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(54) **Blood component spectroscopy analysis system for removing abnormal data**

System zur Spektroskopieanalyse von Blutkomponenten und zum Beseitigen von abnormalen Daten

Systeme d'analyse spectroscopique des composants sanguins pour suppression des donnees anormales

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Description

[0001] The present invention rotates to a blood component analysis system, and more particularly, to a blood component spectroscopy analysis system for removing abnormal data generated due to internal and external vital factors of a human body.

[0002] The measurement of a vital signal using a non-invasive method is an important issue in the field of current medical engineering, and methods of measuring various physiological variables have been developed. In particular, various approaches for analyzing blood components without collecting blood have been published, and studies on analysis of blood components without collecting blood have been undertaken. For example, in a method of analyzing blood components using spectroscopy, without collecting blood, a patient does not suffers pain and is not exposed to an infection, and the result of analysis can be obtained in real time. Due to these advantages and the development of related technology, generalized techniques for conventional equipment for measuring an oxygen saturation have been applied to medical instruments for analyzing blood components such as hemoglobin and glucose. Such medical instruments use a method of analyzing a blood component by measuring a difference in the amount of lights of different wavelengths absorbed by a human body using light having a specific wavelength reacting with the blood component.

[0003] A photo-plethysmographic (PPG) signal generated when spectroscopy is used includes a pulsatile component and a non-pulsatile component. The PPG signal will be described in detail with reference to FIG. 1. In FIG. 1, a reference character Io denotes the amount of light radiated to a human body, a reference character It denotes the amount of light passing through the human body, a reference character Ia denotes the amount of light absorbed by the human body, a reference character To denotes a heart beat period, a reference character Ip denotes the maximum point of a pulsatile component, a reference character Iv denotes the minimum point of the pulsatile component, a reference character P1 denotes a variation of light intensity due to the pulsatile component, i.e., an alternating current (AC) component, and a reference character P2 denotes a variation of light intensity due to a non-pulsatile component, i.e., a direct current (DC) component. Components absorbing the light radiated to the human body are largely divided into non-pulsatile components, i.e., P2 components such as bones and vital tissue which do not change with time, and arterial pulsatile components, i.e., P1 components which change with time due to heart beats.

[0004] Accurately measuring the amount of light absorbed by the pulsatile components changing with time is essential to a method of analyzing a blood component using a ratiometric. However, the amplitude and the base line of the PPG signal frequently change according to an internal vital factor, such as breathing, blood pressure, pulse rate, body temperature, a state of blood vessels, or an autonomic nervous system, and an external vital factor such as a spontaneous or non-spontaneous motion. In quantitative terms, as compared to the amount of light absorbed by a non-pulsatile component, the amplitude of a pulsatile component changes within a range of 2 through 5%, and the base line of the PPG signal changes within a range of 3 through 5%. These changes in the amplitude of the pulsatile component and the base line of the PPG signal due to an internal vital factor causes abnormal data. As a result, an error occurs in the analysis of a blood component using spectroscopy.

[0005] U.S Patent Nos. 5,025,791, 5,517,988, 5,645,060, and 6,393,311 disclose conventional solutions for abnormal data occurring in the PPG signal. In U.S. Patent No. 5,025,791, a motion sensor and an accelerometer are attached to a body portion at which a probe is set, a signal corresponding to a detected a motion exceeding a predetermined limit is transmitted to a microprocessor controlling a system, and data measured during the detection of the motion is excluded from analysis for measuring an oxygen saturation. In this technique, since the motion sensor and the accelerometer are used in addition with an optical unit, the structure of the system is complicated, and the measuring cost increases.

[0006] In U.S. Patent No. 5,517,988, an event indicating that data is caused by a non-physiological factor is generated based on a predetermined criterion, such as a predetermined change in the amplitude of an AC component or a predetermined slope of a DC component, with respect to a PPG signal so that erroneous analysis due to abnormal data can be prevented. However, even when the AC and DC components of the PPG signal are stable, a variable such as a ratio of ratios, which is used in a regressive equation and measured from a pulsatile component during a unit measurement time, changes a lot within a short time due to an internal vital factor.

[0007] In U.S. Patent No. 5,645,060, a ratio of ratios in a Beer-Lambert's equation including motion and noise terms is used in a ratiometric so as to remove the influence of noise. This technique is effective under the assumption that the motion/noise in each wavelength signal is proportional and that a pulsatile component is not affected by motion. However, the pulsatile component greatly changes according to breathing and influences a PPG signal used to calculate the concentration of a blood component, and therefore, the result of the calculation is inaccurate.

[0008] In U.S. Patent No. 6,393,311, a Fourier transform is performed on a single data segment to find a representative frequency, a bandpass filter for extracting only a signal corresponding to the representative frequency is designed, and a signal having removed therefrom a motion-induced noise is extracted. In this technique, the number of calculations for the Fourier transform and the number of taps of a filter for narrow band filtering increase, and therefore, a great amount of data needs to be processed. As a result, it is difficult to continuously implement signal processing in real time.

