Diasensor 2000
Patient Data Analysis
Software Design Description

Contents

1. Introduction

1.1 Purpose

This document describes the design of the Diasensor 2000™ Patient Data Analysis Calibration software. It provides a representation of the software system used to create and update the patient calibration. This document is intended to be a primary medium for communicating software design information.

1.2 Scope

The design description is limited to the Patient Data Analysis Calibration software for the Diasensor 2000™. The software detailed design, interface design, and data definitions are described in this document.

1.3 References

1. 31259-SS *Diasensor 2000* Patient Data Analysis Software Requirements Specification.
2. 31184-FS01 *Diasensor 2000* User Card Format Specification.
3. 32000-PD02 *Diasensor 2000* Algorithm Product Specification.

1.4 Definitions

1.4.1 Calibration

The collection of Calibration Data and the processing of the data to extract a patient's Calibration coefficients. The Calibration process does not include Evaluation and Re-Calibration.

1.4.2 Calibration Coefficients

A set of coefficients used by the measurement algorithm when calculating a glucose measurement. The coefficients are extracted from Calibration Data that is collected from a patient for a single *Diasensor 2000*. This results in a unique set of coefficients for each patient / *Diasensor 2000* combination.

1.4.3 Calibration Data

The spectral, sensor, and time stamp data from the *Diasensor 2000* and the corresponding *HemoCue* monitor's glucose readings collected for the purpose of extracting Calibration coefficients for a glucose measurement algorithm.

1.4.4 Coarse Outlier

A subsession failing the standard deviation check. During Calibration, the Patient Data Analysis Section of Computational Analysis performs the standard deviation check. See the *Diasensor 2000* Algorithm Specification for a complete description of the standard deviation check.

1.4.5 Countable Calibration Session

Session that is valid and with at least one valid subsession that is not a coarse outlier.

1.4.6 Countable Calibration Sitting

Sitting with at least four (4) countable Calibration sessions and a time stamp at least two (2) hours later than the time stamp of the most recent previous successful sitting. At least two (2) of the four (4) sessions must have been collected before the *HemoCue*, and at least two (2) of the four (4) sessions must have been collected after the *HemoCue*.

1.4.7 .hc Object

An electronic file containing one *HemoCue* reading for each *Diasensor 2000* sitting of spectral data, in an S-Plus object format. The actual file extension is ".hc".

1.4.8 HemoCue Reading

The event of performing one measurement on the *HemoCue* monitor. A valid *HemoCue* result is a quantitative reading with a value between 0 and 400 mg/dL (0 to 22.2 mmol/L), the effective measurement range of a *HemoCue* monitor.

1.4.9 Outlier

In a set of data, a value so far removed from other values in the distribution that its presence cannot be attributed to the random combination of chance causes

1.4.10 Re-Calibration

The collection of Re-Calibration Data and the processing of the data to extract updated patient calibration coefficients from both previously collected data and the newly collected Re-Calibration Data. The process of Re-calibration is identical to Calibration, except that the length of time during which data is collected and the amount of data collected are greatly reduced, and the Re-calibration data is concatenated to previously collected data.

1.4.11 Re-Calibration Data

The spectral, sensor, and time stamp data from the *Diasensor 2000* and the corresponding *HemoCue* monitor's glucose readings collected for the purpose of updating the calibration coefficients.

1.4.12 .ska Object

An electronic file containing spectral data from the *Diasensor 2000*, in an S-Plus object format. The actual file extension is ".ska".

1.4.13 Session

The series of events starting when the patient presses the start button <1> on the *Diasensor 2000* and ending after the last action before the patient can press the start button <1> again. From a data acquisition point of view, a session is the time bracketed by two reference measurements and a final local dark measurement.

1.4.14 Sitting

The single event of a patient sitting and collecting data and/or obtaining a glucose reading on the *Diasensor 2000* and the *HemoCue* monitor, when necessary. A sitting in Calibration, Evaluation, and Measurement differs in the nominal number of sessions performed per sitting. During Calibration and Evaluation, there is one *HemoCue* reading for each sitting. During Measurement, there is no HemoCue reading other than normally scheduled quality monitoring.

1.4.15 Subsession

One session may consist of several subsessions. A subsession is the time during which the *Diasensor 2000* collects sixteen (16) individual spectra, each preceded by a single dither.

1.4.16 Valid Session

A session that is not ended prematurely by either the patient or the *Diasensor 2000* and therefore not resulting in a *"Problem Detected"* screen.

1.4.17 Valid Subsession

A subsession of a valid session in which all of the skin spectra time stamps are less than fifteen (15) minutes apart from a valid *HemoCue* time stamp.

1.5 Acronyms

The following abbreviations and acronyms are used in this document.

