METHODS AND SYSTEMS FOR HIGH CONFIDENCE UTILIZATION OF DATASETS

BACKGROUND

The present teachings relate to methods and systems for high-confidence utilization of large-scale datasets.

The recent sequencing of large number of genomes including human and development of arraying and other high-throughput technologies has resulted in increasing utility of these advances to study organismal scale data (cells, tissues, organisms etc.). With these advances and increasing output of large-scale and high-throughput data has increased need for methods and systems to utilize the data with high confidence (i.e., reduce false discovery) to optimally allocate resources for further development of concepts, hypotheses, technologies and products. Many of these technologies have been developed in the last decade and their quality is constantly improving, and so are the tools to utilize the datasets and to further refine the technologies. Here a few concepts and tools are presented that satisfy some of the needs of the latter goals.

Many systems used in large-scale measurements of organismal/cellular state involves multiple independent measurements of each parameter (e.g., genes/transcripts/proteins etc.). Two common forms of this type of technology that are widely used are (i) GeneChip® (Affymetrix, CA), where each transcript of a genome is measured using multiple independent probes, with each probe having a corresponding mismatch probe to estimate cross-hybridization - the former called a perfect match (PM) probe and the latter mismatch probe (MM) – (well described in patents and literature; e.g; U. S. Pat. Nos. 6551784, 6303301) (ii) typical measures of mixtures of proteins as peptide fragments using several variations mass spectrometry (e.g., Washburn et. al., 2001 and many variations for direct and comparative applications). A variety of applications of this type of multiple independent measurements of each parameter are currently in use and can be envisaged. Due to well documented prior knowledge (in literature and in patents) and evolving applications, the use of the technologies and generation of the data are not described here.

Most biological experiments (due to limitations of biological and other resources) utilizing such high-throughput data generation systems are conducted with small number

of replicates. When possible the resultant data is analyzed using statistical or mathematical principles (for example to detect differentials between datasets exploring different conditions) to increase the confidence of the downstream steps used. But, the small number of replicates significantly reduce the statistical power in the analyses. In principle, the utilization of the independent measures of each parameter should alleviate significant part of this problem (at least in terms of improving power with respect to technical aspects of all steps of the process – e.g., manufacturing, handling, hybridization etc.). In the utilization of multiple independent measures there is a need for an understanding of the system specific properties and the behavior of the different parameters used in such analyses with respect to each other. Conversely, understanding properties of such datasets would help design better measurement technologies.

Whether applied to datasets with design principles similar to above example (multiple measures of each parameter under each condition) or otherwise the datasets across different conditions and replications comparable should be available. This step in data analysis is usually termed normalization (in this document used to represent the step after pre-processing data for technological design and data-collection specific effects, e.g., background correction). A good normalization is prerequisite to all further analysis and interpretations of the data.

The above brief background outlines the need i.e., constantly evolving technology and newer algorithms being proposed and no uniform or consensus approach been accepted and even lesser methods are accepted and predictably useful in dealing with multiple independent measures of each parameter (without an intermediate processing into a unified model based summary) highlights the need for improvements that would satisfy the many emerging needs in efficient and productive utilization of the deluge of data being generated in life sciences and other fields, and sets the stage for one kind of dataset being part of the invention.

SUMMARY

In one embodiment, the method of the present teachings includes selecting a metric for determining substantially optimal combination of true positives and false positives in a data set, applying an optimization technique, and obtaining, from the results of the optimization technique, a value for at least one optimization parameter, the value for at least one optimization parameter resulting in substantially optimal combination of true

positives and false positives. A number of true positives and a number of false positives are a function of the one or more optimization parameters.

The system behaviour in terms of true and false positives is typically viewed as an appropriate response surface of the key parameters. In another embodiment, the method of the present teachings for summarizing parameter value includes grouping measurement result from a data set into a number of pairs of measurement results, determining, for each one pair of measurement results, whether predetermined measures for the one pair of measurement results satisfy threshold criteria, classifying a pair of measurement results from the number of pairs of measurement results as not changing if the predetermined measures do not satisfy the threshold criteria; comparing, if the predetermined measures satisfied the threshold criteria, one measurement result in each one pair of measurement results to another measurement result in each one pair of measurement results, classifying, after the comparison, each one pair of measurement results according to result of the comparison. selecting a common set of measurement results from the classified plurality of pairs of measurement result for use with the data set, and providing summary measures for a parameter utilizing the common set. Various embodiments that present parameter estimation methods, data normalization methods and methods for testing quality of analyses are disclosed. In addition, embodiments of systems and computer program products are also disclosed.

For a better understanding of the present invention, together with other and further needs thereof, reference is made to the accompanying drawings and detailed description and its scope will be pointed out in the appended claims.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 depicts a flowchart representation of an embodiment of the method of the present teachings;

FIGS. 2a, 2b depict a flowchart representation of another embodiment of the method of the present teachings;

FIG. 3a, 3b depicts a flowchart representation of the embodiment of the method of the present teachings shown in **FIGS. 2a, 2b**;

FIG. 4 depicts a flowchart representation of a section of the embodiment shown in **FIG. 3a, 3b**;

FIG. 5 depicts a flowchart representation of yet another embodiment of the method of the present teachings.

FIG. 6 and **FIG.7** depict a flowchart representation of a further embodiment of the method of the present teachings;

FIG. 8, FIG. 9 and **FIG. 10** depict an embodiment of the method of the present teachings for expression summary.

FIG. 11 depict another embodiment of the method of the present teachings to estimate fold change..

FIG. 12 depicts a further embodiment of the method of the present teachings to estimate confidence measure.

FIG. 13 depicts yet another embodiment of the method of the present teachings to test quality of data analyses tools used..

FIG. 14 depicts yet a further embodiment of the method of the present teachings in normalizing data.

FIG. 15 depict an embodiment to develop a computer system to practice the present teachings.

FIG. 16 depicts a graphical schematic representation of results from an embodiment of the method of the present teachings;.

FIG. 17 depicts another graphical schematic representation of results from an embodiment of the method of the present teachings;

FIGS. 18A, 18B depict effect of parameters on results of interest in one embodiment of the method of these teachings; and

FIGS. 19 depicts results of an exemplary embodiment of the method of these teachings.

DETAILED DESCRIPTION

In one embodiment, the present teachings include a set of methods and algorithms to aid high-confidence utilization of large-scale datasets, viz., (a) a response surface assisted strategy to study datasets represented by multiple measurements of each parameter (especially using independent aspects of the same parameter) and aid in design of such measurement technologies and schemes, (b) methods for determining data-specific thresholds, (c) to test the efficacy of a selection strategy (statistical and/or mathematical)

in the data analysis scheme, and (d) a new normalizing scheme for making datasets comparable.

Additional information on the data types being discussed and terminology used to describe these teachings is disclosed below.

While attempting to describe the teachings in generic scenario, the Affymetrix GeneChip® technology is used as example often, for convenience. Some design aspects of this technology would serve to highlight, but not limited to, the multiple measures type dataset discussed here. In the GeneChip® system each transcript is represented by eleven or more 25 nucleotide long probes complementary to the mRNA to probe the transcriptional status of the system being studied. A corresponding mismatch probe to represent the cross-hybridization signal (would be considered probe-specific noise) is included in the chip. High feature densities have been achieved and known and predicted transcripts have been arrayed onto one to few chips for human and other organisms. While the mismatch probes is included to represent the cross-hybridization or probe-specific noise signal and is used in that sense in examples described here, other variations (and applications) that do not include these MM probes (e.g., as suggested in dCHIP: www.dchip.org and Irizarry et. al. 2003) are equally well utilized by the approaches described as part of this set of teachings, and advantages if any would directly translate in the outcome.

