

WeQas  
Unit 6, Parc Tŷ Glas  
Llanishen, Cardiff, CF14 5DU

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# WeQas

GLOBAL PROVIDER OF QUALITY  
IN DIAGNOSTIC MEDICINE



EXTERNAL  
QUALITY  
ASSESSMENT



INTERNAL  
QUALITY  
CONTROL



REFERENCE  
MEASUREMENT  
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EDUCATION &  
TRAINING

## POCT EQA Report Interpretation

Gareth Davies

# Overview

- The WeQas Report - Statistical Indices
  - Imprecision
  - Inaccuracy
- How do we set Analytical Performance Specifications (APS) and Target Values
- WeQas Connect Reports
- Problem Solving and Cases
- Case Study Example

# The WeQas Report

## Statistical Indices

- Imprecision:  $S_{y.x}$ ,  $r$ ,  $IS$
- Inaccuracy: Bias plot,  $y=mx+c$

# Interpretation of Imprecision

**S<sub>y,x</sub>** is the deviation around the best fit line and is an indication of scatter. It is used as an index of within run imprecision. This is given in the units of the analyte in question.

Correlation coefficient (**r value**) is also an index of within run imprecision. The closer to 1.0 the value is, the better the precision (less scatter about the best fit line).

**IS** is derived from the correlation coefficient ( $IS = (1-r)*10,000$ ).

<b>'r' value</b>	<b>Imprecision score</b>	
0.9990 to 1.0000	0 to 10	- Good
0.9850 to 0.9989	11 to 150	- Acceptable to Warning level
< 0.9850	> 150	- Unacceptable (including Curvilinear Data)