D2000 -- Diasensor 2000 ™

.hc – S-Plus object of one *HemoCue* reading for each *Diasensor 2000* sitting (see definitions)

I/O -- Input/Output

PCMCIA -- Personal Computer Memory Card International Association

PDA -- Patient Data Analysis

QM -- Quality Monitoring

.ska – Spectral data in S-Plus format (see definitions)

SRS -- Software Requirements Specification

TBD -- To Be Determined

2. Product Perspective

A *Diasensor 2000* must be calibrated for each patient. To accomplish this, data is collected from both a Diasensor and an invasive glucose meter, as directed by the Diasensor 2000 User's Guide. The data is transmitted to Patient Data Analysis. When the specified amount of data has been collected, it is then used as input to the software that forms the Calibration.

After a *Diasensor 2000* is calibrated for a patient, the patient then uses the *Diasensor 2000* to obtain measurements during an Evaluation period, as directed by the Diasensor 2000 User's Guide. The data is transmitted to Patient Data Analysis. When the specified amount of data has been collected, Patient Data Analysis reviews the Evaluation data to ensure the *Diasensor 2000* is successfully calibrated to the patient.

The *Diasensor 2000* is Re-calibrated on a specific time schedule, or when the user experiences repeated Quality Monitoring failures. Re-calibration is identical to Calibration, except that the length of time during which data is collected and the amount of data collected are greatly reduced, and the Re-calibration data is concatenated to previously collected data.

3. Development Environment

The software will be developed and run on a UNIX based system.

The analyst, working from a PC workstation, uses a local area network to gain access to the UNIX system. The UNIX system runs the Solaris operating system.

The standard interface is S-PLUS version 3.3. S-PLUS "wrapper" programs may also be written as user interfaces for C or C++ programs.

4. General Description

The objectives of the D2000 software design are as follows:

1. Provide a software solution that meets software requirements and is verifiable
2. Provide a software solution that meets user needs and can be validated
3. Provide a software design that minimizes the effort required for maintenance throughout the product life-cycle

Risk and hazard management is facilitated by modularizing the design and minimizing the complexity of the individual components.

5. Software Design – All Incoming Data

5.1 Pre-Process Incoming Data

5.1.1 Refers to Software Requirement: 3.1.1

5.1.2 Software Description:

The Pre-Processing software is run on a file of incoming D2000 data. Since there can be up to four patients using an individual Diasensor, the software splits the data into as many as four files, one for each possible patient.

In the process of splitting up the data, if the software finds an Alert record, it also creates an Alert file. The presence of an Alert file informs the Patient Data Analysts that enough data has been collected in the current mode, and will cause the Analyst to take action.

5.1.2.1 Inputs

Data will be uploaded from the Diasensor via the Internet to the directory: /u8/*distributor ID/BICO Login ID/incoming* and the file name will be: mmddhh*mm*.PD.

where:

mm = data transfer month

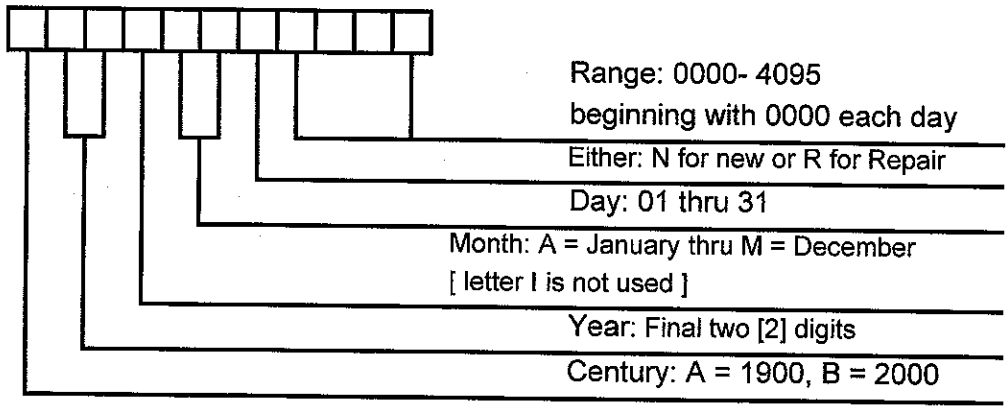
dd = data transfer day

hh = data transfer hour

mm = data transfer minutes

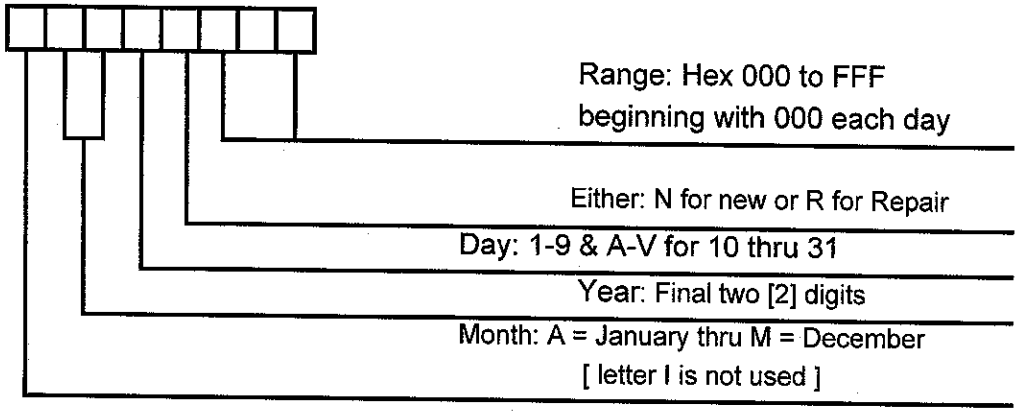
The "BICO Login ID" is a shortened form of the Diasensor serial number. A shortened form of the Diasensor serial number is necessary because only 8 characters or less can currently be accommodated as the Login ID. Below is an explanation of the translation from the *Diasenor 2000* Serial Number to the BICO Login ID:

1. **The Diasensor 2000 serial number is as follows:**



So an example would be: **A99A15N0001**. This new device went through final checkout on 01/15/1999.

2. The BICO Login ID is 8 characters as follows:



5.1.2.2 Processing

Each day, a program will be run to split a file from a single Diasensor into as many as four files: One file of both SPECTRUM and READING data for each of four patients. These files will be built in the directory: /a1c/*distributor ID*/*patient ID*(6 digits max.)/*BICO Login ID*/src and the file name will be: mmddhh*mm*.bin

where:

mm = data transfer month
dd = data transfer day
hh = data transfer hour
mm = data transfer minutes

Some checking of the incoming data will occur. If an error is found, a record is logged in a file. This record shall include the date and time the data was collected, and type of error. The following are the checks:

1. Are the collection date and time stamps out of sequence?
2. Are the incoming sitting counts (records within the sitting) out of sequence?
3. Is there a missing spectral status code?

If an alert record is in the file, create an Alert file in an ASCII text format. The Alert file will be built in the directory: /a1c/*distributor ID*/*patient ID*(6 digits max.)/*BICO Login ID*/src and the file name will be: mmddhh*mm*.alert.txt. The Alert file will contain the following information:

Table 1: Alert File

Column	Field Name	Description	Range
1	distributorId	first 4 digits of the Bico_user_id	4 digits
2	userId	last 6 digits of the Bico_user_id	numeric, 6 digits max.
3	date	Date in the format: yyyymmdd	
4	time	Time in the format: hhmmss	

Column	Field Name	Description	Range
5	mode	instrument operating mode	1 = calibration 2 = evaluation 3 = measurement 4 = recalibration
6	status	alert status code	2 digits

5.1.2.3 Output

An Alert file, when necessary, called: mmddhh*mm*.alert.txt.

A file of the daily incoming data in the correct patient/BICO Login directory, called: mmddhh*mm*.bin.

An entry in an error log file, when necessary.

Note: Each day, each patient's binary files will be zipped into an appropriate file.

5.2 Translate Binary Data into S-Plus format file(s) (objects)

5.2.1 Refers to Software Requirement: 3.1.2

5.2.2 Software Description:

This software is run on the binary files of an individual patient. It translates the binary data to an S-Plus format file. While doing this, it creates separate files (objects) for spectral data and Diasensor 2000 glucose readings, if both exist in the binary file.

5.2.2.1 Inputs

A patient's *Diasensor 2000* data in a binary format, from the file of zipped mmddhh*mm*.bin data.

Part of the output object name, as a parameter, the default being: Fyymmdd where:

"F" = literal, stands for Final.

yymmdd = date that the S-PLUS object was created

The file name will be concatenated with a letter, which indicates the mode the data was collected in as follows:

Mode	Letter
Calibration (1)	C
Evaluation (2)	E
Measurement (3)	M
Re-Calibration (4)	R

The extension of the file will depend upon the type of data that was collected. Spectral data will have the extension ".ska", glucose measurement readings will have the extension ".rdg". The type of data (spectrum or reading) is found in the Object ID of the Object Header.

For example, a file containing Calibration Spectra for a completed (final) calibration would be called: CFyymmdd.ska. A file of Evaluation data may have both an EFyymmdd.ska and an EFyymmdd.rdg.

5.2.2.2 Processing

The analyst unzips the compressed file(s).