[0009] As described above, the conventional techniques are restricted to a method of removing abnormal data gen-

erated due to external vital factors, such as motion-induced noise and an unstable contact of a probe, in a system for measuring an oxygen saturation. Moreover, in the conventional techniques, a physiological signal such as an oxygen saturation signal is measured after a predetermined time has passed until a patient becomes physiologically stable, and therefore, a lot of measuring time is required.

[0010] According to an aspect of the present invention, there is provided a blood component analysis system using spectroscopy, comprising: a light emitter, which comprises at least two light sources emitting light of a wavelength reacting to a particular blood component and radiates light of particular wavelengths on a subject according to predetermined timing; a light receiver, which receives light discharged from the subject and converts the received light into an electrical signal; and a signal processor, which extracts a photo-plethysmographic (PPG) signal corresponding to the particular wavelengths reacting to the particular blood component from the electrical signal received from the light receiver, calculates an average of "*n*" parameters with respect to *"n*" pulses included in the PPG signal corresponding to the wavelengths, which is collected for a predetermined unit period of time, and compares a ratio of the number of parameters whose deviation from the average is greater than a predetermined standard deviation to the "*n*" parameters with a predetermined removal reference value so as to determine whether the "*n*" pulse data is valid, where n is a positive integer.

[0011] Preferably, the signal processor comprises a First In First Out (FIFO) data buffer storing the "*n*" pulse data, and when the "*n*" pulse data is determined as being invalid, divides the "*n*" pulse data into predetermined unit groups, replaces a first predetermined unit group composed of firstly input data with the same amount of new data as the first predetermined unit group, and determines whether new "*n*" pulse data is valid.

[0012] The above and other features and advantages of the present invention will become more apparent by describing in detail preferred embodiments thereof with reference to the attached drawings in which:

FIG. 1 is a graph illustrating a typical photo-plethysmographic (PPG) signal;
FIG. 2 is a block diagram of a blood component spectroscopy analysis system according to an embodiment of the present invention;
FIG. 3 is a flowchart of a method of removing abnormal data; and
FIG. 4 is an example of a graph showing light intensities of a first wavelength and a second wavelength, which define parameters used in each stage of the method shown in FIG. 3.

[0013] Hereinafter, a blood component spectroscopy analysis system according to preferred embodiments of the present invention will be described in detail with reference to the attached drawings.

[0014] FIG. 2 is a block diagram of a blood component spectroscopy analysis system according to an embodiment of the present invention. The blood component spectroscopy analysis system includes a light emitter 21, a subject 22, a light receiver 23, an amplifying and filtering unit 24, a signal processor 25, a storage unit 26, and a display unit 27.

[0015] Referring to FIG. 2, the light emitter 21 includes at least two light sources, for example, light emitting diodes, each of which emits light of a wavelength reacting to a particular blood component. Each light source radiates light of the particular wavelength to the subject 22 according to a timing controlled by the signal processor 25.

[0016] The light receiver 23 receives light transmitted, scattered, or reflected from the subject 22 positioned between the light emitter 21 and the light receiver 23, converts the received light into an electrical signal, and provides the electrical signal to the amplifying and filtering unit 24. The amplifying and filtering unit 24 amplifies the electrical signal to a predetermined level and then filters the amplified electrical signal to remove a noise component from the electrical signal.

[0017] The signal processor 25 extracts a photo-plethysmographic (PPG) signal reacting to a particular blood component from the electrical signal provided from the amplifying and filtering unit 24, converts the PPG signal into digital data, performs signal analysis and processing on the digital data in order to remove abnormal data therefrom, and provides a signal resulting from the signal processing to the storage unit 26 and the display unit 27. The signal processor 25 includes a computer-readable recording medium in which a program for executing a method of removing abnormal data is recorded. Preferably, the signal processor 25 includes a data buffer having a First-In-First-Out (FIFO) structure for storing "*n*" data, where n is a positive integer. Here, when "*n*" data are determined as being removed as the result of the signal analysis and processing, the "*n*" data can be divided into a predetermined number of groups, for example, five groups, and only firstly input *n*/5 data can be updated and applied to signal analysis for removing abnormal data.

[0018] The storage unit 26 stores digital data that is determined as being valid as the result of the processing of the signal processor 25, and the display unit 27 displays the result of the processing of the signal processor 25 to inform a user of it.

[0019] FIG. 3 is a flowchart of a method of removing abnormal data. The method includes collecting data (31), calculating an average of parameters between wavelengths (32 through 35), and determining whether the parameters are valid data using the average of the parameters, a standard deviation, and a predetermined removal reference value (36 through 38). The method shown in FIG. 3 will be described with reference to FIG. 4.

[0020] Referring to FIG. 3, "*n*" pulse data of a PPG signal provided from the amplifying and filtering unit 24 are collected

according to their wavelengths for a predetermined unit period of time, for example, from T1 to T2, in step 31. The "*n*" pulse data may usually have a heartbeat period and may be generated from a modulated signal having a large amplitude due to a change in a blood flow caused by an external pressure.