Due to the physico-chemical properties of the probes and hybridization each probe though representing a single transcript (i.e., transcript expressed at a particular quantal level) has different hybridization intensity levels. This leads to difficulties in direct utilization of the signal levels. One common approach that has been extensively researched on and being continually developed is to use model based approaches to summarize the data represented by multiple probes into a single summary measure for each transcript (see U. S. Pat. No. 6571005, which is incorporated by reference herein). This approach has the advantage of user friendly representation of the data and in ease of utilization in advanced statistical and mathematical applications for the utilization of the data in the context of advancement of knowledge of the system/process being studied (using pattern recognition, classifiers for diagnostics, identification and study of pathways and new processes, lead candidates for product development etc.).

Some conventions used in this description are described herein below.

Throughout this text and in the accompanying figures the term parameter is used in two context specific manner: (i) to describe each experimental feature within a dataset (transcript, protein etc.,), and (ii) thresholds and other calculated numbers used in the process of utilizing the invention(s) in statistical and mathematical sense. In addition the difference between a calculated value and a set of calculated/estimated or designated threshold is differentiated by a superscripted single quote (for example distance designated **d** would be **d'** when used as threshold).

The use of term independent measures simply imply measures of one parameter (transcript etc.,) using entirely different measurement criteria (e.g., different regions of a transcript as probe, different regions of a protein – peptide fragments, more than one antibody to measure a protein etc., - while the different region might have physical overlap it could have different signal properties under the same condition. This explicitly differentiates from the concept of statistical independence. Indeed some of the properties being studied, proposed and advanced here arise due to this difference. The embodiments described herein are not limited to this type of statistical independence.

An embodiment of the method of these teachings, a Response surface aided strategy (also referred to as **ReSurfX**) for the study of datasets is described herein below, where each parameter is measured using multiple independent measurements

FIG.1 illustrates one representative an embodiment of early stage workflow in processing data. In general data are collected from a measurement system step **1002** and pre-processed steps **1004** and **1008**. This pre-processing would depend on the data-collection technology-specific properties and are assumed to be carried out, unless mentioned otherwise (if needed, prior to applying embodiments of the teachings described herein). Such pre-processed datasets are denoted as starter datasets and indicated by letter **D** step **1006** in the rest of the document and in the figures. Some other figures are referred to in this overview depicted in **FIG. 1** (**FIG. 2a**- to **FIG. 4** step **1010**, **FIG. 8** step**1012** and **FIG. 9** step **1014**). Aspects of **FIG. 2a** through **FIG. 4** depict a response surface approach proposed to study the properties of a given data design that would (i) aid high-confidence data analysis, and (ii) conversely, aid development of design principles for a given system using some initial properties of the experimental and technological aspects. **FIG. 14** depicts a new normalization scheme that is motivated by biological invariance principles. **FIG. 9** depicts application of these two above embodiments in combination or using the first aspect alone, together with methods for data specific thresholds for

parameters used in their application in a new summarization scheme as well as in high-confidence differential identification between datasets representing different observations of experimental or natural processes. Variations and details of some individual steps are referred to in those figures as additional figures with appropriate figure numbers. While many of the teachings presented herein relate to large scale datasets with multiple measures of each parameter in each observation set many individual steps such as normalization scheme, the equations used to optimize selection of true and false positives in comparative evaluations, methods for determining data-specific thresholds and evaluating the statistic or mathematical criteria used for identifying differentials are applicable to many other types of datasets that need not involve multiple measurements of each parameter.

FIG. 2a, 2b show an embodiments of the method of these teachings . One instance has a tester system with built-in true and false positives mixed into the system, step **1016**, or to mix an appropriately simulated true and false positives step **1020** (for example using techniques described in developing the methods and algorithms referred to as **DaST** and **SCALEIT**), described below. In one embodiment, the method of this teaching includes optimizing the identification of differentials between datasets maximizing the identification of true positives and minimizing the identification of false positives. In one instance, a metric termed N_{eff} (for effective number of differentials) is utilized. In one embodiment, the following equation is utilized (also used in **FIG. 2b** step **1022**) – alternative forms suited for specific applications can be used for this purpose (**FIG. 2a**, step **1024**).

$$N_{eff} = TP * TP/(TP + FP) * (1 - FP/TP)$$

In one instance, a response surface of **Neff** with differing values of **N** (number of independent measures) of that parameter in that dataset included and any appropriate statistical/mathematical measure of confidence of the determination **F** (i.e., differential against the noise) – e.g., Student's t-test for pair-wise comparison of datasets (with replicates) or Fishers test for comparing multiple groups of data – is a surface with multiple maximum and minimum points on the surface. An example, these teachings not be limited to that example, is shown in **FIG. 16** with GeneChip® datasets and pair-wise comparisons comparing known true positives (**TPs**) of two fold change and a large

number of invariants (false positives- **FPs**) between datasets. In **FIG. 16**, the **Dataset used is** Affymetrix Latin Square Experiments (2 to 7) with three replicates each using U133A-TAG chip (available at http://www.affymetrix.com/support/technical/sample_data/datasets.affx). The normalization used in the results shown in **FIG. 16** was scaling average of all PM and MM intensity values between values 46,000 (saturation) and overall chip background (28) to 500. Intensity measure used in the results shown in **FIG. 16** was PM – MM, for each probe pair. **Parameters** in the results shown in **FIG. 16** are **d' = B'** = 28; **r'** = 1.1 (estimated for use as proof of principle for Response surface strategy). **Statistic used** in the results shown in **FIG. 16** is Student's t-test (t used instead of abbreviation **F'** in text). AvgA and AvgB are used instead of max and min in **FIG. 3a**. **Ranges used** in the results shown in **FIG. 16** are **N** (minimum number of informative probe pairs) = 3 – 11, increments of 1 and a t statisticof 3-10, in increments of 0.5; referred to as **F** and **F'** herein.

The response surface of N_{eff} step **1022**, in **FIG. 16**, indicates a broad range of t statistic and a range of **N** (independent measures included) that gives near maximal value of N_{eff}. In one embodiment, a cost factor involving **N** and **F** (*symbol F is used as the measure of any statistic/mathematical measure of confidence used throughout the document*) is defined. The lower the **F** and **N** that gives the substantially optimal combination of true and false positives, the better the ability to detect small changes with sensitivity. Increased specificity would result from the use of multiple independent measurements in its full form (i.e., without summarizing to a single value) in the analysis schema. It should also be noted at this stage that typically in analysis of large-scale datasets the problem of false positives is more rampant and less desirable than some loss in true positives (which by nature of experimental variability and small number of replicates would even be desirable in some instances). However, it should be noted that these teachings are not limited to the above described typical example. The equation below (also used in **FIG. 2b** step **1026**) proposes one instance of a form of cost, the term **CANeff** for **cost adjusted Neff**), in terms of an additive factor of the statistic and the number of independent measurements included.

$$CAN_{eff} = N_{eff} / (F' + N')$$

As indicated in **FIG. 2a** (step **1028**), other effective forms of cost may be possible and might be desirable in some instances. The calculation of **F'** (the statistical or mathematical confidence threshold) and **N'** are described in **FIG. 3** and figures referenced therein. Use of a set of common **N'** measures for each parameter in all studies relating to a dataset or data from the same application (termed **Chosenset** – step **1122**, **FIG. 10**) is described herein below.. Typically, these teachings not being limited to the typical example, it has been observed that once the parameters for a technological platform has been calculated using well designed true and positives the same set of parameters seem to be applicable for other datasets from that technology (e.g., **FIG. 3**, step **1030**). An alternative strategy that eliminates the need for iteration to determine **F'** as described above but determines a data specific threshold, is described in **FIG. 6** and **FIG. 7**. In the embodiment shown in **FIG. 6** and **FIG. 7**, substantially optimum parameters for **F'** and **N'** would still need to be determined based on knowledge based on test cases run using algorithm in **FIGS. 3a, 3b** starting step **1032** and **FIGS`. 2a, 2b** steps **1026** and **1028**.

