

OUTPUT FORMATS

Pentra DX / DF Nexus

RAA048AEN

Revisions

Table 1: Revisions

| Index | Software revision | Chapter, page | Date |
|-------|-------------------|---------------|------------|
| A | V1.2.0 | All | 15/08/2013 |
| | | | |

Table of contents

- > "Introduction", page 3
- > "Physical connection (RS232)", page 5
- > "ABX Format", page 6

Introduction

ABX Format is currently supported to be compliant with existing connections, but will not be supported on future generation of instrument.

Different protocols can be used on HORIBA Medical instrument, a connection between a computer (host) and an Horiba Medical instrument can be performed when the protocol, the format description and the connection mode are properly set up.

Table 2: Definitions

| Term | Definition |
|-----------------------|---|
| <ACK> | Acknowledgment (ASCII Decimal 6) |
| [C1] | The most significant character of Checksum |
| [C2] | The least significant character of Checksum |
| [DATA] | The data contents of the record |
| <ENQ> | Inquire (ASCII Decimal 5) |
| <ETB> | End of Transmission Block (ASCII Decimal 23). For use only when a single record is too large to fit into one frame. |
| <ETX> | End of Text (ASCII Decimal 3). Required at the end of each record. |
| [frame number] | Single digit frame number "0" to "7", starts with "1". |
| <LF> | Line Feed (ASCII Decimal 10). |
| <NAK> | Negative Acknowledgment (ASCII Decimal 21). |
| <STX> | Start of Frame (ASCII Decimal 2). |
| Communications packet | All framing required for transmission of data. This framing includes: <STX>[frame number][DATA] [<ETB> or <ETX>][C1][C2] <LF> |
| Component Field | One of several related pieces of information within a field. |
| Download | The transmission of data from the LIS to the Pentra Nexus Data Management System. |
| Field | A specific location within a record for a piece of information, indicated by a field delimiter and position. |

Table 2: Definitions

| Term | Definition |
|--------------|--|
| Frame | A complete communications packet. |
| LIS | Laboratory Information System |
| Message | A collection of related information; a group of records that begins with a «Header» record and ends with a «Terminator» record. A single record could theoretically constitute a message, but within this context, a message always contains multiple records. |
| Receiver | The device that responds to the sender. The receiver in this document is either the Pentra Nexus Data Management System or the LIS. |
| <EOT> | End of Transmission (ASCII decimal 4) |
| <CR> | Carriage Return (ASCII decimal 13) |
| Record | In reference to the low level protocol, a record is the message data (shown as [DATA]) as described within the communications packet. If the data is longer than 240 characters, then it must be split into two (or more) parts and sent in two (or more) communications packets. The intermediate packet uses the <ETB> character, and the ending packet uses the <ETX> character. No single communications packet contains more than one record. In reference to the message layer, a record can be one of the following codes: H (header), P (patient), O (order), R (result), L (terminator), C (comment). |
| Repeat Field | An additional field of the preceding type when indicated by a repeat delimiter. The Pentra Nexus Data Management System parses and may produce repeat fields in the Universal Test ID field of a Test Order Record or the Value field of the Result Record, but ignores other occurrences of repeat fields. |
| Sender | The device that has a message to send and initiate the transmission process, in this case between the LIS and the Pentra Nexus Data Management System. The sender in this document is either the Pentra Nexus Data Management System or the LIS. |

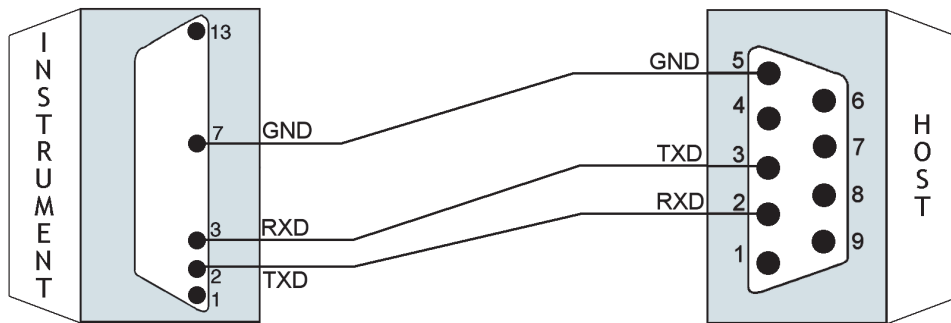
Table 2: Definitions

| Term | Definition |
|---------|--|
| Session | A total unit of communication activity used in this standard to indicate the events starting with the Establishment phase and ending with the Termination phase. |
| Test | A determination of a single analyte or a combination of values from other determinations or observations from which a variable or gradable result is derived. |
| Upload | The transmission of data from the Pentra Nexus Data Management System to the LIS. |

Physical connection (RS232)

Instrument RS DB25

- GND: ground
- TXD: transmission
- RXD: reception



ABX Format

1. Overview

- ABX format supports unidirectional or bidirectional connections.
- ABX format can have a different number of fields according to the transmitted items set up by the user (results, curves, flags, etc...) or according to the type of cycle.
- Fields sequence is not fixed.
- The result identifier is different according to the type of result: patient result («RESULT»), re-run result (RES-RR), QC result (QC-RES) etc... (See 4. "Data transmitted by the host to the analyzer", page 9).

2. Protocol description

2.1. Unidirectional mode

2.1.1. Typical unidirectional transmission from Instrument to Host

Table 3: Typical unidirectional transmission from Instrument to Host

| Instrument | <> | Host | Comment |
|------------------------|----|------|---------|
| <STX> + RESULT + <ETX> | > | | |

2.1.2. Typical unidirectional transmission from Instrument to Host with «SOH»\»EOT»

«SOH»\»EOT» option must be enabled on the instrument.

Table 4: Typical unidirectional transmission with «SOH»\»EOT» from Instrument to Host

| Instrument | <> | Host | Comment |
|------------------------|----|------|---------------------------|
| <SOH> | > | | Instrument takes the Line |
| <STX> + RESULT + <ETX> | > | | |
| | . | | |
| | . | | |
| | . | | |
| <STX> + RESULT + <ETX> | > | | |
| <EOT> | > | | Instrument frees the Line |

2.2. Bidirectionnal mode

2.2.1. Typical bidirectionnal transmission from Host to Instrument

Table 5: Typical transmission from Host to Instrument

| Host | < > | Instrument | Comment |
|----------------------|-----|------------|---------------------|
| <SOH> | > | | Host takes the Line |
| | < | <ENQ> | |
| <STX> + FILE + <ETX> | > | | |
| | < | <ACK> | |
| | . | | |
| | . | | |
| | . | | |
| <STX> + END + <ETX> | > | | Host frees the Line |
| | < | <ACK> | |

2.2.2. Typical bidirectionnal transmission from Instrument to Host

Table 6: Typical transmission from Instrument to Host

| Instrument | < > | Host | Comment |
|------------------------|-----|-------|---------------------------|
| <SOH> | > | | Instrument takes the Line |
| | < | <ENQ> | |
| <STX> + RESULT + <ETX> | > | | |
| | < | <ACK> | |
| | . | | |
| | . | | |

Table 6: Typical transmission from Instrument to Host

| Instrument | < > | Host | Comment |
|---------------------|-----|-------|---------------------------|
| | . | | |
| <STX> + END + <ETX> | > | | Instrument frees the Line |
| | < | <ACK> | |

2.3. Conflict management

Number of transmission if negative answer (NAK): 1
 Timeout: 15s

In case of SOH/SOH conflict, priority is given to Host. After an adjustable delay (8s by default) and if Host has not re-sent a SOH, instrument tries to send SOH again until timeout. This is done until automatic disconnection max. time is reached.