[0021] In step 32, the maximum point I_p and the minimum point I_v of light intensity are obtained for each pulse included in the predetermined unit period of time from the pulse data groups collected according to their wavelengths. In graphs G1 and G2 on the light intensity with respect to a first wavelength and a second wavelength, when "*n*" pulses appear for the time from T1 to T2, the maximum points I_{p11} through I_{p1n} and the minimum points I_{v11} through I_{v1n} of the individual "*n*" pulses on the graph G1 for the first wavelength are obtained, and the maximum points I_{p21} through Ip_{2n} and the minimum points I_{v21} through I_{v2n} of the individual "*n*" pulses on the graph G2 for the second wavelength are obtained.

[0022] In step 33, a logarithmic ratio $\ln(I_p/I_v)$ of the maximum point I_p and the minimum point I_v of each pulse is calculated for each wavelength. In other words, in the graph G1 for the first wavelength, logarithmic ratios $\ln(I_{p11}/I_{v11})$ through $\ln(I_{p1n}/I_{v1n})$ are calculated for first through *n*-th pulses. In the graph G2 for the second wavelength, logarithmic ratios $\ln(I_{p21}/I_{v21})$ through $\ln(I_{p2n}/I_{v2n})$ are calculated for first through n-th pulses.

[0023] In step 34, the logarithmic ratio $\ln(I_p/I_v)$ obtained for each wavelength is used to calculate a parameter, for example, a ratio of ratios (ROR) between the wavelengths, that is, a ratio R_{12} of the logarithmic ratio $\ln(I_{p1k}/I_{v1k})$ of each pulse in the first wavelength (where *k* is 1 through *n*) to the logarithmic ratio $\ln(I_{p2k}/I_{v2k})$ of each pulse in the second wavelength (where *k* is 1 through *n*). The ROR R_{12} between the first and second wavelengths can be expressed by Formula (1).

$$R_{12} = \frac{\ln(I_{p1k} / I_{v1k})}{\ln(I_{p2k} / I_{v2k})} \qquad \ldots(1)$$

[0024] In step 35, an average M_{12} of RORs R_{12} between the first and second wavelengths is calculated according to Formula (2).

$$M_{12} = \frac{\sum_{k=1}^{n} \frac{\ln(I_{p1k} / I_{v1k})}{\ln(I_{p2k} / I_{v2k})}}{n} \qquad \ldots(2)$$

[0025] In step 36, among the "*n*" parameters calculated in step 34, the number "*m*" of parameters, whose deviation from the average M_{12} calculated in step 35 is greater than a standard deviation, is counted. Here, the standard deviation may be set to an optimal value through experiments or simulations. For example, the standard deviation can be set to be different depending on the type of two wavelengths used to obtain the ROR between wavelengths. When the two wavelengths correspond to isobestic point, the standard deviation is set to ±3.5% through ±4.5% and is preferably set to ±4%. When the two wavelengths are in the red or infrared range, the standard deviation is set to ±1.5% through ±2.5% and is preferably set to ±2%.

[0026] In step 37, a ratio of the number "*n*" of all parameters, which is obtained in step 34, to the number *"m"* of parameters whose deviation from the average is greater than the standard deviation, which is obtained in step 36, i.e., *m*/*n,* is compared with a predetermined removal reference value. Here, the removal reference value may be set to an optimal value through experiments or simulations to ensure the accuracy of analysis. As the result of the comparison in step 37, if the ratio *m*/*n* is greater than or equal to the predetermined removal reference value, the currently collected "*n*" data are discarded and excluded from the analysis, and then the method goes back to step 31. Here, in step 31, all of the *"n"* data may be updated with new *"n"* data. Alternatively, the *"n"* data may be divided into predetermined unit groups, a first predetermined unit group composed of firstly input data is replaced with the same amount of new data as the first predetermined unit group.

[0027] If the ratio *m*/*n* is less than the predetermined removal reference value, the *"n"* RORs R_{12} between the first and second wavelengths, which are obtained in step 34, are determined as valid data and stored in the storage unit 26. The average of the valid data stored in the storage unit 26, i.e., the average of the RORs R_{12} between the first and second wavelengths, can be used in, for example, a regressive equation obtained through multivariate linear regressive analysis so as to calculate the concentration of the particular blood component.

[0028] For example, when a regressive equation for calculating the amount (Hb) of hemoglobin is expressed by Formula (3), examples of the average of the RORs between the first and second wavelengths determined as the valid

data in steps 31 through 38 are shown in Table 1.

$$Hb=50.3-21.5\times R_{13}-1.30\times R_{15}-9.00\times R_{45} \quad \ldots(3)$$