# Imprecision indices

Standard deviation

$$SD = \sqrt{\frac{\sum (\bar{y}-y)^2}{d.f.}}$$

where

$y$  = observed value

$\bar{y}$  = expected value

d.f. = degrees of freedom

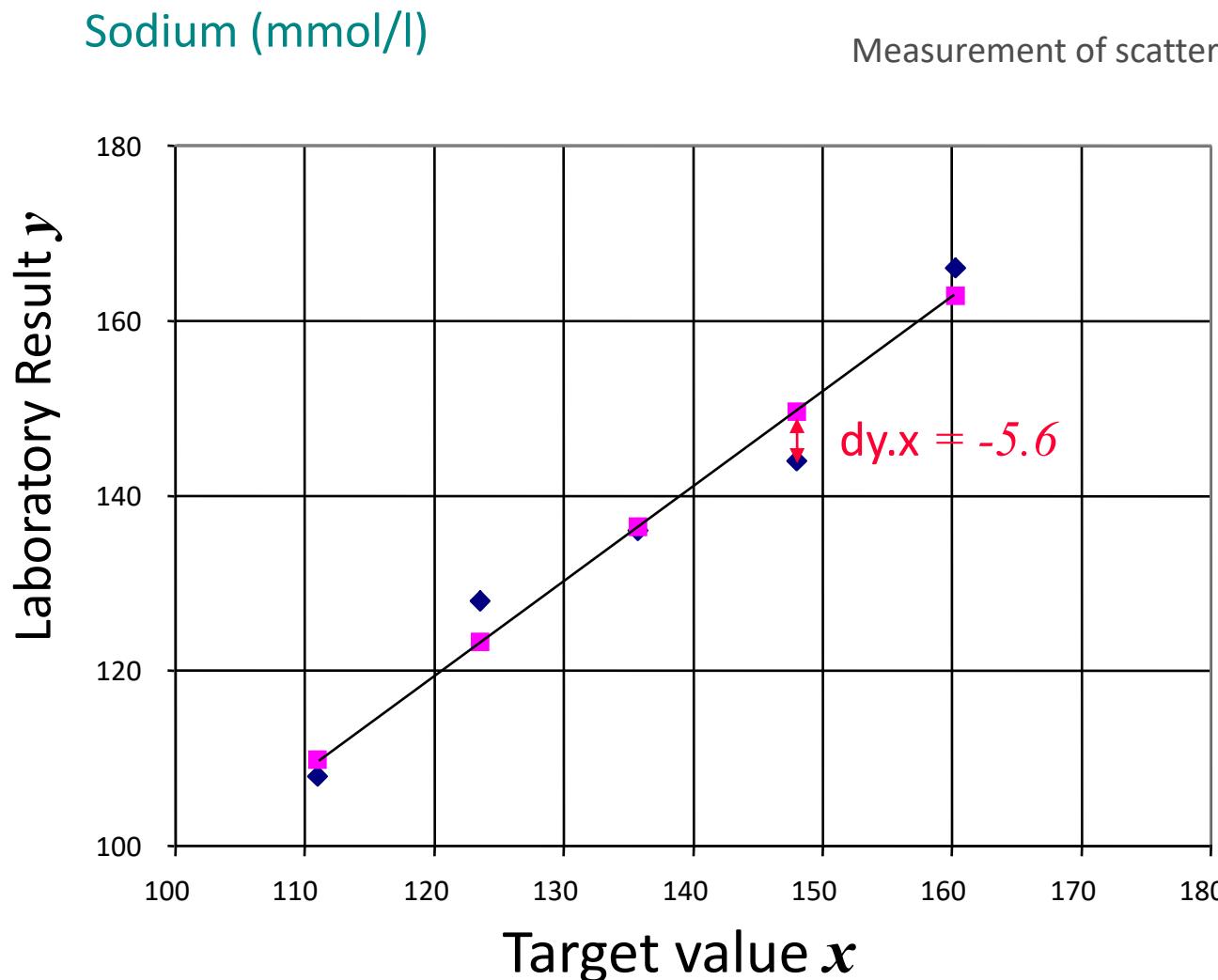
Standard dev of residuals

$$Sy.x = \sqrt{\frac{\sum (\tilde{y}-y)^2}{d.f.}}$$

where

$\tilde{y}$  = the value on the  
line of best fit

# Imprecision – Scatter around the “best fit line”, $S_{y,x}$



All reported results are on the “best fit” line – no scatter

Reported results are scattered around the “best fit” line – standard deviation of 4.1 mmol/L

# Imprecision – how to calculate $S_{y.x}$

Target value <b>x</b>	Lab result <b>y</b>	Line of best fit		$dy.x^2$
		<b>ŷ</b>	$y - \hat{y} = dy.x$	
111	108	109.9	-1.9	3.62
123.5	128	123.3	4.7	21.97
135.7	136	136.4	-0.4	0.16
148	144	149.6	-5.6	31.30
160.3	166	162.8	3.2	10.31
<b>slope</b>	<b>1.07</b>		$\sum dy.x$	$\sum dy.x^2$
<b>int</b>	<b>-9.17</b>		0.0	67.36
		$S_{y.x} = \sqrt{\sum dy.x^2 / df}$	$\sqrt{67.4 / 4}$	4.10

# Interpretation of Inaccuracy

Represents the point at which the line crosses the y axis.  
This is shown in the units of measurement of each analyte.  
If deemed significant, this indicates a constant error.

