers using logistic regression with dropout (CMC/D) (steps 1130, 1132)

Once the filtering of the mCs is complete, the mCs are combined in one master classifier (MC) using a logistic regression trained with the training set labels. To help avoid over-fitting, the regression is regularized using extreme drop out. A total of 5 randomly selected mCs are included in each logistic regression iteration and the weights for the mCs averaged over 10,000 dropout iterations.

Training/Test splits and analysis of master classifier performance (step 1136)

The use of multiple training/test splits in loop 1136 avoids selection of a single, particularly advantageous or difficult, training set for classifier creation and avoids bias in performance assessment from testing on a test set that could be especially easy or difficult to classify. Accordingly, loop 1136 was taken 301 times in Example 2, resulting in 301 different master classifiers (MCs), one per loop. A final classifier is defined at step 1144 from the 301 MCs by taking a majority vote over the MCs. For each approach above this process is described in more detail:

Approach 1. A total of 12 samples from the "High" group and 11 samples from the "Low" group are randomly assigned, in each realization, to the training set while the remaining samples are used in the test set (11 for each of the groups). Each training/test split produces a MC which is applied to the test set at step 1134. At step 1134, the Hazard Ratio is assessed taking into consideration the risk groups defined by the Modified Majority Vote (MMV) classifications.

Approach 2. When the process loops back to step 1108, and samples from patients leaving the study without progression are fed into the development set with risk labels guessed from the results of approach 1, a total of 21 samples from the "High" group and 20 samples from the "Low" group are randomly assigned, in each realization, to the training set 1112 while 30 from the "High" group and 20 for the "Low" are designated as members of the test set 1110 and used for testing at step 1134. The Hazard Ratio is then assessed considering the MMV labels.

Approach 3. At step 1140, one other advantage of these multiple training/test splits is that it might allow for the refinement of the initial assignment of High and Low group labels for the development set at step 1102. In particular, for the training/test splits where a particular sample from the development set is in the test set, the MMV label is obtained. If the sample persistently misclassifies relative to the initial guess as to the risk group, the sample can be moved from the "High" into the "Low" group, or vice versa. Carrying out this procedure for all samples in the development set produces a new, possibly refined version of the group label definitions (1102) which are the starting point for a second iteration of the CMC/D process. This refinement process can be iterated so that the risk groups are determined at the same time as a classifier is constructed, in an iterative way.

In our development of the CMC/D classifier, we performed three different iterations of loop 1142 after the initial iteration (iteration 0):

Iteration 1: The labels of the patients for which the classification MMV Label (from approach 2) was mismatching the initial guess (9 patients from the "High" group and 11 patients from the "Low" group) were flipped and a new CMC/D iteration (steps 1102, 1108, 1120, 1126, 1130, 1134, 1136) was run. After this label flipping, 53 patients were classified as belonging to the "High" group and 38 to the "Low" group. The 301 test/training splits randomly took 18 patients from the "High" group and 19 from the "Low" group to the training set, while leaving the remaining patients in the test set.

Iteration 2: The labels of 6 patients from the "High" group and 1 patient from the "Low" group, whose MMV label didn't match the initial guess were flipped and a new CMC/D iteration was run. After label flipping, 48 patients were classified as belonging to the "High" group and 43 to the "Low" group. The 301 test/training splits randomly took 24 patients from the "High" group and 22 from the "Low" to the training set, while leaving the remaining patients in the test set.

Iteration 3: The labels of 5 patients from the "High" group and 1 patient from the "Low" group were flipped and a new CMC/D iteration was run. After label flipping, 44 patients were classified as belonging to the "High" group and 47 to the "Low" group. The 301 test/training splits randomly took 22 patients from the "High" group and 24 from the "Low" group to the training set, while leaving the remaining patients in the test set.

Results (Example 2)

Approach 1. The final CMC/D classifier, defined at step 1144 as a MMV over all the 301 master classifiers using "Approach 1" above, is characterized in terms of patient outcome by the Kaplan-Meier survival curve shown in Figure 7. The curve is obtained by comparing the groups defined by the samples that were classified with "High" or "Low" MMV labels and the associated time to progression (TTP) from the clinical data associated with the development sample set 1100. The final CMC/D classifier does not seem to be able to distinguish between patients who progressed early and those who progressed later, with the Kaplan-Meier curves for TTP being similar for both groups. The log-rank test gives a p-value of 0.51 and the log-rank Hazard Ratio (HR) is 1.34 with a 95% Confidence Interval (CI) of 0.56 – 3.14. The accuracy metrics of this classifier do not show any particularly interesting performance.

Accuracy	Sensitivity (Positive = "High")	Specificity (Negative = "Low")
0.56	0.68	0.41

While the CMC/D classifier seems to give a sensitivity better than a coin-flip, it seems to do poorly with the "Low" risk patients, misidentifying more than half of them as "High" risk (low specificity).

Regarding the patients left out of the training / test sets (those who left the study without progression), 25 were classified with the label "High" and 21 with the label "Low". Figure 8 is a plot of the Kaplan-Meier curves for TTP for the classifications obtained in Approach 1, including half (46) of the patients who dropped out of the study. For the patients who were used in the test/training splits, the MMV label is taken. For those patients who dropped out of the study (code "8"), the normal Majority Vote of all the 301 MCs is used. Log-rank test p-value = 0.42, log-rank HR = 1.42 with a 95% CI = [0.61 – 3.33].

Approach 2. The final CMC/D classifier obtained for "approach 2" is characterized by the Kaplan-Meier curves shown in Figure 9. The log-rank test gives a p-value of 0.037 and the log-rank Hazard Ratio (HR) is 2.74 with a 95% Confidence Interval (CI) of 1.05 – 5.49. The distribution of the HRs of the 301 MCs is shown in Figure 10 and shows a "well behaved" shape, with a very small fraction of the MCs having a HR ratio lower than 1. The

percent progression free for each classified risk group at 3, 4 and 5 years after study entry is shown in the following table 12:

Table 12

Time on study [years]	Percent Progression Free [%]	
	High	Low
3	63.9	87.3
4	58.8	82.9
5	58.8	82.9

The accuracy metrics (using the MMV labels) are also quite promising in this approach:

Accuracy	Sensitivity (Positive = "High")	Specificity (Negative = "Low")
0.78	0.82	0.73

The distributions of each of these metrics across the created 301 MCs is shown in Figures 11A-11C. The performance of this classifier is fairly good in terms of overall accuracy as well as accuracy within each risk group ("High" and "Low"). In addition, the distributions of the metrics for the 301 MCs are well behaved and centered on the average values.

One hypothesis for this significantly better performance relative to Approach 1 has to do with the bigger training set (24 samples for "High" and 22 for "Low") used in Approach 2 while only 11 of each group were used in Approach 1.

The statistically significant difference between the two Kaplan-Meier curves ("High" and "Low), as demonstrated in Figure 9, supported by the accuracy performances, points to a good discrimination power of the classifier. Taking the development set, those patients classified (by MMV) as "Low" have 87.3 % probability of not progressing in a period of 3 years or 82.9 % in a period of 4 years. This compares to a probability of not progressing of 63.9 % and 58.8 % in a period of 3 and 4 years, respectively, for the patients classified as "High" risk.

Approach 3. The label flip process explained above in Approach 3 did not significantly improve the overall discrimination power of the classifier as compared to Approach 2, as assessed on the associated test sets. However, based on our experience with other projects, we expect the generalization power of a test derived from a convergence of label flips to be better than one derived without label flips. The Kaplan-Meier curves constructed using the MMV labels after each iteration are shown in the Figure 12, along with the outcome statistical metrics. Like the Kaplan-Meier plot of Figure 9, the plots of Figure 12 show a clear separation of the TTP curves between those samples testing Low and High.

t-SNE Visualization

t-Distributed Stochastic Neighbor Embedding (t-SNE) is a tool that allows the visualization of high-dimensional data in a 2D or 3D-map, and is introduced previously in Example 1. Figure 13 shows the 2D maps of the data obtained through t-SNE for the initial assignment of group labels for the development set and for the final classification labels, for each of approaches 1, 2 and 3 described above. Each point is represented with a marker that identifies to which risk label it was assigned ("High" or "Low"). Note that the t-SNE map for the final classification in each of the approaches is more ordered with clustering of the high and low classification labels as compared to the maps of the initial assignments.

Assessment of the final classifier on the 46 patients reserved in the "validation set" cohort did not prove to be informative on the accuracy of the above classifier performance estimates, as analysis was limited by the lack of any progression events in this subgroup. Hence, the 46 patients not included in classifier development were simply combined with the development set to assess the performance of the classifier on the full study population. The results are shown in Figure 14. In particular, Figure 14 shows the Kaplan-Meier curves for TTP using classification labels obtained in Approach 2 and including the classification of the patients of the "validation set". For the patients that were used in the test/training splits the MMV label is taken. For the "validation set" patients, the normal majority vote of all the 301 MCs is used. The log-rank p-value is 0.025 and the log-rank Hazard Ratio 2.95 with a 95% CI of [1.13,5.83]. A table showing the percent progression free for each classified risk group at 3, 4 and 5 years on study is also shown in Figure 14. Again, like Figure 9 and 12, the Kaplan-Meier plot of TTP in Figure 14 shows clear separation of the High and Low groups.

Assessment of correlation of the classification groups with TGS and PSA

It is interesting to assess if the classification groups ("High" and "Low") resulting from the classifier developed in Approach 2 (the one with best performance) are correlated with the Total Gleason Score (TGS) values and PSA baseline levels determined at the beginning of the study. Note that baseline PSA level was available for only 119 of the 137 patients and TGS only for 133 patients.

The distribution of the baseline PSA levels (taken at the beginning of the study) of both the "High" and the "Low" groups as classified in approach 2 are shown in Figure 15. Figure 15 are Box and Whisker plots of the distribution of the PSA baseline levels (taken at the beginning of the study) of the two classification groups (approach 2). For the patients that were used in the test/training splits the MMV label is taken. For the "validation set" patients, the normal majority vote of all the 301 MCs is used. The median PSA of the "High" group is 6.15 ng/ml and that of the "Low" group is 7.42 ng/ml. An unpaired Mann-Whitney test, which compares the ranks of the two groups, gives a p-value of 0.19, which indicates that the PSA distributions of the two groups are not significantly different. Thus, no correlation between the baseline PSA level and the cancer progression risk as given by the classifier is evident. This indicates that the classifier of this Example 2 is, in some sense, an orthogonal measurement to PSA as a predictor of risk of prostate cancer progression.

The distribution of the TGS values of both the "High" and the "Low" groups after classification in Approach 2 is shown in Figure 16. In particular, in Figure 16 for the patients that were used in the test/training splits the MMV label is taken. For the "validation set" patients, the normal majority vote of all the 301 MCs is used. Only the 133 patients (from the development and validations sets) for whom TGS was available are considered in this plot. A Fisher's exact test applied to the table shown in Figure 16 gives a p-value of 0.61 for getting the observed correlation or stronger, assuming that there is no correlation between the TGS values and the classification labels. Thus, the null-hypothesis cannot be rejected and there is no evidence for a correlation between TGS and progression risk category, as given by the developed classifier. Again, this indicates that the classifier of this Example 2 is, in some sense, an orthogonal measurement to TGS as a predictor of risk of prostate cancer progression.

The classifier developed in Approach 2 discriminates fairly well between "High" and "Low" prostate cancer progression risk as evaluated considering the outcome data of the patients. However, neither the TG scores nor the PSA baseline values, which constitute the

only available additional clinical data in the studied data set, seem to be correlated with such risk, as labeled by the classifier. It is possible that other clinical data could show some significant correlation, but this could only be assessed with a more complete data set containing other relevant baseline prognostic factors.

Conclusions for Example 2

Three different approaches were tried in order to develop a CMC/D classifier capable of assessing the aggressiveness or indolence of a patient's cancer in a population with low Total Gleason Score (TGS<8) and in watchful waiting. A development set of MALDI mass spectra obtained from plasma samples from 137 patients was used. Two of the approaches were different in terms of the chosen initial risk group definitions, while the third one consisted of a sequence of label flip iterations. The performance of the CMC/D classifiers was evaluated in terms of the hazard ratio between the two classification groups ("High" risk and "Low" risk) using the outcome data (inferred Time to Progression) available in the data set, as well as in terms of overall accuracy, sensitivity and specificity in terms of predicting a progression within the time of the study.

The best classifier (from Approach 2) is characterized by a hazard ratio of 2.74 with a 95% CI of 1.05 – 5.49, indicating a significantly better prognosis for patients assigned to the "Low" risk group. Our data hint at a better effect size than two commercially available sets: 1. Genomic Health, see Klein, A.E., et al. A 17-gene Assay to Predict Prostate Cancer Aggressiveness in the Context of Gleason Grade Heterogeneity, Tumor Multifocality, and Biopsy Undersampling Euro Urol 66, 550-560 (2014), Odds Ratio ~ 2.1 – 2.3 , in the correct population, but might be because they only have TGS <=6; and 2. Myriad (Cooperberg, M.R., et al. Validation of a Cell-Cycle Progression Gene Panel to Improve Risk Stratification in a Contemporary Prostatectomy Cohort, J Clin Oncol 31, 1428-1434 (2013) in a radical prostatectomy population, Odds Ratio 2.1 -2.3). When considering the whole population of the sample set, the percent progression free in the "High" risk group is 73 % and 69 % at 3 and 4 years, respectively, while in the "Low" group the percent of patients progression free is 92 % and 88 % for the same times after study entry. Although this remains to be validated on an internal validation set (step 1146, Figure 1, which was not available due to the small number of samples available) or, better, an independent validation set from a separate study (step 1148 of Figure 1), these classifier performance estimates are promising: they could possibly lead to a test that would guide actions to take regarding prostate cancer patients with

low TGS. Further investigation of CMC/D classification within this prostate cancer indication is definitely worthwhile.

Example 3: Tyrol Prostate Cancer Screening Demonstration Project Data Set and Deep-MALDI Spectra

A third example of a method for generating a classifier for predicting aggressiveness or indolence of prostate cancer from a multitude of blood-based samples obtained from prostate cancer patients will be described in this section. The methodology of classifier generation is similar to that described above in Examples 1 and 2, see Figure 1. However, in this example we obtained mass spectral data from the samples using a method we refer to as "Deep MALDI", see US patent application publication 2013/0320203 of H. Roder et al., inventors. The description of mass spectral acquisition and spectral data processing set forth in the '203 application publication is incorporated by reference. Additionally, there were some differences in the patient population and course of treatment in this data set as compared to the sets of Examples 1 and 2. Nevertheless, in this section we describe several classifiers that we developed which can be used to predict aggressiveness or indolence of prostate cancer.

The samples analyzed in this study were collected as part of the Tyrol Prostate Cancer Screening Demonstration Project. See Bartsch G, Horninger W, Klocker H, Pelzer A, Bektic J, Oberaigner W et al., *Tyrol Prostate Cancer Demonstration Project: early detection, treatment, outcome, incidence and mortality.* BJU Int 2008: 101(7):809–816. doi: 10.1111/j.1464-410x.2008.07502.x. This is an exemplary study of the use of PSA measurement for prostate cancer screening. The Tyrol region of Austria, with a population of around 7.8 million, is geographically compact, with most of the population within 100 km of the main health care center of Innsbruck. This geographical situation and the willingness of the well-educated population to participate in preventative screening programs make this an ideal location for a population-wide screening study. PSA testing is freely available and encouraged for all men in Tyrol aged between 45 and 75 (and to men over 40 years old with a family history of prostate cancer) at the University Hospital of Innsbruck. Patients taking part in screening could volunteer to participate in the Tyrol Prostate Cancer Screening Demonstration Project (TPCSDP), which implemented an early detection algorithm, which was updated to keep pace with advances in clinical practice during the course of more than 20

years. In addition to collecting samples in the screening setting, the study continued to collect samples from patients once a diagnosis of prostate cancer was made and through various stages of treatment. In addition, clinical, treatment and outcome data were collected. The biobank created as part of the TPCSDP and the associated well-curated clinical data is an invaluable resource for studies aimed at understanding all stages of prostate cancer and its treatment, including investigations directed at the development of test and biomarkers that could improve patient care.

The aim of the study of Example 3 was to develop a blood-based test for prognosis in patients with detected prostate cancer classified as low risk based on Gleason scores obtained from diagnostic biopsy. Here, the term "test for prognosis" is used to interchangeably with a test for whether the patient's prostate cancer is indolent or aggressive, as explained previously in this document. Previous work on plasma samples obtained from a cohort of patients in a "watchful waiting" protocol (Example 2, "low risk" patients with Gleason scores of 7 or lower assigned to a protocol of monitoring rather than immediate radical prostatectomy (RPE)) had shown the potential for such a blood test with clinical relevant performance, as explained in Examples 1 and 2 above. While the group of patients with a Gleason score of six or lower is at relatively low risk of aggressive prostate cancer with quick disease progression and associated impact on survival, the cancer of some patients within this group is aggressive and does progress quickly. It is of clinical relevance to be able to identify which patients within this general low risk category are indeed at higher risk of quick progression of aggressive disease so that these patients can be directed to immediate intervention with appropriate therapies, which patients at genuine low risk can still be assigned to a watchful waiting or active surveillance protocol and avoid possibilities of side effects of unnecessary treatment. Hence, the test described in this Example is of clinical significance.

The option of active surveillance was not commonly offered in Tyrol during the period for which the TPCSDP has adequate follow up for collected samples to be of use for this study. Hence, this project involves analysis of samples collected from patients at time points close to their diagnosis with prostate cancer (diagnosis was always confirmed by biopsy) with Gleason scores of 6 or lower, who went on to undergo radical prostatectomy (RPE). The relative level of aggression of disease could then be assessed by the time to relapse of prostate cancer following RPE.

Samples

Serum samples from prostate cancer patients enrolled in the TPCSDP study were provided and used in this project. For classifier development, only patients were considered who underwent biopsy and RPE within a year of the sample collection. Thus, at the time the patients' blood samples were taken the patients had been diagnosed with prostate cancer but had not yet undergone RPE. In addition, generated mass spectra of the serum samples had to pass quality controls, and clinical data (outcome as well as PSA, %fPSA, and age) had to be available. This left a total of 124 samples for classifier development. The clinical characteristics of the development set of samples are summarized in table 13. All the samples were obtained from prostate cancer patients who, at the time the sample was obtained, had a total Gleason score of 6 or lower.

Table 13: Clinical characteristics of patients with samples used in the development set

		Median (Range)
PSA		3.85 (1.30-8.72)
%fPSA		15.8 (5.7-47.1)
Age at diagnosis		60.5 (42.9-74.3)
		n (%)
Total Gleason Score (biopsy)	2	1 (1)
	3	0 (0)
	4	1 (1)
	5	3 (2)
	6	119 (96)
Gleason Score 1 (biopsy)	1	1 (1)
	2	3 (2)
	3	120 (97)
Gleason Score 2 (biopsy)	1	1 (1)
	2	2 (2)
	3	121 (98)

Total Gleason Score (RPE)	4	1 (1)
	5	24 (19)
	6	40 (32)
	7	51 (41)
	8	6 (5)
	9	1 (1)
	NA	1 (1)
Gleason Score 1 (RPE)	2	7 (6)
	3	108 (87)
	4	8 (6)
	NA	1 (1)
Gleason Score 2 (RPE)	2	20 (16)
	3	48 (39)
	4	49 (40)
	5	5 (4)
	NA	2 (2)
pT Staging (RPE)	2a	18 (15)
	2b	3 (2)
	2c	85 (69)
	3a	17 (14)
	NA	1 (1)

Sample preparation

Samples were thawed and 3 µl aliquots of each test sample (serum from patients with prostate cancer) and quality control serum (a pooled sample obtained from serum of five healthy patients, purchased from ProMedDx, "SerumP3") were spotted onto VeriStrat ® serum cards (Therapak). The cards were allowed to dry for 1 hour at ambient temperature

after which the whole serum spot was punched out with a 6mm skin biopsy punch (Acuderm). Each punch was placed in a centrifugal filter with 0.45 μm nylon membrane (VWR). One hundred μl of HPLC grade water (JT Baker) was added to the centrifugal filter containing the punch. The punches were vortexed gently for 10 minutes then spun down at 14,000 rcf for 2 minutes. The flow-through was removed and transferred back on to the punch for a second round of extraction. For the second round of extraction, the punches were vortexed gently for 3 minutes then spun down at 14,000 rcf for 2 minutes. Twenty microliters of the filtrate from each sample was then transferred to a 0.5 ml eppendorf tube for MALDI analysis.

All subsequent sample preparation steps were carried out in a custom designed humidity and temperature control chamber (Coy Laboratory). The temperature was set to 30 °C and the relative humidity at 10%.

An equal volume of freshly prepared matrix (25 mg of sinapinic acid per 1 ml of 50% acetonitrile:50% water plus 0.1% TFA) was added to each 20μl serum extract and the mix vortexed for 30 sec. The first three aliquots (2 x 2μl) of sample:matrix mix were discarded into the tube cap. Eight aliquots of 2μl sample:matrix mix were then spotted onto 8 different sample spot locations of a stainless steel MALDI target plate (SimulTOF). The MALDI target was allowed to dry in the chamber before placement in the MALDI mass spectrometer.

This set of samples was processed for MALDI analysis in 6 batches. QC samples were added to the beginning (2 preparations) and end (2 preparations) of each batch run.

Spectral acquisition

MALDI spectra were obtained using a MALDI-TOF mass spectrometer (SimulTOF 100 from Virgin Instruments, Sudbury, MA, USA). The instrument was set to operate in positive ion mode, with ions generated using a 349 nm, diode-pumped, frequency-tripled Nd:YLF laser operated at a laser repetition rate of 0.5 kHz. External calibration was performed using a mixture of standard proteins (Bruker Daltonics, Germany) consisting of insulin (m/z 5734.51), ubiquitin (m/z 8565.76), cytochrome C (m/z 12360.97), and myoglobin (m/z 16952.30).

Spectra from each MALDI spot were collected as 800 shot spectra that were 'hardware averaged' as the laser fires continuously across the spot while the stage is moving at a speed of 0.25 mm/sec. A minimum intensity threshold of 0.01 V was used to discard any

'flat line' spectra. All 800 shot spectra with intensity above this threshold were acquired without any further processing. The spectral acquisition used a raster scanning method which is described in U.S. patent application publication 2013/0320203 of H. Roder et al., inventors.

Raster Spectral Preprocessing

Raster spectra rescaling by batch

A coarse alignment step was performed to overcome shifts in the m/z grid resulting from instrument calibration. As the instrument is recalibrated prior to batch acquisition, rescaling was performed independently by batch. An m/z grid shift factor was determined for each batch by comparing peaks in the first acquired reference spectrum to a historical reference spectrum. The m/z grid from the historical reference was applied to the newly acquired spectra with the calculated shift.

Alignment and filtering of raster spectra

This workflow performs a ripple filter, as it was observed that using this procedure improved the resulting averages in terms of noise. The spectra were then background subtracted and peaks were found in order to perform alignment. The spectra that were used in averaging were the aligned ripple filtered spectra without any other preprocessing. The calibration step used a set of 43 alignment points listed below in table 14. Additional filtering parameters required that the spectra had at least 20 peaks and that at least 5 of the alignment points were used in alignment.

Table 14 Alignment points used to align the raster spectra

m/z
3168
4153
4183
4792
5773
5802
6433
6631
7202
7563
7614

7934
8034
8206
8684
8812
8919
8994
9133
9310
9427
10739
10938
11527
12173
12572
12864
13555
13763
13882
14040
14405
15127
15263
15869
17253
18630
21066
23024
28090
28298
33500
67150

Raster Spectra Averaging

Averages were created from the pool of rescaled, aligned and filtered raster spectra. We collected multiple 800 shot spectra per spot, so that we end up with a pool in excess of 500 in number of 800 shot raster spectra from the 8 spots from each sample. We randomly select 500 from this pool, which we average together to create a final 400,000 shot average deep MALDI spectrum.

Pre-Processing of Averaged Spectra

Background estimation and subtraction

Details regarding background subtraction are known in the art and describe in US Patent 7,736,905, the content of which is incorporated by reference. Estimation of background was performed with additional consideration for the high mass region. The two window method of background estimation and subtraction was used (Table 15).

Table 15: Background estimation windows

Wide windows	m/Z	width
	3000	80000
	30000	80000
	31000	160000
Medium windows		
	3000	5000
	30000	5000
	31000	10000

Normalization of spectra

A normalization scalar was determined for each spectrum using a set of normalization windows. These windows were taken from the bin method parameters from a pre-existing project using Deep-MALDI. While a new set of windows was investigated for this Example dataset, a superior set was not found. The normalization was performed in a two stage process. First, the spectra were normalized using the windows found in table 16. Following, the spectra were normalized using the windows found in table 17.

Table 16: Step 1 normalization windows

Left	Right
3530.679	3784.658
3785.029	4078.739
4220.21	4323.065
4875.581	4943.903
5260.635	5435.524
5436.47	5682.433
6050.421	6376.807
6510.852	6601.081
7751.414	7898.826
10606.12	10897.2

10908.61	11356.51
12425.27	12527.26
17710.35	18504.69
19212.92	20743.82
22108.95	22959.15
23738.5	24739.04

Table 17: Step 2 normalization windows

Left	Right
4168.226	4219.839
4875.581	4943.903
4946.131	5077.576
5080.918	5259.892
5260.635	5435.524
6510.852	6601.081
7751.414	7898.826
10606.12	10897.2
10908.61	11356.51

The normalization scalars that were found for each average were compared by t-test by clinical group Relapse (patients relapsing after RPE) versus NoRelapse (patients not relapsing after RPE). As shown in Figure 17, the scalars were not found to be significantly associated with patient relapse status. (Note, at this point we have not yet initiated the classifier development process of Figure 1 and hence have not yet generated or assigned class labels for the samples. We just used the Relapse and NoRelapse labels to confirm that our normalization scalars were acceptable.)

Average spectra alignment

The peak alignment of the average spectra is typically very good; however, a fine-tune alignment step was performed to address minor differences in peak positions in the spectra. A set of alignment points was identified and applied to the analysis spectra (table 18).

Table 18: Calibration points used to align the spectral averages

m/Z
3315
4153

4457
4710
5066
6433
6631
7934
8916
9423
9714
12868
13766
14045
14093
15131
15872
16078
17256
17383
18631
21069
21168
28084
28293
67150

Feature definitions

Feature definitions (i.e., selection of features or m/z ranges to use for classification) were selected interactively by viewing the spectra. The left and right boundaries were assigned manually using an overlay of many spectra. The process was performed iteratively over batches to ensure that the boundaries and features were representative of the whole dataset. A final iteration was performed using the class labels assigned to the spectra of 'Relapse' and 'No Relapse' to ensure selected features were appropriately assigned considering these clinical groupings. A total of 329 features were identified to use in the new classifier development project. These feature definitions were applied to all spectra to create a feature table of feature values. An example of the selected features is shown in Figure 18. The full list of feature definitions can be found in Example 3 Appendix A, table A1. After the feature definitions are assigned, a feature table is created by computing the integrated intensity value of the spectra over each of the features listed in the Example 3 Appendix A table A1.