3. Message structure

3.1. Lines structure

HEADER:

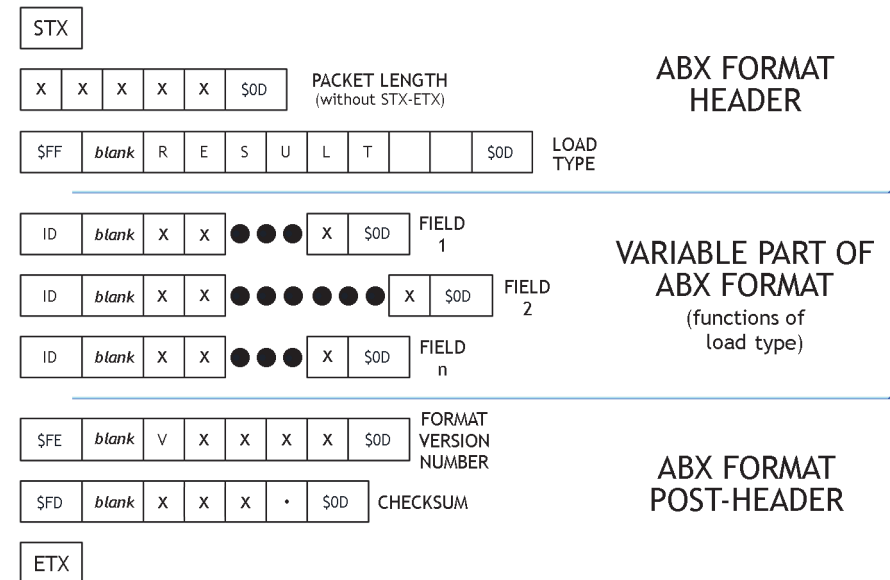
- STX
- Size + carriage return (Size: 5 bytes representing the total amount of the data except STX and ETX).
- Identifier followed by a Load Type + carriage return (Load: 8 character string preceded by a blank indicating the type of data).

VARIABLE PART:

- Identifier followed by the Information associated to the Load Type + carriage return (Identifier: 1 byte moving about \$21 to \$FF, it describes the information type which follows this indicator, always followed by a blank character \$20).
- Remainder of the other Identifiers and Information associated to the Load Type + carriage returns.
- Other Load Type blocs + Associated Information

POST-HEADER:

- Identifier followed by CheckSum + carriage return (CheckSum: Sum modulo 65536 of all characters except ETX, STX and all information about checksum (identifier - space - checksum - carriage return) in the hexadecimal format on 4 bytes, preceded by a blank character \$20).
- ETX



Diag.1: ABX format line structure

3.2. Control characters

Table 7: Standard control characters

| Control String | Hexadecimal value |
|----------------|-------------------|
| <ENQ> | \$05 |
| <ACK> | \$06 |
| <NAK> | \$15 |
| <STX> | \$02 |
| <ETX> | \$03 |

Table 7: Standard control characters

| Control String | Hexadecimal value |
|----------------|-------------------|
| <CR> | \$0D |
| <LF> | \$0A |
| <EOT> | \$04 |
| <SOH> | \$01 |

4. Data transmitted by the host to the analyzer

Data packet files are available only if the instrument has been set up with the remote controlled mode.

"FILE" request:

The data packet "FILE" is followed by \$75 or \$76 representing the patient file to obtain the type of test to be run on the corresponding sample.

Table 8: Example of transmission between Host and Instrument

| Flow | Dataflow | Comments |
|-----------------|---|---|
| Instrument>Host | \$01 | Pentra sends SOH |
| Host>Instrument | \$05 | Host responds ENQ |
| Instrument>Host | \$02\$FF FILE \$0D \$75 123456789012 \$0D \$03 | Pentra sends STX + First Query Message + ETX... |
| Host>Instrument | \$06 | Host responds ACK |
| Instrument>Host | | Pentra sends STX + Next Query Message + ETX |
| Host>Instrument | \$06 | Host responds ACK |
| Instrument>Host | | Pentra sends STX + Last Query Message + ETX |
| Host>Instrument | \$06 | Host responds ACK |
| Instrument>Host | \$0200043\$0D \$FF END \$0D \$03 | Pentra sends STX + Free line + ETX |
| Host>Instrument | \$06 | Host responds ACK |

Each data packet "FILE" is preceded and followed by STX and ETX.

Several requests of this type can be chained between a line bid and a line free in order to organize the grouping of the requests for the instruments equipped with an automatic sampling mode.

Table 9: Data packet strings

| Data packet string | Use |
|--------------------|-------------------|
| FILE | Patient file |
| END | Line free message |

Patient identification:

- All the described fields have a fixed size character string type and are completed with blanks on the right side for the non-significant information.
- n= number
- c= character

Table 10: Identifier list (Host to Instrument)

| Identifier | Correspondance | Example | Length | Format | Transmission | See Note |
|------------|---------------------|-------------------------------|--------|-------------------|--------------|----------|
| \$70 p | Analyzer number | 01 | 2+2+1 | Integers | required | |
| \$75 u | Id # or sample id. | 1450302154275-42 | 2+16+1 | String(16) | required | |
| \$76 v | Id. or patient name | SMITH Ronald | 2+30+1 | String(30) | required | |
| \$77 w | Birth date | YYYYMMDD | 2+8+1 | nnnnnnnn | optional | 1 |
| \$78 x | Age | 7d or 4w or 10m or 54y or 100 | 2+3+1 | String(3) | advised | 2 |
| \$79 y | Sex | 0, 1 or 2 | 2+1+1 | String(1) | advised | 3 |
| \$7A z | Origin | x | 2+1+1 | String(1) | optional | |
| \$7B { | Doctor | Dr Jones | 2+15+1 | String(15) | optional | |
| \$7C | Department | Cardiology | 2+10+1 | String(10) | optional | |
| \$7D } | Collection date | 06/08/99 13h15 | 2+14+1 | nn/nn/nn nnhnn | optional | |
| \$7E ~ | Comments | | 2+32+1 | String(32) | optional | |
| \$7F | Blood type | man | 2+16+1 | String(16) | optional | 4 |

Table 10: Identifier list (Host to Instrument)

| Identifier | Correspondance | Example | Length | Format | Transmission | See Note |
|------------|------------------------|---|--------|------------|--------------|----------|
| \$80 ç | Analysis type | defined on 1 character (see description). ' A ' : analysis CBC ' B ' : analysis DIF ' C ' : analysis RET ' E ' : analysis CBR ' F ' : analysis DIR ' G ' : no analysis (smearing SPS only) ' H ' : ERB ' I ' : CBE ' J ' : CBF | 2+1+1 | String(1) | advised | 5 |
| \$89 ë | SPS smearing mode | ECC | 2+3+1 | String(3) | optional | 6 |
| \$8A è | SPS smearing profile | 65G4 | 2+4+1 | String(4) | optional | 7 |
| \$8B ï | Patient identification | 200205125751 | 2+30+1 | String(30) | advised | 8 |



• NOTE 1 (\$77)

No check on \$77 compared to \$78.

• NOTE 2 (\$78)

\$78 is a 3 characters string completed on the right side by blanks.

If age > 99 years, the 3 characters are used for the age without unit (ex: 102).

• NOTE 3 (\$79)

0 or Blank: Unspecified, 1: Male, 2: Female

• NOTE 4 (\$7F)

\$7F must be one of the instrument blood type list. If not, it is generated according to the age (\$78) or for adults according to the sex (\$79).