Table 1

Pulse index	R_{13}	R_{15}	R_{45}
1	1.11935	1.56065	1.37540
2	1.13040	1.51785	1.28079
3	1.11839	1.55493	1.32513
4	1.15221	1.51489	1.29946
5	1.16072	1.57932	1.33420
6	1.15716	1.49149	*1.25697*
7	1.19721	1.52200	*1.26801*
8	*1.09604*	1.45250	1.30688
9	*1.08103*	1.56253	1.32151
10	1.11863	1.55737	1.32719
11	1.11456	1.50028	1.31471
12	1.17718	1.59165	1.36132
13	1.13893	1.59417	*1.40585*
14	1.11350	1.53898	1.36942
15	1.11424	1.52678	1.30636
16	1.18262	1.60972	1.34542
17	1.18803	*1.66496*	1.45322
18	1.17468	1.59366	1.36323
19	1.17791	1.63599	1.38658
20	1.12564	1.63940	1.38449
21	1.15660	1.59757	1.38367
22	1.12855	1.58233	1.35407
23	1.11076	1.62814	1.42659
24	1.19795	1.59025	1.35692
25	1.16404	1.59834	1.37347
26	1.12490	1.55290	1.28225
27	1.12226	1.50934	1.34515
28	1.16658	1.55562	1.32509
29	1.13476	1.58237	1.35572
30	1.10259	1.62487	1.39802
Average	1.14158	1.56769	1.34624

[0029] Here, the number "*n*" of pulses included in a the predetermined unit period of time is 30, R_{13} denotes an ROR between a wavelength of 569 nm and a wavelength of 805 nm, R_{15} denotes an ROR between a wavelength of 569 nm

and a wavelength of 970 nm, and R_{45} denotes an ROR between a wavelength of 940 nm and a wavelength of 970 nm. The concentration of hemoglobin can be estimated by applying the average of RORs between two wavelengths to R_{13}, R_{15}, or R_{45}. the RORs being determined as valid data according to the present invention.

[0030] The method can be realized as a code which is recorded on a computer-readable recording medium and can be read by a computer. For example, a method of removing abnormal data can be implemented by recording on a computer-readable recording medium a first program for calculating "*n*" parameters with respect to "*n*" pulses included in a PPG signal corresponding to the first and second wavelengths, the PPG signal being collected for a predetermined unit period of time; and a second program for calculating an average of the "*n*" parameters and comparing a ratio of the number of parameters whose deviation from the average is greater than a predetermined standard deviation to the *"n"* parameters with a predetermined removal reference value so as to determine whether the "n" pulse data is valid. In the meantime, the computer-readable recording medium may be any type of medium on which data which can be read by a computer system can be recorded, for example, a ROM, a RAM, a CD-ROM, a magnetic tape, a floppy disc, or an optical data storage device. The method can also be realized as carrier waves (for example, transmitted through Internet). Alternatively, computer-readable recording media are distributed among computer systems connected through a network so that the method can be realized as a code which is stored on the recording media and can be read and executed in the computers. Functional programs, codes, and code segments for implementing the method can be easily inferred by programmers.

<Experiment>

[0031] In order to obtain quantitative results of a method of removing abnormal data, data was continuously collected for 10 minutes from 30 subjects lying on their back and having a hemoglobin concentration of 10.5-16.5 g/dl. The population composed of 30 subjects was divided at a ratio of 2 to 1, and a regressive equation was obtained through multivariate linear regressive analysis having 20 subjects as a calibration model. The regressive equation was applied to the data collected from the rest 10 subjects so as to calculate the result for a prediction model. Hemoglobin values of all the subjects to be used as references were measured using HemoCue AB (Sweden), an apparatus for invasively measuring hemoglobin using a cuvette.

[0032] In order to determine whether parameters, i.e., RORs between wavelengths, were abnormal data, a standard deviation for a ratio R_{13} of a logarithmic ratio with respect to a wavelength of 569 nm to a logarithmic ratio with respect to a wavelength of 805 nm and a standard deviation for a ratio R_{45} of a logarithmic ratio with respect to a wavelength of 940 nm to a logarithmic ratio with respect to a wavelength of 970 nm were increased by 2% and 1%, respectively. A removal reference value was set to 20%, and a unit period of time for the determination was set to 1 minute. As the standard deviation was small, a correlation coefficient was high, but the number N of subjects satisfying the standard deviation decreased, not allowing much data to be analyzed. The correlation coefficient was in inverse proportion to the number N of subjects satisfying the standard deviation. Accordingly, the standard deviations for R_{13} and R_{45} were optimally set to 4% and 2%, respectively. Table 2 shows correlation coefficients and the number N of subjects to be analyzed in the calibration model and the prediction model with respect to R_{13} and R_{45}.

Table 2

Standard deviation		Calibration model			Prediction model		
R_{13} (%)	R_{45} (%)	Correlation coefficient (R)	Standard deviation (g/dl)	Number of subjects (N)	Correlation coefficient (R)	Standard deviation (g/dl)	Number of subjects (N)
2	1	0.71	1.2	15	0.65	1.4	6
4	2	0.71	1.3	20	0.61	1.7	10
6	3	0.59	1.5	20	0.39	2.05	10
8	4	0.53	1.82	20	0.3	2.34	10
The invention applied	present is not	0.51	1.9	20	0.3	2.4	10

[0033] Referring to Table 2, when a method of removing abnormal data using the optimal standard deviations and the predetermined removal reference value to determine whether the collected data would be used to non-invasively measure a hemoglobin concentration in blood was applied to the 30 subjects, a correlation coefficient of 0.71 was obtained with

respect to the calibration model, and a correlation coefficient of 0.61 was obtained with respect to the prediction model. As compared to the results of analysis performed without using a method where a correlation coefficient of 0.51 was obtained with respect to the calibration model and a correlation coefficient of 0.3 was obtained with respect to the prediction model, the method improved the results of analysis. Accordingly, it was proved that the system of the present invention is effective to minimize an influence due to a change in a pulsatile component, which is caused by an internal vital factor, such as breathing, blood pressure, pulse rate, body temperature, a state of blood vessels, or an autonomic nervous system, and an influence due to an external vital factor, such as motion-induced noise or an unstable contact of a probe, on a physiological signal.

