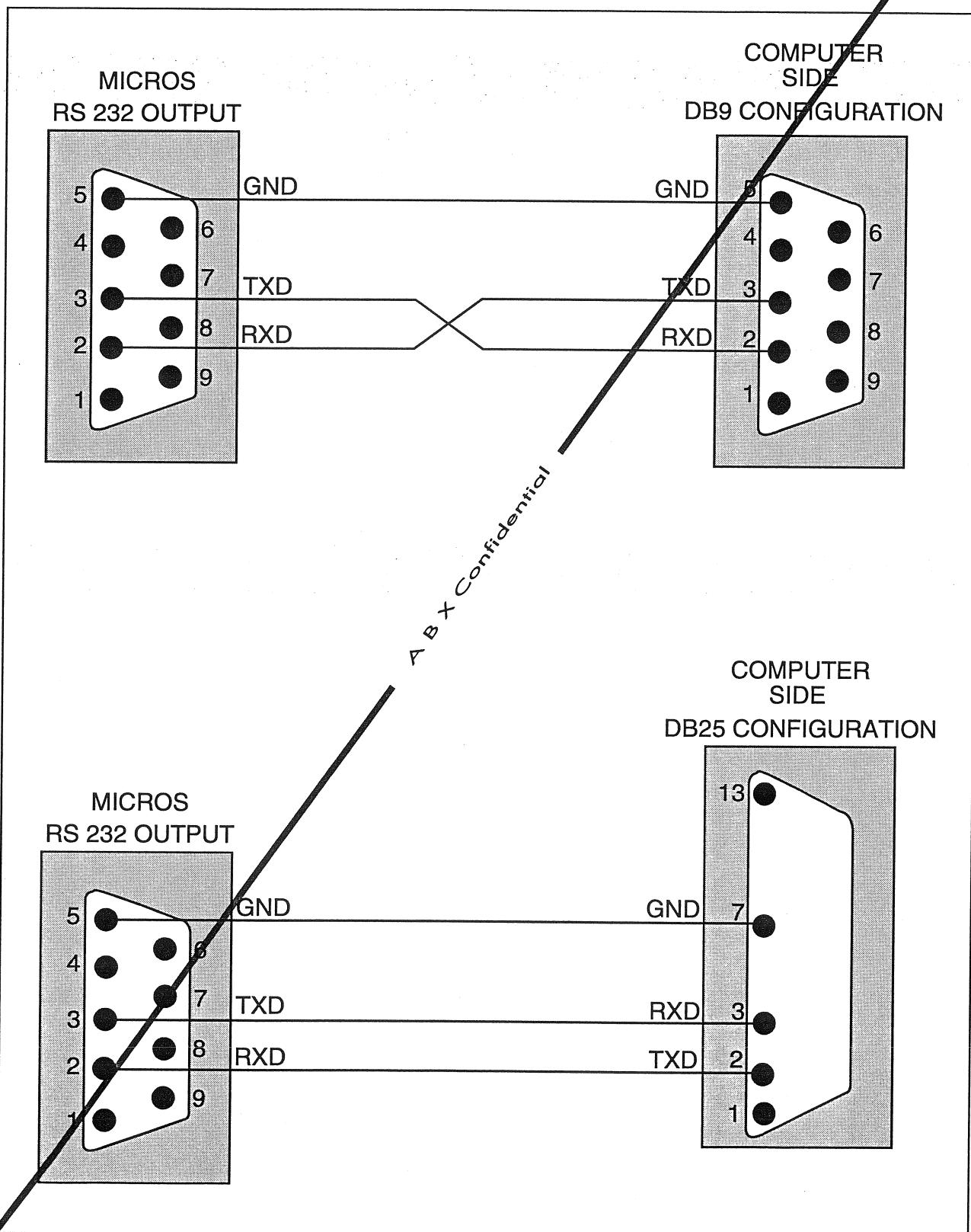


# 5 DATA OUTPUT FORMAT

scil Vet abc

## Table of Content

1. - Message Structure .....	4
2. - Details about the structure .....	4
3. - Identifier list and their formats.....	4
3.1.      Hematologic numeric parameters .....	4
3.1.1.     Format description.....	4
3.1.1.1.    Numerical field .....	4
3.1.1.2.    Parameter status .....	4
3.1.1.3.    Example .....	4
3.1.2.     Identifier list .....	5
3.2.      Pathology.....	6
3.2.1.     Flags associated with parameters .....	6
3.2.1.1.    Format description .....	6
3.2.1.2.    Identifier list.....	6
3.2.2.     Pathological messages .....	6
3.2.2.1.    Format description .....	6
3.2.2.2.    Identifier list.....	7
3.3.      Histograms and matrix.....	7
3.3.1.     Format description.....	7
3.3.1.1.    Histograms .....	7
3.3.1.2.    Matrix.....	7
3.3.1.3.    Separation thresholds .....	7
3.3.2.     Identifier list .....	7
3.3.3.     Format description of the threshold transmission .....	8
3.3.3.1.    WBC identifier.....	8
3.3.3.2.    RBC identifier .....	8
3.3.3.3.    PLT identifier.....	8
3.3.3.4.    Basophil identifier.....	8
3.3.3.5.    Eryne matrix identifier.....	9
3.3.3.6.    Reticulocyte matrix identifier.....	9
3.4.      Patient result identification .....	10
3.4.1.     Format description .....	10
3.4.2.     Identifier list .....	10
4. - Packet type .....	11
4.1.     Identifiers List .....	11