• NOTE 5 (\$80)

Table 11: Test compatibility

| Instrument | CBC | DIFF | RET | CBR | DIR | ERB | CBE | CBF | SPS |
|-----------------------|-----|------|-----|-----|-----|-----|-----|-----|-----|
| Pentra DX Nexus | X | X | X | X | X | X | X | X | |
| Pentra DX Nexus + SPS | X | X | X | X | X | X | X | X | X |
| Pentra DF Nexus | X | X | | | | | | | |
| Pentra DF Nexus + SPS | X | X | | | | | | | X |

• NOTE 6 (\$89)

First character is blank +3 characters ECC:

E: Smearing

C: Staining

C: Criteria

When the file is received without \$89, the default type is applied.

Table 12: ECC combinations

| E | C | C | Action |
|-------|-------|-------|--|
| E | C | C | A slide for Smearing and Staining is done before test. A slide could be done after test, according to instrument Reflex testing conditions |
| E | C | blank | A slide for Smearing and Staining is done before test. Reflex testing conditions are inhibited |
| E | blank | blank | A slide for Smearing is done before test. Reflex testing conditions are inhibited |
| E | blank | C | A slide for Smearing is done before test. A slide could be done after test, according to instrument Reflex testing conditions |
| blank | blank | C | No Slide Before test. A slide could be done after test, according to instrument Reflex testing conditions |
| blank | blank | blank | No Slide Before test. Reflex testing conditions are inhibited |

• NOTE 7 (\$8A)

\$8A must be one of the Smearing profiles: drop volume, angle and speed.

• NOTE 8 (\$8B)

The Patient ID field can be transmitted, but it will be ignored by the instrument.

5. Data transmitted by the analyzer to the host

5.1. Packet type

The information described in the packet type allows the specification of the global message content: hematological routine results or statistic results.

Table 13: Packet type list

| Data packet string (8 characters) | Use |
|-----------------------------------|---|
| RESULT | Hematological result transmission on a routine mode |
| RES-RR | Hematological result transmission on automatic re-sampling mode |
| RES-BLK | Hematological result transmission on blank cycle |
| QC-RES-H | Result transmission of a high level control blood |
| QC-RES-M | Result transmission of a median level control blood |
| QC-RES-L | Result transmission of a low level control blood |
| FILE | Patient file request |
| QC-PRG-H | Patient File Query for High level control |
| QC-PRG-M | Patient File Query for Medium level control |
| QC-PRG-L | Patient File Query for Low level control |
| END | Connection end |

5.2. Identifier list (Instrument to Host)

Table 14: Identifier list (Instrument to Host)

| Identifier | Correspondance | Example | Length | Format | See Note |
|------------|--------------------------|--|----------|----------------------------|----------|
| \$6B k | Reagents list | | 2+168 +1 | String | 9 |
| \$6C l | Instrument Serial number | | 2+20+1 | String | |
| \$70 p | Analyzer number | 01 | 2+2+1 | Integers | |
| \$71 q | Analysis date and time | 03/01/05 13h15mn31s | 2+19+1 | String(19) | |
| \$72 r | Analyzer run number | 115 or 005CBC06 | 2+16+1 | String(16) | 10 |
| \$73 s | Analyzer sequence number | 0128: analysis counter since instrument starts | 2+4+1 | 2+16+1 | |
| \$74 t | Sampling mode | M: manual (open tube) R: rack (close tube) | 2+1+1 | String(1) | |
| \$75 u | Id # or sample id. | 1450302154275-42 | 2+16+1 | String(16) | |
| \$76 v | Id. or patient name | SMITH Ronald | 2+30+1 | String(30) | |
| \$77 w | Birth date | 16/03/72 or 03161972 | 2+8+1 | nn/nn/nn or nnnnnnnn | 10 |
| \$78 x | Age | 7d or 4w or 10m or 54y | 2+3+1 | String(3) | 11 |
| \$79 y | Sex | 0, 1 or 2 | 2+1+1 | String(1) | 12 |
| \$7A z | Origin | x | 2+1+1 | String(1) | |
| \$7B { | Doctor | Dr Jones | 2+15+1 | String(15) | |
| \$7C | Department | Cardiology | 2+10+1 | String(10) | |
| \$7D } | Collection date | 06/08/99 13h15 | 2+14+1 | nn/nn/nn nnhnn | |
| \$7E ~ | Comments | | 2+32+1 | String(32) | |
| \$7F | Blood type | man | 2+16+1 | String(16) | 13 |

Table 14: Identifier list (Instrument to Host)

| Identifier | Correspondance | Example | Length | Format | See Note |
|------------|------------------|---|--------|-----------|----------|
| \$80 ç | Analysis type | defined on 1 character (see description). 'A': analysis CBC 'B': analysis DIF 'C': analysis RET 'E': analysis CBR 'F': analysis DIR 'G': without analysis (smearing SPS only) 'H': ERB 'I': CBE 'J': CBF | 2+1+1 | String(1) | |
| \$81 ü | Sample rack type | 0: 10 positions 1: 15 positions 2: 32 positions | 2+1+1 | Integer | |
| \$82 é | Number of runs | 0, 1, ... | 2+1+1 | Integer | |
| \$83 â | Operator code | Bob | 2+3+1 | String(3) | |



• NOTE 9 (\$6B)

The Reagents list is on the following format: lot# (9 characters), space, installation of the reagent on the instrument (AAAMMJ), space, time of the reagent installation (HH:MM:SS) and space.

This format is equivalent for all the reagents.

• NOTE 10: (\$72)

Rack Mode: indicates «number of runs on a rack + Rack test mode + Tube position» with number of runs from 0 to 9, Rack number from 01 to 99 (according to the Instrument settings), Test (CBC, DIF, RET, ERB, DIR, CBR or CBE), position from 01 to 10

Stat Mode: contains a single number on 4 digits. This number automatically increments on each new stat analysis.

• NOTE 11 (\$78)

\$78 is a 3 characters string completed on the right handside by «spaces». If age exceeded 99 years, the 3 characters of the string are used for the age without unit (example: 102).

• NOTE 12 (\$79)

0 or blank: Unspecified, 1: Male, 2: Female

• NOTE 13 (\$7F)

\$7F must be one of the instrument blood type list. If not, it will be generated according to the age (\$78) or for adults by the sex (\$79).

5.2.1. Numerical result fields

- Units are standard units.
- If one parameter cannot be calculated by the analyzer, the field is replaced with --.--

Parameter status:

Following the numerical field, a first digit gives the counting rejection status or the suspicion, a second one gives the parameter value status according to high and low normalities, to high and low extreme values and to the overloading capacities.

Table 15: Identifier First digit

| First digit (letter) | Correspondance |
|----------------------|---|
| R | Parameter rejected for a counting default |
| S | Suspicious parameter value |
| D | Value obtained by dilution |
| blank | No anomaly observed |

Table 16: Identifier Second digit

| Second digit (letter) | Correspondance |
|-----------------------------------|--|
| B (french) or L (other languages) | Parameter < to the lower extreme value |
| b (french) or l (other languages) | Parameter < to the low normal value |
| blank | Parameter normal value |
| h | Parameter > to the high normal value |
| H | Parameter > to the high extreme value |
| C | Platelet concentrate |
| O | Parameter exceeding the capacity |

Example: 5.5 millions RBC with a counting error in the standard units:

\$32 \$20 \$30 \$35 \$2E \$35 \$30 \$52 \$68 \$0D or «2 05.50Rh» + carriage return.