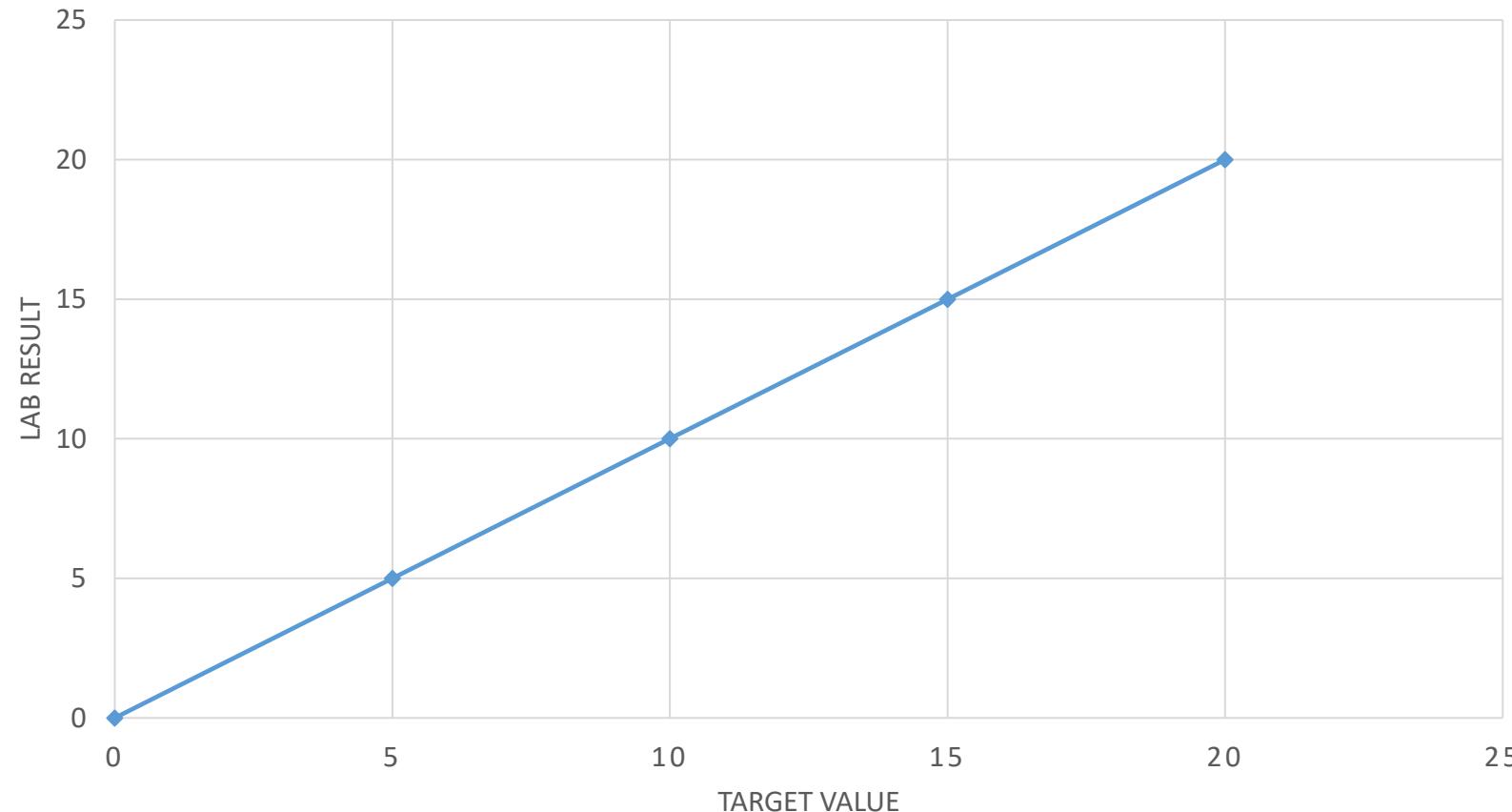
$$y = mx + c$$

Represents the slope. If deemed significant -  
indicates a proportional error.

