

Section overview

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9. General (V02)

This section describes the serial data format as well as other 'data' issues like software upgrading and printer selection. The reader must have basic understanding of serial data communication, printer- and XML protocol in case of host programming.

9.1 Serial output (hardware)

The connections from the BM800 to an external PC must be according to the drawing below:

PC Computer using a 25 pin RS232

Cable end BM800
9 Pin Female DSUB

Cable end 'standard' PC
25 Pin Female DSUB

2-----	3
3-----	2
5-----	7
7-----	4
8-----	5

PC Computer using a 9 pin RS232

Cable end BM800
9 Pin Female DSUB

Cable end PC
9 Pin Female DSUB

2-----	2
3-----	3
5-----	5
7-----	7
8-----	8

The pinning on the 9 Pin BM800 female connector is as follows:

1.	N. C.
2.	$\overline{\text{TX}}$ -OUTPUT
3.	$\overline{\text{RX}}$ -INPUT
4.	N.C.
5.	GND
6.	N.C.
7.	CTS-INPUT
8.	RTS-OUTPUT
9.	N.C.

The in- and output follows strictly the RS232 specifications.

Serial parameters are set to fixed values within the BM800:

Baud rate = 19.200

Bits = 8

Parity = None

Start/Stop bits = 1

9.2 Serial output format

The BM800 is capable to send the measured data to the serial output. This can be done sample by sample, using the 'auto-send' function, or batch-wise from the 'Send' menu. The transmitted data to the serial output contain measured parameters including flagging, abnormalities etc. and might contain technical parameters if selected in the Setup menu.

Note:

At current software versions, no commands via an host can be send to the BM800.

Below, a typical data-set from a sample is shown. Regarding explanation see section 9.3.

```
<!--:Begin:Chksum:1:-->
<!--:Begin:Msg:3:0:-->
<sample>
<ver>0.1</ver>
<instrinfo>
<p><n>PRDI</n><v>BM800</v></p>
<p><n>FIWV</n><v>1.0.1</v></p>
<p><n>SNO</n><v>0</v></p>
<p><n>BRND</n><v>M</v></p>
<p><n>IAPL</n><v>V</v></p>
<p><n>IID</n><v>10005</v></p>
</instrinfo>
<mpinfo>
<p><n>ID</n><v>0502011+</v></p>
<p><n>SEQ</n><v>166</v></p>
<p><n>DATE</n><v>2005-08-29T09:39:55</v></p>
<p><n>APNU</n><v>#</v></p>
<p><n>APNA</n><v>10502011</v></p>
<p><n>ASPM</n><v>OT</v></p>
```

```
<p><n>ASPS</n><v>1</v></p>
<p><n>SORC</n><v>0</v></p>
<p><n>BLNK</n><v>0</v></p>
<p><n>STYP</n><v>0</v></p>
<p><n>RPD</n><v>0</v></p>
<p><n>RPDL</n><v>15</v></p>
<p><n>RPDH</n><v>30</v></p>
<p><n>WDMS</n><v>1</v></p>
<p><n>WDMA</n><v>0</v></p>
<p><n>WDLL</n><v>40</v></p>
<p><n>WDLH</n><v>330</v></p>
</smpinfo>
<smpresults>
<p><n>RBC</n><v>4.19</v><l>2.32</l><h>2.56</h></p>
<p><n>MCV</n><v>86.7</v><l>55.9</l><h>63.9</h></p>
<p><n>HCT</n><v>36.4</v><l>12.6</l><h>16.6</h></p>
<p><n>MCH</n><v>28.5</v><l>20.3</l><h>23.3</h></p>
<p><n>MCHC</n><v>32.9</v><l>34.1</l><h>38.5</h></p>
<p><n>RDWR</n><v>14.5</v><l>14.0</l><h>20.0</h></p>
<p><n>RDWA</n><v>64.2</v><l>0.0</l><h>0.0</h></p>
<p><n>PLT</n><v>251</v><l>78</l><h>108</h></p>
<p><n>MPV</n><v>10.5</v><l>9.5</l><h>12.5</h></p>
<p><n>PCT</n><v>0.26</v><l>0.00</l><h>0.00</h></p>
<p><n>PDW</n><v>10.6</v><l>0.0</l><h>0.0</h></p>
<p><n>LPCR</n><v>32.9</v><l>0.0</l><h>0.0</h></p>
<p><n>HGB</n><v>12.0</v><l>5.0</l><h>5.6</h></p>
<p><n>WBC</n><v>8.7</v><l>2.4</l><h>3.0</h></p>
<p><n>LA</n><v>4.5</v><l>0.5</l><h>1.3</h></p>
<p><n>MA</n><v>0.6</v><l>0.0</l><h>0.6</h></p>
<p><n>GA</n><v>3.6</v><l>0.7</l><h>2.3</h></p>
<p><n>LR</n><v>52.3</v><l>27.8</l><h>41.8</h></p>
<p><n>MR</n><v>5.8</v><l>6.5</l><h>14.5</h></p>
<p><n>GR</n><v>41.9</v><l>47.7</l><h>61.7</h></p>
</smpresults>
<tparams>
<p><n>RCT</n><v>13870</v></p>
<p><n>WCT</n><v>11131</v></p>
<p><n>aspt</n><v>1230</v></p>
<p><n>xfrt</n><v>3353</v></p>
<p><n>acps</n><v>0</v></p>
<p><n>asl1</n><v>0</v></p>
<p><n>asl2</n><v>0</v></p>
<p><n>rdmx</n><v>19</v></p>
<p><n>rdmn</n><v>514</v></p>
<p><n>rdbl</n><v>2048</v></p>
<p><n>rrmn</n><v>1375</v></p>
<p><n>rrmx</n><v>1850</v></p>
<p><n>rrmd</n><v>1651</v></p>
<p><n>rrdp</n><v>804</v></p>
<p><n>rpds</n><v>125</v></p>
<p><n>rpdt</n><v>1195</v></p>
<p><n>rpdd</n><v>149</v></p>
<p><n>rpus</n><v>1475</v></p>
```