Batch correction of spectra

SerumP3 Analysis

Two preparations of the reference sample, SerumP3, were plated at the beginning (1, 2) and end (3, 4) of each run. The purpose of these samples is to ensure that variations by batch due to slight changes in instrument performance (for example, aging of the detector) can be corrected for. The section below describes the batch correction procedure. To perform batch correction, one spectrum must serve as the reference for the batch which is an average of one of the preparations from the beginning and one from the end of the batch. A procedure for selecting the pair is first described.

The reference samples were preprocessed as described above. All 329 features were used to evaluate the possible combinations (1-3, 1-4, 2-3, 2-4). We compared each possible combination of replicates using the function:

$$A = \min(\text{abs}(1-\text{ftrval1}/\text{ftrval2}), \text{abs}(1-\text{ftrval2}/\text{ftrval1}))$$

where ftrval1 (ftrval2) is the value of a feature for the first (second) replicate of the replicate pair. This quantity A gives a measure of how similar the replicates of the pair are. For each feature, A is reported. If the value is >0.5, then the feature is determined to be discordant, or 'Bad'. A tally of the bad features is reported for each possible combination. If the value of A is <0.1, then the feature is determined to be concordant and reported as 'Good'. A tally of the Good features is reported for each possible combination. Using the tallies of Bad and Good features from each possible combination, we computed the ratio of Bad/Good. The combination with the lowest ratio was reported as the most similar combination and unlikely to contain any systematic or localized outlier behavior in either of the reference spectra. Finally, if no ratio can be found that is less than 0.25, then the batch is a failure. This threshold was easily met for all batches. The highest threshold was 0.125.

Batch Correction

Batch 1 was used as the baseline batch to correct all other batches. The reference sample was used to find the correction coefficients for each of the batches 2-6 by the following procedure.

Within each batch j ($2 \leq j \leq 6$), the ratio $\hat{r}_i^j = \frac{A_i^j}{A_i^1}$ and the average amplitude $\bar{A}_i^j = \frac{1}{2}\left(A_i^j + A_i^1\right)$ are defined for each i^{th} feature centered at $(m/z)_i$, where A_i^j is the average reference spectra amplitude of feature i in the batch being corrected and A_i^1 is the reference spectra amplitude of feature i in batch 1 (the reference standard). It is assumed that the ratio of amplitudes between two batches follows the dependence

$$r\left(\bar{A}, (m/z)\right) = \left(a_0 + a_1 \ln(\bar{A})\right) + \left(b_0 + b_1 \ln(\bar{A})\right)(m/z) + c_0 (m/z)^2 .$$

On a batch to batch basis, a continuous fit is constructed by minimizing the sum of the square residuals, $\Delta^j = \sum_i \left(\hat{r}_i^j - r^j(a_0, a_1, b_0, b_1, c_0)\right)^2$, and using the experimental data of the reference sample. The SerumP3 reference samples are used to calculate the correction function. Steps were taken to not include outlier points in order to avoid bias in the parameter estimates. The values of the coefficients a_0, a_1, b_0, b_1 and c_0, obtained for the different batches are listed in Example 3 Appendix B (table B.1). The projection in the $\hat{r}_i^j$ versus $(m/z)_i$ plane of the points used to construct the fit for each batch of reference spectra, together with the surface defined by the fit itself, is shown in figure B.1 of Appendix B.

Once the final fit, $r^j\left(\bar{A}, (m/z)\right)$, is determined for each batch, the next step is to correct, for all the samples, all the features (with amplitude A at (m/z)) according to $A_{\text{corr}} = \frac{A}{r^j(\bar{A}, (m/z))}$. After this correction, the corrected $\left(\bar{A}_i^j, (m/z)_i, \hat{r}_i^j\right)$ feature values calculated for reference spectra lie around the horizontal line defined by $r = 1$, as shown in Figure B.2 of Example 3 Appendix B. Post correction coefficients are calculated to compare to quality control thresholds. These coefficients can be found in Example 3 Appendix B table B.2 and the corresponding plots in Figure B.2 of the appendix.

Final feature table assembly

Normalization by Partial Ion Current (PIC) method

The batch corrected feature table was examined to find regions on intrinsic stability to use as the final normalization windows. First, the univariate p values were found by comparing the clinical groups Relapse and No Relapse. Features with p values less than 0.15 were excluded from the PIC analysis as these features may contribute meaningful information

in test development. A set of 188 features were used in the PIC analysis, of which 13 features were used in normalization (see table 19).

Table 19: Features used in the final normalization

PIC Features
4459
4718
4818
4856
6612
6634
8928
9430
9641
9721
12873
12968
13081

Partial ion current normalization of spectra is known in the art, see e.g., U.S. patent 7,736,905, therefore a detailed description is omitted for the sake of brevity.

The normalization scalars computed using the features found in table 19 were compared by clinical group (Relapse, NoRelapse) to ensure normalization would not impede the new classifier development effort. As shown in Figure 19, no association was found between the scalars and the clinical group.

Following PIC normalization, the feature table was finalized for use in the classifier development process described below. That is, integrated intensity values of the features selected for classification was computed and stored in a table for each of the spectra in the development set.

SerumP3 analysis of features

As a final assessment of the preprocessing procedure, the Serum P3 samples were analyzed across all batches in the initial feature table and following the PIC normalization. Prior to batch correction, the median and average CVs were 14.2% and 17.5% respectively. Following batch correction and the final normalization, the median and average CVs for the

SerumP3 samples were 13.7% and 17.4%. These modest improvements reflect the relatively small role of batch correction in the processing of data and demonstrate that little variability is introduced across batches.

Classifier development for Example 3

The new classifier development process was carried out using the platform/methodology shown in Figure 1, and described previously at some length, which we have termed "Diagnostic Cortex"™ . The methodology of Figure 1 is particularly useful for constructing a classifier and building a prognostic test where it is not *a priori* obvious which patients should be assigned to the better or worse prognosis groups (Low and High Risk, or Early and Late relapse/progression, respectively in Figure 1, blocks 1104 and 1106). The risk of overfitting to the data is minimized by regularization (step 1132) and the use of majority voting or average probability cutoff in the selection or definition of the final classifier at step 1144. Confidence in performance metrics for a classifier generated by the method of Figure 1 is enhanced by the observation of many master classifiers (MCs) with similarly good performance and the use of out-of-bag estimates for performance metrics.

The classifier generation procedure is described in some detail in Examples 1 and 2 above. The reader is also directed to the US patent application publication no. 2015/0102216, H. Roder et al. inventors, for a further description and examples of the methodology. The following discussion will provide further explanations of the method in the present Example 3.

Definition of class labels

As shown in Figure 1 step 1102, an initial class label assignment is made for each of the samples in the development set 1100, in this example the 124 blood-based samples that passed QC filtering and for which patient clinical data was available. In this example, we are trying to assign the correct class label for each sample, either Low Risk or High Risk (or, equivalently, Late or Early, respectively), with Low Risk or the equivalent signifying good prognosis, indolence, and late progression of disease and High Risk or the equivalent signifying relatively poor prognosis, aggressiveness of the prostate cancer, and early progression of disease. Time-to-event data, in this case time from sample collection to relapse after RPE was used for assigning the initial class label and classifier training. In this situation, class labels are not obvious and, as shown in Figure 1, the method uses an iterative

method to refine class labels at the same time as creating the classifier. See loop 1142. An initial guess is made for the class labels at step 1102. The samples are sorted on time to relapse and half of the samples with the lowest time-to-event outcome are assigned the "Early" class label (early relapse, i.e. poor outcome, high risk) while the other half are assigned the "Late" class label (late relapse, i.e. good outcome, low risk). A classifier is then constructed using the outcome data and these class labels. This classifier can then be used to generate classifications for all of the development set samples and these are then used as the new class labels for a second iteration of the classifier construction step. This process is iterated until convergence (i.e., the number of persistently misclassified samples is minimized at step 1140 after multiple iterations through the process of Figure 1 including loop 1142).

Creation and Filtering of Mini-Classifiers (steps 1120 and 1126)

The development set samples 1100 were split into training and test sets in multiple different random realizations. See Step 1108, Figure 1 and loop 1136. Six hundred and twenty five realizations (iterations through loop 1136) were used.

In step 1120, many k-nearest neighbor (kNN) mini-classifiers (mCs) that use the training set as their reference set were constructed using subsets of features. In this project we tried two different approaches in terms of the nature of features used by the mini-classifiers. In approach (1), see description below, we used only mass spectral features while in approach (2), see description below, in addition to those mass spectral features, we also used age, PSA and % fPSA as features for classification by the mini-classifiers.

To be able to consider subsets of single, two, or three features and improve classifier performance, it was necessary to deselect features that were not useful for classification from the set of 329 features of Example 3 Appendix A. Feature deselection was carried out using the bagged method outlined in Example 3 Appendix C. In the case of approach (2), age, PSA and % fPSA did not pass the filtering criteria of the bagged method more times than the applied threshold, but we kept these three features for classifier training nevertheless. The methodology of deselection of features is disclosed in U.S. provisional application of J. Röder et al., serial no. 62/154,844 filed April 30, 2015, the contents of which is incorporated by reference herein.

To target a final classifier that has certain performance characteristics, these mCs are filtered at step 1126. Each mC is applied to its training set and performance metrics are

calculated from the resulting classifications of the training set. Only mCs that satisfy thresholds on these performance metrics pass filtering to be used further in the process. The mCs that fail filtering are discarded. For this project only hazard ratio filtering was used, i.e. the classifier was applied to the training set of samples and the hazard ratio calculated between the time to relapse for the two classification groups had to lie within a preset range for the mC to pass filtering. The filtering options used in this project are listed in table 20

Table 20 Filtering parameters used in step 1126 Figure 1

Iteration of loop 1142 of Figure 1	Approach (1)		Approach (2)	
	k	HR filtering range	k	HR filtering range
0	7	3.0 - 10.0	7	3.0 – 10.0
1	7	2.5 – 10.0	7	2.0 – 10.0
2	7	2.5 – 10.0	7	2.5 – 10.0

Here in Table 20 and below, "iteration" means an exercise of classifier generation using the through the loop 1142 of Figure 1 with "iteration 0" referring to an initial iteration through the process, "iteration 1" referring to a second iteration, etc. It will be appreciated that by experimenting with the parameters for the classifier generation process, such as for example filtering parameters for the mini-classifiers, the number of features used by the mini-classifiers, or inclusion of additional non-mass spectral features for classification such as PSA level, age, etc., and performing the process of Figure 1 many times, one can explore the performance of classifiers generated using the process of Figure 1 to find one that has optimal performance.

Combination of mini-classifiers using logistic regression with drop-out

Once the filtering step 1126 is complete, at step 1130, the mini-classifiers are combined into one master classifier using logistic regression trained using the training set labels as indicated 1132 in Figure 1. To help avoid overfitting the regression is regularized using extreme drop out with only a small number of the mCs chosen randomly for inclusion

in each of the logistic regression iterations. The number of dropout iterations in step 1132 was selected based on the typical number of mCs passing filtering to ensure that each mC was likely to be included within the drop out process multiple times. For this project 10 mCs were randomly selected for each drop out iteration. The number of drop out iterations that were carried out in each iteration are listed in table 21.

Table 21: Number of drop out iterations used

Iteration (of loop 1142 of Figure 1)	Approach (1)	Approach (2)
0	300,000	300,000
1	250,000	300,000
2	250,000	200,000

Training/test set splits (loop 1136)

The use of multiple training/test splits (loop 1136) and evaluation of Master Classifier (MC) performance on the new test set in each iteration) avoids selection of a single, particularly advantageous or difficult, training set for classifier creation and avoids bias in performance assessment from testing on a test set that could be especially easy or difficult to classify.

The output of the logistic regression performed at step 1132 that defines each MC is a probability of being in one of the two training classes (Early or Late). During the iterative classifier construction and label refinement process, classifications were assigned by majority vote of the individual MC labels obtained with a cutoff of 0.5 applied to the logistic regression output. This process was modified to incorporate only MCs where the sample was not in the training set (modified, or "out-of-bag" majority vote, MMV).

Example 3 Results

The performance of the classifiers was assessed using Kaplan-Meier plots of time to relapse (time between sample collection and relapse after RPE), TTR, of samples classified as Early and Late, together with corresponding hazard ratios (HRs) and log-rank p values.

Kaplan-Meier plots corresponding to the data in table 22 are shown in Figure 20. The classifications per sample are listed in Example 3 Appendix E. Note in Figure 20 that the classifiers generated in both approaches show a clear separation in time to relapse between the Early and Late class label groups. The results are summarized in table 22.

Table 22: Performance summary for time to relapse (Early vs Late)

	#Early/#Late	HR (95% CI)	log-rank p
Approach (1)	56/68	2.38 (1.08-5.73)	0.035
Approach (2)	55/69	2.49 (1.13-6.07)	0.026

Table 23: Percent relapse free for each classification risk group at 3, 4 and 5 years after sample collection

Time on study [years]	Approach (1)		Approach (2)	
	Early (%)	Late (%)	Early (%)	Late (%)
3	81	94	81	94
4	79	92	79	92
5	77	92	77	92
10	59	83	59	83

Table 24: Multivariate analysis of time to relapse

	Approach (1)		**Approach (2)**	
Covariate	**HR (95% CI)**	**P value**	**HR (95% CI)**	**P value**
Late vs Early	2.41 (1.00-5.82)	0.050	2.64 (1.08 – 6.44)	0.033
PSA	1.18 (0.94-1.47)	0.150	1.18 (0.95 – 1.48)	0.142
fPSA	1.00 (0.94-1.06)	0.983	1.00 (0.94 – 1.06)	0.955
Age (50-59 .vs. <50)	0.94 (0.12-7.59)	0.955	0.98 (0.12 – 7.88)	0.984
Age (60-69 .vs. <50)	0.65 (0.08-5.67)	0.699	0.62 (0.07 – 5.41)	0.665
Age (>70 .vs. <50)	0.59 (0.05-7.08)	0.673	0.57 (0.05 – 6.86)	0.656

Baseline clinical characteristics are summarized by classification group in table 25.

Table 25: Clinical characteristics by classification group

	Approach (1)		Approach (2)	
	Early (N=56)	Late (N=68)	Early (N=55)	Late (N=69)
	Median (Range)			

PSA		3.96 (1.65-8.72)	3.67 (1.3-8.4)	3.99 (1.65-8.72)	3.7 (1.3-8.4)
%fPSA		15.18 (6.2-47.1)	15.88 (5.7-33.1)	15.5 (6.2-47.1)	15.85 (5.7-33.1)
Age at diagnosis		62.0 (46.8-74.3)	59.5 (42.9-72.2)	62.2 (46.8-74.3)	59.5 (42.9-72.2)
		n (%)			
Total Gleason Score (biopsy)	2	1 (2)	0 (0)	1 (2)	0 (0)
	3	0 (0)	0 (0)	0 (0)	0 (0)
	4	0 (0)	1 (1)	0 (0)	1 (1)
	5	1 (2)	2 (3)	1 (2)	2 (3)
	6	54 (96)	65 (96)	53 (96)	66 (96)
Gleason Score 1 (biopsy)	1	1 (2)	0 (0)	1 (2)	0 (0)
	2	1 (2)	2 (3)	1 (2)	2 (3)
	3	54 (96)	66 (97)	53 (96)	67 (97)
Gleason Score 2 (biopsy)	1	1 (2)	0 (0)	1 (2)	0 (0)
	2	0 (0)	2 (3)	0 (0)	2 (3)
	3	55 (98)	66 (97)	54 (98)	67 (97)
Total Gleason Score (RPE)	4	0 (0)	1 (1)	0 (0)	1 (1)
	5	8 (14)	16 (24)	9 (16)	15 (22)
	6	16 (29)	24 (35)	15 (27)	25 (36)
	7	27 (48)	24 (35)	26 (47)	25 (36)
	8	5 (9)	1 (1)	5 (9)	1 (1)
	9	0 (0)	1 (1)	0 (0)	1 (1)
	NA	0 (0)	1 (1)	0 (0)	1 (1)
Gleason Score 1 (RPE)	2	2 (4)	5 (7)	2 (4)	5 (7)
	3	48 (86)	60 (88)	47 (85)	61 (88)
	4	6 (11)	2 (3)	6 (11)	2 (3)
	NA	0 (0)	1 (1)	0 (0)	1 (1)
Gleason Score 2 (RPE)	2	6 (11)	14 (21)	7 (13)	13 (19)
	3	22 (39)	26 (38)	21 (38)	27 (39)
	4	25 (45)	24(35)	24 (44)	25 (36)
	5	3 (5)	2 (3)	3 (5)	2 (3)
	NA	0 (0)	2 (3)	0 (0)	2 (3)
pT Staging (RPE)	2a	5 (9)	13 (19)	5 (9)	13 (19)
	2b	2 (4)	1 (1)	2 (4)	1(1)
	2c	42 (75)	43 (63)	41 (75)	44 (64)
	3a	7 (13)	10 (15)	7 (13)	10 (14)
	NA	0 (0)	1 (1)	0 (0)	1 (1)

The sample classifications were identical for the two approaches except for three samples which swapped classifications between the two. Inclusion of PSA, %fPSA and age may improve classification (Approach 2), but any improvement seems to be quite marginal. This is consistent with the lack of significance of PSA, %fPSA, and age as predictive factors for outcome in the multivariate analysis of table 25. Test classification remains a significant predictor of TTR and is the only available significantly predictive factor of TTR in multivariate analysis. While there is an indication that patients with higher TGS from RPE tend to be assigned an Early classification (5/6 patients with TGS 8 from RPE are classified as Early), larger sample numbers would be required to demonstrate this conclusively. As the

vast majority of patients in this study had TGS by biopsy of 6, it is clear that the classifications obtained from the mass spectral analysis provide information in addition to Gleason score at time of diagnosis, before additional, more reliable tumor staging can be obtained after RPE. Furthermore, this information is independent of PSA and %fPSA measurements as shown by Mann-Whitney tests performed to assess association between these variables and the classification groups (table 26).

Table 26: Mann-Whitney test p-values

	Mann-Whitney test p-value	
	Approach (1)	Approach (2)
PSA	0.105	0.118
% fPSA	0.474	0.767
age	0.111	0.052

Conclusions and clinical significance of classifier generated in Example 3

Applying the procedure of Figure 1 to the feature table obtained from Deep MALDI spectra generated from serum samples collected from low risk prostate cancer patients and associated outcome data, it was possible to create a test able to stratify patients into two groups with better and worse prognosis following RPE, thus differentiating indolent from aggressive prostate cancer using a blood-based sample prior to RPE. The difference in TTR between the two classification groups was statistically significant and clinically meaningful, with a hazard ratio of around 2.5. See Figure 20 and Tables 22-25. Slightly less than half of the patients were assigned to the poor prognosis group (Early). Five years after sample collection (at least 4 years after RPE), 92% of the patients in the good prognosis group were disease free compared with only 77% in the poor prognosis group (Late). This difference increased at ten years post sample collection, with 83% of patients relapse-free in the good prognosis group compared with 59% in the poor prognosis group.

The next step in the development of this potentially clinically useful test is to validate the current results in an independent cohort of patients in a similar indication. (See Figure 1

step 1148). This is planned using an additional sample set collected from patients in the TPCSDP.

These results are in line with previous work on low risk prostate cancer based on plasma samples collected from patients in a watchful waiting protocol. See Examples 1 and 2. In the case of Example 2 (cohort of patients on watchful waiting with TGS of 7 or lower) at five years after sample collection, 88% of patients were progression-free in the good prognosis group compared with 69% of patients in the poor prognosis group, and the hazard ratio for time to progression between good and poor prognosis groups was 2.95 (95% CI: 1.13-5.83). In the present study, the indication was similar (low risk prostate cancer with Gleason score of 6 or below); however, in this present cohort all patients underwent RPE soon after diagnosis. As one would expect that this latter treatment paradigm should improve outcomes for the poor prognosis group more than the good prognosis group, one would expect that the hazard ratio in the present setting should be smaller than that in the watchful waiting setting. The consistency between the two development projects adds to our confidence in the classifiers described in this disclosure and their performance estimates.

As watchful waiting or active surveillance protocols are now becoming more widely applied to these "low risk" prostate cancer patients (see Klotz L, Zhang L, Lam A, et al, Long-term follow up of a large active surveillance cohort of patients with prostate cancer J. Clin. Oncol. 2015 (33):272-277; Morash C, Tey R, Agbassi C, et al., Can Urol Assoc 2015: 9(5-6): 171-178) and there are recognized issues determining whether all these patients should be considered as really "low risk" (see Cooperberg M., Long-Term Active Surveillance for Prostate Cancer: Answers and Questions. J. Clin. Oncol. 2015: 33 (3): 238-240), it would seem that clinical utility of the test in Example 3 may lie more in the prediction of outcomes following diagnosis of prostate cancer with Gleason score from biopsy of 6 or lower in an active surveillance setting, than in prediction of outcomes following RPE in this population. The test could indicate which patients in this "low risk" setting are really good candidates for active surveillance/watchful waiting and which patients should go straight on to more aggressive treatment regimens such as immediate RPE. Acquiring a set of serum samples from an active surveillance population to test performance of this test in that setting is therefore an important next step. As explained above, one might expect an even better separation in outcomes between classification groups in the active surveillance setting.

In addition, as this test is prognostic of relapse following RPE, it could be useful to predict prognosis of patients with higher risk prostate cancer who undergo immediate RPE. Presumably the test should still have some predictive power for time to relapse even in the setting of patients with higher biopsy Gleason scores and it may be able to provide additional information to physicians trying to assess how aggressive a patient's prostate cancer is prior to RPE and possibly indicate the need for additional supportive therapies.

Testing system

After a classifier for predicting indolence or aggressiveness of prostate cancer has been generated and defined as explained in Examples 1-3 (including specifying the feature table with intensity values, final classifier definition, mini-classifier parameters including filtering etc.), it is now ready for use to classify a blood-based sample from a prostate cancer patient to assign a class label for the sample as either Early (high risk of relapse/aggressive) or Late (low risk/indolence). The class label is provided to the medical practitioner ordering the test. The class label can be used to guide treatment, for example initiating more aggressive treatment if the class label is Early or the equivalent.

Figure 21 is an illustration of a system for processing a test sample (in this example a blood-based sample from a prostate cancer patient) using a classifier generated in accordance with Figure 1. The system includes a mass spectrometer 2106 and a general purpose computer 2110 implementing a final classifier 2120 coded as machine-readable instructions and a constitutive mass spectral data set including a feature table 2122 of class-labeled mass spectrometry data stored in memory 2114. It will be appreciated that the mass spectrometer 2106 and computer 2110 of Figure 21 could be used to generate the classifier in accordance with the classifier development process of Figure 1.

The operation of the system of Figure 21 will be described in the context of a predictive test for indolence or aggressiveness of prostate cancer as explained in the above Examples, but it will be appreciated that the methodology described in this section can be used in other examples.

The system of Figure 21 obtains a multitude of samples 2100, e.g., blood-based samples (serum or plasma) from diverse prostate cancer patients. The samples 2100 are used by the classifier (implemented in the computer 2110) to make predictions as to whether the

patient providing the sample is likely to have aggressive or indolent prostate cancer, and typically will be have just been diagnosed with "low risk" prostate cancer (TGS <7) with the physician deciding whether watchful waiting/active surveillance is an appropriate treatment protocol or maybe in an indication ready to undergo RPE and the physician may require additional prognostic information to plan additional supportive therapy post RPE. The outcome of the test is a binary class label, such as Low Risk, Low, Late, or the equivalent, or High Risk, High, Early or the equivalent, with Low or the equivalent indicating that the patient is likely to have an indolent form of the cancer and High meaning that the patient is likely to have an aggressive form of the cancer. The particularly moniker for the class label is not important and could be in accordance any binary system.

The samples may be obtained on serum cards or the like in which the blood-based sample is blotted onto a cellulose or other type card. The obtaining of the mass spectra and the pre-processing of the spectra will normally follow the methods used in generating the classifier in accordance with Figure 1 and described in the Examples. As one possible example, in which typical "Dilute and Shoot" ~ 2000 shot spectra are acquired for each sample, three aliquots of the sample are obtained. The three aliquots of the sample are spotted onto a MALDI-ToF sample "plate" 2102 and the plate inserted into a MALDI-ToF mass spectrometer 2106. The mass spectrometer 2106 acquires a mass spectrum 2108 from each of the three aliquots of the sample. The mass spectra are represented in digital form and supplied to a programmed general purpose computer 2110. The computer 2110 includes a central processing unit 2112 executing programmed instructions. The memory 2114 stores the data representing the mass spectra 2108.

The memory 2114 also stores a final classifier 2120 defined as per the procedure of Figure at step 1144, which includes a) a constitutive mass spectral data set 2122 in the form of a feature table of N class-labeled spectra, where N is some integer number, in this example a development set used to develop the classifier as explained in Examples 1-3. The final classifier 2120 includes b) code 2124 representing a KNN classification algorithm (which is implemented in the mini-classifiers as explained above in Figure 1, as well as values defining the parameters of the mini-classifiers such as features to use, etc.), c) program code 2126 for executing the final classifier generated in accordance with Figure 1 on the mass spectra of patients, including logistic regression weights and data representing master classifier(s) forming the final classifier, and d) a data structure 2128 for storing classification results, including a final class label for the test sample. The memory 2114 also stores program code

2130 for implementing the processing shown at 2150, including code (not shown) for acquiring the mass spectral data from the mass spectrometer in step 2152; a pre-processing routine 2132 for implementing the background subtraction, normalization and alignment step 2154 (details explained above), a module (not shown) for calculating integrated intensity values at predefined m/Z positions in the background subtracted, normalized and aligned spectrum (step 2156), and a code routine 2138 for implementing the final classifier 2120 using the dataset 2122 on the values obtained at step 2156. The process 2158 produces a class label at step 2160. The module 2140 reports the class label as indicated at 2160 (i.e., "low", "Late" or the equivalent).

The program code 2130 can include additional and optional modules, for example a feature correction function code 2136 (described in co-pending US patent application serial no. 14/486,442) for correcting fluctuations in performance of the mass spectrometer, a set of routines for processing the spectrum from a reference sample to define a feature correction function, a module storing feature dependent noise characteristics and generating noisy feature value realizations and classifying such noisy feature value realizations, modules storing statistical algorithms for obtaining statistical data on the performance of the classifier on the noisy feature value realizations, or modules to combine class labels defined from multiple individual replicate testing of a sample to produce a single class label for that sample. Still other optional software modules could be included as will be apparent to persons skilled in the art.

The system of Figure 21 can be implemented as a laboratory test processing center obtaining a multitude of patient samples from oncologists, patients, clinics, etc., and generating a class label for the patient samples as a fee-for-service. The mass spectrometer 2106 need not be physically located at the laboratory test center but rather the computer 2110 could obtain the data representing the mass spectra of the test sample over a computer network.