Reverse application of the above described teaching would be to collect/simulate preliminary measures using multiple measures for each parameter (typically more than estimated need) in one or more likely scenarios of the use of that technology platform or a data collection strategy and based on calculated values of **d'**, **r'** and **F'**, and additionally using required confidence for that application, the optimal number of **N** (multiple independent measures) would be designed in the technology or the data collection strategy. An embodiment of the method for the devising of measurements includes obtaining a relationship between one or more preselected parameters and one or more performance indicators for the measurement of the data set, selecting a metric based on the at least one performance indicator, applying an optimization technique, and obtaining, from the results of the optimization technique, one or more substantially optimal values of the one or more parameters. The one or more substantially optimal values of the one or more parameters enables devising the measurement/collection strategy of the data set.

FIG. 3a and FIG. 3b depict an algorithm to study these behaviors and iteration over the parameters to determine the substantially optimal threshold. The method described in **FIG. 3a** and **FIG. 3b** includes iterating over possible values of **N** (number of independent measures included, steps **1032** and **1032b**) and over a range of user determined confidence threshold of **F** (when there are more than one replicated group, **FIG. 3b** – step **1032b**). The datasets could, in one instance, be composed of two or more

observations, or groups of replicated dataset representing properties of different process states. The increment for iteration over **N** (N_{inc}) would be 1 (as this represents the number of measures), and for **F** (F_{inc}) – step **1032** and **1032b**, **FIG. 3a** and **FIG. 3b**, respectively - would be determined by the user based on computational and other resources and the goals of the data analyses. Each parameter (i) is evaluated to satisfy a set of noise threshold criteria and confidence measures on a comparative basis (i.,e between two observations or between sets of replicated observations classified into groups) as decribed below. In one instance, only measures that satisfies the noise control criteria mentioned below and in **FIG. 3a** step **1036** and **FIG. 3b** step **1036** and step **1046** are used.

$$[\sum_{j=1}^{M}(x \mid F >= F',\ x_{jA}/\ x_{jB} >= r',\ |x_{jA} - x_{jB}| >= d')\ ] >= N'$$

(It should be noted that other predetermined criteria are also within the scope of this teachings.) where x_{jA} and x_{jB} above refers to signal of that measure for that parameter being evaluated (**x**) between two conditions designated **A** and **B**, and **j** running over the **M** measures of that parameter **i**. **F** applies to cases with replicated groups in the dataset (step **1046**). In **FIG. 3a** and **FIG. 3b** the terms **max** and **min** are used in step **1036** to represent a general case where **max** refers to maximum and **min** the minimum of the two values in case of single values being compared, maximum/minimum of two averages or medians or maximum/minimum of the group with the lower average or median. In all the examples used in the document to demonstrate the utility of these teachings, average is used when groups are being compared. Optionally, when all the data points of a measure **j** of that parameter being evaluated for differential are below a calculated or estimated overall background noise (**B'** – typically determined below which most data collected represent parameters below reliable detection threshold of that measurement system under the conditions used), they are eliminated from analysis step **1048**. These thresholds (**d'**, **r'** and **B'**) avoid differentials in the noise range – this aspect is discussed in more detail in a future section. The algorithm for calculating dataset-specific thresholds on distance (**d'**) and ratio (**r'**) are described in **FIG. 5**. When the evaluation of a measure satisfy these criteria it is used in the measures included in the analysis (step **1050**) and the next measure is evaluated. This is repeated for all the measures of a parameter (step **1034**). When the number of measures passing the above criteria exceeds the threshold number of measures

for that iteration (step **1052**), then that parameter is considered differential between the observations (or groups) being compared. When all the parameters are evaluated the results are for that set of threshold used in that iteration are recorded (step **1054**) and the values of the parameter thresholds are incremented and used for the next iteration (step **1058**). Once the range of iterations are covered using the increments specified all the stored results are used to select the substantially optimal combination of **N'** - and **F'** in case of multiple replicated groups as in **FIG. 3b** - (step **1056**), one embodiment of which is described in **FIG. 2**, using known or simulated differentials.

FIG. 3b, which is an extension of **FIG. 3a** deals with the case of multiple replicated groups involves optimization of two parameters, the number of measures of that parameter (**N'**) and a confidence measure (**F'**). The use of the confidence measure based on replicated observations in combination with multiple measures substantially improves the comparative analyses of the data. In this case the iterations are carried out similar to that of **FIG. 3a** but for each increment of **F** in the range selected (i.e., **F'** for that iteration), the values as described in **FIG. 3a** above are calculated for the whole range of **N** through iterative loop with changing **N'** (steps **1032b** and **1058b**). The specifics of the strategy are nearly identical except that for each measure and for each evaluation cycle the confidence measure **F** (step **1044**) that is calculated on a comparative basis between two replicates should also exceed the threshold **F'** (step **1046**).

FIG. 4 (optional step **1040**, **FIG. 3b**) depicts a strategy that eliminates some groups (in multi-group comparisons) based on these thresholding strategies and allows varying group number based differential identification for each measure to be evaluated. In this case the noise thresholding is based on comparison of average values over all G groups (termed AvgT step **1060**) to that of individual group for each parameter i. As in the previous case average could be replaced by median or maximum and minimum of the groups or over all groups as described for **FIG. 3**.

FIG. 17 depicts an example of the behavior of $\mathbf{CAN_{eff}}$ with varying values of measurements included (**N**) and of the statistic (t-statistic in this case) for the same comparison shown in **FIG.16**. It can be seen from **FIG. 16** and **Table 1** that (i) the nearly flat surface in **FIG. 16** of the response surface of $\mathbf{N_{eff}}$ can now be reduced to a few distinct peaks, and (ii) the statistical threshold is much lower than that of commonly used data analysis threshold for p value of 0.05.

	3,6	3,7	4,6	4,7	6,6	7,5	12,6	7.71,6
0*	1	0	0	0	0	0	0	0
0.125	4	1	3	1	3	3	1	2
0.25	3	1	3	1	1	1	1	1
0.5	1	1	1	1	1	1	0	1
1	5	5	5	5	5	5	4	4
2	7	6	6	6	6	6	5	6
4	8	8	8	8	8	8	6	8
8	8	8	8	7	7	8	7	7
16	8	8	8	8	8	8	8	8
32	9	9	9	9	9	9	9	9
64	9	9	9	9	9	9	9	9
128	9	9	9	9	9	9	9	9
256	9	8	8	8	8	8	6	8
512*	9	9	9	9	9	9	9	9
CR†	5	4	5	4	4	5	3	4
Total identified	95	86	91	85	87	89	77	85
Total present	135	135	135	135	135	135	135	135
FP	16	2	5	0	0	1	0	0
PPV	0.86	0.98	0.95	1.00	1.00	0.99	1.00	1.00
Sensitivity	0.70	0.64	0.67	0.63	0.64	0.66	0.57	0.63

Table 1 - An example of the effect of different statistical threshold (F') and number of independent measurements used (N') on the true and false positives (of two fold change) identified

Indicated, in Table 1, are the number of spike-ins of two fold difference identified at each threshold (out of 9, three in each comparison for three individual comparisons). The concentration of the spike-in (in pM) are indicated in the leftmost column in each case the concentration of the spike-in in the other dataset is twice this amount (except as indicated below). The threshold of t-statistic (F') and number of valid probe-pairs (N') is indicated in the first row as (F',N'). FP is number of false positives, PPV is positive prediction value [TP/(TP+FP)], sensitivity is [TP/(TP + FN)]. * 0 pM spike-in was compared to 0.125 pM spike-in, and 512 pM spike-in is compared to 0 pM spike-in. † CR indicates cross-reactive transcripts/probesets with homology to spike-ins (out of 9, three in each comparison for three individual comparisons). The dataset are the same as used in example shown in **FIG. 16** and **FIG. 17**. (**Note that, in FIG. 17, t** used instead of **F'** above and that **N'** is equal to the number of probe pairs.)

The example shown in **Table 2** demonstrate the significant advantages of these findings, i.e., ability to select true positives without much impact on the number of false positives identified even at lower confidence thresholds. Further this precludes the need for guessing the threshold. Strategies for estimating data-specific thresholds are described later (**FIG. 5, FIG. 6** and **FIG. 7**). Some aspects of applications of this invention in the context of gene expression measurements using GeneChip® technology are described in Gopalan, *Genome Biology* 2004 5:p14, which is incorporated by reference herein.

