(54) Title: MEANS AND METHODS FOR DETECTING BACTERIA IN A SAMPLE
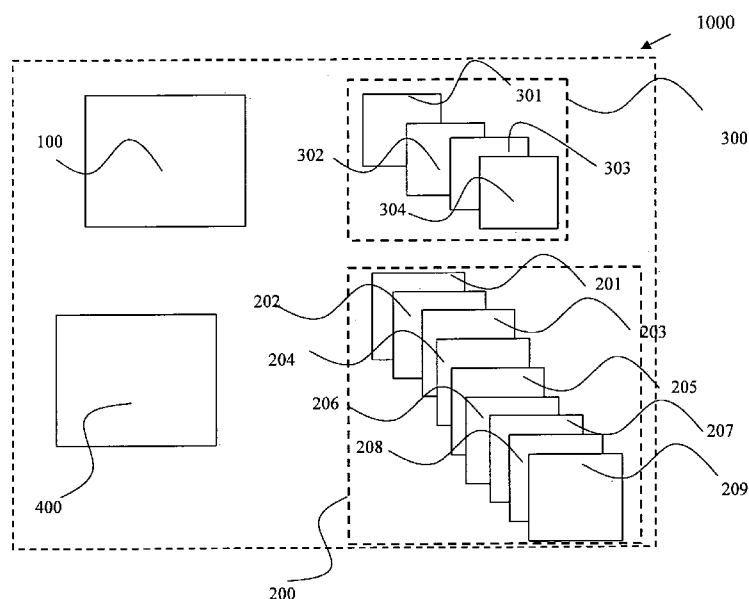
Fig. 1

(57) Abstract: The present invention provides a method for detecting and/or identifying specific bacteria within an uncultured sample. The method comprises steps selected inter alia from (a) obtaining an absorption spectrum (AS) of said uncultured sample; (b) acquiring the n dimensional volume boundaries for said specific bacteria; (c) data processing said AS; and, (d) detecting and/or identifying said specific bacteria if said m1 statistical correlation and/or said m features are within said n dimensional volume.

MEANS AND METHODS FOR DETECTING BACTERIA IN A SAMPLE

FIELD OF THE INVENTION

The present invention relates to the field of spectroscopic medical diagnostics of specific bacteria within a sample. More particularly, the present invention provides a means and methods for detecting different kinds of bacteria in a sample by using spectroscopic measurements. The detection can be used for both medical and non-medical applications, such as detecting bacteria in water, beverages, food production, sensing for hazardous materials in crowded places etc.

BACKGROUND OF THE INVENTION

The identification of microorganisms is clearly of great importance in the medical fields. Furthermore, in recent years the need for efficient and relatively rapid identification techniques has become even more pressing owing to the remarkable expansion of environmental and industrial microbiology. One field in which it there is an urgent need for a rapid and accurate identification of bacteria is in the respiratory diseases.

Respiratory disease is an umbrella term for diseases of the lung, bronchial tubes, trachea and throat. These diseases range from mild and self-limited (coryza -or common cold) to being life-threatening, (bacterial pneumonia, or pulmonary embolism for example).

Respiratory diseases can be classified as either obstructive or restrictive. Obstructive is a condition which impede the rate of flow into and out of the lungs (e.g, asthma); and restrictive is a condition which cause a reduction in the functional volume of the lungs (e.g., pulmonary fibrosis).

Respiratory disease can be further classified as either upper or lower respiratory tract (most commonly used in the context of infectious respiratory disease), parenchymal and vascular lung diseases.

Infectious Respiratory Diseases are, as the name suggests, typically caused by one of many infectious agents able to infect the mammalian respiratory system, the etiology can be viral or bacterial (for example the bacterium Streptococcus pneumoniae).

A patient who suffers from infectious respiratory diseases will usually endure sore throat and have trouble swallowing. However, these sympthoms might indicate also a flu.

Usually a throat culture is taken from the patient, that is suspected to have strep, in order to correctly diagnose the infection and to give the proper treatment.

The throat culture and bacterial analysis will usually take about three days. Moreover, the test causes some inconvience to the patient.

The bacterial analysis will determine what is the desired and correct treatment and medication.

Another kind of tests are the "rapid" strep tests. In these tests a throat swab is inserted into a reagent and the presence of the bacteria is determined according to the chemical reaction between the bacteria and the reagent. Although these test give fast results (10 to 30 minutes) their sensitivity is very poor and they are not user friendly. Therfore they are not commonly used by the medical stuff.

Usually the physician desires to know if the bacteria is present and then perscribe antibiotics. Therefore, it will be beneficial for the doctor and the patient alike to get an immidiate response for the throat sample.

An immindiate response might be obtained by sampling the exhaled debrit (exhaled gases and micro fluids) of coughing or other human fluids (saliva, mucos etc.) and optically characterizing their content. Optically characterizing the sample will likely be more convinient for the patient than the usual throat culturing.

Some spectroscopic techniques already known in the art. For example, PCT No. WO 98/41842 to NELSON, Wilfred discloses a system for the detection of bacteria antibody complexes. The sample to be tested for the presence of bacteria is placed in a medium which contains antibodies attached to a surface for binding to specific bacteria to form an antigen - antibody complex. The medium is contacted with an incident beam of light energy. Some of the energy is emitted from the medium as a lower resonance enhanced Raman backscattered energy. The detection of the presence or absence of the microorganism is based on the characteristic spectral peak of said microorganism. In other words PCT No. WO 98/41842 uses UV resonance Raman spectroscopy.

US patent No. 6,599,715 to Laura A. Vanderberg relates to a process for detecting the presence of viable bacterial spores in a sample and to a spore detection system. The

process includes placing a sample in a germination medium for a period of time sufficient for commitment of any present viable bacterial spores to occur. Then the sample is mixed with a solution of a lanthanide capable of forming a fluorescent complex with dipicolinic acid. Lastly, the sample is measured for the presence of dipicolinic acid.

US patent No. 4,847,198 to Wilfred H. Nelson; discloses a method for the identification of a bacterium. Firstly, taxonomic markers are excited in a bacterium with a beam of ultra violet energy. Then, the resonance enhance Raman back scattered energy is collected substantially in the absence of fluorescence. Next, the resonance enhanced Raman back scattered energy is converted into spectra which corresponds to the taxonomic markers in said bacterium. Finally, the spectra are displayed and thus the bacterium may be identified.

US patent No. 6,379,920 to Mostafa A. El-Sayed discloses a method to analyze and diagnose specific bacteria in a biologic sample by using spectroscopic means. The method includes obtaining the spectra of a biologic sample of a non-infected patient for use as a reference, subtracting the reference from the spectra of an infected sample, and comparing the fingerprint regions of the resulting differential spectrum with reference spectra of bacteria. Using this diagnostic technique, patent 6,379,920 claims to identify specific bacteria without culturing.

Naumann et al had demonstrated bacteria detection and classification in dried samples using FTIR spectroscopy [Naumann D. et al., "Infrared spectroscopy in microbiology", Encyclopedia of Analytical Chemistry, R.A. Meyers (Ed.) pp. 102–131, John Wiley & Sons Ltd, Chichester, 2000.]. Marshall et al had identifies live microbes using FTIR Raman spectroscopy [Marshall et al " Vibrational spectroscopy of extant and fossil microbes: Relevance for the astrobiological exploration of Mars", Vibrational Spectroscopy 41 (2006) 182–189]. Others methods involve fluorescence spectroscopy of a combination of the above.

None of the prior art literature discloses means and method that can quickly (without culturing) and accurately detect bacteria from a sample, and none demonstrates identification within a wet sample. Furthermore, non of the prior art literature discloses means and method that can eliminate the water influence from the sample so as to better detect the bacteria. Moreover all of the above require a skilled operator and/or the use of reagents or a complicated sample preparation for the detection of bacteria.

Thus, there is a long felt need for means and method for an accurate bacteria identification from an uncultured sample especially wet samples without the use of reagents and/or complicated sample preparation.

SUMMARY OF THE INVENTION

It is one object of the present invention to provide a method for detecting and/or identifying specific bacteria within an uncultured sample. The method comprises steps selected inter alia from:

    a. obtaining an absorption spectrum (AS) of said uncultured sample;

    b. acquiring the n dimensional volume boundaries for said specific bacteria by

        i. obtaining at least one absorption spectrum (AS2) of samples containing said specific bacteria;

        ii. extracting x features from said AS2 selected from a group consisting of peaks wavelength, peaks height and widths, different peaks' intensity ratios or any combination thereof; said x is an integer higher or equal to one;

        iii. calculating at least one derivative of said AS2;

        iv. dividing said AS2 into several segments according to said x features;

        v. calculating the y statistical correlation of each of said segment; said y is an integer higher or equal to one;

        vi. defining n dimensional space; n equals the sum of said x features and said y statistical correlations;

        vii. assigning each one of said x feature and each one of said y correlation to said specific bacteria;

        viii. calculating the Gaussian distribution for each of said x feature and/or for each of said y statistical correlations; said Gaussian distributions defined the n dimensional volume in said n dimensional space;

        ix. determining said boundaries of said n dimensional volume by using technique selected from a group consisting of quadratic

Gaussian classifier, k nearest neighbor, Bayesian classification or any combination thereof;

c. data processing said AS;

    i. noise reducing by using different smoothing techniques selected from a group consisting of running average savitzky-golay or any combination thereof;

    ii. extracting m features from said AS selected from a group consisting of peak's width, intensity, the ratio width/intensity, peak's wavelength, different peaks' intensity ratios, or any combination thereof; said m is an integer higher or equal to one;

    iii. dividing said AS into several segments according to said m features;

    iv. calculating the m_1 statistical correlation of each of said segment; said m_1 is an integer higher or equal to one; and,

d. detecting and/or identifying said specific bacteria if said m_1 statistical correlation and/or said m features are within said n dimensional volume.

It is another object of the present invention to provide the method as defined above, wherein said step (c) of data processing said AS additionally comprising steps of:

    i. calculating at least one of the oth derivative of said AS; said o is an integer greater than or equals 1;

    ii. extracting m_2 features from said o^{th} derivative selected from a group consisting of peak's width, intensity, the ratio width/intensity, different peaks' intensity ratios, peak's wavelength or any combination thereof;

    iii. dividing said o^{th} derivative into several segments according to said m_2 features;

    iv. calculating the m_3 statistical correlation in each of said segments; and,

    v. detecting and/or identifying said specific bacteria if said m_1 and/or m_3 statistical correlation and/or said m and/or said m_2 features are within said n dimensional volume.

It is another object of the present invention to provide the method as defined above, wherein said step of calculating the statistical correlation of each of said segment is performed by using Pearson's correlation coefficient.

It is another object of the present invention to provide the method as defined above, additionally comprising the step of selecting said specific bacteria selected from a group consisting of *Streptococcus Pyogenes, Group C and G beta-hemolytic streptococci, Corynebacterium haemolyticum, Diphtheria and Ulcerans, Neisseria Gonorrhoeae, Mycoplasma Pneumoniae, Yersinia Enterocolitica, Mycobacterium tuberculosis, Chlamydia Trachomatiss and Pneumoniae, Bordetella Pertussis, Legionella spp, Pneumocystis Carinii, Nocardia, Histoplasma Capsulatum, Coccidioides Immitis, Haemophilus influenza group A beta hemolytic* and *staphylococcus Aureus.*

It is another object of the present invention to provide the method as defined above, wherein said step of obtaining the AS additionally comprising steps of:

    a. providing at least one optical cell accommodates said uncultured sample;

    b. providing p light source selected from a group consisting of laser, lamp, LEDs tunable lasers, monochrimator, p is an integer equal or greater than 1; said p light source are adapted to emit light to said optical cell;

    c. providing detecting means for receiving the spectroscopic data of said sample;

    d. emitting light from said light source at different wavelength to said optical cell; and,

    e. collecting said light exiting from said optical cell by said detecting means; thereby obtaining said AS.

It is another object of the present invention to provide the method as defined above, wherein said step of emitting light is performed at the wavelength range of UV, visible, IR, mid-IR, far-IR and terahertz.

It is another object of the present invention to provide the method as defined above, additionally comprising the step of detecting said bacteria by analyzing said AS in the region of about 3000-3300 cm^{-1} and/or about 850-1000 cm^{-1} and/or about 1300-1350 cm^{-1}.

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It is another object of the present invention to provide a method for detecting and/or identifying specific bacteria within an uncultured sample. The method comprises steps selected inter alia from:

    a. obtaining an absorption spectrum (AS) of said uncultured sample; said AS containing water influence;

    b. acquiring the n dimensional volume boundaries for said specific bacteria by

        i. obtaining at least one absorption spectrum (AS2) of samples containing said specific bacteria;

        ii. extracting x features from said AS2 selected from a group consisting of peaks wavelength, peaks height and widths, different peaks' intensity ratios or any combination thereof; said x is an integer higher or equal to one;

        iii. calculating at least one derivative of said AS2;

        iv. dividing said AS2 into several segments according to said x features;

        v. calculating the y statistical correlation of each of said segment; said y is an integer higher or equal to one;

        vi. defining n dimensional space; n equals the sum of said x features and said y statistical correlations;

        vii. assigning each one of said x feature and each one of said y correlation to said specific bacteria;

        viii. calculating the Gaussian distribution for each of said x feature and/or for each of said y statistical correlations; said Gaussian distributions defined the n dimensional volume in said n dimensional space;

        ix. determining said boundaries of said n dimensional volume by using technique selected from a group consisting of quadratic Gaussian classifier, k nearest neighbor, Bayesian classification or any combination thereof;

    c. eliminating said water influence from said AS;

        i. providing the absorption intensity at each of wavenumber (x) within said AS ($Sig_{with\ water}(x)$);

        ii. dividing said AS into at least two wavenumber ranges;

    iii. calculating the correction factors (CF) at each wavenumber (x) within said least two ranges ($CF(x)$);

    iv. acquiring from said AS at least one absorption intensity that is mainly influenced by said water $Sig_{water\ only}(x1)$ and the corresponding wavenumbers ($x1$);

    v. calculating at least one correction factor of said water ($CF_{water\ only}\ (x1)$) at said at least one wavenumber ($x1$);

    vi. dividing said at least one $Sig_{water\ only}(x1)$ by said at least one CF_{water} (i.e., $Sig_{water\ only}(x1)\ /\ CF_{water\ only}\ (x1)$) at said at least one wavenumber ($x1$);

    vii. calculating the average of step (vi) ($AVG[Sig_{water\ only}(x1)\ /\ CF_{water\ only}\ (x1)]$);

    viii. multiplying said $AVG[Sig_{water\ only}(x1)\ /\ CF_{water\ only}]\ (x1)$ by said $CF(x)$ for each of said wavenumber (x) within said AS; and,

    ix. subtracting the result of step (viii) from said ($Sig_{with\ water}(x)$) at each of said wavenumber(x) within said AS;

d. data processing said AS without said water influence by

    i. noise reducing by using different smoothing techniques selected from a group consisting of running average savitzky-golay or any combination thereof;

    ii. extracting m features from said AS selected from a group consisting of peak's width, intensity, the ratio width/intensity, peak's wavelength, different peaks' intensity ratios, or any combination thereof; said m is an integer higher or equal to one;

    iii. dividing said AS into several segments according to said m features;

    iv. calculating the m_1 statistical correlation of each of said segment; said m_1 is an integer higher or equal to one; and,

e. detecting and/or identifying said specific bacteria if said m_1 statistical correlation and/or said m features are within said n dimensional volume.

It is another object of the present invention to provide the method as defined above, wherein said step (c) of data processing said AS without said water influence, additionally comprising steps of:

    i. calculating at least one of the oth derivative of said AS; said o is an integer greater than or equals 1;

    ii. extracting m_2 features from said o^{th} derivative selected from a group consisting peak's width, intensity, the ratio width/intensity, different peaks' intensity ratios, peak's wavelength or any combination thereof;

    iii. dividing said o^{th} derivative into several segments according to said m_2 features;

    iv. calculating the m_3 statistical correlation in each of said segments; and,

    v. detecting and/or identifying said specific bacteria if said m_1 and/or m_3 statistical correlation and/or said m and/or said m_2 features are within said n dimensional volume.

It is another object of the present invention to provide the method as defined above, wherein said step of calculating the statistical correlation in each of said segments is performed by using Pearson's correlation coefficient.

It is another object of the present invention to provide the method as defined above, additionally comprising the step of selecting said specific bacteria selected from a group consisting of *Streptococcus Pyogenes, Group C and G beta-hemolytic streptococci, Corynebacterium haemolyticum , Diphtheria and Ulcerans ,Neisseria Gonorrhoeae, Mycoplasma Pneumoniae, Yersinia Enterocolitica, Mycobacterium tuberculosis, Chlamydia Trachomatiss and Pneumoniae, Bordetella Pertussis,Legionella spp, Pneumocystis Carinii, Nocardia, Histoplasma Capsulatum, Coccidioides Immitis, Haemophilus influenza group A beta hemolytic* and *staphylococcus Aureus.*

It is another object of the present invention to provide the method as defined above, wherein said step of obtaining the AS additionally comprising steps of:

    a. providing at least one optical cell accommodating said uncultured sample;

    b. providing p light source selected from a group consisting of laser, lamp, LEDs tunable lasers, monochrimator, p is an integer equal or

    greater than 1; said p light source are adapted to emit light to said optical cell;

    c. providing detecting means for receiving the spectroscopic data of said sample;

    d. emitting light from said light source at different wavelength to said optical cell;

    e. collecting said light exiting from said optical cell by said detecting means; thereby obtaining said AS.

It is another object of the present invention to provide the method as defined above, wherein said step of emitting light is performed at the wavelength range of UV, visible, IR, mid-IR, far IR and terahertz.

It is another object of the present invention to provide a system 1000 adapted to detect and/or identify specific bacteria within a sample. The system comprises:

    a. means 100 for obtaining an absorption spectrum (AS) of said sample;

    b. statistical processing means 200 for acquiring the n dimensional volume boundaries for said specific bacteria; said means 200 are characterized by

        i. means 201 for obtaining at least one absorption spectrum (AS2) of samples containing said specific bacteria;

        ii. means 202 for extracting x features from said AS2 selected from a group consisting of peaks wavelength, peaks height and widths, different peaks' intensity ratios or any combination thereof; said x is an integer higher or equal to one;

        iii. means 203 for calculating at least one derivative of said AS2;

        iv. means 204 for dividing said AS2 into several segments according to said x features;

        v. means 205 for calculating the y statistical correlation of each of said segment; said y is an integer higher or equal to one;

        vi. means 206 for defining n dimensional space; n equals the sum of said x features and said y statistical correlations;

        vii. means 207 for assigning each one of said x feature and each one of said y correlation to said specific bacteria;

        viii. means 208 for calculating the Gaussian distribution for each of said x feature and/or for each of said y statistical correlations;

said Gaussian distributions defined the n dimensional volume in said n dimensional space;

ix. means 209 for determining said boundaries of said n dimensional volume by using technique selected from a group consisting of quadratic Gaussian classifier, k nearest neighbor, Bayesian classification or any combination thereof;

c. means 300 for data processing said AS; said means 300 are characterized by

i. means 301 for noise reducing by using different smoothing techniques selected from a group consisting of running average savitzky-golay or any combination thereof;

ii. means 302 for extracting m features from said AS selected from a group consisting of peak's width, intensity, the ratio width/intensity, peak's wavelength, different peaks' intensity ratios, or any combination thereof; said m is an integer higher or equal to one;

iii. means 303 for dividing said AS into several segments according to said m features;

iv. means 304 for calculating the m_1 statistical correlation of each of said segment; said m_1 is an integer higher or equal to one; and,

d. means 400 for detecting and/or identifying said specific bacteria if said m_1 statistical correlation and/or said m features are within said n dimensional volume.

It is another object of the present invention to provide the system as defined above, wherein said means 300 for data processing said AS additionally characterized by:

i. means 305 for calculating at least one of the oth derivative of said AS; said o is an integer greater than or equals 1;

ii. means 306 for extracting m_2 features from said o^{th} derivative selected from a group consisting of peak's width, intensity, the ratio width/intensity, different peaks' intensity ratios, peak's wavelength or any combination thereof;

iii. means 307 for dividing said o^{th} derivative into several segments according to said m_2 features;

iv. means 308 for calculating the m_3 statistical correlation in each
of said segments; and,

v. means 309 for detecting and/or identifying said specific
bacteria if said m_1 and/or m_3 statistical correlation and/or said m
and/or said m_2 features are within said n dimensional volume.

It is another object of the present invention to provide the system as defined above,
wherein said means 308 or 304 for calculating the statistical correlation is selected
from a group consisting of Pearson's correlation coefficient.

It is another object of the present invention to provide the system as defined above,
wherein said specific bacteria is selected from a group consisting of *Streptococcus
Pyogenes, Group C and G beta-hemolytic streptococci, Corynebacterium
haemolyticum, Diphtheria and Ulcerans, Neisseria Gonorrhoeae, Mycoplasma
Pneumoniae, Yersinia Enterocolitica, Mycobacterium tuberculosis, Chlamydia
Trachomatiss and Pneumoniae, Bordetella Pertussis, Legionella spp, Pneumocystis
Carinii, Nocardia, Histoplasma Capsulatum, Coccidioides Immitis, Haemophilus
influenza group A beta hemolytic* and *staphylococcus Aureus*.

It is another object of the present invention to provide the system as defined above,
wherein said means 100 for obtaining an absorption spectrum (AS) of said sample
additionally comprising:

a. at least one optical cell for accommodating said uncultured sample;

b. p light source selected from a group consisting of laser, lamp, LEDs
tunable lasers, monochrimator, p is an integer equal or greater than 1; said
p light source are adapted to emit light at different wavelength to said
optical cell; and,

c. detecting means for receiving the spectroscopic data of said sample exiting
from said optical cell.

It is another object of the present invention to provide the system as defined above,
wherein said p light source are adapted to emit light at wavelength range selected
from a group consisting of UV, visible, IR, mid-IR, far-IR and terahertz.

It is another object of the present invention to provide a system 2000 adapted to detect
and/or identify specific bacteria within an uncultured sample; wherein said system
2000 comprising:

a. means 100 for obtaining an absorption spectrum (AS) of said uncultured
sample; said AS containing water influence;

   b. statistical processing means 200 for acquiring the n dimensional volume
       boundaries for said specific bacteria; said means 200 are characterized
       by

              i.   means 201 for obtaining at least one absorption spectrum (AS2)
                   of samples containing said specific bacteria;

              ii. means 202 for extracting x features from said AS2 selected
                   from a group consisting of peaks wavelength, peaks height and
                   widths, different peaks' intensity ratios or any combination
                   thereof; said x is an integer higher or equal to one;

             iii. means 203 for calculating at least one derivative of said AS2;

              iv. means 204 for dividing said AS2 into several segments
                   according to said x features;

              v.   means 205 for calculating the y statistical correlation of each of
                   said segment; said y is an integer higher or equal to one;

              vi. means 206 for defining n dimensional space; n equals the sum
                   of said x features and said y statistical correlations;

             vii. means 207 for assigning each one of said x feature and each
                   one of said y correlation to said specific bacteria;

            viii. means 208 for calculating the Gaussian distribution for each of
                   said x feature and/or for each of said y statistical correlations;
                   said Gaussian distributions defined the n dimensional volume
                   in said n dimensional space;

              ix. means 209 for determining said boundaries of said n
                   dimensional volume by using technique selected from a group
                   consisting of quadratic Gaussian classifier, k nearest neighbor,
                   Bayesian classification or any combination thereof;

   c. means 300 for eliminating said water influence from said AS; said means
       300 having:

              i.   means 301 for providing the absorption intensity at each of
                   wavenumber (x) within said AS ($Sig_{with\ water}(x)$);

              ii. means 302 for dividing said AS into at least two wavenumber
                   ranges;

             iii. means 303 for calculating the correction factors (CF) at each
                   wavenumber (x) within said least two ranges ($CF(x)$);

iv. means 304 for acquiring from said AS at least one absorption intensity that is mainly influenced by said water $Sig_{water\ only}(x1)$ and the corresponding wavenumbers $(x1)$;

v. means 305 for calculating at least one correction factor of said water $(CF_{water\ only}\ (x1))$ at said at least one wavenumber $(x1)$;

vi. means 306 for dividing said at least one $Sig_{water\ only}(x1)$ by said at least one CF_{water} (i.e., $Sig_{water\ only}(x1)\ /\ CF_{water\ only}\ (x1)$) at said at least one wavenumber $(x1)$;

vii. means 307 for calculating the average of step (vi) $(AVG[Sig_{water\ only}(x1)\ /\ CF_{water\ only}\ (x1)]\ )$;

viii. means 308 for multiplying said $AVG[Sig_{water\ only}(x1)\ /\ CF_{water\ only}]\ (x1)$ by said $CF(x)$ for each of said wavenumber (x) within said AS; and,

ix. means 309 for subtracting the result of step (viii) from said $(Sig_{with\ water}(x))$ at each of said wavenumber(x) within said AS;

d. means 400 for data processing said AS without said water influence; said means 400 are characterized by

i. means 401 for noise reducing by using different smoothing techniques selected from a group consisting of running average savitzky-golay or any combination thereof;

ii. means 402 for extracting m features from said AS selected from a group consisting of peak's width, intensity, the ratio width/intensity, peak's wavelength, different peaks' intensity ratios, or any combination thereof; said m is an integer higher or equal to one;

iii. means 403 for dividing said AS into several segments according to said m features;

iv. means 404 for calculating the m_1 statistical correlation of each of said segment; said m_1 is an integer higher or equal to one; and,

e. means 500 for detecting and/or identifying said specific bacteria if said m_1 statistical correlation and/or said m features are within said n dimensional volume.