4.2.     Data exported by the analyzer.....	11
4.3.     Errors List .....	11
4.4.     Data interpreted by the analyzer .....	12

2. PIN ASSIGNMENTS

## 5 - DATA OUTPUT FORMAT

### 3.3.3. Format description of the threshold transmission

#### 3.3.3.1. WBC identifier

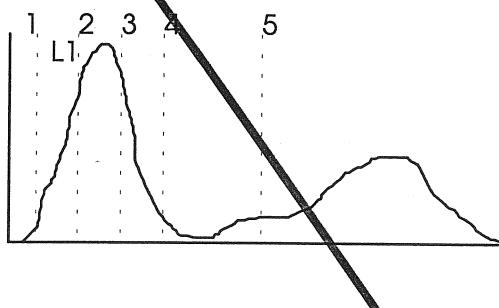
Separation thresholds 1-2-3 allow the L1 flag determination. For the analyzers in LMG mode, the 4-5 thresholds allow the separation of the 3 populations Lymphocytes, Monocytes, Granulocytes.

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

"**) 000 000 000 040 060**" + carriage return.

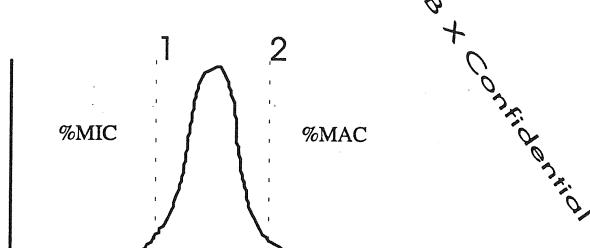
Example 2 : output format of the WBC curve thresholds for CBC and DIFF sampling. In this 5 parts DIFF analyzer, the LMG is not measured, the 4-5 thresholds are not significant.

"**) 005 008 020 000 000**" + carriage return.



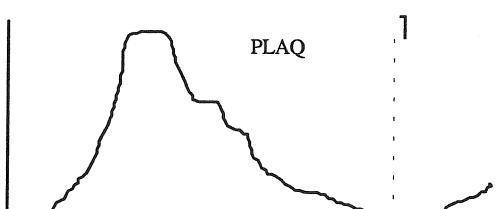
#### 3.3.3.2. RBC identifier

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



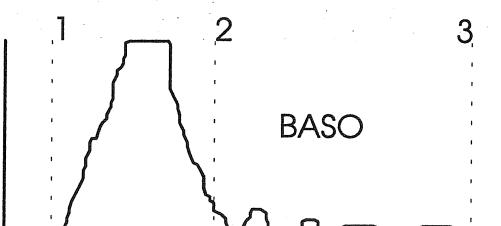
#### 3.3.3.3. PLT identifier

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



#### 3.3.3.4. Basophil identifier

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



### 3.3.3.5. Lmne matrix identifier

The 11 resistive thresholds are transmitted in the following order : NoI, Non, Noe, Ln, Rn, Li, Al, Lm, Lmn, Mn, Rm. The 3 absorbance thresholds are following : NI, Ne, Rmrn.