[0034] As described above, according to the present invention, a blood component analysis system using spectroscopy calculates parameters of a regressive equation from a PPG signal generated from a subject, analyzes abnormal data of the parameters for a predetermined unit period of time, and excludes a data group including abnormal data whose proportion is equal to or greater than a predetermined removal reference value from the analysis, thereby minimizing an influence of a change in a pulsatile component due to an internal vital factor as well as an influence due to an external vital factor without separately adding hardware systems, such as a motion sensor and an accelerometer. As a result, the accuracy of the analysis can be increased without increasing the manufacturing cost of a blood component analysis system.

[0035] Moreover, time taken for preparing a patient in a stable status required for general test of a physiological signal is removed or minimized, so that entire time for analysis can be reduced. In addition, removal or non-removal of abnormal data can be automatically and objectively determined compared to conventional subjective analysis depending on a tester, so that the accuracy of analysis can be maintained constant.

Claims

1. A blood component analysis system using spectroscopy, comprising:

a light emitter (21) comprising at least two light sources emitting light of a wavelength reacting to a particular blood component and radiating light of particular wavelengths on a subject according to predetermined timing;
a light receiver (23) adapted to receive light discharged from the subject and to convert the received light into an electrical signal; and
a signal processor (25); **characterized by** the signal processor being adapted to extract a photo-plethysmographic (PPG) signal corresponding to the particular wavelengths reacting to the particular blood component from the electrical signal received from the light receiver to calculate an average of "*n*" parameters with respect to "*n*" pulses included in the PPG signal corresponding to the wavelengths, being collected for a predetermined unit period of time, and to compare a ratio m/n of the number m of parameters whose deviation from the average is greater than a predetermined standard deviation to the "*n*" parameters with a predetermined removal reference value so as to determine whether the "*n*" pulse data is valid, where *n* is a positive integer.

2. The blood component analysis system of claim 1, wherein the signal processor comprises a First In First Out (FIFO) data buffer storing the "*n*" pulse data, and when the "*n*" pulse data is determined as being invalid, divides the "*n*" pulse data into predetermined unit groups, replaces a first predetermined unit group composed of firstly input data with the same amount of new data as the first predetermined unit group, and determines whether new "*n*" pulse data is valid.

3. The blood component analysis system of claim 1 or 2, wherein the standard deviation is determined according to the first and second wavelengths.

4. The blood component analysis system of claim 3, wherein when the first and second wavelengths correspond to an isobestic point, the standard deviation is set to $\pm$3.5% through $\pm$4.5%.

5. The blood component analysis system of claim 3 wherein when the first and second wavelengths are in a red range or an infrared range, the standard deviation is set to $\pm$1.5% through $\pm$2.5%.

6. The blood component analysis system of any of claims 1 to 5, wherein the "*n*" pulse data are generated from a modulated signal influenced by a change in a blood flow caused by an external pressure.

Patentansprüche

1. Analysesystem für Blutkomponenten unter Verwendung von Spektroskopie umfassend:

einen Lichtemitter (21) umfassend mindestens zwei Lichtquellen, die Licht einer Wellenlänge emittieren, das mit einer speziellen Blutkomponente reagiert und Licht spezieller Wellenlängen nach einem bestimmten Zeitplan auf ein Prüfobjekt einstrahlt;
einen Lichtempfänger (23), geeignet zum Empfangen von Licht, das vom Prüfobjekt ausgegeben ist, und zum Konvertieren des empfangenen Lichts in ein elektrisches Signal; und
einen Signalprozessor (25);

dadurch gekennzeichnet, dass
der Signalprozessor geeignet ist, ein photo-plethysmographisches (PPG) Signal entsprechend der speziellen Wellenlängen, die mit der speziellen Blutkomponente reagieren, aus dem elektrischen Signal zu extrahieren, das vom Lichtempfänger empfangen ist, um einen Mittelwert von "n" Parametern bezüglich "n" Impulsen zu berechnen, die im PPG-Signal enthalten sind, entsprechend der Wellenlängen, die über eine bestimmte Zeiteinheit gesammelt wurden, und das Verhältnis m/n der Anzahl von m Parametern, deren Abweichung vom Mittelwert größer ist als eine bestimmte Standardabweichung, mit den "n" Parametern mit einem bestimmten Eliminierungsreferenzwert zu vergleichen, um zu bestimmen, ob die "n" Impulsdaten gültig sind, wo n eine positive ganze Zahl ist.