It is another object of the present invention to provide the system as defined above, wherein said means 400 for data processing said AS without said water influence additionally comprising:

    i.   means 405 for calculating at least one of the oth derivative of said AS; said o is an integer greater than or equals 1;

    ii.   means 406 for extracting m_2 features from said o^{th} derivative selected from a group consisting peak's width, intensity, the ratio width/intensity, different peaks' intensity ratios, peak's wavelength or any combination thereof;

    iii.   means 407 for dividing said o^{th} derivative into several segments according to said m_2 features;

    iv.   means 408 for calculating the m_3 statistical correlation in each of said segments; and,

    v.   means 409 for detecting and/or identifying said specific bacteria if said m_1 and/or m_3 statistical correlation and/or said m and/or said m_2 features are within said n dimensional volume.

It is another object of the present invention to provide the system as defined above, wherein said means 408 and/or 404 for calculating the statistical correlation in each of said segments is selected form a group consisting of Pearson's correlation coefficient.

It is another object of the present invention to provide the system as defined above, wherein said specific bacteria is selected from a group consisting of *Streptococcus Pyogenes, Group C and G beta-hemolytic streptococci, Corynebacterium haemolyticum, Diphtheria* and *Ulcerans, Neisseria Gonorrhoeae, Mycoplasma Pneumoniae, Yersinia Enterocolitica, Mycobacterium tuberculosis, Chlamydia Trachomatiss and Pneumoniae, Bordetella Pertussis,Legionella spp, Pneumocystis Carinii, Nocardia, Histoplasma Capsulatum, Coccidioides Immitis, Haemophilus influenza group A beta hemolytic* and *staphylococcus Aureus.*

It is still an object of the present invention to provide the system as defined above, wherein said means 100 for obtaining an absorption spectrum (AS) of said sample additionally comprising:

    a.   at least one optical cell for accommodating said uncultured sample;

    b. p light source selected from a group consisting of laser, lamp, LEDs tunable lasers, monochrimator, p is an integer equal or greater than 1;

said *p* light source are adapted to emit light at different wavelength to said optical cell; and,

c. detecting means for receiving the spectroscopic data of said sample exiting from said optical cell.

It is lastly an object of the present invention to provide the system as defined above, wherein said *p* light source are adapted to emit light at wavelength range selected from a group consisting of UV, visible, IR, mid-IR, far-IR and terahertz.

BRIEF DESCRIPTION OF THE FIGURES

In order to understand the invention and to see how it may be implemented in practice, a plurality of embodiments will now be described, by way of non-limiting example only, with reference to the accompanying drawings, in which

Figs. 1-2 illustrate a system 1000 and 2000 adapted to detect and/or identify bacteria within a sample according to preferred embodiments of the present invention.

Figs. 3-4 illustrate an absorption spectrum prior to the water correction (figure 3) and after the water correction (figure 4).

Fig. 5 is an example of the absorption peaks of streptococcus.

Fig. 6 illustrates the absorption signal of a dry sample containing 100% streptococcus prior to and after the noise was reduced.

Fig. 7 illustrates the first derivative of the absorption signal in a dry sample containing 100% streptococcus prior to and after the noise was reduced.

Figs. 8-12 illustrate the absorption spectrum of a sample and a reference sample at wavenumber range of 950 cm^{-1} to 1200 cm^{-1} and the corresponding statistical correlation. Figures 8-12 also present the first derivative of the spectrum at the same range and the corresponding statistical correlation.

Figs. 13-17 illustrate the absorption spectrum of a sample and a reference sample at wavenumber range of 1220 cm^{-1} to 1380 cm^{-1} and the corresponding statistical correlation. Figures 13-17 also present the first derivative of the spectrum at the same range and the corresponding statistical correlation.

Fig 18 schematically illustrates the boundaries of a two dimensions area that identifies the bacteria within a dry sample.

Fig. 19 illustrates the absorption signal of a sample containing 100% streptococcus prior to and after the noise was reduced.

Fig. 20 illustrates the first derivative of the absorption signal in a sample containing 100% streptococcus prior to and after the noise was reduced.

Figs. 21-23 illustrate the first derivative of the absorption spectrum of a reference sample containing 100% Streptococcus, a sample containing 100% Streptococcus and the corresponding statistical correlations.

Figs. 24-26 illustrate the first derivative of the absorption spectrum of a reference sample containing 100% Streptococcus and a solution containing 100% Staphylococcus and the correlation coefficient between them.

Figs. 27-29 illustrate the first derivative of the absorption spectrum of a reference sample 100% Streptococcus and a solution containing 50% Staphylococcus and 50% Streptococcus and the correlation coefficient between them.

Figs. 30-32 illustrate the first derivative of the absorption spectrum of a reference sample 100% Streptococcus and a solution containing 25% Staphylococcus and 75% Streptococcus and the correlation coefficient between them.

Figs. 33-35 illustrate the first derivative of the absorption spectrum of a reference sample 100% Streptococcus and a solution containing 75% Staphylococcus and 25% Streptococcus and the correlation coefficient between them.

Fig. 36 schematically illustrates the boundaries of a two dimensions area that identifies the bacteria within a solution.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

The following description is provided, alongside all chapters of the present invention, so as to enable any person skilled in the art to make use of said invention and sets forth the best modes contemplated by the inventor of carrying out this invention. Various modifications, however, will remain apparent to those skilled in the art, since the generic principles of the present invention have been defined specifically to provide means and methods for detecting bacteria within a sample by using Spectroscopic measurements.

Spectroscopic measurements, whether absorption fluorescence Raman, and scattering are the bases for all optical sensing devices. In order to identify a hazardous material (for example a bacteria) a sample that might contain the material is placed inside a spectrometer and the absorption spectrum of the sample is then analyzed to verify whether the spectral signature of the hazardous material is recognized.

The present invention provides means and methods for detection or identification of bacteria by analyzing the absorption spectra of a sample which might contain bacteria.

The term **"sample"** refers herein to either an aerosol sample or a liquid sample. The present invention provides detection means that enable the detection of bacteria in liquids as well as in aerosol. The detection means can be used for medical or non-medical applications. Furthermore, the detection means can be used, for example, in detecting bacteria in water, beverages, food production, sensing for hazardous materials in crowded places etc.

The term **"Pearson's correlation coefficient"** refers hereinafter to the correlation between two variables that reflects the degree to which the variables are related. Pearson's correlation reflects the degree of linear relationship between two variables. It ranges from +1 to -1. A correlation of -1 means that there is a perfect negative linear relationship between variables. A correlation of 0 means there is no linear relationship between the two variables. A correlation of 1 means there is a complete linear relationship between the two variables.

A commonly used formula for computing Pearson's correlation coefficient r is the following one:

$$r = \frac{\sum XY - \frac{\sum X \sum Y}{N}}{\sqrt{(\sum X^2 - \frac{(\sum X)^2}{N})(\sum Y^2 - \frac{(\sum Y)^2}{N})}}$$

The term **"about"** refers hereinafter to a range of 25% below or above the referred value.

The term **"segments"** refers hereinafter to wavelength ranges within the absorption spectrum.

The term **"*n* dimensional volume"** refers hereinafter to a volume in an n dimensional space that is especially adapted to identify the bacteria under consideration. The *n* dimensional volume is constructed by extracting features and statistical correlations from the absorption spectrum or its derivatives.

The term **"*n* dimensional space"** refers hereinafter to a space where each coordinate is a feature or a statistical correlation extracted from the bacteria spectral signature or a calculated statistical correlation calculated out of the spectrum and its derivatives or from a segment of the spectrum and/or its derivatives

The term **"*n* dimensional volume boundaries"** refers hereinafter to a range that includes about 95% of the bacteria under consideration possible features and correlation values.

Methods and means for bacteria detection adapted to utilize the unique spectroscopic signature of microbes/bacteria/hazardous materials and thus enables the detection of the microbes/bacteria/hazardous materials within a sample are provided by the present invention.

Reference is now made to figure 1, illustrating a system 1000 adapted to detect and/or identify specific bacteria within a sample according to one preferred embodiment of the present invention. System 1000 comprises:

    a.   means 100 for obtaining an absorption spectrum (AS) of the sample;

    b.   statistical processing means 200 for acquiring the *n* dimensional volume boundaries for the specific bacteria, having:

        i.   means 201 for obtaining at least one absorption spectrum (AS2) of samples containing the specific bacteria;

        ii.   means 202 for extracting *x* features from the AS2 selected from a group consisting of peaks' wavelength, peaks height and widths, different peaks' intensity ratios or any combination thereof; *x* is an integer higher or equal to one;

        iii.   means 203 for calculating at least one derivative of the AS2;

        iv.   means 204 for dividing the AS2 into several segments according to the *x* features;

        v.   means 205 for calculating the *y* statistical correlation of each of the segment; *y* is an integer higher or equal to one;

        vi.   means 206 for defining *n* dimensional space; *n* equals the sum of the *x* features and the *y* statistical correlations;

    vii.   means 207 for assigning each of the x feature and the y correlation to the specific bacteria;

    viii. means 208 for calculating the Gaussian distribution for each of the x feature and/or for each of the y statistical correlations; the Gaussian distributions defined the n dimensional volume in the n dimensional space;

    ix.   means 209 for determining the boundaries of the n dimensional volume by using technique selected from a group consisting of quadratic Gaussian classifier, k nearest neighbor, Bayesian classification or any combination thereof;

c. means 300 for data processing the AS, having:

    i.   means 301 for noise reducing by using different smoothing techniques selected from a group consisting of running average savitzky-golay or any combination thereof;

    ii. means 302 for extracting m features from the AS selected from a group consisting of peak's width, intensity, the ratio width/intensity, peak's wavelength, different peaks' intensity ratios, or any combination thereof; m is an integer higher or equal to one;

    iii. means 303 for dividing the AS into several segments according to the m features;

    iv. means 304 for calculating the m_1 statistical correlation of each of the segment; m_1 is an integer higher or equal to one; and,

d. means 400 for detecting and/or identifying the specific bacteria if the m_1 statistical correlation and/or the m features are within the n dimensional volume.

According to another embodiment of the present invention, means 300 (in system 1000) for data processing the AS additionally characterized by:

    i.   means 305 for calculating at least one of the oth derivative of the AS; o is an integer greater than or equals 1;

    ii. means 306 for extracting m_2 features from the oth derivative selected from a group consisting of peak's width, intensity, the ratio width/intensity, different peaks' intensity ratios, peak's wavelength or any combination thereof;

iii. means 307 for dividing the oth derivative into several segments according to the m_2 features;

iv. means 308 for calculating the m_3 statistical correlation in each of the segments; and,

v. means 309 for detecting and/or identifying the specific bacteria if the m_1 and/or m_3 statistical correlation and/or the m and/or the m_2 features are within the n dimensional volume.

According to another embodiment of the present invention, means 308 or 304 (in system 1000) for calculating the statistical correlation is selected from a group consisting of Pearson's correlation coefficient.

According to yet another embodiment of the present invention, the specific bacteria to be identified by system 1000 is selected from a group consisting of *Streptococcus Pyogenes, Group C and G beta-hemolytic streptococci, Corynebacterium haemolyticum, Diphtheria and Ulcerans, Neisseria Gonorrhoeae, Mycoplasma Pneumoniae, Yersinia Enterocolitica, Mycobacterium tuberculosis, Chlamydia Trachomatiss* and *Pneumoniae, Bordetella Pertussis, Legionella spp, Pneumocystis Carinii, Nocardia, Histoplasma Capsulatum, Coccidioides Immitis, Haemophilus influenza group A beta hemolytic* and *staphylococcus Aureus*.

According to another embodiment of the present invention, the means 100 for obtaining an absorption spectrum (AS) of the sample (in system 1000), additionally comprising:

a.   at least one optical cell for accommodating the sample;

b. p light source selected from a group consisting of laser, lamp, LEDs tunable lasers, monochrimator, p is an integer equal or greater than 1; the p light source are adapted to emit light at different wavelength to the optical cell; and,

c.   detecting means for receiving the spectroscopic data of the sample exiting from the optical cell.

According to yet another embodiment of the present invention, the p light source (in system 1000) are adapted to emit light at wavelength range selected from a group consisting of UV, visible, IR, mid-IR, far-IR and terahertz.

Reference is now made to figure 2, illustrating a system 2000 adapted to detect and/or identify specific bacteria within a sample, according to another preferred embodiment of the present invention. System 2000 comprises:

a.   means 100 for obtaining an absorption spectrum (AS) of the sample; the AS containing water influence;

b.   statistical processing means 200 for acquiring the n dimensional volume boundaries for the specific bacteria, having:

        i.   means 201 for obtaining at least one absorption spectrum (AS2) of samples containing the specific bacteria;

        ii.   means 202 for extracting x features from the AS2 selected from a group consisting of peaks wavelength, peaks height and widths, different peaks' intensity ratios or any combination thereof; x is an integer higher or equal to one;

        iii.   means 203 for calculating at least one derivative of the AS2;

        iv.   means 204 for dividing the AS2 into several segments according to the x features;

        v.   means 205 for calculating the y statistical correlation of each of the segment; y is an integer higher or equal to one;

        vi.   means 206 for defining n dimensional space; n equals the sum of the x features and the y statistical correlations;

        vii.   means 207 for assigning each of the x feature and the y correlation to the specific bacteria;

        viii.   means 208 for calculating the Gaussian distribution for each of the x feature and/or for each of the y statistical correlations; the Gaussian distributions defined the n dimensional volume in the n dimensional space;

        ix.   means 209 for determining the boundaries of the n dimensional volume by using technique selected from a group consisting of quadratic Gaussian classifier, k nearest neighbor, Bayesian classification or any combination thereof;

c.   means 300 for eliminating the water influence from the AS, comprising:

        i.   means 301 for providing the absorption intensity at each of wavenumber (x) within said AS ($Sig_{with\ water}(x)$);

        ii.   means 302 for dividing said AS into at least two wavenumber ranges;

iii. means 303 for calculating the correction factors (CF) at each wavenumber (x) within said least two ranges ($CF(x)$);

iv. means 304 for acquiring from said AS at least one absorption intensity that is mainly influenced by said water $Sig_{water\ only}(x1)$ and the corresponding wavenumbers ($x1$);

v. means 305 for calculating at least one correction factor of said water ($CF_{water\ only}\ (x1)$) at said at least one wavenumber ($x1$);

vi. means 306 for dividing said at least one $Sig_{water\ only}(x1)$ by said at least one CF_{water} (i.e., $Sig_{water\ only}(x1)\ /\ CF_{water\ only}\ (x1)$) at said at least one wavenumber ($x1$);

vii. means 307 for calculating the average of step (vi) ($AVG[Sig_{water\ only}(x1)\ /\ CF_{water\ only}\ (x1)]$);

viii. means 308 for multiplying said $AVG[Sig_{water\ only}(x1)\ /\ CF_{water\ only}]\ (x1)$ by said $CF(x)$ for each of said wavenumber (x) within said AS; and,

ix. means 309 for subtracting the result of step (viii) from said ($Sig_{with\ water}(x)$) at each of said wavenumber(x) within said AS;

d.   means 400 for data processing the AS without the water influence, characterized by:

i. means 401 for noise reducing by using different smoothing techniques selected from a group consisting of running average savitzky-golay or any combination thereof;

ii. means 402 for extracting m features from the AS selected from a group consisting of peak's width, intensity, the ratio width/intensity, peak's wavelength, different peaks' intensity ratios, or any combination thereof; m is an integer higher or equal to one;

iii. means 403 for dividing the AS into several segments according to the m features;

iv. means 404 for calculating the m_1 statistical correlation of each of the segment; m_1 is an integer higher or equal to one; and,

e.   means 500 for detecting and/or identifying the specific bacteria if the m_1 statistical correlation and/or the m features are within the n dimensional volume.

According to another embodiment of the present invention, means 400 (in system 2000) for data processing the AS without the water influence additionally comprising:

  i.   means 405 for calculating at least one of the oth derivative of the AS; o is an integer greater than or equals 1;

  ii.   means 406 for extracting m_2 features from the oth derivative selected from a group consisting peak's width, intensity, the ratio width/intensity, different peaks' intensity ratios, peak's wavelength or any combination thereof;

  iii. means 407 for dividing the oth derivative into several segments according to the m_2 features;

  iv.   means 408 for calculating the m_3 statistical correlation in each of the segments; and,

  v.   means 409 for detecting and/or identifying the specific bacteria if the m_1 and/or m_3 statistical correlation and/or the m and/or the m_2 features are within the n dimensional volume.

According to another embodiment of the present invention, means 408 and/or 404 within system 2000, for calculating the statistical correlation in each of said segments is selected form a group consisting of Pearson's correlation coefficient.

According to another embodiment of the present invention, the specific bacteria (in system 2000) is selected from a group consisting of *Streptococcus Pyogenes, Group C and G beta-hemolytic streptococci, Corynebacterium haemolyticum, Diphtheria and Ulcerans, Neisseria Gonorrhoeae, Mycoplasma Pneumoniae, Yersinia Enterocolitica, Mycobacterium tuberculosis, Chlamydia Trachomatiss and Pneumoniae, Bordetella Pertussis,Legionella spp, Pneumocystis Carinii, Nocardia, Histoplasma Capsulatum, Coccidioides Immitis, Haemophilus influenza group A beta hemolytic* and *staphylococcus Aureus*.

According to another embodiment of the present invention, means 100 for obtaining an absorption spectrum (AS) of the sample additionally comprising:

  a.   at least one optical cell for accommodating the sample;

  b. p light source selected from a group consisting of laser, lamp, LEDs tunable lasers, monochrimator, p is an integer equal or greater than 1; p light source are adapted to emit light at different wavelength to the optical cell; and,

c. detecting means for receiving the spectroscopic data of the sample exiting from the optical cell.

According to yet another embodiment of the present invention, the p light source are adapted to emit light at wavelength range selected from a group consisting of UV, visible, IR, mid-IR, far-IR and terahertz.

Yet another object of the present invention is to provide a method for detecting and/or identifying specific bacteria within a sample. The method comprises step selected inter alia from:

a. obtaining an absorption spectrum (AS) of the sample;

b. acquiring the n dimensional volume boundaries for the specific bacteria by:

i. obtaining at least one absorption spectrum (AS2) of samples containing the specific bacteria;

ii. extracting x features from the AS2 selected from a group consisting of peaks wavelength, peaks height and widths, different peaks' intensity ratios or any combination thereof; x is an integer higher or equal to one;

iii. calculating at least one derivative of the AS2;

iv. dividing the AS2 into several segments according to the x features;

v. calculating the y statistical correlation of each of the segment; y is an integer higher or equal to one;

vi. defining n dimensional space; n equals the sum of the x features and the y statistical correlations;

vii. assigning each of the x feature and the y correlation to the specific bacteria;

viii. calculating the Gaussian distribution for each of the x feature and/or for each of the y statistical correlations; the Gaussian distributions defined the n dimensional volume in the n dimensional space;

ix. determining the boundaries of the n dimensional volume by using technique selected from a group consisting of quadratic Gaussian classifier, k nearest neighbor, Bayesian classification or any combination thereof.

   c. data processing the AS;

       i. noise reducing by using different smoothing techniques selected from a group consisting of running average savitzky-golay or any combination thereof;

      ii. extracting m features from the AS selected from a group consisting of peak's width, intensity, the ratio width/intensity, peak's wavelength, different peaks' intensity ratios, or any combination thereof; m is an integer higher or equal to one;

     iii. dividing the AS into several segments according to the m features;

     iv. calculating the m_1 statistical correlation of each of the segment; m_1 is an integer higher or equal to one; and,

   d. detecting and/or identifying the specific bacteria if the m_1 statistical correlation and/or the m features are within the n dimensional volume.

It should be pointed out that in each of the systems as described above (either 1000 or 2000), the statistical processing means 200 is used only once for each specific bacteria. Once the boundaries were provided by the statistical processing means 200 the determination whether the specific bacteria is present in a sample is performed by verifying whether the m_1 and/or m_3 statistical correlation and/or the m and/or m_2 features are within the boundaries. Furthermore, once the boundaries were provided, there exists no need for the statistical processing of the same specific bacteria again.

Yet another object of the present invention is to provide a method for detecting and/or identifying specific bacteria within a sample. The method comprises steps selected inter alia from:

   a. obtaining an absorption spectrum (AS) of the sample; the AS containing water influence;

   b. acquiring the n dimensional volume boundaries for the specific bacteria by:

       i. obtaining at least one absorption spectrum (AS2) of samples containing the specific bacteria;

      ii. extracting x features from the AS2 selected from a group consisting of peaks wavelength, peaks height and widths,

different peaks' intensity ratios or any combination thereof; x is an integer higher or equal to one;

iii. calculating at least one derivative of the AS2;

iv. dividing the AS2 into several segments according to the x features;

v. calculating the y statistical correlation of each of the segment; y is an integer higher or equal to one;

vi. defining n dimensional space; n equals the sum of the x features and the y statistical correlations;

vii. assigning each of the x feature and the y correlation to the specific bacteria;

viii. calculating the Gaussian distribution for each of the x feature and/or for each of the y statistical correlations; the Gaussian distributions defined the n dimensional volume in the n dimensional space;

ix. determining the boundaries of the n dimensional volume by using technique selected from a group consisting of quadratic Gaussian classifier, k nearest neighbor, Bayesian classification or any combination thereof;

c. eliminating the water influence from the AS by:

i. providing the absorption intensity at each of wavenumber (x) within said AS $(Sig_{with\ water}(x))$;

ii. dividing said AS into at least two wavenumber ranges;

iii. calculating the correction factors (CF) at each wavenumber (x) within said least two ranges $(CF(x))$;

iv. acquiring from said AS at least one absorption intensity that is mainly influenced by said water $Sig_{water\ only}(x1)$ and the corresponding wavenumbers $(x1)$;

v. calculating at least one correction factor of said water $(CF_{water\ only}(x1))$ at said at least one wavenumber $(x1)$;

vi. dividing said at least one $Sig_{water\ only}(x1)$ by said at least one CF_{water} (i.e., $Sig_{water\ only}(x1)\ /\ CF_{water\ only}(x1)$) at said at least one wavenumber $(x1)$;

vii. calculating the average of step (vi) $(AVG[Sig_{water\ only}(x1)\ /$ $CF_{water\ only}(x1)]\ )$;

viii. multiplying said $AVG[Sig_{water\ only}(x1)\ /\ CF_{water\ only}]\ (x1)$ by said $CF(x)$ for each of said wavenumber (x) within said AS; and,

ix. subtracting the result of step (viii) from said $(Sig_{with\ water}(x))$ at each of said wavenumber(x) within said AS;

d. data processing the AS without the water influence by:

i. noise reducing by using different smoothing techniques selected from a group consisting of running average savitzky-golay or any combination thereof;

ii. extracting m features from the AS selected from a group consisting of peak's width, intensity, the ratio width/intensity, peak's wavelength, different peaks' intensity ratios, or any combination thereof; m is an integer higher or equal to one;

iii. dividing the AS into several segments according to the m features;

iv. calculating the m_1 statistical correlation of each of the segment; m_1 is an integer higher or equal to one; and,

e. detecting and/or identifying the specific bacteria if the m_1 statistical correlation and/or the m features are within the n dimensional volume.

In each of the methods as described above, the statistical processing is used only once for each specific bacteria. Once the boundaries were provided by the statistical processing the determination whether the specific bacteria is present in a sample is performed by verifying whether the m_1 statistical correlation and/or said m features are within the boundaries. Furthermore, once the boundaries were provided, there exists no need for the statistical processing of the same specific bacteria again.

According to another embodiment of the present invention step (c) of data processing the AS, in the methods as described above, additionally comprising steps of:

i. calculating at least one of the oth derivative of the AS; o is an integer greater than or equals 1;

ii. extracting m_2 features from the oth derivative selected from a group consisting of peak's width, intensity, the ratio width/intensity, different peaks' intensity ratios, peak's wavelength or any combination thereof;

    iii.   dividing the oth derivative into several segments according to the m_2 features;

    iv.   calculating the m_3 statistical correlation in each of the segments; and,

    v.   detecting and/or identifying the specific bacteria if the m_1 and/or m_3 statistical correlation and/or the m and/or the m_2 features are within the n dimensional volume.

According to another embodiment of the present invention, the step of calculating the statistical correlation of each of said segment, in the methods as described above, is performed by using Pearson's correlation coefficient.

According to another embodiment of the present invention, the methods as described above, additionally comprising the step of selecting the specific bacteria selected from a group consisting of *Streptococcus Pyogenes, Group C and G beta-hemolytic streptococci, Corynebacterium haemolyticum, Diphtheria and Ulcerans, Neisseria Gonorrhoeae, Mycoplasma Pneumoniae, Yersinia Enterocolitica, Mycobacterium tuberculosis, Chlamydia Trachomatiss and Pneumoniae, Bordetella Pertussis, Legionella spp, Pneumocystis Carinii, Nocardia, Histoplasma Capsulatum, Coccidioides Immitis, Haemophilus influenza group A beta hemolytic* and *staphylococcus Aureus.*

According to another embodiment of the present invention, the step of obtaining the AS, in the methods as described above, additionally comprising the following steps:

    a.   providing at least one optical cell accommodates the sample;

    b.   providing p light source selected from a group consisting of laser, lamp, LEDs tunable lasers, monochrimator, p is an integer equal or greater than 1; p light source are adapted to emit light to the optical cell;

    c.   providing detecting means for receiving the spectroscopic data of the sample;

    d.   emitting light from the light source at different wavelength to the optical cell; and,

    e.   collecting the light exiting from the optical cell by the detecting means; thereby obtaining the AS.

According to another embodiment of the present invention, the step of emitting light is performed at the wavelength range of UV, visible, IR, mid-IR, far-IR and terahertz.

According to another embodiment of the present invention, the methods as defined above, additionally comprising the step of detecting the bacteria by analyzing the AS in the region of about 3000-3300 cm^{-1} and/or about 850-1000 cm^{-1} and/or about 1300-1350 cm^{-1}.

According to yet another embodiment of the present invention, the absorption spectra, in any of the systems (1000 or 2000) or for any of the methods as described above, is obtained using an instrument selected from the group consisting of a Fourier transform infrared spectrometer, a fluorometer and a Raman spectrometer.