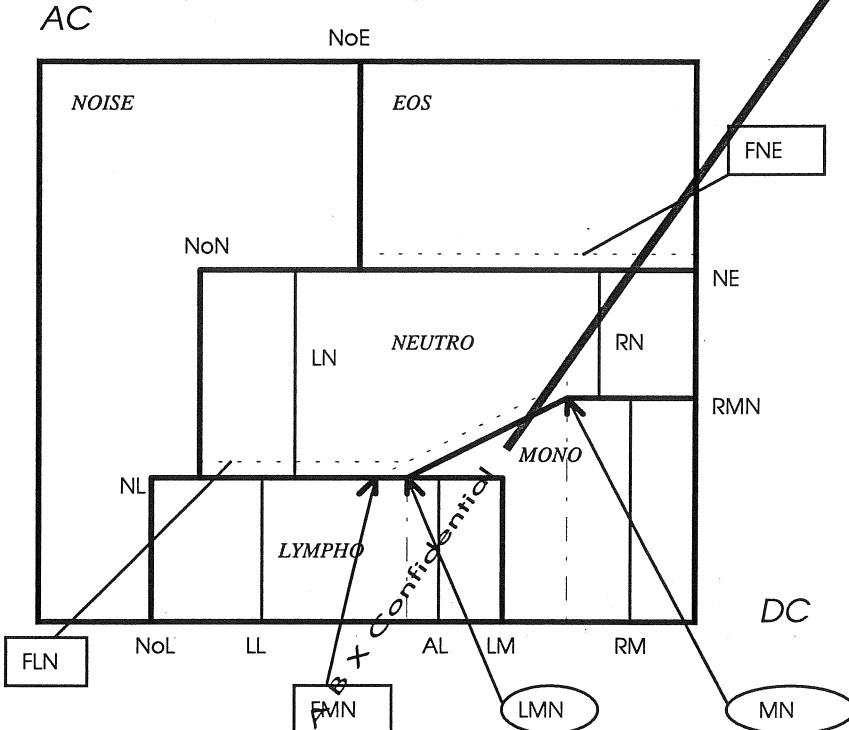
At the end the width of the areas (in channel number) describing the proximity flags : Fne, Fmn, Fln are transmitted .

#### Caption:

The position of the miscellaneous populations given in the differential are shown in italic.

Framed items are the proximity flags.

Surrounded items are inflexion points similar to separation thresholds.

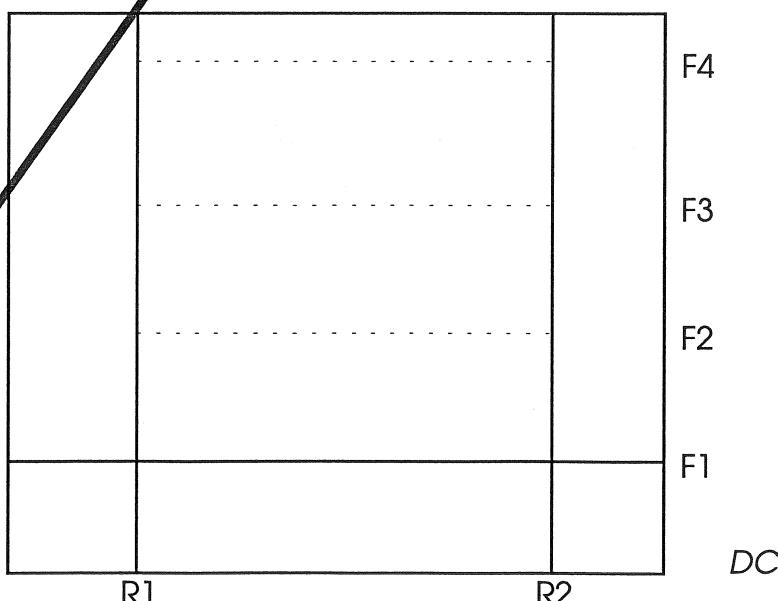


### 3.3.3.6. Reticulocyte matrix identifier

The 2 resistive thresholds are transmitted in the following order : R1, R2.