The analyst concatenates the appropriate mmddhh*mm*.bin files into a concatenated file, named mmdd.cat.bin, where:

mm = month the concatenated file was created
dd = day the concatenated file was created
.cat = literal, indicates this is a concatenated file

Translate the Diasensor binary spectral data from the concatenated file into an S-PLUS object, as follows:

Table 2: SKA Structure Format

Column	Field Name	Description	Range
1	spectrumType	Type of spectrum in data buffer. Type 3 = index is not really a spectrum type. It is used by protomgr for indexing.	0 = spectrum_status 1 = control 2 = dark 3 = index 4 = reference 5 = skin 6 =control_absorbance 7 = dark_absorbance 8 = ref._absorbance 9 = skin_absorbance
2	distributorId	first 4 digits of the Bico_user_id	4 digits, 0-4294
3	userId	last 6 digits of the Bico_user_id	numeric, 6 digits max. 0-967295
4	date	Date in the format: yyyymmdd	numeric
5	time	Time in the format: hhmmss	numeric warning: no leading zeros
6	invasive	Corresponding invasive meter reading	0 to 65,535
7	mode	instrument operating mode	1 = calibration 2 = evaluation 3 = measurement 4 = recalibration
8	sittCount	Sitting count. (the number of good spectrum status records for all the data (e.g. a whole Calibration)) or if all data is wanted, the number of spectrum status records.	1 – 65,535 The sitting number while using this mode of operation. (normally, cal. sittings would be 1-120).
9	sessCount	Session count	1 – 6 for Cal. or Re-cal., 1-1 for Evaluation or Measurement mode. The session number within the above sitting.
10	todCode	Time-Of-Day class code.	1 = before breakfast 2 = after breakfast 3 = before lunch 4 = after lunch 5 = before dinner 6 = after dinner 7 = bedtime 8 = night

Column	Field Name	Description	Range
			9 = other
11	spectrum[1]	Spectral data of spectrum_type	up to 15 digits
12	spectrum[2]	Spectral data of spectrum_type	up to 15 digits
13-73	spectrum[3 to 63]	Spectral data of spectrum_type	up to 15 digits
74	spectrum[64]	Spectral data of spectrum_type	up to 15 digits
75	sensor[1]	sensor data	up to 15 digits
76	sensor[2]	sensor data	up to 15 digits
77-84	sensor[3 to 10]	sensor data	up to 15 digits
85	statusCode	error code from spectrum status	2 digits

Translate the Diasensor binary glucose measurement data from the concatenated file into an S-PLUS object, as follows:

Table 3: RDG Structure

Column	Field Name	Description	Range
1	distributorId	first 4 digits of the Bico_user_id	4 digits
2	userId	last 6 digits of the Bico_user_id	numeric, 6 digits max
3	mode	Instrument operating mode	1 = calibration 2 = evaluation 3 = measurement 4 = recalibration
4	date	Date in the format: yyyymmdd	numeric
5	time	Time in the format: hhmmss	numeric warning: no leading zeros
6	glucose	measured blood glucose (mg/dL)	-32,768 to 32,767
7	control	control sample (absorbance * 100,000)	-32,768 to 32,767
8	invasive	invasive meter measurement (mg/dL)	-32,768 to 32,767
9	todCode	Time-Of-Day class code	1 = before breakfast 2 = after breakfast 3 = before lunch 4 = after lunch 5 = before dinner 6 = after dinner 7 = bedtime 8 = night 9 = other
10	qmFlag	quality monitoring indicator; if nonzero, then this reading was used for QM purposes	0 or 1
11	status	measurement algorithm completion status code	Usage specific
12	correction	bias correction value used to get this measurement. in units of mg/dL	-32,768 to 32,767

Normally, only data from sittings with a status code indicating that the data is good is converted into S-PLUS object(s). Good glucose measurement readings are defined as having a status code of zero(0), eighteen(18), and nineteen(19).

However, we also need an option to build S-PLUS object(s) that contain all the data, both good and bad data.

Other Checks:

1. Warn the analyst if the data collection time stamps are out of sequence, and display what the date and time is.
2. If the incoming sitting counts (records within the sitting) are out of sequence, warn the analyst and display the date and time where this occurs.
3. If there is a missing spectral status code, warn the analyst and display the date and time where this occurs.

5.2.2.3 Output

Diasensor 2000 data in S-PLUS format file(s) (objects). These objects will be stored in the following directory: /a1c/*distributor ID*/*patient ID*(6 digits max.)/*BICO Login ID.*

If necessary, warnings that the data checks failed.