According to yet another embodiment of the present invention, the uncultured sample, in any of the systems (1000 or 2000) or for any of the methods as described above, is selected from fluid originated from the human body such as blood, saliva, urine, bile, vaginal secretions, middle ear aspirate, pus, pleural effusions, synovial fluid, abscesses, cavity swabs, and serum.

In the foregoing description, embodiments of the invention, including preferred embodiments, have been presented for the purpose of illustration and description. They are not intended to be exhaustive or to limit the invention to the precise form disclosed. Obvious modifications or variations are possible in light of the above teachings. The embodiments were chosen and described to provide the best illustration of the principals of the invention and its practical application, and to enable one of ordinary skill in the art to utilize the invention in various embodiments and with various modifications as are suited to the particular use contemplated. All such modifications and variations are within the scope of the invention as determined by the appended claims when interpreted in accordance with the breadth they are fairly, legally, and equitably entitled.

EXAMPLES

Examples are given in order to prove the embodiments claimed in the present invention. The examples describe the manner and process of the present invention and set forth the best mode contemplated by the inventors for carrying out the invention, but are not to be construed as limiting the invention.

EXAMPLE 1 - Water influence

One of the major problems in identifying bacteria from a fluid sample's spectrum (and especially an aerosol spectrum) is the water influence (i.e., the water noise which masks the desired spectrum by the water spectrum).

The water molecule may vibrate in a number of ways. In the gas state, the vibrations involve combinations of symmetric stretch ($v1$), asymmetric stretch ($v3$) and bending ($v2$) of the covalent bonds. The water molecule has a very small moment of inertia on rotation which gives rise to rich combined vibrational-rotational spectra in the vapor containing tens of thousands to millions of absorption lines. The water molecule has three vibrational modes x, y and z. The following table (table 1) illustrates the water vibrations, wavelength and the assignment of each vibration:

Table 1: water vibrations, wavelength and the assignment of each vibration

Wavelength	cm-1	Assignment
0.2 mm	50	intermolecular bend
55 µm	183.4	intermolecular stretch
25 µm	395.5	L1, librations
15 µm	686.3	L2, librations
6.08 µm	1645	v2, bend
4.65 µm	2150	v2 + L2 b
3.05 µm	3277	v1, symmetric stretch
2.87 µm	3490	v3, asymmetric stretch
1900 nm	5260	av1 + v2 + bv3; a+b=1
1470 nm	6800	av1 + bv3; a+b=2
1200 nm	8330	av1 + v2 + bv3; a+b=2
970 nm	10310	av1 + bv3; a+b=3
836 nm	11960	av1 + v2 + bv3; a+b=3
739 nm	13530	av1 + bv3; a+b=4
660 nm	15150	av1 + v2 + bv3; a+b=4
606 nm	16500	av1 + bv3; a+b=5
514 nm	19460	av1 + bv3; a+b=6
a and b are integers; ≥ 0 ms.		

The present invention provides a method for significantly reducing and even eliminating the water influence within the absorption spectra.

Reference is now made to figures 3 and 4 which illustrate an absorption spectrum of a sample with and without the water influence. Example for a spectrum without the water influence is given in figure 4. Figure 3 represents a spectrum prior to the water correction.

The method for eliminating the water influence contains the following steps:

First the absorption spectrum was divided in several segments (i.e, wavelength ranges). The spectrum was divided to segments (wavenumber ranges) of about 1800 cm^{-1} to about 2650 cm^{-1}, about 1400 cm^{-1} to about 1850 cm^{-1}, about 1100 cm^{-1} to about 1450 cm^{-1}, about 950 cm^{-1} to about 1100 cm^{-1}, about 550 cm^{-1} to about 970 cm^{-1}.

The segments were determined according to (i) different intensity peaks within the water's absorption spectrum; and, (ii) the signal's trends.

Next, each segment was eliminated from the water influence in the following manner:

(a) providing the absorption intensity at each of wavenumber (x) within the absorption spectrum (refers hereinafter as $Sig_{with\ water}(x)$);

(b) calculating the correction factors (CF) at each wavelength (refers hereinafter as x) within each segment (refers hereinafter as $CF(x)$);

(c) acquiring from the absorption spectrum, at least one absorption intensity that is mainly influenced by water (refers hereinafter as $Sig_{water\ only}(x1)$) at the corresponding wavenumbers (x1);

(d) calculating at least one correction factor of the water ($CF_{water\ only}$ (x1)) at said at least one wavenumber (x1);

(e) dividing at least one $Sig_{water\ only}(x1)$ by at least one CF_{water} (i.e., $Sig_{water\ only}(x1)$ / $CF_{water\ only}$ (x1)) at said at least one wavenumber (x1);

(f) calculating the average of the results of step (e) (refers hereinafter as $AVG[Sig_{water\ only}(x1)$ / $CF_{water\ only}$ (x1)]);

(g) multiplying the $AVG[Sig_{water\ only}(x1)$ / $CF_{water\ only}]$ (x1) by $CF(x)$ for each wavenumber (x); and,

(h) Subtracting each result of step (g) from $Sig_{with\ water}(x)$ per each (x).

In other words, each absorption intensity within the spectrum is eliminated from the water influence according to the following equation:

$Sig_{with\ water}(x)-(CF(x) * AVG [Sig_{water\ only}(x1)$ / $CF_{water\ only} (x1)]$)

Calculating the correction factors

The correction factors (*CF*) depends on the wavelength range, the water absorption peak's shape at each wavelength, peak's width, peak's height, absorption spectrum trends and any combination thereof. The following series were used as a correction factor (x – denote the wavenumber in cm^{-1})

1. Wavelength range 1846 cm^{-1} to 2613 cm^{-1}

Coefficients:

```
a11  =        137.2;

b11  =         2170;
c11  =        224.3;
a21  =        19.02;
b21  =         2063;
c21  =        37.53;
a31  =       0.7427;
b31  =         2224;
c31=             13;
a41  =        98.33;
b41  =         2124;
c41=          109.8;
a51  =       -4.988;
b51=           2192;
c51  =        33.87;
a61  =        20.19;
b61  =         1998;
c61  =        40.22;
a71  =        228.3;
b71  =         1496;
c71  =         1329;
a81  =    6.751e+012;
b81  =        -1226;
c81  =        592.1;
```

$$CF(x) = a11*e^{(-((x-b11)/c11)^2)} + a21*e^{(-((x-b21)/c21)^2)} + a31*e^{(-((x-b31)/c31)^2)} + a41*e^{(-((x-b41)/c41)^2)} + a51*e^{(-((x-b51)/c51)^2)} + a61*e^{(-((x-b61)/c61)^2)} + a71*e^{(-((x-b71)/c71)^2)} + a81*e^{(-((x-b81)/c81)^2)}$$

2. Wavelength range 1461 cm^{-1} to 1846 cm^{-1}

```
a12  =       -300.2;
b12  =         1650;
c12  =        13.65;
a22  =       -51.65;
b22  =         1665;
c22  =         6.48;
a32  =        142.4;
b32  =         1623;
c32  =        7.584;
a42  =         1450;
b42  =         1649;
```

```
c42  =        32.62;
a52  =        96.34;
b52  =         1617;
c52  =        2.387;
a62  =          608;
b62  =         1470;
c62  =        369.3;
a72  =            0;
b72  =         1873;
c72  =        2.625;
a82  =         1037;
b82  =         1644;
c82  =        76.21;
```

$$CF(x) = a12*e^{(-((x-b12)/c21)^2)} + a22*e^{(-((x-b22)/c22)^2)} + a32*e^{(-((x-b32)/c32)^2)} + a42*e^{(-((x-b42)/c42)^2)} + a52*e^{(-((x-b52)/c52)^2)} +$$

$$a62*e^{(-((x-b62)/c62)^2)} + a72*e^{(-((x-b72)/c72)^2)} + a82*e^{(-((x-b82)/c82)^2)}$$

3. Wavelength range 1111 cm^{-1} to 1461 cm^{-1}

```
a13  =         1368;
b13  =         2167;
c13  =          767;
a23  =        80.67;
b23  =         1356;
c23  =        68.83;
a33  =        36.85;
b33  =         1307;
c33  =        33.79;
a43  =        142.5;
b43  =         1244;
c43  =        67.19;
a53  =        260.4;
b53  =         1130;
c53  =        88.91;
a63  =        66.54;
b63  =         1093;
c63  =           31;
a73  =        7.126;
b73  =         1345;
c73  =         20.9;
a83  =        4.897;
b83  =         1280;
c83  =        11.05;
```

$$CF(x) = a13*e^{(-((x-b13)/c13)^2)} + a23*e^{(-((x-b23)/c23)^2)} + a33*e^{(-((x-b33)/c33)^2)} + a43*e^{(-((x-b43)/c43)^2)} + a53*e^{(-((x-b53)/c53)^2)} +$$

$$a63*e^{(-((x-b63)/c63)^2)} + a73*e^{(-((x-b73)/c73)^2)} + a83*e^{(-((x-b83)/c83)^2)}$$

4. Wavelength range 961 cm^{-1} to 1111 cm^{-1}

```
a14  =        692.6;
b14  =          952;
```

35

```
c14  =        31.04;
a24  =        48.46;
b24  =        983.2;
c24  =        15.72;
a34  =        287.5;
b34  =        994.6;
c34  =        27.98;
a44  =        434.9;
b44  =         1032;
c44  =        40.86;
a54  =        17.05;
b54  =         1052;
c54  =        13.55;
a64  =        48.61;
b64  =         1068;
c64  =        16.56;
a74  =        70.71;
b74  =         1086;
c74  =        21.23;
a84  =        497.3;
b84  =         1124;
c84  =        64.42;
```

$$CF(x) = a14*e^{(-((x-b14)/c14)^2)} + a24*e^{(-((x-b24)/c24)^2)} + a34*e^{(-((x-b34)/c34)^2)} + a44*e^{(-((x-b44)/c44)^2)} + a54*e^{(-((x-b54)/c54)^2)} +$$
$$a64*e^{(-((x-b64)/c64)^2)} + a74*e^{(-((x-b74)/c74)^2)} + a84*e^{(-((x-b84)/c84)^2)}$$

Wavelength range 570 cm^{-1} to 961 cm^{-1}

```
a15  =  -2877;
b15  =        36.23;
c15  =        29.09;
a25  =            0;
b25  =       -124.3;
c25  =        22.09;
a35  =       -190.7;
b35  =        18.97;
c35  =        16.45;
a45  =    1.589e+004;
b45  =       -3.427;
c45  =        56.25;
a55  =  -1.352e+004;
b55  =       -5.861;
c55  =        40.75;
a65  =        476.7;
b65  =        82.38;
c65  =        17.29;
a75  =         1286;
b75  =        62.29;
c75  =        180.3;
a85  =        802.9;
b85  =        102.8;
```

c85   =   18.79;

$$CF(x) = a15 * e^{(-((x-b15)/c15)^2)} + a25 * e^{(-((x-b25)/c25)^2)} + a35 * e^{(-((x-b35)/c35)^2)} + a45 * e^{(-((x-b45)/c45)^2)} + a55 * e^{(-((x-b55)/c55)^2)} +$$
$$a65 * e^{(-((x-b65)/c65)^2)} + a75 * e^{(-((x-b75)/c75)^2)} + a85 e^{(-((x-b85)/c85)^2)}$$

<u>Absorption intensity mainly influenced by water</u>

Reference is made again to figure 3 which illustrate the absorption spectrum prior to eliminating the water influence.

As can be seen from the figure, the absorption intensity that is mainly influenced by the water is the wavenumber region of 2000 cm^{-1} and above. The intensity at that region is about 0.2 absorption units. In the present example, $x1$ is 2000 and $Sig_{water\ only}(x1)$ is 0.2.

Reference is made again to figure 4, which illustrate the absorption spectrum of a sample after the influence of the water was eliminated.

It should be pointed out that for the purpose of obtaining a better resolution both graphs (3 and 4) are normalized to 2 (i.e., multiplied by 2).

<u>EXAMPLE 2 - Bacteria's absorption spectrum</u>

Each type of bacteria has a unique spectral signature. Although many types of bacteria have similar spectral signatures there are still some spectral differences that are due to different proteins on the cell membrane and differences in the DNA/ RNA structure. The following table, table 2, lists the wavelengths in the IR region that can be used to identify a bacterium.

Table 2: bacterium wavelengths in the IR region

Wavelength [nm]	Wavenumber [cm^{-1}]	Assignment
2857	3500	O-H stretch etch of hydroxyl groups
3125	3200	N-H stretch (amide A) of proteins
3379	2959	C-H stretch (asymmetric) of -CH3
3408	2934	C-H stretch (asymmetric) of >CH2
3423	2921	C-H stretch (asymmetric) of >CH2 in fatty acids
3450	2898	C-H stretch of C-H methine
3481	2872	C-H stretch (symmetric) of CH3
3506	2852	C-H stretch (symmetric) of >CH2 in fatty acids
5743	1741	>C=O stretch of esters
5830	1715	>C=O stretch of esters, RNA/DNA, OH-C=O
5899	1695	Amide I band components
5934	1685	resulting from antiparallel
5970	1675	pleated sheets and b-turns of proteins
6042	1655	Amide I of a-helical stretch uctures

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6108	1637	Amide I of b-pleated sheet stretch uctures
6459	1548	Amide II
6600	1515	"Tyrosine" band
6811	1468	C-H def of >CH2
7142	1400	C=O stretch (symmetric) of COO⁻
7633-8064	1310-1240	Amide III band components of proteins
8000-8190	1250-1220	P=O stretch (asymmetric) of >PO2⁻ hosphodiesters
8333-11111	1200-900	C-O-C, C-O dominated by ring vibrations of carbohydrates C-O-P, P-O-P
9216	1085	P=O stretch (symmetric) of >PO$_2$⁻
13888	720	C-H rocking of >CH$_2$
11111-16666	900-600	Specific bacteria bonds

The table was taken from Naumann D., "Infrared spectroscopy in microbiology", *Encyclopedia of Analytical Chemistry*, R.A. Meyers (Ed.) pp. 102–131, John Wiley & Sons Ltd, Chichester, 2000.

The following table, table 3, and figure 5 is an example of the absorption peaks of streptococcus payogenous. Some of the peaks could be related to the peaks in table 2. Others, such as peak number 1, 2, 9, 12, 13 and 14 are specific streptococcus payogenous peaks discovered in the present invention and are used for the detection and identification.

Table 3: streptococcus' absorption peaks

Peak numbe r	Wavenumber [cm⁻¹]	Absorbanc e	Weightin g factor	Assignment
1	3286	0.3638	0.09	Specific bacteria characteristics
2	3077	0.2852	0.1	Specific bacteria characteristics
3	2962	0.2875	0.1	C-H stretch (asymmetric) of -CH3
4	2933	0.2785	0.09	C-H stretch (asymmetric) of >CH2
5	1648	0.5245	0.01	Amide I of a-helical stretch uctures
6	1548	0.4029	0.01	Amide II
7	1452	0.2235	0.15	C-H def of >CH2
8	1405	0.2920	0.15	C=O stretch (symmetric) of COO⁻
9	1348	0.1763	0.15	Specific bacteria characteristics
10	1245	0.1589	0.15	P=O stretch (asymmetric) of >PO$_2$⁻
11	1076	0.2159	0.15	P=O stretch (symmetric) of >PO$_2$⁻
12	989	0.0957	0.05	Specific bacteria characteristics
13	925	0.0821	0.05	Specific bacteria characteristics

| 14 | 850 | 0.0828 | 0.05 | Specific bacteria characteristics |

EXAMPLE 3 - Distinguishing between two bacteria in a dry mixture

The following ex-vivo example provides a method to distinguish between two bacteria within a dry mixture of - Streptococcus payogenes and Staphylococcus aureus and to identify and/or determine whether Streptococcus is present within the sample.

Five mixtures of - Streptococcus payogenes and Staphylococcus aureus were prepared according to the following protocol:

1. The following solutions of Strep. β hemolytic (cat number-ATCC 19615) and Staphylococcus aureus (Cat. Number ATCC 25923) were prepared:

Total volume	Strep Pyogenes CFU/160 µL	Staph Aurous CFU/160 µL
60	12	0
60	9	3
60	6	6
60	3	9
60	0	12
Total	**150 µL**	**150 µL**

2. 30 µL of each solution was placed on one marked slot on an optical plate (ZnSe). Another slot contained 30 µl ddH2O for reference.

3. The plate was placed in a desiccator (Dessicator 250 mm polypropylene, Yavin Yeda, Israel) in the presence of several petri plates having a desiccant agent (Phosphorus Pentoxide cat #79610 Sigma Aldrich).

4. The desiccator was vacuumed for about 30 minutes.

Then the samples were placed inside a FTIR spectrometer (Bruker) and the spectral response of the samples was acquired (spectral range 4000cm^{-1} to 400cm^{-1}).

The absorption spectra of each sample were applied with Blackman-Harris 3-term apodization function (see the following equation):

$$w(n) = a_0 - a_1 \cos\left(\frac{2\pi n}{N-1}\right) + a_2 \cos\left(\frac{4\pi n}{N-1}\right) - a_3 \cos\left(\frac{6\pi n}{N-1}\right)$$

$$a_0 = 0.35875; \quad a_1 = 0.48829; \quad a_2 = 0.14128; \quad a_3 = 0.01168$$

In which $w(n)$ is the Blackman-Harris 3-term apodization; n is integer between 0 to N-1; and, N is the range at which the Blackman-Harris 3-term apodization function was applied.

Next, the sample was scanned sufficient number of times (64 scans) in order to reach a signal to noise ratio greater than 3000:1.

The identification and/or detection of specific bacteria was as follows:

(a) the noise in each of the absorption spectra was reduced by using Savitzky-Golay smoothing;

(b) the signal's first derivative was calculated;

(c) *m* features such as, but not limited to, peaks wavelength, peaks height and widths, peaks height ratio etc. were extracted from the spectra. A total of *m* features were extracted. *m* is an integer higher or equals 1;

(d) the signal and/or its first derivative were divided into several regions (segments, i.e., several wavenumber regions) according to said *m* features;

(e) m_l statistical correlation were calculated for (i) the spectral signal at each region; and for (ii) the signal derivatives at each region. A total of m_l statistical correlations were extracted. m_l is an integer higher or equals 1. The statistical correlation for the each region (the signal's and its derivatives) was calculated by using Pearson's correlation coefficient;

(f) the m features and the m_l statistical correlation were examined and checked whether they are within the n dimensional volume boundaries (which acquired by the statistical processing);

(g) the identification of the specific bacteria was determined as positive if the *m* features and/or the m_l statistical correlation were within the n dimensional volume boundaries.

Statistical processing

The statistical processing is especially adapted to provide the n dimensional volume boundaries. For each specific bacterium the statistical processing was performed only once, for obtaining the boundaries. Once the boundaries were provided, the

determination whether the specific bacteria is present in a sample was as explained above (i.e., verifying whether the features or correlation are within the boundaries). Furthermore, once the boundaries were provided, there exists no need for the statistical processing of the same specific bacteria again.

The statistical processing for each specific bacterium is performed in the following manner:

(a) obtaining several absorption spectrum (AS2) of samples containing the specific bacteria;

(b) extracting x features such as, but not limited to, peaks wavelength, peaks height and widths, different peaks' intensity ratios etc. were extracted from the spectra. A total of x features. x is an integer higher or equals 1;

(c) calculating the signal's first derivative;

(d) dividing the signal and/or its first derivative into several regions (segments) according to said x features;

(e) Calculating the y correlation for the different segments within the absorption spectrums;

(f) Defining n dimensional space. n equals the sum of the x features and the y statistical correlations;

(g) Assigning and/or interlinking each one of the x feature, and each one of the y correlation to the specific bacteria which its identification is required;

(h) Calculating the Gaussian distribution for (i) each of the x feature; and/or for (ii) each of the y statistical correlations. All the calculated Gaussian distributions constitute an n dimensional volume in the n dimensional space; and,

(i) Determining the boundaries of each volume by using quadratic Gaussian classifier or similar method (for example k nearest neighbor, Bayesian classification et cetera).

If the features and correlation (extracted from the spectrum) are within the n dimensional volume boundaries, the specific bacteria are identified. Otherwise the bacteria are not identified.

Alternatively or additionally, each of the x feature and/or for the y statistical correlations is given a weighting factor. The weighting factor is determined by the

examining how each feature or correlation improves the bacteria detection prediction (for example by using maximum likelihood or Bayesian estimation). Once the weighting factor is assigned to each one of the x feature and the y statistical correlations, the boundaries are determined for the features and/or the statistical correlations having the most significant contribution to the bacteria prediction.

Alternatively or additionally, the AS2 is smoothed by reducing the noise. The noise reduction is obtained by different smoothing techniques selected from a group consisting of running average savitzky-golay or any combination thereof.

We'll first present an example for the smoothing technique. For that the entire signal and its first derivative prior to and after the noise are presented.

Then will give examples for the deviation of the spectrum. And lastly an example of the boundaries is given. It should be pointed put that for demonstrating purposes the boundaries were calculated according to the features and/or statistical correlations which had the most significant contribution are given for the samples.

Furthermore, the object of the following examples is to identify streptococcus.

Smoothing of the spectrum

Reference is now made to figure 6 illustrating the absorption signal of a sample containing 100% streptococcus prior to and after the noise was reduced (recorded signal vs. smoothed signal).

Reference is now made to figure 7 illustrating the signal's first derivative of a sample containing 100% streptococcus prior to and after the noise was reduced (recorded signal vs. smoothed signal).

Dividing the absorption spectrum and its first derivative

The absorption spectrum of different samples (having different amount of streptococcus and Staphylococcus) and the first derivative are given. The absorption spectrum and the first derivative are given as example in two selected segments (950 cm^{-1} to 1200 cm^{-1}; and, 1230 cm^{-1} to 1360 cm^{-1}).

The entire segments (as divided both for the signal and the first derivative) are listed in table 3 and 4 along with the correlations.

Reference is now made to figures 8-12 which illustrate the absorption spectrum of a sample (solid line) and a reference sample (dotted line) at wavenumber range of 950 cm^{-1} to 1200 cm^{-1} and the corresponding statistical correlation. Figures 8-12 also present the first derivative of the spectrum at the same range and the corresponding statistical correlation.

Each of the absorption spectra was smoothed (i.e., noise reduction) by using different techniques (such as running average, Savitzky-Golay etcetera).

Figure 8 represents a reference sample having 100% streptococcus (dotted line) and a sample having 100% streptococcus (solid line);

Figure 9 represents a reference sample having 100% streptococcus (dotted line) and a sample having 100% Staphylococcus (solid line);

Figure 10 represents a reference sample having 100% streptococcus (dotted line) and a sample having 50% streptococcus and 50% Staphylococcus (solid line);

Figure 11 represents a reference sample having 100% streptococcus (dotted line) and a sample having 75% streptococcus and 25% Staphylococcus (solid line);

Figure 12 represents a reference sample having 100% streptococcus (dotted line) and a sample having 25% streptococcus and 75% Staphylococcus (solid line).

Reference is now made to figures 13-17 which illustrate the first derivative of an absorption spectrum of a sample (solid line) and a reference sample (dotted line) at wavenumber range of 1220 cm^{-1} to 1380 cm^{-1} and the corresponding statistical correlation. Figures 13-17 also present the first derivative of the spectrum at the same range and the corresponding statistical correlation.

Each of the absorption spectra was smoothed (i.e., noise reduction) by using different techniques (such as running average, Savitzky-Golay etcetera).

Figure 13 represents the first derivative of a reference sample having 100% streptococcus (dotted line) and the first derivative of a sample having 100% streptococcus (solid line);

Figure 14 represents the first derivative of a reference sample having 100% streptococcus (dotted line) and the first derivative of a sample having 100% Staphylococcus (solid line);

Figure 15 represents the first derivative of a reference sample having 100% streptococcus (dotted line) and the first derivative of a sample having 50% streptococcus and 50% Staphylococcus (solid line);

Figure 16 represents the first derivative of a reference sample having 100% streptococcus (dotted line) and the first derivative of a sample having 75% streptococcus and 25% Staphylococcus (solid line);

Figure 17 represents the first derivative of a reference sample having 100% streptococcus (dotted line) and the first derivative of a sample having 25% streptococcus and 75% Staphylococcus (solid line).

The _m_ features extracted from the spectrum

The following features were extracted peaks wavelength, peaks height and widths, different peaks' intensity ratios, peaks height ratio. The signal and the signal's first derivative were divided to the above mentioned segments according to said features due to the fact that in that region there were differences between the specific bacteria to be detected (i.e., streptococcus) and other bacteria (e.g., Staphylococcus).

The m_l statistical correlation of each segment and the weighting factor

The following table, table 4 illustrates the m_l statistical correlation of the signal's first derivative for each segment. The wavenumber ranges are in cm^{-1} and are mentioned in the brackets. Table 4 also presents the weighting factor for each.

Table 4: signal's first derivative correlation table

sample	Correlation 1 [1190:990]	Correlation 2 [1363:1235]	Correlation 3 [1650:1550]	Correlation 4 [1780:1720]	Correlation 5 [2995:2836]
Strep. 100%	0.9966	0.988	0.9987	0.5004	0.9987
Staph. 100%	0.7845	0.7467	0.996	0.3735	0.9826
Strep. 75%	0.9167	0.978	0.998	0.8102	0.9892
Strep 50%	0.9753	0.9016	0.9993	0.7703	0.9888
Strep. 25%	0.9646	0.8246	0.9979	0.4362	0.9901
weighting factor	0.31	0.3	0.02	0.001	0.019

The following table, table 5 illustrates the m_l statistical correlation of the signal for each segment. The wavenumber ranges are in cm^{-1} and are mentioned in the brackets. Table 5 also presents the weighting factor for each.