	1.5	2	3	4
3,5	9287	13595	18001	19251
3,6	8548	11031	15101	16657
4,6	7553	12753	16947	18287
4,7	6927	10333	13965	15431
6,6	7418	11444	15235	16677
7,5	8588	13500	17426	18690
12,6	5164	8993	12204	13596
7.71,6	6634	10584	14111	15600

Table 2- Application of data-scaling strategy (SCALEIT) to identify utility of the Response surface assisted strategy

Indicated in Table 2 are the number of probesets (average of three independent comparisons) detected (out of possible 22,301) at the given thresholds of t statistic cut-off (F') and minimum number of probe-pairs (N') satisfying this F', indicated as (F',N') in column 1. For the purpose of this evaluation three replicates were compared to three other independent replicates essentially representing the same samples scaled to the given differential (indicated in first row), and the values indicated are averages of three such independent evaluations. Again, the dataset used are the same as used in example shown in **FIG. 16** and **FIG. 17**.

Embodiments of the method of this teachings which utilize (and are utilized in) the above described Response surface assisted thresholding strategy (**ReSurfX**) embodiment for identification of differentials using data-specific thresholds are described below.

Some of the embodiments described above utilized a dataset specifically designed for such purposes. Many currently existing datasets seldom are designed with built-in true and false positives, or not in sufficient number and variety. One embodiment , for the instance in which there is not a sufficient number of variety of true and false-positives utilizes a tester dataset as above to determine thresholds that could be used with that type of data generation technology. The use of distance and ratio thresholds have already been demonstrated in several conventional analyses schemes, but, in this teachings, algorithms for determining data-specific thresholds of these parameters are disclosed.

Ebodiment for determining data-specific thresholds (**DaST**) of distance, ratio and statistic to avoid differentials in the noise range are disclosed herein below.

Different data collection platforms, pre-processing schemes (background correction, normalization etc.) and experimental systems have different levels of inherent and other handling based noise/variability (typically observed when comparing data between replicates).

FIG. 5 depicts a schema that determines data-specific thresholds for distance (**d**) (i.e., numerical difference between the two values or two groups) and ratio (**r**) that would typically lie within noise level for that data. In one embodiment, a percentile is determined at which these values **d** and **r** would be optimum based on the ability to detect substantially optimal combination of true and positives from a tester dataset, e.g., using N_{eff} step **1022**. For this purpose, a large enough random sampling of the data – step **1062** (or the whole data, step **1064**) is selected and the distance and ratio are determined between the maximum and minimum for each selected measure for example within replicates (thus capturing the noise component of the data, step **1066**). The calculated distances and ratios (individually) are sorted in ascending order of values (of **d** and **r**) and values of **d** and **r** at different percentiles on the ordered set of values are chosen as thresholds (**d'** and **r'**) – step **1072** - and used as described in applications described in previous sections or in determining thresholds for many data analyses scheme (either for selection or for elimination to avoid dealing with data just in noise range). The different thresholds are tested on a training set and optimum value chosen (for example by using equation for N_{eff}). This percentile value can be used to determine **d'** and **r'** (the selected thresholds – **DaSTd'** and **DaSTr'**) step **1074**. When additional specificity or safeguard is warranted scaled up versions of the determined values of **d'** and **r'**, or a percentile threshold above that determined as optimum using the algorithm in **FIG. 5** can be used to

increase the confidence level. Dynamic thresholds can also be determined by using similar strategies on a data ranked by values of the measures at different points along the distribution and assuming piecewise linearity (step **1076**).

FIG. 6 and **FIG. 7** describes similar embodiments, but with additional intricacies for the determination of data-specific threshold of **F** (the measure of confidence used) to avoid differentials primarily within the range of noise (hence few true positives in those ranges). In this instance, a large enough sample of parameters and all its replicates are used and additional values within the range of values represented by the replicates are simulated, step **1080**. As warranted, this range can be scaled up by a factor, termed **vibrate factor - v** (e.g., **v = r'**, would imply find enough number of random values between **r'** times the maximum value and (1/**r'**) times the minimum value) – step **1082**. Using just the maximum and minimum value as range would be equivalent to using a vibrate factor of 1.0. The values for that parameter and the random values within (inclusive of the end points) are sorted to form enough groups, step **1084**, with appropriate number of replicates and the measure of confidence calculated, step **1090**. In case of multiple independent measurements of the parameter, as is the main theme of this section, this process is repeated **N'** (threshold number of measurements) times and minimum value is stored as one value of the dataset to be used for determining the substantially optimal threshold step **1092**. The collected minimum values are sorted descending and the value of **F** is chosen at a user determined confidence threshold, **DaSTF'** (e.g., 95% confidence level would be vale at 95th percentile), step **1094**. This value can either be chosen on user determined confidence level or iterated for using a training set, step **1096**. The noise range elimination strategies described earlier steps **1036** and **1048** (steps **1086** and **1088** in this algorithm) could optionally included in calculating **DaSTd'**, **DaSTr'** and **DaSTF'**. Alternate manifestations of step **1092** could include median or any other percentile of values calculated for the **N'** measures of each parameter, rather than the minimum over the **N'** values of **F**.

When informative **N** is greater than **N'** the statistical threshold can be relaxed (for more sensitive identification of differentials), using basic statistical principle of independence (viz., $\mathbf{p}^{N'} = \mathbf{p_1}^{N}$). As mentioned before these data types do not exactly satisfy statistical independence principle, but the advantage obtained through this adjustment does not seem to come at recognizable cost in cases tested.

The above embodiment has been applied to a published defined dataset (as an example, embodiments not to be limited to applications or datasets of type used in this example) with large number of differential and invariant parameters without iterating over range of **N** and **F** values as in example 1, with good success (**FIG.16**), by using the strategies described in **FIG. 5, FIG. 6 and FIG. 7** and applying the results to **FIG. 4.** For this purpose **N'** value was set as 50% of all probesets (independent measures) available, based on prior trials with data used in example results shown in **Tables 1** and **2** (**Table 3**).

	Choe et. al., Design	ResurfX identified	
		TPs	FPs
Chip type	DrosGenome1		
Total probesets used	3919		
Total non-differential	2588		
Total differential	1331	937	73
>= 2 fold	781	732	
>= 1.5 fold	1129	921	
< 1.5 fold	202	16	
Total probesets not used	10091		

Table 3- Application of data-specific thresholding strategy (**FIG. 5 - FIG. 7**), **BINorm** scheme (**FIG. 14**), and **ReSurfX** (**FIG. 3**) on a test dataset with large number of true and false positives.

The dataset used is from Choe et. al., [*Genome Biology (2005) 6:R16*], which is incorporated by reference herein. The parameters used are

B'=107 (calculated, data not shown)

d' = 57 (Figure 5, at 50th percentile)

r' = 1.162(Figure 5, at 50th percentile)

N' = 7 (estimated - prior art)

F' = 1.65 (t-statistic – Figure 6)

Intensity measure used is PM – MM, for each probe pair. **Normalization used is** BINorm at 25% middle values in each subset using known spiked-in invariant set built-in the data. AvgA and AvgB are used instead of max and min in Figure 3.

While both these applications are depicted for multiple independent measurements it has a broad utility even in datasets with each parameter represented by a single value. This can simply be achieved by setting **N' = 1** in both these cases.