Then the 4 fluorescent thresholds are following : F1, F2, F3, F4.

#### Fluorescence



## 5 - DATA OUTPUT FORMAT

### 3.4. Patient result identification

#### 3.4.1. Format description

All the described fields have a fixed size character chain type and are completed with spaces for the non significant informations.

#### 3.4.2. Identifier list

94/Mo/Day

Identifiers	Correspondance	Formats	Length
\$70 p	Analyzer number	01	2 + 2 + 1
\$71 q	Analysis date and time	94/06/06 13h15mn31s	2 + 19 + 1
\$72 r	Analyzer run number	94/06/06-0001001 or 0115	2 + 16 + 1
\$73 s	Analyzer sequence number	0128	2 + 4 + 1
\$74 t	Sampling mode	'O' : open tube 'C' : close tube	2 + 1 + 1
\$75 u	Identification number	1450302154275-42	2 + 16 + 1
\$76 v	Identification	SMITH Ronald	2 + 30 + 1
\$77 w	Birth date	yy/mm/dd	2 + 8 + 1
\$78 x	Age	7d, 4w, 10m, 54y	2 + 3 + 1
\$79 y	Sex	2	2 + 1 + 1
\$7A z	Origin	F	2 + 1 + 1
\$7B {	Doctor	Dr; Jones	2 + 15 + 1
\$7C l	Department	Hemato	2 + 10 + 1
\$7D }	Sampling date	94/06/06 13h15	2 + 14 + 1
\$7E ~	Comments		2 + 32 + 1
\$7F	Blood type	Cat	2 + 16 + 1
\$80 ç	Analysis type	'G' : CBC 'F' : CBC & Differential 'R' : Reticulocytes 'L' : LMG	2 + 1 + 1
\$81 ü	Sample rack type	'0' : 10 positions '1' : 15 positions '2' : 32 positions	2 + 1 + 1
\$82 é	Number of runs	'0' : first run '1' : second run etc...	2 + 1 + 1

#### 4. - Packet type

The information described in the packet type allows the specification of the global message content; Analyzers being able to communicate in the bidirectional mode and supporting the remote control mode, this string of characters can be presented under several forms. Its length is 8 characters.

The version number is linked to the development of the hematological message identifiers.

An error number is also available. It codifies some events which happened on the analyzer (see error number list here below).

##### 4.1. Identifiers List

Identifier	Correspondance	Format	Length
\$FC	Error number	4 decimal bytes	2 + 4 + 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
\$FF	type of data packet	String of characters	2 + 8 + 1

##### 4.2. Data exported by the analyzer

Data packet string (8 char.)	Use
RESULT	Hematological result transmission on a routine mode
RES-RR	Hematological result transmission on a re-sampling mode
RES-BLK	Result transmission on a blank sampling mode
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
QC-TAR-H	Target transmission of a high level control blood
QC-TAR-M	Target transmission of a median level control blood
QC-TAR-L	Target transmission of a low level control blood
FILE	Patient file request
LINE	Connection request
END	End of the connection
BUSY	Analyzer not available
WHAT?	Response to a non registered request