Further considerations:

Deep-MALDI spectra

As explained in Example 3, it is possible to obtain much more spectral information from the samples used in generation of the classifier using the techniques termed "Deep-MALDI" described in the pending application of Roder et al., serial no. 13/836,436 filed

March 15, 2013, the content of which is incorporated by reference herein. In that technique, more than 100,000 laser shots, and potentially hundreds of thousands or even millions of laser shots, are applied to the MALDI plate spot containing the sample (or as a sum from shots on several such MALDI plate spots). This technique produces a vastly increased amount of spectral information than obtained from typical 2,000 shot "dilute and shoot" spectra. If this technique is used, during the classifier development process there may be many dozens, if not hundreds or even thousands of potential m/z features which can be used for classifier generation. All of these features may be used for classifier development, or a statistical analysis of the features may be performed to identify those features that are most discriminatory or differentially expressed in the Low and High risk patients. If Deep MALDI is used for generating the classifier then the same procedures are used for obtaining spectral data from the sample under test. For example, the methods described in Example 3 are used in both classifier generation and in the testing environment at Figure 21, step 2150, and in the pre-processing steps 2154.

Reselection of feature values during iterative development of the classifier

We have found from other exercises of classifier development using the procedure of Figure 1 that when we have a feature space with a large number of features (typically hundreds or even thousands, as is often the case particular when you use Deep MALDI) and where there is some inherent ambiguity or uncertainty in the initial definition of the class labels during classifier development (as here), it can be advantageous to not only perform label flipping during iterations of the classifier development process of Figure 1 (step 1140) but also at the same time use the new class label groupings to reselect features from the available feature space for classification (again, using the statistical methods for feature selection). This technique is explained in some detail in the related US application serial no. 14/486,442 filed September 15, 2014. In essence, and with reference to Figure 1, when the loop 1142 is entered and new groupings defined at the new iteration of step 1102, at the same time new features are selected in the feature space of available mass spectrometry features using statistical analysis of the features for each of the group labels in the development set. Then, in the subsequent iteration of the step 1120 the mini-classifiers are constructed and executed using the redefined group labels and new features. Repeated iteration of this

process tends to converge on a generalizable and unique definition of both group labels and classification features.

m/z features

Note that, in the above classifier development process and in applying a final classifier to a test sample, we have not found it necessary to correlate the m/z features we use for classification to particular proteins or biomarkers circulating in blood. The validity of the classifier is established by whether it works or not and whether it is generalizable to new samples. The methods we have described demonstrate that the classifier works and is generalizable.

Constitutive set for classification of test samples

Once the classifier generation process of Figure 1 is followed and a final classifier defined for future testing, the data set of class-labeled spectra used in generating the classifier (and in particular a feature table of intensity values at particular m/z ranges) is stored and then used as a reference set for classification using the testing procedure of Figure 21. As noted, this "constitutive set" of spectra is obtained from blood-based samples of humans diagnosed with prostate cancer and includes patients both with indolent cancer and with aggressive cancer. This constitutive set can consist of spectra from all of the samples in a classifier development sample set (1100) or some subset thereof.

The appended claims are offered as further descriptions of the disclosed inventions.

Appendices

Example 1 Appendix A: Feature Definitions Used in New Classifier Development for Prostate Cancer

All feature definitions

Left m/z	Center m/z	Right m/z
3081.583	3090.249	3098.915
3308.621	3329.648	3350.675
4145.045	4160.911	4176.776
4177.923	4197.23	4216.536
4446.822	4468.04	4489.258
4556.927	4572.41	4587.894
4694.939	4717.304	4739.669
4772.094	4790.636	4809.178
4809.56	4824.661	4839.762
4846.644	4860.598	4874.552
4880.493	4896.55	4912.607
5053.678	5071.264	5088.85
5090.762	5109.303	5127.845
5279.182	5292.874	5306.565
6376.924	6430.949	6484.973
6576.342	6590.984	6605.625
6606.408	6652.759	6699.111
6782.803	6797.117	6811.43
6822.441	6835.653	6848.866
6849.6	6859.632	6869.663
6870.397	6891.073	6911.748
6928.141	6946.736	6965.332
7018.671	7055.25	7091.829
7370.816	7387.447	7404.077
7405.224	7419.56	7433.897
7514.946	7556.617	7598.289
7658.311	7681.058	7703.805
7893.703	7945.124	7996.544
7999.22	8034.583	8069.947
8181.751	8209.468	8237.185
8551.43	8562.293	8573.157
8574.723	8589.795	8604.867
8666.721	8691.776	8716.831
8730.019	8759.869	8789.72
8792.411	8818.347	8844.283
8859.941	8870.798	8881.656

8883.796	8923.25	8962.704
9043.529	9067.232	9090.935
9092.465	9154.245	9216.026
9265.334	9282.308	9299.283
9324.362	9346.077	9367.792
9368.098	9381.861	9395.624
9398.071	9433.855	9469.639
9471.168	9487.836	9504.505
9617.762	9641.159	9664.556
9690.553	9717.467	9744.382
9777.537	9793.747	9809.957
9902.628	9935.506	9968.385
10325.87	10347.13	10368.38
10430.11	10453.51	10476.9
11502.59	11525.29	11547.99
11642.19	11673.55	11704.91
11709.09	11730.3	11751.51
12525.06	12571.66	12618.25
12808.63	12864.18	12919.74
13676.71	13706.17	13735.63
13737.77	13758.42	13779.07
13781.02	13797.76	13814.5
13825.46	13839.55	13853.64
13855.09	13877.11	13899.13
13899.72	13913.81	13927.91
13928.52	13939.29	13950.05
13958.08	13970.19	13982.3
14026.12	14041.39	14056.66
14056.69	14066.96	14077.23
14612.46	14676.26	14740.06
15010.07	15126.44	15242.8
15269.09	15291.55	15314.01
15315.44	15345.55	15375.65
15724.22	15852.06	15979.89
16008.09	16031.26	16054.44
16056.83	16093.15	16129.47
16605.01	16682.66	16760.32
17091.97	17138.56	17185.16
17223.02	17266.27	17309.52
17333.41	17393.86	17454.31
17563.93	17601.92	17639.91
18598.12	18640.3	18682.49
21007.96	21074.42	21140.87
21949.42	22238.76	22528.1
27742.59	27978.55	28214.5

28227.94	28314.56	28401.17
28793.87	28909.23	29024.6
29572.29	29667.12	29761.95

Example 1 Appendix B: Samples from the Oregon Prostate Cancer data set used in Classifier Development

Samples used in the Classifier Development and clinical data available

Patient ID	Primary Gleason Score	Secondary Gleason Score	Total Gleason Score
2	3	3	6
3	3	3	6
9	3	3	6
10	3	3	6
15	3	3	6
18	3	3	6
19	3	3	6
20	3	3	6
21	3	3	6
26	3	3	6
29	3	3	6
32	3	3	6
22--EB	3	3	6
N--04--1	3	3	6
N--06--0	3	3	6
N--15--0	3	3	6
N--18--0	3	3	6
OET	3	3	6
5	3	4	7
6	3	4	7
7	3	4	7
11	3	4	7
13	3	4	7
14	3	4	7
16	3	4	7
17	3	4	7
25	3	4	7
27	3	4	7
13 --WFG	3	4	7
N--07--0	3	4	7
N--08--0	3	4	7
N--19--1	3	4	7
N--22--0	3	4	7

N--27--0	3	4	7
N--31--1	3	4	7
N--39--1	3	4	7
UW-01	3	4	7
UW-12	3	4	7
KP-02	4	3	7
KP-03	4	3	7
KP-04	4	3	7
N--03--0	4	3	7
N--23--0	4	3	7
UW-09	4	3	7
UW-10	4	3	7
UW-11	4	3	7
8	4	4	8
33	4	4	8
N--01--0	4	4	8
N--02--0	4	4	8
N--10--0	5	3	8
N--13--1	4	4	8
N--16--1	4	4	8
N--21--0	4	4	8
N--24--0	4	4	8
N--32--1	4	4	8
N--35--1	4	4	8
N--36--1	3	5	8
UW-06	5	3	8
UW-08	4	4	8
UW-16	4	4	8
UW-17	4	4	8
1	4	5	9
23	4	5	9
N--11--0	4	5	9
N--14--1	4	5	9
N--25--0	4	5	9
N--28--0	4	5	9
N--34--0	4	5	9
N--5--1	5	4	9
UW-03	4	5	9
UW-07	4	5	9
UW-13	4	5	9
UW-18	4	5	9
KP-05	5	5	10

Example 1 Appendix C: MMV labels attributed to each patient after 3 label flips

Risk levels as defined in Table 1 are also included.

Patient ID	Final MMV Label	Definition (as in Table 1)
1	High	High
10	Low	Low
11	High	Int
13	Low	Int
13-WFG	Low	Int
14	Low	Int
15	High	Low
16	Low	Int
17	Low	Int
18	Low	Low
19	Low	Low
2	High	Low
20	High	Low
21	Low	Low
22-EB	Low	Low
23	High	High
25	Low	Int
26	Low	Low
27	High	Int
29	High	Low
3	High	Low
32	High	Low
33	High	High
5	Low	Int
6	Low	Int
7	High	Int
8	High	High
9	Low	Low
KP-02	High	Int
KP-03	High	Int
KP-04	Low	Int
KP-05	Low	High
N-01-0	Low	High
N-02-0	High	High
N-03-0	Low	Int
N-04-1	High	Low
N-06-0	Low	Low
N-07-0	High	Int
N-08-0	Low	Int
N-10-0	Low	High
N-11-0	Low	High

N-13-1	Low	High
N-14-1	Low	High
N-15-0	Low	Low
N-16-1	High	High
N-18-0	High	Low
N-19-1	Low	Int
N-21-0	High	High
N-22-0	High	Int
N-23-0	Low	Int
N-24-0	High	High
N-25-0	High	High
N-27-0	High	Int
N-28-0	Low	High
N-31-1	High	Int
N-32-1	High	High
N-34-1	High	High
N-35-1	High	High
N-36-1	High	High
N-39-1	High	Int
N-5-1	Low	High
OET	Low	Low
UW-01	Low	Int
UW-03	High	High
UW-06	High	High
UW-07	Low	High
UW-08	Low	High
UW-09	High	Int
UW-10	High	Int
UW-11	Low	Int
UW-12	Low	Int
UW-13	High	High
UW-16	High	High
UW-17	High	High
UW-18	High	High

Example 2 appendices

Appendix A: Feature Definitions Used in New Classifier Development for Prostate Cancer

All feature definitions

Left m/z	Center m/z	Right m/z
3153.208	3164.868	3176.529
3353.837	3372.531	3391.224
3419.727	3442.492	3465.257
3473.03	3490.798	3508.566
4055.23	4068.741	4082.252
4137.036	4153.693	4170.351
4170.721	4190.155	4209.588
4698.8	4712.168	4725.537
4759.221	4802.16	4845.099
4983.911	5008.526	5033.142
5053.501	5069.418	5085.336
5090.443	5104.695	5118.946
5121.167	5133.938	5146.708
5525.044	5570.204	5615.365
5843.444	5879.72	5915.996
5978.924	6000.949	6022.974
6366.989	6387.348	6407.707
6409.047	6457.28	6505.514
6518.615	6532	6545.385
6623.863	6631.566	6639.268
6566.766	6632.507	6698.248
6785.31	6794.313	6803.315
6826.591	6838.081	6849.57
6850.447	6859.449	6868.452
6870.181	6882.263	6894.346
6916.615	6940.779	6964.943
7459.185	7488.68	7518.175
7526.229	7562.357	7598.486
7601.624	7617.379	7633.133
7657.771	7674.354	7690.938
7887.538	7929.737	7971.936
7976.674	7990.148	8003.622
8005.695	8033.827	8061.96
8188.822	8205.257	8221.693
8226.727	8238.276	8249.825
8651.726	8684.856	8717.985
8726.499	8759.074	8791.648
8797.941	8827.554	8857.167
8887.061	8931.11	8975.16
9041.789	9061.223	9080.657
9084.787	9147.53	9210.273
9281.714	9303.369	9325.024
9329.466	9346.308	9363.151
9366.482	9382.584	9398.686

9400.788	9437.805	9474.821
9623.278	9643.606	9663.934
9693.159	9709.261	9725.363
9727.954	9747.388	9766.821
9917.122	9933.965	9950.807
10045.12	10073.81	10102.5
10130.62	10227.42	10324.21
10326.06	10342.54	10359.01
10409.79	10460.69	10511.59
10610.05	10649.29	10688.53
10778.11	10838.26	10898.41
11501.77	11535.78	11569.79
11653.08	11680.38	11707.67
11713.23	11736.36	11759.5
12524.61	12570.59	12616.58
12768.69	12848.51	12928.32
13256.1	13278.08	13300.06
13490.6	13556.3	13622.01
13660.37	13699.01	13737.65
13740.89	13760.09	13779.29
13781.6	13794.79	13807.98
13825.56	13840.37	13855.17
13857.95	13878.31	13898.67
13901.91	13915.09	13928.28
13928.74	13942.62	13956.51
13960.21	13979.18	13998.15
14020.82	14048.12	14075.42
14078.2	14103.42	14128.63
14130.48	14156.63	14182.77
14339.49	14402.65	14465.81
14830.89	14885.25	14939.62
14941.47	14989.6	15037.72
15039.57	15067.33	15095.09
15096.02	15155.01	15214.01
15270.23	15291.74	15313.26
15314.65	15346.57	15378.5
15705.12	15736.59	15768.05
15769.44	15801.13	15832.83
15833.76	15867.07	15900.39
15901.31	15925.14	15948.97
15951.75	15981.59	16011.43
16014.21	16034.34	16054.47
16055.85	16088.94	16122.02
16125.23	16148	16170.78
16175.11	16204.76	16234.4
16600.22	16666.38	16732.53

17222.34	17246.92	17271.5
17272.23	17288.13	17304.04
17358.26	17377.42	17396.58
17398.03	17417.91	17437.79
17852.61	17901.41	17950.21
18594.98	18622.82	18650.65
18652.82	18677.4	18701.98
20902.69	20954.66	21006.62
21011.14	21064.46	21117.78
23258.31	23571.9	23885.49
27660.21	27839.26	28018.31
28019.44	28098.51	28177.59
28227.29	28315.97	28404.65
28815.5	28888.93	28962.36

Example 2

Appendix B: Samples from the Oregon Prostate Cancer data set used in Classifier Development

Samples used in the Classifier development and clinical data available

PatientID	Code	TGS	PSA baseline	TimeToProgression [days]	Censor	Set
WW001354	8	7	4.69	714	0	Development
WW001537	99	6	5.85	824	1	Development
WW001578	8	6	10.43	83	0	Development
WW001636	99	Unknown	3.75	985	1	Development
WW001826	99	6	19.88	207	1	Development
WW001883	8	5	Unknown	1325	0	Development
WW001990	99	7	Unknown	1279	1	Development
WW002048	99	6	Unknown	644	1	Development
WW002055	99	3	Unknown	917	1	Development
WW002063	8	6	Unknown	412	0	Development
WW002089	99	6	Unknown	99	1	Development
WW002097	99	5	Unknown	810	1	Development
WW040139	8	6	8.11	1918	0	Development
WW040220	8	6	6.6	1286	0	Development
WW040238	8	6	6.3	1106	0	Development
WW040261	8	6	6.7	1895	0	Development
WW040295	8	5	1	91	0	Development
WW040303	8	6	9.2	1726	0	Development
WW040311	8	6	7.9	1820	0	Development
WW040360	8	6	14.1	165	0	Development

WW040386	8	6	10	1650	0	Development
WW040444	99	6	4.4	350	1	Development
WW040451	99	6	8.6	986	1	Development
WW040469	99	6	Unknown	461	1	Development
WW040527	8	4	8.6	1701	0	Development
WW040543	8	7	3.1	1705	0	Development
WW040550	99	6	24.8	889	1	Development
WW040683	99	3	5.5	769	1	Development
WW040709	8	6	3.1	1509	0	Development
WW040717	99	6	10.5	1210	1	Development
WW040790	8	6	11.5	1432	0	Development
WW040873	8	6	4.1	1363	0	Development
WW040899	99	6	9.1	455	1	Development
WW040907	99	6	1.7	355	1	Development
WW040931	8	5	7.8	362	0	Development
WW040980	99	6	6	1013	1	Development
WW041020	8	6	4.7	1098	0	Development
WW041046	8	6	8.8	90	0	Development
WW041053	99	6	5.4	909	1	Development
WW041145	8	6	4	96	0	Development
WW041194	8	5	0.4	912	0	Development
WW001180	99	6	26.6	609	1	Development
WW001198	99	6	13.82	581	1	Development
WW001313	99	7	12.68	512	1	Development
WW001438	8	5	9.7	447	0	Development
WW001495	99	6	7.5	1365	1	Development
WW001958	8	6	Unknown	1573	0	Development
WW001966	8	6	Unknown	560	0	Development
WW040030	99	6	18.6	176	1	Development
WW040758	8	6	8.2	275	0	Development
WW001016	90	5	2.75	1813	0	Development
WW001131	90	6	15.36	1723	0	Development
WW001719	90	5	8.14	1825	0	Development
WW001727	90	6	8.8	1638	0	Development
WW001909	90	6	0.5	1840	0	Development
WW001982	90	4	Unknown	1832	0	Development
WW002014	90	4	Unknown	1819	0	Development
WW002071	90	5	Unknown	1807	0	Development
WW040014	90	6	1.35	1714	0	Development
WW040097	90	5	6.93	2010	0	Development
WW040345	8	6	6.2	1826	0	Development
WW001115	8	6	10.21	1018	0	Development
WW001214	8	6	8.92	801	0	Development
WW001222	8	6	15.06	761	0	Development
WW001230	8	5	9.11	71	0	Development
WW001255	90	4	9.29	1736	0	Development

WW001339	8	6	6.96	506	0	Development
WW001396	90	6	7.33	1911	0	Development
WW001404	8	3	1.84	490	0	Development
WW001446	90	5	10.13	1818	0	Development
WW001487	90	6	2.8	1897	0	Development
WW001503	8	7	8.89	303	0	Development
WW001545	8	Unknown	2.12	1553	0	Development
WW001586	90	6	8.32	1817	0	Development
WW001594	8	6	4.71	1204	0	Development
WW001701	90	6	4.31	1748	0	Development
WW001735	90	6	10.48	1839	0	Development
WW001768	90	6	8.07	1900	0	Development
WW001792	90	6	4.28	1871	0	Development
WW001875	90	4	0.76	1827	0	Development
WW002105	90	4	Unknown	1846	0	Development
WW040022	90	6	11.4	1826	0	Development
WW040048	8	6	5.34	1034	0	Development
WW040188	8	6	25.7	295	0	Development
WW040352	8	7	9.2	1367	0	Development
WW040436	8	7	5.4	1722	0	Development
WW040634	8	6	0.5	1672	0	Development
WW040642	8	5	8.3	1469	0	Development
WW040667	8	6	4.9	999	0	Development
WW040725	8	7	9.1	1461	0	Development
WW001800	8	5	2.98	91	0	Validation
WW001842	8	5	3.41	442	0	Validation
WW002006	8	5	Unknown	119	0	Validation
WW002030	8	5	Unknown	507	0	Validation
WW002113	8	6	13.9	1654	0	Validation
WW040055	8	4	2.26	1981	0	Validation
WW040121	8	6	8.67	364	0	Validation
WW040170	8	6	12.8	909	0	Validation
WW040246	8	6	16.3	1728	0	Validation
WW040287	8	5	4.4	1872	0	Validation
WW040337	8	6	6.6	1848	0	Validation
WW040378	8	6	5.4	555	0	Validation
WW040493	8	7	15.1	1715	0	Validation
WW040501	8	7	12.1	761	0	Validation
WW040519	8	6	15.2	1716	0	Validation
WW040659	8	6	4.5	1597	0	Validation
WW040691	8	6	5.3	1286	0	Validation
WW040733	8	Unknown	6.1	629	0	Validation
WW040741	8	6	3.7	652	0	Validation
WW040816	8	7	5.9	1426	0	Validation
WW040915	8	6	1.1	1363	0	Validation
WW040949	8	6	1.8	292	0	Validation

WW040972	8	6	13.4	95	0	Validation
WW041103	8	6	6.1	186	0	Validation
WW041129	8	4	1.2	93	0	Validation
WW041152	8	6	6.5	97	0	Validation
WW041186	8	6	4.3	1096	0	Validation
WW001321	8	6	6.74	1485	0	Validation
WW001420	8	6	9.81	763	0	Validation
WW001511	8	5	11.29	1406	0	Validation
WW001644	8	6	19.47	476	0	Validation
WW001677	8	6	6.17	1825	0	Validation
WW001859	8	7	3.5	1658	0	Validation
WW001917	8	6	Unknown	1099	0	Validation
WW001974	8	3	Unknown	368	0	Validation
WW040105	8	6	7.1	1903	0	Validation
WW040147	8	6	7.12	87	0	Validation
WW040162	8	6	4.68	1967	0	Validation
WW040600	8	6	5	1003	0	Validation
WW040618	8	6	19.1	1568	0	Validation
WW040675	8	7	5.5	442	0	Validation
WW040824	8	7	3	1281	0	Validation
WW040832	8	6	3.3	1279	0	Validation
WW041038	8	5	5.8	1181	0	Validation
WW041095	8	6	0.8	1197	0	Validation
WW041160	8	6	7.1	1026	0	Validation

Example 3

Appendix A: Feature Definitions

Table A.1 Feature definitions n=329

Left	Center	Right
3073.625	3085.665	3097.705
3098.586	3109.891	3121.197
3123.546	3138.669	3153.793
3190.793	3210.615	3230.436
3230.73	3242.623	3254.516
3255.103	3264.647	3274.191
3296.802	3316.77	3336.739
3349.072	3363.608	3378.144
3380.2	3391.946	3403.692
3405.16	3420.283	3435.407
3435.7	3445.097	3454.494
3454.788	3465.359	3475.931
3490.725	3508.305	3525.884
3531.431	3553.896	3576.36
3581.059	3593.099	3605.138
3665.631	3679.286	3692.941
3693.94	3712.036	3730.132
3745.211	3754.755	3764.299
3764.592	3775.604	3786.616
3798.592	3814.263	3829.933
3831.545	3841.53	3851.514
3876.474	3887.486	3898.499
3898.583	3906.18	3913.777
3914.356	3928.158	3941.959
3942.253	3953.412	3964.571
3994.23	4008.619	4023.008
4024.182	4031.67	4039.159
4039.452	4050.464	4061.476
4086.437	4098.77	4111.104
4111.308	4118.525	4125.742
4126.043	4133.109	4140.176
4198.812	4209.788	4220.764
4241.573	4249.445	4257.316
4258.28	4265.83	4273.38
4273.837	4286.166	4298.495
4328.264	4340.217	4352.17
4352.32	4360.815	4369.31
4369.611	4380.962	4392.314
4393.817	4408.627	4423.436
4424.789	4431.179	4437.569
4437.87	4459.22	4480.57
4496.507	4506.58	4516.654
4552.738	4564.991	4577.245
4577.384	4592.602	4607.819
4616.938	4625.282	4633.627
4633.927	4643.324	4652.721
4664.148	4675.274	4686.4
4690.609	4717.673	4744.736
4746.54	4756.162	4765.785
4766.386	4773.152	4779.918
4780.218	4791.194	4802.17
4802.621	4817.881	4833.142
4836.299	4855.995	4875.691
4880.953	4891.177	4901.401
4909.52	4918.316	4927.111
4927.261	4937.636	4948.01
4948.16	4963.045	4977.93
4987.552	4998.979	5010.405
5011.007	5020.103	5029.199
5029.65	5041.077	5052.504
5053.556	5067.839	5082.123
5087.535	5104.074	5120.613
5121.383	5134.355	5147.326
5149.837	5156.322	5162.808
5164.9	5181.637	5198.375
5209.77	5223.753	5237.736
5238.036	5247.734	5257.432
5275.624	5289.757	5303.89
5347.191	5358.543	5369.894
5370.646	5377.186	5383.726
5383.877	5389.815	5395.754
5395.905	5403.422	5410.94
5411.09	5416.277	5421.464
5421.615	5429.809	5438.003
5439.807	5449.204	5458.601
5463.713	5472.057	5480.402
5481.454	5495.813	5510.171
5510.472	5521.222	5531.972
5535.439	5557.829	5580.219
5663.828	5675.387	5686.946
5696.097	5709.823	5723.549
5740.923	5748.044	5755.165
5756.127	5762.381	5768.636
5769.502	5776.671	5783.84
5787.496	5795.483	5803.469
5803.95	5815.979	5828.007
5828.68	5842.055	5855.431
5856.297	5867.218	5878.14

5879.39	5889.157	5898.924
5899.02	5910.808	5922.595
5924.106	5934.47	5944.834
5946.068	5961.861	5977.654
5978.694	5997.458	6016.222
6016.895	6026.806	6036.717
6052.178	6074.758	6097.337
6099.552	6108.597	6117.642
6161.136	6170.373	6179.611
6184.807	6192.938	6201.069
6201.261	6209.585	6217.908
6218.004	6226.039	6234.074
6245.993	6254.58	6263.166
6273.718	6283.244	6292.771
6292.867	6301.238	6309.61
6321.927	6331.742	6341.556
6349.371	6357.324	6365.277
6379.18	6386.108	6393.037
6393.229	6399.965	6406.7
6408.625	6437.829	6467.033
6467.129	6485.171	6503.214
6520.161	6531.72	6543.279
6548.095	6556.042	6563.989
6577.691	6589.431	6601.17
6603.961	6611.61	6619.26
6620.319	6634.319	6648.32
6648.512	6657.076	6665.64
6668.623	6680.651	6692.68
6700.438	6707.101	6713.764
6719.237	6731.65	6744.063
6744.599	6755.677	6766.754
6767.638	6773.171	6778.704
6786.982	6792.762	6798.542
6799.97	6808.919	6817.868
6824.892	6836.679	6848.467
6848.948	6859.629	6870.31
6873.797	6881.433	6889.07
6890.609	6897.599	6904.589
6914.565	6921.586	6928.606
6933.102	6941.477	6949.853
6950.469	6956.75	6963.032
6963.34	6970.545	6977.75
6978.92	6992.222	7005.524
7014.269	7022.06	7029.85
7029.912	7034.592	7039.272
7039.395	7045.154	7050.912
7067.293	7073.79	7080.287
7119.824	7147.228	7174.633
7177.589	7188.951	7200.314
7232.783	7257.933	7283.084
7292.812	7300.633	7308.454
7316.187	7321.946	7327.705
7327.772	7333.817	7339.863
7339.896	7346.093	7352.29
7352.819	7360.754	7368.688
7379.768	7393.009	7406.249
7406.3	7419.793	7433.287
7433.608	7447.584	7461.56
7463.692	7479.362	7495.032
7497.824	7510.356	7522.889
7731.041	7738.801	7746.561
7761.341	7779.077	7796.813
7808.996	7828.02	7847.044
7849.362	7871.424	7893.485
7904.954	7912.836	7920.719
8007.424	8015.07	8022.717
8134.028	8157.158	8180.287
8195.752	8206.991	8218.23
8238.737	8253.917	8269.098
8304.472	8328.669	8352.866
8353.406	8363.536	8373.667
8380.133	8391.495	8402.857
8404.767	8413.388	8422.01
8422.133	8430.231	8438.33
8457.421	8464.072	8470.723
8470.846	8477.558	8484.271
8497.292	8508.651	8520.011
8520.544	8531.198	8541.852
8554.723	8564.761	8574.799
8575.476	8585.268	8595.06
8618.77	8631.702	8644.635
8649.87	8660.554	8671.239
8671.855	8696.119	8720.383
8720.568	8728.512	8736.456
8736.518	8745.817	8755.116
8756.348	8770.604	8784.861
8791.574	8796.962	8802.351
8802.474	8822.181	8841.887
8861.964	8871.848	8881.732
8883.826	8890.538	8897.251