Table 17: CBC numerical result fields list

| Identifier | Correspondance | Example | Format (Length) |
|------------|----------------|---------|-----------------|
| \$21 ! | WBC | 07.40 | 2+String(7)+1 |
| \$32 2 | RBC | 04.64 | 2+String(7)+1 |
| \$33 3 | Hgb | 14.17 | 2+String(7)+1 |
| \$34 4 | Hct | 43.95 | 2+String(7)+1 |
| \$35 5 | MCV | 94.68 | 2+String(7)+1 |
| \$36 6 | MCH | 30.53 | 2+String(7)+1 |
| \$37 7 | MCHC | 32.24 | 2+String(7)+1 |
| \$38 8 | RDW | 12.98 | 2+String(7)+1 |
| \$40 @ | PLT | 00401 | 2+String(7)+1 |
| \$41 A | MPV | 07.94 | 2+String(7)+1 |
| \$42 B | THT | 0.318 | 2+String(7)+1 |
| \$43 C | PDW | 13.50 | 2+String(7)+1 |

Table 18: DIF numerical result fields list

| Identifier | Correspondance | Example | Format (Length) |
|------------|--------------------------|---------|-----------------|
| \$21 ! | WBC | 07.40 | 2+String(7)+1 |
| \$22 " | Lymphocytes (#) | 02.03 | 2+String(7)+1 |
| \$23 # | Lymphocytes (%) | 27.40 | 2+String(7)+1 |
| \$24 \$ | Monocytes (#) | 00.70 | 2+String(7)+1 |
| \$25 % | Monocytes (%) | 09.40 | 2+String(7)+1 |
| \$28 (| Neutrophils (#) | 04.51 | 2+String(7)+1 |
| \$29) | Neutrophils (%) | 60.90 | 2+String(7)+1 |
| \$2A * | Eosinophils (#) | 00.13 | 2+String(7)+1 |
| \$2B + | Eosinophils (%) | 01.70 | 2+String(7)+1 |
| \$2C , | Basophils (#) | 00.04 | 2+String(7)+1 |
| \$2D - | Basophils (%) | 00.60 | 2+String(7)+1 |
| \$2E . | Atypical Lymphocytes (#) | 00.11 | 2+String(7)+1 |
| \$2F / | Atypical Lymphocytes (%) | 01.49 | 2+String(7)+1 |
| \$30 0 | Large Immature Cells (#) | 00.03 | 2+String(7)+1 |
| \$31 1 | Large Immature Cells (%) | 00.43 | 2+String(7)+1 |
| \$32 2 | RBC | 04.64 | 2+String(7)+1 |
| \$33 3 | Hgb | 14.17 | 2+String(7)+1 |
| \$34 4 | Hct | 43.95 | 2+String(7)+1 |
| \$35 5 | MCV | 94.68 | 2+String(7)+1 |
| \$36 6 | MCH | 30.53 | 2+String(7)+1 |
| \$37 7 | MCHC | 32.24 | 2+String(7)+1 |
| \$38 8 | RDW | 12.98 | 2+String(7)+1 |
| \$40 @ | PLT | 00401 | 2+String(7)+1 |
| \$41 A | MPV | 07.94 | 2+String(7)+1 |
| \$42 B | THT | 0.318 | 2+String(7)+1 |
| \$43 C | PDW | 13.50 | 2+String(7)+1 |

Table 19: RET numerical result fields list

| Identifier | Correspondance | Example | Format (Length) |
|------------|----------------------------|---------|-----------------|
| \$32 2 | RBC | 04.64 | 2+String(7)+1 |
| \$3B ; | Reticulocytes (#) | 0656 | 2+String(7)+1 |
| \$3C < | Reticulocytes (%) | 01.41 | 2+String(7)+1 |
| \$3D = | Reticulocytes Low (%) | 80.34 | 2+String(7)+1 |
| \$3E > | Reticulocytes Median (%) | 14.96 | 2+String(7)+1 |
| \$3F ? | Reticulocytes High (%) | 04.90 | 2+String(7)+1 |
| \$47 G | Retic Immatures | 00.02 | 2+String(7)+1 |
| \$48 H | Mean fluorescent index (%) | 17.97 | 2+String(7)+1 |
| \$49 I | Mean reticulocyte vol. | 107.5 | 2+String(7)+1 |
| \$4A J | Corrected ret. count (%) | 01.38 | 2+String(7)+1 |
| \$4C L | IRF | .0500 | 2+String(7)+1 |

Table 20: ERB numerical result fields list

| Identifier | Correspondance | Example | Format (Length) |
|------------|----------------|---------|-----------------|
| \$21 ! | WBC | 04.64 | 2+String(7)+1 |
| \$BA | ERB% | 07.20 | 2+String(7)+1 |
| \$BB | ERB# | 01.70 | 2+String(7)+1 |
| \$BE | CWBC | 24.30 | 2+String(7)+1 |

Table 21: CBR numerical result fields list

| Identifier | Correspondance | Example | Format (Length) |
|------------|----------------|---------|-----------------|
| \$21 ! | WBC | 07.40 | 2+String(7)+1 |
| \$32 2 | RBC | 04.64 | 2+String(7)+1 |
| \$33 3 | Hgb | 14.17 | 2+String(7)+1 |

Table 21: CBR numerical result fields list

| Identifier | Correspondance | Example | Format (Length) |
|------------|----------------------------|---------|-----------------|
| \$34 4 | Hct | 43.95 | 2+String(7)+1 |
| \$35 5 | MCV | 94.68 | 2+String(7)+1 |
| \$36 6 | MCH | 30.53 | 2+String(7)+1 |
| \$37 7 | MCHC | 32.24 | 2+String(7)+1 |
| \$38 8 | RDW | 12.98 | 2+String(7)+1 |
| \$3B ; | Reticulocytes (#) | .0656 | 2+String(7)+1 |
| \$3C < | Reticulocytes (%) | 01.41 | 2+String(7)+1 |
| \$3D = | Reticulocytes Low (%) | 80.34 | 2+String(7)+1 |
| \$3E > | Reticulocytes Median (%) | 14.96 | 2+String(7)+1 |
| \$3F ? | Reticulocytes High (%) | 04.90 | 2+String(7)+1 |
| \$40 @ | PLT | 00401 | 2+String(7)+1 |
| \$41 A | MPV | 07.94 | 2+String(7)+1 |
| \$42 B | THT | 0.318 | 2+String(7)+1 |
| \$43 C | PDW | 13.50 | 2+String(7)+1 |
| \$47 G | Retic Immatures | 00.02 | 2+String(7)+1 |
| \$48 H | Mean fluorescent index (%) | 17.97 | 2+String(7)+1 |
| \$49 I | Mean reticulocyte vol. | 107.5 | 2+String(7)+1 |
| \$4A J | Corrected ret. count (%) | 01.38 | 2+String(7)+1 |
| \$4C L | IRF | .0500 | 2+String(7)+1 |

Table 22: CBE numerical result fields list

| Identifier | Correspondance | Example | Format (Length) |
|------------|----------------|---------|-----------------|
| \$21 ! | WBC | 07.40 | 2+String(7)+1 |
| \$32 2 | RBC | 04.64 | 2+String(7)+1 |
| \$33 3 | Hgb | 14.17 | 2+String(7)+1 |
| \$34 4 | Hct | 43.95 | 2+String(7)+1 |

Table 22: CBE numerical result fields list

| Identifier | Correspondance | Example | Format (Length) |
|------------|----------------|---------|-----------------|
| \$35 5 | MCV | 94.68 | 2+String(7)+1 |
| \$36 6 | MCH | 30.53 | 2+String(7)+1 |
| \$37 7 | MCHC | 32.24 | 2+String(7)+1 |
| \$38 8 | RDW | 12.98 | 2+String(7)+1 |
| \$40 @ | PLT | 00401 | 2+String(7)+1 |
| \$41 A | MPV | 07.94 | 2+String(7)+1 |
| \$42 B | THT | 0.318 | 2+String(7)+1 |
| \$43 C | PDW | 13.50 | 2+String(7)+1 |
| \$BA | ERB% | 07.20 | 2+String(7)+1 |
| \$BB | ERB# | 01.70 | 2+String(7)+1 |
| \$BE | CWBC | 24.30 | 2+String(7)+1 |