##### 4.3. Errors List

Error N°	event linked to the analyzer
0001	Operating temperature out of limits

## 5 - DATA OUTPUT FORMAT

### 4.4. Data interpreted by the analyzer

Data packet string (8 char.)	Use
FILE	Patient file reception
AUTO	Start of an automatic sampling mode (piercer)
STEP	Start of an automatic sampling mode (piercer) with the choice of the tube position number to be sampled
NO:xx	Sampling request of a tube in the position xx: 01 to 32
MANUAL	Start of a manual sampling mode (open tube)
STOP	Emergency stop
STOPAUTO	Stop of an automatic sampling cycle (piercer)
DILUENT	Diluent rinse cycle
LYSE	Lyse priming cycle
CLEANER	Cleaning cycle
EOSINO	Eosinofix priming cycle
BASO	Basolyse priming cycle
RETIC	Retix priming cycle
CLRNEEDL	Needle cleaning cycle
BCKFLUSH	Backflush cycle
DRAIN	Drain chamber cycle
CONTROL	Autocontrol cycle
STARTUP	Startup cycle
SHUTDOWN	Shutdown cycle
SETCBC	Setup in the CBC analysis mode
SET5D	Setup in the Differential analysis mode
SETRET	Setup in the Reticulocytes analysis mode
SETLMG	Setup in the LMG mode
REMOTE	Run in the remote control mode
STANDARD	End of the remote control mode

## 5 - DATA OUTPUTFORMAT

### 1. - Message Structure

STX

Size + carriage return.

Identifier followed by a space then the Load Type + carriage return.

Identifier followed by a space then the Information + carriage return.

Remainder of the other Identifiers and Informations + carriage returns.

Identifier followed by a space then the CheckSum + carriage return.

ETX

### 2. - Details about the structure

Size : 5 bytes representing the total amount of the data except STX and ETX.

Load : A character chain indicating that this load is a result type.

Identifier : 1 byte (moving about \$21 to \$FF, it describes the information type which follows this indicator).

CheckSum : Sum modulo 65535 of all the characters except ETX and STX in the hexadecimal format on 4 bytes.

### 3. - Identifier list and their formats

#### 3.1. Hematology numeric parameters

##### 3.1.1. Format description

###### 3.1.1.1. Numerical field

For all indicated parameters from \$21 to \$43, the format is a numerical field of 5 digits completed with zeros on the left side (ex. : 04.55).

The unit is the one chosen by the operator.

When the parameter cannot be calculated by the analyzer, the field is replaced with (---).

###### 3.1.1.2. 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.

First digit (letter)	correspondance
R	Parameter rejected for a counting default
B	Incorrect balance between the counting methods
S	Suspicious parameter value
'space'	No anomaly observed

Second digit (letter)	correspondance
L	Parameter < to the lower extreme value
I	Parameter < to the low normal value
'space'	Parameter normal value
h	Parameter > to the high normal value
H	Parameter > to the high extreme value
O	Parameter exceeding the capacity

###### 3.1.1.3. Example

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

\$32\$20\$30\$35\$2E\$35\$30\$52\$68\$0D ou "0 05.5Rh" + carriage return.

The length is fixed and is worth 2+7+1, that is to say 10 bytes for one parameter.

## 3.1.2. Identifier list

Identifiers		Parameters	Units
\$21	!	WBC	Standard - SI g/dl - SI mmoles
\$22	"	Lymphocytes	(#)
\$23	#		(%)
\$24	\$	Monocytes	(#)
\$25	%		(%)
\$26	&	Granulocytes	(#)
\$27	'		(%)
\$28	(	Neutrophils	(#)
\$29	)		(%)
\$2A	*	Eosinophils	(#)
\$2B	+		(%)
\$2C	,	Basophils	(#)
\$2D	-		(%)
\$2E	.	Atypical Lymphocytes	(#)
\$2F	/		(%)
\$30	0	Large Immature Cells	(#)
\$31	1		(%)

Identifiers		Parameters	Units
\$32	2	RBC	Standard - SI g/dl - SI mmoles
\$33	3	HGB	
\$34	4	HCT	
\$35	5	MCV	+ Confidential
\$36	6	MCH	♦
\$37	7	MCHC	
\$38	8	RDW	
\$39	9	reserved	
\$3A	:	reserved	
\$3B	:	Reticulocytes	(#)
\$3C	<		(%)
\$3D	=	Reticulocytes Low	(%)
\$3E	>	Reticulocytes Median	(%)
\$3F	?	Reticulocytes High	(%)

Identifiers		Parameters	Units
\$40	@	PLT	Standard - SI g/dl - SI mmoles
\$41	A	MPV	
\$42	B	THT	
\$43	C	PDW	

## 5 - DATA OUTPUT FORMAT

### 3.2. Pathology

#### 3.2.1. Flags associated with parameters

##### 3.2.1.1. Format description

Flags are transmitted in a comprehensive mode (same presentation than on the screen, that is to say dependant from the language) 2 characters which are replaced with spaces when the flag has not been detected.