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Table 5: signal correlation table

sample	Correlation1 [1190:990]	Correlation 2 [1363:1235]	Correlation 3 [1650:1550]	Correlation 4 [1780:1720]	Correlation 5 [2995:2836]
Strep. 100%	0.99887	0.99417	0.99985	0.99697	0.99987
Staph. 100%	0.8719	0.97454	0.9978	0.98574	0.99703
Strep. 75%	0.91777	0.98977	0.99901	0.99817	0.99775
Strep.50%	0.99542	0.987	0.99982	0.99563	0.99697
Strep. 25%	0.98933	0.98857	0.99739	0.98584	0.99598
weighting factor	0.18	0.09	0.04	0.02	0.02

The weighting factors of each feature or correlation was determined by the maximum likelihood method.

As can be seen from the tables (4 & 5) correlation 1 and correlation 2 have the largest weighting factor both in the signal and its first derivative. Hence, we will illustrate the calculated boundaries for those correlations.

Boundaries calculation

As explained above, the boundaries are calculated according to the features and/or statistical correlations which had the most significant contribution for the specific bacteria identification in the sample.

Reference is now made to figure 18 which illustrate the boundaries of a two dimensions area which enable the identification of bacteria. The boundaries were calculated based on the two features or correlation having the significant contribution to the bacteria prediction – correlation 1 (for the wavenumber ranges of 990 cm^{-1} - 1190 cm^{-1}) and correlation 2 (for the wavenumber ranges of 1235 cm^{-1} -1363 cm^{-1}) calculated from the first derivative. The specific bacteria to be identified are streptococcus.

As can be seen from figure 18, when streptococcus is present in the sample, it is possible to optically determine and identify its presence within the sample.

Verification whether the features or correlation are within the boundaries

Once a sample for detection is obtained (for example, a sample containing 50% strep), the absorption signal is read, the first derivative is calculated and data processed. Then, according to the correlations and/or features one can determine whether strep. is present in the sample. The correlations presented in figure 18 are the 1st and the 2nd correlation.

As can be seen from figure 15, the 2nd correlation (the correlation calculated from the wavenumber range of 1235 cm^{-1} - 1363 cm^{-1}) of the first derivative is 0.9016, the 1st correlation (the correlation calculated from the wavenumber range of 990 cm^{-1} - 1190 cm^{-1}) of the first derivative is 0.9753 (figure 10).

Referring again to figure 18, it can be seen that the point (0.9016, 0.9753) is in the Strep. region – and hence we can inform the patient that strep. is present in the sample.

Let us look at another sample – 100% Staph (i.e., no streptococcus).

As can be seen from figure 14, the 2nd correlation (the correlation calculated from the wavenumber range of 1235 cm^{-1} - 1363 cm^{-1}) of the first derivative is 0.7467, the 1st correlation (the correlation calculated from the wavenumber range of 990 cm^{-1} - 1190 cm^{-1}) of the first derivative is 0.7845 (figure 9).

And from figure 18, one can observe that the point (0.7467, 0.7845) is in the Staph. region –hence we can inform the patient that strep. is not present in the sample.

Interlinking between the *m* feature and the *m$_l$* correlation to the specific bacteria

The following feature and correlations were linked to streptococcus:

peaks 1, 2, 9, 12 13 and 14 from table 3 and the first derivative correlations in the range 990cm^{-1} to 1190cm^{-1} and 1235cm^{-1} to 1363cm^{-1}.

It should be pointed out that the present invention detects bacteria as whole and not just single proteins on the membrane.

EXAMPLE 4 - Distinguishing between two bacteria in a solution

The following ex-vivo example provides a method to distinguish between two bacteria within a solution. The solution contained a mixture of - Streptococcus payogenes and Staphylococcus aureus. Furthermore, the ex-vivo example provides a

method to identify and to determine whether Streptococcus is present within the sample.

The following example provides a method to distinguish between two bacteria in a solution. The solution contained a mixture of - Streptococcus payogenes and Staphylococcus aureus.

Five mixtures of - Streptococcus payogenous and Staphylococcus aurus were prepared. The first derivative of the sample's spectroscopic absorption spectrum was then analyzed in different wavelength regions by using Pearson's correlation coefficient as described above.

The mixtures were prepared as follows:

Strep. β hemolytic (lot number 6919) and Staphylococcus Aureus (lot number 6985) after third transfer (*note: two extra transfers are acceptable before mutations*) were purchased (from HY Labs (08-9366475. www.hylabs.co.il))

Next, two eppendorf tubes were weighted. Then, one stoke solution per brand was prepared. The total volume was of 160 μl + 10 swipes with a quadloop from each plat in the two measured plates.

Next, 30 μL of the solutions was put on one marked slot on an optical plate (ZnSe): one slot for the 30 μl *Strep* and one slot for 30 μl ddH$_2$O. Then, 30 μL of the solution was put on one marked slot on another optical plate (ZnSe): one slot for the 30 μl *Staph* and one slot for 30 μl ddH$_2$O.

Next, the plates were placed in a desiccator (Dessicator 250 mm polypropylene, Yavin Yeda) in the presence of several petri plates with a desiccant agent (Phosphorus Pentoxide cat #79610 Sigma Aldrich) and vacuum was used for 30 minutes.

Next, the two tubes were centrifuged at 14,0000RPM (HSIANGTAI CNM2000) for 5 minutes. And the supernatant was aspirated. Then, the tubes were weighted and an even concentration was adjusted by diluting the dry bacteria with ddH2O.

The following calculations were recorded:

	Weight empty tube	Weight tube+bacteria	Bacteria weight mg	Water added
Streptococcus Pyogenes	1.05167	1.05814	6.47	150μl

Staphylococcus Aureus	1.06035	1.07268	12.33	300μl

Next, 5 solutions were prepared according to the following table:

Total volume μl	Strep Pyogenes % (amount to take from master solution in μl)	Staph Aurous CFU/160 μL (amount to take from master solution)
60	100% (60μL)	0% (0μL)
60	75% (45μL)	25% (15μL)
60	50% (30μL)	50% (30μL)
60	25%(15μL)	75% (45μL)
60	0 (0μL)	0 (0μL)
Total	**μL 150**	**μL 150**

Then, the tubes were centrifuged at 140,000RPM (HSIANGTAI CNM2000) for 5 minutes; and the supernatant was aspirated. Next, 2-3 1 μL droplets were placed on both sides of an optical plate and the spectral signature was read.

The identification and/or detection of specific bacteria was as follows:

(a) the noise in each of the absorption spectra was reduced by using Savitzky-Golay smoothing;

(b) the signal's first derivative was calculated;

(c) m features such as, but not limited to, peaks wavelength, peaks height and widths, peaks height ratio etc. were extracted from the spectra. A total of m features were extracted. m is an integer higher or equals 1;

(d) the signal and/or its first derivative were divided into several regions (segments) according to said m features;

(e) m_l statistical correlation were calculated for (i) the spectral signal at each region; and for (ii) the signal derivatives at each region. A total of m_l statistical correlations were extracted. m_l is an integer higher or equals 1. The statistical correlation for the each region (the signal's and its derivatives) was calculated by using Pearson's correlation coefficient;

(f) the m features and the m_l statistical correlation were examined and checked whether they are within the n dimensional volume boundaries (which acquired by the statistical processing);

(a) the identification of the specific bacteria was determined as positive if the m features and/or the m_l statistical correlation were within the n dimensional volume boundaries.

Statistical processing

The statistical processing is especially adapted to provide the n dimensional volume boundaries. For each specific bacterium the statistical processing was performed only once, for obtaining the boundaries. Once the boundaries were provided, the determination whether the specific bacteria is present in a sample was as explained above (i.e., verifying whether the features or correlation are within the boundaries). Furthermore, once the boundaries were provided, there exists no need for the statistical processing of the same specific bacteria again.

The statistical processing for each specific bacterium is performed in the following manner:

(a) obtaining several absorption spectrum (AS2) of samples containing the specific bacteria;

(b) extracting x features, from said AS2, such as, but not limited to, peaks wavelength, peaks height and widths, different peaks' intensity ratios etc. were extracted from the spectra. A total of x features. x is an integer higher or equals 1;

(c) calculating the signal's first derivative;

(d) dividing the signal and/or its first derivative into several regions (segments) according to said x features;

(e) Calculating the y correlation for the different segments within the absorption spectrums;

(f) Defining n dimensional space. n equals the sum of the x features and the y statistical correlations;

(g) Assigning and/or interlinking each one of the x feature, and each one of the y correlation to the specific bacteria which its identification is required;

(h) Calculating the Gaussian distribution for (i) each of the x feature; and/or for (ii) each of the y statistical correlations. All the calculated Gaussian

distributions constitute an *n* dimensional volume in the n dimensional space; and,

(i) Determining the boundaries of each volume by using quadratic Gaussian classifier or similar method (for example *k* nearest neighbor, Bayesian classification et cetera).

If the features and correlation (extracted from the spectrum) are within the *n* dimensional volume boundaries, the specific bacteria are identified. Otherwise the bacteria are not identified.

Alternatively or additionally, each of the *x* feature and/or for the *y* statistical correlations is given a weighting factor. The weighting factor is determined by the examining how each feature or correlation improves the bacteria detection prediction (for example by using maximum likelihood or Bayesian estimation). Once the weighting factor is assigned to each one of the *x* feature and the *y* statistical correlations, the boundaries are determined for the features and/or the statistical correlations having the most significant contribution to the bacteria prediction.

Alternatively or additionally, the AS2 is smoothed by reducing the noise. The noise reduction is obtained by different smoothing techniques selected from a group consisting of running average savitzky-golay or any combination thereof.

We'll first present an example for the smoothing technique. For that the entire signal and its first derivative prior to and after the noise are presented.

Then will give examples for the deviation of the spectrum. And lastly an example of the boundaries is given. It should be pointed put that for demonstrating purposes the boundaries were calculated according to the features and/or statistical correlations which had the most significant contribution are given for the samples.

Furthermore, the object of the following examples is to identify streptococcus.

Smoothing of the spectrum

Reference is now made to figure 19 illustrating the absorption signal of a sample containing 100% streptococcus prior to and after the noise was reduced (recorded signal vs. smoothed signal).

Reference is now made to figure 20 illustrating the signal's first derivative of a sample containing 100% streptococcus prior to and after the noise was reduced (recorded signal vs. smoothed signal).

Dividing the absorption spectrum and its first derivative

The first derivative of an absorption spectrum of different samples (having different amount of streptococcus and Staphylococcus) are given. The first derivatives are given as example in three selected segments (950 cm^{-1} to 1200 cm^{-1}; 1220 cm^{-1} to 1380 cm^{-1}; and 1710 cm^{-1} to 1780 cm^{-1}).

The entire segments (as divided both for the signal and the first derivative) are listed in table 5 and 6 along with the correlations.

Reference is now made to figures 21-23 which illustrate the first derivative of the absorption spectrum of a reference sample containing 100% Streptococcus (dotted line), a sample containing 100% Streptococcus(solid line), and the corresponding statistical correlations.

Figure 21 illustrates the reference sample's and sample's first derivative in the first range region of 950 cm^{-1} to 1200 cm^{-1}. Figure 22 illustrates the reference sample's and the sample's first derivative in the second region of 1220 cm^{-1} to 1380 cm^{-1}. Figure 23 illustrates the reference sample's and the sample's first derivative in the third region of 1710 cm^{-1} to 1780 cm^{-1}.

Reference is now made to figures 24-26 which illustrate the first derivative of the absorption spectrum of a reference sample containing 100% Streptococcus (dotted line) and a sample containing 100% Staphylococcus (solid line). The figures also present the corresponding statistical correlations.

Figure 24 illustrates the reference sample's and the sample's first derivative in the first range region of 950 cm^{-1} to 1200 cm^{-1}.

Figure 25 illustrates the reference sample's and the sample's first derivative in the second region of 1220 cm^{-1} to 1380 cm^{-1}.

Figure 26 illustrates the reference sample's and the sample's first derivative in the third region of 1710 cm^{-1} to 1780 cm^{-1}.

Reference is now made to figures 27-29 which illustrate the first derivative of the absorption spectrum of a reference sample containing 100% Streptococcus (dotted

line) and a sample containing 50% Staphylococcus and 50% Streptococcus (solid line). The figures also present the corresponding statistical correlations.

Figure 27 illustrates the reference sample's and the sample's first derivative in the first range region of 950 cm⁻¹ to 1200 cm⁻¹.

Figure 28 illustrates the reference sample's and the sample's first derivative in the second region of 1220 cm⁻¹ to 1380 cm⁻¹.

Figure 29 illustrates the reference sample's and the sample's first derivative in the third region of 1710 cm⁻¹ to 1780 cm⁻¹.

Reference is now made to figures 30-32 which illustrate the first derivative of the absorption spectrum of a reference sample containing 100% Streptococcus (dotted line) and a sample containing 25% Staphylococcus and 75% Streptococcus (solid line). The figures also present the corresponding statistical correlations.

Figure 30 illustrates the reference sample's and the sample's first derivative in the first range region of 950 cm⁻¹ to 1200 cm⁻¹.

Figure 31 illustrates the reference sample's and the sample's first derivative in the second region of 1220 cm⁻¹ to 1380 cm⁻¹.

Figure 32 illustrates the reference sample's and the sample's first derivative in the third region of 1710 cm⁻¹ to 1780 cm⁻¹.

Reference is now made to figures 33-35 which illustrate the first derivative of the absorption spectrum of a reference sample containing 100% Streptococcus (dotted line) and a sample containing 75% Staphylococcus and 25% Streptococcus (solid line). The figures also present the corresponding statistical correlations.

Figure 33 illustrates the reference sample's and the sample's first derivative in the first range region of 950 cm⁻¹ to 1200 cm⁻¹.

Figure 34 illustrates the reference sample's and the sample's first derivative in the second region of 1220 cm⁻¹ to 1380 cm⁻¹.

Figure 35 illustrates the reference sample's and the sample's first derivative in the third region of 1710 cm⁻¹ to 1780 cm⁻¹.

The *m* features extracted from the spectrum

The following features were extracted peaks wavelength, peaks height and widths, different peaks' intensity ratios, peaks height ratio. The signal and the signal's first derivative were divided to the above mentioned segments according to said features

due to the fact that in that region there were differences between the specific bacteria to be detected (i.e., streptococcus) and other bacteria (e.g., Staphylococcus).

The m_l statistical correlation of each segment and the weighting factor

The following table, table 6 illustrates the m_l statistical correlation of the signal's first derivative for each segment. The wavenumber ranges are in cm^{-1} and are mentioned in the brackets. Table 6 also presents the weighting factor for each.

Table 6: signal's first derivative correlation table

sample	Correlation1 [1190:990]	Correlation 2 [1363:1235]	Correlation 3 [1650:1550]	Correlation 4 [1780:1720]	Correlation 5 [2995:2836]
Strep. 100%	0.99719	0.99517	0.98354	0.99716	0.99794
Staph. 100%	0.89313	0.91064	0.89163	-0.43181	0.98581
Strep. 75%	0.98223	0.98223	0.98703	0.86995	0.99619
Strep.50%	0.91633	0.95679	0.83732	-0.1747	0.98709
Strep. 25%	0.90358	0.93308	0.83065	-0.19636	0.99509
weighting factor	0.27	0.18	0.01	0.3	0.05

The following table, table 7 illustrates the m_l statistical correlation of the signal for each segment. The wavenumber ranges are in cm^{-1} and are mentioned in the brackets. Table 7 also presents the weighting factor for each.

sample	Correlation1 [1190:990]	Correlation 2 [1363:1235]	Correlation 3 [1650:1550]	Correlation 4 [1780:1720]	Correlation5 [2995:2836]
Strep. 100%	0.99097	0.99954	0.99237	0.99997	0.99923
Staph. 100%	0.97118	0.99099	0.90992	0.99441	0.99516
Strep. 75%	0.98197	0.9858	0.93361	0.99329	0.99692
Strep.50%	0.98696	0.99762	0.99266	0.99921	0.99983
Strep. 25%	0.96841	0.98883	0.85486	0.99385	0.98444
weighting factor	0.09	0.005	0.005	0.01	0.09

The weighting factors of each feature or correlation was determined by the maximum likelihood method.

As can be seen from the tables (6 & 7) correlation 1 and correlation 4 have the largest weighting factor both in the signal and its first derivative. Hence, we will illustrate the calculated boundaries for those correlations.

Boundaries calculation

As explained above, the boundaries are calculated according to the features and/or statistical correlations which had the most significant contribution for the specific bacteria identification in the samples.

Reference is now made to figure 36 which illustrate the boundaries of a two dimensions area which enable the identification of bacteria. The boundaries were calculated based on the two features or correlation having the significant contribution to the bacteria prediction – correlation 1 (for the wavenumber ranges of 990 cm^{-1} - 1190 cm^{-1}) and correlation 2 (for the wavenumber ranges of 1235 cm^{-1} -1363 cm^{-1}) calculated from the first derivative. The specific bacteria to be identified are streptococcus.

As mentioned, the boundaries of the correlation values as well as for the other features are determined by the quadratic Gaussian classifier or similar method.

Again, as can be seen from figure 36 and as was demonstrated in the dry samples, when streptococcus is present in the sample, it is possible to optically determine and identify its presence within the sample.

Verification whether the features or correlation are within the boundaries

Once a sample for detection is obtained (for example, a sample containing 25% strep), the absorption signal is read, the first derivative is calculated and data processed. Then according to the correlations and/or features one can determine whether strep. is present in the sample. The correlations presented in figure 36 are the 1st and the 4th correlation.

As can be seen from figure 35, the 4th correlation (the correlation calculated from the wavenumber range of 1720 cm^{-1} - 1780 cm^{-1}) of the first derivative is -0.1936, the 1st

correlation (the correlation calculated from the wavenumber range of 990 cm^{-1} - 1190 cm^{-1}) of the first derivative is 0.90358 (figure 33).

Referring again to figure 36, it can be seen that the point (-0.1936, 0.90358) is in the Strep. region – and hence we can inform the patient that strep. is present in the sample.

Let us look at another sample – 100% Staph (i.e., no streptococcus).

As can be seen from figure 26, the 4th correlation (the correlation calculated from the wavenumber range of 1720 cm^{-1} - 1780 cm^{-1}) of the first derivative is -0.43181, the 1st correlation (the correlation calculated from the wavenumber range of 990 cm^{-1} - 1190 cm^{-1}) of the first derivative is 0.89313 (figure 24).

And from figure 36, one can observe that the point (-0.43181, 0.89313) is in the Staph. region –hence we can inform the patient that strep. is not present in the sample.

Interlinking between the *m* feature and the m_l correlation to the specific bacteria

The following feature and correlations were linked to streptococcus peaks 1, 2, 9, 12 13 and 14 from table 3 and the first derivative correlations in the range 990cm^{-1} to 1190cm^{-1} and 1235cm^{-1} to 1363cm^{-1}.

It should be pointed out that the present invention detects bacteria as whole and not just single proteins on the membrane.

Furthermore, it should be pointed out that in this specific example the water influence was not eliminated. And hence, it is within the scope of the present invention to identify bacteria without eliminating the water influence.

CLAIMS

1. A method for detecting and/or identifying specific bacteria within an uncultured sample; wherein said method comprising:

    a. obtaining an absorption spectrum (AS) of said uncultured sample;

    b. acquiring the n dimensional volume boundaries for said specific bacteria by

        i. obtaining at least one absorption spectrum (AS2) of samples containing said specific bacteria;

        ii. extracting x features from said AS2 selected from a group consisting of peaks wavelength, peaks height and widths, different peaks' intensity ratios or any combination thereof; said x is an integer higher or equal to one;

        iii. calculating at least one derivative of said AS2;

        iv. dividing said AS2 into several segments according to said x features;

        v. calculating the y statistical correlation of each of said segment; said y is an integer higher or equal to one;

        vi. defining n dimensional space; n equals the sum of said x features and said y statistical correlations;

        vii. assigning each one of said x feature and each one of said y correlation to said specific bacteria;

        viii. calculating the Gaussian distribution for each of said x feature and/or for each of said y statistical correlations; said Gaussian distributions defined the n dimensional volume in said n dimensional space;

        ix. determining said boundaries of said n dimensional volume by using technique selected from a group consisting of quadratic Gaussian classifier, k nearest neighbor, Bayesian classification or any combination thereof;

    c. data processing said AS;

        i. noise reducing by using different smoothing techniques selected from a group consisting of running average savitzky-golay or any combination thereof;

ii. extracting m features from said AS selected from a group consisting of peak's width, intensity, the ratio width/intensity, peak's wavelength, different peaks' intensity ratios, or any combination thereof; said m is an integer higher or equal to one;

iii. dividing said AS into several segments according to said m features;

iv. calculating the m_1 statistical correlation of each of said segment; said m_1 is an integer higher or equal to one; and,

d. detecting and/or identifying said specific bacteria if said m_1 statistical correlation and/or said m features are within said n dimensional volume.

2. The method for detecting and/or identifying specific bacteria within an uncultured sample according to claim 1, wherein said step (c) of data processing said AS additionally comprising steps of:

i. calculating at least one of the oth derivative of said AS; said o is an integer greater than or equals 1;

ii. extracting m_2 features from said o^{th} derivative selected from a group consisting of peak's width, intensity, the ratio width/intensity, different peaks' intensity ratios, peak's wavelength or any combination thereof;

iii. dividing said o^{th} derivative into several segments according to said m_2 features;

iv. calculating the m_3 statistical correlation in each of said segments; and,

v. detecting and/or identifying said specific bacteria if said m_1 and/or m_3 statistical correlation and/or said m and/or said m_2 features are within said n dimensional volume.

3. The method for detecting and/or identifying specific bacteria within an uncultured sample according to either one of claims 1 or 2, wherein said step of calculating the statistical correlation of each of said segment is performed by using Pearson's correlation coefficient.

4. The method for detecting and/or identifying specific bacteria within an uncultured sample according to either one of claims 1-3, additionally comprising

the step of selecting said specific bacteria selected from a group consisting of *Streptococcus Pyogenes, Group C and G beta-hemolytic streptococci, Corynebacterium haemolyticum, Diphtheria and Ulcerans, Neisseria Gonorrhoeae, Mycoplasma Pneumoniae, Yersinia Enterocolitica, Mycobacterium tuberculosis, Chlamydia Trachomatiss and Pneumoniae, Bordetella Pertussis, Legionella spp, Pneumocystis Carinii, Nocardia, Histoplasma Capsulatum, Coccidioides Immitis, Haemophilus influenza group A beta hemolytic* and *staphylococcus Aureus.*

5. The method for detecting and/or identifying specific bacteria within an uncultured sample according to either one claims 1-4, wherein said step of obtaining the AS additionally comprising steps of:

   a. providing at least one optical cell accommodates said uncultured sample;

   b. providing p light source selected from a group consisting of laser, lamp, LEDs tunable lasers, monochrimator, p is an integer equal or greater than 1; said p light source are adapted to emit light to said optical cell;

   c. providing detecting means for receiving the spectroscopic data of said sample;

   d. emitting light from said light source at different wavelength to said optical cell; and,

   e. collecting said light exiting from said optical cell by said detecting means; thereby obtaining said AS.

6. The method for detecting and/or identifying specific bacteria within an uncultured sample according to claim 5, wherein said step of emitting light is performed at the wavelength range of UV, visible, IR, mid-IR, far-IR and terahertz.

7. The method for detecting and/or identifying specific bacteria within an uncultured sample according to either one of claims 1-6, additionally comprising the step of detecting said bacteria by analyzing said AS in the region of about 3000-3300 cm^{-1} and/or about 850-1000 cm^{-1} and/or about 1300-1350 cm^{-1}.

8. A method for detecting and/or identifying specific bacteria within an uncultured sample; wherein said method comprising:

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a. obtaining an absorption spectrum (AS) of said uncultured sample; said AS containing water influence;

b. acquiring the n dimensional volume boundaries for said specific bacteria by

  i. obtaining at least one absorption spectrum (AS2) of samples containing said specific bacteria;

  ii. extracting x features from said AS2 selected from a group consisting of peaks wavelength, peaks height and widths, different peaks' intensity ratios or any combination thereof; said x is an integer higher or equal to one;

  iii. calculating at least one derivative of said AS2;

  iv. dividing said AS2 into several segments according to said x features;

  v. calculating the y statistical correlation of each of said segment; said y is an integer higher or equal to one;

  vi. defining n dimensional space; n equals the sum of said x features and said y statistical correlations;

  vii. assigning each one of said x feature and each one of said y correlation to said specific bacteria;

  viii. calculating the Gaussian distribution for each of said x feature and/or for each of said y statistical correlations; said Gaussian distributions defined the n dimensional volume in said n dimensional space;

  ix. determining said boundaries of said n dimensional volume by using technique selected from a group consisting of quadratic Gaussian classifier, k nearest neighbor, Bayesian classification or any combination thereof;

c. eliminating said water influence from said AS;

  i. providing the absorption intensity at each of wavenumber (x) within said AS $(Sig_{with\ water}(x))$;

  ii. dividing said AS into at least two wavenumber ranges;

  iii. calculating the correction factors (CF) at each wavenumber (x) within said least two ranges $(CF(x))$;

    iv. acquiring from said AS at least one absorption intensity that is mainly influenced by said water $Sig_{water\ only}(x1)$ and the corresponding wavenumbers $(x1)$;

    v. calculating at least one correction factor of said water ($CF_{water\ only}(x1)$) at said at least one wavenumber $(x1)$;

    vi. dividing said at least one $Sig_{water\ only}(x1)$ by said at least one CF_{water} (i.e., $Sig_{water\ only}(x1) / CF_{water\ only}(x1)$) at said at least one wavenumber $(x1)$;

    vii. calculating the average of step (vi) ($AVG[Sig_{water\ only}(x1) / CF_{water\ only}(x1)]$);

    viii. multiplying said $AVG[Sig_{water\ only}(x1) / CF_{water\ only}](x1)$ by said $CF(x)$ for each of said wavenumber (x) within said AS; and,

    ix. subtracting the result of step (viii) from said ($Sig_{with\ water}(x)$) at each of said wavenumber(x) within said AS;

d. data processing said AS without said water influence by

    i. noise reducing by using different smoothing techniques selected from a group consisting of running average savitzky-golay or any combination thereof;

    ii. extracting m features from said AS selected from a group consisting of peak's width, intensity, the ratio width/intensity, peak's wavelength, different peaks' intensity ratios, or any combination thereof; said m is an integer higher or equal to one;

    iii. dividing said AS into several segments according to said m features;

    iv. calculating the m_1 statistical correlation of each of said segment; said m_1 is an integer higher or equal to one; and,

e. detecting and/or identifying said specific bacteria if said m_1 statistical correlation and/or said m features are within said n dimensional volume.