<p><n>rpua</n><v>13870</v></p>
<p><n>rput</n><v>15345</v></p>
<p><n>rpud</n><v>462</v></p>
<p><n>rbrn</n><v>0</v></p>
<p><n>rpdb</n><v>0</v></p>
<p><n>rpdp</n><v>0</v></p>
<p><n>rpdo</n><v>0</v></p>
<p><n>rpub</n><v>0</v></p>
<p><n>rpup</n><v>0</v></p>
<p><n>rpu1</n><v>0</v></p>
<p><n>rpu2</n><v>0</v></p>
<p><n>rpud</n><v>0</v></p>
<p><n>wdmx</n><v>5</v></p>
<p><n>wdmn</n><v>989</v></p>
<p><n>wdbl</n><v>1024</v></p>
<p><n>wrmn</n><v>425</v></p>
<p><n>wrmx</n><v>503</v></p>
<p><n>wrmd</n><v>458</v></p>
<p><n>wrpd</n><v>919</v></p>
<p><n>wpds</n><v>113</v></p>
<p><n>wpdt</n><v>953</v></p>
<p><n>wpdd</n><v>95</v></p>
<p><n>wpus</n><v>1444</v></p>
<p><n>wpua</n><v>11131</v></p>
<p><n>rput</n><v>12574</v></p>
<p><n>rpud</n><v>371</v></p>
<p><n>rbrn</n><v>0</v></p>
<p><n>rpdb</n><v>0</v></p>
<p><n>rpdp</n><v>0</v></p>
<p><n>rpdo</n><v>0</v></p>
<p><n>rpub</n><v>0</v></p>
<p><n>rpup</n><v>0</v></p>
<p><n>rpu1</n><v>0</v></p>
<p><n>rpu2</n><v>0</v></p>
<p><n>rpud</n><v>0</v></p>
<p><n>dpds</n><v>111</v></p>
<p><n>dpdt</n><v>3202</v></p>
<p><n>dpdd</n><v>0</v></p>
<p><n>dpus</n><v>1</v></p>
<p><n>dput</n><v>1745</v></p>
<p><n>dpud</n><v>0</v></p>
<p><n>dpdb</n><v>0</v></p>
<p><n>dpdp</n><v>0</v></p>
<p><n>dpdo</n><v>0</v></p>
<p><n>dpup</n><v>0</v></p>
<p><n>dpuo</n><v>0</v></p>
<p><n>ipds</n><v>130</v></p>
<p><n>ipdt</n><v>4001</v></p>
<p><n>ipdd</n><v>0</v></p>
<p><n>ipus</n><v>121</v></p>
<p><n>iput</n><v>5197</v></p>
<p><n>ipud</n><v>0</v></p>
<p><n>ipdb</n><v>0</v></p>

```
<p><n>ipdp</n><v>0</v></p>
<p><n>ipdo</n><v>0</v></p>
<p><n>ipup</n><v>0</v></p>
<p><n>ipuo</n><v>0</v></p>
<p><n>lpds</n><v>109</v></p>
<p><n>lpdt</n><v>3490</v></p>
<p><n>lpdd</n><v>0</v></p>
<p><n>lpus</n><v>214</v></p>
<p><n>lput</n><v>5665</v></p>
<p><n>lpud</n><v>0</v></p>
<p><n>lpdb</n><v>0</v></p>
<p><n>lpdp</n><v>0</v></p>
<p><n>lpdo</n><v>0</v></p>
<p><n>lpup</n><v>0</v></p>
<p><n>lpuo</n><v>0</v></p>
</tparams>
<hgrams>
<hgram>
<n>PLT</n><m>30</m><k>80</k><w>0</w><d>67</d><hgdata>
<v>
0 0 0 0 0 1 1 2 2 3 4 5 7 8 10
12 14 16 19 21 22 24 25 26 26 26 25 24 23 22
20 19 17 16 14 13 12 10 9 8 7 6 5 5 4 3
3 2 2 2 1 1 1 1 1 1 1 0 1 1 1 1
1 1 1 1 1 1 1 0 0 0 0 0 0 0 0
</v>
</hgdata>
</hgram>
<hgram>
<n>RBC</n><m>250</m><k>80</k><w>0</w><d>8</d><hgdata>
<v>
6 21 42 55 49 31 14 5 3 4 6 8 12 16 23 34
51 74 104 138 174 208 235 251 254 249 238 224 209 192 173 154
136 119 105 93 82 73 64 56 47 41 34 28 23 19 17 14
12 11 9 8 7 6 5 5 4 4 3 3 3 3 2 2
1 1 1 1 1 1 0 0 0 0 0 0 0 1 2
</v>
</hgdata>
</hgram>
<hgram>
<n>WBC</n><m>450</m><k>80</k><w>4</w>
<hgdata>
<n>LYM</n><v>
0 1 3 6 11 17 25 32 38 43 45 45 42 37 32 26
20 15 11 9 7 5 3 2 1 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
</v>
</hgdata>
<hgdata>
<n>MID</n><v>
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
```

```
0000112334332222
1111111100000000
0000000000000000
0000000000000000
</v>
</hgdata>
<hgdata>
<n>GRA</n><v>
0000000000000000
0000000000000000
01112234567910111112
121313131313121212111110101099
8877776666666555
</v>
</hgdata>
</hgram>
</hgrams>
</sample>
<!--:End:Msg:3:0:-->
<!--:End:Chksum:1:47:11:-->
```

9.3 XML serial output format description

This section describes the XML format for all parameters described in section 9.2 above.

Sample Data Basic Structure

Overall structure.

```
<sample>
  <ver>
    <!-- Version number of XML sample data format -->
  </ver>
  <instrinfo>
    <!-- Information about the instrument. -->
  </instrinfo>
  <smppinfo>
    <!--Sample Information parameter values -->
  </smppinfo>
  <smppresults>
    <!--Sample Result parameter values -->
  </smppresults>
  <tparams>
    <!-- Technical (troubleshooting) parameter values (optional) --
  >
  </tparams>
  <hgrams>
    <!-- Histograms (optional) -->
  </hgrams>
  <rawdata>
    <!-- Raw data (optional) -->
  </rawdata>
  <scatter>
    <!-- Scatter data (optional) -->
  </scatter>
</sample>
```

Common Parameter Format

All parameters have the following common structure:

```
<p><n>NAME</n><!-- value and/or other stuff --></p>
```

By convention, sample result parameter names use only upper case.

The "<n>" (name) tag is the first one. The order of the following tags is not fixed.

The "<v>" tag is the parameter value. It is present if a valid value of the parameter exists.

Parameters that could be present are present with their names even if they have no value. Parameters are not present if:

- 1) The parameter is not included in the BM800 model, or
- 2) The parameter is blocked by the user.

Examples:

A parameter without any value etc.


```
<p><n>MCV</n></p>
```

A parameter with a value

```
<p><n>RBC</n><v>4.56</v></p>
```

The common parameter format is extended for result parameters and technical parameters.

<ver> - Data Format Version

The "<ver>" tag identifies the version of the BM800 XML format spec used. The used version denotation is *{major.minor}*. It is supposed that the major number is changed when incompatible changes have been implemented. The minor number is changed for backward-compatible changes like adding parameters and tags.

The "<ver>" tag is first to make it possible to change the interpretation of the rest of the sample dump depending on this version number.

<instrinfo> - Instrument Information

The instrument information parameters are formatted according to the common parameter format. The structure of the instrument information parameters is as follows:

```
<instrinfo>
  <p><n>PRDI</n><v> ... </v></p>
  <p><n>SNO</n><v> ... </v></p>
  <p><n>SWI</n><v> ... </v></p>
  <p><n>L</n><v> ... </v></p>
  <p><n>IID</n><v> ... </v></p>
</instrinfo>
```

Static Instrument Parameters

The static instrument parameters are parameters that are always the same during the instrument life cycle. The combination of the PRDI and SNO parameters expresses a unique identifier (primary key) of an individual instrument.

PRDI - Product Identifier

The PRDI parameter identifies the instrument as for example a BM800. Its format is not further defined here.

```
<p><n>PRDI</n><v>BM800</v></p>
```

SNO - Serial Number

The SNO parameter is the serial number of the instrument. This number is supposed to be unique for a certain instrument chassis.

Value range: 1 – 65534.

```
<p><n>SNO</n><v>10001</v></p>
```

BRND – Instrument Brand

The brand parameter indicates marketing brand of the instrument.

Value range: M - for Medonic, S - for Swelab.

```
<p><n>BRND</n><v>M</v></p>
```

Instrument Configuration Parameters

The instrument configuration parameters are "semi-static" instrument parameters. The parameters are probably the same during the instrument life cycle, but they may change, for example at a software upgrade.