##### 3.2.1.2. Identifier list

Identifiers	R	Parameters	Formats	Length
\$50	R	WBC or LMG	L1M1M2G1G2G3	2 + 12 + 1
\$51	Q	Differential	CoMbLLNIMnLnRmRnNoNeLb	2 + 22 + 1
\$52	R	RBC	MiMa	2 + 4 + 1
\$53	S	PLT	PcScMc	2 + 6 + 1

#### 3.2.2. Pathological messages

##### 3.2.2.1. Format description

Each pathology is described by a group of 4 letters preceding a space. The content of the pathology is dependent from the chosen language. Messages are divided in 3 groups. Only the detected pathologies are transmitted. A common header to the 3 groups indicates that the pathological interpretation has not been determined by the analyzer.

Populations	Messages	Signification
WBC	GRA+ GRA- LEU+ LEU- LYM+ LYM- NEU+ NEU- EOS+ MYEL LIMC ALYM LSHT NRBC MON+	Granulocytosis Granulopenia Leukocytosis Leukopenia Lymphocytosis Lymphopenia Neutrophilia Neutropenia Eosinophilia Myelemia Large Immature Cells Atypic Lymphocytes Left shift Nucleated RBCs Monocytosis
RBC	ANEM ANI1, ANI2, ANI3 MIC1, MIC2, MIC3 MAC1, MAC2, MAC3 HCR1, HCR2, HCR3 POI1, POI2, POI3 ERYT	Anemia Anisocytosis level 1, 2, 3 Microcytosis     "     " Macrocytosis     "     " Hypochromia     "     " Poikilocytosis     "     " Erythrocytosis     "     "
PLT	THR+ THR- AGPL MPEC MICC SCHI	Thrombocytosis Thrombopenia Platelet aggregates Small cells Microcytes Schizocytes
All populations	???? PANC	No interpretation Pancytopenia

### 3.2.2.2. Identifier list

Identifiers		Parameters	Formats	Length
\$54	T	WBC	String of characters	2 + ..... + 1
\$55	U	RBC	String of characters	2 + ..... + 1
\$56	V	PLT	String of characters	2 + ..... + 1

### 3.3. Histograms and matrix

#### 3.3.1. Format description

##### 3.3.1.1. Histograms

Histograms are transmitted on 128 or 256 channels. They are automatically rescaled to a 223 maximum amplitude value. The zero amplitude value is \$20, the maximum amplitude value is \$FF.

##### 3.3.1.2. Matrix

2048 bytes matrix are transmitted on 4096 bytes giving by group of 2 bytes the value of 1 screen bitmap byte represented from the left to the right and from the top to the bottom of the screen (principles of the recovery of the 128x16 matrix bitmap on the VEGA LCD board).

##### 3.3.1.3. Separation thresholds

It is the channel number enclosing areas on the histograms or on the matrix. Each threshold is transmitted on 3 bytes preceeded by a space (max. : 255).

#### 3.3.2. Identifier list

Identifiers		Parameters	Formats	Length
\$57	W	WBC	Amplitude of each channel	2 + 128 + 1
\$58	X	RBC	"	"
\$59	Y	PLT	"	"
\$5A	Z	Basophils	"	"
\$5B	(	Lmne matrix	Screen bitmap	2 + 4096 + 1
\$5C	\	Reticulocyte matrix	Screen bitmap	2 + 4096 + 1
\$5D	)	WBC thresholds	5 thresholds	2 + 19 + 1
\$5E	^	RBC thresholds	2 thresholds	2 + 7 + 1
\$5F	-	PLT thresholds	1 threshold	2 + 3 + 1
\$60	-	Basophil thresholds	3 thresholds	2 + 11 + 1
\$61	a	Lmne matrix thresholds	11 RES thresholds, 6 ABS thresholds	2 + 67 + 1
\$62	b	Reticulocyte matrix thresholds	2 RES thresholds, 4 ABS thresholds	2 + 23 + 1