2. Analysesystem für Blutkomponenten nach Anspruch 1, worin der Signalprozessor einen FIFO-Datenpuffer (first in first out) umfasst, der die "n" Impulsdaten speichert, und wenn die "n" Impulsdaten als ungültig bestimmt werden, die "n" Impulsdaten in bestimmte Einheitengruppen teilt, eine erste bestimmte Einheitengruppe gebildet aus zuerst eingegebenen Daten durch die selben Menge an neuen Daten wie die erste bestimmte Einheitengruppe ersetzt und bestimmt, ob neue "n" Impulsdaten gültig sind.

3. Analysesystem für Blutkomponenten nach Anspruch 1 oder 2, worin die Standardabweichung entsprechend der ersten und zweiten Wellenlänge bestimmt wird.

4. Analysesystem für Blutkomponenten nach Anspruch 3, worin, wenn die erste und zweite Wellenlänge einem isobestischen Punkt entsprechen, die Standardabweichung auf $\pm$ 3,5 % bis $\pm$ 4,5 % gesetzt ist.

5. Analysesystem für Blutkomponenten nach Anspruch 3, worin, wenn die erste und zweite Wellenlänge in einem roten Bereich oder einem infraroten Bereich sind, die Standardabweichung auf $\pm$ 1,5 % bis $\pm$ 2,5 % gesetzt ist.

6. Analysesystem für Blutkomponenten nach einem der Ansprüche 1 bis 5, worin die "n" Impulsdaten aus einem modulierten Signal erzeugt werden, das von einer Veränderung in einem Blutstrom beeinflusst ist, die durch einen externen Druck ausgelöst ist.

Revendications

1. Système d'analyse de composants sanguins utilisant la spectroscopie, comprenant :

■ un émetteur de lumière (21) comprenant au moins deux sources lumineuses émettant de la lumière d'une longueur d'onde qui réagit à un composant sanguin particulier et rayonnant de la lumière ayant des longueurs d'onde particulières sur un sujet selon une synchronisation prédéterminée ;
■ un récepteur de lumière (23) adapté pour recevoir de la lumière émise à partir du sujet et pour convertir la lumière reçue en un signal électrique ; et
■ un processeur de signal (25) ;

caractérisé en ce que
le processeur de signal est adapté pour extraire un signal photopléthysmographique (PPG) correspondant aux longueurs d'onde particulières réagissant au composant sanguin particulier à partir du signal électrique venant du récepteur de lumière afin de calculer une moyenne de "*n*" paramètres relatifs à "*n*" impulsions comprises dans le signal PPG correspondant aux longueurs d'onde qui sont collectées pendant une durée unitaire prédéterminée et pour comparer le ratio *m*/*n* du nombre de paramètres *m* dont l'écart par rapport à la moyenne est supérieur à un écart type prédéterminé par rapport aux "*n*" paramètres ayant une valeur de référence de suppression prédéterminée

de façon à déterminer si les "*n*" données impulsionnelles sont valides, n étant un nombre entier positif.

2. Système d'analyse de composants sanguins selon la revendication 1, dans lequel le processeur de signal comprend un tampon de données premier entré - premier sorti ("FIFO") stockant les "*n*" données impulsionnelles et, lorsque les "*n*" données impulsionnelles sont déterminées comme étant invalides, divise les "*n*" données impulsionnelles en groupes unitaires prédéterminés, remplace un premier groupe unitaire prédéterminé composé des données entrées en premier par la même quantité de nouvelles données que le premier groupe unitaire prédéterminé et détermine si les "*n*" nouvelles données impulsionnelles sont valides ou non.

3. Système d'analyse de composants sanguins selon la revendication 1 ou la revendication 2, dans lequel l'écart type est déterminé en fonction des première et deuxième longueurs d'onde.

4. Système d'analyse de composants sanguins selon la revendication 3, dans lequel, lorsque les première et deuxième longueurs d'onde correspondent à un point isobestique, l'écart type est fixé à une valeur dans la plage de ± 3,5% à ± 4,5%.

5. Système d'analyse de composants sanguins selon la revendication 3, dans lequel, lorsque les première et deuxième longueurs d'onde se situent dans le domaine du rouge ou dans le domaine de l'infrarouge, l'écart type est fixé à une valeur dans la plage de ± 1,5% à ± 2,5%.

6. Système d'analyse de composants sanguins selon l'une quelconque des revendications 1 à 5, dans lequel les "*n*" données impulsionnelles sont générées à partir d'un signal modulé qui est influencé par une variation du débit sanguin provoquée par une pression externe.