Table 23: DIR numerical result fields list

| Identifier | Correspondance | Example | Format (Length) |
|------------|-----------------|---------|-----------------|
| \$21 ! | WBC | 07.40 | 2+String(7)+1 |
| \$22 " | Lymphocytes (#) | 02.03 | 2+String(7)+1 |
| \$23 # | Lymphocytes (%) | 27.40 | 2+String(7)+1 |
| \$24 \$ | Monocytes (#) | 00.70 | 2+String(7)+1 |
| \$25 % | Monocytes (%) | 09.40 | 2+String(7)+1 |
| \$28 (| Neutrophils (#) | 04.51 | 2+String(7)+1 |
| \$29) | Neutrophils (%) | 60.90 | 2+String(7)+1 |
| \$2A * | Eosinophils (#) | 00.13 | 2+String(7)+1 |
| \$2B + | Eosinophils (%) | 01.70 | 2+String(7)+1 |
| \$2C , | Basophils (#) | 00.04 | 2+String(7)+1 |
| \$2D - | Basophils (%) | 00.60 | 2+String(7)+1 |

Table 23: DIR numerical result fields list

| Identifier | Correspondance | Example | Format (Length) |
|------------|--------------------------|---------|-----------------|
| \$2E . | Atypical Lymphocytes (#) | 00.11 | 2+String(7)+1 |
| \$2F / | Atypical Lymphocytes (%) | 01.49 | 2+String(7)+1 |
| \$30 0 | Large Immature Cells (#) | 00.03 | 2+String(7)+1 |
| \$31 1 | Large Immature Cells (%) | 00.43 | 2+String(7)+1 |
| \$B4 ´ | IML (%) | 000.5 | 2+String(7)+1 |
| \$B5 µ | IML (#) | 00.05 | 2+String(7)+1 |
| \$B6 ¶ | IMM (%) | 000.5 | 2+String(7)+1 |
| \$B7 · | IMM (#) | 00.05 | 2+String(7)+1 |
| \$B8 ¸ | IMG (%) | 000.5 | 2+String(7)+1 |
| \$B9 ¹ | IMG (#) | 00.05 | 2+String(7)+1 |
| \$32 2 | RBC | 04.64 | 2+String(7)+1 |
| \$33 3 | Hgb | 14.17 | 2+String(7)+1 |
| \$34 4 | Hct | 43.95 | 2+String(7)+1 |
| \$35 5 | MCV | 94.68 | 2+String(7)+1 |
| \$36 6 | MCH | 30.53 | 2+String(7)+1 |
| \$37 7 | MCHC | 32.24 | 2+String(7)+1 |
| \$38 8 | RDW | 12.98 | 2+String(7)+1 |
| \$3B ; | Reticulocytes (#) | 0656 | 2+String(7)+1 |
| \$3C < | Reticulocytes (%) | 01.41 | 2+String(7)+1 |
| \$3D = | Reticulocytes Low (%) | 80.34 | 2+String(7)+1 |
| \$3E > | Reticulocytes Median (%) | 14.96 | 2+String(7)+1 |
| \$3F ? | Reticulocytes High (%) | 04.90 | 2+String(7)+1 |
| \$40 @ | PLT | 00401 | 2+String(7)+1 |
| \$41 A | MPV | 07.94 | 2+String(7)+1 |
| \$42 B | THT | 0.318 | 2+String(7)+1 |
| \$43 C | PDW | 13.50 | 2+String(7)+1 |



• NOTE 14:

«RUO message» is a warning message, transmitted always in english language. Its content and size depend on the instrument.

5.2.3. Pathology messages fields

Each pathology is described by a group of 4 characters followed by a blank, except for the last one.

The content of the pathology depends of the chosen language.

Only detected pathologies are transmitted. A common header (????) to the 4 Pathology message groups, indicates that the pathological interpretation is impossible.

Table 27: Identifier list

| Identifier | Parameter | Format | Length |
|------------|-----------|---|--------------------|
| \$54 T | WBC | String of characters | 1 + 12x5 + 1 (max) |
| \$55 U | RBC | String of characters | 1 + 7x5 + 1 (max) |
| \$56 V | PLT | String of characters | 1 + 4x5 + 1 (max) |
| \$69 i | RET | String of characters | 1 + 2x5 + 1 (max) |
| \$C5 Å | ERB | String of characters Reserved but not sent | 0 |

When there is no pathological message, length is: 2+0+1

Table 28: Pathological format description (English and other languages)

| Population | Message | Signification |
|------------|-----------------|------------------------------|
| WBC | LEU+ or LEU- | Leukocytosis Leukopenia |
| | LYM+ or LYM- | Lymphocytosis Lymphopenia |
| | NEU+ or NEU- | Neutrophilia Neutropenia |

Table 28: Pathological format description (English and other languages)

| Population | Message | Signification |
|------------|----------------------------|--|
| | EOS+ | Eosinophilia |
| | MYEL | Myelemia |
| | LIMC | Large Immature Cells |
| | ALYM | Atypic Lymphocytes |
| | LSHT | Left shift |
| | NRBC | Nucleated Red Blood Cells |
| | MON+ | Monocytosis |
| | BAS+ | Basophilia |
| | BLST | Blasts |
| RBC | ANEM | Anemia |
| | ANI1 or ANI2 or ANI3 | Anisocytosis level 1 Anisocytosis level 2 Anisocytosis level 3 |
| | MIC1 or MIC2 or MIC3 | Microcytes level 1 Microcytes level 2 Microcytes level 3 |
| | MAC1 or MAC2 or MAC3 | Macrocytes level 1 Macrocytes level 2 Macrocytes level 3 |
| | MICR | Microcytosis |
| | MACR | Macrocytosis |
| | HCR1 or HCR2 or HCR3 | Hypochromia level 1 Hypochromia level 2 Hypochromia level 3 |
| | CAGG | Cold agglutinin |
| | ERYT | Erythrocytosis |
| Plt | THR+ | Thrombocytosis |
| | THR- | Thrombopenia |

Table 28: Pathological format description (English and other languages)

| Population | Message | Signification |
|-----------------|-----------------|----------------------------------|
| | PLAG | Platelet aggregates |
| | SCEL | Small cells |
| | MICC | Microcytes |
| | SCHI | Schizocytes |
| | MAPL | Macro platelet |
| Reticulocytes | IMMT | Immature reticulocytes |
| | RET+ or RET- | Reticulocytosis Reticulopenia |
| All populations | ???? | No interpretation |
| | PANC | Pancytopenia |

Table 29: Pathological format description (French)

| Population | Messages | Signification |
|------------|-----------------|-----------------------------|
| GB | LEU+ or LEU- | Leucocytose Leucopénie |
| | LYM+ or LYM- | Lymphocytose Lymphopénie |
| | NEU+ or NEU- | Neutrophilie Neutropénie |
| | EOS+ | Eosinophilie |
| | MYEL | Myélémie |
| | GCIM | Grandes Cellules Immatures |
| | LYAT | Lymphocytes atypiques |
| | FORG | Formule gauche |
| | MON+ | Monocytose |
| | BAS+ | Basophilie |
| | BLST | Blastes |