## Technical Note content:

### A- Main V2.40 software evolutions:

- 1- «CAT» type: Creation of AG1% & AG2% alarms.
- 2- DIL Alarm management.
- 3- Specie Card Management: Modification of the specie card reading in two times during an analysis;  
Management of the «CAMEL» specie card.
- 4- LMGE results computation and display:  
Determination of LMGE populations;  
LMGE results & curves conditions for printout, emission and display.
- 5- Creation of the «COMPLETE» RS output format.
- 6- Instrument new default values.
- 7- Latex targets modification.

### B- Installation procedure

#### A- Main V2.40 software evolutions:

##### 1- «CAT» type: Creation of AG1% & AG2% alarms

NOTE: AG1% and AG2% alarms are adjustable by menu **SETUP/CHGT LAB. LIMITS/FLAGS LIMITS**; but are activated only with the CAT type.

###### Computation:

According to the following formula:

$$X = \frac{\text{Number of particles counted from channel } 255 \times 100}{\text{Sum of the counted particles from channel C3 to C13 included}}$$

This formula gives a percentage, alarms activation depends on AG1% and AG2% sensitivity level enter by user (see following table).

###### AG1% or AG2% triggering off conditions:

CONDITIONS	
X < AG1% Sensitivity level	No alarm
X > AG1% Sensitivity level & X < AG2% Sensitivity level	AG1% alarm activated
X > AG2% Limit	AG2% alarm activated

###### Printout management:

AG1% and AG2% alarms are printed out in the animal limits and in «WBC Alarms» area of the result printout.

#### RS output management:

AG1% and AG2% alarms are managed by **FORMAT 1**, **STANDARD** and **COMPLETE** RS formats, they use previous G1 and G2 alarm locations.

#### RS FORMAT 1:

Each letter corresponds to one alarm, WBC alarms are in the LMMGGG sequence:

«ABCDEFGHIJKLMNPQRSTUVWXYZ», «LMMGGG»

L:	Not managed (=0)
M:	Not managed (=0)
M:	Not managed (=0)
G:	AG1 alarm 1 for activated alarm.
G:	AG2 alarm 1 for activated alarm.
G:	Not managed (=0)

#### RS COMPLETE or STANDARD format:

Alarm is emitted in the sequence: **PL1M1M2G1G2G3** (where AG1% is emitted instead of G1 and AG2% is emitted instead of G2).

#### Specie card management:

AG1% and AG2% alarm sensitivity level values are recorded on «CAT» type specie card in the previous G1 and G3 locations. Default values must be initialized to **0.5%** for AG1% and **2%** for AG2%. See installation procedure.

## 2- DIL alarm management

#### DIL alarm (WBC, RBC, Plt -> MPV, Hgb, Hct):

- Display: Values for all these parameters are not displayed, «DIL» is displayed instead.
- Printout: Values for all these parameters are not printed out, «---- D» is printed instead.

## 3- Specie cards management

#### Modification of the specie card reading in two times during an analysis

The specie type used by the instrument can be changed by the user before each analysis by inserting a different specie card type in the reader.

When a specie card is present in the reader and a cycle is started:

- If it is the same specie card type as in the instrument current setting, the specie card will not be read.
- If it is not the same specie card type, the specie card is read in two times to save time on sampling.

#### NOTE:

If the user removes or replaces the specie card between the start of the cycle and the blood sampling, the instrument will display the following message:

ENGLISH	«ERROR: INCOMPATIBLE CARD»
FRENCH	«ERREUR: CARTE INCOMPATIBLE»
GERMAN	«ERROR: CHIPKARTE INCOMPATIBLE»
SPANISH	«ERROR: SMARTCARD INCOMPATIBLE»

After user validates the error, a rinse cycle is automatically started.