Embodiments of the method of the present teachings for summarizing parameter value includes grouping measurement result from a data set into a number of pairs of measurement results, determining, for each one pair of measurement results, whether predetermined measures for the one pair of measurement results satisfy threshold criteria, classifying a pair of measurement results from the number of pairs of measurement results as not changing if the predetermined measures do not satisfy the threshold criteria; comparing, if the predetermined measures satisfied the threshold criteria, one measurement result in each one pair of measurement results to another measurement result in each one pair of measurement results, classifying, after the comparison, each one pair of measurement results according to result of the comparison. For replicated data sets, the embodiment includes the steps of averaging the measurement results over replications and grouping the averaged measurement results into a number of pairs of averaged measurement results. The method proceeds similar to the preceding embodiment, utilizing pairs of averaged measurement results instead of pairs of results. An embodiment of such method of these teachings, EMINE: An Explicit Model INdependent Expression measure, for summarizing parameter value when represented by multiple independent measures is disclosed below.

As described above, conventional summarized values for multiple independent measures are model based. While such conventionally used model based approaches have significant advantages they may not always be desirable for all datasets. As described above, use of all independent measures directly confers significant advantage of specificity when identifying differentials between datasets. But such methodology has to be adapted for use with other well established advanced statistical and mathematical methods of analysis for pattern recognition etc, especially when the dimensions classifying the observations and the interactions of interest in the dataset gets higher. And embodiment of a explicit model independent expression summary method is disclosed, where the computational and adaptation costs for using the multiple measures of each parameter does not outweigh the disadvantages.

FIG. 9 and **FIG. 10** describe an embodiment of the method of these teachings for summary measure using groups of data (typically replicates of observations in a dataset),

while **FIG. 8** and **FIG. 10** describe a similar algorithm but for dealing with each observation as single unit (typically unreplicated observations). Each independent measure satisfying noise threshold criteria i.e., steps **1100, 1102, 1110, 1112** and **1114** (as in steps **1036** and **1048**) of a parameter is classified as no change (**NC**), increase (**I**) or decrease (**D**) i.e., steps **1104, 1106, 1108, 1116, 1118, 1120** based on pair-wise comparisons, step **1098**. Based on as many comparisons possible (or a minimum number of comparisons when large number of combinations are available) the independent measurements satisfying the specified criteria in the pairs over a particular threshold of datasets and as many independent measurements having uniform classification for that parameter are chosen for each parameter step **1122**. When the number of independent measurements chosen for each parameter is above **N'** the values based one reference chip or a set of chips are ordered and the middle **N'** measurements are used for calculation of expression summaries for all datasets step **1128**. Some alternate purpose/technology specific embodiments would include ordering the usable parameters **N** based on purpose specific criteria (e.g., along a predicted transcript and using a set that maximizes chances of detecting a variant of the transcript of interest among possible alternatively spliced forms). When the number of measurements chosen are below **N'** and the threshold on the number of pair-wise comparison could not be relaxed further without deterioration of quality (step **1124**) all **N** measurements satisfying minimum criteria are used (step **1126**), sorted and measurements representing middle **N'** values chosen. The expression summary could be a simple measure such as weighted average with outlier correction or any other established or modified summary measures step **1130**. When a number of measurements are available such **N'** measurements that have uniform property over many comparisons (usually can be set as a threshold percentage of comparisons available to determine this property) a common set for use with that type of dataset for most uses beyond available or used for this step can be chosen and stored for future use. The use of such uniform set of measurements for each parameter for all datasets, termed the **Chosenset** step **1122**, makes the summarized values have naturally better quality than using all or variable number of informative measurements. Use of an additional appropriate normalization after **EMINE** may be advantageous in some instances. One advantage of **EMINE** is the minimal use of numerical correction criteria.

In the context of biological applications, with the development of large scale dataset, a universal set of uniform measurements for **EMINE** can be devised and used. The strategy devised above can be interpreted as an approach to directly achieve this goal.

Embodiment of the method of these teachings for estimating fold change confidence estimates of differentials for Response surface based data analysis are disclosed herein below.

FIG. 11 and **FIG. 12** depict embodiments for determining estimates of ratio of differential (in pair-wise comparisons) and estimate of confidence for differentials when using Response surface assisted strategy, respectively. In the simplest form estimate of ratio is obtained by taking pair-wise ratio for each selected measurement (selection is either based on noise threshold elimination strategies, step **1132**) similar to steps **1036** and **1048**, using all **N** passing threshold elimination, the **Chosenset** strategy (step **1134**), or the **N'** values nearest to median (step **1136**), as described below and in step **1042**) of that parameter followed by a summary metric – step **1138** - (e.g., weighted average with outlier correction as in step **1130**). When **N** failing noise threshold elimination strategy is greater than **N'** (step **1140**) the failed ones can be used for summary measure. When needed middle **N'** ratios as in step **1136** can be used. The spread of the estimated ratio for each parameter over the number of measures used is used to determine and report an estimate of the ratio. The measure of confidence uses similar techniques (steps **1144** and **1146**) except that a minimum value is used to give the most conservative measure of confidence, other variations based on percentiles of all confidence measures from informative measurements of that parameter in that comparison could also be used. When informative **N** is greater than threshold **N'**, an alternative is to use the middle **N'** values of a sorted (descending) array of **F** values – step **1148**. The confidence measure can then be used as in the cost factor as an additive measure of **N'** and **F'** (step **1026**) or can be converted to a p-value from a standard statistic or bootstrap based statistics and presented in desirable format (some usable forms are proposed in **FIG. 12**, step **1150**). In the case of using **EMINE** summarized values, standard mathematical and/or statistical can be applied – steps **1142** and **1152**.

An embodiment of a data-scaling method for testing efficacy of differential selection scheme used in analyses of datasets (referred to as **SCALEIT**) is disclosed herein below.

As has been used extensively in the above sections, a well designed tester dataset would be of extreme value in development and validation of algorithms used in various steps of the workflow. But, such well designed tester sets are seldom available that is appropriate for an experimental scenario, or some times limited by resources. Numerous data analysis schemes are used to glean useful information from datasets. Different schemes result in different degree of success (identifying true and false changes and relationships between parameters and/or different observations/conditions being studied). A simulation method that utilizes the variances structures present in the whole dataset to evaluate the efficacy of the data analysis scheme applied in a specific experimental situation is conceived, tested, and described below.

FIG. 13 describes an embodiment of the method of these teachings using a data-scaling approach **(SCALEIT)**, and an example of its utility provided.

Briefly, this embodiment, **SCALEIT,** involves scaling the whole dataset and its replicates to varying extent (e.g., 1.2, 1.5, 2 times etc.,) – step **1154** - and application of the data analysis/differential identification scheme – step **1156**. The advantage with this approach being the utilization of all possible variance structures inherent to the system. An example of this approach in the context of Response surface assisted method to identify differentials at various thresholds – step **1158** - is shown in **Table 2**. Some forms of data analysis schemes would be better tested by modifications of this unidirectional scaling strategy, for example bidirectional changes or mixture of such changes suitably combined with original dataset.

An embodiment of the method of these teachings for normalizing data from a data set includes the steps of sorting data from the data set according to measurement value, selecting, according to a predetermined criterion, reference subsets, the reference subsets having at least one reference measurement value, selecting, from the sorted data, data elements having measurement values substantially equivalent to the one or more reference measurement values, sorting the data elements having substantially equivalent measurement values, the sorted data elements comprising a sorted substantially equivalent subset, and utilizing the one or more reference measurement values and the sorted substantially equivalent subset to normalize the data set.. An embodiment of such

teachings motivated by principles of biological invariance to normalize data, referred to as **BINorm**, is disclosed herein below.

Array based as well as many other technologies rely highly on normalization (or some form of numerical equivalency of data) between datasets within a platform and across platforms. Most normalization used to date relies on ordering of datasets and correcting systematic variations in a intensity dependent manner either using the whole data based distributions, or in spatially separated groups as in print-tip normalizations (e.g., lowess). Invariably a rank based assumption is built-into the system including nearly exact distribution of datasets, or ordering the whole datasets and choosing rank based invariant sets between a reference and a target dataset (e.g., U. S. Patent No. 6571005, which is incorporated by reference herein) or a more recently proposed variant of the latter method where the dataset is divided into ranges of expression values and invariant sets chosen by rank equivalence (U. S. Patent Application Pub. No. 2005/0038839A1, which is incorporated by reference herein). Example of other commonly used methods include extensive application of principles of variance distributions and attempts to reduce their systematic component using transformations or modeling). Improper use of normalization scheme can at times introduce artificial bias and error in datasets. An embodiment of the method of these teachings, which is motivated by fundamental behavior of biological systems, is disclosed below and shown in **FIG. 14**.