8897.436	8901.654	8905.873
8905.934	8928.258	8950.582
8967.272	8974.415	8981.559
8988.149	8997.971	9007.794
9010.011	9020.295	9030.58
9030.764	9038.216	9045.668
9055.367	9062.134	9068.902
9069.184	9079.194	9089.205
9091.547	9097.798	9104.049
9115.171	9134.336	9153.501
9196.082	9206.437	9216.792
9217.991	9226.317	9234.643
9234.742	9244.546	9254.35
9254.941	9263.932	9272.924
9273.256	9291.73	9310.203
9310.761	9318.865	9326.969
9344.962	9359.289	9373.615
9387.662	9395.293	9402.923
9410.817	9430.014	9449.211
9475.524	9484.41	9493.296
9494.536	9504.042	9513.549
9520.898	9534.803	9548.707
9559.484	9576.179	9592.874
9615.006	9641.179	9667.352
9689.387	9720.901	9752.414
9784.265	9793.021	9801.777
9840.895	9862.594	9884.294
9908.49	9918.931	9929.371
9929.66	9941.495	9953.331
10002.41	10012.36	10022.32
10066.88	10079.24	10091.61
10091.7	10102.24	10112.77
10120.09	10135.29	10150.49
10150.78	10162.62	10174.45
10174.65	10185.23	10195.82
10195.91	10210.35	10224.78
10225.16	10236.04	10246.91
10250.09	10263.03	10275.97
10276.55	10285.11	10293.68
10295	10313.15	10331.3
10333.03	10346.26	10359.49
10359.69	10365.85	10372
10408.98	10420.87	10432.75
10436.76	10448.55	10460.34
10472.41	10480.21	10488.01

10488.32	10503.84	10519.36
10521.66	10532.67	10543.68
10543.99	10551.18	10558.36
10573.66	10589.18	10604.71
10615.84	10636.81	10657.79
10705.55	10734.07	10762.59
10773.07	10782.59	10792.12
10792.19	10804.96	10817.72
10827.72	10846.77	10865.83
10912.98	10923.56	10934.15
10954.02	10965.58	10977.14
11035.47	11057.93	11080.38
11092.07	11107.19	11122.31
11137.08	11149.06	11161.04
11288.09	11306.44	11324.78
11357.26	11375.9	11394.54
11396.27	11410.09	11423.9
11425.13	11447.54	11469.96
11505.19	11532.05	11558.92
11613	11627.24	11641.47
11642.18	11654.28	11666.38
11666.74	11688.44	11710.15
11712.08	11733.43	11754.78
11756.23	11786.66	11817.09
11817.93	11834.77	11851.61
11868.93	11898.52	11928.11
11928.7	11944.87	11961.05
12143.52	12158.28	12173.04
12271.47	12290.85	12310.22
12400.43	12412.62	12424.81
12433.83	12457.39	12480.94
12489.93	12507.27	12524.61
12536.4	12565.8	12595.2
12597.2	12613.41	12629.61
12647.98	12674.21	12700.44
12716.47	12738.02	12759.57
12761.24	12785.79	12810.35
12829.73	12873.16	12916.59
12935.63	12967.54	12999.44
13051.23	13080.96	13110.69
13117.71	13134.41	13151.12
13225.86	13241.27	13256.68
13258.69	13274.73	13290.77
13304.99	13318.16	13331.32
13347.56	13364.6	13381.64

13402.57	13413.92	13425.28
13510.26	13524.96	13539.66
13551.35	13567.72	13584.09
13597.13	13624.17	13651.21
13703.7	13721.07	13738.44
13740.45	13762.16	13783.88
13784.55	13798.24	13811.94
13826.64	13842.84	13859.05
13864.06	13882.93	13901.81
13903.15	13916.01	13928.87
13929.87	13943.07	13956.27
13958.61	13983.66	14008.72
14015.73	14042.8	14069.86
14076.2	14097.59	14118.97
14124.31	14149.03	14173.76
14178.77	14198.98	14219.19
14231.55	14254.61	14277.66
14281.33	14306.56	14331.78
14461.45	14515	14568.55
14751.73	14784.47	14817.21
14857.63	14884.53	14911.42
14949.73	14975.44	15001.15
15009.14	15028.79	15048.44
15527.48	15563.22	15598.97
15713.63	15753.95	15794.27
16465.93	16502.17	16538.42
16610.92	16630.13	16649.34
16999.46	17032.54	17065.61
17104.03	17148.13	17192.23
17225.64	17270.91	17316.18
17318.65	17335.6	17352.55
17359.48	17401.7	17443.93
17445.13	17476.37	17507.61
17569.08	17604.33	17639.57
17774.54	17815.47	17856.39
17982.34	18031.12	18079.9
18232.58	18275.34	18318.1
18593.72	18636.99	18680.25
18816.22	18850.13	18884.04
19339.07	19373.15	19407.22
19407.56	19463.85	19520.15
19522.82	19575.27	19627.72
20740.85	20811.99	20883.14
20886.89	20945.69	21004.49
21005.16	21061.95	21118.75
21119.42	21170.37	21221.31
21221.98	21275.44	21328.89
21330.89	21377.17	21423.44
21428.09	21475.32	21522.55
21642.26	21687.7	21733.13
21733.61	21755.74	21777.87
21778.15	21807.79	21837.44
21837.72	21862.69	21887.65
21887.93	21917.15	21946.37
22967.23	23036.05	23104.87
23110.29	23160.86	23211.44
23212.98	23256.28	23299.59
23407.68	23468.85	23530.03
27630.18	27715.9	27801.62
27874.33	27944.17	28014.01
28015.03	28082.32	28149.61

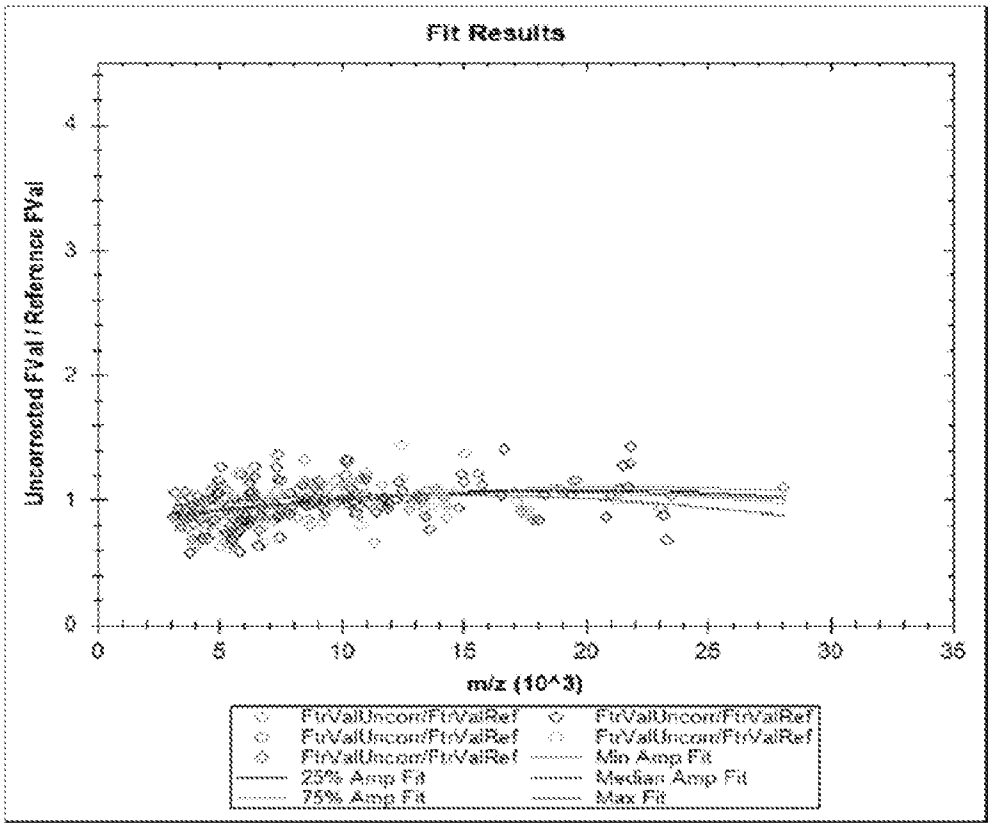
Example 3 Appendix B: Batch Correction

Table B.1 Batch correction coefficients

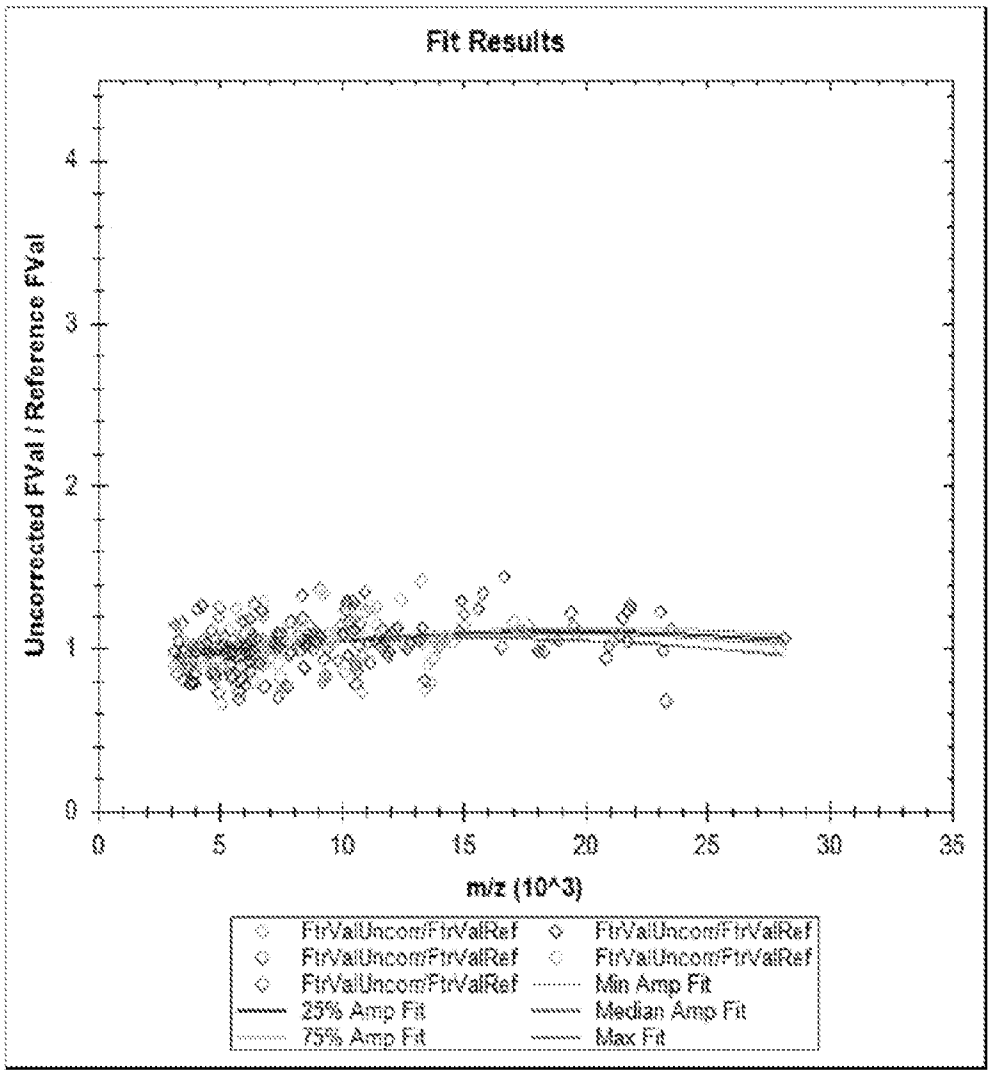
Model	A0	A1	B0	B1	C
Batch2	7.86E-01	1.97E-02	3.04E-05	-1.53E-06	-7.82E-10
Batch3	8.76E-01	6.70E-03	2.45E-05	-7.89E-07	-6.40E-10
Batch4	8.41E-01	-4.54E-03	2.64E-05	-6.29E-08	-6.92E-10
Batch5	8.69E-01	2.57E-02	2.87E-05	-3.49E-06	-8.96E-10
Batch6	8.43E-01	-1.51E-02	3.66E-05	1.52E-06	-1.23E-09

Figure B.1 Batch correction plots pre-correction

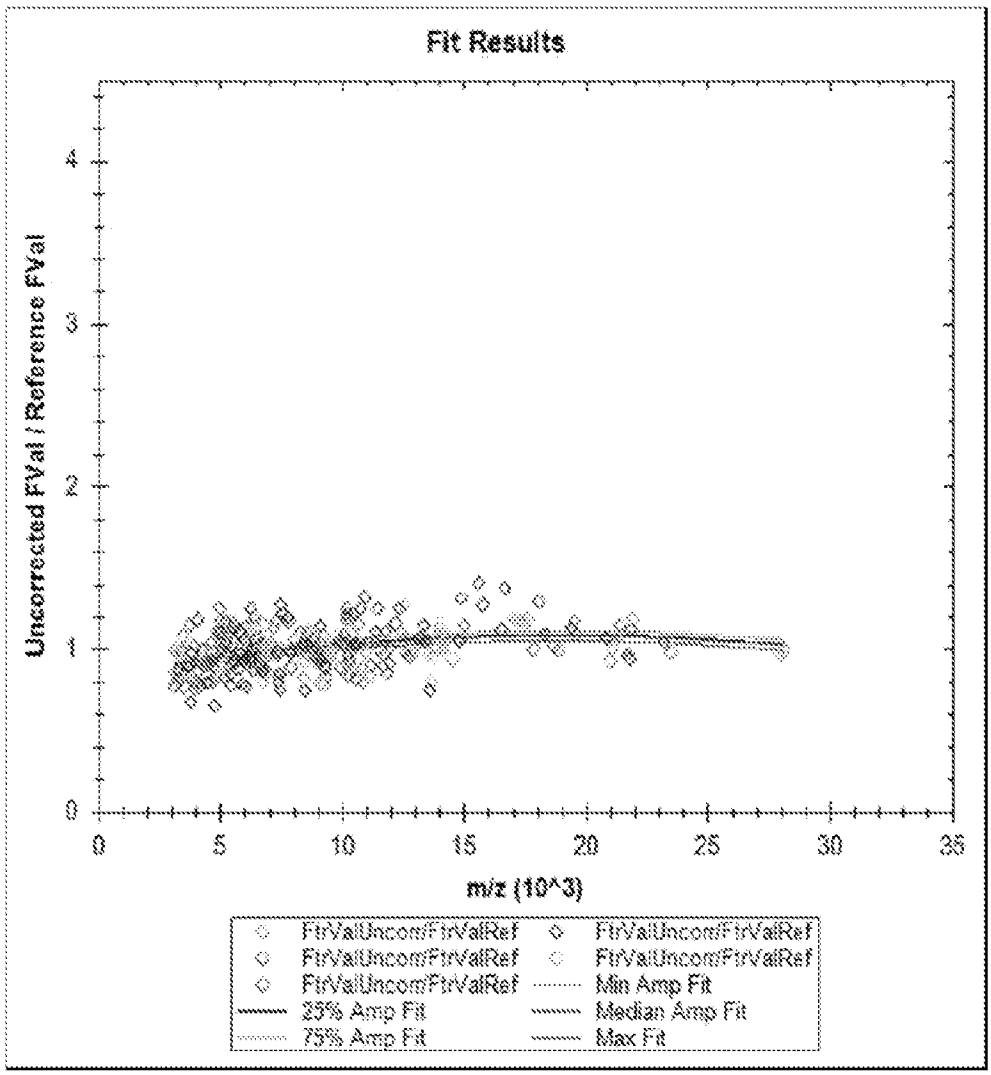
Batch 2 Pre Correction



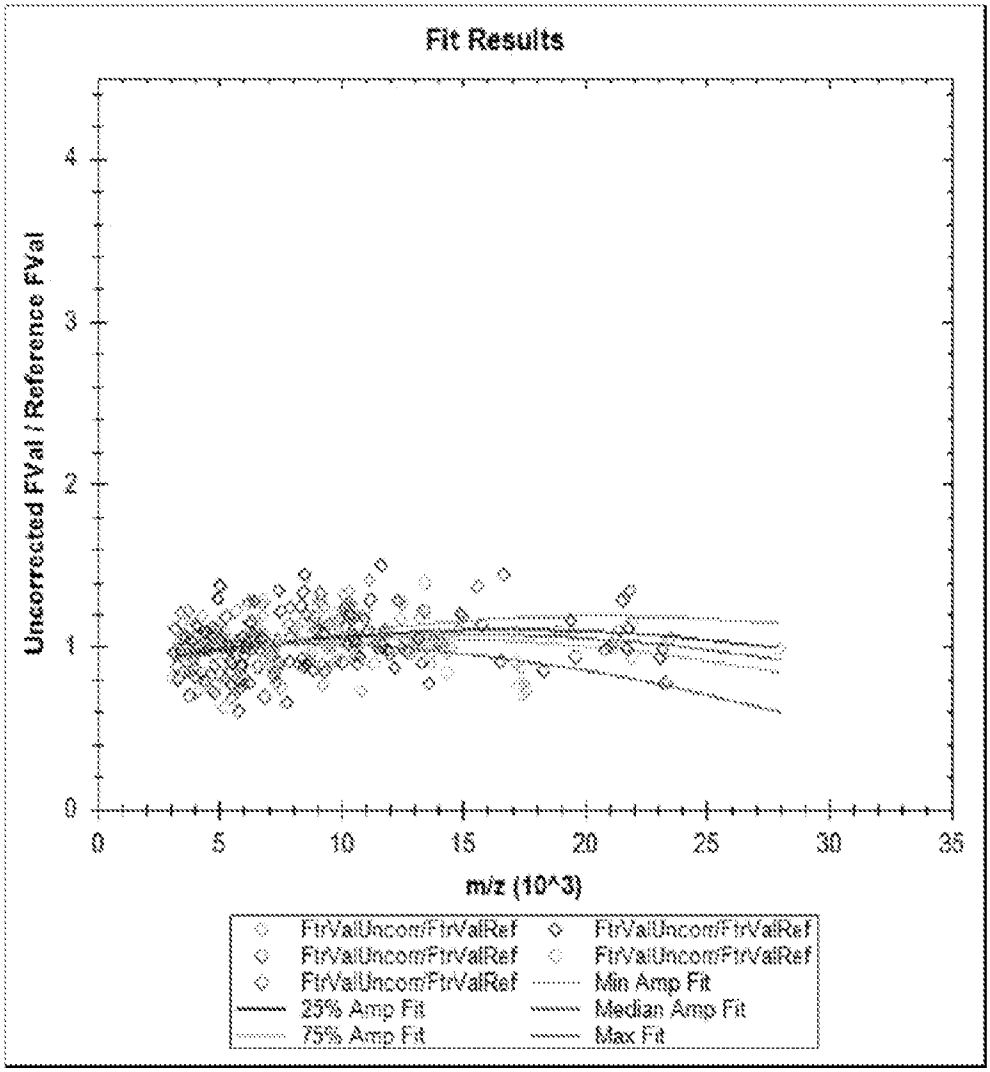
Batch 3 Pre Correction



Batch 4 Pre Correction



Batch 5 Pre Correction



Batch 6 Pre Correction

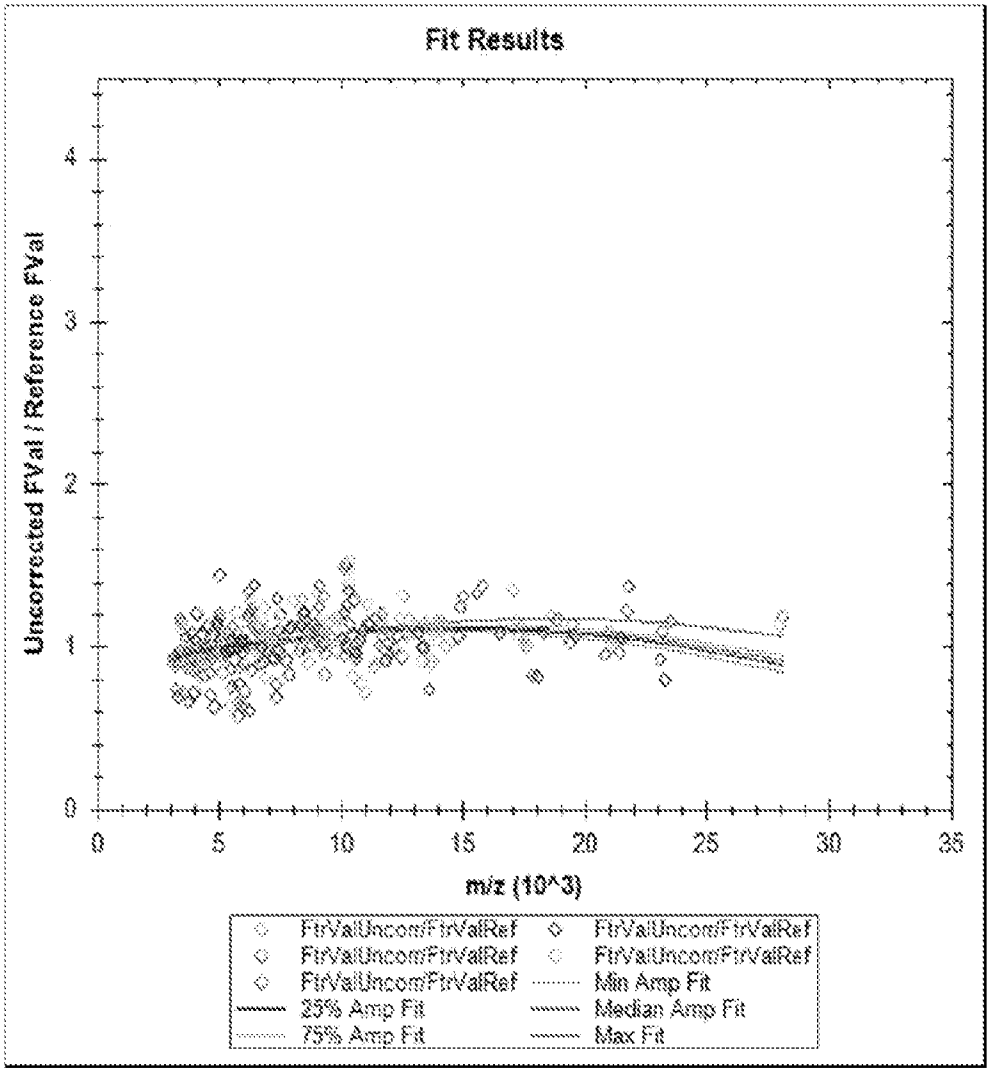
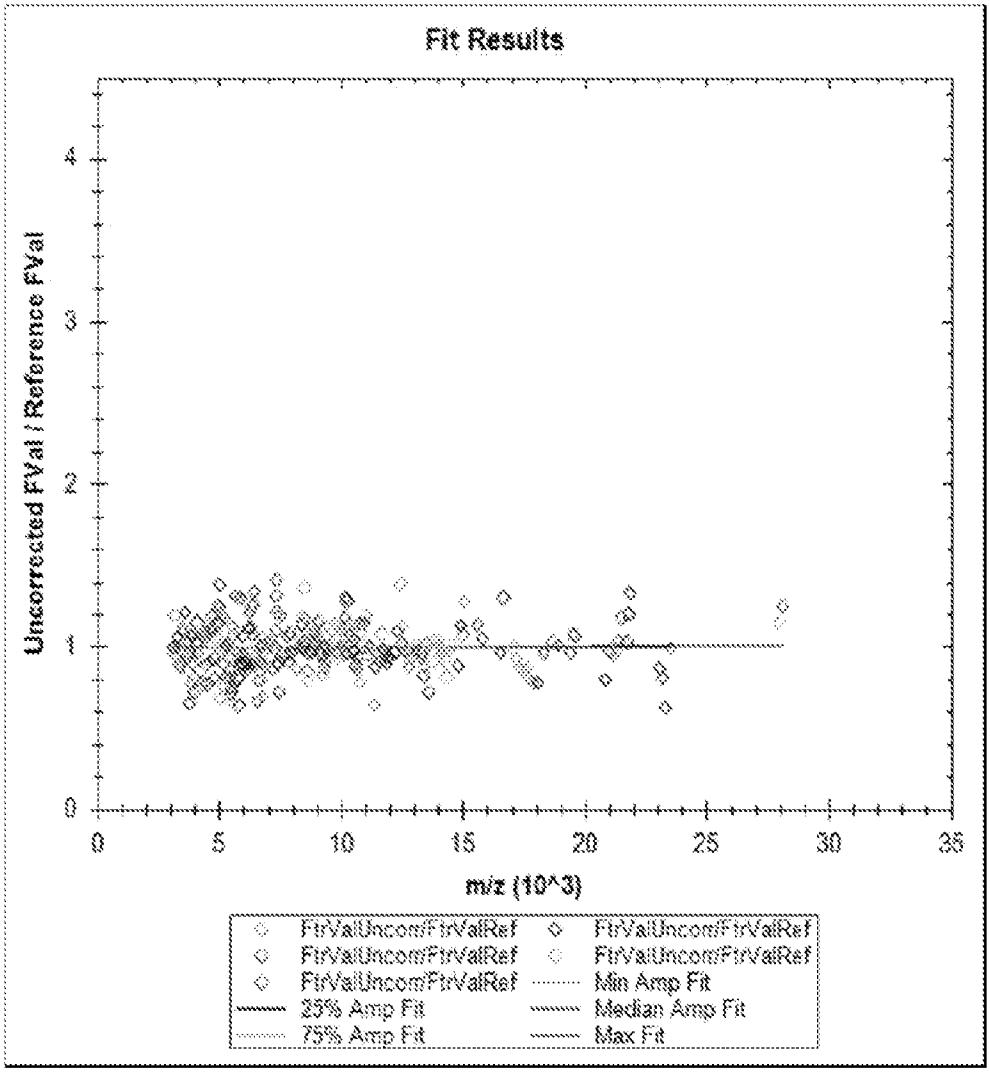