**ATTENTION:** The reading of the specie card has not been completed so datas related to specie in the instrument current setting are not coherent and must be re-initialized. The instrument will automatically load DOG type default values.

#### Management of the «CAMEL» specie card:

The V2.40 release allows the management of a new «CAMEL» specie card, this specie card will be available soon.

## 4- LMGE results computation and display

### Determination of LMGE populations:

Calculation of L% and M% proportions are related to the total WBC count in the distribution curve (WBC count starts at the same cursor than the Lymphocytes).

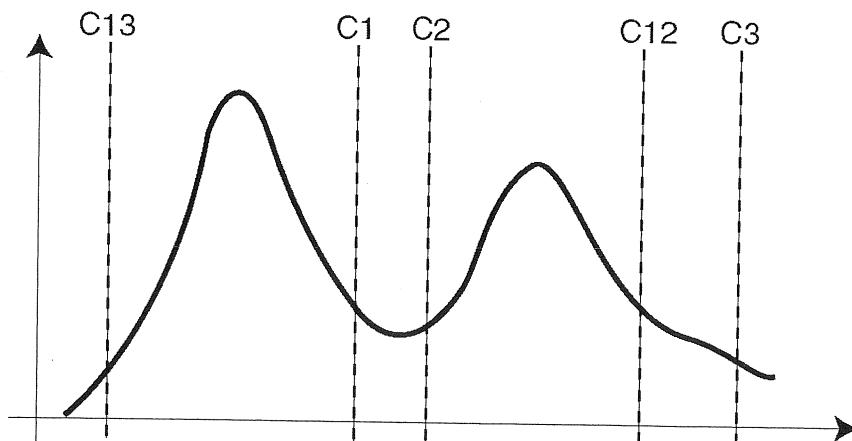
#### Formula used:

**Lym** calculation from **C13** cursor included to **C1** cursor not included on smoothed distribution.

**Mon** calculation from **C1** cursor included to **C2** cursor not included on smoothed distribution.

**Gra** calculation from **C2** cursor included to **C3** cursor included on smoothed distribution.

**Eos** calculation from **C12** cursor included to **C3** cursor included on raw distribution.



### LMGE results & curves conditions for printout, emission and display:

CONDITIONS	WBC<1000	REJECT ON WBC (*)	3 WBC COUNTS (\$)	3 WBC COUNTS & WBC<1000
Curves (RS)	Yes	No	Yes	Yes
Results (RS)	No (LMGE)	No	Yes	No (LMGE)
Display	No	No	Yes	No
Print out	No	No	Yes	No

## 5- Creation of the «COMPLETE» RS output format: ABX format including raw curves transmission

### Curves transmission:

LMGE cursors are transmitted on 256 channels, transmission of raw curves (512 octets table) in accordance with V3.00 ABX format:

CODE	IDENTIFIER	CURVE
\$6C	I	WBC curve
\$6D	m	RBC curve
\$6E	n	Plt curve

The 512 octets table is coded before transmission as follows:

code, space, type of coding on 8 characters (MICROSRD), space, length of datas coded on 5 characters, space, datas then carriage return.

#### ► Example of a WBC curve emitted in «COMPLETE» RS format:

#### ◆ Transmission:

\$6C \$20 MICROS RD \$20 00724 \$20 datas \$0D

## • Datas:

Each channel is coded in ASCII code and separated by a '{' character.

#### • Example of coded raw curve:

## ❖ «I» Identifier:

## MICROSRD: type of coding.

00684: Length of datas on 5 characters.

then values for each channel seperated by a '{' character are following.

## **6- Instrument new default values**

#### Modification of instrument default configuration:

<b>IDENTIFICATION</b>	<b>DEFAULT CONFIGURATION</b>
Type of Micros	Vet
Reagent pack	Yes
Analysis mode (US or STD)	STD
Date format	DD.MM.YY
Curves printing	Yes
Default Vet animal type	Dog
LMGE results printout	Yes
Limit printout	Yes

## **7- Latex targets modification**

#### ▼ New target values:

• Lym: 78 +/-1

• Gra: 206 +/- 5