FIG. 1

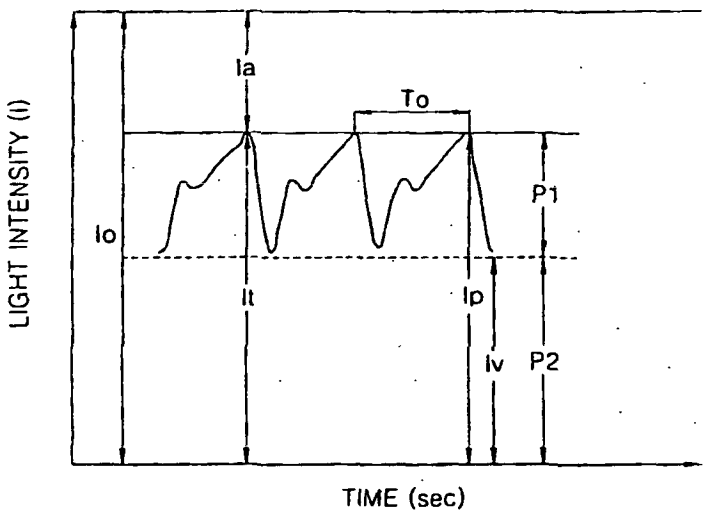


FIG. 2

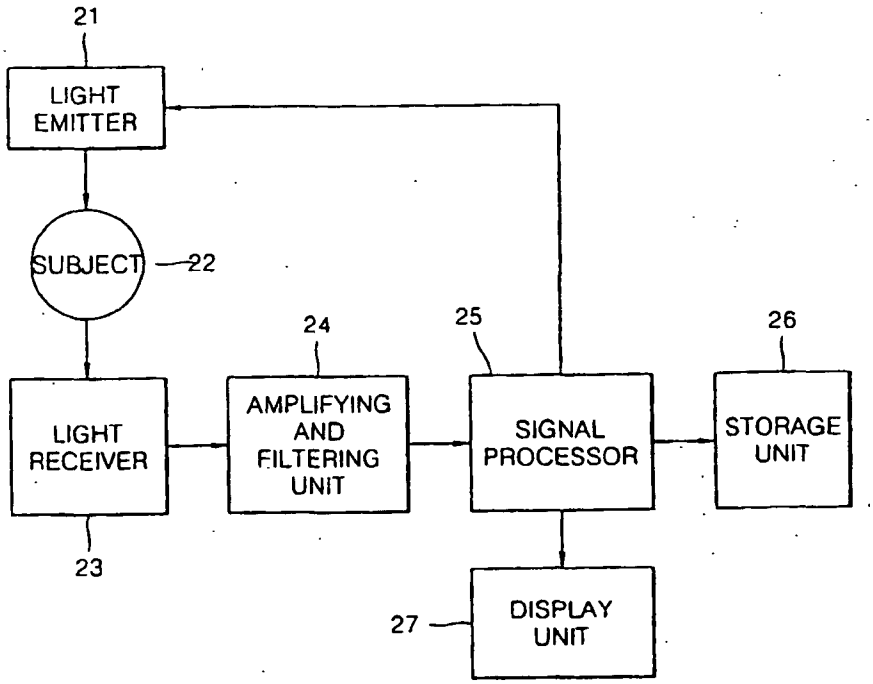

21
LIGHT EMITTER
SUBJECT
22
24
25
26
LIGHT RECEIVER
AMPLIFYING AND FILTERING UNIT
SIGNAL PROCESSOR
STORAGE UNIT
23
27
DISPLAY UNIT