Table B.2 Batch correction coefficients on corrected tables

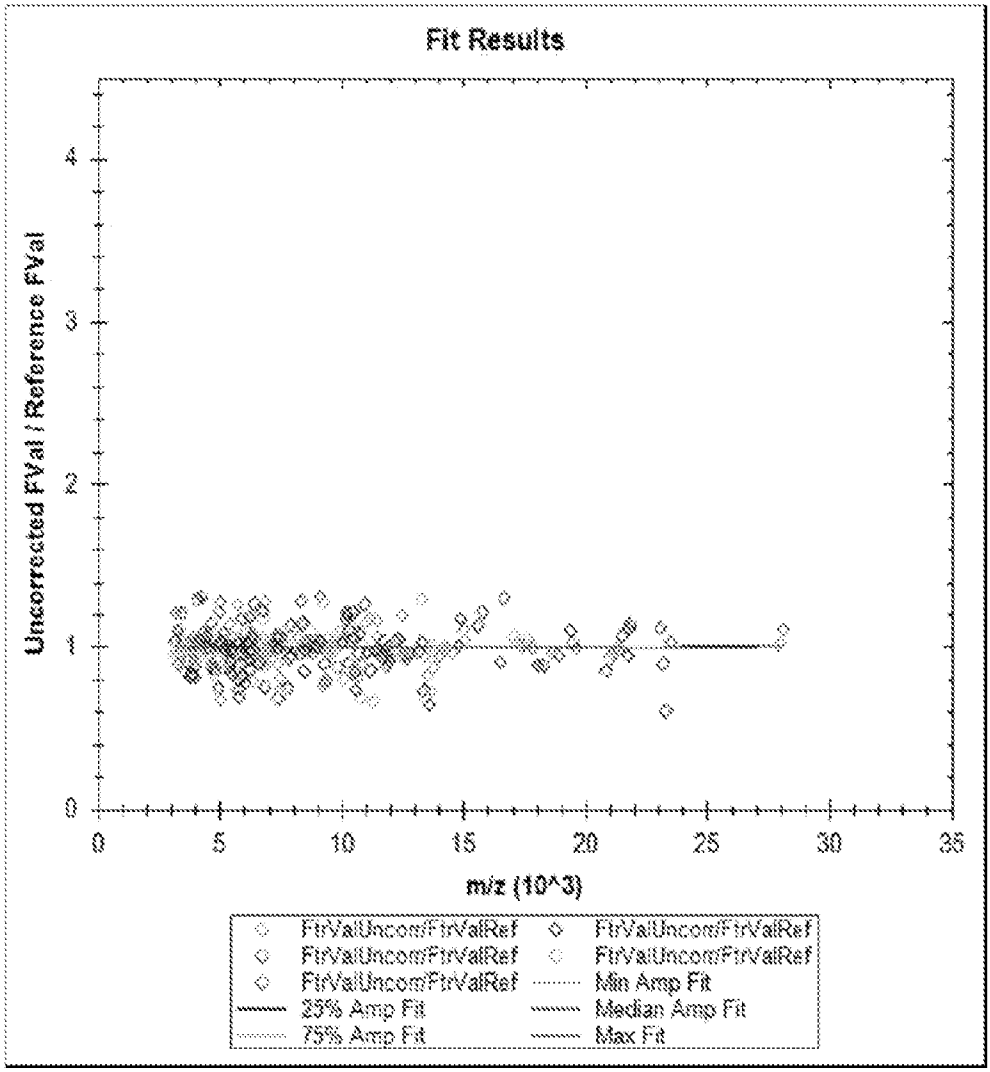
Model	A0	A1	B0	B1	C	ResSD
Batch2	1.00E+00	-7.90E-05	-4.00E-07	7.28E-08	2.14E-11	1.40E-01
Batch3	1.01E+00	8.79E-04	-2.03E-06	3.78E-08	7.00E-11	1.23E-01
Batch4	9.95E-01	-5.85E-04	8.10E-07	4.13E-08	-2.76E-11	1.15E-01
Batch5	1.03E+00	-1.12E-02	-5.79E-06	1.06E-06	2.03E-10	1.50E-01
Batch6	9.90E-01	-2.56E-04	2.06E-06	-1.19E-07	-5.97E-11	1.41E-01

Figure B.2 Batch correction plots post-correction

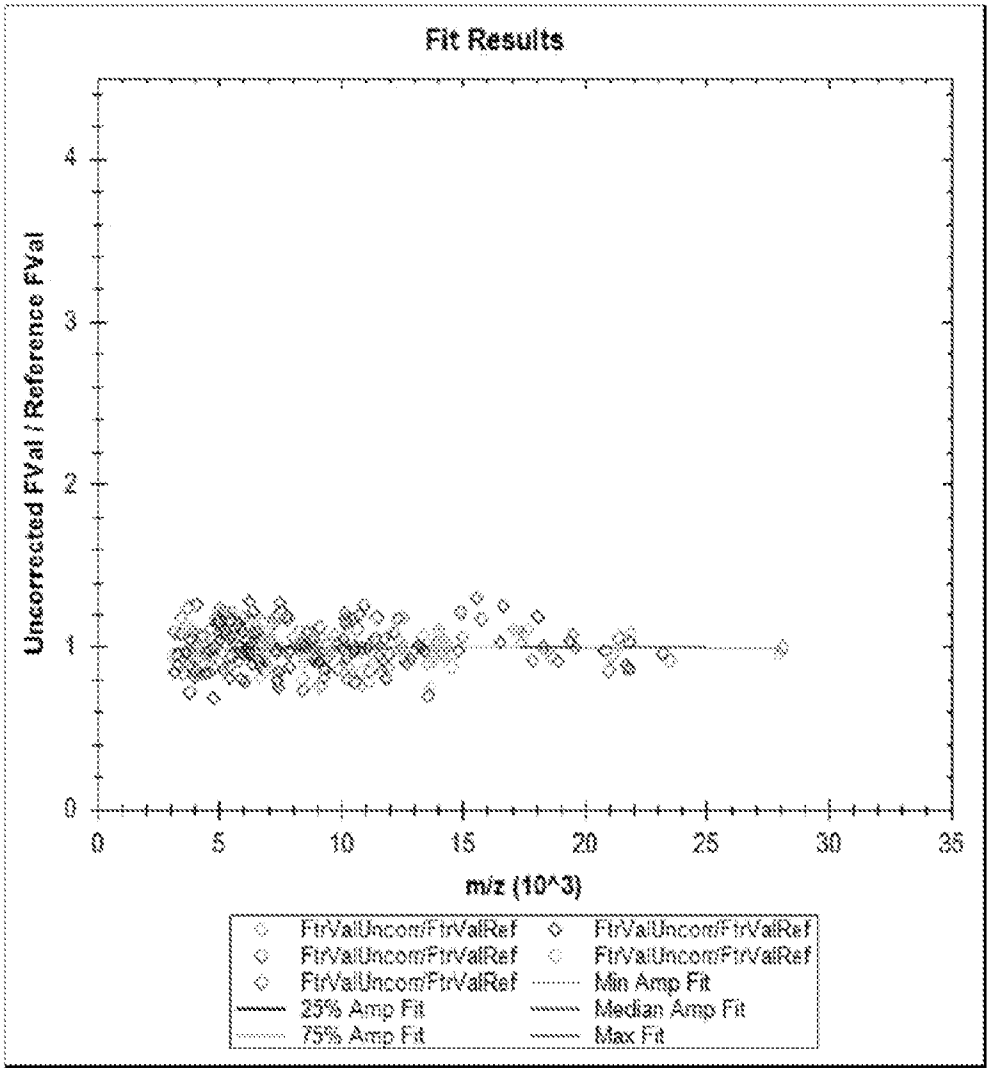
Batch 2 Post Correction



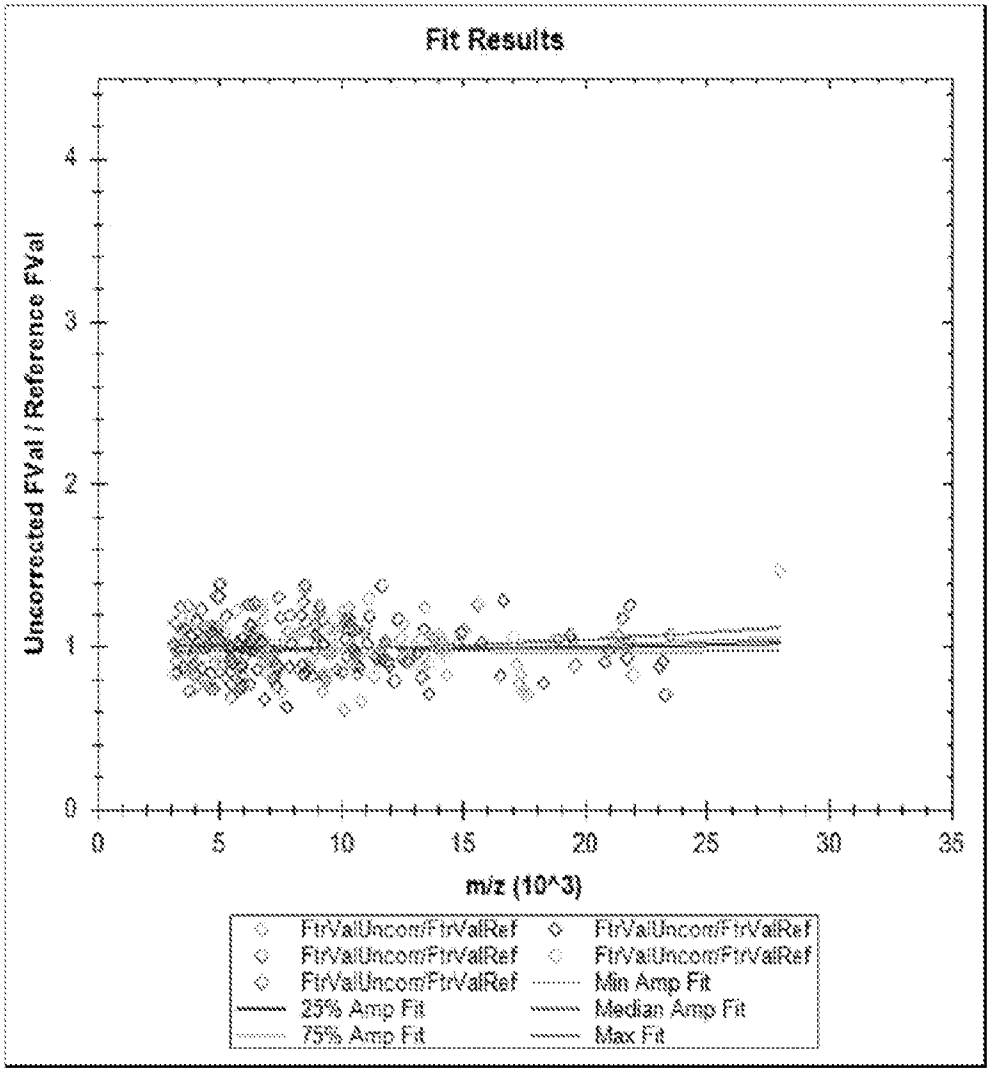
Batch 3 Post Correction



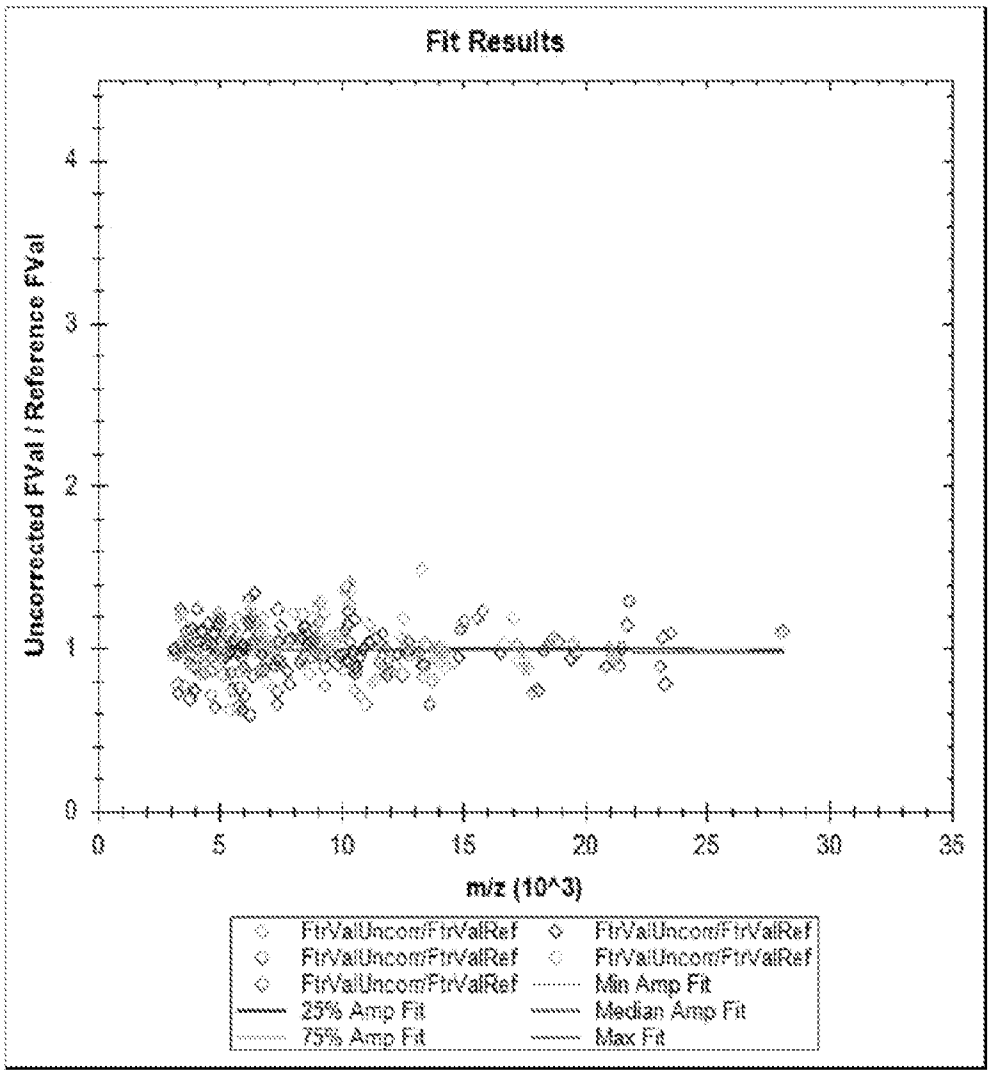
Batch 4 Post Correction



Batch 5 Post Correction



Batch 6 Post Correction



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Example 3 Appendix C: Feature Deselection Method

A multitude of splits (a total of 625) of the development set samples into two subsets is created. One of the subsets is used for feature (de)selection and the remainder is left aside.

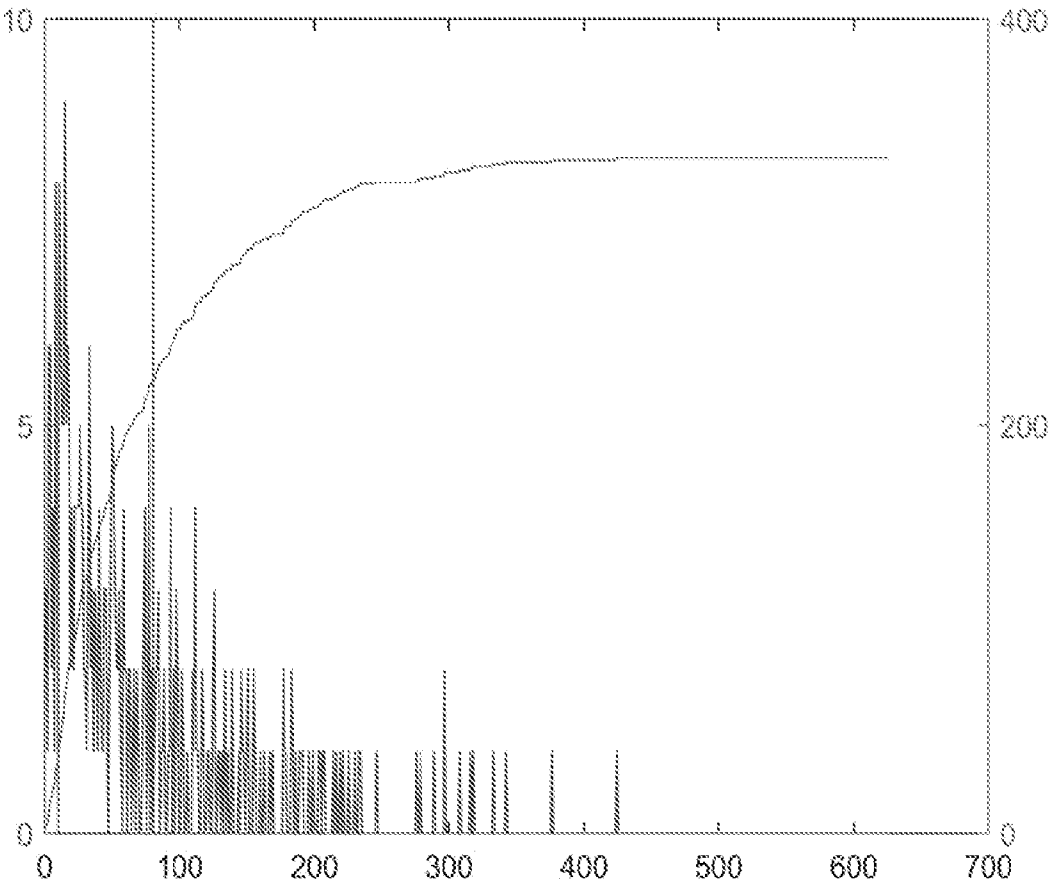
For each split a kNN classifier is created using the given subset as the training set of the classifier and one single feature. For this project k = 7 was used. The created classifier is applied to the training subset and the classifier performance is assessed in terms of hazard ratio between classification groups (Early vs Late). A filter is applied to these performance estimates, such that the feature only passes filtering if the classifier using this sample subset for training has adequate performance. For the approaches used in this report, the feature deselection step used K = 7 for the kNN classifiers and a hazard ratio range for filtering between 2.5 and 10.0, for both approaches in all label flip iterations.

All features that pass filtering for a given subset choice are added to a list. This is repeated for all the subset realizations generated. The lists of features passing filtering are then compiled across the subset realizations to determine how often a feature passes filtering. Features that pass filtering in most of the subsets are likely to be useful and robust for the question being addressed, as they are not dependent on any particular sample subset. Features that pass filtering for very few subset realizations are likely to have been overfitted to those few subsets and are not likely to be useful.

Figure C.1 shows an example of the distribution of how many features pass filtering in how many subset realizations.

It is apparent that the distribution falls off quite quickly with a tail containing features that occur in a relatively large proportion of subset realizations, which are those which are likely to be most useful for classifier development.

Figure C.1: Number of features passing filtering for a given number of subset realizations (y axis) vs. the number of subset realizations. (Red line shows the cut off for which features were deselected for that specific iteration)



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Example 3 Appendix D: Features used in final classifiers

Approach (1)	Approach (2)
3110	3110
3211	3243
3243	3265
3265	3317
3317	3554
3554	3755
3755	3776
3776	3887
3887	4099
3953	4266
4099	4286
4266	4431
4286	4643
4431	4718
4593	4756
4718	4891
4756	4918
4891	4938
4938	5068
5041	5156
5068	5182
5156	5224
5182	5675
5224	5710
5675	5748
5710	5777
5748	5816
5777	5997
5816	6210
5997	6332
6109	6634
6210	6657
6283	6773
6332	6860
6438	6881
6634	6898
6657	6971
6756	6992
6773	7074
6793	7258

6860	7322
6881	7334
6898	7346
6971	7420
6992	7448
7074	7779
7258	7871
7322	8391
7334	8464
7346	8509
7420	8531
7448	8565
7479	8632
7779	8661
7871	8729
8391	8746
8464	8771
8509	8902
8531	8998
8565	9079
8632	9206
8661	9264
8696	9359
8729	9430
8746	10079
8771	10421
8891	10533
8902	10734
8998	11306
9079	12507
9098	12613
9206	13275
9264	13624
9359	13943
9430	13984
9641	14043
9721	15029
9793	17033
10079	17148
10421	17271
10449	17336
10533	18850
10734	19464

11306	19575
11448	20812
11945	20946
12507	21062
12613	21917
13275	23036
13624	27716
13883	27944
13943	28082
13984	30001 *
14043	30002 *
14199	30003 *
14784	
15029	
16630	
17033	
17148	
17271	
17336	
18850	
19464	
19575	
20812	
20946	
21062	
21475	
23036	
23256	
27716	
27944	
28082	

* 30001: Age at diagnosis; 30002: PSA (ng / ml); 30003: fPSA (%). All other features refer to m/z values.

Example 3 Appendix E: Classifications by sample

Filename	SampleID	Classification (Approach (1))	Classification (Approach (2))
Average_00001_100070597.txt	100070597	Early	Early
Average_00001_101051627.txt	101051627	Late	Late
Average_00001_108429555.txt	108429555	Late	Late
Average_00001_112805.txt	112805	Early	Early
Average_00001_118508.txt	118508	Early	Early
Average_00001_157578.txt	157578	Late	Late
Average_00001_157590.txt	157590	Late	Late
Average_00001_158292.txt	158292	Late	Late
Average_00001_180920.txt	180920	Late	Late
Average_00001_182834.txt	182834	Late	Late
Average_00001_183488.txt	183488	Early	Early
Average_00001_190911.txt	190911	Late	Late
Average_00001_209775.txt	209775	Early	Early
Average_00001_223900.txt	223900	Late	Late
Average_00001_224788.txt	224788	Late	Late
Average_00001_226786.txt	226786	Late	Late
Average_00001_226987.txt	226987	Early	Early
Average_00001_228905.txt	228905	Late	Late
Average_00001_229360.txt	229360	Early	Early
Average_00001_239074.txt	239074	Late	Late
Average_00001_241112.txt	241112	Late	Late
Average_00001_241121.txt	241121	Late	Late
Average_00001_241122.txt	241122	Late	Late
Average_00001_255951.txt	255951	Late	Late
Average_00001_255985.txt	255985	Early	Early
Average_00001_260476.txt	260476	Early	Early
Average_00001_273316.txt	273316	Early	Early
Average_00001_274982.txt	274982	Late	Late
Average_00001_278636.txt	278636	Early	Early
Average_00001_286982.txt	286982	Early	Early
Average_00001_287874.txt	287874	Early	Early
Average_00001_287880.txt	287880	Late	Late
Average_00001_289609.txt	289609	Late	Late
Average_00001_294677.txt	294677	Early	Early
Average_00001_294981.txt	294981	Late	Late
Average_00001_296404.txt	296404	Late	Early
Average_00001_296417.txt	296417	Late	Late
Average_00001_296898.txt	296898	Late	Late
Average_00001_296944.txt	296944	Late	Late

Average_00001_307920.txt	307920	Early	Early
Average_00001_310070.txt	310070	Late	Late
Average_00001_310370.txt	310370	Early	Early
Average_00001_312967.txt	312967	Late	Late
Average_00001_313197.txt	313197	Early	Early
Average_00001_313595.txt	313595	Early	Early
Average_00001_316897.txt	316897	Late	Late
Average_00001_319783.txt	319783	Early	Early
Average_00001_319933.txt	319933	Early	Early
Average_00001_319953.txt	319953	Early	Early
Average_00001_319978.txt	319978	Late	Late
Average_00001_323657.txt	323657	Late	Late
Average_00001_323670.txt	323670	Early	Late
Average_00001_323914.txt	323914	Early	Early
Average_00001_325081.txt	325081	Late	Late
Average_00001_326057.txt	326057	Early	Early
Average_00001_326060.txt	326060	Early	Early
Average_00001_326316.txt	326316	Late	Late
Average_00001_326450.txt	326450	Late	Late
Average_00001_327622.txt	327622	Early	Early
Average_00001_327684.txt	327684	Early	Early
Average_00001_328489.txt	328489	Early	Early
Average_00001_328957.txt	328957	Late	Late
Average_00001_329385.txt	329385	Late	Late
Average_00001_330169.txt	330169	Early	Early
Average_00001_332082.txt	332082	Late	Late
Average_00001_332578.txt	332578	Late	Late
Average_00001_334141.txt	334141	Early	Early
Average_00001_334255.txt	334255	Early	Early
Average_00001_336363.txt	336363	Late	Late
Average_00001_336955.txt	336955	Early	Early
Average_00001_339433.txt	339433	Late	Late
Average_00001_341209.txt	341209	Late	Late
Average_00001_341734.txt	341734	Late	Late
Average_00001_341925.txt	341925	Late	Late
Average_00001_342099.txt	342099	Early	Early
Average_00001_342860.txt	342860	Late	Late
Average_00001_342985.txt	342985	Late	Late
Average_00001_343874.txt	343874	Late	Late
Average_00001_344282.txt	344282	Late	Late
Average_00001_344289.txt	344289	Late	Late
Average_00001_344939.txt	344939	Late	Late
Average_00001_345168.txt	345168	Early	Early

Average_00001_346821.txt	346821	Late	Late
Average_00001_347163.txt	347163	Early	Early
Average_00001_348382.txt	348382	Early	Early
Average_00001_350235.txt	350235	Early	Early
Average_00001_353843.txt	353843	Late	Late
Average_00001_354225.txt	354225	Early	Early
Average_00001_354400.txt	354400	Late	Late
Average_00001_355346.txt	355346	Early	Early
Average_00001_355914.txt	355914	Late	Late
Average_00001_361015.txt	361015	Late	Late
Average_00001_363529.txt	363529	Early	Early
Average_00001_363749.txt	363749	Late	Late
Average_00001_370511.txt	370511	Early	Early
Average_00001_371762.txt	371762	Early	Early
Average_00001_5704021811.txt	5704021811	Early	Early
Average_00001_5802062717.txt	5802062717	Late	Late
Average_00001_5836060014.txt	5836060014	Early	Early
Average_00001_5913033212.txt	5913033212	Late	Late
Average_00001_601870.txt	601870	Early	Early
Average_00001_610232.txt	610232	Late	Late
Average_00001_610772.txt	610772	Late	Late
Average_00001_613294.txt	613294	Early	Early
Average_00001_622251.txt	622251	Late	Late
Average_00001_623716.txt	623716	Early	Early
Average_00001_626399.txt	626399	Early	Early
Average_00001_628652.txt	628652	Late	Late
Average_00001_630085.txt	630085	Late	Late
Average_00001_636662.txt	636662	Late	Late
Average_00001_637317.txt	637317	Early	Late
Average_00001_640612.txt	640612	Late	Late
Average_00001_640794.txt	640794	Early	Early
Average_00001_641548.txt	641548	Late	Late
Average_00001_649071.txt	649071	Late	Late
Average_00001_660326.txt	660326	Early	Early
Average_00001_661812.txt	661812	Late	Late
Average_00001_662523.txt	662523	Early	Early
Average_00001_663348.txt	663348	Early	Early
Average_00001_665928.txt	665928	Late	Late
Average_00001_669710.txt	669710	Early	Early
Average_00001_672480.txt	672480	Early	Early
Average_00001_676629.txt	676629	Early	Early
Average_00001_89287.txt	89287	Late	Late

------ end of appendices ------

Claims

We claim:

1. A method for predicting the aggressiveness or indolence of prostate cancer in a patient previously diagnosed with prostate cancer, comprising the steps of:

obtaining a blood-based sample from the prostate cancer patient;

conducting mass spectrometry of the blood-based sample with a mass spectrometer and thereby obtaining mass spectral data including intensity values at a multitude of m/z features in a spectrum produced by the mass spectrometer;

performing pre-processing operations on the mass spectral data;

classifying the sample with a programmed computer implementing a classifier operating on the intensity values of the sample after the pre-processing operations are performed and a set of stored intensity values of m/z features from a constitutive set of mass spectra obtained from blood-based samples of a multitude of prostate cancer patients;

wherein the classifier produces a class label for the blood based sample of High, Early, or the equivalent signifying the patient is at high risk of early progression/relapse of the prostate cancer indicating aggressiveness of the prostate cancer, or Low, Late or the equivalent, signifying that the patient is at low risk of early progression/relapse of the prostate cancer indicating indolence of the prostate cancer.