FIWV - Firmware Version

The FIWV parameter identifies the software used in the instrument. Its format is not further defined here.

```
<p><n>FIWV</n><v>v1.2.1</v></p>
```

IAPL – Instrument Application

The instrument application parameter describes the application configuration of the instrument, i.e. if it is a human, veterinary or blood bank instrument.

Value range: H – Human, V- Veterinary, B – Blood Bank.

```
<p><n>IAPL</n><v>H</v></p>
```

IID - User-Settable Instrument ID

The IID parameter identifies the individual BM800 instrument. It is a user-settable string of 1-15 characters. The parameter value is only present if the ID is given.

```
<p><n>IID</n><v>12345</v></p>
```

<smppinfo> Sample Information Parameter Values

Sample information parameter values identify the sample run.

The parameter order below is not fixed. The parameters might be in another order. Be prepared for newly defined parameters.

```
<smppinfo>
  <p><n>ID</n>...</p>
  <p><n>SEQ</n>...</p>
  <p><n>DATE</n>...</p>
  <p><n>SORC</n>...</p>
  <p><n>STYP</n>...</p>
  <p><n>ASPM</n>...</p>
  <p><n>ASPS</n>...</p>
  <p><n>BLNK</n>...</p>
  <p><n>ASWN</n>...</p>
  <p><n>ASWP</n>...</p>
  <p><n>RPD</n>...</p>
  <p><n>RPDL</n>...</p>
  <p><n>RPDH</n>...</p>
  <p><n>WDMA</n>...</p>
  <p><n>WDMS</n>...</p>
  <p><n>WDLL</n>...</p>
  <p><n>WDLH</n>...</p>
  <p><n>WLGL</n>...</p>
  <p><n>WDIL</n>...</p>
  <p><n>WDIH</n>...</p>
  <p><n>SWM</n>...</p>
  <p><n>SWF</n>...</p>
  <p><n>CAPL</n>...</p>
  <p><n>CLVL</n>...</p>
```

```
<p><n>CLOT</n> . . . </p>
<p><n>CEXP</n> . . . </p>
<p><n>CEXT</n> . . . </p>
<p><n>CDSC</n> . . . </p>
<p><n>PNAM</n> . . . </p>
<p><n>PDOB</n> . . . </p>
<p><n>PAGE</n> . . . </p>
<p><n>PSEX</n> . . . </p>
<p><n>PDOC</n> . . . </p>
<p><n>PREF</n> . . . </p>
<p><n>APNU</n> . . . </p>
<p><n>APNA</n> . . . </p>
<p><n>XLT</n> . . . </p>
</smpinfo>
```

ID – Blood Sample ID

ID is the identification of the blood sample. This parameter is always present, but the value is absent for "blank" ID:s.

Value range: 1 - 15 characters .

Note that non-numeric characters are allowed in the ID..

All control blood sample ID:s today have a trailing "+" after a number, both generic control blood (AKA fixed ID) and the reference range control blood (e.g. input via barcode).

"Blank" ID

```
<p><n>ID</n></p>
```

Numeric ID

```
<p><n>ID</n><v>12356</v></p>
```

Non-numeric ID

```
<p><n>ID</n><v>0412-042+</v></p>
```

SEQ – Sample Run Sequence Number

The sequence number of the run. This parameter is always present with a value.

Value range: 1 - 9999 (as of this writing, could be increased)

Note that SEQ numbers are not unique in samples from one instrument! They can be set by the user, and they wraps around.

```
<p><n>SEQ</n><v>444</v></p>
```

DATE – Sample Run Date and Time

The date and time of the sample run. This parameter is always present with a value except when the date and time is not set in the instrument. The value is always formatted according to ISO 8601. See example below.

The date and time is always in the local time zone. There is never any time zone info.

```
<p><n>DATE</n><v>2004-05-06T07:08:09</v></p>
```

SORC – Sample or Control

This flag indicates if it is a normal sample run or a control sample run. This parameter is always present with a value.

Value range:

- 0: normal sample
- 1: generic (also known as fixed ID) control sample
- 2: control sample with reference ranges (e.g. input via barcode)

<p><n>SORC</n><v>0</v></p>

STYP – Sample Type

This flag indicates the sample type, i.e. if the run was a blood or a PLT concentrate sample. Only present if the sample can be anything else than blood, i.e. it is present in blood bank models where platelet concentrate may be analyzed.

Value range:

- 0: blood
- 1: PLT concentrate

<p><n>STYP</n><v>1</v></p>

ASPM - Aspiration Mode

The aspiration mode for the analysis. This parameter is always present with a value. The value is one of the values listed below **Fel! Hittar inte referenskälla..**

Value	Description
"OT"	Open Tube
"PD"	Prediluted sample
"CT"	Closed Tube = Cap piercer
"MC"	Micro capillary = MPA
"AS"	Auto sampler

<p><n>ASPM</n><v>OT</v></p>

ASPS – Aspiration Status

The aspiration status for the analysis. This parameter is always present with a value.

The value is a status flag indicating if blood was detected during aspiration.

Value range:

- 0: no blood (or other) detected
- 1: blood (or other) detected
- 2: indeterminate due to e.g. timed aspiration

<p><n>ASPS</n><v>1</v></p>

BLNK - Blank Sampl

This flag indicates the analysis was regarded as a background count by the instrument. This parameter is always present with a value.

Value range:

- 0: not a blank
- 1: a blank

The definition of a blank today is $RBC < 1.00$, but this can change.

<p><n>BLNK</n><v>0</v></p>

ASWN - Autosampler Wheel Number

The wheel number for an autosampler run. This parameter is only present if the instrument has an autosampler. The value is only present for autosampler samples.

Value range:

- 1 – 2 (TBD)

<p><n>ASWN</n><v>1</v></p>

ASWP - Autosampler Wheel Position

The wheel position for an autosampler run. This parameter is only present if the instrument has an autosampler. The value is only present for autosampler samples.

Value range:

- 1 - 20.

<p><n>ASWP</n><v>17</v></p>

Differentiation – Red Cells-Platelets

The differentiation between red cells and platelets is realised with a method that uses floating discriminators. The search range for a minimum between the populations is limited by a low and a high limit.

The floating discriminator is denoted RPD, the low and the high limits are denoted RPDL and RPDH.

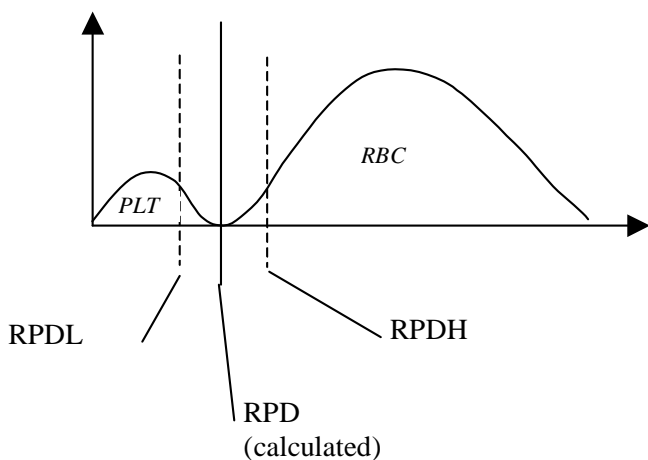


Fig. 9:1

RPD - RBC/PLT Floating Discriminator

This is position of the floating RBC/PLT discriminator. This parameter is always present with a value. The value is given in the unit *fl*.

Value range: 0 - 99

Note that the position of this discriminator is included in the PLT and RBC histograms too, but in that case as histogram bin indices.