## ERRORS IN ACCURACY

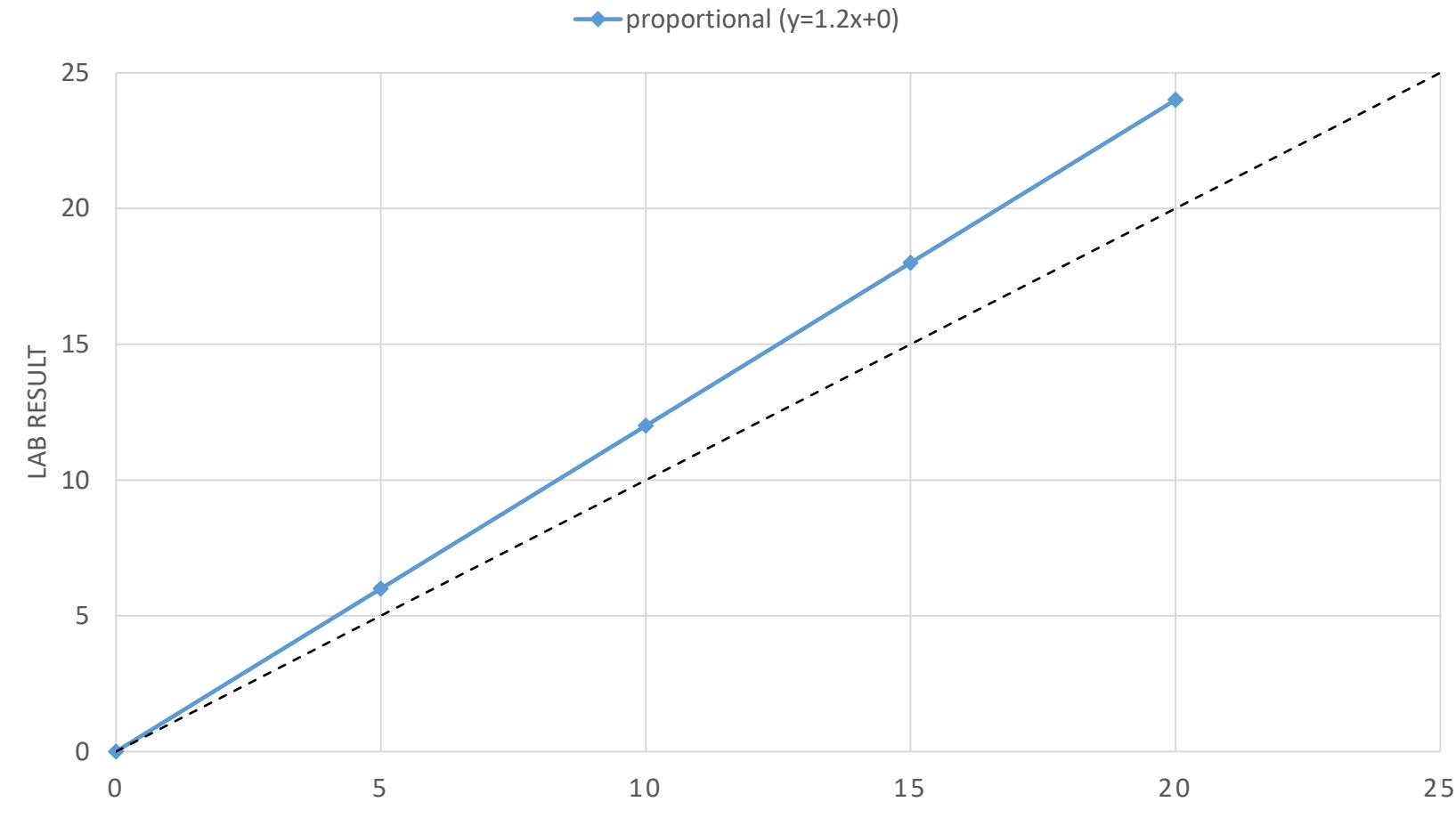
### 1. NO ERROR

—●—  $y = 1x + 0$