FIG. 3

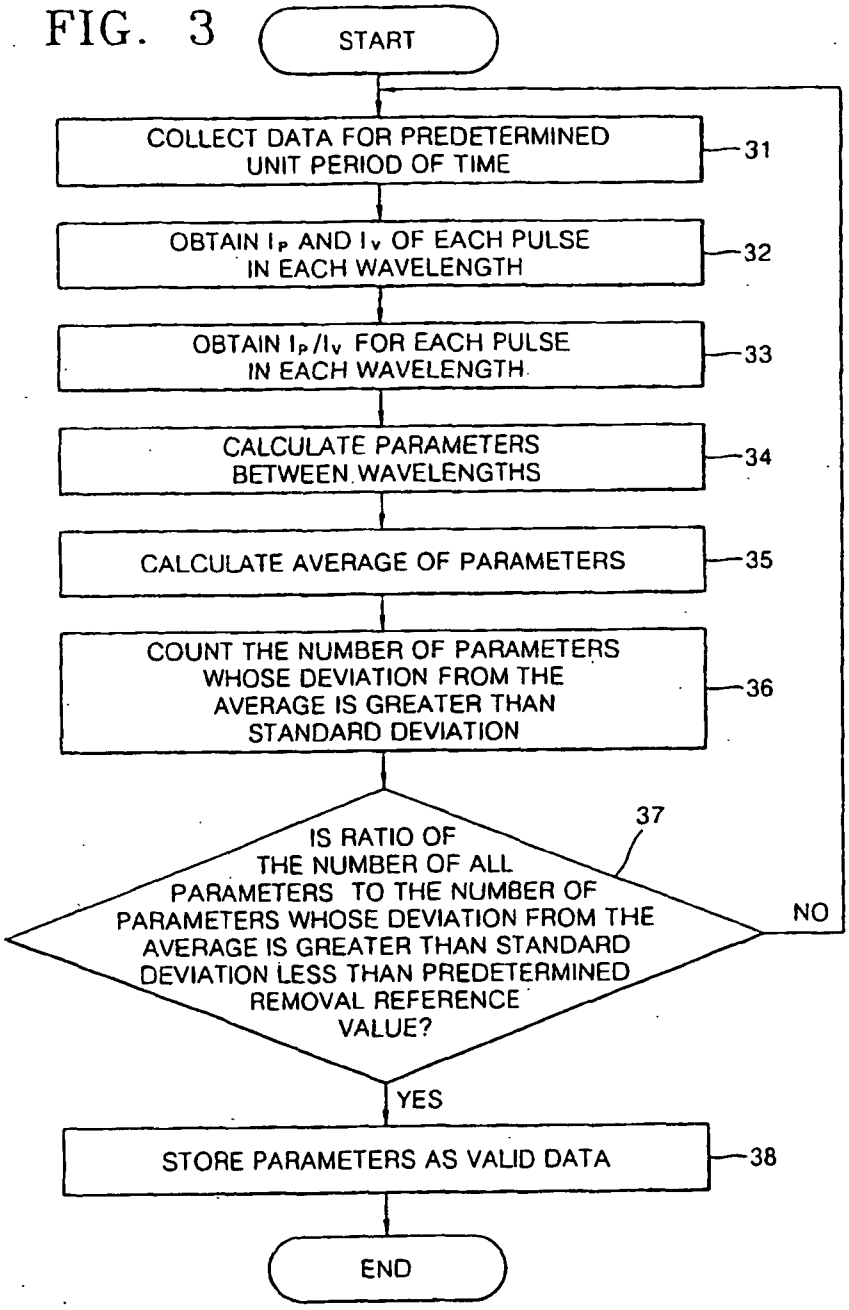
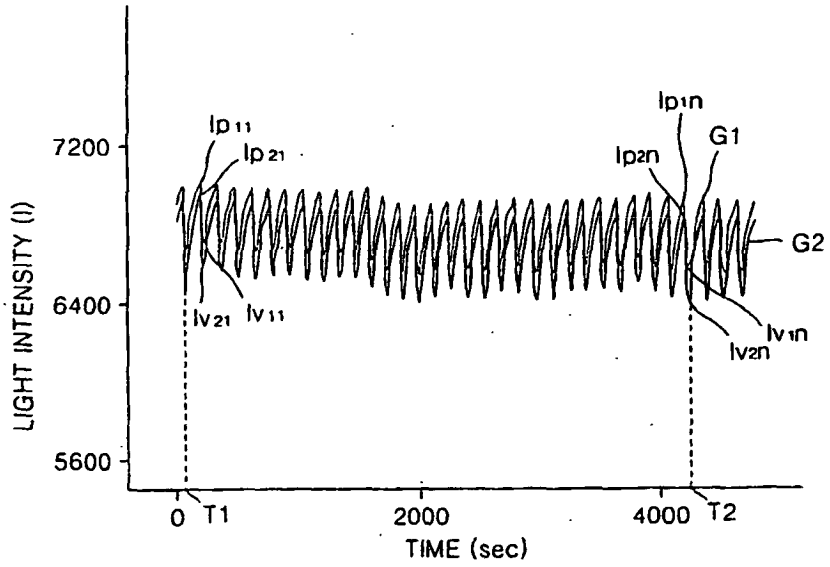

START
COLLECT DATA FOR PREDETERMINED UNIT PERIOD OF TIME
31
OBTAIN I_P AND I_V OF EACH PULSE IN EACH WAVELENGTH
32
OBTAIN I_P/I_V FOR EACH PULSE IN EACH WAVELENGTH
33
CALCULATE PARAMETERS BETWEEN WAVELENGTHS
34
CALCULATE AVERAGE OF PARAMETERS
35
COUNT THE NUMBER OF PARAMETERS WHOSE DEVIATION FROM THE AVERAGE IS GREATER THAN STANDARD DEVIATION
36
37
IS RATIO OF THE NUMBER OF ALL PARAMETERS TO THE NUMBER OF PARAMETERS WHOSE DEVIATION FROM THE AVERAGE IS GREATER THAN STANDARD DEVIATION LESS THAN PREDETERMINED REMOVAL REFERENCE VALUE?
NO
YES
STORE PARAMETERS AS VALID DATA
38
END

FIG. 4


LIGHT INTENSITY (I)
7200
6400
5600
0
T1
2000
4000
T2
TIME (sec)
Ip11
Ip21
Ip1n
Ip2n
G1
G2
Iv21
Iv11
Iv1n
Iv2n

专利名称(译)	用于去除异常数据的血液成分光谱分析系统		
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摘要(译)

提供了一种使用光谱学去除异常数据的方法和血液成分分析系统。使用光谱法去除血液成分分析系统中的异常数据的方法包括：（a）收集对应于第一和第二波长的PPG信号达预定单位时间段，（b）计算“n”参数，相对于“n“收集的PPG信号中包含的脉冲数据，其中n是正整数，（c）计算”n“参数的平均值，（d）比较偏离平均值的参数数量的比率比具有预定移除参考值的“n”参数的预定标准偏差，以便确定“n”脉冲数据是否有效。

(1)