<p><n>RPD</n><v>24</v></p>

RPDL - RBC/PLT Floating Discriminator Low Range Limit

This is the low range limit for the floating RBC/PLT discriminator. This parameter is always present with a value. The value is given in the unit *fl*.

The operator of the instrument setup sets the value of this parameter.

Value range: 0 - 99

<p><n>RPDL</n><v>12</v></p>

RPDH - RBC/PLT Floating Discriminator High Range Limit

This is the high range limit for the floating RBC/PLT discriminator. This parameter is always present with a value. The value is given in the unit *fl*.

The operator of the instrument setup sets the value of this parameter.

Value range: 0 - 99

<p><n>RPDH</n><v>27</v></p>

Differentiation – White Cells

WDMA - WBC Diff Method Actual

This indicates the floating WBC diff method actually used during the calculations. Only present in instruments with WBC diff.

Value range:

- 1: DM1 human floating
- 2: DM2 fixed
- 4: DM4 vet floating

<p><n>WDMA</n><v>2</v></p>

WDMS - WBC Diff Method Set

This indicates the WBC diff method selected in the instrument setup. Only present in instruments with WBC diff.

The operator of the instrument setup sets the value of this parameter.

Note: WDMA and WDMS have the same value, except when a “fallback” from the selected WBC diff method to another one occurs. This happens when it isn’t possible to calculate a WBC diff using the selected method, but it is possible with the fallback method..

Value range:

- 1: DM1 human floating
- 2: DM2 fixed
- 4: DM4 vet floating

<p><n>WDMS</n><v>1</v></p>

WDLL - WBC Floating Discriminator Low Range Limit

This is the low range limit for the floating WBC discriminator (LYM-L). The value is given in the unit *fl*.

The parameter is only present in models where a floating differentiation method (e.g. "DM1" or "DM4") can be chosen. The value present only if a floating differentiation method is used.

The operator of the instrument setup sets the value of this parameter.

Value range:

0 - 999

<p><n>WDLL</n><v>40</v></p>

WDLH - WBC Floating Discriminator High Range Limit

This is the high range limit for the floating WBC discriminator (GRAN-H). The value is given in the unit *fl*.

The parameter is only present in models where a floating differentiation method (e.g. "DM1" or "DM4") can be chosen. The value present only if a floating differentiation method is used.

The operator of the instrument setup sets the value of this parameter.

Value range:

0 - 999

<p><n>WDLH</n><v>330</v></p>

WLGL – WBC DM4 LYM/GRAN Limit

This is the hard limit between LYM and GRAN populations for the floating WBC discriminator (GRAN-H). The hard limit is used when the floating differentiation method cannot find two peaks. The parameter is only present in models where "DM4" can be chosen. The value is present if "DM4" is used.

The operator of the instrument setup sets the value of this parameter.

Value range:

0 – 999

Not DM4:

<p><n>WLGL</n></p>

DM4:

<p><n>WLGL</n><v>150</v></p>

WDIL - WBC Fixed Discriminator Low

This is the low range limit for the fixed WBC discriminator (LYM-L). The parameter is only present in models where a differentiation method with fixed discriminators (e.g. "DM2") can be chosen or is automatically used in a 'fallback' case.

Value range:
0 - 999

<p><n>WDIL</n><v>110</v></p>

WDIH - WBC Fixed Discriminator High

This is the high range limit for the fixed WBC discriminator (GRAN-H).

The parameter is only present in models where a differentiation method with fixed discriminators (e.g. "DM2") can be chosen or is automatically used in a fallback situation. The value present only if a differentiation method with fixed discriminators is used.

Value range:
0 - 999

<p><n>WDIH</n><v>130</v></p>

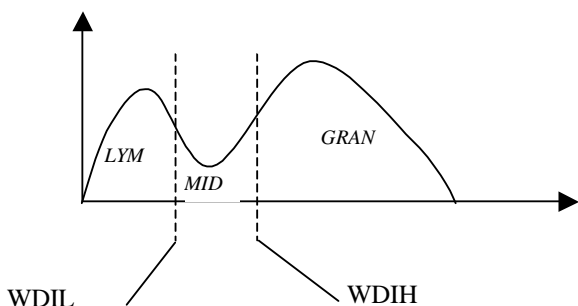


Fig. 9:2

SWM - WBC Software Discriminator Mode - WBC Debris Discriminator Mode

This parameter indicates the used debris subtraction mode used during the WBC calculations. Only present in vet models.

Value range:

- 0: fixed
- 1: floating 1
- 2: floating 2

<p><n>SWM</n><v>0</v></p>

SWF - WBC Fixed Software Discriminator WBC Debris Discriminator Position

This indicates the WBC fixed debris subtraction discriminator setting used during the calculations. Only present in vet models.

Value range:

- 0 – 999

<p><n>SWF</n><v>45</v></p>

Control Blood with Reference Ranges

CAPL – Control Blood Application

The application (human/vet/blood bank) of a control blood with reference ranges. This parameter is only present if the instrument has at least one control blood with reference ranges defined. The value is only present if the run was a control blood with reference ranges.

The value is a one character string: "H" for human, "V" for vet and "B" for blood bank.

Note: This information is included in the current control blood reference range bar code sheets.

<p><n>CAPL</n><v>H</v></p>

CLVL – Control Blood Level

The level (normal/low/high/calibrator) of a control blood with reference ranges. This parameter is only present if the instrument has at least one control blood with reference ranges defined. The value is only present if the analysis was a control blood with reference ranges.

The value is a one-character string: "N" for normal level, "L" for low level, "H" for high level, and "C" for calibrator.

Note: This information is included in the current control blood reference range bar code sheets.

<p><n>CLVL</n><v>N</v></p>

CLOT - Lot identifier of a Control Blood with Reference Ranges

The lot identifier of a control blood with reference ranges. This parameter is only present if the instrument has a least one control blood with reference ranges defined. The value is only present if the run was a control blood with reference ranges.

The lot identifier uniquely identifies one lot of control blood with reference ranges.

The value is string of up to 15 characters. Treat it as an "atomic unit".

Note: this information is not explicitly included in the current control blood reference range bar code sheets, but a numeric lot number is included in both the ID (followed by "+"), and the description (prefixed by level).

```
<p><n>CLOT</n><v>0410042</v></p>
```

CEXP - Expiry Date of a Control Blood with Reference Ranges

The expiry date of a control blood with reference ranges. This parameter is only present if the instrument has a least one control blood with reference ranges defined. The value is only present if the run was a control blood with reference ranges.

The value is a date, always formatted according to ISO 8601. See example below.

```
<p><n>CEXP</n><v>2005-03-09</v></p>
```

CEXT - Extra Control Blood Information for a Control Blood with Reference Ranges

Extra control blood info for a control blood with reference ranges. This parameter is only present if the instrument has a least one control blood with reference ranges defined. The value is only present if the run was a control blood with reference ranges, and there is some extra information.

Value range:

TBD

Note: this information might be included in the current (or future) control blood reference range bar code sheets.

No extra info:

```
<p><n>CEXT</n></p>
```

Some extra info:

```
<p><n>CEXT</n><v>1</v></p>
```

CDSC - Descriptive Text of a Control Blood with Reference Ranges

The descriptive text of a control blood with reference ranges. This parameter is only present if the instrument has a least one control blood with reference ranges defined. The value is only present if the analysis was a control blood with reference ranges.

The descriptive text is output on the display as a control ID entry confirmation.

The value is a string of up to 15 characters. It can contain white space. "Strip"/"Trim" leading and trailing white space, keep internal white space.