2. The method of claim 1, wherein the mini-classifiers execute a K-nearest neighbor classification algorithm on a set of features selected from the list of features set forth in Example 1 Appendix A, Example 2 Appendix A, or Example 3 Appendix A.

3. The method of claim 1, wherein the classifier is defined from one or more master classifiers generated by conducting logistic regression with extreme drop-out on a multitude of mini-classifiers which meet predefined filtering criteria.

4. The method of claim 1, wherein non-mass spectral information on the patient whose sample is tested in claim 1 is obtained, including at least one of age, PSA and % fPSA, wherein such non-mass spectral information is also obtained for each prostate cancer patient whose blood-based sample is a member of the constitutive set and stored in a computer memory, and wherein the final classifier uses such non-mass spectral information in addition to the mass spectral data when generating a class label for the sample.

5. The method of claim 1, wherein each prostate cancer patient whose sample is a member of the constitutive set supplied the sample after diagnosis with prostate cancer but before radical prostatectomy (RPE).

6. The method of claim 1, wherein each prostate cancer patient whose sample is a member of the constitutive set has a Total Gleason Score of 6 or lower at the time the blood-based sample from such patient was obtained.

7. A system for prostate cancer aggressiveness or indolence prediction, comprising:

a computer system including a memory storing a final classifier in memory defined from one or more master classifiers generated by conducting logistic regression with extreme drop-out on a multitude of mini-classifiers which meet predefined filtering criteria, a set of mass spectrometry feature values for a constitutive set for classification, the set of mass spectrometry feature values obtained from blood-based samples of prostate cancer patients, a classification algorithm and a set of logistic regression weighting coefficients derived from a combination of filtered mini-classifiers with dropout regularization;

the computer system including program code for executing the final classifier on a set of mass spectrometry feature values obtained from mass spectrometry of a blood-based sample of a human with prostate cancer.

8. The computer system of claim 7. wherein non-mass spectral information for each prostate cancer patient whose blood-based samples are in the constitutive set is stored in the memory, including at least one of age, PSA and % fPSA.

9. The computer system of claim 7, wherein each prostate cancer patient whose sample is a member of the constitutive set supplied the sample after diagnosis with prostate cancer but before radical prostatectomy (RPE).

10. The computer system of claim 7, wherein each prostate cancer patient whose sample is a member of the constitutive set has a Total Gleason Score of 6 or lower at the time the blood-based sample from such patient was obtained.

11. A laboratory test system for conducting a test on a blood-based sample from a prostate cancer patient to predict aggressiveness or indolence of the prostate cancer comprising, in combination:

a mass spectrometer conducting mass spectrometry of the blood-based sample with a mass spectrometer and thereby obtaining mass spectral data including intensity values at a multitude of m/z features in a spectrum produced by the mass spectrometer; and

a programmed computer including code for performing pre-processing operations on the mass spectral data and classifying the sample with a final classifier defined by one or more master classifiers generated as a combination of filtered mini-classifiers with regularization, the final classifier operating on the intensity values of the sample after the pre-processing operations are performed and a set of stored values of m/z features from a constitutive set of mass spectra obtained from blood-based samples of prostate cancer patients;

the programmed computer producing a class label for the blood-based sample of High, Early or the equivalent signifying the patient is at high risk of early progression/relapse of the prostate cancer indicating aggressiveness of the prostate cancer, or Low, Late or the

equivalent, signifying that the patient is at low risk of early progression/relapse of the prostate cancer indicating indolence of the cancer.

12. The system of claim 11, wherein the m/z features are selected from the list of features comprising Example 1 Appendix A, Example 2 Appendix A, or Example 3 Appendix A.

13. The system of claim 11, wherein the mass spectrum of the blood-based sample is obtained from at least 100,000 laser shots applied to the blood-based sample using MALDI-TOF mass spectrometry.

14. The method of claim 1, wherein the mass spectrum of the blood-based sample is obtained from at least 100,000 laser shots applied to the sample using MALDI-TOF mass spectrometry

15. A programmed computer operating as a classifier for predicting prostate cancer aggressiveness or indolence, comprising a processing unit and a memory storing a final classifier in the form of a set of feature values for a set of mass spectrometry features forming a constitutive set of mass spectra obtained from blood-based samples of prostate cancer patients, and a final classifier defined as a majority vote or average probability cutoff, of a multitude of master classifiers constructed from a combination of mini-classifiers with dropout regularization.

Fig. 1

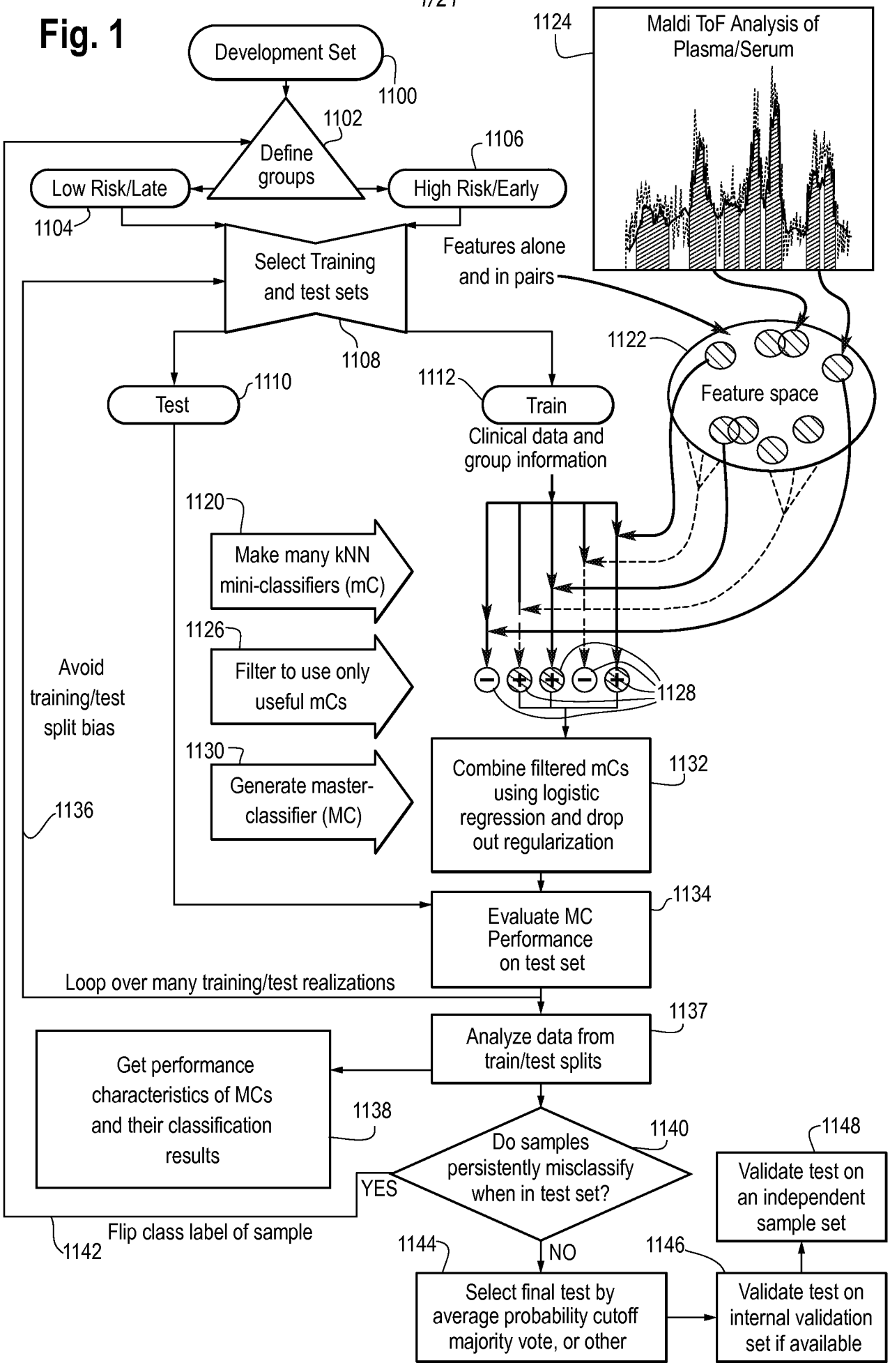

Development Set
1100
Define groups
1102
Low Risk/Late
1104
High Risk/Early
1106
1124
Maldi ToF Analysis of Plasma/Serum
Select Training and test sets
1108
Features alone and in pairs
1122
Feature space
Test
1110
1112
Train
Clinical data and group information
1120
Make many kNN mini-classifiers (mC)
1126
Filter to use only useful mCs
1128
Avoid training/test split bias
1130
Generate master-classifier (MC)
1136
Combine filtered mCs using logistic regression and drop out regularization
1132
Evaluate MC Performance on test set
1134
Loop over many training/test realizations
1137
Analyze data from train/test splits
Get performance characteristics of MCs and their classification results
1138
Do samples persistently misclassify when in test set?
1140
YES
Flip class label of sample
1142
NO
1144
Select final test by average probability cutoff majority vote, or other
1146
Validate test on internal validation set if available
1148
Validate test on an independent sample set

Fig. 2A

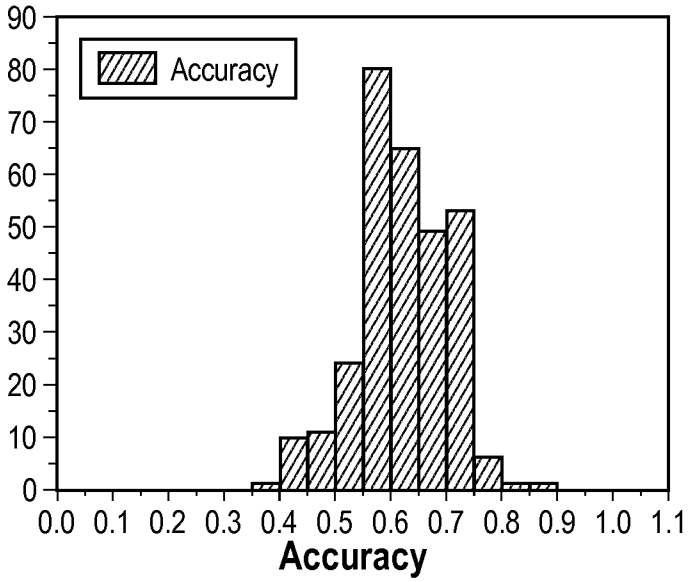


Fig. 2B

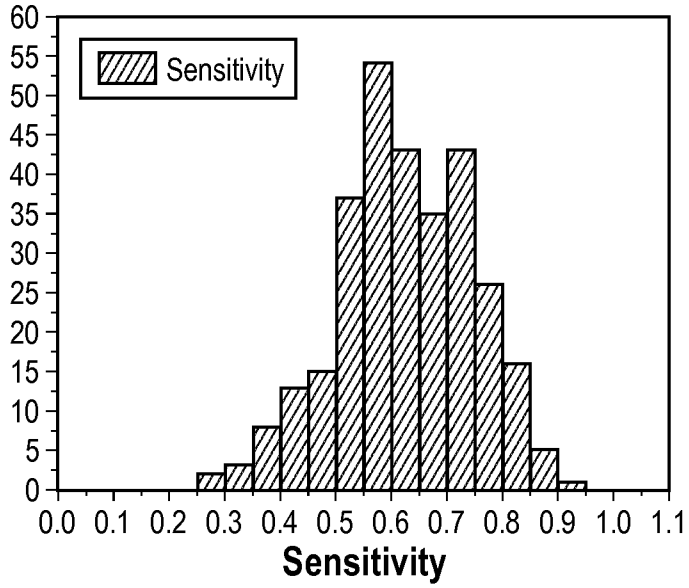


Fig. 2C

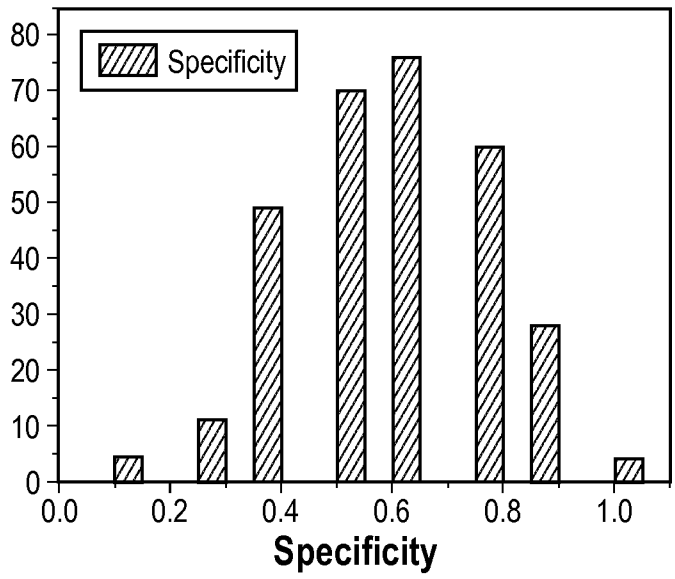


Fig. 3A

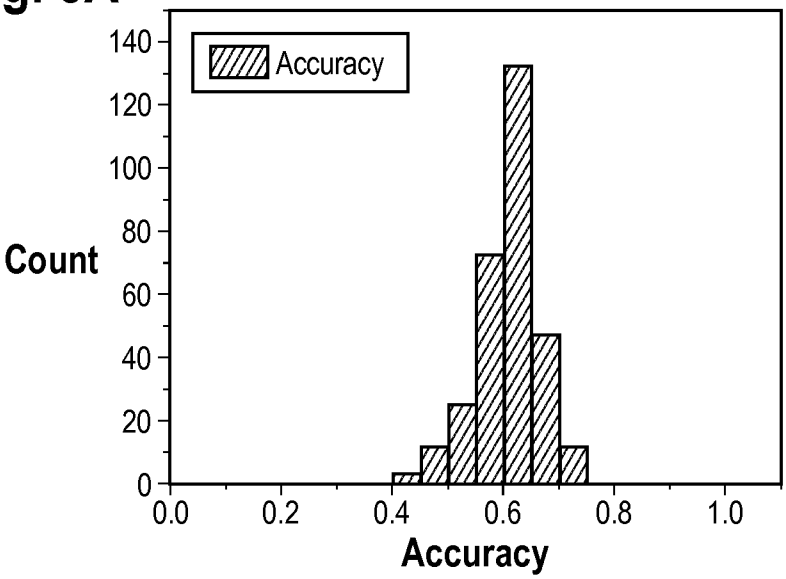


Fig. 3B

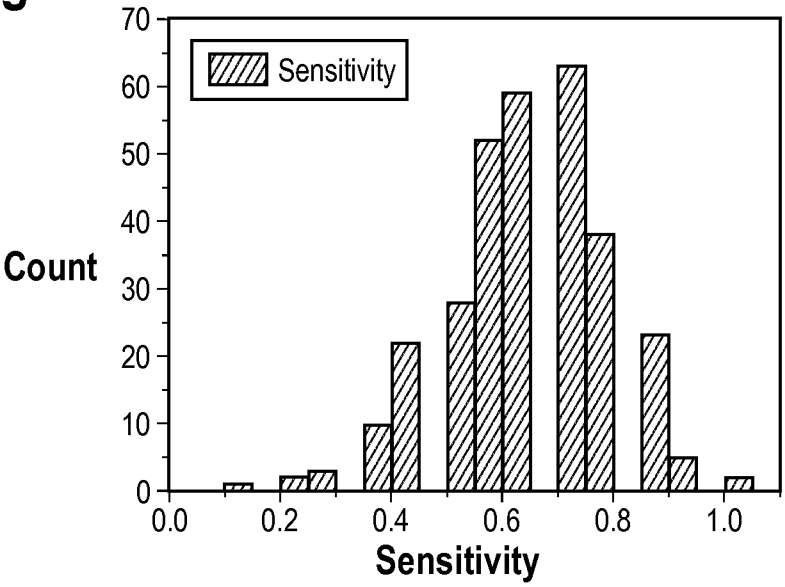
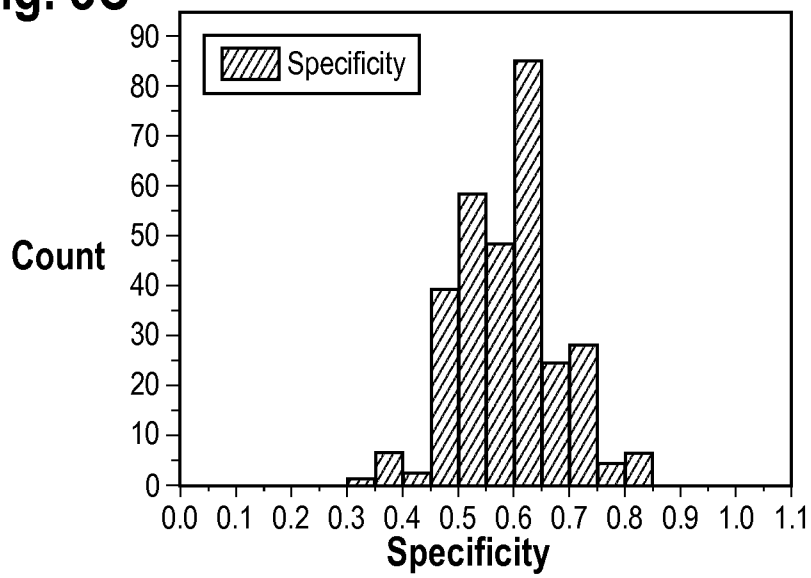


Fig. 3C



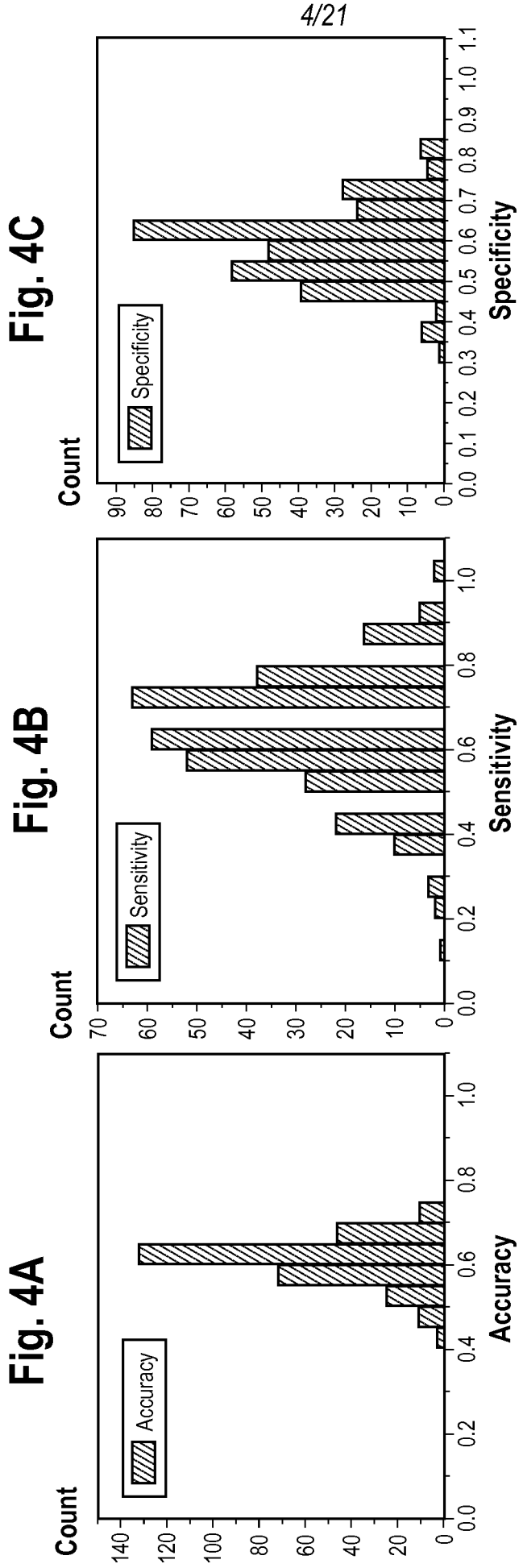


Fig. 4A
Count
Accuracy
0.0 0.2 0.4 0.6 0.8 1.0
0 20 40 60 80 100 120 140
Fig. 4B
Count
Sensitivity
0.0 0.2 0.4 0.6 0.8 1.0
0 10 20 30 40 50 60 70
Fig. 4C
Count
Specificity
0.0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1.0 1.1
0 10 20 30 40 50 60 70 80 90

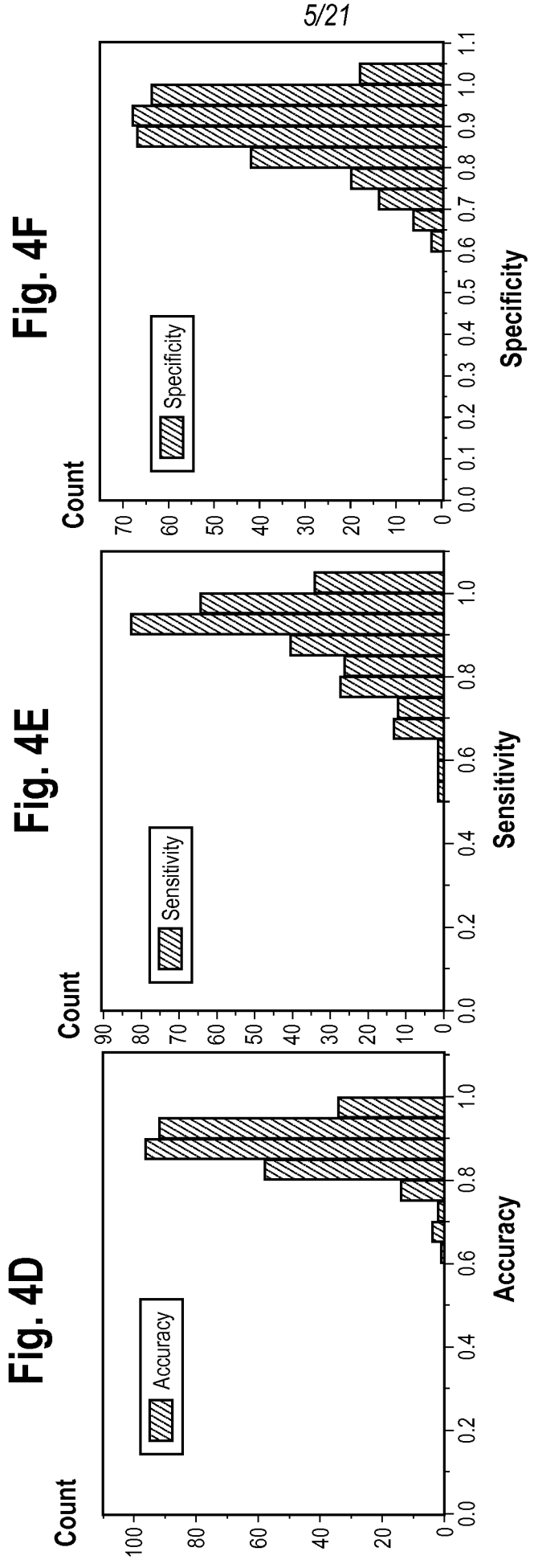


Fig. 4D
Count
Accuracy
Accuracy
0.0
0.2
0.4
0.6
0.8
1.0
0
20
40
60
80
100
Fig. 4E
Count
Sensitivity
Sensitivity
0.0
0.2
0.4
0.6
0.8
1.0
0
10
20
30
40
50
60
70
80
90
Fig. 4F
Count
Specificity
Specificity
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
1.1
0
10
20
30
40
50
60
70