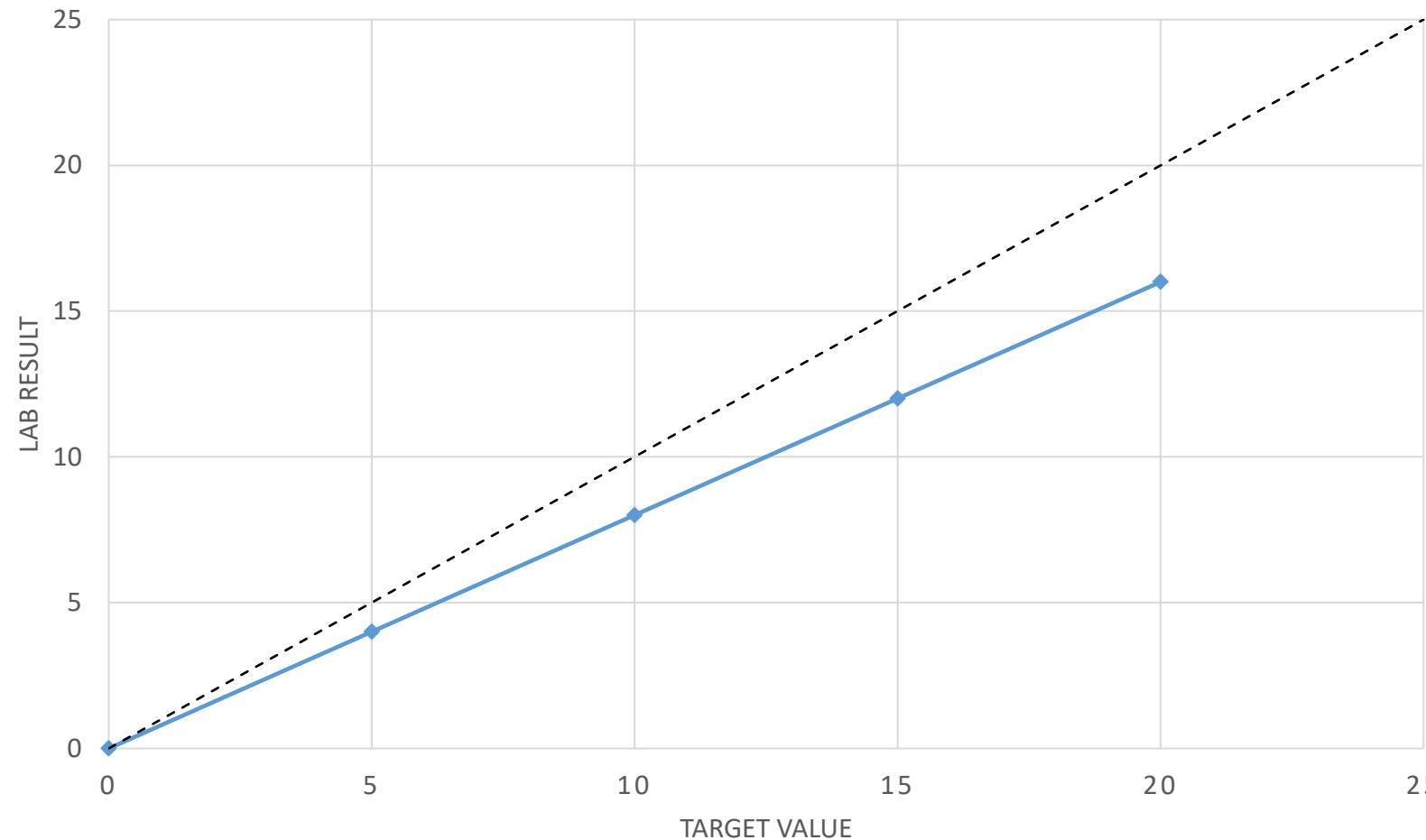
## ERRORS IN ACCURACY

### 2. SYSTEMATIC PROPORTIONAL (POSITIVE BIAS)

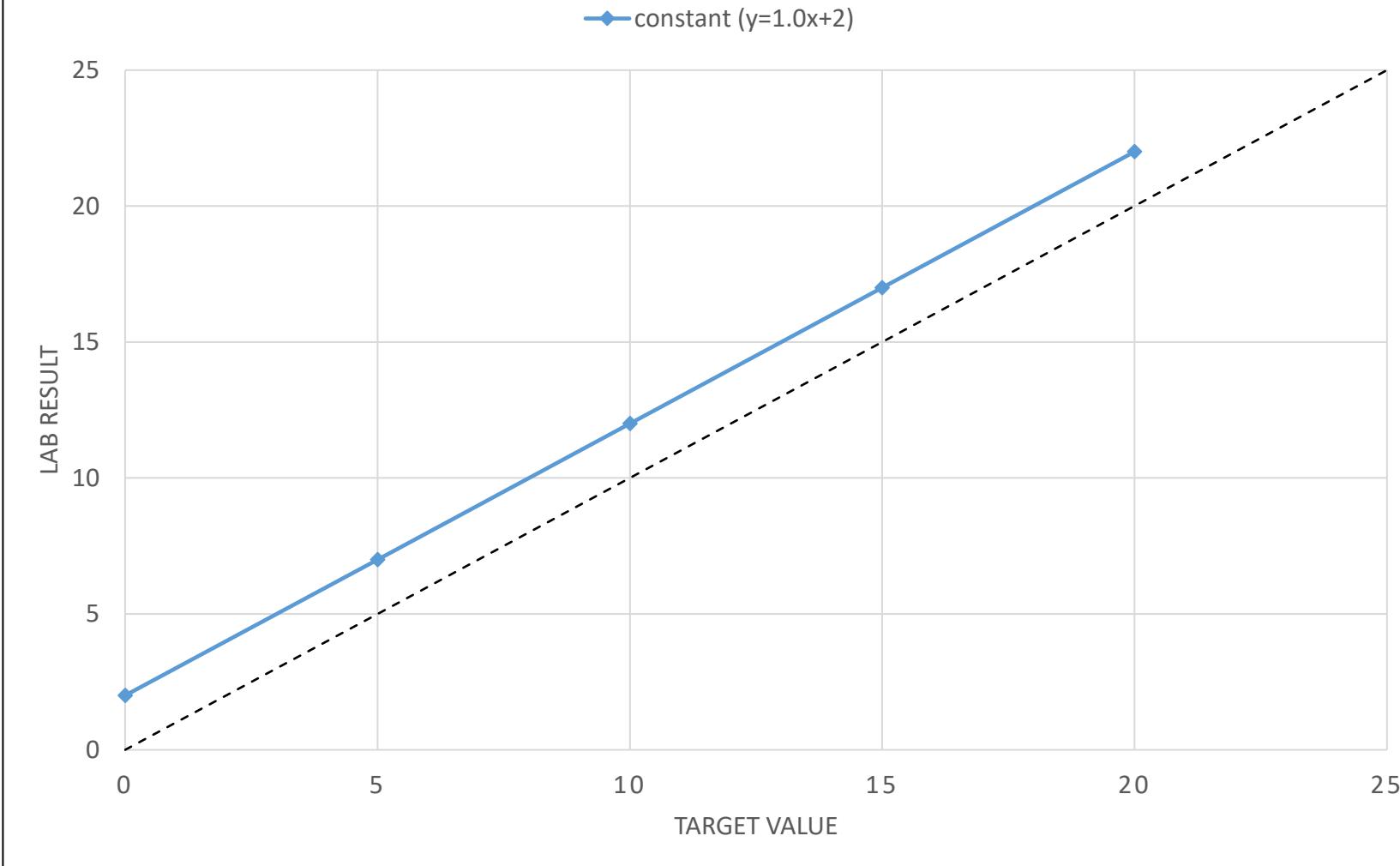


## ERRORS IN ACCURACY

## 3. SYSTEMATIC PROPORTIONAL (NEGATIVE BIAS)

proportional ( $y=0.8x+0$ )