Note: this information is explicitly included in the current control blood reference range bar code sheets.

```
<p><n>CDSC</n><v>NORM 0410042</v></p>
```

Patient Information

NOTE: The instrument does NOT manage a patient database, i.e. there is no way to relate samples to a certain patient record. The patient information is only textual information entered by the operator and hence its consistency cannot be guaranteed. Therefore no patient field or combination of fields can be considered as unique for a certain patient (i.e. no “primary key” exists).

PNAM - Patient's Name

The patient's name. This parameter is only present if the instrument is configured to handle patient info. The value is only present if the info was input during the run.

Value:

string 1 - TBD.

```
<p><n>PNAM</n><v>Scrouge McDuck</v></p>  
<p><n>PNAM</n><v>Socks</v></p>
```

PDOB - Patient's Day of Birth

The patient's day of birth. This parameter is only present if the instrument is configured to handle patient info. The value is only present if the info was input during the run.

Note that the value of this parameter basically says the same as the parameter PAGE below. The instrument only outputs what the operator inputs. It does not check these two parameters for consistency, or calculate the other when one is input.

The value is a date, always formatted according to ISO 8601. See example below.

```
<p><n>PDOB</n><v>2000-02-29</v></p>
```

PAGE - Patient's Age

The patient's age. This parameter is only present if the instrument is configured to handle patient info. The value is only present if the info was input during the run.

Note that the value of this parameter basically says the same as the parameter PDOB above. The instrument only outputs what the operator inputs. It does not check these two parameters for consistency, or calculate the other when one is input.

The value is a number of years, with decimals.

Patient is 18 months = 1.5 years old:

```
<p><n>PAGE</n><v>1.5</v></p>
```

PSEX - Patient's Sex

The patient's sex. This parameter is only present if the instrument is configured to handle patient info. The value is only present if the info was input during the run.

Value range:

- 0: not specified, not an issue, unknown.
- 1: female
- 2: male

```
<p><n>PSEX</n><v>2</v></p>
```

PDOC - Name of Patient's Physician, Doctor, Veterinarian etc

Name of patient's physician, doctor, veterinarian etc. This parameter is only present if the instrument is configured to handle patient info. The value is only present if the info was input during the run.

Value:

string 1 - TBD.

```
<p><n>PDOC</n><v>Dr Huckstable</v></p>
```

```
<p><n>PDOC</n><v>DVM Smith</v></p>
```

PREF - Patient's Reference Information

Other reference info about the patient, not further defined here. This parameter is only present if the instrument is configured to handle patient info. The value is only present if the info was info during the run.

Value:

string 1 - TBD.

```
<p><n>PREF</n><v>Bill account #12345</v></p>
```

```
<p><n>PREF</n><v>Call (212)555-1234</v></p>
```

Analysis Settings

APNU – Analysis Profile Number

The number of the Analysis Profile (species) selected for the analysis. This parameter is always present. The value is present if the blood was not a control blood with reference ranges.

Value range: 1 - TBD.

```
<p><n>APNU</n><v>1</v></p>
```

APNA – Analysis Profile Name

The name (if defined) of the Analysis Profile (species) selected for the analysis. This parameter is always present. The value is present if a name is defined for the selected Analysis Profile (species), and if the blood was not a control blood with reference ranges.

The value is a string of 1 to TBD with non-whitespace characters.

APNA without name:

```
<p><n>APNA</n></p>
```

APNA with name:

```
<p><n>APNA</n><v>DOG</v></p>
```

XLT - Extra Lyzing Time

This indicates the use of a longer lyzing time than standard. Only present in vet models. Value only present if a longer lyzing time used.

Value range:

Seconds with one decimal, 0.0 – 19.9

No extra lyze time:

```
<p><n>XLT</n></p>
```

Extra lyze time:

```
<p><n>XLT</n><v>5.0</v></p>
```

<smprresults> Sample Result Parameter Values

Sample result parameter values are the measured and calculated hematology parameters from a sample run.

The parameter order below is not fixed. The parameters might be in another order. Be prepared for new parameter definitions.

Note: If a parameter is not present in the instrument, or if it is blocked by the user, then it is not output at all.

```
<smprresults >
  <p><n>RBC</n>...</p>
  <p><n>MCV</n>...</p>
  <p><n>HCT</n>...</p>
  <p><n>MCH</n>...</p>
  <p><n>MCHC</n>...</p>
  <p><n>RDWR</n>...</p> <!-- RDW% -->
  <p><n>RDWA</n>...</p> <!-- RDWa -->
  <p><n>PLT</n>...</p>
  <p><n>MPV</n>...</p>
  <p><n>PCT</n>...</p>
  <p><n>PDW</n>...</p>
  <p><n>LPCR</n>...</p>
  <p><n>HGB</n>...</p>
  <p><n>WBC</n>...</p>
  <p><n>LA</n>...</p> <!-- LYM# -->
  <p><n>MA</n>...</p> <!-- MID# -->
  <p><n>GA</n>...</p> <!-- GRAN# -->
  <p><n>LR</n>...</p> <!-- LYM% -->
  <p><n>MR</n>...</p> <!-- MID% -->
  <p><n>GR</n>...</p> <!-- GRAN% -->
</smprresults >
```

Result Parameter Format

A result parameter always has a name and a normal / reference range. It could also have a value or a out-of-range flag, and an error flag.

<v> - Parameter Value

The "<v>" tag is the normal parameter value. It is present if a valid value was calculated for the analysis.

For example if the instrument counts RBC as 0.00, then there is not enough cells to calculate an acceptable MCV. The instrument reports the RBC value as 0.00, since it did actually not count any cells, but the MCV value is absent.

The value range and the number of decimals depend of the parameter [ZZZ and the unit]. (The BM800 stores each parameter internally as a 16-bit scaled integer, so the "mantissa range" is 0 - 65535.)

The "<v>" and "<r>" tags are mutually exclusive. A value is either not calculated (neither "<v>" nor "<r>"), calculated ("<v>" only), or out-of-range ("<r>" only).

<r> - Parameter Out-of-Range

The "<r>" tag is only present if the parameter value is either completely out-of-range, or could not be determined for some unusual reason. For example, if the MCV value is absent due to a blank run, then there is no "<r>" tag. But if the RBC value is absent due to a ridiculously high count (currently above 14 in human models), then we have "<r>H<r>".

The "<r>" tag can take the values "H" (value too high) or "L" (value too low).

The "<r>" and "<v>" tags are mutually exclusive. A value is either not calculated (neither "<v>" nor "<r>"), calculated ("<v>" only), or out-of-range ("<r>" only).

<f> - Parameter Error Flag

The "<f>" tag is an optional parameter error flag. Some errors block the calculation of a parameter value, others provide additional information.

The error flag is always two upper-case letter. The list of possible values is not included here. Be prepared for any combination of two uppercase letters.

Only these parameters can have an error flag: RBC, MCV [MCV flag is currently not in use] PLT, HGB, WBC, and the LYM, MID, GRAN parameters. The latter three have one common error flag.

<l> - Parameter Normal/Reference Range Low

The "<l>" tag is always present. Its value is the low end of the normal / reference(*) range. If the parameter value is exactly equal to "<l>", then it is within the normal / reference range.

(* It is called the normal range for normal blood and generic (AKA fixed ID) control blood, and reference range for reference range control blood (f.ex. input via barcode).)