Frequently, in biological systems studying variation of all parameters in one or more experimental conditions there are always a proportion of randomly distributed invariant values in any given sample of the dataset. In addition in many systems the variation (or differentials) between experimental conditions and technical variations are random, bidirectional and randomly distributed. Such systems and systems with small number of real differences are amenable to this normalization scheme, termed, **BINorm** – to indicate **b**iological **i**nvariance motivated **norm**alization. This schema requires designation of one observation as reference – step **1160** - and all other observations are normalized with reference to this dataset. Cyclical normalization, i.e., all against all in pair-wise manner might be of use in some instances.

The reference data is ordered by measured values – step **1162** - and subsets are chosen along the total distribution of the data, termed **Iref**, step **1164**. The measures equivalent to each subset (i.e., indexes of the data points in the subset are used) are chosen from the target data and this subset sorted, termed **Itarget**, step **1166**. In its simplest form

with the above stated assumption not significantly violated the middle **x** % of values in the target subset should have equivalent values of the subset from reference array – simplified version of step **1168** - (e.g., middle 10% in a 100 point subset of **Iref** and **Itarget**). Thus the average (or median) of the **x** values in **Itarget** will be equivalent to **Iref**. The equivalence determined this way along the whole dataset would then be used to normalize using a piecewise linear functionality. The value of **x** would vary with the percentage of invariance and can be iterated upon, step **1176**, after the above step or on another embodiment depicted in the picture after iterating on regional equivalence of values in **Itarget** as described below. As long as the percentage of invariance between the datasets is above **x**, there should be no degradation of quality even when much lower percentage, than actual invariance in the data is used. Variations in regional selection of invariance are needed when unidirectional skew in differentials is present between datasets. One embodiment to deal with such cases, represented in steps **1168** and **1170**, is to iterate over the equivalent region by scaling the **x**% of ordered measurements of **Itarget** at different at different percentiles on the ordered data (e.g., **x**% starting at 10^{th} percentile rather then the middle) and scaling the value to the middle **x**% of **Iref**. A built-in training set, a large enough putative invariant set (see description below) can be used to test the quality of the normalization to particular datasets – step **1172** – or using an appropriate test scheme for equivalence. Thus after iterating over the range of percentiles on ordered **Itarget**, the equivalent range chosen to scale the whole data would be the one that gives the best concordance between the two datasets as determined with the test using known/simulated invariants or another test scheme for equivalence – step **1174**. **BINorm** scheme has the advantage of simple correction of systematic changes while preserving variability inherent in the experimental design, thus improving specificity and confidence in the utilization of resultant inferences from the analyses. An example of such usage with a perfect invariant set is shown in **Table 3,** though these teachings not being limited to such an example.

When data from multiple measurement platforms or variations in the measurement system of the same platform are used, a large enough presence of common link terms for the identifiers of the parameters should suffice to make the measurement values in between the datasets equivalent and comparable.

As mentioned above, the availability of large scale datasets for each organism and platform a large enough putative invariant parameters can be chosen and used for general purpose analyses of various kinds. While not all parameters may be truly invariant in all

conditions being tested a majority should be useful. When most are not utilizable either the normalization scheme is not applicable to those datasets or that system is uniquely different.

It should also be noted that though this type of invariance is prevalent in biological systems, any experimental system or datasets having such properties are amenable to this normalization schema.

A system and computer program product that integrates the above described teachings to current databases and other software utilities is described below.

As can be seen in the Figures and the above description, the teachings and concepts presented hereinabove are presented directly in the form of algorithms that are directly amenable to development of computer software – step **1182** - (in any of the computer languages and user-interface tools) that can be integrated with databases and data warehouses – step **1178** and **1180** - as well as ability to use output for other applications using other software or use as input methods/algorithms available in other software packages in conjunction with these teachings – step **1184**, **1186**, **1188** and **1190**. A computer usable medium **1179** has computer readable code embodied therein, where the computer readable code is capable of causing the computer system **1175** to execute the methods of these teachings. Indeed, several of the teachings presented above were tested using software codes built in the C++ language. (However, the methods and systems of these teachings are not limited to any one computer language.) In addition these concepts individually can also be used as functions integrated inside other packages. A simple schema of an embodiment of a system of these teachings is presented in **FIG. 15**.

The teachings presented here have the advantage of minimal assumptions and numerical treatments in most cases thus adding to the goal of high confidence utilization of large-scale and many high-throughput data – step **1192**. The concepts and algorithms for applicability for multiple independent measures of a parameter also would have applications in many other scenario (e.g., certain kinds of analysis of time course data, collection of meta-data as each parameter). While the utility are discussed in the context of high-throughput and large-scale organismal (or genome wide) data in biological contexts it should have utility in variety of other contexts where the possibility of application of the concepts and algorithms exist.

In order to better describe these teachings, the following exemplary embodiment, these teachings not limited to that embodiment, is presented below. The GeneChip expression data set used in these analyses is from the Affymetrix dataset released for purposes of algorithm development, and based on HG-U133A-Tag arrays Experiments 2 through 5, replicates R1 through R3 (http://www.affymetrix.com/support/technical/sample_data/datasets.affx). This data setwas generated using a hybridization cocktail consisting of specific RNA spike-ins of known concentration mixed with total cRNA from HeLa cell line, by Affymetrix. All probesets starting with AFFX not part of the spike-ins of known concentration were removed for calculation of true and false positives involving spike-ins, since some of them had obviously discernible differences. Three probesets were reported to have perfect homology of 5 or more probe-pairs thus leaving 45 true positives and 22,185 false positives for each comparison in the dataset. Unless mentioned otherwise, values represented are based on average of three comparisons between experiments differing in spike-ins with two fold difference in concentration viz., experiments 2 with 3, 3 with 4 and 4 with 5. Probe level data were extracted from Cell files (using tiling coordinates defined by probesequence information supplied for the chip type – U133A-Tag by Affymetrix) and the mean of all signal values (of perfect matches and mismatches that were between the value 28 (the lowest background in the chips used) and a saturation value of 46,000) were scaled to target value of 500.

b is the background of that chip (as determined by Microarray Suite 5.0). When more than 11 probe-pairs represented a probeset only the first 11 (in their order of listing in Affymetrix probesequence file) were extracted and used. The difference between perfect match and mismatch value for each probe-pair was used for all further evaluations. Zero or negative differences were set to background.

The signal values were extracted using Microarray Suite 5.0 (Affymetrix, CA) with the trimmed mean (top and bottom 2% signal values are trimmed) for each array scaled to a target intensity of 500, for representation in Figure 3. Standard definitions for sensitivity and positive prediction value (PPV) were used. Sensitivity was calculated as sn = TP /(TP + FN); PPV was calculated as: PPV = TP /(TP + FP), where TP is true positives, FPis false positives, and FN is false negatives. Typically, variance weighted average were used, as mentioned.

For the preliminary evaluation on biological replicates, the data from human patients with aortic stenosis (samples JB-as_0806, JB-as_1504 and JB-as_1805 were comparedagainst JB-as_2111, JB-as_2604 and JB-as_2708, hybridized to U75-Av2 chips), from Genomics of Cardiovascular Development, Adaptation, and Remodeling site. NHLBI Program for Genomic Applications, Harvard Medical School. URL: http://www.cardiogenomics.org [*accessed 28 May, 2004*]. This chip consisted of 16 probe-pairs for most transcripts and the average background was used as 60 .Calculations were performed using C++ on MS-Developer environment in Windows XP background.