6. Software Design – Process Calibration Data

6.1 Create an S-PLUS object (.hc object) that contains one HemoCue reading per sitting of spectral data.

6.1.1 Refers to Software Requirement: 3.1.3

6.1.2 Software Description:

This software is run on the spectral data of an individual patient (.ska file). It creates a single S-PLUS object containing one HemoCue reading for each sitting of spectral data.

6.1.2.1 Inputs

The S-PLUS object of spectral data (.ska object)

The output object name, as a parameter.

The Distributor ID.

The Patient ID.

6.1.2.2 Processing

Create an S-PLUS object containing a vector of one HemoCue reading for each sitting of spectral data.

6.1.2.3 Output

One *HemoCue* reading for each sitting of spectral data, in an S-PLUS format file (.hc object).

This object will be stored in the following directory: /a1c/*distributor ID*/*patient ID*(6 digits max.)/*BICO Login ID*.

6.2 Software to create preliminary plots.

6.2.1 Refers to Software Requirement: 3.1.4

6.2.2 Software Description:

This software creates several plots from *Diasensor 2000* spectral data and the associated HemoCue readings.

6.2.2.1 Inputs

The spectral data and associated HemoCue readings in S-PLUS format (the .ska object).

6.2.2.2 Processing

The following plots will be created:

1) A histogram of the HemoCue
2) HemoCue readings vs. data collection time
3) Raw Diasensor skin data vs. channel
4) Mean Diasensor skin data vs. channel
5) Standard deviation of Diasensor skin data vs. channel
6) Diasensor skin absorbance data vs. channel (every 100^{th} row)
7) Mean Diasensor skin absorbance data vs. channel
8) Standard deviation of Diasensor skin absorbance data vs. channel
9) Raw Reference data vs. channel

10) Mean Reference data vs. channel
11) Standard deviation of Reference data vs. channel
12) Reference absorbance data vs. channel
13) Mean absorbance of reference data vs. channel
14) Standard deviation of reference absorbance data vs. channel
15) Dark spectra vs. channel
16) Temperature sensors vs. time

6.2.2.3 Outputs

Several plots, as described above.

6.3 Calculate the Standard Deviation of the HemoCue Readings

6.3.1 Refers to Software Requirement: 3.1.6

6.3.2 Software Description:

This software calculates and displays the standard deviation of the HemoCue readings collected during Calibration. If the HemoCue standard deviation is not greater than or equal to 40 mg/dL, the analyst will discontinue processing.

6.3.2.1 Inputs

The HemoCue readings in S-PLUS format (the .hc object).

6.3.2.2 Processing

Use one HemoCue reading per sitting to calculate the standard deviation of the HemoCue readings. Display the standard deviation of the HemoCue readings.

6.3.2.3 Outputs

Display the standard deviation of the HemoCue readings.

6.4 Remove Standard Deviation Failures, and Ensure that there is still Sufficient Data

6.4.1 Refers to Software Requirement(s): 3.1.5, 3.1.7

6.4.2 Software Description:

This software performs a Standard Deviation check on the spectra by subsession and removes the subsessions that do not pass. It then checks to ensure that less than or equal to 30% of all the data was removed due to Standard Deviation errors.

The software then ensures that there is still enough data available after the Standard Deviation check on the spectra to continue forming a Calibration.

6.4.2.1 Inputs

The spectral data in S-PLUS format (the .ska object).

A parameter indicating whether or not to check the Sufficient Data Criteria, default set to True.

A parameter for the Standard Deviation acceptance cutoff, default set to 0.009.
Parameter for the percent of Standard Deviation failure, default set to 30%.

A parameter for the Distributor ID.

A parameter for the Patient ID.

A parameter containing the name of the file of S-PLUS spectra to be used (.ska file).

6.4.2.2 Processing

Perform the Standard Deviation Check:

Let M denote the number of skin spectra in the set. Let S_{ij} denote a particular skin spectra pixel, where i denotes the spectra number {1..M} and j denotes the pixel number {1..64}.

Perform the Standard Deviation Check as follows.

1. Compute standard deviations of individual pixels: σ_j = STDEV (S_{1j}, S_{2j}, ... $S_{M,j}$) for j = 1 to 64.
2. Compute the average of the 64 standard deviations, denoted as σ_{AVG}.
3. If $\sigma_{AVG} < 0.009$, accept the sub-session. Otherwise, reject the sub-session.

Also, the number of subsessions failing the standard deviation check (Coarse Outliers) must be less than or equal to 30% of the total valid subsessions. For example:

invalid $\leq$ 0.3 * total

Display the total number of subsessions, the number of subsessions that failed the standard deviation check, and whether this check passed. Discontinue processing if the Standard Deviation Check failed.

Check if there is enough Calibration Data to continue:

Perform tests to check the Sufficient Calibration Data Criteria as follows:

The number of countable Calibration sessions must be greater than or equal to 600.