Table 29: Pathological format description (French)

| Population | Messages | Signification |
|--------------------|----------------------------|--|
| GR | ANEM | Anémie |
| | ANI1 or ANI2 or ANI3 | Anisocytose niveau 1 Anisocytose niveau 2 Anisocytose niveau 3 |
| | MIC1 or MIC2 or MIC3 | Microcytes niveau 1 Microcytes niveau 2 Microcytes niveau 3 |
| | MAC1 or MAC2 or MAC3 | Macrocytes niveau 1 Macrocytes niveau 2 Macrocytes niveau 3 |
| | MICR | Microcytose |
| | MACR | Macrocytose |
| | HCR1 or HCR2 or HCR3 | Hypochromie niveau 1 Hypochromie niveau 2 Hypochromie niveau 3 |
| | AGGF | Agglutinine froide |
| | POLY | Erythrocytose |
| Pla | THR+ | Thrombocytose |
| | THR- | Thrombopénie |
| | AGPL | Agrégats plaquettaires |
| | PECL | Petits éléments cellulaires |
| | MICC | Microcytes |
| | SCHI | Schizocytes |
| | MAPL | Macro plaquettes |
| Réticulocytes | IMMT | Réticulocytes immatures |
| | RET+ or RET- | Réticulocytose Réticulopénie |
| Toutes populations | ???? | Pas d'interprétation possible |
| | PANC | Pancytopénie |

5.2.4. Histograms

5.2.4.1. Histograms

Histograms are transmitted on 128 channels, preceded by a blank. They are automatically rescaled to a 223 maximum amplitude value. The zero amplitude value is \$20, the maximum amplitude value is \$FF.

Extended format:

The extended format includes all the height information relative to each channel. It is constituted by a chart of 256 [RES] entries of 16 bits each.

These 512 bytes chart is encoded before being transmitted. The format is as follows: identifier, space, encoding type on 8 characters (od or uuencode), space, encoded data size on 5 characters, space, data then carriage return.

5.2.4.2. Separation thresholds

It is the channel number (decimal value) enclosing areas on the histograms or on the matrix. Each threshold is transmitted on 3 bytes preceded by a blank.

5.2.4.3. Format description of the threshold transmission

A. WBC thresholds

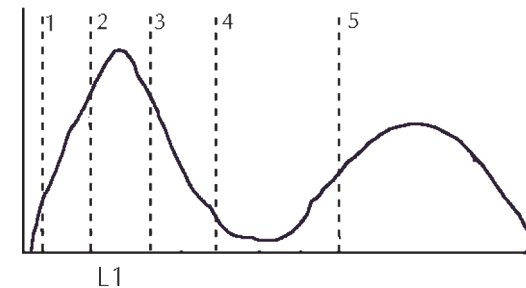
Separation thresholds 1-2-3 allow the L1 flag determination. For the analyzers in LMG mode, the 4-5 thresholds allow the separation of the 3 populations Lymphocytes, Monocytes, Granulocytes.

Example 1: output format of the WBC curve thresholds for an LMG sampling. In this example, the analyzer does not send the calculation thresholds of the L1 flag.

«] 000 000 000 040 060» + carriage return.

Example 2: output format of the WBC curve thresholds for CBC and DIFF sampling. In this 5 parts DIFF analyzer, the LMG is not measured, the 4-5 thresholds are not significant.

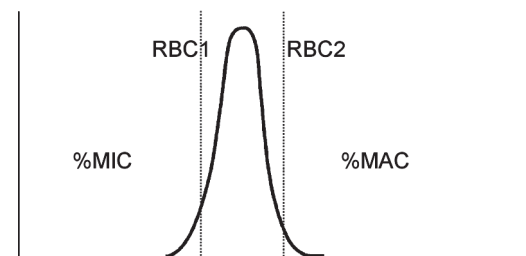
«] 005 008 020 000 000» + carriage return.



Diag.2: WBC histogram

B. RBC thresholds

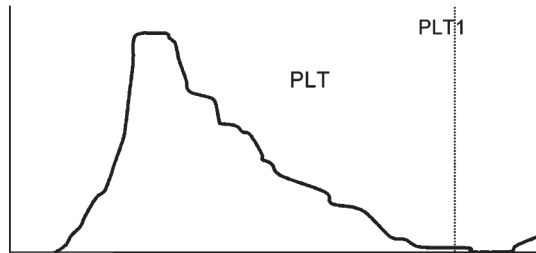
Separation thresholds 1-2 allow the calculation of the microcytic and macrocytic cell proportions.



Diag.3: RBC histogram

C. PLT thresholds

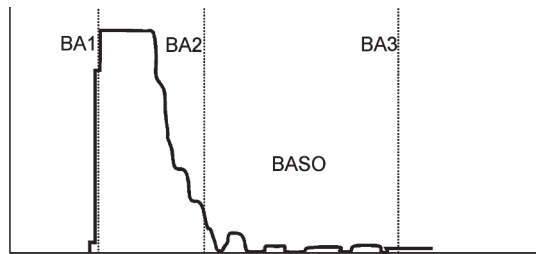
The threshold 1 is the number of the last channel used to calculate the PLT number.



Diag.4: Plt histogram

D. Basophil thresholds

Thresholds 1-2-3 allow the determination of the basophil proportion regarding the total number of WBCs.



Diag.5: BASO histogram

Table 30: Histogram format description

| Identifier | Parameter | Format | Length |
|------------|-----------|---------------------------|---------|
| \$57 W | WBC | Amplitude of each channel | 2+128+1 |
| \$58 X | RBC | Amplitude of each channel | 2+128+1 |
| \$59 Y | Plt | Amplitude of each channel | 2+128+1 |

Table 30: Histogram format description

| Identifier | Parameter | Format | Length |
|------------|---------------------|---------------------------|---------|
| \$5A Z | Basophils | Amplitude of each channel | 2+128+1 |
| \$5D] | WBC thresholds | 5 thresholds | 1+20+1 |
| \$5E ^ | RBC thresholds | 2 thresholds | 1+8+1 |
| \$5F _ | PLT thresholds | 1 threshold | 1+4+1 |
| \$60 ' | Basophil thresholds | 3 thresholds | 1+12+1 |

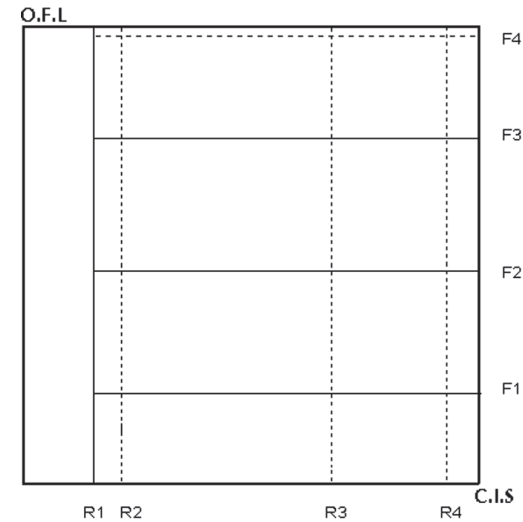
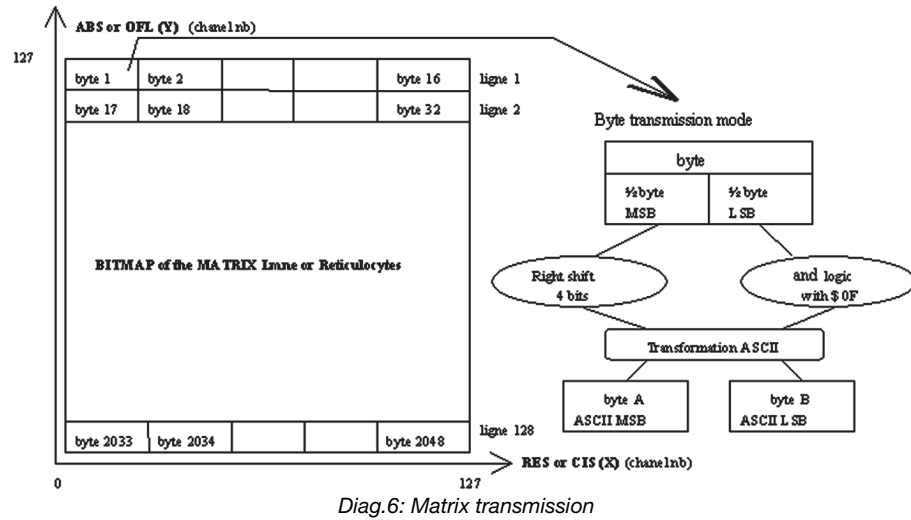
5.2.5. Matrix principles

A. ERB-RETIC Matrix principles

Screen bitmap: 2048 graphic bytes matrix are transmitted on 4096 ASCII bytes, preceded by a space. Each group of 2 ASCII bytes is the value of 1 graphic byte represented from the left to the right and from the top to the bottom of the screen. The matrix ERB-RET [128(ABS) x 128(RES)] is transmitted according to the same process.