9. The method for detecting and/or identifying specific bacteria within an uncultured sample according to claim 8, wherein said step (c) of data processing said AS without said water influence, additionally comprising steps of

    i. calculating at least one of the oth derivative of said AS; said o is an integer greater than or equals 1;

    ii. extracting m_2 features from said o^{th} derivative selected from a group consisting peak's width, intensity, the ratio width/intensity, different peaks' intensity ratios, peak's wavelength or any combination thereof;

    iii. dividing said o^{th} derivative into several segments according to said m_2 features;

    iv. calculating the m_3 statistical correlation in each of said segments; and,

    v. detecting and/or identifying said specific bacteria if said m_1 and/or m_3 statistical correlation and/or said m and/or said m_2 features are within said n dimensional volume.

10. The method for detecting and/or identifying specific bacteria within an uncultured sample according to either one of claims 8 or 9, wherein said step of calculating the statistical correlation in each of said segments is performed by using Pearson's correlation coefficient.

11. The method for detecting and/or identifying specific bacteria within an uncultured sample according to either one claims 8-10, additionally comprising the step of selecting said specific bacteria selected from a group consisting of *Streptococcus Pyogenes, Group C and G beta-hemolytic streptococci, Corynebacterium haemolyticum , Diphtheria and Ulcerans ,Neisseria Gonorrhoeae, Mycoplasma Pneumoniae, Yersinia Enterocolitica, Mycobacterium tuberculosis, Chlamydia Trachomatiss and Pneumoniae, Bordetella Pertussis,Legionella spp, Pneumocystis Carinii, Nocardia, Histoplasma Capsulatum, Coccidioides Immitis, Haemophilus influenza group A beta hemolytic* and *staphylococcus Aureus*.

12. The method for detecting and/or identifying specific bacteria within an uncultured sample according to claim either one claims 8-11, wherein said step of obtaining the AS additionally comprising steps of:

    a. providing at least one optical cell accommodating said uncultured sample;

b. providing *p* light source selected from a group consisting of laser, lamp, LEDs tunable lasers, monochrimator, *p* is an integer equal or greater than 1; said *p* light source are adapted to emit light to said optical cell;

c. providing detecting means for receiving the spectroscopic data of said sample;

d. emitting light from said light source at different wavelength to said optical cell;

e. collecting said light exiting from said optical cell by said detecting means; thereby obtaining said AS.

13. The method for detecting and/or identifying specific bacteria within an uncultured sample according to claim 12, wherein said step of emitting light is performed at the wavelength range of UV, visible, IR, mid-IR, far IR and terahertz.

14. A system 1000 adapted to detect and/or identify specific bacteria within an uncultured sample; wherein said system comprising:

a. means 100 for obtaining an absorption spectrum (AS) of said uncultured sample;

b. statistical processing means 200 for acquiring the *n* dimensional volume boundaries for said specific bacteria; said means 200 are characterized by

   i. means 201 for obtaining at least one absorption spectrum (AS2) of samples containing said specific bacteria;

   ii. means 202 for extracting *x* features from said AS2 selected from a group consisting of peaks wavelength, peaks height and widths, different peaks' intensity ratios or any combination thereof; said *x* is an integer higher or equal to one;

   iii. means 203 for calculating at least one derivative of said AS2;

   iv. means 204 for dividing said AS2 into several segments according to said *x* features;

   v. means 205 for calculating the *y* statistical correlation of each of said segment; said *y* is an integer higher or equal to one;

   vi. means 206 for defining *n* dimensional space; *n* equals the sum of said *x* features and said *y* statistical correlations;

      vii. means 207 for assigning each one of said x feature and each one of said y correlation to said specific bacteria;

      viii. means 208 for calculating the Gaussian distribution for each of said x feature and/or for each of said y statistical correlations; said Gaussian distributions defined the n dimensional volume in said n dimensional space;

      ix. means 209 for determining said boundaries of said n dimensional volume by using technique selected from a group consisting of quadratic Gaussian classifier, k nearest neighbor, Bayesian classification or any combination thereof;

c. means 300 for data processing said AS; said means 300 are characterized by

      i. means 301 for noise reducing by using different smoothing techniques selected from a group consisting of running average savitzky-golay or any combination thereof;

      ii. means 302 for extracting m features from said AS selected from a group consisting of peak's width, intensity, the ratio width/intensity, peak's wavelength, different peaks' intensity ratios, or any combination thereof; said m is an integer higher or equal to one;

      iii. means 303 for dividing said AS into several segments according to said m features;

      iv. means 304 for calculating the m_l statistical correlation of each of said segment; said m_l is an integer higher or equal to one; and,

d. means 400 for detecting and/or identifying said specific bacteria if said m_l statistical correlation and/or said m features are within said n dimensional volume.

15. The system 1000 according to claim 14, wherein said means 300 for data processing said AS additionally characterized by:

      i. means 305 for calculating at least one of the oth derivative of said AS; said o is an integer greater than or equals 1;

      ii. means 306 for extracting m_2 features from said o^{th} derivative selected from a group consisting of peak's width, intensity, the

ratio width/intensity, different peaks' intensity ratios, peak's wavelength or any combination thereof;

   iii. means 307 for dividing said o^{th} derivative into several segments according to said m_2 features;

   iv. means 308 for calculating the m_3 statistical correlation in each of said segments; and,

   v. means 309 for detecting and/or identifying said specific bacteria if said m_1 and/or m_3 statistical correlation and/or said m and/or said m_2 features are within said n dimensional volume.

16. The system 1000 according to either one of claims 14 or 15, wherein said means 308 or 304 for calculating the statistical correlation is selected from a group consisting of Pearson's correlation coefficient.

17. The system 1000 according to either one of claims 14-16, wherein said specific bacteria is selected from a group consisting of *Streptococcus Pyogenes, Group C and G. beta-hemolytic streptococci, Corynebacterium haemolyticum, Diphtheria and Ulcerans, Neisseria Gonorrhoeae, Mycoplasma Pneumoniae, Yersinia Enterocolitica, Mycobacterium tuberculosis, Chlamydia Trachomatiss and Pneumoniae, Bordetella Pertussis, Legionella spp, Pneumocystis Carinii, Nocardia, Histoplasma Capsulatum, Coccidioides Immitis, Haemophilus influenza group A beta hemolytic* and *staphylococcus Aureus*.

18. The system 1000 according to either one of claims 14-16, wherein said means 100 for obtaining an absorption spectrum (AS) of said sample additionally comprising:

   a. at least one optical cell for accommodating said uncultured sample;

   b. p light source selected from a group consisting of laser, lamp, LEDs tunable lasers, monochrimator, p is an integer equal or greater than 1; said p light source are adapted to emit light at different wavelength to said optical cell; and,

   c. detecting means for receiving the spectroscopic data of said sample exiting from said optical cell.

19. The system 1000 according to claim 18, wherein said p light source are adapted to emit light at wavelength range selected from a group consisting of UV, visible, IR, mid-IR, far-IR and terahertz.
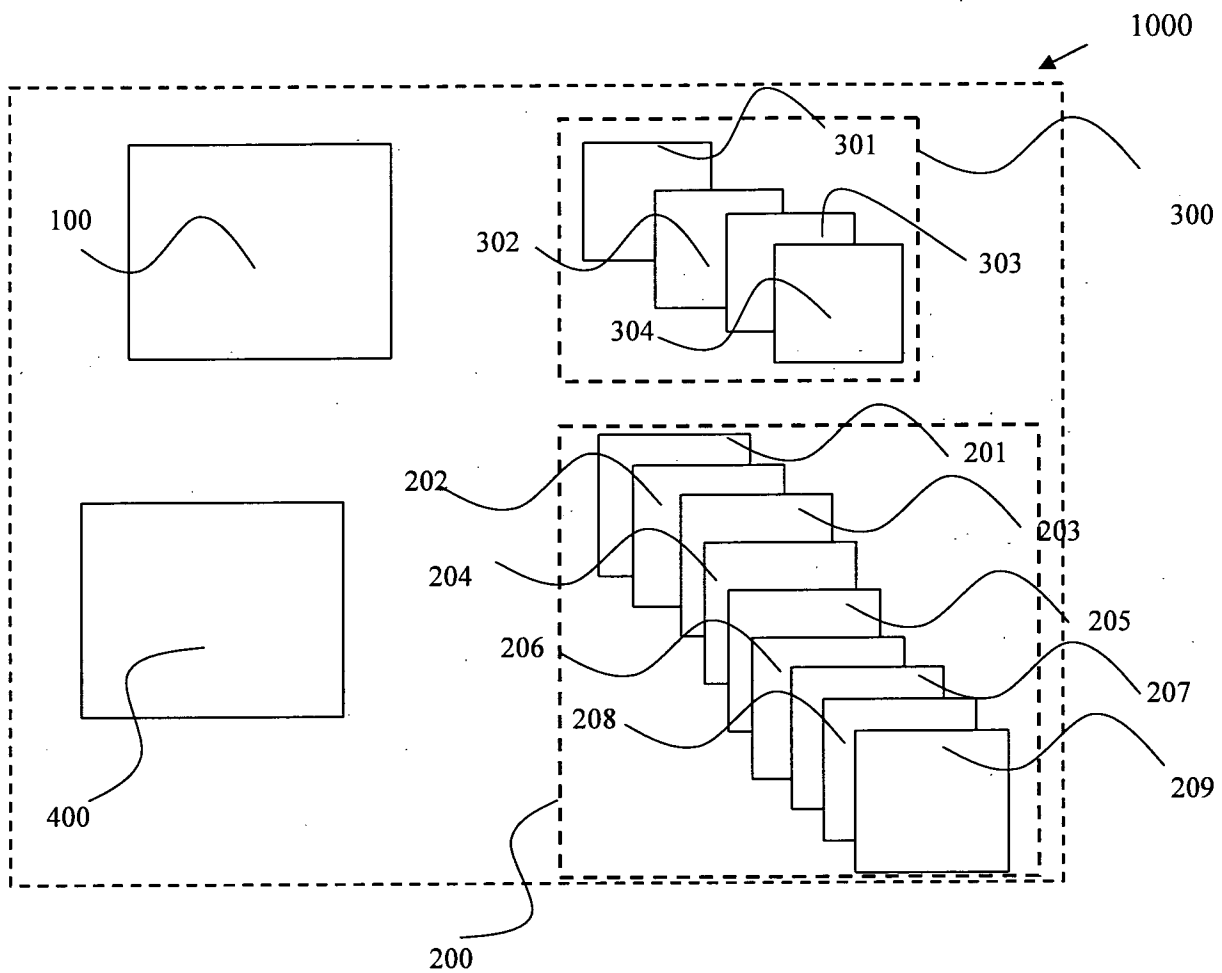
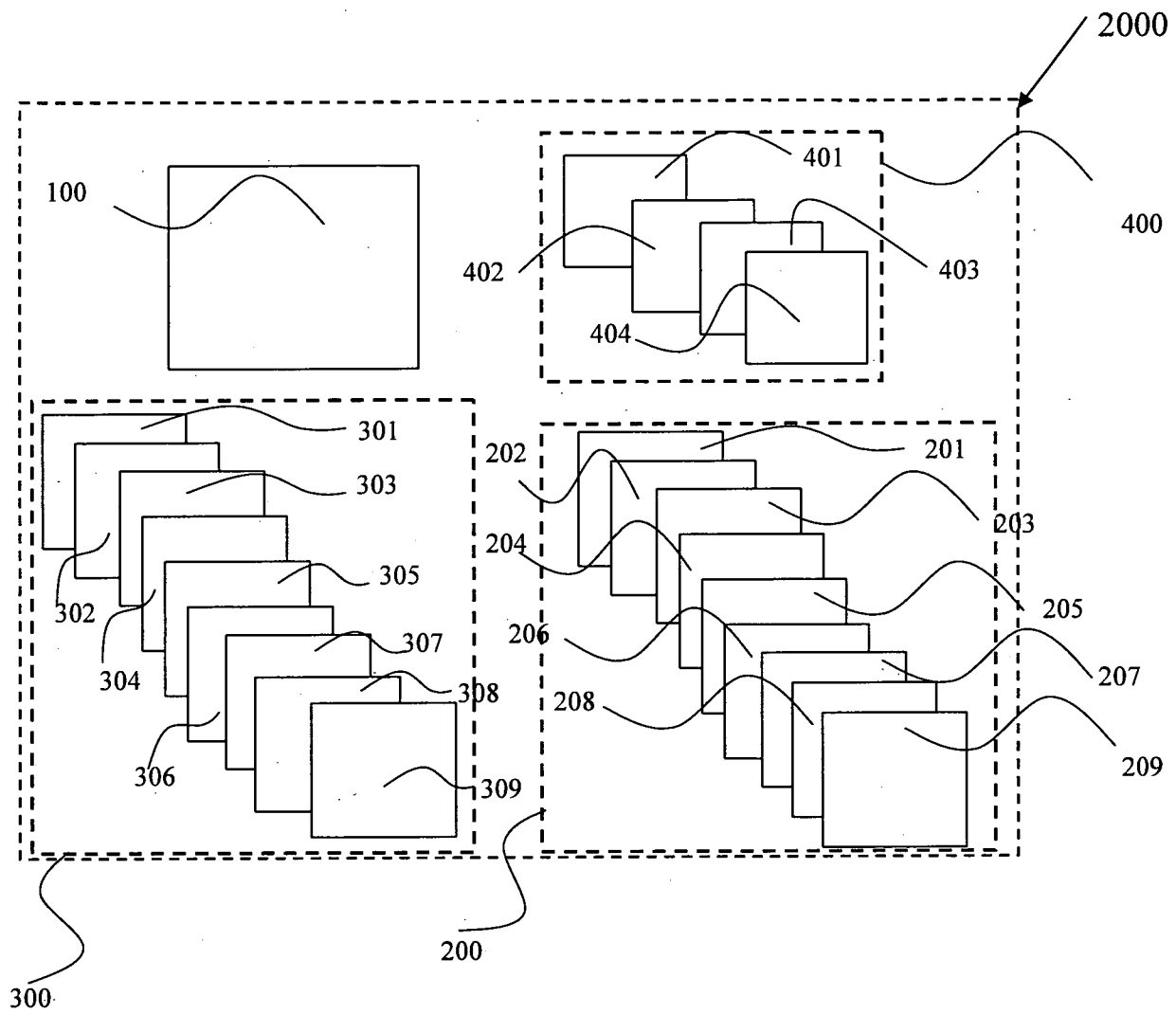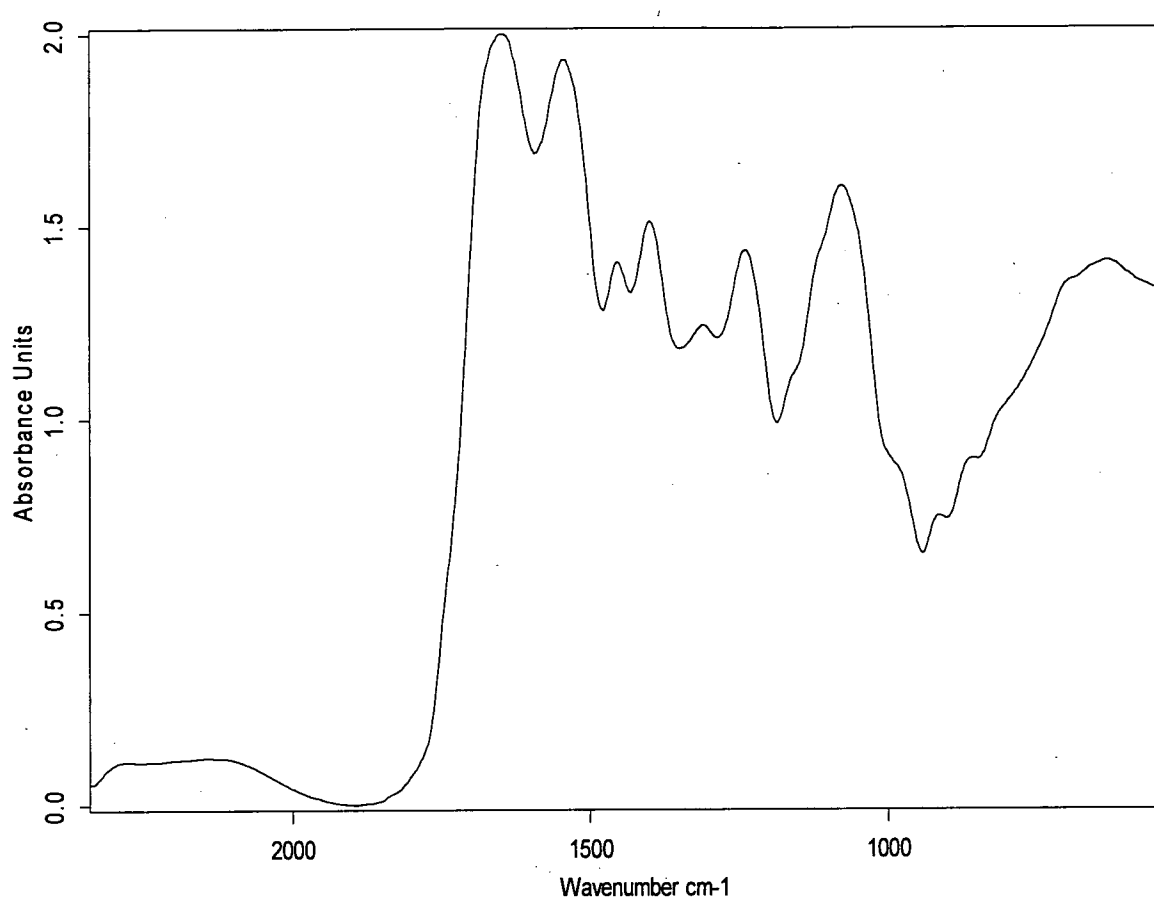20. A system 2000 adapted to detect and/or identify specific bacteria within an uncultured sample; wherein said system 2000 comprising:

a. means 100 for obtaining an absorption spectrum (AS) of said uncultured sample; said AS containing water influence;

b. statistical processing means 200 for acquiring the n dimensional volume boundaries for said specific bacteria; said means 200 are characterized by:

   i. means 201 for obtaining at least one absorption spectrum (AS2) of samples containing said specific bacteria;

   ii. means 202 for extracting x features from said AS2 selected from a group consisting of peaks wavelength, peaks height and widths, different peaks' intensity ratios or any combination thereof; said x is an integer higher or equal to one;

   iii. means 203 for calculating at least one derivative of said AS2;

   iv. means 204 for dividing said AS2 into several segments according to said x features;

   v. means 205 for calculating the y statistical correlation of each of said segment; said y is an integer higher or equal to one;

   vi. means 206 for defining n dimensional space; n equals the sum of said x features and said y statistical correlations;

   vii. means 207 for assigning each one of said x feature and each one of said y correlation to said specific bacteria;

   viii. means 208 for calculating the Gaussian distribution for each of said x feature and/or for each of said y statistical correlations; said Gaussian distributions defined the n dimensional volume in said n dimensional space;

   ix. means 209 for determining said boundaries of said n dimensional volume by using technique selected from a group consisting of quadratic Gaussian classifier, k nearest neighbor, Bayesian classification or any combination thereof;

c. means 300 for eliminating said water influence from said AS; said means 300 having:

   i. means 301 for providing the absorption intensity at each of wavenumber (x) within said AS ($Sig_{with\,water}(x)$);

    ii. means 302 for dividing said AS into at least two wavenumber ranges;

    iii. means 303 for calculating the correction factors (*CF*) at each wavenumber (*x*) within said least two ranges (*CF(x)*);

    iv. means 304 for acquiring from said AS at least one absorption intensity that is mainly influenced by said water $Sig_{water\ only}(x1)$ and the corresponding wavenumbers (*x1*);

    v. means 305 for calculating at least one correction factor of said water ($CF_{water\ only}(x1)$) at said at least one wavenumber (*x1*);

    vi. means 306 for dividing said at least one $Sig_{water\ only}(x1)$ by said at least one CF_{water} (i.e., $Sig_{water\ only}(x1) / CF_{water\ only}(x1)$) at said at least one wavenumber (*x1*);

    vii. means 307 for calculating the average of step (vi) ($AVG[Sig_{water\ only}(x1) / CF_{water\ only}(x1)]$);

    viii. means 308 for multiplying said $AVG[Sig_{water\ only}(x1) / CF_{water\ only}]$ (*x1*) by said *CF(x)* for each of said wavenumber (*x*) within said AS; and,

    ix. means 309 for subtracting the result of step (viii) from said ($Sig_{with\ water}(x)$) at each of said wavenumber(*x*) within said AS;

d. means 400 for data processing said AS without said water influence; said means 400 are characterized by:

    i. means 401 for noise reducing by using different smoothing techniques selected from a group consisting of running average savitzky-golay or any combination thereof;

    ii. means 402 for extracting *m* features from said AS selected from a group consisting of peak's width, intensity, the ratio width/intensity, peak's wavelength, different peaks' intensity ratios, or any combination thereof; said *m* is an integer higher or equal to one;

    iii. means 403 for dividing said AS into several segments according to said *m* features;

    iv. means 404 for calculating the m_1 statistical correlation of each of said segment; said m_1 is an integer higher or equal to one; and,

e. means 500 for detecting and/or identifying said specific bacteria if said m_1 statistical correlation and/or said m features are within said n dimensional volume.

21. The system 2000 according to claim 20, wherein said means 400 for data processing said AS without said water influence additionally comprising:

i. means 405 for calculating at least one of the oth derivative of said AS; said o is an integer greater than or equals 1;

ii. means 406 for extracting m_2 features from said o^{th} derivative selected from a group consisting peak's width, intensity, the ratio width/intensity, different peaks' intensity ratios, peak's wavelength or any combination thereof;

iii. means 407 for dividing said o^{th} derivative into several segments according to said m_2 features;

iv. means 408 for calculating the m_3 statistical correlation in each of said segments; and,

v. means 409 for detecting and/or identifying said specific bacteria if said m_1 and/or m_3 statistical correlation and/or said m and/or said m_2 features are within said n dimensional volume.

22. The system 2000 according to either one of claims 20 or 21, wherein said means 408 and/or 404 for calculating the statistical correlation in each of said segments is selected form a group consisting of Pearson's correlation coefficient.

23. The system 2000 according to either one of claims 20 -22, wherein said specific bacteria is selected from a group consisting of *Streptococcus Pyogenes, Group C and G beta-hemolytic streptococci, Corynebacterium haemolyticum, Diphtheria* and *Ulcerans, Neisseria Gonorrhoeae, Mycoplasma Pneumoniae, Yersinia Enterocolitica, Mycobacterium tuberculosis, Chlamydia Trachomatiss and Pneumoniae, Bordetella Pertussis,Legionella spp, Pneumocystis Carinii, Nocardia, Histoplasma Capsulatum, Coccidioides Immitis, Haemophilus influenza group A beta hemolytic* and *staphylococcus Aureus.*

24. The system 2000 according to either one of claims 20-23, wherein said means 100 for obtaining an absorption spectrum (AS) of said sample additionally comprising:

a. at least one optical cell for accommodating said uncultured sample;

b. *p* light source selected from a group consisting of laser, lamp, LEDs tunable lasers, monochrimator, *p* is an integer equal or greater than 1; said *p* light source are adapted to emit light at different wavelength to said optical cell; and,

c. detecting means for receiving the spectroscopic data of said sample exiting from said optical cell.

25. The system 2000 according to claim 24, wherein said *p* light source are adapted to emit light at wavelength range selected from a group consisting of UV, visible, IR, mid-IR, far-IR and terahertz.