Typical analysis of GeneChip data for identification of differentials between datasets involve extraction of the probe level data using an unified expression index signifying the estimated level of expression of that transcript summarizing the information in the eleven or more probe-pairs, following normalization or scaling. Some common methods used for this purpose are dCHIP , RMA and MAS (Microarray Suite, currently version 5,0, Affymetrix, CA). The use of unified expression index is advantageous in terms of computational simplicity and easy adaptation of statistical methods to high dimensional datasets. But, due the extremely variable behavior inherent to each probe representing the transcript the unified expression index do not always perform satisfactorily. Consequently, statistical approach to reduction of false positives based on ordered statistics or other Bayesian approaches does not satisfactorily address the issue of false positives. This aspect has recently been evaluated for a few test datasets such as the one used herein. While improvements in the aforementioned aspects are constantly being proposed, statistics applied directly to probe-level data is an attractive alternative. As discussed earlier, several biological and sequence related issues complicate simple selection of a statistical threshold such as a p-value when using the Student's t-test. The following approach is motivated by the fact that the multiple independent features measured signifying the expression level of a transcript should in principle allow selection of a threshold that is appropriate to the noise in a particular data set. In many well behaved dataset this threshold should be lower than a commonly acceptable threshold, e.g., t signifying $p <= 0.05$.

In order to study the performance of differential expression measured at probe level the response surface of sensitivity, positive prediction value, number of true positives and number of false positives were evaluated as a function of number of valid probe-pairs

and a range of values for t (the Student's t statistic). This was done with triplicate datasets that had spike-ins of two fold difference with different probesets in concentration ranges (0 – 512 pM) between the two datasets. A valid probe-pair was defined as one that has a minimum difference of average signal value (difference between signal for perfect match and mismatch) above background, and the ratio of averages is at least 1.1 (selected intuitively, but can be determined empirically for different datasets) and above threshold t, to avoid values in very close range. In addition, a condition that there are no more than one-fifth the probesets that had change in opposite direction was enforced. In general this latter condition was never a determining factor in selection of differentials in this dataset. This selection criteria for can be expressed as:

$$[\sum_{i=1}^{m}(n \mid t >= t', x_{ie}/x_{ib} >= 1.1, (x_{ie} - x_{ib}) >= b)\,] >= np \qquad [3]$$

where n is the number of probe-pairs satisfying the conditions, t' is the threshold for t statistic, np is the threshold for number of valid probe-pairs, xie and xib is the signal value for probe-pair i, in experimental and baseline chips, respectively. The above equation represents selection of probesets where the chip designated the experimental chip has higher value than the chip designated the baseline chip, the equation for probesets with value for baseline chip higher can be obtained by interchanging xie and xib. For example for a probeset that satisfies the threshold of 6 valid probe-pairs and t value of 7.0, at least 6 probe-pairs representing that probeset will individually have a t-statistic of 7.0 or above - all having the same direction of change. As can be seen from **FIG. 18A**, and as expected, with increasing threshold of t and probe-pair threshold the positive prediction value (PPV) increases i.e., a decreasing number of false positives are identified and sensitivity decreases i.e., lesser number of true positives are identified as differentials. **FIG. 18B**, shows the decrease of true and false positives with increasing threshold of t and np.

The above problem can in principle be viewed as area under the Receiver operating characteristic (ROC) curve problem with two dimensions t threshold as one dimension and number of valid probe-pair number as another dimension. In this kind of situation, one would expect multiple thresholds involving the two dimensions that would have optimal area under the ROC curve. Alternatively, this can be viewed as an optimization problem with the goal of detecting as many true positives with optimal combination sensitivity and

positive prediction value. In other words this can be written mathematically as, termed effective number of positives identified (Neff):

$$N_{eff} = TP * TP/(TP + FP) * (1 - FP/TP) \quad [4]$$

FIG. 16 shows the response surface of this effective number of positives as a function of t and number of valid probe-pairs (np). It can be seen from the figure that a range of t and np can result in comparable Neff, with top two Neff at (t',np) of (7,5) and (6,6) with (true positives, false positives) of (91,1),(89,1) and (87,0), respectively. The total possible number of true positives and false positives were 135, and 66,555, respectively. It should be noted that the lowest differential (two fold) was used from the dataset, higher differentials would lead to identification of higher number of true positives. The presence of a large portion of the surface across a range of t and np having similar Neff in **FIG. 16** suggests that it would be possible to achieve good sensitivity and selectivity for many np and t values thus potentially increasing the sensitivity of detection of small differentials and differentials in transcripts expressed at low levels. This can be achieved in principle by defining a cost factor consisting of the two parameters being tested. One form of defining such a cost adjusted effective number of positives picked (CANeff) would be:

$$CAN_{eff} = N_{eff} /(t' + np) \quad [5]$$

The response surface for CANeff as a function of t' and np is shown in **FIG. 17**. It can be seen from the surface of CANeff (**FIG. 17**) that the largely flat area near the peak of Neff (in **FIG. 16**) can now be reduced to a few distinct and narrow peaks. The (t',np) values yielding the top three CANeff are (3,7), (4,6) and (4,7) with (true positives, false positives) (86, 2), (91,5) and (85,0), respectively. It should be highlighted that these values of true and false positives selected at this threshold are comparable to that of the maximum Neff mentioned before. For comparison, at t signifying $p <= 0.05$ and a threshold of six valid probesets the (true positives,false positives) was (85,0). The number of true and false positives identified and the concentration range of the spike-in positives for a selected set of t' and np values are summarized in **Table 1**. The possibility of selecting a lower

threshold and still being able to maintain high selectivity would especially be of interest (i) with certain datasets where there is a large increase in positives with a small reduction in threshold, whereas the training dataset indicative of variability in the experiment suggest that this would result in a very small number increase in selection of false positives, and (ii) for sensitive identification of small differentials without significant loss of selectivity (illustrated in the next section with some test cases).

The methodology outlined above is termed ResurfP, for Response surface assisted Parametic test. It should be noted that lower the threshold that can give good selectivity, the better it is to select small differentials and differentials in transcripts with low expression levels. Thus, the advantage of the lowered threshold were evaluated by scaling one of the two datasets (i.e., the probe level data extracted as outlined herein) used in above comparison to varying extents (1.5, 2, 3 and 4 fold) and comparing to the other dataset. This should allow comparison of data classes with wider variety of variances as opposed to a few signified by the spike-ins. Further, this should also reveal the sensitivity of the methodology in the context of technical replicates, thus revealing the maximum achievable sensitivity. The results for this evaluation at the thresholds yielding the top two CANeff, t signifying $p <= 0.05$, and the threshold specifying the top Neff are represented in **Table 2**. As expected, the lower thresholds lead to higher sensitivity of detection at any given level. It should be noted that even at the lower threshold (t', np) of (3,6), the differentials (average of three comparisons compared to maximum identifiable differentials defined below) identified were only 42%, 61%, 81% and 86% of 1.5, 2, 3 and 4 fold respectively, which further emphasizes the need for and importance of the proposed approach. At a threshold of (7.71, 6) these values were significantly lower viz., 30%, 47%, 63% and 70%, respectively. For the purpose of calculating percentage of differentials identified the maximum identifiable differentials was set at 21,485, which is the differentials (average of three comparisons) identified at the threshold of (t' = 4, np = 5) with a scaling factor of 10. A steep decline face on the surface of **FIG 17** (right hand side) with increasing probe-pair threshold together with results indicated in Table 2 also indicate a higher penalty for increasing the probe-pair threshold than for increasing t statistic threshold. Additionally, these data indicate that an appropriate choice of a lower probe-pair threshold can lead to significantly higher number of true differentials without concomitant increase in false positives. In order to have a preliminary characterization of the nature of probesets/transcripts that are selected and are missed in this study, the

distribution of the expression indices (to simplify the representation) of these probesets for one of the thresholds (t',np) of (3,7) is shown in **FIG. 19**. As can be seen from **FIG. 19** and as expected the distribution of the expression indices of probesets, low expressors are detected better at higher differential ratios. Conversely, almost all the probesets missed at higher differential ratios were low expressors, which is consistent with observations that there is high variability in the low detection ranges.