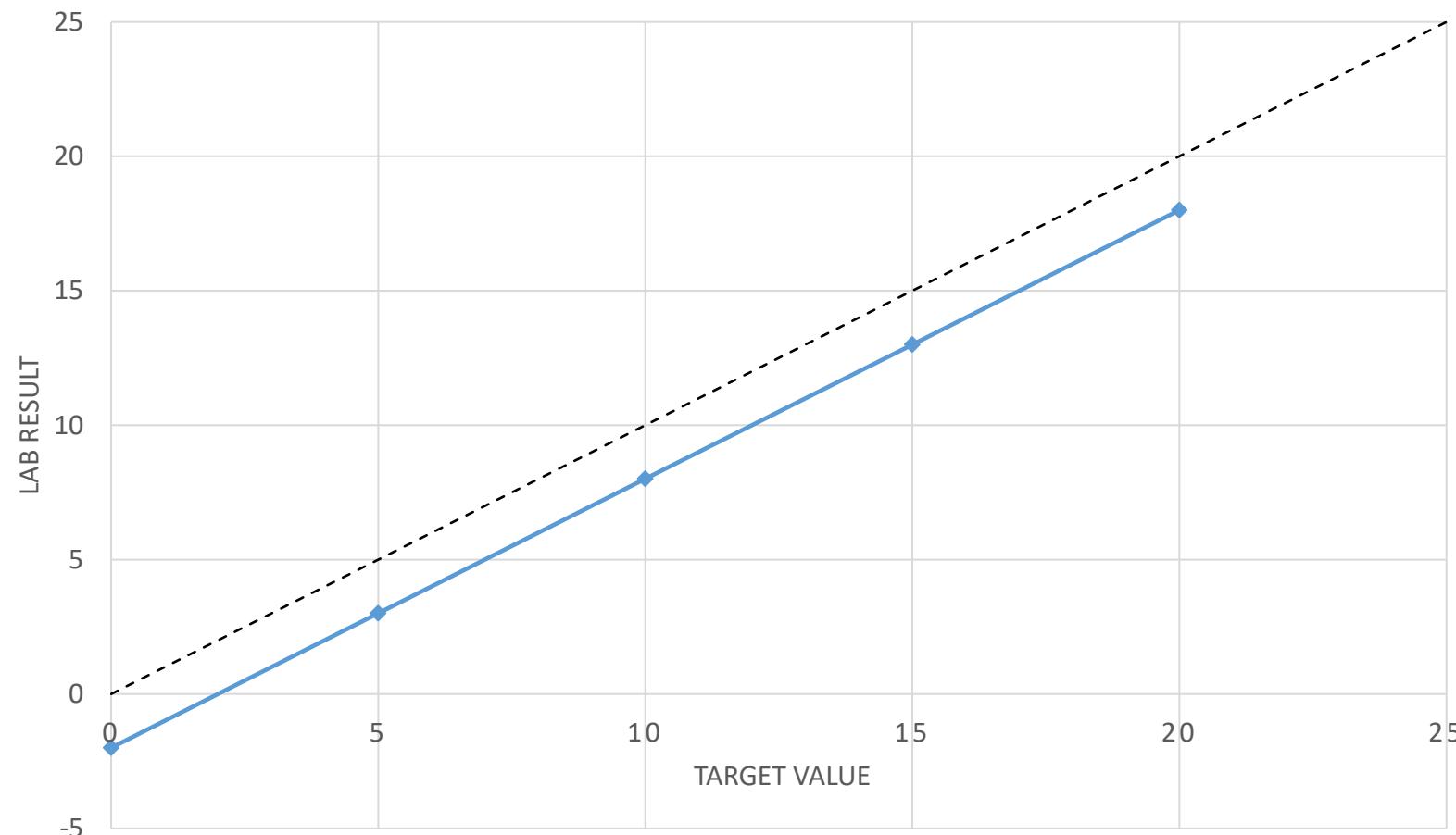
**ERRORS IN ACCURACY**  
**4. CONSTANT (POSITIVE BIAS)**



## ERRORS IN ACCURACY