Fig. 1

Fig. 2

Fig. 3

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Fig. 4

Fig. 5

Fig. 6

Fig. 7

Fig 8

Fig 9

**Smoothed Signal Correlation=
0.99542**

**Smoothed First Derivarive Correlation=
0.9753**
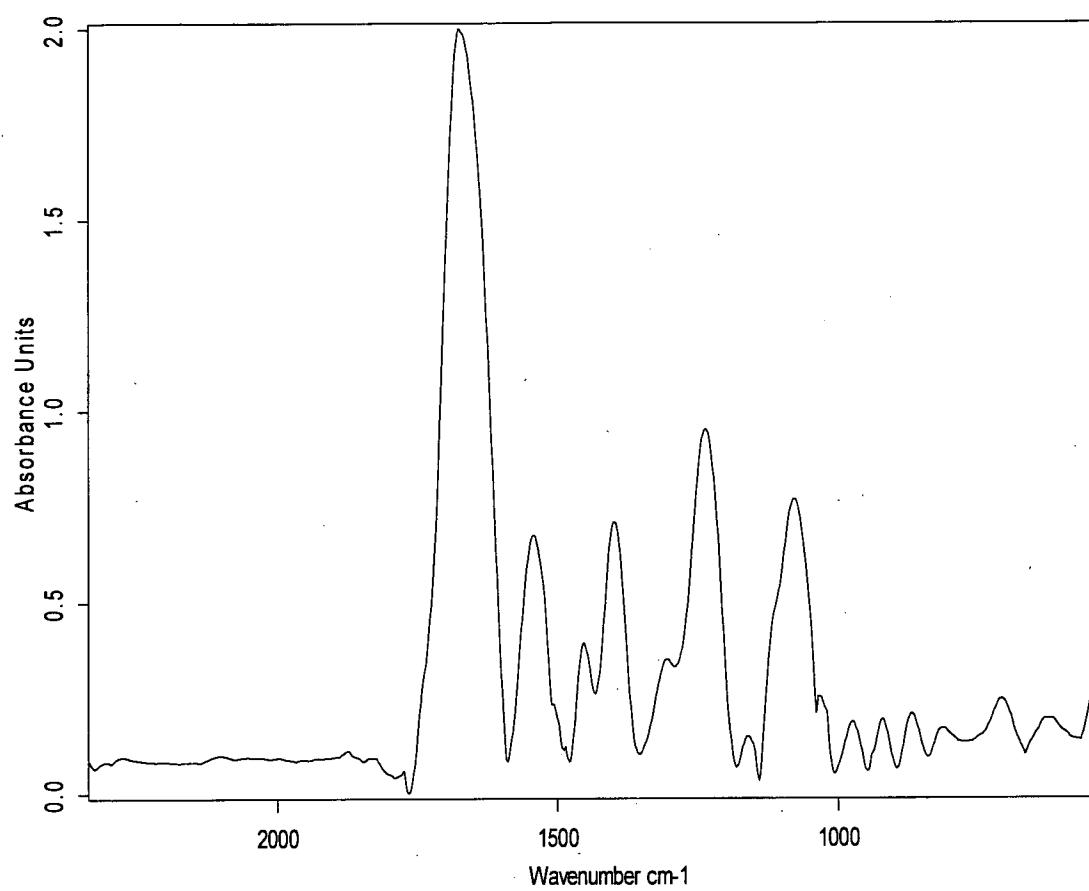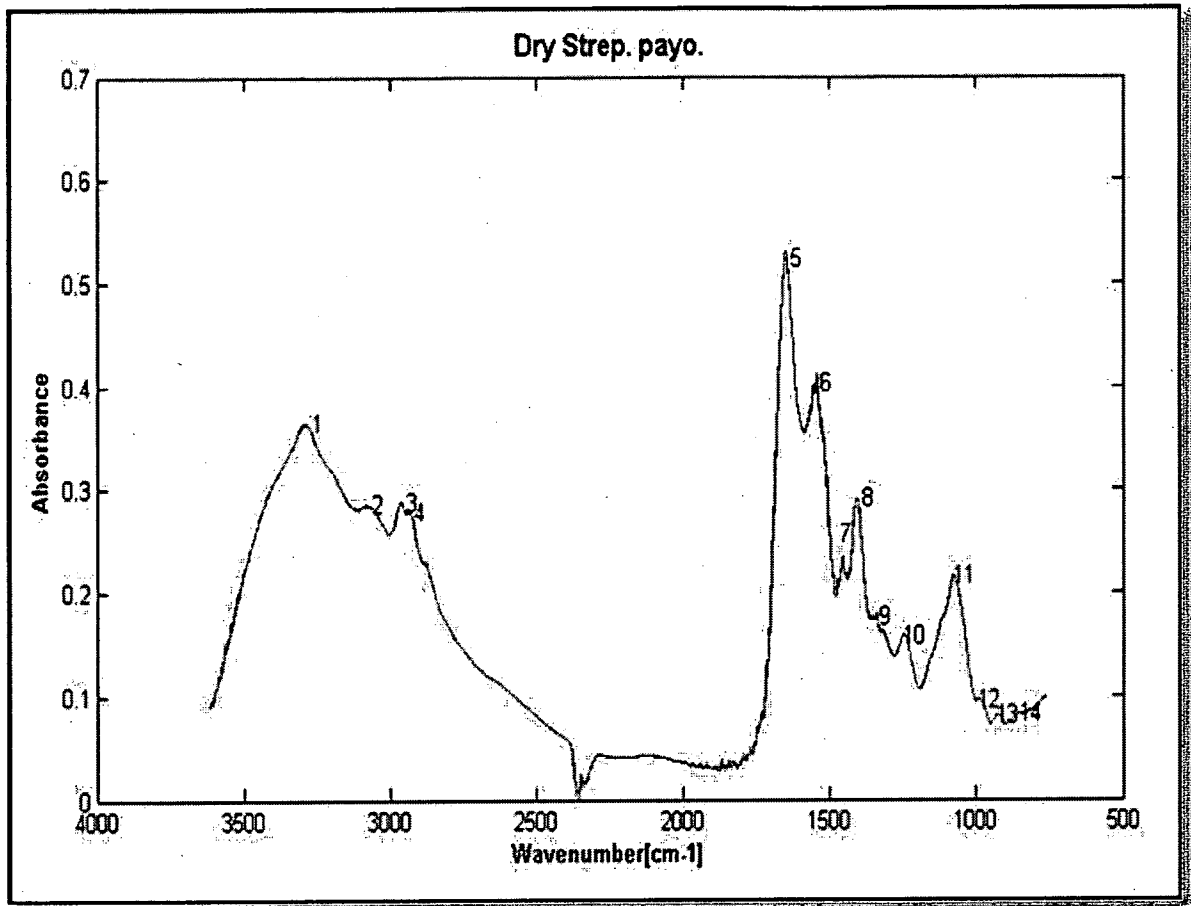
Fig 10.
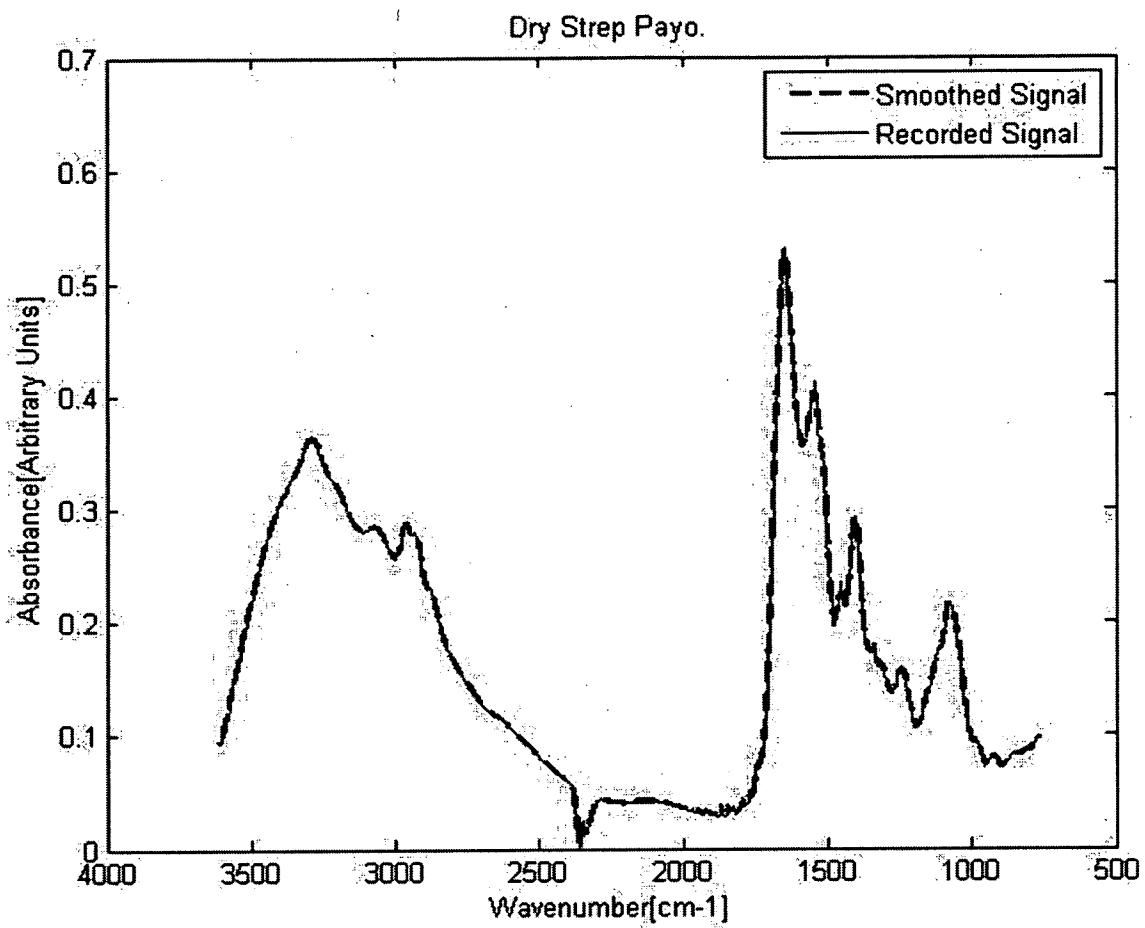
Fig. 11

Fig. 12
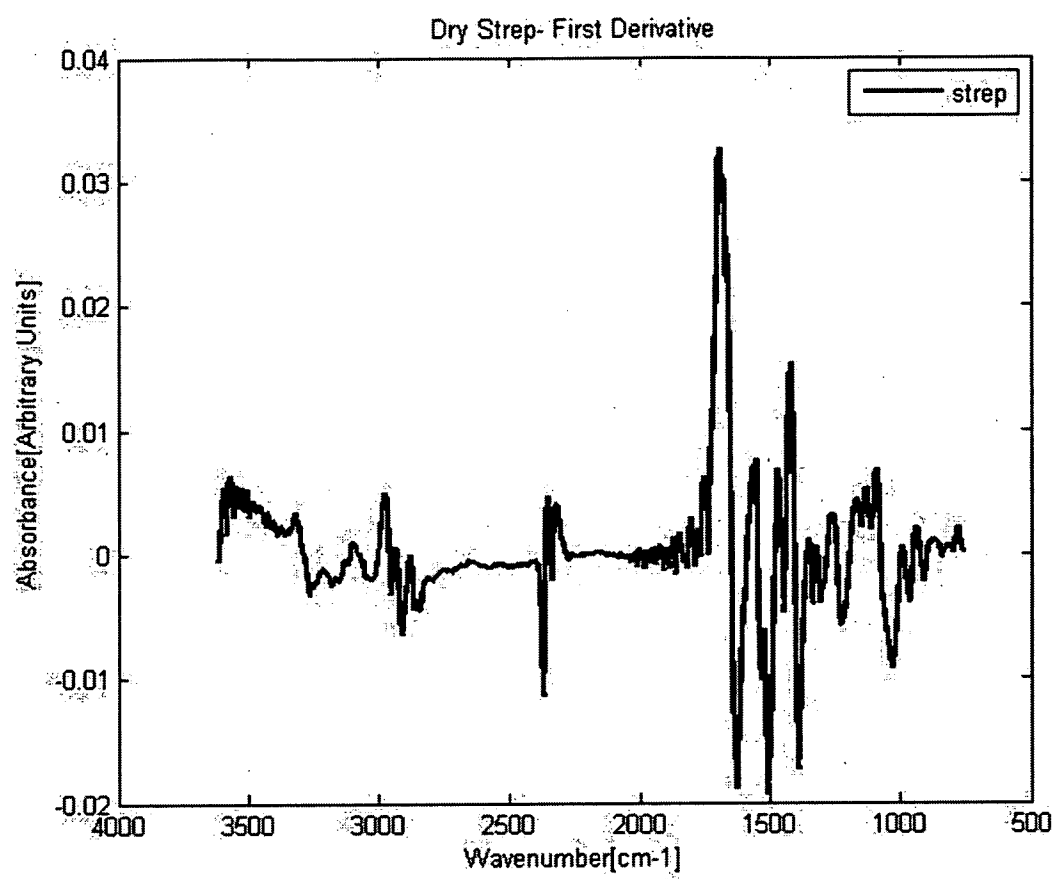
Fig. 13
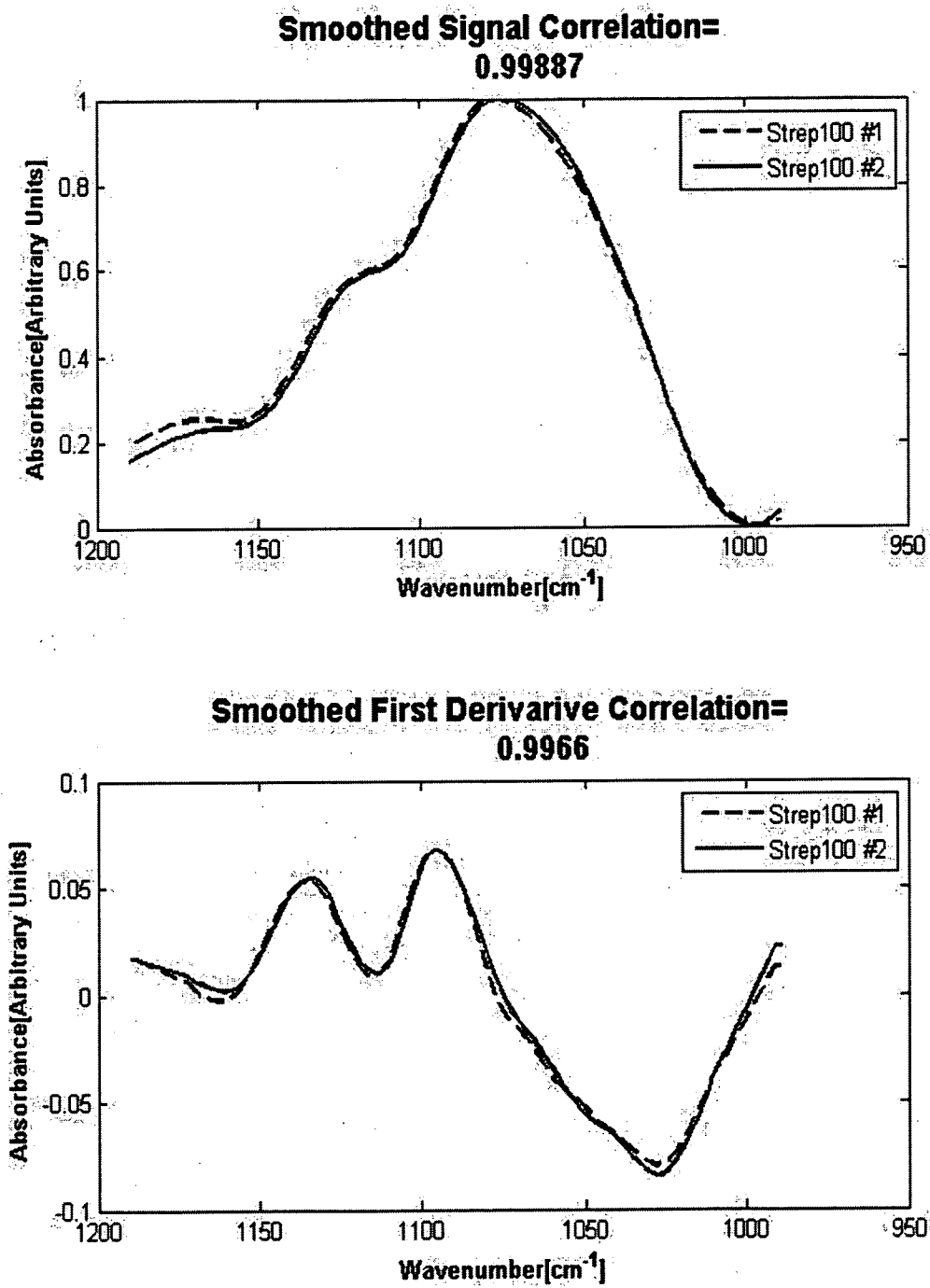
Smoothed Signal Correlation= 0.97454
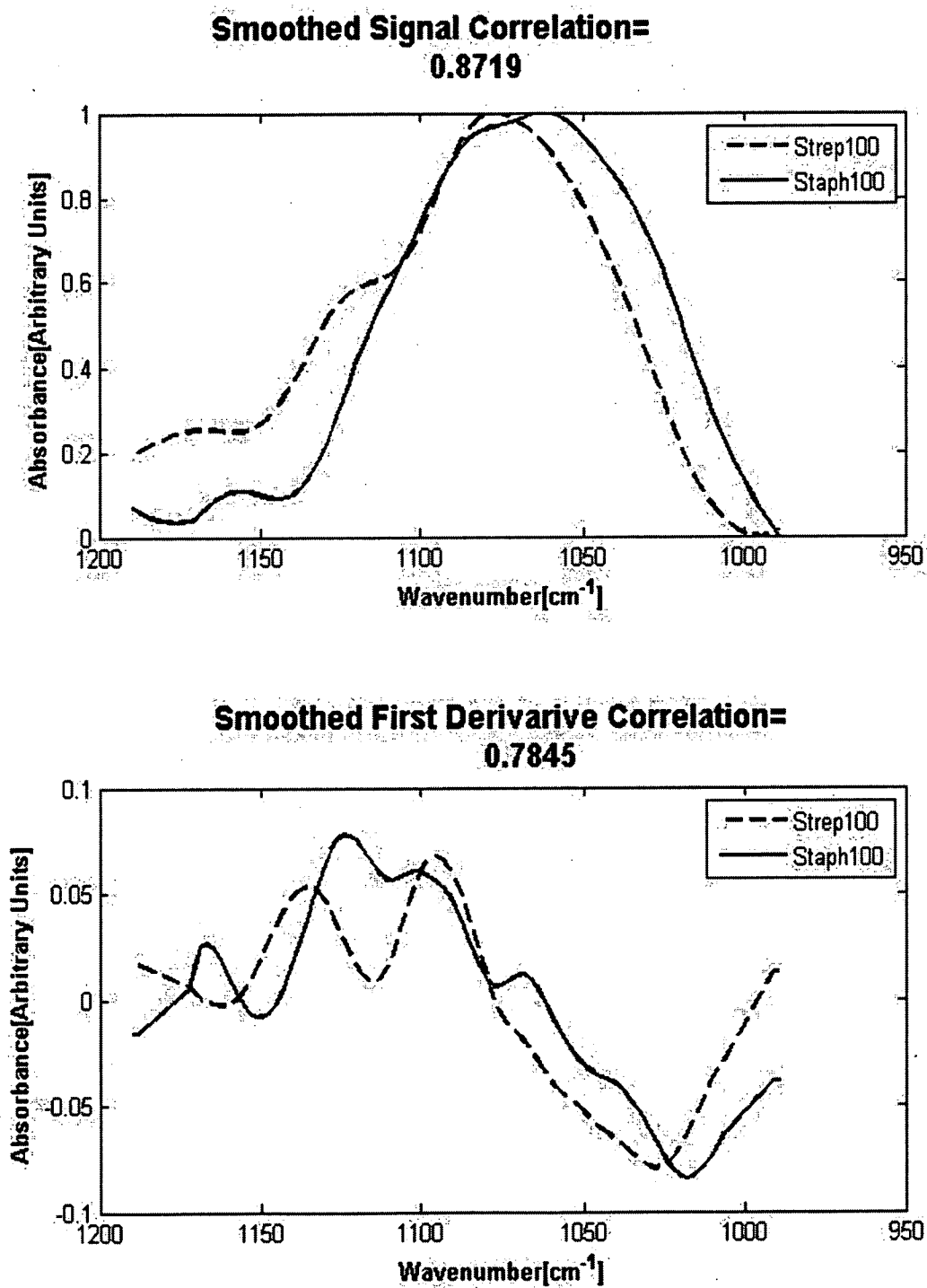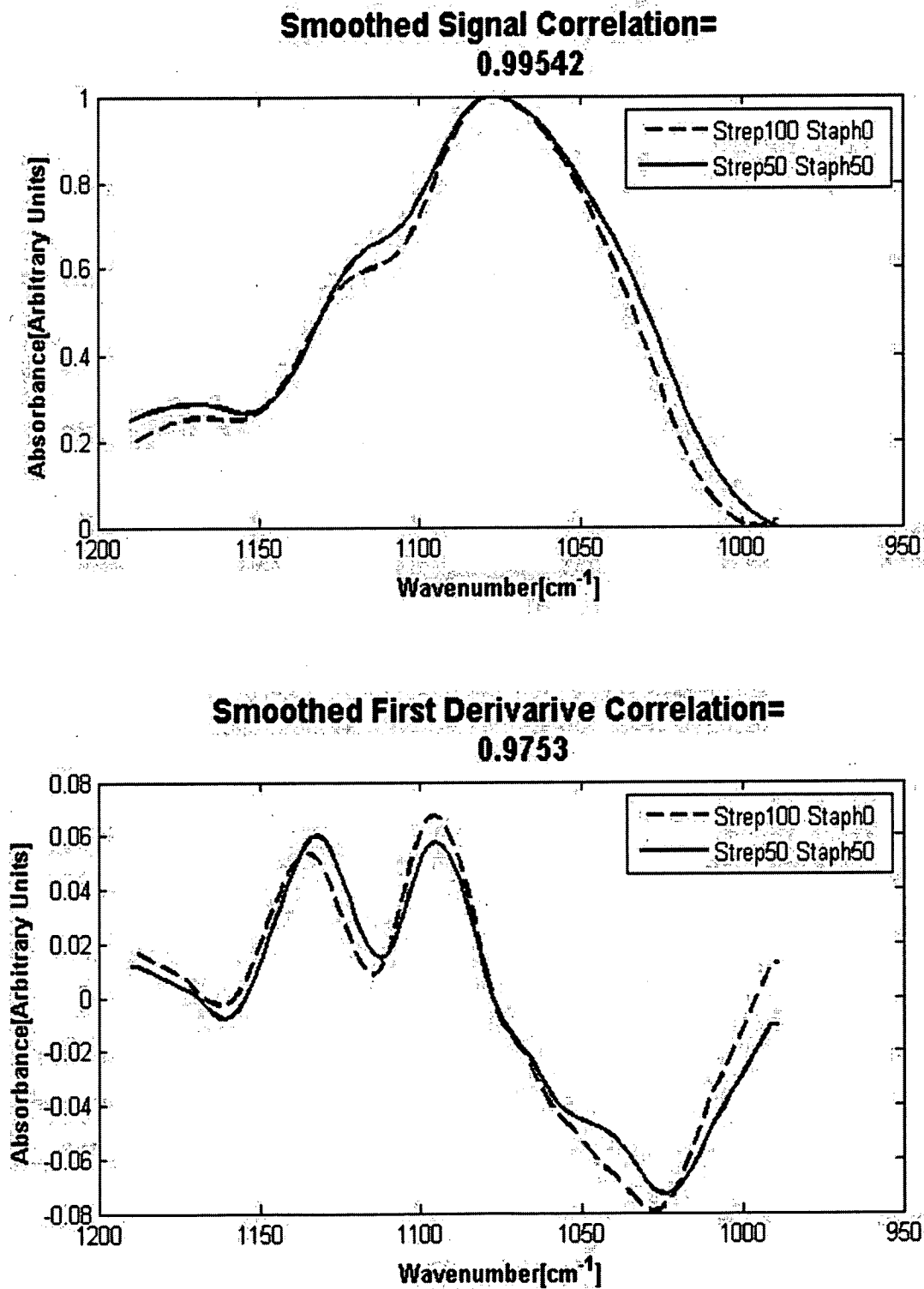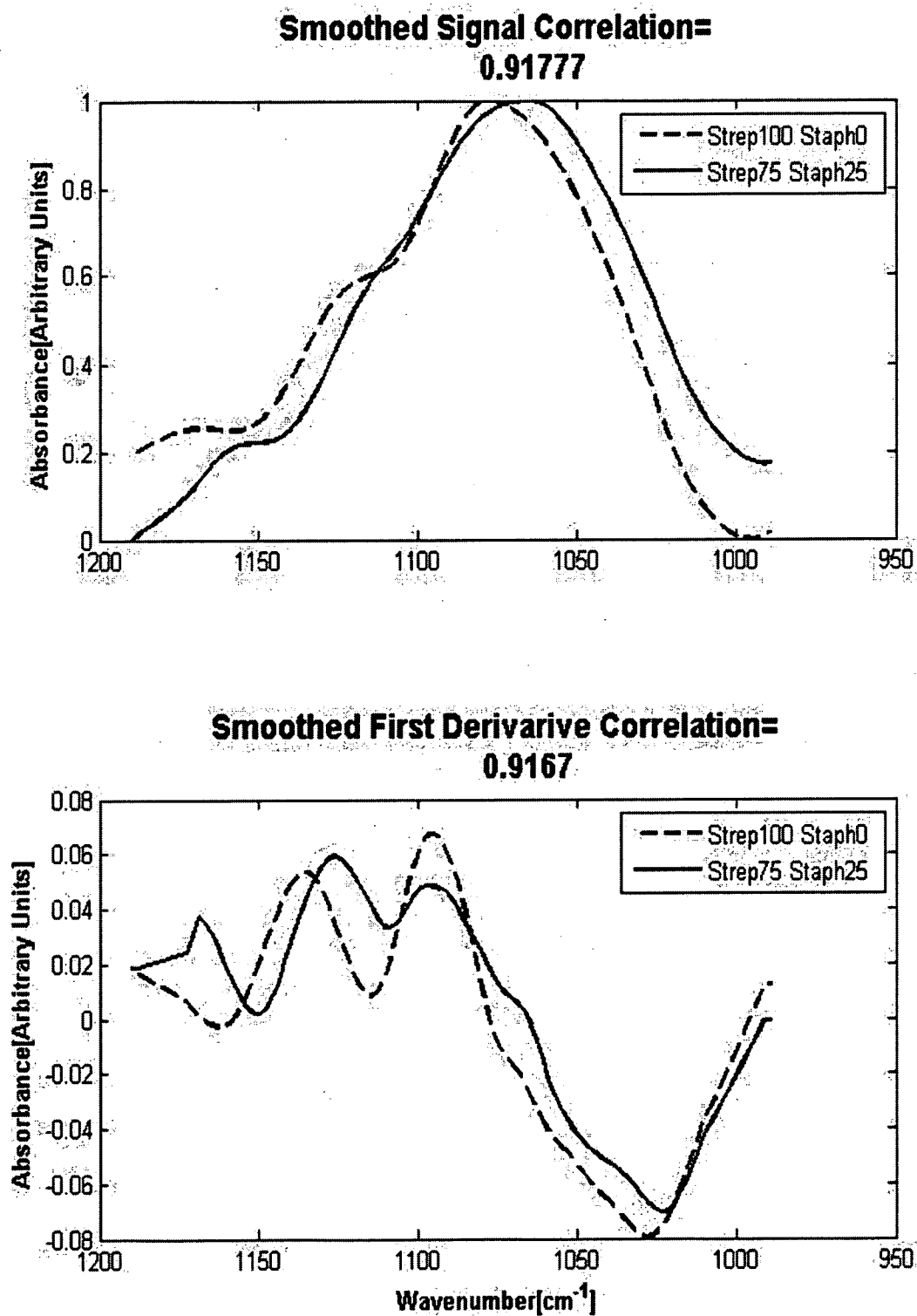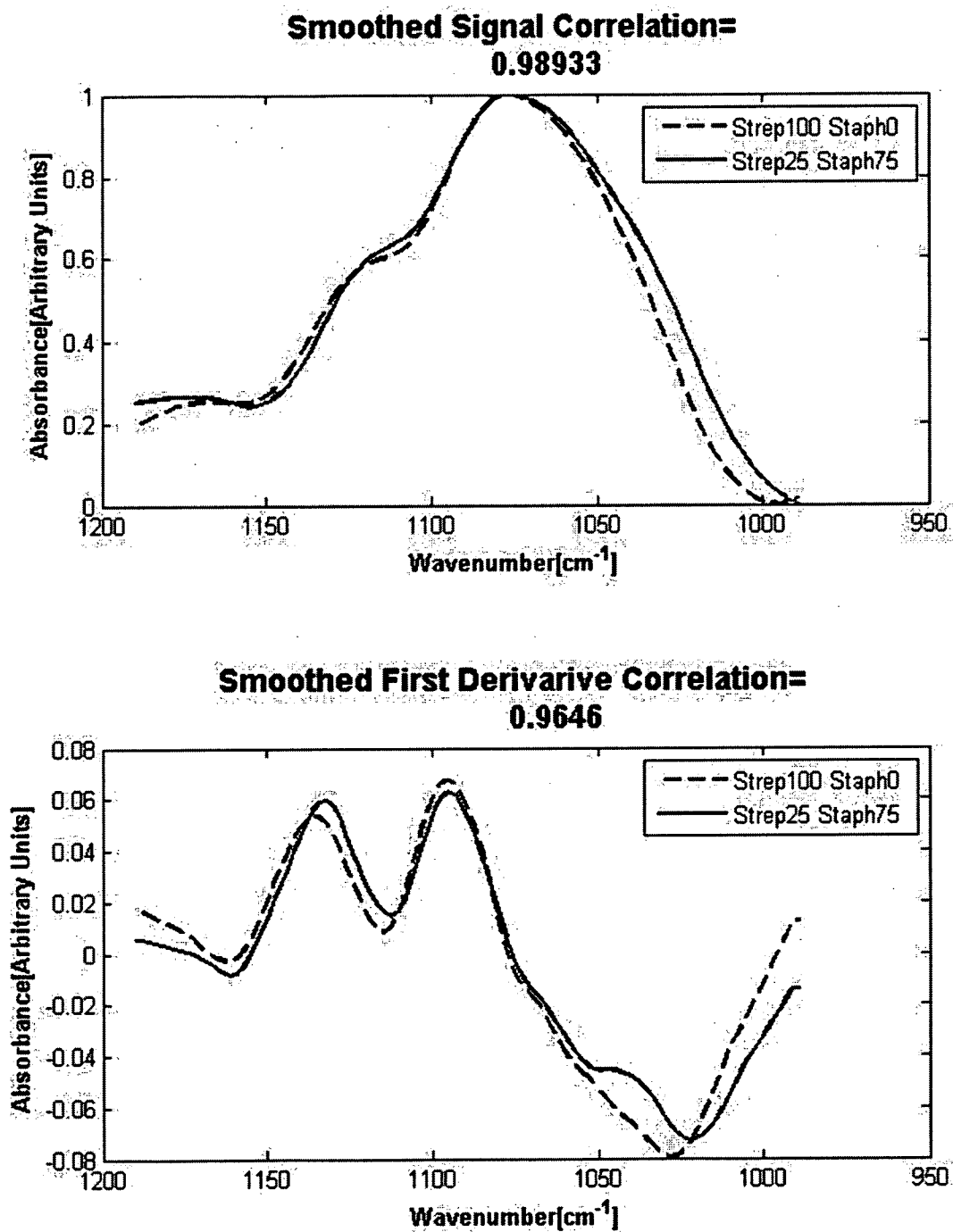
Smoothed First Derivarive Correlation= 0.7467

