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Method for the Discovery of Biomarkers

Stanford Reference: S07-242

Abstract

Stanford researchers have discovered a unique biomarker platform integrating technologies of sample processing, label free MALDI Mass spectrometer profiling, biomarker differentiation algorithms, and biomarker database mining web services. Our biomarker discovery platform pioneers the application of quantitative mass spectrometry for biomarker discovery. The discovery platform and subsequent discoveries of biomarkers from current Stanford/LPCH projects will revolutionize disease management through the enabling of technologies for personalized medicine. Furthermore, the utilities of our discovery platform and biomarker probes will greatly expand biological research, accelerate therapeutics development, and reduce the astronomical cost of current drug discovery and clinical trials.

Applications

- Discovery of peptide or protein biomarkers for disease management, including diagnosis, prognosis, and prediction of response to treatment.

Advantages

- Multi-dimensional HPLC fractionation.
- Sensitivity of the Mass spec instrument.
- Use of spiked in calibration standard leads to tight mass accuracy.
- Rigorous data mining process, resulting in substantially larger feature space for biomarker discovery than that seen in the current community, including various commercial turnkey solutions like SELDI.

Related Web Links

- [Pediatric biotech core biomarker database](#)

Innovators & Portfolio

- Bruce Xuefeng Ling [more technologies from Bruce Xuefeng Ling »](#)
- James Schilling [more technologies from James Schilling »](#)

Date Released: 06/20/2011

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Related Keywords

[diagnostic](#), [diagnostic: assay](#), [diagnostic: detection](#), [diagnostic: marker](#), [immune](#), [MALDI-TOF MS](#), [proteomics](#), [software](#), [software: bioinformatics](#), [software: optimization](#)

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Method for the Discovery of Biomarkers

Web Disclosure

General Information

Title: Method for the Discovery of Biomarkers

Submitted: 08/07/07 By James Schilling

VA or HHMI: VA Percentage:

About the Invention

Purpose:

Discovery of peptide or protein biomarkers for disease management, including diagnosis, prognosis, and prediction of response to treatment.

Technical Description (Abstract):

Unique biomarker discovery platform integrating technologies of sample processing, label free MALDI Mass spectrometer profiling, biomarker differentiation algorithms, and biomarker database mining web services.

Applications:

Potential Licensees:

1. Diagnostic companies
2. Biotech/pharmaceutical companies

Advantages:

Multi-dimensional HPLC fractionation.

Sensitivity of the Mass spec instrument.

Use of spiked in calibration standard leads to tight mass accuracy

Rigorous data mining process, resulting in substantially larger feature space for biomarker discovery than that seen in the current community, including various commercial turnkey solutions like SELDI.

Variations:

The plug-in of different mass spec technologies, including electrospray, to complement the currently applied mass spec platform.

New Features:

1. Use of label free MALDI to allow the quantitative comparative analysis of disease categories.
2. Data mining algorithms lead to substantial larger biomarker feature space and integration of robust statistical packages for differential biomarker identification.
3. Formal introduction of False Discovery Rate to evaluate the statistical contexts of the discovered biomarkers.
4. Develop computing algorithms for multi-stage multi-hypothesis data mining purpose in the evaluation of statistical effect of pooling and subsequent individual sampling analysis.

Related Patents:

Critical Solution:

1. Diagnostic needs for any preventive disease management
2. Prognostic needs for chronic disease management
3. Surrogate markers for clinical trial of new therapies

Related Invention:

Continued Research:

1. Continue to refine the discovery platform, including the sample processing technique as well as the data mining algorithms
2. Continue the application of the platform for queued projects of diagnostic/prognostic/drug response analysis
3. Extend the current platform to include other emerging mass spec technologies

In Software: yes

Formulas:

1. Database technologies including MySQL data processing and data modeling
2. Statistical algorithm integration including false discovery rate evaluation, supporting vector machines, SAM/PAM, CART etc.
3. Two dimensional clustering for feature space definition and segregation.
4. Mass spec peak find algorithms
5. Web services for corroboration of data mining and data publishing

When Licensable:

Not Now Due To:

Marketing Abstract

Our biomarker discovery platform pioneers the application of quantitative mass spectrometry for biomarker discovery. The discovery platform and subsequent discoveries of biomarkers from current Stanford/LPCH projects will revolutionize disease management in general through the enabling of technologies for personalized medicine. Furthermore, the utilities of our discovery platform and biomarker probes will greatly expand biological research, accelerate therapeutics development, and reduce the astronomical cost of current drug discovery and clinical trials.

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None

Sponsors

None

Material Transfer

MTA: no

MTA Company:

Events

Initial Idea Date: 04/13/2006

Ling notebook 1 page 60

First Description Date: 04/13/2006

Ling notebook 1 page 60

First Demo Date: 06/19/2006

Ling notebook 2 page 107

First Publication Date: 00/00/0000

None

External Date:

Attachments

None

Keywords

MALDI-TOF MS; proteomics; diagnostic: marker; diagnostic: detection; diagnostic: assay; software: optimization; software: bioinformatics; immune

Web Links

<http://biomarker.stanford.edu>

Digital Signatures

Main Digital Signature: By: James Schilling On: 20070807142423

Witness Digital Signature: unsigned...

James Schilling Signed On: 20070807142423

Bruce Xuefeng Ling unsigned...

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