See the <v> tag above for information about values ranges

<h> - Parameter Normal/Reference Range High

The "<h>" tag is always present. Its value is the high end of the normal / reference range. If the parameter value is exactly equal to "<h>", then it is within the normal / reference range.

See the <v> tag above for information about values ranges

Examples:

A result parameter could be without any value, f.ex. if the value could not be calculated:

<p><n>MCV</n><l>70.0</l><h>100.0</h></p>

Normally, a result parameter has a value:

<p><n>RBC</n><v>4.56</v><l>3.50</l><h>5.50</h></p>

Or it could have a value and an error flag:

<p><n>PLT</n><v>234</v><f>FD</f><l>100</l><h>400</h></p>

Or an error flag only:

<p><n>WBC</n><f>TU</f><l>5.5</l><h>8.5</h></p>

Or it could have an out-of-range flag instead of a value (possibly with an error flag too).

<p><n>HGB</n><r>H</r><l>12.5</l><h>16.5</h></p>

Description of the Sample Result Parameters

Result Parameter	Description	Unit	Comments
RBC	Red blood cell concentration	10 ¹² /l	
MCV	Mean Cell Volume	fl	
HCT	Hematocrit value	%	
MCH	Mean Cell Hemoglobin	pg	
MCHC	Mean Cell Hemoglobin Concentration	g/dl	
RDWR	Red blood cell distribution width, relative. Note: RDW relative is the commonly accepted RDW value.	%	
RDWA	Red blood cell distribution width, absolute.	fl	
PLT	Platelet concentration (trombocytes).	10 ⁶ /l	
MPV	Mean Platelet Volume.	fl	
PCT	Platelet Crit. As HCT but for platelets (PLT).	%	
PDW	Platelet distribution width.	%	
LPCR	Large Platelet Concentration Ratio. (PLT > 12 fl / PLT _{tot})	%	
HGB	Hemoglobin concentration.	g/dl	
WBC	White blood cell concentration	10 ⁹ /l	
LA	Lymphocyte concentration	10 ⁹ /l	
MA	Mid concentration	10 ⁹ /l	
GA	Granulocyte concentration.	10 ⁹ /l	

LR	Lymphocyte concentration, relative. Given in percent (%).	%	
MR	Mid concentration, relative total WBC. Given in percent (%).	%	
GR	Granulocyte concentration, relative total WBC. Given in percent (%).	%	

< tparams> Technical (troubleshooting) Parameter Values

Note:

Technical (troubleshooting) parameter values describe results about the run itself and not about the blood. They can be used for troubleshooting purposes. Hence, these parameters are not absolute necessary to be handled by any host system.

The parameter order below is not fixed. The parameters might be in another order. Be prepared for newly defined parameters.

Please note: the technical parameters might not be present for all samples in the sample memory to conserve space, but rather for, say, the last 20 samples. Or some of them could be present for all samples. Be prepared for this.

```
<tparams>
  <p><n>RCT</n>...</p>
  <p><n>WCT</n>...</p>
  <p><n>RPUT</n>...</p>
  <p><n>WPUT</n>...</p>
  <p><n>RPDT</n>...</p>
  <p><n>WPDT</n>...</p>
  <p><n>ASPT</n>...</p>
  <p><n>STT</n>...</p>
  <p><n>LPET</n>...</p>
  <p><n>LPFT</n>...</p>
  <p><n>DPET1</n>...</p>
  <p><n>DPFT1</n>...</p>
  <p><n>DPET2</n>...</p>
  <p><n>DPFT2</n>...</p>
  <!-- ZZZ more to come? ... -->
</tparams>
```

Technical Parameter Format

A technical parameter has a name (“<n>”), an optional value (“<v>”) and an optional error flag (“<f>”).

A technical parameter could be without any value, e.g. when a value could not be calculated:

```
<p><n>RCT</n></p>
```


<v> - Technical Parameter Value

The "<v>" tag is the value of the technical parameter. It is present if a valid value was calculated for the run.

Normally, a technical parameter has a value:

```
<p><n>WCT</n><v>10.23</v></p>
```

<f> - Technical Parameter Error Flag

The "<f>" tag is an optional technical parameter error flag. Some errors block the calculation of a parameter value, others provide additional information.

The error flag is always two upper-case letters. The list of possible values is not included here.

Examples:

A value and an error flag:

```
<p><n>RPUT</n><v>42</v><f>FD</f></p>
```

An error flag only:

```
<p><n>RCT</n><f>TU</f></p>
```

RCT - Red Counting Time

The time the instrument counts cells on the red side. (=The time from the lower to the upper detector)

Unit: seconds with two decimals.

This parameter could have an error flag with the values "LO" or "HI", or could have an out-of-range flag with the values "L" or "H" instead of a value. The latter indicates serious abnormalities during the sample analysis.

WCT - White Counting Time

The time the instrument counts cells on the white side. (=The time from the lower to the upper detector)

Unit: seconds with two decimals.

This parameter could have an error flag with the values "LO" or "HI", or could have an out-of-range flag with the values "L" or "H" instead of a value. The latter indicates serious abnormalities during the sample run.

RPUT - Red Pillar Up Time

The time from the opening of the red pillar valve to the pillar reaches the upper detector. (Note the difference from RCT.)

Unit: seconds with two decimals.

This parameter could have an error flag with the values "LO" or "HI", or could have an out-of-range flag with the values "L" or "H" instead of a value. The latter indicates serious abnormalities during the sample run.

WPUT - White Pillar Up Time

The time from the opening of the white pillar valve to the pillar reaches the upper detector. (Note the difference from WCT.)

Unit: seconds with two decimals.

This parameter could have an error flag with the values "LO" or "HI", or could have an out-of-range flag with the values "L" or "H" instead of a value. The latter indicates serious abnormalities during the sample run.

RPDT - Red Pillar Down Time

The time from the opening of the red pillar valve to the pillar reaches the lower detector.

Unit: seconds with two decimals.

This parameter could have an error flag with the values "LO" or "HI", or could have an out-of-range flag with the values "L" or "H" instead of a value. The latter indicates serious abnormalities during the sample run.

WPDT - White Pillar Down Time

The time from the opening of the white pillar valve to the pillar reaches the lower detector.

Unit: seconds with two decimals.

This parameter could have an error flag with the values "LO" or "HI", or could have an out-of-range flag with the values "L" or "H" instead of a value. The latter indicates serious abnormalities during the sample run.

ASPT - Aspiration Time

The time from the opening of the aspiration valve to blood is detected by the blood detector.

Unit: seconds with two decimals.

See also: ASPF parameter above.

This parameter could have an error flag with the values "LO" or "HI". (The latter is also indicated with "ASPF=0".

STT - Sample Transfer Time

The time from the opening of the sample transfer valve(s) to air is detected by the beaker detector.

Unit: seconds with two decimals.

This parameter could have an error flag with the values "LO" or "HI", or could have an out-of-range flag with the values "L" or "H" instead of a value. The latter indicates serious abnormalities during the sample analysis.

LPET - Lyze Pipette Emptying Time

The time for the emptying of the lyze pipette.

Unit: seconds with two decimals.

This parameter could have an error flag with the values "LO" or "HI", or could have an out-of-range flag with the values "L" or "H" instead of a value. The latter indicates serious abnormalities during the sample run.

LPFT - Lyze Pipette Filling Time

The time for the first filling of the lyze pipette.

Unit: seconds with two decimals.

This parameter could have an error flag with the values "LO" or "HI", or could have an out-of-range flag with the values "L" or "H" instead of a value. The latter indicates serious abnormalities during the sample run.