Fig. 14
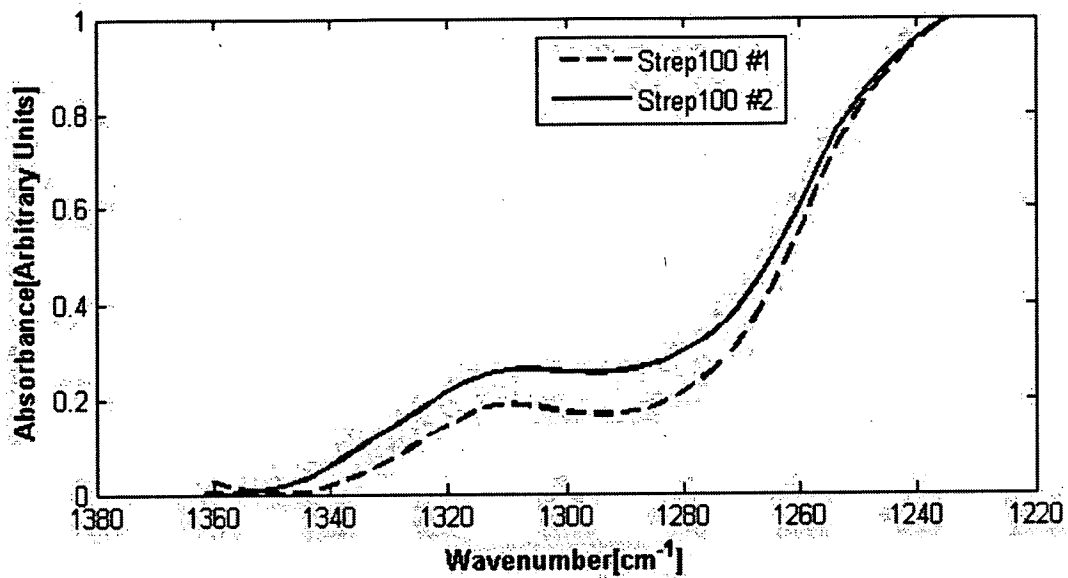
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Smoothed Signal Correlation= 0.987

Smoothed First Derivarive Correlation= 0.9016
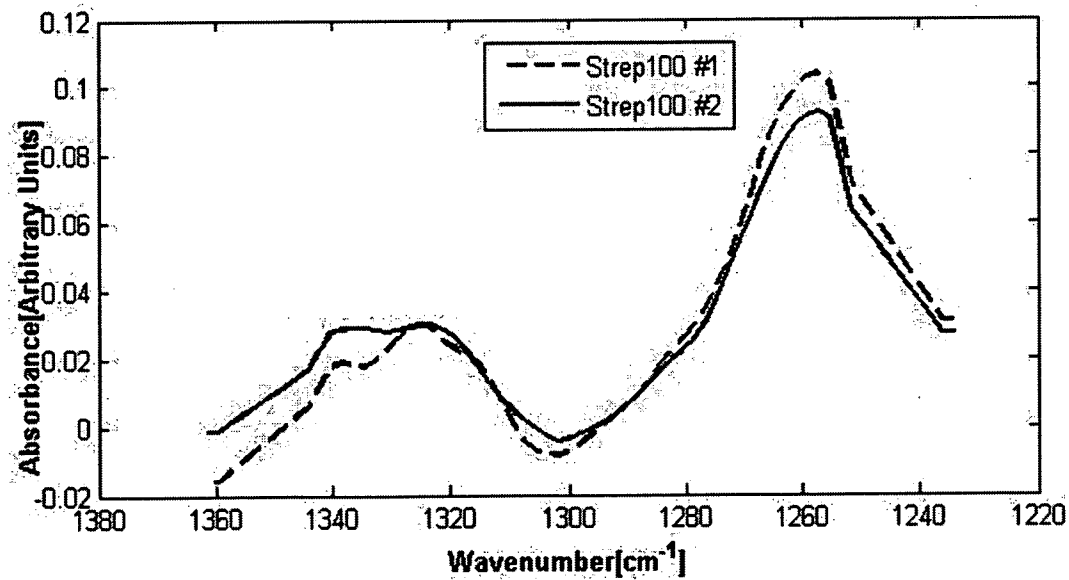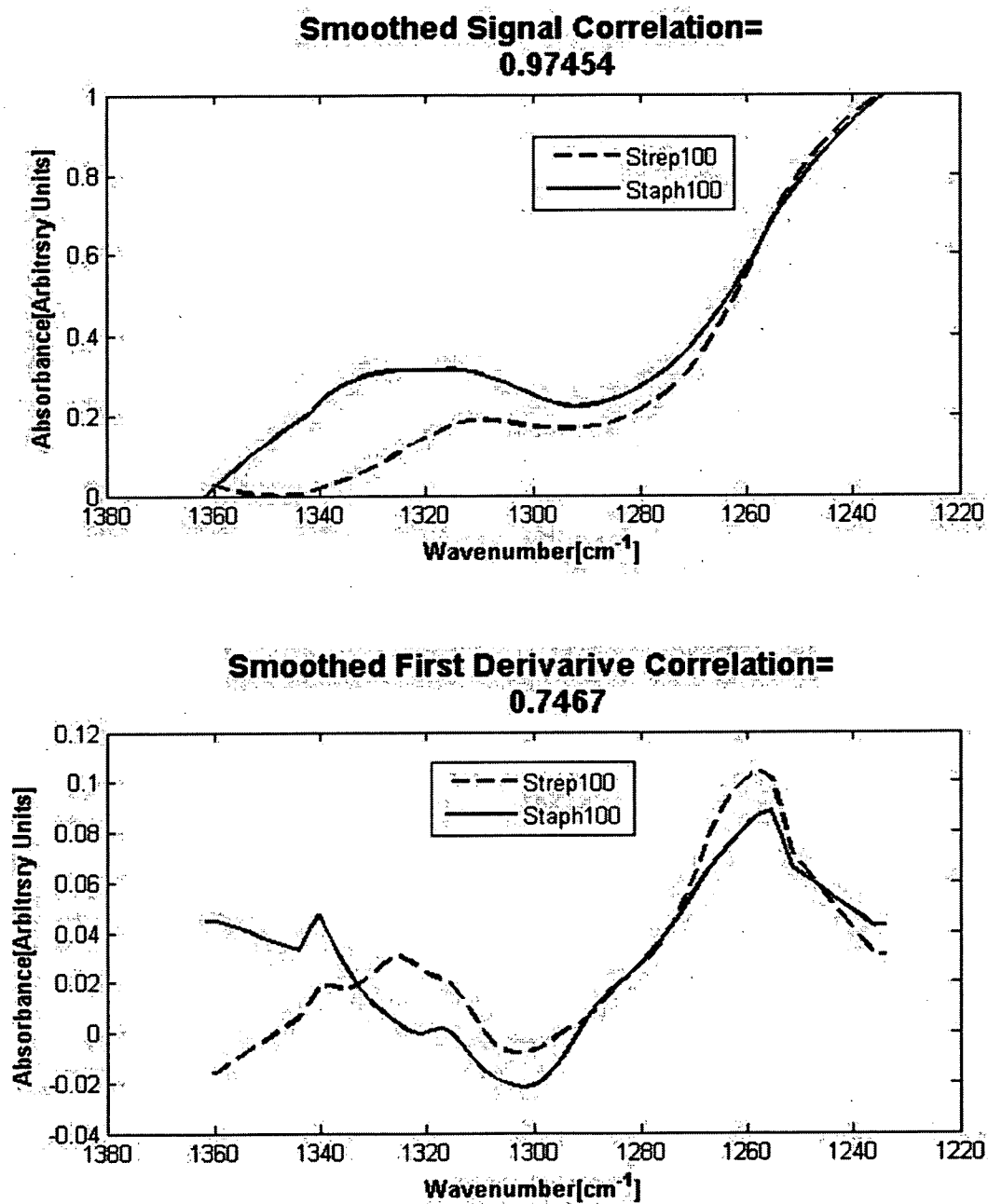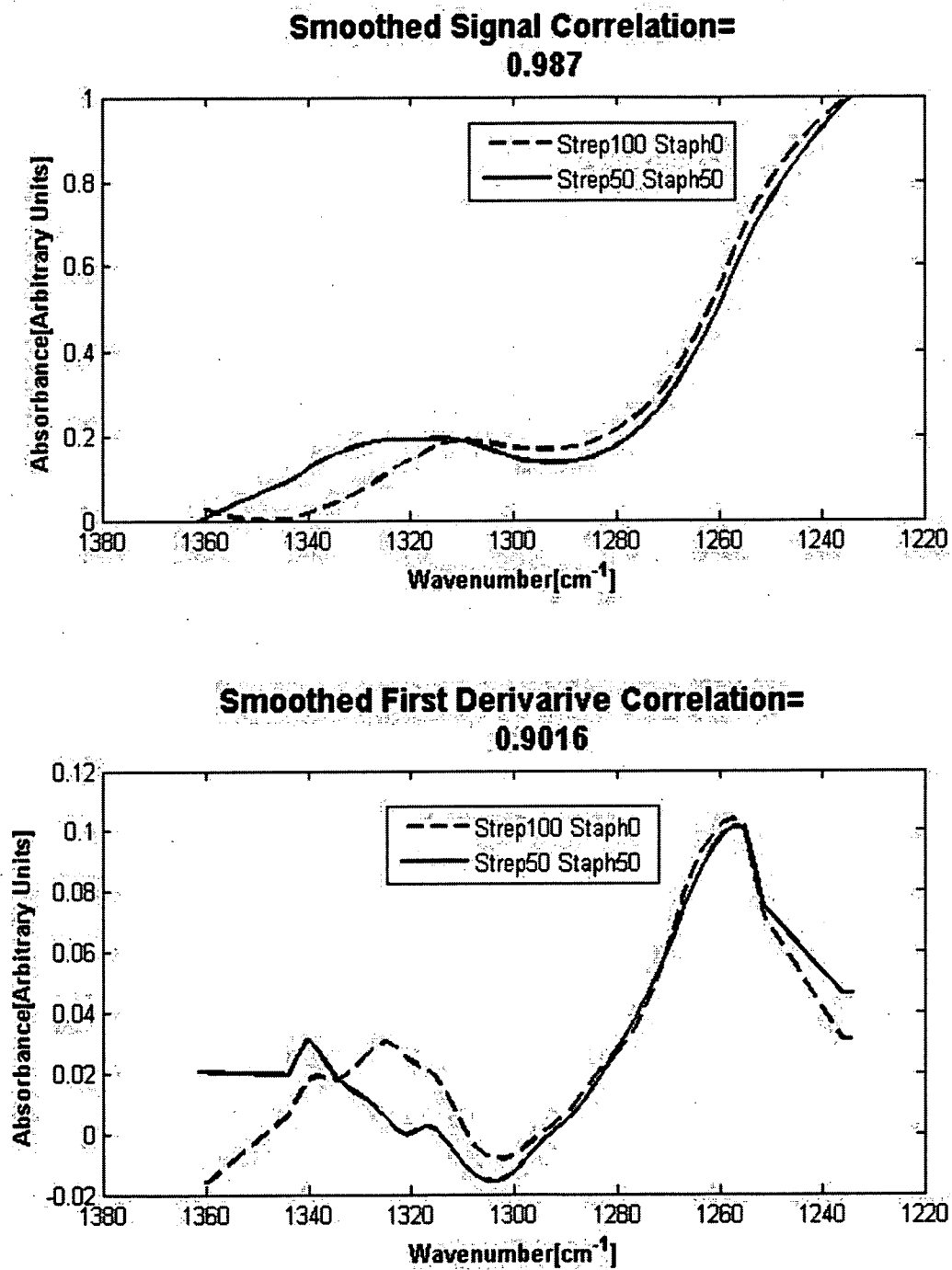
Fig. 15