The number of countable Calibration sittings must be greater than or equal to 108. To count, a sitting must have at least 4 sessions that have at least one subsession each.

The number of days with at least 1 countable Calibration sitting must be greater than or equal to 54.

Display to the analyst: the number of countable Calibration sessions, the number of countable Calibration sittings, the number of days with at least 1 countable Calibration sitting, and the number of each that is still needed to pass the sufficient Calibration data criteria. Discontinue processing if the data did not pass the sufficient Calibration data criteria.

6.4.2.3 Outputs

The spectral data that has had the standard deviation errors removed (cleaned .ska data.)

Displays to the Analyst indicating if there is enough data to procede with a Calibration.

6.5 Average the Skin Spectra and Create the Absorbance Object.

6.5.1 Refers to Software Requirement: 3.1.8

6.5.2 Software Description:

If there is enough data, the software averages the skin spectra in each subsession, so there is a maximum of four skin spectra per session. The software then converts each average skin spectrum to absorbance units, and writes this to a new S-PLUS object.

6.5.2.1 Inputs

The spectral data in S-PLUS format (the .ska object).

The output file name, as a parameter, the default being the same file name as the .ska object used as input, except with a ".abs" extension. For example, if the input .ska object is named: CF000415.ska, the default name for the output absorbance object is: CF000415.abs.

6.5.2.2 Processing

Average the skin spectra in each subsession (16 spectra) to give a maximum of four spectra per session. Each average spectrum will contain the sensor readings and time stamp of the last un-averaged spectrum collected in the subsession.

Convert each average skin spectrum to absorbance units by using the following equation:

$$\text{absorbance} = \log_{10}\left(\frac{\text{first reference reading}}{\text{skin reading}}\right)$$

6.5.2.3 Outputs

An absorbance object of averaged skin spectra, in the same format as the .ska object (see table 2). This object is stored in the following directory: /a1c/*distributor ID*/*patient ID*(6 digits max.)/*BICO Login ID*.

6.6 Produce a Calibration Vector Using the Slope Intercept Corrected (SIC) Calibration Method.

6.6.1 Refers to Software Requirement: 3.1.9

6.6.2 Software Description:

This software performs PLS Decomposition, then performs Slope Intercept Correction (SIC) and updates the Calibration vector.

6.6.2.1 Inputs

The absorbance object (.abs object).

A parameter to indicate how many of the PLS Loadings should be saved.

6.6.2.2 Processing

See the *Diasensor 2000* Algorithm Product Specification, sections on PLS Decomposition and Slope and Intercept Correction Calibration Method for the details of performing the PLS decomposition and updating the calibration vector using SIC.

6.6.2.3 Outputs

The Calibration vector and Calibration constant. The PLS Loadings (one for each rank up to the parameter), and the SVD Load Vector. All of these are so they can be input into the skin library program without re-creating them.

Three objects, one for the Calibration constant and Calibration vector, one for the PLS Loadings, and one for the SVD Load Vector, are stored in the following directory: /a1c/*distributor ID*/*patient ID*(6 digits max.)/*BICO Login ID*.

The Calibration constant and Calibration vector are stored in an object named: cal.vec. The first column in cal.vec is the Calibration constant, the Calibration vector is stored in columns 2 through 65.

The PLS Loadings are stored in an object named: pls.load. There is one row for each rank up to the parameter number. The first column in each row of pls.load is the constant, the PLS Loadings are stored in columns 2 through 65.

The SVD Load vector is stored in an object named: svd.load, in columns 1 through 64.

6.7 Print an Error Grid of Calibration Self-Predictions and record the Quality Monitoring Cutoff.

6.7.1 Refers to Software Requirement: 3.1.10

6.7.2 Software Description:

Prints a Clarke error grid comparing the Calibration self-predictions and the actual HemoCue readings and creates a file containing the QM Cutoff value to be used in the skin library.

6.7.2.1 Inputs

The absorbance object (.abs object).

The Calibration Vector and Calibration Constant (cal.vec).

6.7.2.2 Processing

Print a Clarke error grid, comparing the Calibration self-predictions with the actual HemoCue readings. On the error grid, display the calculated correlation coefficient, the RMSEC (Root Mean Square Error of Calibration), the slope, and the Quality Monitoring Cutoff (QM Acceptable Range).

The correlation coefficient will allow the patient data analyst to determine if the correlation is $\geq$ 0.7. The Quality Monitoring Cutoff is used when the Skin Library is created.