B. LMNE matrix principles

Screen bitmap: 4096 graphic bytes matrix are transmitted on 8192 ASCII bytes, preceded by a space. Each group of 2 ASCII bytes is the value of 1 graphic byte represented from the left to the right and from the top to the bottom of the screen. The double matrix Lmne [128(ABS) x 256(RES)] is transmitted according to the same process.



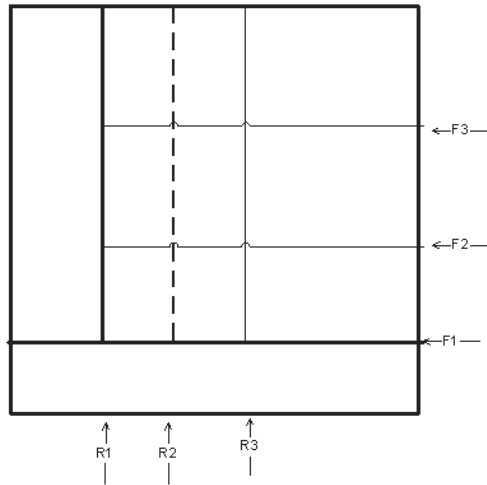
5.2.6. Matrix thresholds

A. Reticulocyte matrix thresholds

The 4 resistive thresholds are transmitted in the following order: R1, R2, R3, R4. Then the 4 fluorescent thresholds are following: F1, F2, F3, F4.

B. ERB matrix thresholds

The 3 CIS thresholds are transmitted in the following order: R1, R2, R3. Then the 3 OFL thresholds are following: F1, F2, F3.



Diag.8: ERB matrix thresholds

C. LMNE matrix thresholds

The 12 resistive thresholds are transmitted in the following order: BFL, BFN, BFE, NG, ND, LG, LYA, LMN, LI, MI, MDI, IGI.

The 11 absorbance thresholds are transmitted in the following order: NL, NE, MND, LMI, MMD, IB, IH, IGIB, IGIH, GIB, GIH.

The width of the areas (002 channels) describing the proximity thresholds (ANE, AMN, ALN) are also transmitted.

Table 31: Channel Numbers for Resistive Thresholds

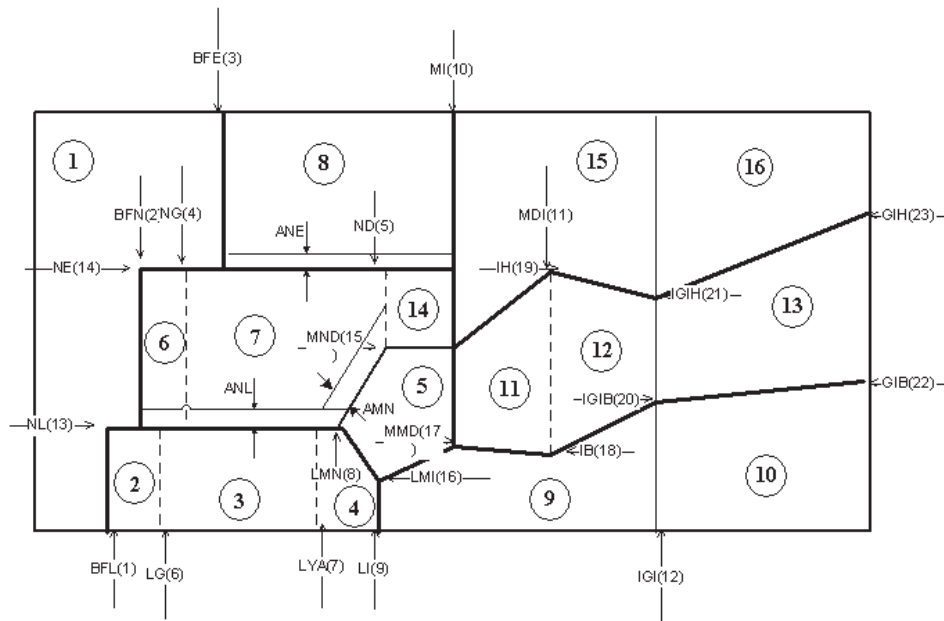
| Thresholds | BFL | BFN | BFE | NG | ND | LG | LYA | LMN | LI | MI | MDI | IGI |
|-----------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Channel numbers | 022 | 025 | 048 | 037 | 100 | 030 | 067 | 068 | 088 | 127 | 145 | 190 |

Table 32: Channel Numbers for Absorbance Thresholds

| Thresholds | NL | NE | MND | LMI | MMD | IB | IH | IGIB | IGIH | GIB | GIH |
|-----------------|-----|-----|-----|-----|-----|-----|-----|------|------|-----|-----|
| Channel numbers | 031 | 069 | 050 | 021 | 026 | 028 | 055 | 031 | 070 | 037 | 095 |

Table 33: Histogram & Matrix format description

| Identifier | Parameter | Format | Length |
|------------|--------------------------------|--|----------|
| \$5C \ | Reticulocyte matrix | Screen bitmap | 2+4096+1 |
| \$C6 Æ | ERB matrix | Screen bitmap | 2+4096+1 |
| \$63 c | Double matrix Lmne | screen bitmap | 2+8192+1 |
| \$C8 È | Lmne matrix thresholds | 12 RES thresholds /11 ABS thresholds 3 proximity thresholds | 1+104+1 |
| \$62 b | Reticulocyte matrix thresholds | 4 CIS thresholds, 4 OFL thresholds | 1+32+1 |
| \$C9 É | ERB matrix thresholds | 3 CIS thresholds, 3 OFL thresholds | 1+24+1 |



Diag.9: Lmne matrix thresholds

5.2.7. Other identifiers

Identifier \$FB: Identifies the analyzer type when communicating.

Identifier \$FC: This identifier allows the transmission of a number which can be an error number, a position number, a burn-in sequence number or a status in hexadecimal mode (Not available yet).

Identifier \$FD: Checksum value (see section on the message structure).

Identifier \$FE: The version number is linked to the development of the hematological message identifiers.



Identifier \$FC: The error list is dedicated to the "remote" mode. For \$FB and \$FF, the strings having less than 8 characters are completed on the right side by blanks.

Table 34: Other identifiers

| Identifier | Correspondance | Format | Length |
|------------|-------------------------------|-----------------------------|---------|
| \$8C | Message content | Character string | 2+512+1 |
| \$FB | Analyzer name | Character string | 2+8+1 |
| \$FC | Number | 8 decimal bytes | 2+8+1 |
| \$FD | 16 bits check sum value | 4 hexadecimal bytes | 2+4+1 |
| \$FE | Version N° of Identifier list | String of characters: Vx.xx | 2+5+1 |

6. Query mode

6.1. Sending orders

Requests sent by the host when the line is free.