Smoothed Signal Correlation= 0.98977
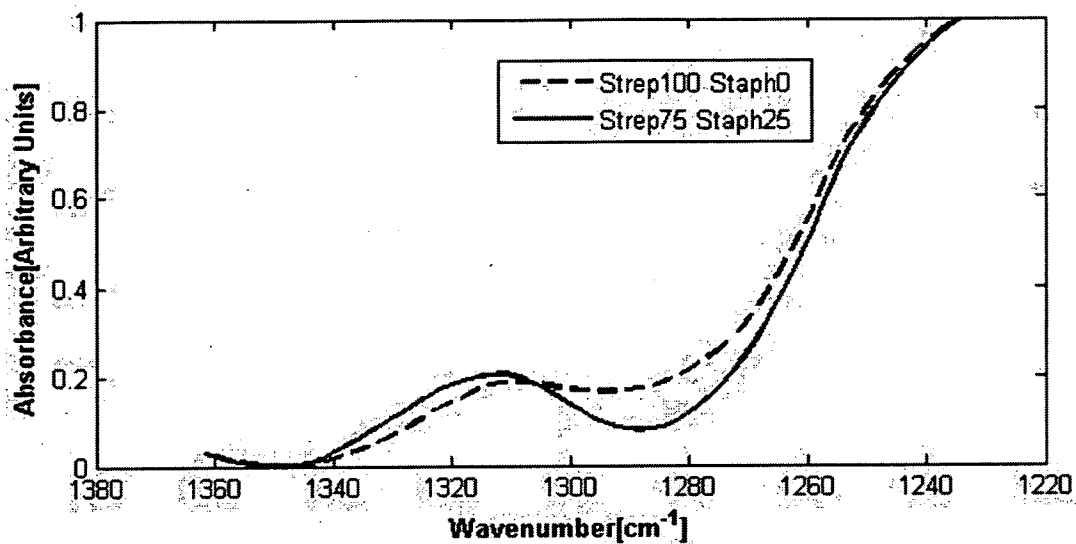
Smoothed First Derivarive Correlation= 0.978
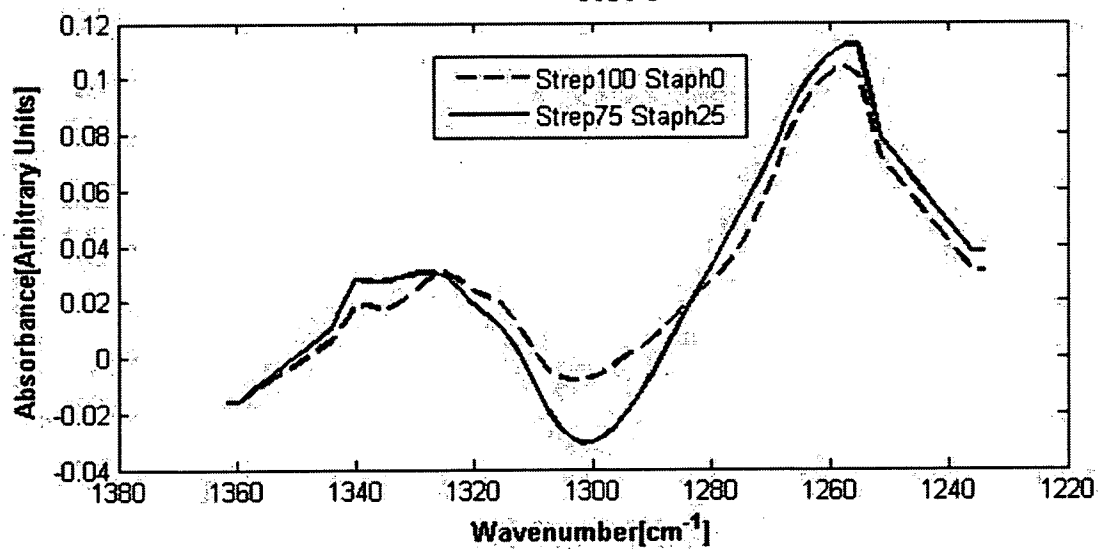
Fig. 16
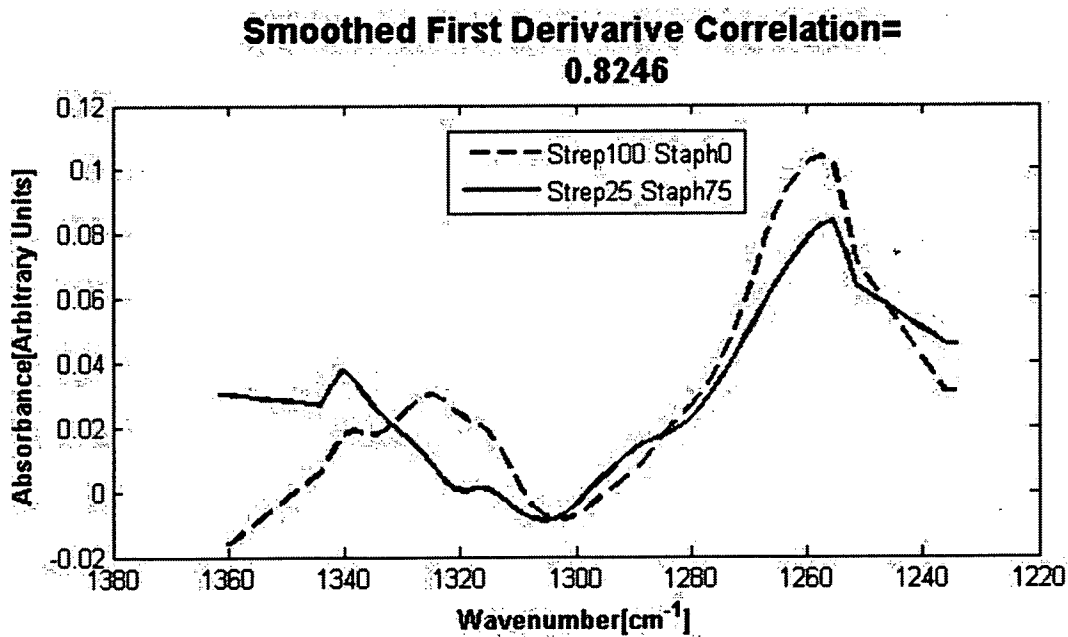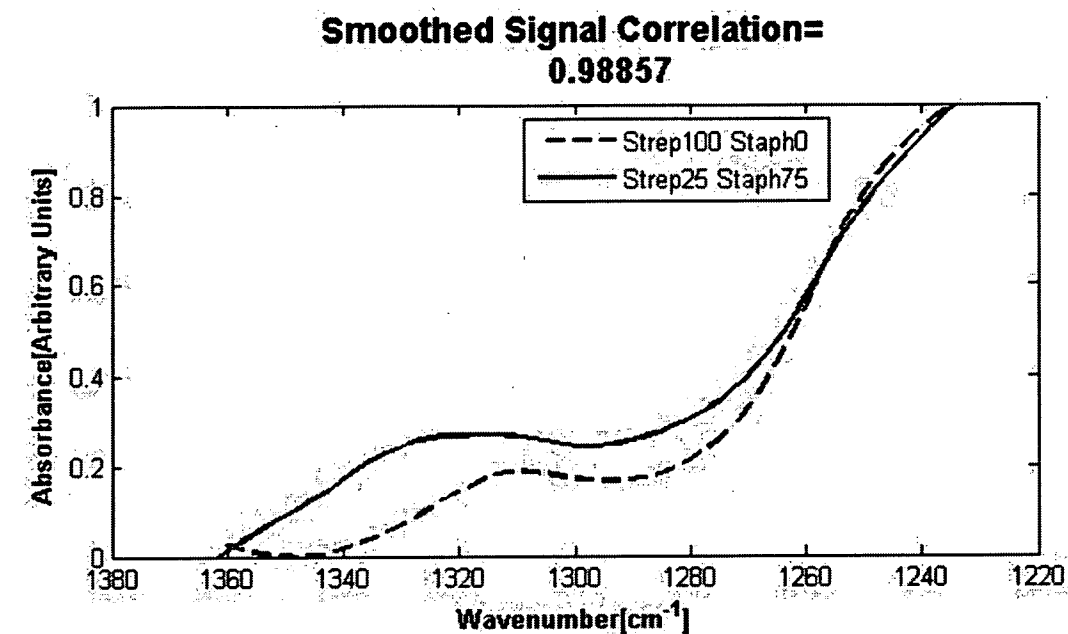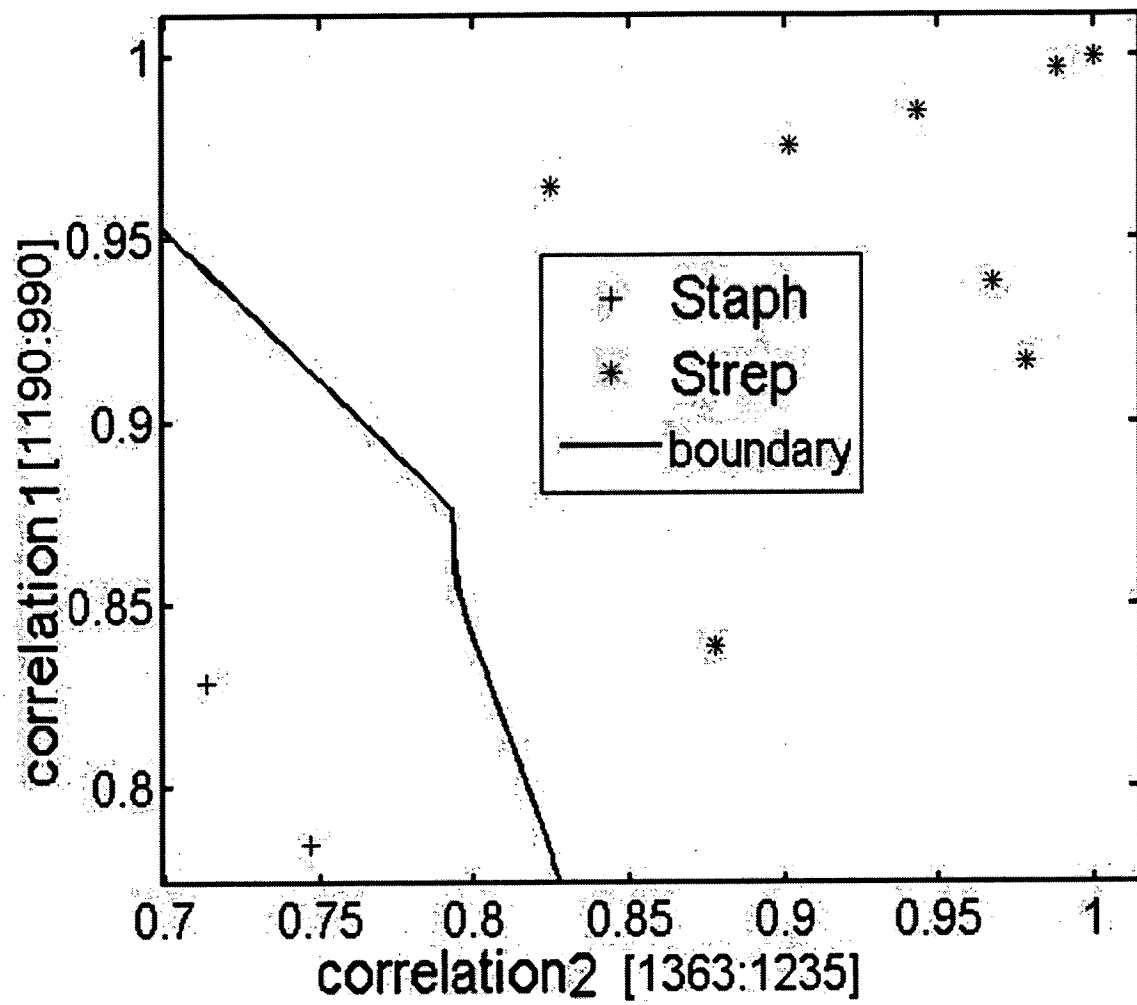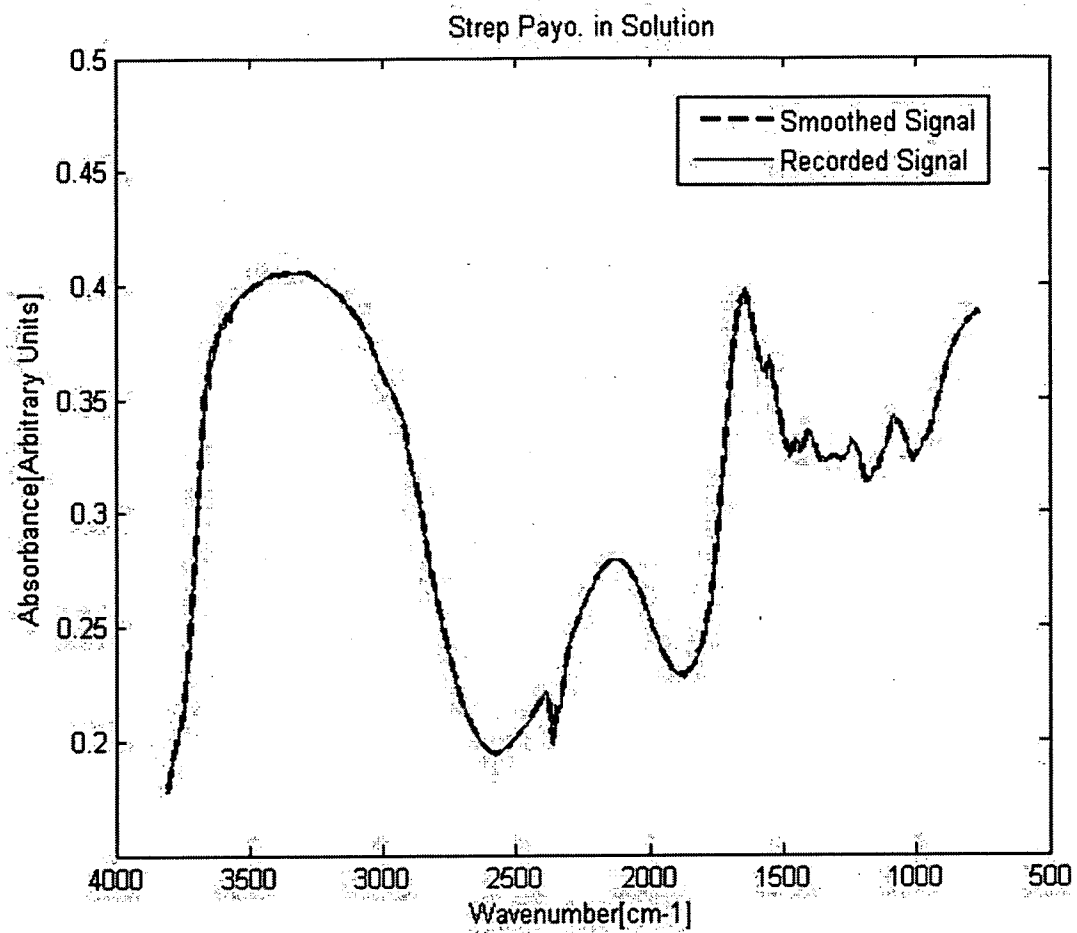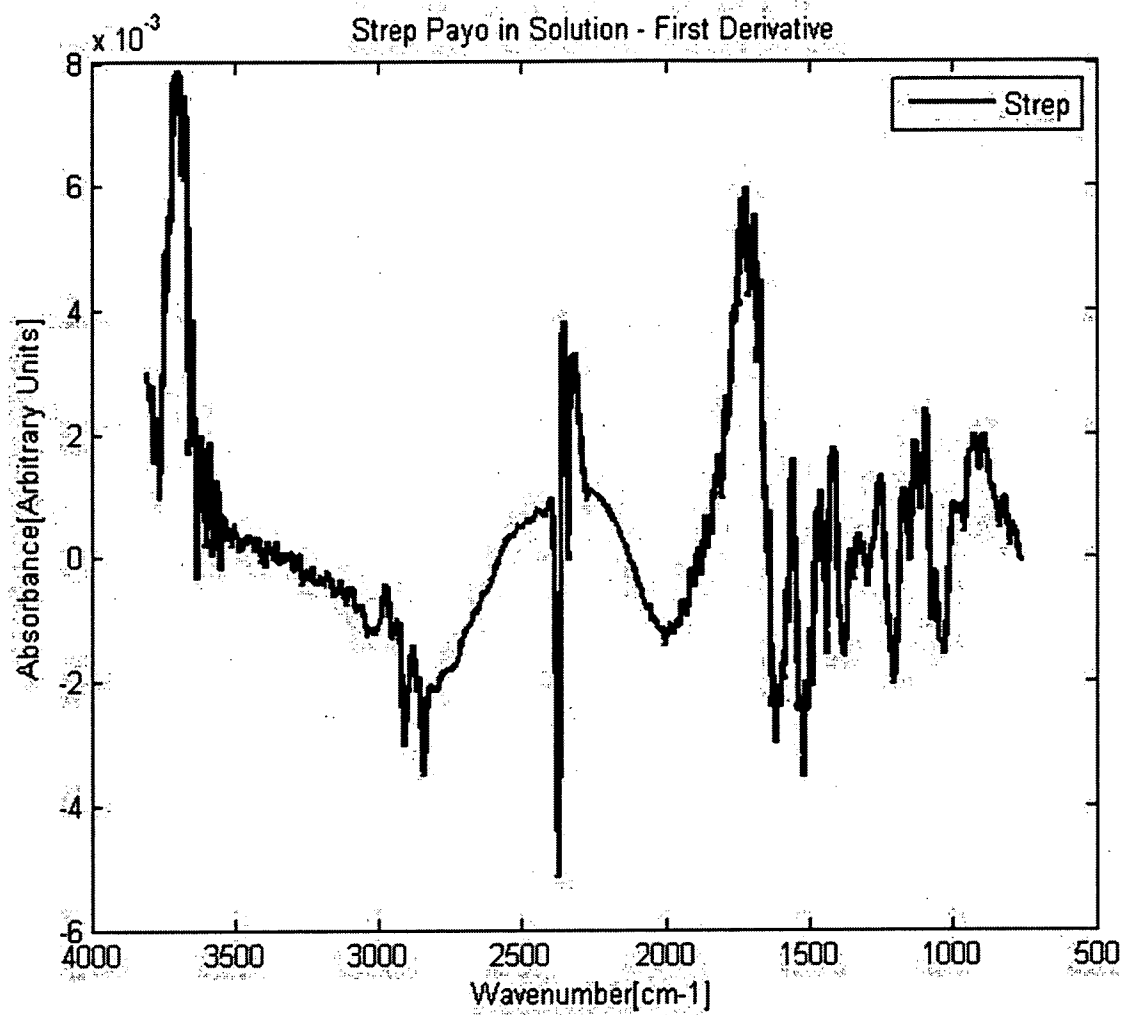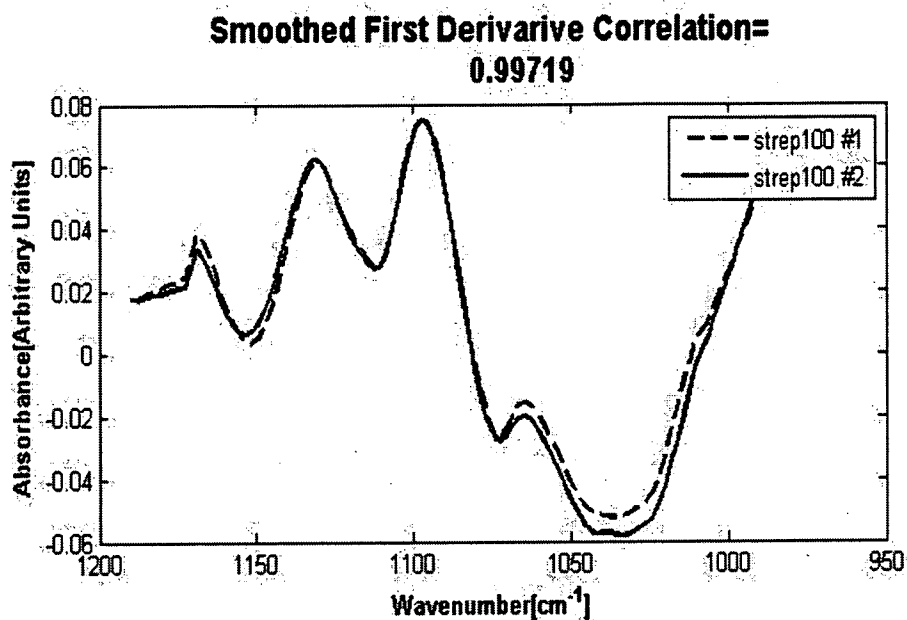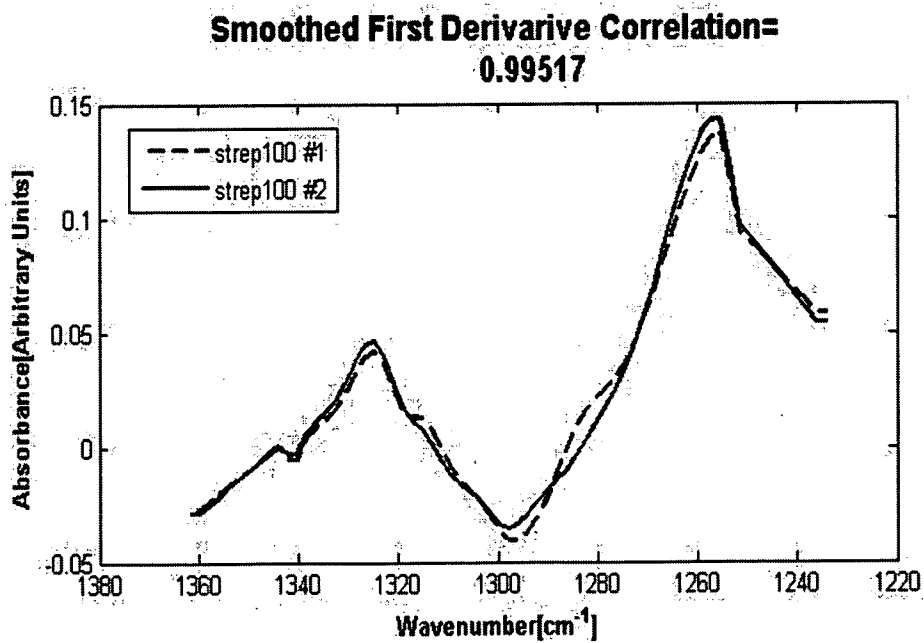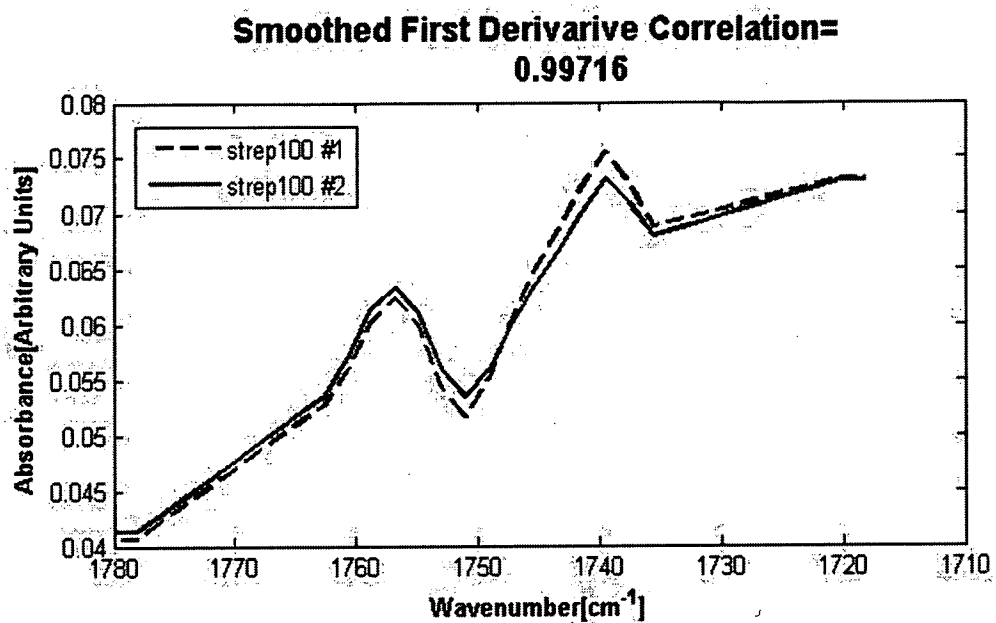
Smoothed Signal Correlation= 0.98857

Smoothed First Derivarive Correlation= 0.8246

Fig. 17

Fig. 18

Fig. 19

Fig. 20

Smoothed First Derivarive Correlation= 0.99719

Fig. 21

Smoothed First Derivarive Correlation= 0.99517

Fig. 22

Smoothed First Derivarive Correlation= 0.99716

Fig. 23

Smoothed First Derivarive Correlation= 0.89313

Fig. 24

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**Smoothed First Derivarive Correlation=
0.91064**

Fig. 25

**Smoothed First Derivarive Correlation=
-0.43181**

Fig. 26

Smoothed First Derivarive Correlation=
0.91633
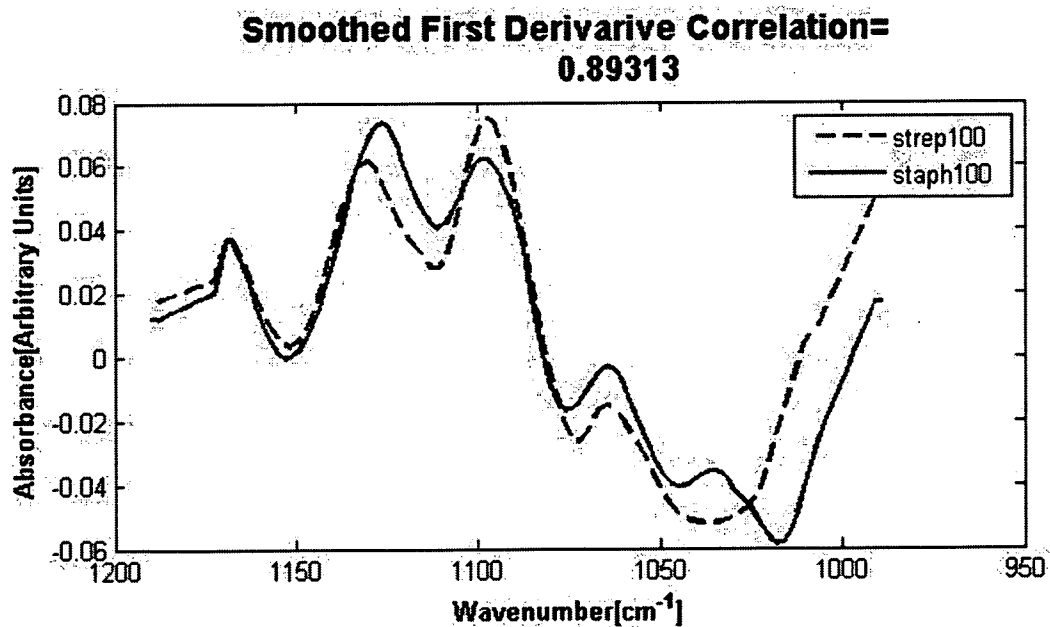
Fig. 27

Smoothed First Derivarive Correlation=
0.95679
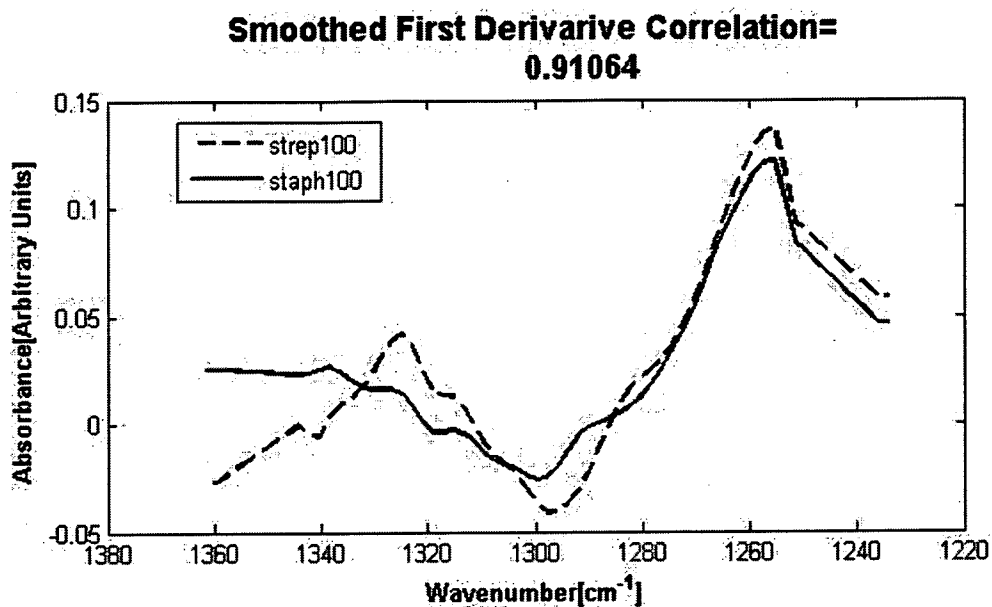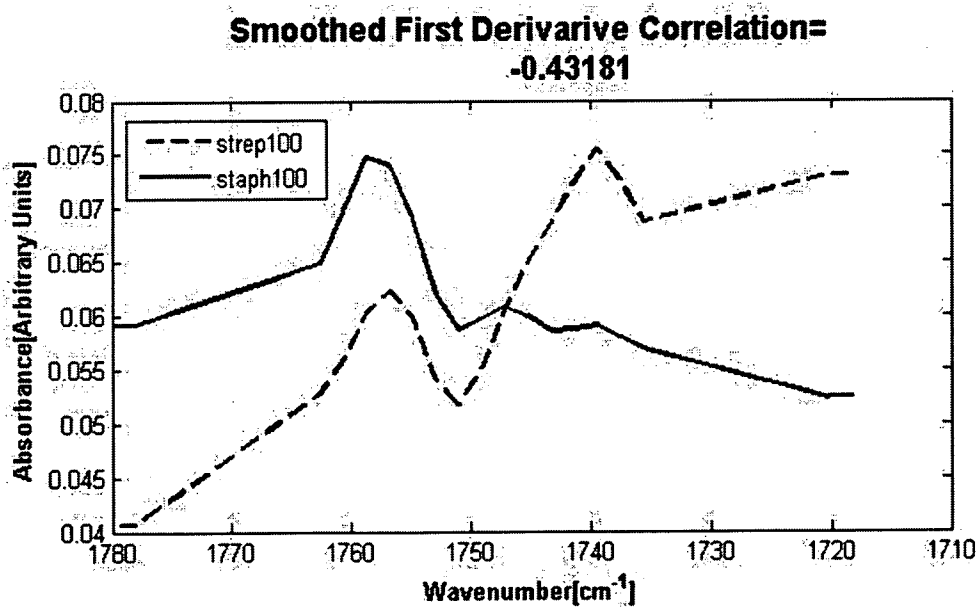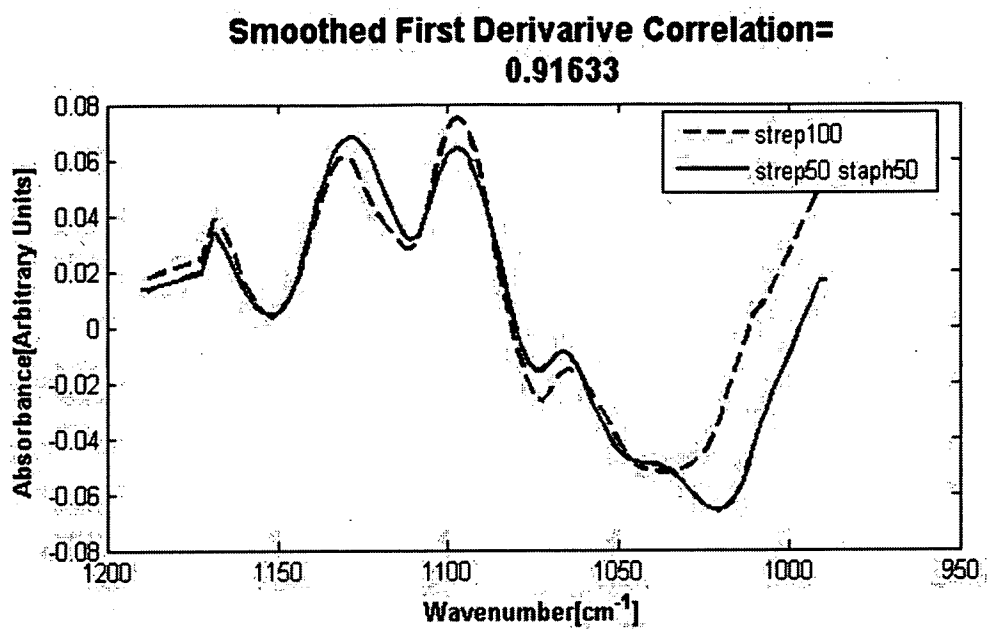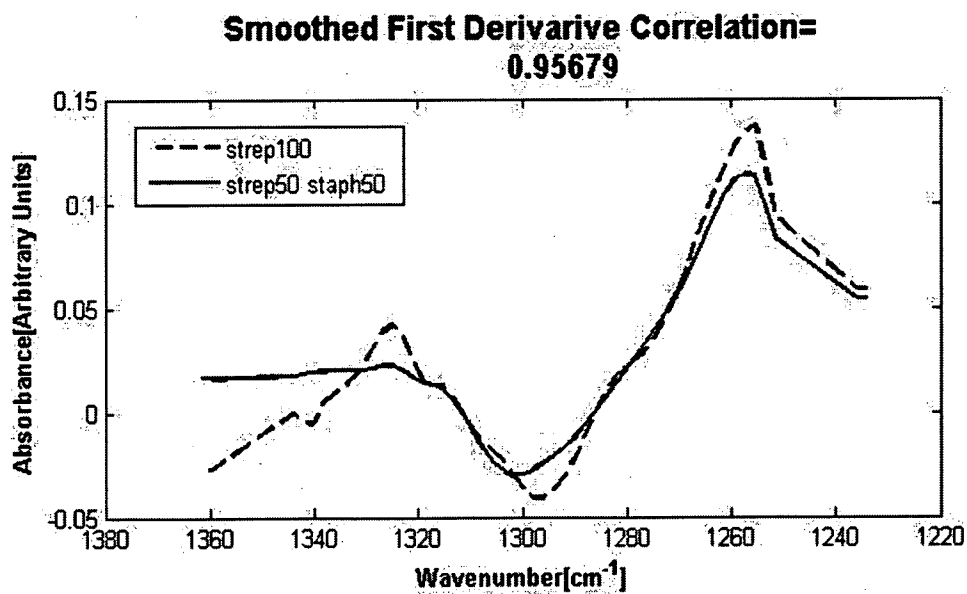
Fig. 28

Smoothed First Derivarive Correlation=
-0.1747

Fig. 29

Fig. 30

Fig. 31

**Smoothed First Derivarive Correlation=
0.86995**

Fig. 32

**Smoothed First Derivarive Correlation=
0.90358**

Fig. 33

**Smoothed First Derivarive Correlation=
0.93308**

Fig. 34

**Smoothed First Derivarive Correlation=
-0.19636**

Fig. 35

Fig. 36