Determine the Quality Monitoring Cutoff Value as follows:

For paired Diasensor measurement (x_i) and HemoCue value (y_i) for data collected during calibration, define a root mean square (RMS) error as follows.

$$\mathbf{RMS}_{\mathbf{Diasensor}} = \sqrt{\frac{1}{\mathbf{M}}\sum_{i=1}^{\mathbf{M}}(\mathbf{y_i} - \mathbf{x_i})^2}$$ where M is the number of paired results

$$QM\ cutoff\ value = 2 * RMS_{Diasensor}$$

6.7.2.3 Outputs

A Clarke error grid, which shows the calculated correlation coefficient, the RMSEC, the slope, and the QM Cutoff (QM Acceptable Range).

A file called qm.cutoff which contains the QM Cutoff value, stored in the following directory: /a1c/*distributor ID*/*patient ID*(6 digits max.)/*BICO Login ID*.

6.8 Create a Patient Skin Library.

6.8.1 Refers to Software Requirement: 3.1.11

6.8.2 Software Description:

This software enables the analyst to create a patient skin library, which contains the patient's Calibration coefficients and other information the *Diasensor 2000* needs to function in Measurement mode.

6.8.2.1 Inputs

The absorbance object (.abs object).

The .ska object (used for the Control data only).

The Calibration vector, and Calibration constant from cal.vec.

The PLS Loadings and constants (one for each rank up to the Calibration rank used) from pls.load.

The SVD Load Vector from svd.load.

The QM Cutoff value (QM Acceptable Range) from qm.cutoff.

Parameters:

1. The 4-digit distributor ID and 6-digit user ID, used for naming the output file only.
2. The channel numbers to be used. The default will be 1 through 57. Fill the unused channels with zeros so there is a placeholder for all 64 channels.
3. The total number of channels, default to 64.
4. The calibration coefficient rank, default of 25.
5. Quality Monitoring flag, default = "T"
6. The prediction limit low and high limit, default 0-400.
7. The clinical alert limit low and high range, default 40-400.
8. The deviation that the current Control pixel measurements may drift from the maximum and minimum values of the Control average absorbance (ctrlRefLimit). The default is 0.003.

6.8.2.2 Processing

The software must build the patient skin library. Components of the skin library include all the contents of cal.vec, pls.load, svd.load, and qm.cutoff. The skin library also includes the parameters except the first, plus the following:

General:

1. The Calibration Date, use the current date.
2. The Sensor Ranges (rangeSensors), low and high point pre-set to 99.
3. Leverage tolerance, pre-set to 1.
4. LOF tolerance, pre-set to 1.
5. Distance tolerance, pre-set to 0.
6. A slope correction number, pre-set to 1.
7. A bias correction number, pre-set to 0.

Control Data:

1. Average Absorbance of control data. Calculate the average absorbance of the control data as detailed in the Calibration section of the Control Standard Check in the *Diasensor 2000* Algorithm Product Specification.
2. The Average sensor spectral readings collected at the same time the control data was collected.

Skin Data

1. Calculate the Mean of the Calibration Skin Spectra, which is the average of all the columns of absorbance data.

6.8.2.3 Outputs

The patient's skin library, as detailed in the Diasensor 2000 User Card Format Specification in the following directory:

/a1c/*distributor ID*/*patient ID*(6 digits max.)/*BICO Login ID.*

The file naming convention will be: *patient ID*(6 digits max.).slb

7. Software Design – Process Evaluation Data

7.1 Ensure that there is Sufficient Data to Evaluate the Calibration.

7.1.1 Refers to Software Requirement(s): 3.1.12

7.1.2 Software Description:

The software ensures that there is enough data available to continue the process of Evaluation.

7.1.2.1 Inputs

Diasensor 2000 measurements in an S-PLUS format file (.rdg object).

(See the section "Translate Binary Data into S-Plus format file(s) (objects)" for a file layout.)

7.1.2.2 Processing

Perform tests to check if there is sufficient Evaluation data as follows:

Number of days with at least one (1) countable Evaluation sitting should be greater than or equal to twenty-five (25).

Number of countable Evaluation sittings should be greater than or equal to forty-nine (49).

Sittings with a status code other than zero(0), eighteen(18), and nineteen(19) are not countable.

7.1.2.3 Outputs

Display to the analyst: the number of countable Evaluation sittings, the number of days with at least 1 countable Evaluation sitting, and the number of each still needed to pass the sufficient Evaluation data criteria. The analyst will record this information in a patient spreadsheet. Discontinue processing if the data did not pass the sufficient Evaluation data criteria.

7.2 Perform the Evaluation

7.2.1 Refers to Software Requirement(s): 3.1.13

7.2.2 Software Description:

The software calculates the mean of the absolute values of the differences between the paired *HemoCue* and *Diasensor 2000* measurements. The software calculates a 95% confidence interval and compares the result to a threshold of 90, beyond which the Evaluation is said to have failed.