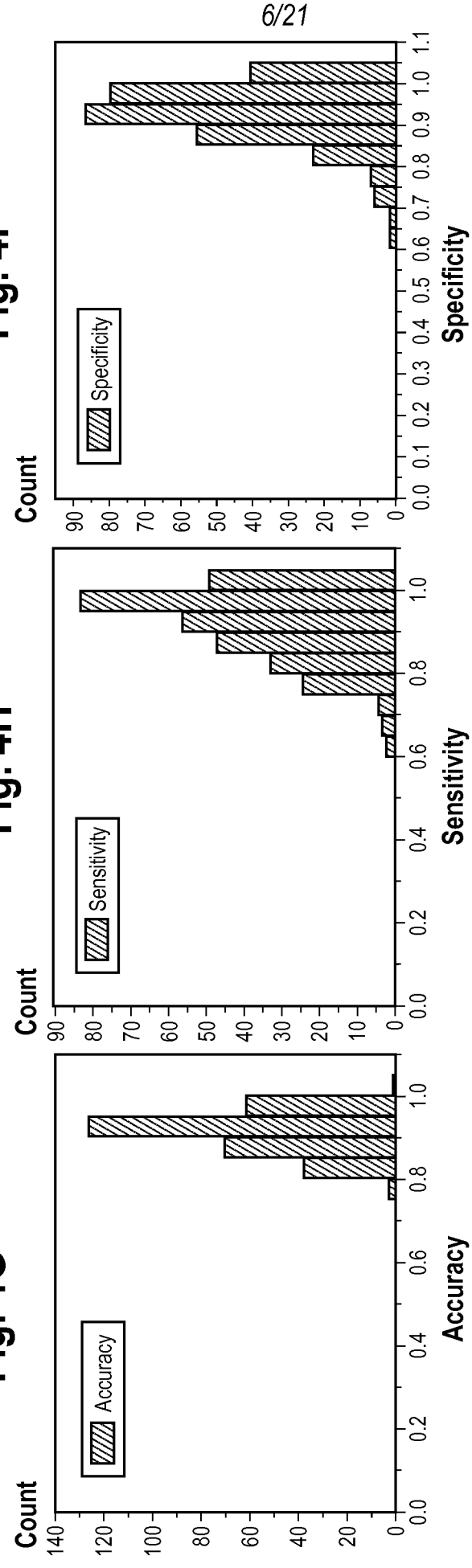


Fig. 4G

Fig. 4H

Fig. 4I

Fig. 4J

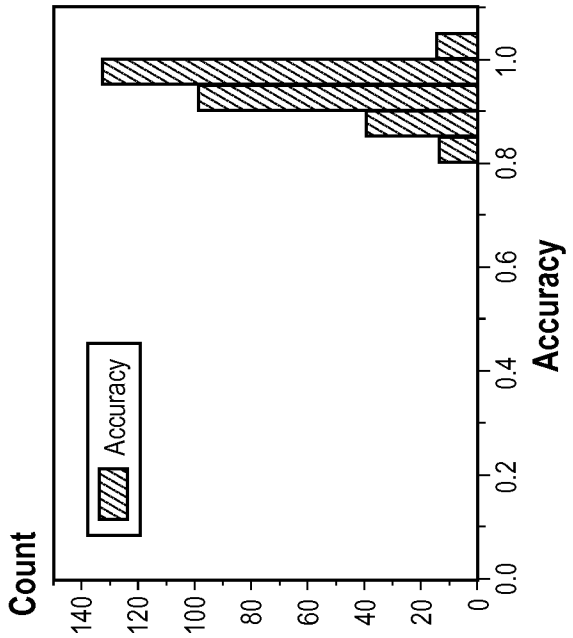


Fig. 4K

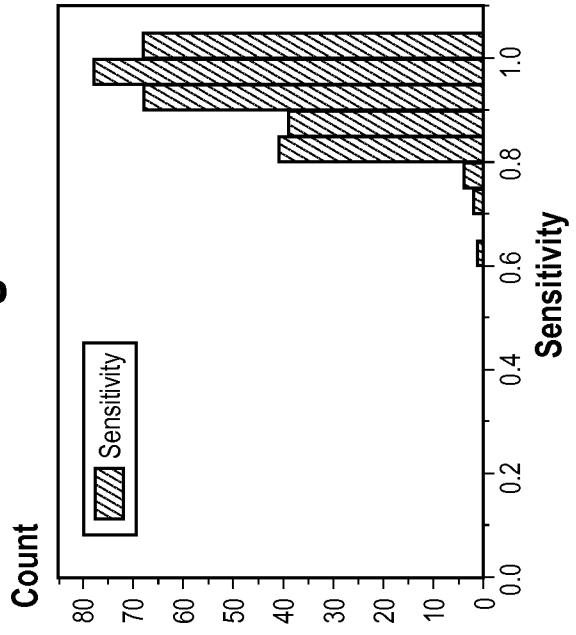


Fig. 4L

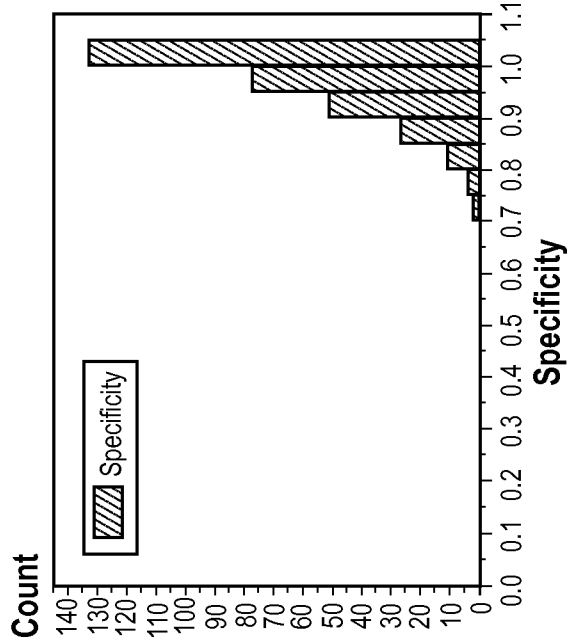


Fig. 5A

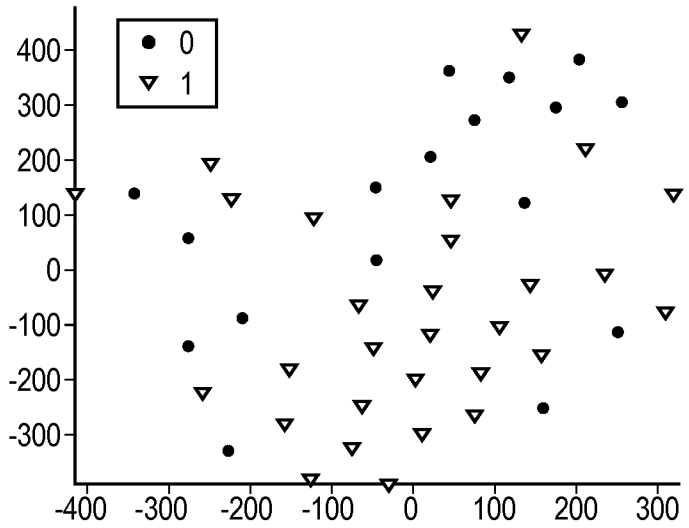


Fig. 5B

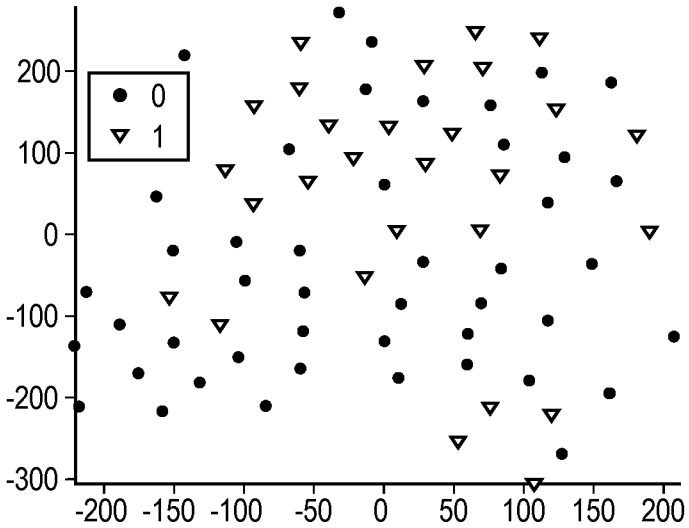


Fig. 5C

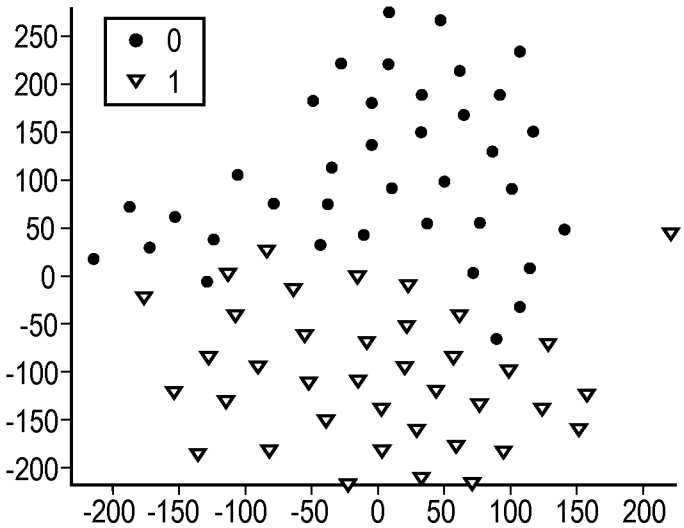


Fig. 6

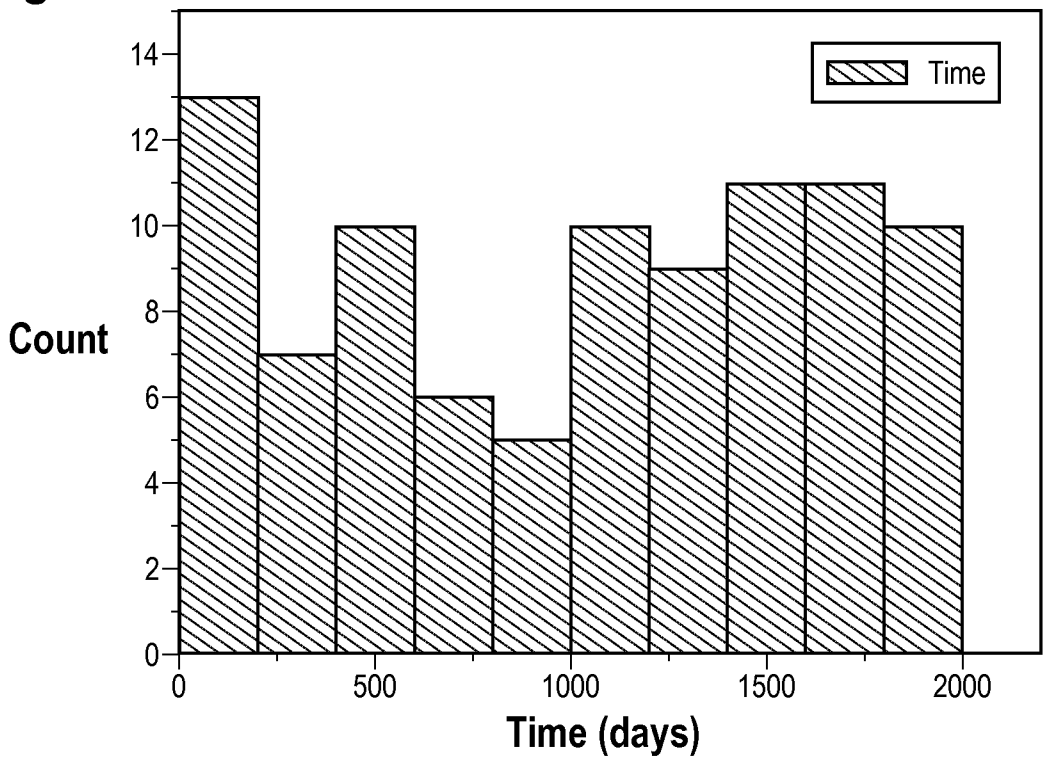

Time
Count
14
12
10
8
6
4
2
0
0
500
1000
1500
2000
Time (days)

Fig. 7

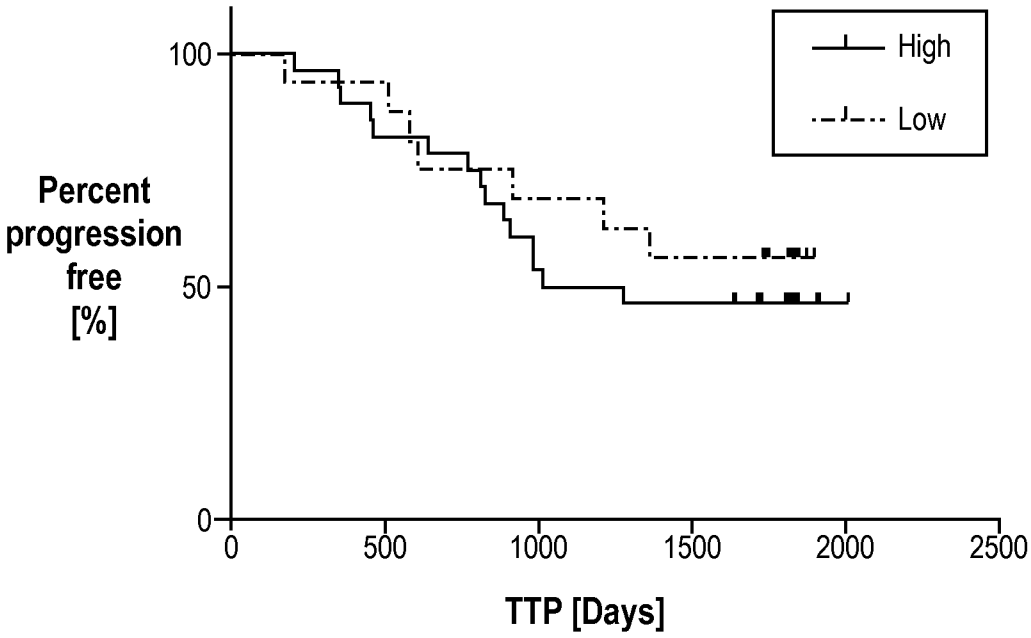

High
Low
Percent progression free [%]
100
50
0
0
500
1000
1500
2000
2500
TTP [Days]

Fig. 8

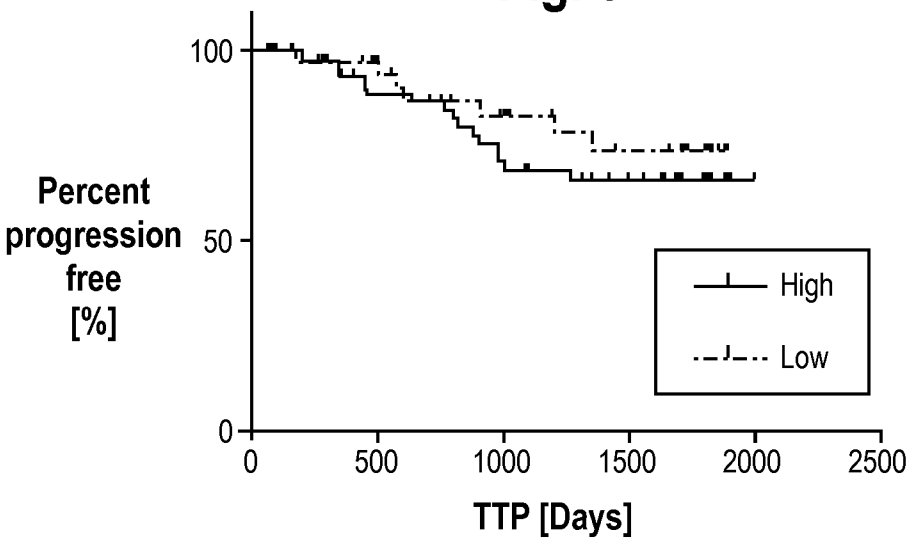

Percent progression free [%]
100
50
0
0
500
1000
1500
2000
2500
TTP [Days]
High
Low

Fig. 9

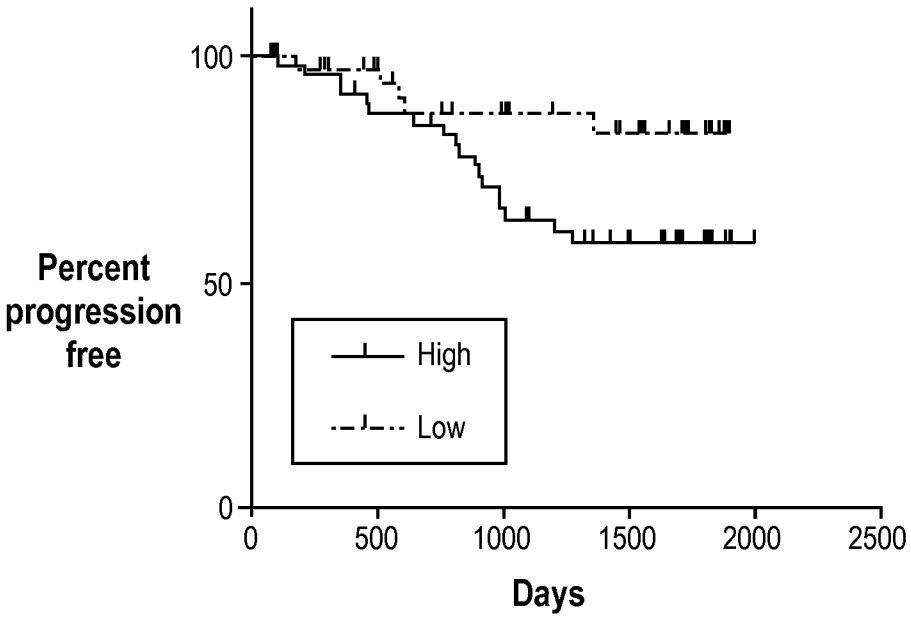

Percent progression free
100
50
0
0
500
1000
1500
2000
2500
Days
High
Low

Fig. 10

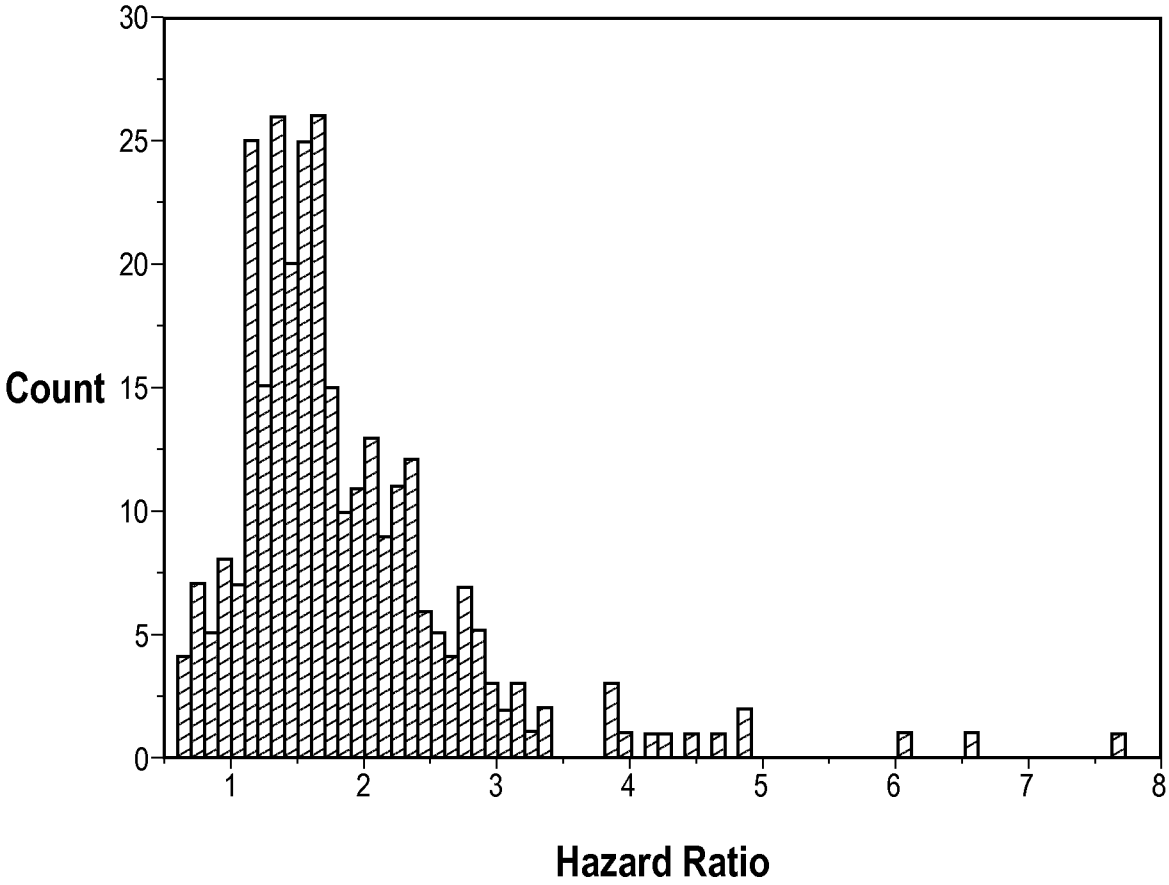


Fig. 11A

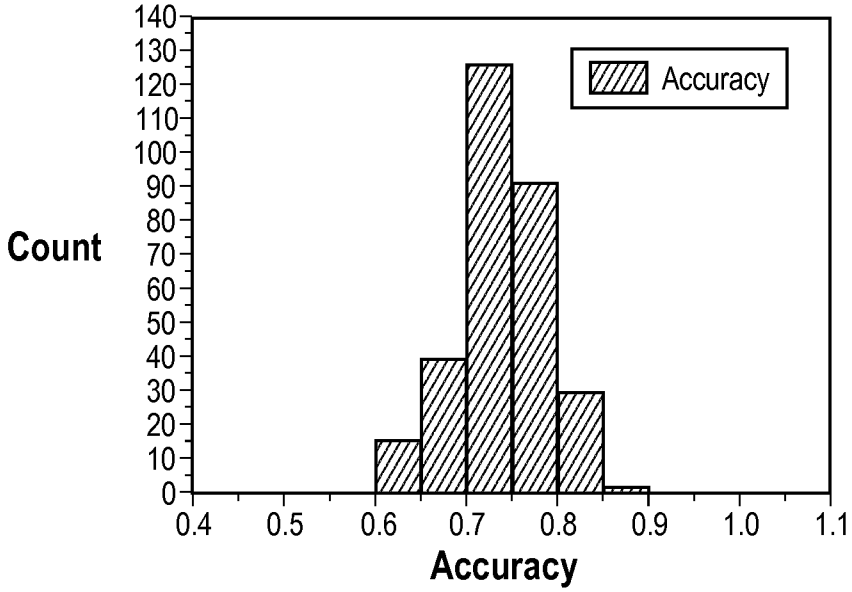


Fig. 11B

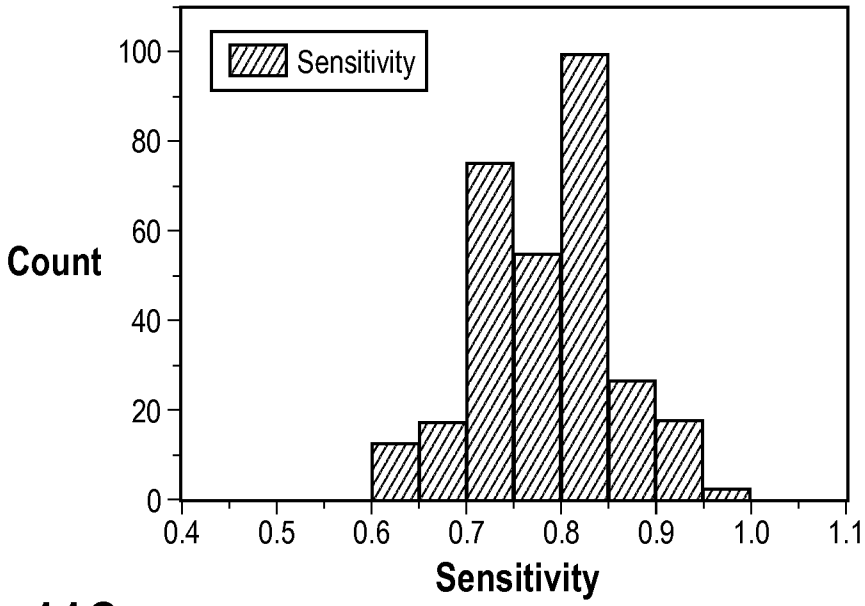


Fig. 11C

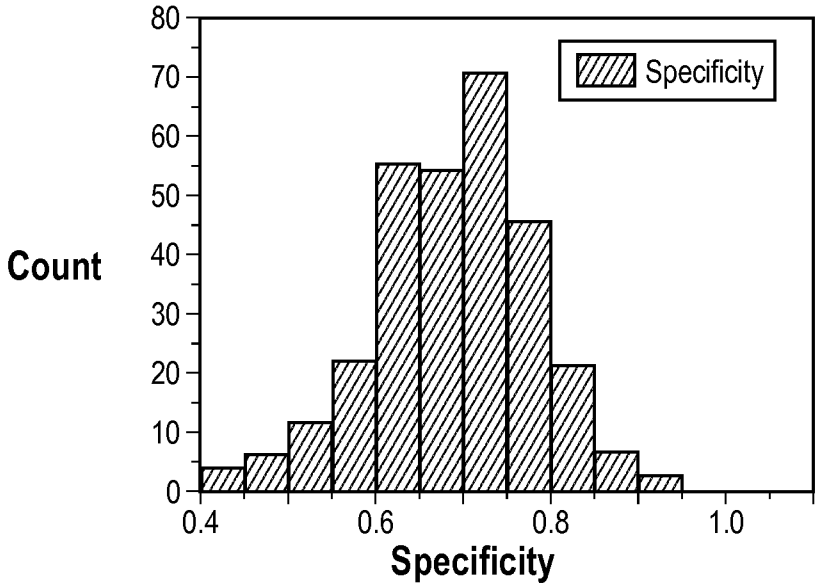


Fig. 12

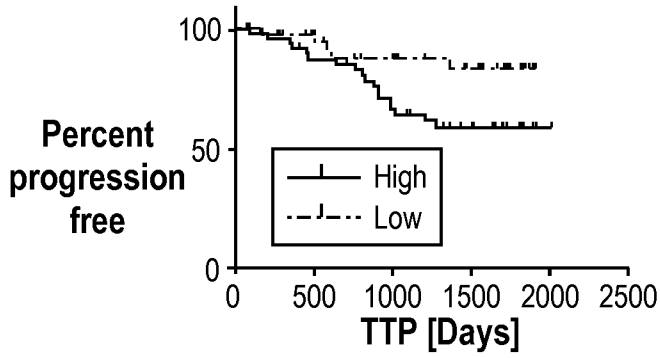
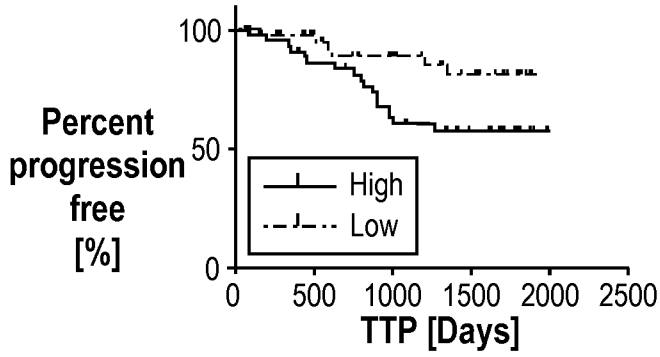
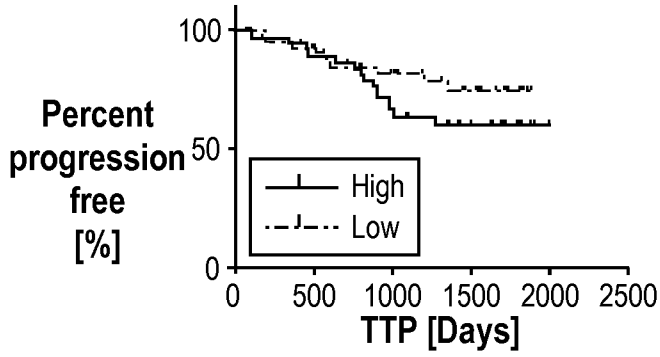
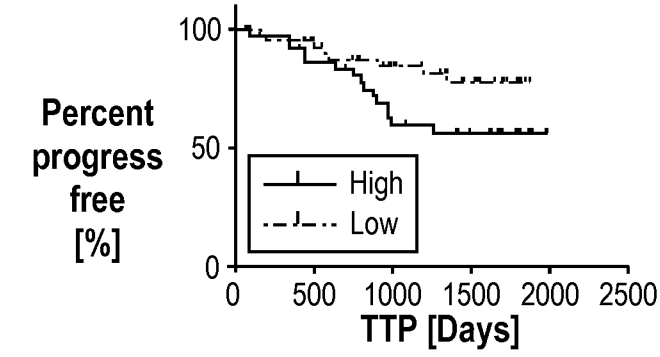
Iteration	Kaplan-Meier Curve	Outcome Metrics
0		p-value = 0.037 HR (log-rank) = 2.74 HR 95% CI: [1.05;5.49]
1		p-value = 0.021 HR (log-rank) = 2.85 HR 95% CI: [1.16;5.94]
2		p-value = 0.199 HR (log-rank) = 1.72 HR 95% CI: [0.75;3.88]
3		p-value = 0.046 HR (log-rank) = 2.38 HR 95% CI: [1.02;5.26]