DPET1 - Diluent Pipette Emptying Time #1

The time for the first emptying of the diluent pipette.

Unit: seconds with two decimals.

This parameter could have an error flag with the values "LO" or "HI", or could have an out-of-range flag with the values "L" or "H" instead of a value. The latter indicates serious abnormalities during the sample run.

DPFT1 - Diluent Pipette Filling Time #1

The time for the first filling of the diluent pipette.

DPFT2 - Diluent Pipette Filling Time #2

The time for the second filling of the diluent pipette.

<hgrams> Histograms

Note about terminology: We could call our graphical results histograms or graphs (with plotted curves). Histograms are used in statistics to show the relative frequency of discrete "bins" of some underlying measurement. Graphs are used for example in mathematics to show continuous curves over function values. In a way, a graphical representation of our raw data would be a histogram, while a graphical representation of filtered data would be more like a curve in a graph. Messy. Lets call them histograms. (And lets separate out the actual graphical representation from the data representation here. The data here is just a vector of values.)

The whole "<hgrams>" part is optional. The control sample memory has no histograms, and the user might choose not to include histograms in the dumps.

The histogram order below is not fixed. The histograms might be in another order. Be prepared for newly defined histograms.

There are two variants of histogram layouts.

Variant 1: 3 numbers of diff histograms (LYM, MID, GRA), which should be overlaid to create one WBC histogram with 3 populations. We use the multiple <hgdata> nodes in the <hgram> construct to indicate this. The <hgdata> then also has a <n> that indicates the name of each histogram vector that is a part of the overlaid histogram.

```
<hgrams>
  <hgram>
    <n>PLT</n><m>30</m><k>80</k><w>0</w><d>64</d>
    <hgdata>
      <v>
        0 0 2 5 7 ... <!-- 80 numbers in total, separated by white
space -->
      </v>
    </hgdata>
  </hgram>
  <hgram>
    <n>RBC</n><m>250</m><k>80</k><w>0</w><d>8</d>
    <hgdata>
      <v>
        0 1 3 1 ... <!-- 80 numbers in total, separated by white
space -->
      </v>
    </hgdata>
  </hgram>
  <hgram>
    <n>WBC</n><m>400</m><k>80</k><w>0</w><d>12</d><d>54</d>
    <hgdata>
      <n>LYM</n>
      <v>
        0 0 1 3 5 ... <!-- 80 numbers in total, separated by white
space -->
      </v>
    </hgdata>
    <hgdata>
      <n>MID</n>
      <v>
        0 0 0 0 0 ... <!-- 80 numbers in total, separated by white
space -->
      </v>
    </hgdata>
    <hgdata>
      <n>GRA</n>
      <v>
        0 0 0 0 0 ... <!-- 80 numbers in total, separated by white
space -->
      </v>
    </hgram>
</hgrams>
```

Variant 2, One WBC histogram with 2 (optional) discriminator lines.

```
<hgrams>
  <hgram>
    <n>PLT</n><m>30</m><k>80</k><w>0</w><d>64</d>
    <hgdata>
      <v>
        0 0 2 5 7 ... <!-- 80 numbers in total, separated by white
space -->
      </v>
```

```
</hgdata>
</hgram>
<hgram>
  <n>RBC</n><m>250</m><k>80</k><w>0</w><d>8</d>
  <hgdata>
    <v>
      0 1 3 1 ... <!-- 80 numbers in total, separated by white
space -->
    </v>
  </hgdata>
</hgram>
<n>WBC</n><m>400</m><k>80</k><w>0</w><d>22</d><d>26</d>
<hgdata>
  <v>
    0 0 1 3 5 ... <!-- 80 numbers in total, separated by white
space -->
  </v>
</hgdata>
</hgram>
</hgrams>
```

<hgrams> - Histograms

Histogram Format

All tags are present and in this order, exceptions for:

- 1) The discriminator tag "<d>" that may be present zero, one or more than one times.
- 2) The histogram data vector tag <hgdata> that may be present one or more than one times.

```
<hgram>
  <n>PLT</n>
  <min>5</min>   <!-- Optional. If not present the min range is 0.
-->
  <m>30</m>
  <k>80</k>
  <d>64</d>
  <hgdata>
    <v>
      0 0 2 5 7 ...
    </v>
  </hgdata>
</hgram>
```

<n> – Histogram Name

The "<n>" tag specifies the name of histogram.

<min> - Histogram Min Range

The "<min>" tag specifies the cell volume of the cells that are represented by the bin at the left end of the histogram, i.e. the smallest cells. (Min value of x-axis).

This parameter is optional. If it does not exist, the default minimum value is 0.

Unit: fl (femtoliter).

<m> - Histogram Max Range

The "<m>" tag specifies the cell volume of the cells that are represented by the bin at the right end of the histogram, i.e. the largest cells. (Max value of x-axis).

Unit: fl (femtoliter).

<k> - Histogram Number of Bins

The "<k>" tag specifies the number of data points (bins) in the histogram.

Note 1: There has always been 80 data points in all our histograms, but do not bet that this is fixed for the future!

Note 2: Do not even bet that all histograms in one sample have the same number of data points!
Exception: the "LYM", "MID", "GRA" histograms must of course have the same number of data points, since they are overlaid to create a single three-population histogram.

<w> - Histogram Filter Factor

The "<w>" tag is specifies the filter factor and indicates how hard the instrument has filtered the histogram. The values 0 and 1 mean no filtering while 2, 3, 4, ... mean increasingly harder filtering.

<d> - Histogram Discriminator Index

The "<d>" tag(s) optionally specifies the indices of the bins where the discriminators are positioned in the histogram. This tag is optional. A histogram may have more than one discriminator, so the tag may be present more than once.

The histogram discriminator index is zero-based.

Unit: data point index. In the example above 64 for "PLT" gives a scale value of $\text{<d>} * (\text{<m>} / \text{<k>}) = 64 * (30/80) = 24$.

Note 1: Do not assume that the maximum number of discriminator lines always is 2.

Note 2: Do not assume that the discriminators are output with ascending positions.

Note 3: Try to visually separate the different discriminator lines during graphical presentation, e.g. by the use of different line styles.

Note 4: The discriminator for the PLT and RBC histograms is also included as "RPD".

<hgdata> - Histogram Data Vector

The <hgdata> element represents a histogram data vector, i.e. the values for each bin in the histogram

Each histogram, <hgram>, may have one or more histogram data vectors. The latter case with more than one data vector represents an "overlay" histogram, i.e. a histogram with more than one data vectors drawn in the same histogram.

```
<hgdata>
  <n>LYM</n>
  <v>
    0 0 2 5 7 ...
  </v>
</hgdata>
```

<n> - Histogram Data Vector Name

The "<n>" tag specifies the name of the histogram data vector. The name is optional if there is only one data vector present in a single histogram, but it is mandatory if there is more than one data vector in a single histogram.

<v> - Histogram Data Vector Values

The "<v>" tag specifies the data points (bin values) of the histogram as a data vector. The vector values are represented as a list of numbers, separated by at least one character of white space.

Value range of a vector value:

0 - 255

Index range:

0 - "<k>-1"

Note: Try to apply some formatting to the data point numbers. For instance output 80 data points as 5 rows with 16 data points each.

<rawdata> - Raw Data

Raw data are data as measured by the BM800. It can be used for analysis and/or later recalculations. To be able to perform a correct recalculation of the result parameter, the following information is needed:

- The measured raw data, i.e. the values from the A/D converters.
- The calibration factors.
- For red raw data the MCV temperature compensation is needed.