7.2.2.1 Inputs

Diasensor 2000 measurements in an S-PLUS format file (.rdg object). This file also contains the corresponding *HemoCue* reading.

The threshold of 90, as a parameter.

The output file name, as a parameter. The default will be: evl_ddddpppppp.txt where:

dddd	4-digit distributor ID
pppppp	6-digit user ID

7.2.2.2 Processing

z_α is such that the integral of the standard normal density from $z_{\alpha/2}$ to infinity equals $\alpha/2$.

$\bar{\mu}$ is the estimate of the mean absolute value of the error.

σ is the sample variance.

Assuming that the absolute value of the error is:

$$x_m = |Diasensor - HemoCue|$$

The estimate of the mean absolute value of the error is:

$$\bar{\mu} = \frac{1}{M}\sum_{m=1}^{M}|x_m|$$

The sample variance is:

$$\sigma = \sqrt{\frac{\sum_{m=1}^{M}(x_m)^2 - M(\bar{\mu})^2}{M-1}}$$

The upper boundary of the confidence interval must be less than the threshold to pass Evaluation:

$$\bar{\mu} + z_\alpha \frac{\sigma}{\sqrt{n}} < threshold$$

7.2.2.3 Outputs

Display the upper boundary of the confidence interval.

Display a Pass or Fail status to the analyst, based on whether the confidence interval was less than the threshold. The pass or fail is included in the Physician's report.

Create a text file, named according to an input parameter, in the following directory: /a1c/*distributor ID*/*patient ID*(6 digits max.)/*BICO Login ID*

The text file will contain the following:

Distributor ID, User ID

.rdg file name

Threshold used

Confidence Interval calculated

"Evaluation Status:" (Pass or Fail)

7.3 Calculate Data for a Physician's report

7.3.1 Refers to Software Requirement(s): 3.1.14

7.3.2 Software Description:

Calculates or creates, then saves several items to be included on the Physician's report. The report is created as a Word document (for format), and the file that is generated by this software is included.

7.3.2.1 Inputs

Diasensor 2000 measurements in an S-PLUS format file (.rdg object). This file also contains the corresponding *HemoCue* reading.

7.3.2.2 Processing

Calculate and save the following, so they may be included on the Physician's report:

1. An analysis of the relative error between the average *Diasensor 2000* and *HemoCue* readings.
2. A regression analysis of the *Diasensor 2000* vs. *HemoCue* individual readings.
3. The Correlation Coefficient, Standard Error, Slope, Intercept, and the number of glucose readings.

7.3.2.3 Outputs

A file containing the above data to be included in a Physician's report, in the directory: /a1c/*distributor ID*/*patient ID*(6 digits max.)/*BICO Login ID*. The file name will be: rep_*ddddpppppp*.txt, where:

dddd	4-digit distributor ID
pppppp	6-digit user ID

8. Software Design – Miscellaneous Software

8.1 Software Used to Attach to the Correct Patient Directory

8.1.1 Refers to Software Requirement(s): None

8.1.2 Software Description:

This software attaches the analyst to the directory where the patient data is stored. It was developed to reduce the risk of the analyst accidentally using the wrong data or storing a file in the wrong directory.

8.1.2.1 Inputs

4-digit Distributor ID, a parameter.

6-digit Patient ID, a parameter.

Subdirectory, an optional parameter defaulted to null.

Return directory, a parameter defaulted to "F". If the parameter is used as "T", do not attach to the directory, just return it to the calling program.

The master list containing the patient directory information. The master list file, named d2k.master.list, located in the Splus source file directory, has the following file format:

Table 5: d2k.master.list Structure Format

Column	Field Name	Description	Range
1	distributorId	First 4 digits of the Bico_user_id	numeric, 4 digits max., 0-4294
2	userId	Last 6 digits of the Bico_user_id	numeric, 6 digits max. 0-967295
3	BicoLogin	A translated form of the device Serial Number	8 alphanumeric
4	TopLevelDir	Top level directory	Alphanumeric, length varies

8.1.2.2 Processing

Check to see if there are multiple BICO login ID's for the Distributor ID/User ID combination. If there are, display a list of the available BICO login ID's and ask the analyst to choose one. Retrieve the Top Level Directory. If the Return Directory parameter = "F", attach to that directory, or subdirectory, if specified. If the Return Directory parameter = "T", return the directory or subdirectory to the calling program.

8.1.2.3 Outputs

An attachment to the correct directory, or the path of the directory if the Return Directory parameter = "T".

9. Revisions

Rev.	Description	Author	Effective Date
AA	Initial Issue of Document	D. Griffith	04-25-00