Fig. 13

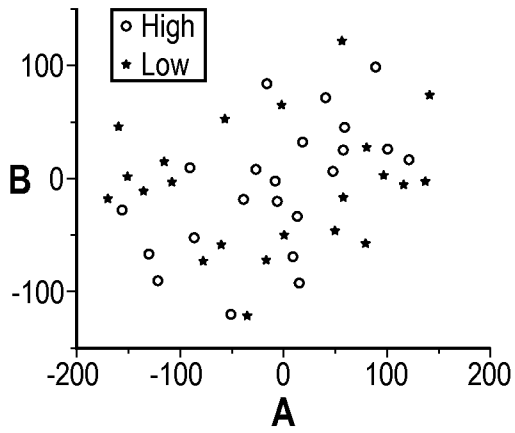
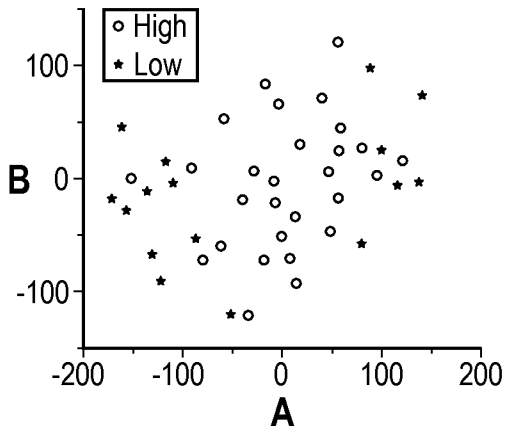
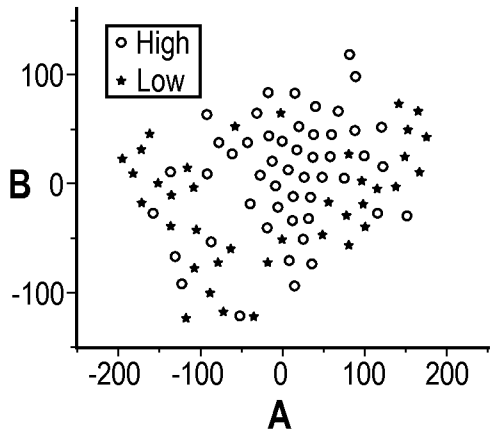
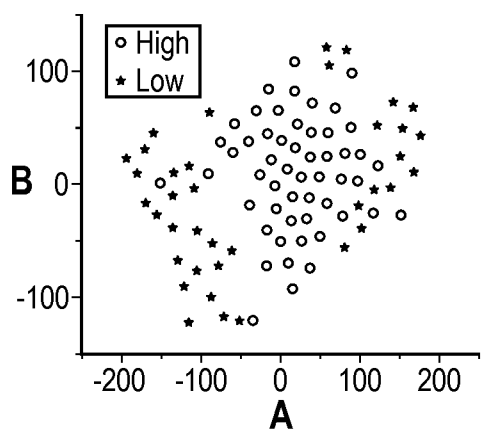
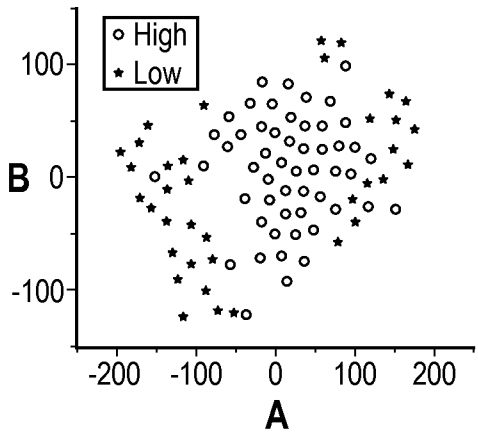
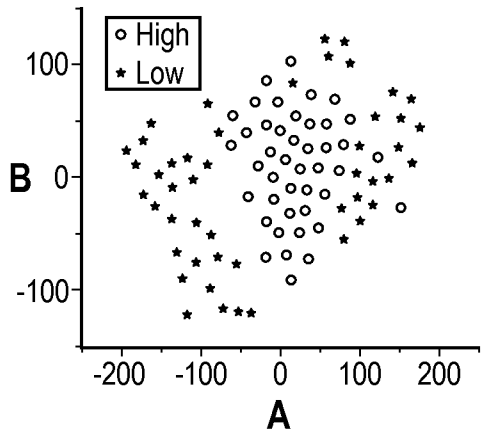
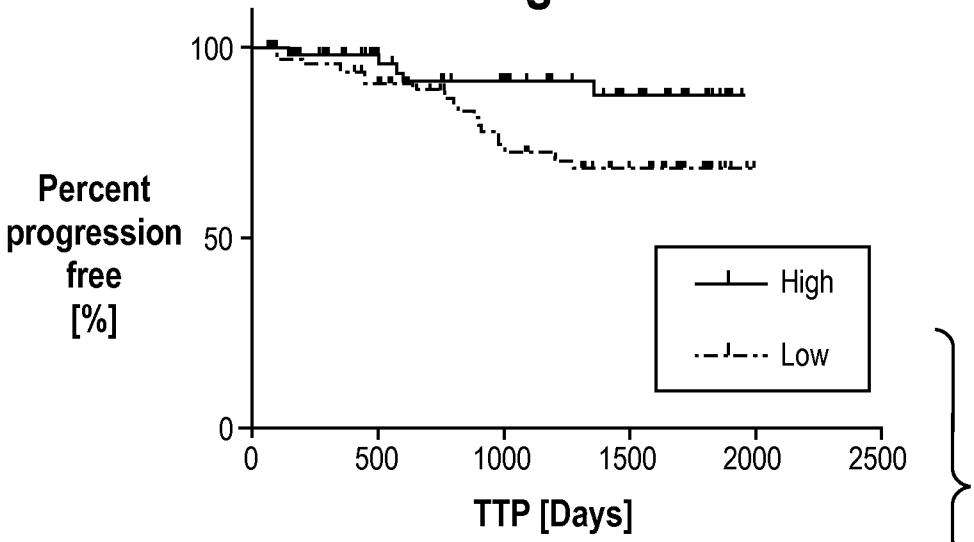
Approach	Initial Definition	Final Classification
1		
2		
3	 (before iteration 1)	 (after iteration 3)

Fig. 14



Time on Study [years]	Percent Progression Free [%]	
	High	Low
3	72.9	91.5
4	68.8	88.1
5	68.8	88.1

Fig. 15

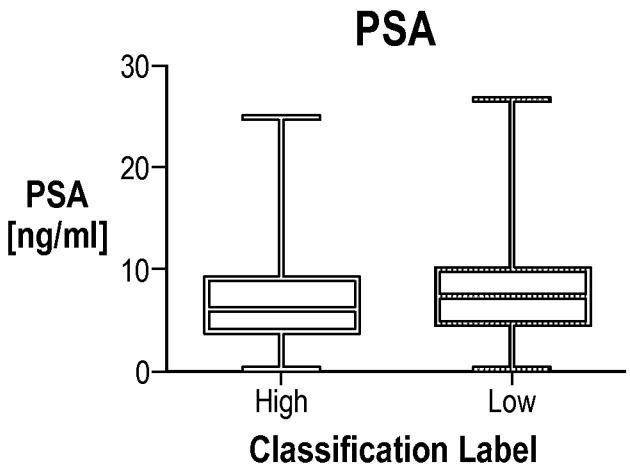
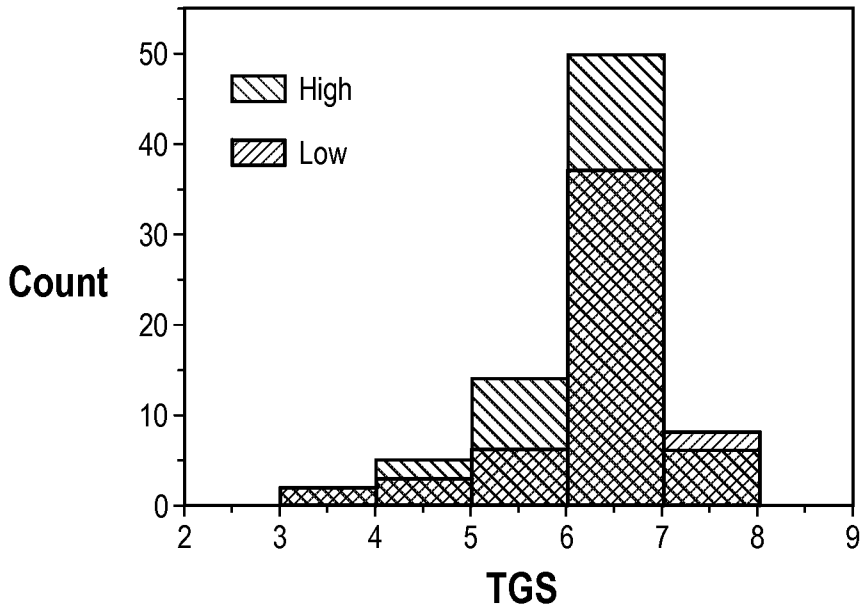
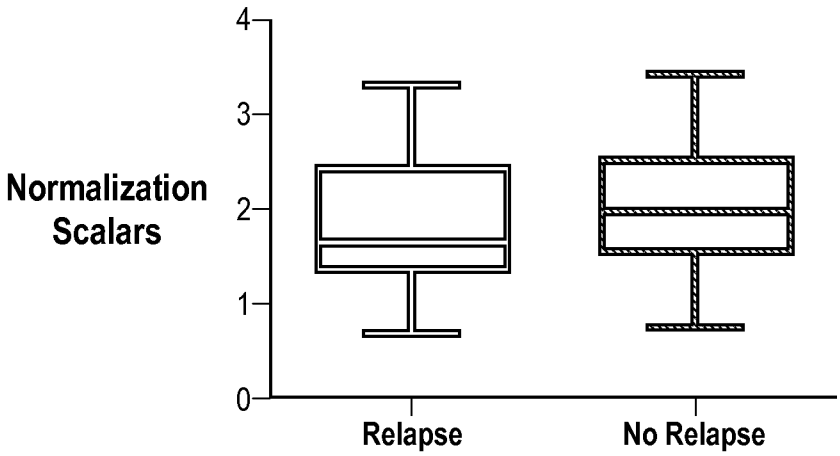


Fig. 16



TGS	MMV Label		Totals
	High	Low	
3	2	2	4
4	5	6	8
5	14	6	20
6	50	37	87
7	6	8	14
Totals	77	56	133

Fig. 17



Unpaired t test	
P value	0.1532

Mann Whitney test	
P value	0.1147

Fig. 18

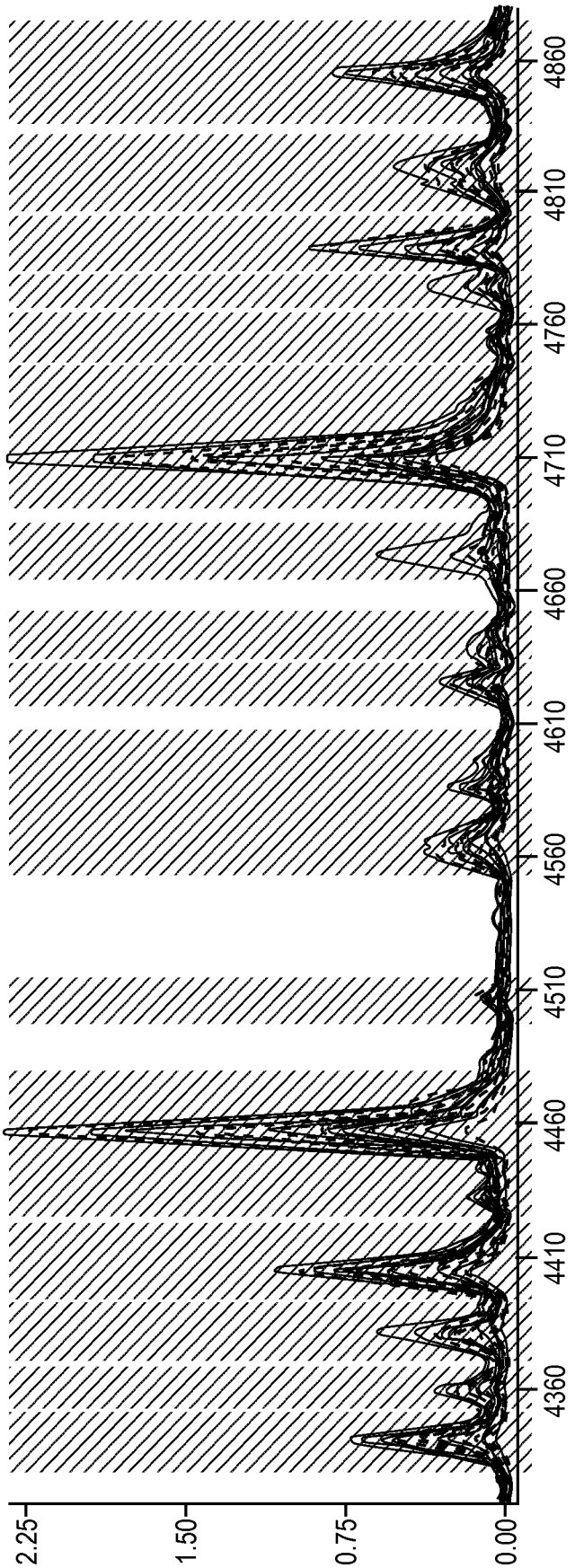
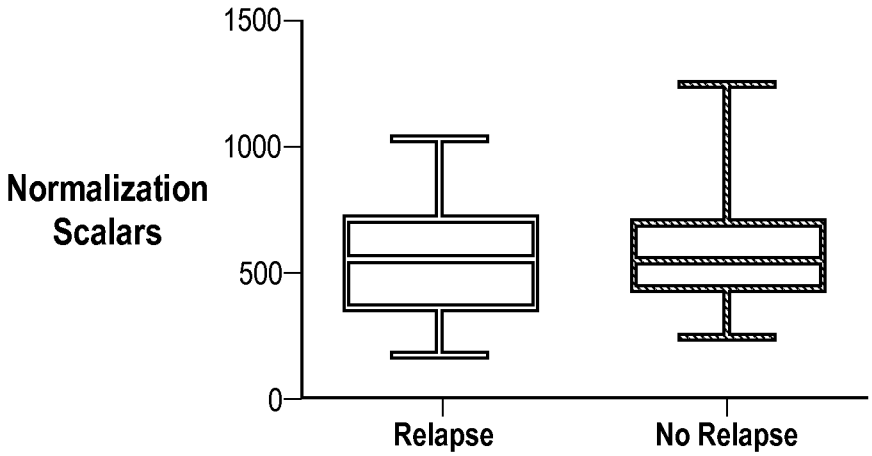

2.25
1.50
0.75
0.00
4360
4410
4460
4510
4560
4610
4660
4710
4760
4810
4860

Fig. 19



Unpaired t test	
P value	0.4963

Mann Whitney test	
P value	0.5267

Fig. 20A

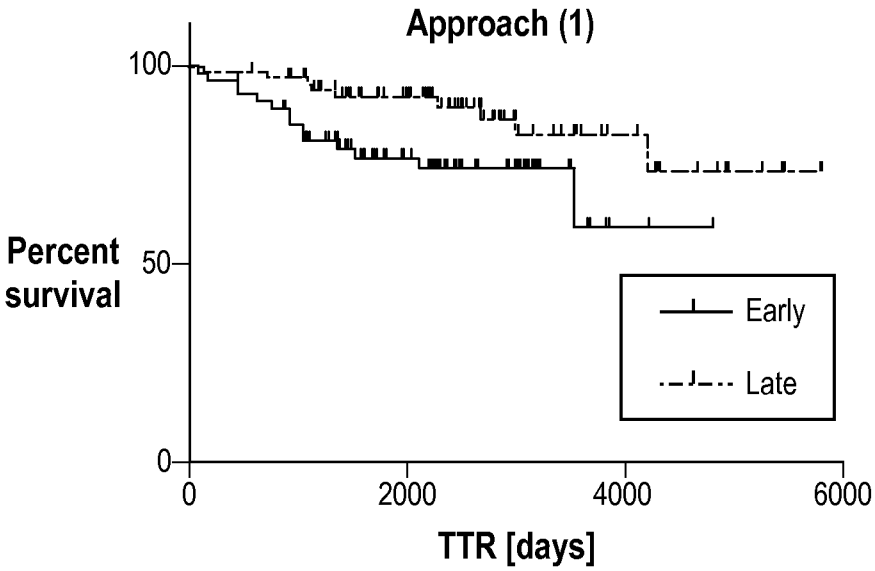


Fig. 20B

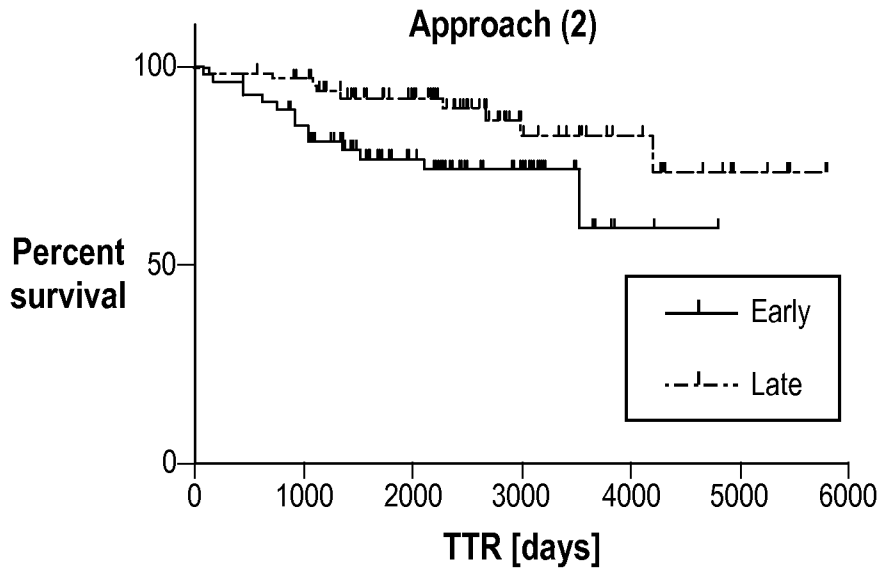
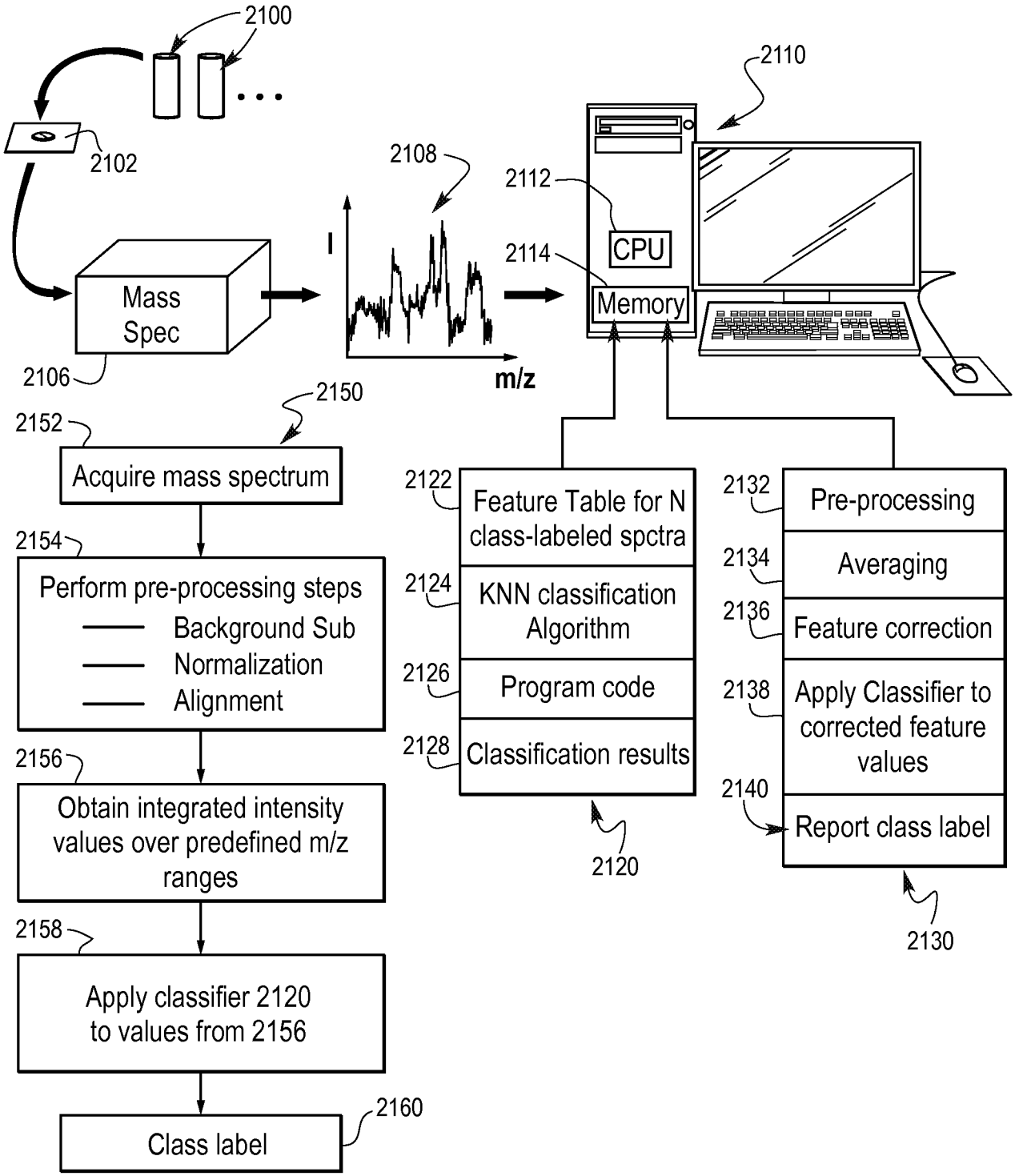


Fig. 21


2100
2102
2108
2110
2112
2114
CPU
Memory
Mass Spec
2106
I
m/z
2150
2152
Acquire mass spectrum
2154
Perform pre-processing steps
Background Sub
Normalization
Alignment
2156
Obtain integrated intensity values over predefined m/z ranges
2158
Apply classifier 2120 to values from 2156
2160
Class label
2122
Feature Table for N class-labeled spctra
2124
KNN classification Algorithm
2126
Program code
2128
Classification results
2120
2132
Pre-processing
2134
Averaging
2136
Feature correction
2138
Apply Classifier to corrected feature values
2140
Report class label
2130

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2015/052927

A. CLASSIFICATION OF SUBJECT MATTER
IPC(8) - G06F 19/24 (2015.01)
CPC - H01J 49/00 (2015.12)
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC(8) - A61K 39/02; A61P 35/00, 35/02, 35/04; C07K 14/255; C12N 15/00, 15/10; C12Q 1/68; G01N 33/53, 33/574; G06F 19/10, 19/24; H01J 49/40 (2015.01)
CPC - C12Q 2600/112, 2600/118, 2600/158; G01N 2800/50, 2800/52, 2800/7028; H01J 49/00 (2015.12)

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
CPC - C12Q 2600/112, 2600/118, 2600/158; G01N 2800/50, 2800/52, 2800/7028; H01J 49/00 (2015.12) (keyword delimited)
USPC - 250/282; 424/133.1; 435/6.9, 29, 69.9; 436/86; 506/13; 706/47, 61

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
PatBase, Orbit, Google Patents, Google Scholar, Google
Search terms used:

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	US 2012/0121618 A1 (KANTOFF et al) 17 May 2012 (17.05.2012) entire document	1, 3-6, 10, 14
Y	US 2014/0284468 A1 (BIODESIX, INC.) 25 September 2014 (25.09.2014) entire document	1, 3-6, 11, 13, 14
Y	US 2014/0106369 A1 (JOHNS HOPKINS UNIVERSITY et al) 17 April 2014 (17.04.2014) entire document	1, 3-11, 13-15
Y	US 8,731,839 B2 (BHANOT et al) 20 May 2014 (20.05.2014) entire document	3, 7-10, 15
Y	SRIVASTAVA, N. "Improving Neural Networks with Dropout" University of Toronto, Department of Computer Science, Thesis, 18 February 2013 (18.02.2013), Pgs. 1-26. Retrieved from the Internet: <www.cs.toronto.edu/~nitish/msc_thesis.pdf> on 23 December 2015 (23.12.2015). entire document	3, 7-10, 15
Y	US 2005/0282199 A1 (SLAWIN et al) 22 December 2005 (22.12.2005) entire document	4, 8
Y	US 2011/0142301 A1 (BOROCZKY et al) 16 June 2011 (16.06.2011) entire document	4
Y	LADJEVARDI et al. "Prostate Biopsy Sampling Causes Hematogenous Dissemination of Epithelial Cellular Material," Disease Markers, 28 January 2014 (28.01.2014), Vol. 2014, Pgs. 1-6. entire document	5, 9
Y	WO 2014074821 A1 (DANA-FARBER CANCER INSTITUTE, INC. et al) 15 May 2014 (15.05.2014) entire document	5, 9
Y	US 2011/0218950 A1 (MIROWSKI et al) 08 September 2011 (08.09.2011) entire document	7-11, 13, 15

☒ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

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"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
23 December 2015	02 FEB 2016
Name and mailing address of the ISA/ Mail Stop PCT, Attn: ISA/US, Commissioner for Patents P.O. Box 1450, Alexandria, VA 22313-1450 Facsimile No. 571-273-8300	Authorized officer Blaine R. Copenheaver PCT Helpdesk: 571-272-4300 PCT OSP: 571-272-7774

Form PCT/ISA/210 (second sheet) (January 2015)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2015/052927

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	US 6,578,003 B1 (CAMARDA et al) 10 June 2003 (10.06.2003) entire document	7-10
Y	FARIA et al. "Use of low free to total PSA ratio in prostate cancer screening: detection rates, clinical and pathological findings in Brazilian men with serum PSA levels < 4.0 ng/mL," BJU International, 01 December 2012 (01.12.2012), Vol. 110, Pgs. E653-E657. entire document	8
Y	US 2013/0320203 A1 (BIODESIX, INC.) 05 December 2013 (05.12.2013) entire document	13, 14