The whole "<rawdata>" part is optional.

Note that BM800 might only store raw data for some of the last samples. Compare "<tparams>".

This paper does not discuss the rawdata format as it is only used at Boule for detailed data/sample analysis. Also, enabling the rawdata mode in the Setup menu, will limit the number of samples in memory to approx. 60 samples.

Checksum issues

When parsing a package it is important to know where a package starts and ends. Therefore package "begin" and "end" delimiters are used.

Package begin token:

```
<!--:Begin:Checksum:
```

Package end token:

```
<!--:End:Checksum:
```

Since we use serial communication and serial communication is not 100% safe, we add a generic check summing mechanism to the BM800 XML communication.

The data that is subject for checksum control is delimited by checksum begin and end tokens and data according to the following:

Checksum begin:

```
<!--:Begin:Checksum:{Algorithm ID}:-->
```

Checksum end:

```
<!--:End:Checksum:{Algorithm ID}:{Checksum byte 1}:{Checksum byte 2}:-->
```

{Algorithm ID} Corresponds to an integer that identifies what checksum algorithm that has been used.

{Checksum byte 1} Is the first byte of the calculated checksum. The value is in the range 0 – 255.

{Checksum byte 2} Is the second byte of the calculated checksum. The value is in the range 0 – 255.

Example:

```
<!--:Begin:Checksum:1:-->
  {Data to be check summed.}
<!--:End:Checksum:1:105:246:-->
```

The checksum tokens have the syntax of an XML comment (that is delimited by the “<!--“ and “-->“ tokens).

The checksum is calculated for every character (byte) that exist after the “>” character in the checksum begin token and up to but not including the “<” character in the checksum end token. This means that white spaces and new lines also are included in the checksum calculation. Notice though that new lines are handled according to the XML standard, i.e. they are always replaced with the line feed character (ASCII 10) ..

The data between checksum begin and end tokens should be considered as a “byte stream” and hence the format of the data is irrelevant. Note that therefore should in our case no XML parsing of the data be performed before the checksum calculation.

New Line handling

In the checksum calculation we have to handle the different ways of representing a new line. We therefore adopt the line ending handling in the XML standard: a “\n” not followed by a “\r” is treated as it is, the character pair “\r\n” is treated as a single “\n”, and a “\r” not followed by a “\n” is also treated as a single “\n”.

Checksum algorithm

An ID of the used checksum algorithm is given in the checksum tokens. The table below describes the different checksum algorithms and their IDs.

(Currently there exists only one checksum algorithm in the BM800.)

Checksum algorithm ID	Description
0	No checksum
1	“Easy calculation”.

“Easy calculation” checksum algorithm (ID=1)

This checksum algorithm is very easy to calculate, and even easier to verify. Currently used in the BM800

C code sample:

The basic check calculation for a sequence of bytes looks like this in C. The actual checksum is placed in the two last bytes.

```
void
cs_calc( const unsigned char buf[], // Pointer to buffer
         unsigned start, // Index of first check summed byte
         unsigned lim, // Index of last+1 check summed byte
         unsigned char cs[2] ) // Output checksum
{
    unsigned char cs1 = 0, cs2 = 0;
    for( ; start < lim; ++start ){
        cs1 += buf[start];
        cs2 += c1;
    }
    cs[0] = cs1;
    cs[1] = cs2;
}
```

The correct result when checking check summed data is "cs[0]==0 && cs[1]==0".

This is how you set the checksum in the two last bytes:

```
void
cs_set( unsigned char buf[], // Pointer to buffer (2 bytes changed)
        unsigned start, // Index of first check summed byte
        unsigned lim ) // Index of last+1 check summed byte
{
    // precondition: start+2 <= lim
    unsigned char cs[2];
    buf[ lim-2 ] = buf[ lim-1 ] = 0; // Init checksum bytes for
    calc
    cs_calc( buf, start, lim, cs );
    buf[ lim-2 ] = cs[0] - cs[1];
    buf[ lim-1 ] = cs[1] - 2*cs[0];
}
```

C# Code sample:

The data to be check summed is stored in the msg string variable. The two checksums are returned in the out parameters checksum1 and checksum2.

```
private void CalcCheckSum(string msg, out byte checksum1, out byte
checksum2)
{
    byte cs1 = 0;
    byte cs2 = 0;

    // Always use "\n" as line break when calculating the checksum.
    msg = msg.Replace("\r\n", "\n"); // Find and replace CR LF with
LF
    msg = msg.Replace("\r", "\n"); // Find and replace CR with LF.

    for (int i = 0; i < msg.Length; i++)
    {
        cs1 += (byte) msg[i];
        cs2 += cs1;
    }

    checksum1 = cs1;
    checksum2 = cs2;
}
```

We then add the checksums read from the transferred package to the calculated checksums in the following way:

```
checksum1 += transferredChecksum1;
checksum2 += checksum1;
checksum1 += transferredChecksum2;
checksum2 += checksum1;
```

The values of checksum1 and checksum2 should now be 0.

9.4 Upgrading software

The application software in the BM800 is stored in flash-memory and can be upgraded any time. New versions will be available on the Boule support site.

To upgrade, please follow the procedure below:

0. Do a 'Print All Settings' (P.A.S) and 'Print Instrument Log' (P.I.L.)
1. Be sure to have a cable according to 9.1 above and connect it to the BM800 <-> PC
2. Use a terminal program in the PC set to 19.2K Baud, 8 bits, No parity and Start/stop=1. A typical Win-PC terminal program is as standard available called 'Hyperterm'. On Linux, use 'Minicom'. Start the serial communication program in the PC.
3. Start the BM800 (switch ON)
4. The PC will show: "**BM800 boot monitor V2.0.0 , press @ to login**"
5. Press the @ symbol within 5 seconds, otherwise the application will start. In case the 5 seconds limit is missed type 'restart' and try again..
6. After a successful login, the BM800 asks for 'User:'. Type 'upgrade' within 10 seconds and press <Enter>. The BM800 responds with '**Login successful**' and **BM800 boot>**

Type : erase <Enter>. The BM800 responds with:

Eraseing flash, please wait

BM800 boot>

7. Type: 'load' and press <Enter>
8. Send the file from the PC as a xx file to the BM800 , e.g. '**Main-board.XX**'
9. This takes approx. 10-15 minutes, where after the BM800 responds with **Programming completed, starting application**"
10. Repeat (0) above and check that the Instrument Setup is identical. If not; make the necessary adjustments in the Setup menu.

Notes:

Typing 'help' at the BM800 boot> prompt will give a short list of available commands. Typing 'log' will display possible errors.

Possible error messages are listed below:

ErrorCode #	Text	Description/cause
001	System halted	The application start point could not be validated. This check is performed after reset and/or after completed downloads.
002	Download failure, aborting	Below checks can be generated during download <ul style="list-style-type: none">- A line in the upgrade file has a faulty CRC.- Missing or bad sections- Validation key is bogus, e.g. length is out of range- "Write" address points outside of application code area
003	FLASH is not erased, aborting	A location in the flash memory has not been erased prior to programming. Download will be aborted.
004	System failure	Internal error, receive buffer overrun
005	FLASH malfunction	Internal error, flash memory is not responding to an erase or program operation
006	System subcomponent failure	Internal HW error, no communication with the PIC subcomponent or the PIC subcomponent version is not supported