The optimal application of ResurfP on biological samples with different properties need additional testing with an independent confirmation using another technology. Nevertheless, the results of a preliminary evaluation to test if the lower threshold identified by ResurfP would lead high false positives when tested on biological replicates are very encouraging. For this purpose (t',np) thresholds of (3,6) and (3,8) were tested on one set of biological replicates from cardiogenomics website (see methods). For this purpose, data from six human patients with aortic stenosis were split into two groups (of triplicates) and the method was evaluated. This lead to identification of only 52 and 21 of 12,624 probesets at (3,6) and (3,8), respectively, even though this chip type consisted of 16 probe-pairs for most probesets/transcripts.

It should be noted that the above exemplary embodiment is presented to better illustrate some of the embodiments of these teachings and does not limit these teachings nor does the above exemplary embodiment illustrate all of the above described embodiments.

The techniques described above may be implemented in one or more computer programs executing on a programmable computer including a processor, a storage medium readable by the processor (including, for example, volatile and non-volatile memory and/or storage elements), and, in some embodiments, also including at least one input device, and/or at least one output device. Program code may be applied to data entered using the input device (or user interface) to perform the functions described and to generate output information. The output information may be applied to one or more output devices.

Elements and components described herein may be further divided into additional components or joined together to form fewer components for performing the same functions.

Each computer program may be implemented in any programming language, such as assembly language, machine language, a high-level procedural programming language, an object-oriented programming language, or a combination thereof. The programming language may be a compiled or interpreted programming language.

Each computer program may be implemented in a computer program product tangibly embodied in a computer-readable storage device for execution by a computer processor. Method steps of the invention may be performed by a computer processor executing a program tangibly embodied on a computer-readable medium to perform functions of the invention by operating on input and generating output. Other methods and/or computer codes can provide input to these programs based on combinations of components herein or take output from these combinations as input. Combinations of input and output, i.e., communicative and integrative use of components described herein and other methods or computer codes could also be implemented.

Common forms of computer-readable (computer usable) media include, for example, a floppy disk, a flexible disk, hard disk, magnetic tape, or any other magnetic medium, a CDROM, any other optical medium, punched cards, paper tape, any other physical medium with patterns of holes or other patterns, a RAM, a PROM, and EPROM, a FLASH-EPROM, any other memory chip or cartridge, a carrier wave, such as electromagnetic radiation or electrical signals, or any other medium from which a computer can read.

Although the invention has been described with respect to various embodiments, it should be realized this invention is also capable of a wide variety of further and other embodiments within the spirit and scope of the appended claims.

CLAIMS

1. A method for summarizing parameter value, the method being implemented in a computer and comprising the steps of:

grouping measurement result from a data set into a plurality of pairs of measurement results;

determining, for said each one pair of measurement results, whether predetermined measures for said each one pair of measurement results satisfy threshold criteria;

classifying a pair of measurement results from said plurality of pairs of measurement results as not changing if the predetermined measures do not satisfy the threshold criteria;

comparing, if the predetermined measures satisfied the threshold criteria, one measurement result in said each one pair of measurement results to another measurement result in said each one pair of measurement results;

classifying, after the comparison, said each one pair of measurement results according to result of the comparison;

selecting a common set of measurement results from the classified plurality of pairs of measurement result for use with the data set; and

providing summary measures for a parameter utilizing the common set;

said determining, classifying, comparing, selecting and providing being performed by means of a computer usable medium having computer readable code that causes the computer to perform said steps;

whereby the data set includes data obtained from large-scale measurements of organismal and cellular state involving multiple independent measurements of each parameter, said parameters including genes, transcripts and proteins; and

wherein the summarized parameter values are utilized for decision making to increase confidence on the use of the data in activities including manufacturing, handling, hybridization and gene expression.

2. The method of claim 1 further comprising the steps of:

providing summary measures of predetermined quantities utilizing the common set.

3. The method of claim 2 wherein one of the predetermined quantities is a confidence measure.

4. The method of claim 1 wherein the data set is a replicated data set; and wherein the method further comprises the step of:

averaging, as a first step, the measurement results over replications; averaged measurement results constituting said measurement results.

5. The method of claim 4 further comprising the step of:

providing summary measures of predetermined quantities utilizing the common set.

6. The method of claim 5 wherein one of the predetermined quantities is a statistical measure.

7. A method for determining efficacy of a data set analyses techniques, the method being implemented in a computer and comprising the steps of:

scaling a data set and replicates of the data set;

comparing the scaled data set to predetermined groups of original data sets in order to test a predetermined analysis results;

wherein efficacy can be determined;

said scaling and comparing being performed by means of a computer usable medium having computer readable code that causes the computer to perform said steps;

whereby the data set being analyzed includes data obtained from large-scale measurements of organismal and cellular state involving multiple independent measurements of each parameter, said parameters including genes, transcripts and proteins; and

wherein the efficacy of a data set analyses techniques is utilized for decision making to increase confidence on the use of the data in activities including manufacturing, handling, hybridization, gene expression.

8. A method for normalizing data from a data set, the method being implemented in a computer and comprising the steps of:

sorting data from the data set according to measurement value;

selecting, according to a predetermined criterion, reference subsets, the reference subsets having at least one reference measurement value;

selecting, from the sorted data, data elements having measurement values substantially equivalent to said at least one reference measurement value;

sorting the data elements having substantially equivalent measurement values, the sorted data elements comprising a sorted substantially equivalent subset; and

utilizing the at least one reference measurement value and the sorted substantially equivalent subset to normalize the data set;

said selecting, sorting and normalizing being performed by means of a computer usable medium having computer readable code that causes the computer to perform said steps;

whereby the data set being analyzed includes data obtained from large-scale measurements of organismal and cellular state involving multiple independent measurements of each parameter, said parameters including genes, transcripts and proteins;

wherein the normalized data set analyses techniques is utilized for decision making to increase confidence on the use of the data in activities including manufacturing, handling, hybridization, gene expression.

9. The method of claim 8 wherein the step of utilizing the at least one reference measurement value on the sorted substantially equivalent subset to normalize the data set comprises the step of utilizing a predetermined combination of the at least one reference value and the sorted substantially equivalent subset in order to establish a distribution curve.

10. The method of claim 9 wherein the step of utilizing a predetermined combination of the at least one reference value and the sorted substantially equivalent subset comprises the steps of:

iterating over portions of the sorted substantially equivalent subset in order to obtain the predetermined combination of the at least one reference value and the sorted substantially equivalent subset.

11. A computer program product comprising a computer usable medium having computer readable code embodied therein; said computer readable code being capable of causing a computer system to:

scale a data set and replicates of the data set; and

compare the scaled data set to predetermined groups of original data sets in order to test a predetermined analysis results;

wherein efficacy can be determined;

whereby the data set being analyzed includes data obtained from large-scale measurements of organismal and cellular state involving multiple independent measurements of each parameter, said parameters including genes, transcripts and proteins; and

wherein the efficacy of a data set analyses techniques is utilized for decision making to increase confidence on the use of the data in activities including manufacturing, handling, hybridization and gene expression.

12. A computer program product comprising a computer usable medium having computer readable code embodied therein; said computer readable code being capable of causing a computer system to:

sort data from the data set according to measurement value;

select, according to a predetermined criterion, reference subsets, the reference subsets having at least one reference measurement value;

select, from the sorted data, data elements having measurement values substantially equivalent to set at least one reference measurement value;

sort the data elements having substantially equivalent measurement values, the sorted data elements comprising a sorted substantially equivalent subset; and

utilize the at least one reference measurement value and the sorted substantially equivalent subset to normalize the data set;

whereby the data set being analyzed includes data obtained from large-scale measurements of organismal and cellular state involving multiple independent measurements of each parameter, said parameters including genes, transcripts and proteins; and

wherein the normalized data set analyses techniques is utilized for decision making to increase confidence on the use of the data in activities including manufacturing, handling, hybridization and gene expression.