Query mode:

- This optional mode allows the Host to selectively load the working list of each sample, once the barcode of the sample is read and a Query request is emitted by the instrument.
- This mode is of particular interest when the Host system manages several instruments analysers. In this case, the Query request transmitted by one of the analysers allows the Host system to load the working list on the instrument identified by the presence of the sample on this analyzer.
- The Query request is a 'FILE' type message and encapsulates 1 or several blocks surrounded by STX & ETX including the '\$75' type line followed by the identification of the sample (barcodes) (Maximum 10 Blocks per Query request).
- Transmission of the Query requests is carried out by instrument immediately after the tray of 10 samples is read. Only the samples identified by a barcode, and for which instrument did not receive a working list are transmitted in the QUERY request.
- The Host system has an answering delay which is adjustable on the analyzer (25 seconds by default). This delay is fixed after transmission of the last Query message, in order to return the message to load the working list of the sample or the samples concerned. Once the delay has been respected and in the case where no message is received by the analyzer, the rack of samples is automatically discharged without carrying out tests.
- The adjustment of the answering delay of the Host system is ideally fixed at 25 seconds by default. It is possible to change the value of this parameter, however, from 30 seconds on the analyser generates a supplementary waiting cycle of 30 seconds, or 2 waiting cycles from 60 seconds, involving a reduction of the analytical output capacity.

Table 35: QUERY request line structure

| Identifier | Correspondance | Format | Length |
|------------|------------------|------------------|--------|
| \$FF y | Data Packet | Character string | 2+8+1 |
| \$75 u | Identification # | Character string | 2+16+1 |

Loading protocol of a working list in answer to a QUERY request:

Table 36: Instrument transmits to the Host a QUERY request

| Flow | Dataflow | Comments |
|-----------------|--|--|
| Instrument>Host | \$01 | Pentra sends SOH |
| Host>Instrument | \$05 | Host responds ENQ |
| Instrument>Host | \$02\$FF FILE \$OD \$75 123456789012 \$OD \$03 | Pentra sends STX + First Query Message + ETX |
| Host>Instrument | \$06 | Host responds ACK |
| Instrument>Host | | Pentra sends STX + Next Query Message + ETX |
| Host>Instrument | \$06 | Host responds ACK |
| Instrument>Host | | Pentra sends STX + Last Query Message + ETX |
| Host>Instrument | \$06 | Host responds ACK |
| Instrument>Host | \$02 00043\$OD \$FF END \$OD \$03 | Pentra sends STX + Free line + ETX |
| Host>Instrument | \$06 | Host responds ACK |

Once the Host receives a Query type message, it returns a message to load the working list for the sample or samples concerned, respecting the delay programmed on the instrument (25 seconds by default).

6.2. Resampling and reflex testing

- This optional mode offers the possibility to the Host system of returning the re-sampling request to the analyser, according to a decision algorithm calculated by the Host system and in answer to an analytical result transmitted by the analyser.
- The request of re-sampling allows for the carrying out of the same tests as those requested during the former sampling procedure, or any other test amongst those available. It is therefore possible for example to carry out a request for complementary tests during the re-sampling procedure.
- When the remote controlled re-sampling mode is activated and after transmission of each result the analyser waits for the re-sampling decision message from the Host system. Whatever decision is taken by the Host system, it returns a message, either a re-sampling request, or when the result obtained does not require re-sampling the freeing of the blood sample without re-sampling.
- The Host system has an answering delay which is adjustable on the analyser (25 seconds by default). This delay is fixed after transmission of the last result in order to return the re-sampling request or the message to free the sample. Once the delay has been respected and in the case where no message is received by the analyser, the rack of samples is automatically discharged without re-sampling .
- The adjustment of the answering delay of the Host system is ideally fixed at 25 seconds by default. It is possible to change the value of this parameter, however, from 30 seconds on the analyser generates a supplementary waiting cycle of 30 seconds, or 2 waiting cycles from 60 seconds involving consequently a reduction of the analytical output capacity.

Table 37: Structure of lines included in the message «re-sampling request»

| Identifier | Correspondance | Format | Length |
|------------|----------------|-------------------------------------|--------|
| \$FF ÿ | Data Packet | Character string | 2+8+1 |
| \$75 u | Identification | Character string | 2+16+1 |
| \$80 Ç | Analysis type | Defined on 1 character (See Note 5) | 2+1+1 |

Table 38: Structure of lines included in the message «end of re-sampling»

| Identifier | Correspondance | Format | Length |
|------------|----------------|------------------|--------|
| \$FF ÿ | Data Packet | Character string | 2+8+1 |
| \$75 u | Identification | Character string | 2+16+1 |
| \$80 Ç | Analysis type | '@' | 2+1+1 |

Table 39: Transmission of results protocol and insertion of automatic re-sampling

| Flow | Dataflow | Comments |
|-----------------|---|---------------------------------|
| Instrument>Host | \$01 | Pentra sends SOH |
| Host>Instrument | \$05 | Host responds ENQ |
| Instrument>Host | \$0205395\$OD \$FF RESULT \$OD \$03 | Pentra sends STX + Result + ETX |

Table 39: Transmission of results protocol and insertion of automatic re-sampling

| Flow | Dataflow | Comments |
|-----------------|---|------------------------------------|
| Host>Instrument | \$06 | Host responds ACK |
| Instrument>Host | \$02 00043\$OD \$FF END \$OD \$03 | Pentra sends STX + Free line + ETX |
| Host>Instrument | \$06 | Host responds ACK |

Once the line is free the Host returns a re-sampling message in a delay of <25s ideally.

Table 40: Host sends «re-sampling message»

| Flow | Dataflow | Comments |
|-----------------|---|----------------------------------|
| Host>Instrument | \$01 | Host sends SOH |
| Instrument>Host | \$05 | Pentra responds ENQ |
| Host>Instrument | \$02\$FF FILE \$OD \$75 123456789012 \$80 B \$OD \$03 | Host sends STX + ReRun + ETX |
| Instrument>Host | \$06 | Pentra responds ACK |
| Host>Instrument | \$02 00043\$OD \$FF END \$OD \$03 | Host sends STX + Free line + ETX |
| Instrument>Host | \$06 | Pentra responds ACK |

...or the Host returns a message «end of re-sampling»

Table 41: Host sends «end of re-sampling»

| Flow | Dataflow | Comments |
|-----------------|---|---------------------------------------|
| Host>Instrument | \$01 | Host sends SOH |
| Instrument>Host | \$05 | Pentra responds ENQ |
| Host>Instrument | \$02\$FF FILE \$OD \$75 123456789012 \$80 @ \$OD \$03 | Host sends STX + No more RerRun + ETX |
| Instrument>Host | \$06 | Pentra responds ACK |
| Host>Instrument | \$02 00043\$OD \$FF END \$OD \$03 | Host sends STX + Free line + ETX |
| Instrument>Host | \$06 | Pentra responds ACK |

6.3. QC Query mode

The communication from Pentra ML to Analyzer allows to receive an order in the quality Control mode.

- The \$FF field becomes "QC-PRG-H", "QC-PRG-M" or "QC-PRG-L" according to the quality control level.
- The \$75 field (identification number defined on 16 characters) and the \$80 field (Analysis Type defined on 1 character) are mandatory otherwise the string is rejected.
- The analysis Type must be: CBC or DIF or RET or ERB

Example of a DIF Low QC sample with identification number PX088-L :

\$FF \$20 QC-PRG-L \$0D \$75 \$20 PX088-L \$20 \$20 \$20 \$20 \$20 \$20 \$20 20 \$0D
\$80 \$20 B \$0D