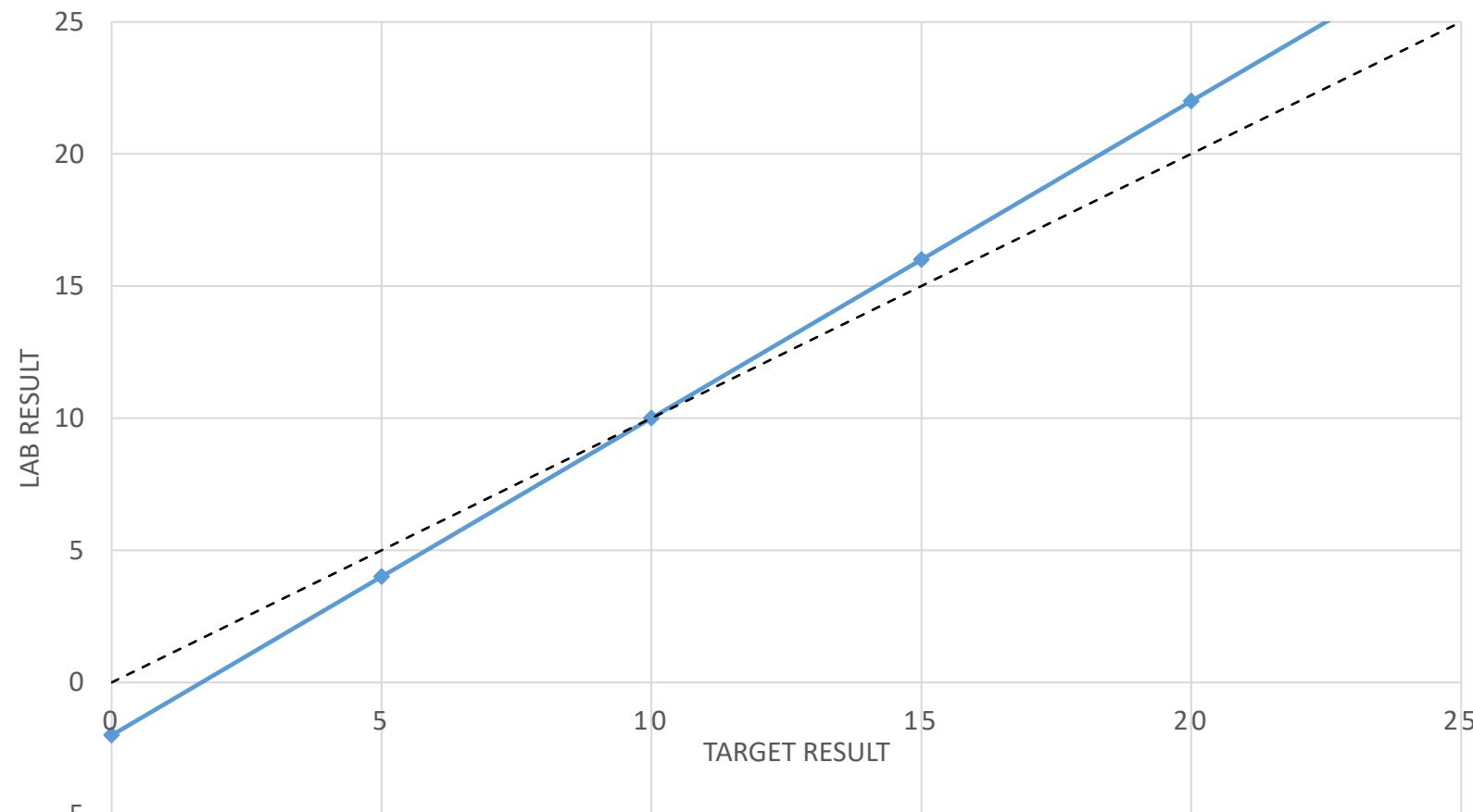
### 5. CONSTANT (NEGATIVE BIAS)

constant ( $y=1x-2$ )



**ERRORS IN ACCURACY**  
**6. MIXED**

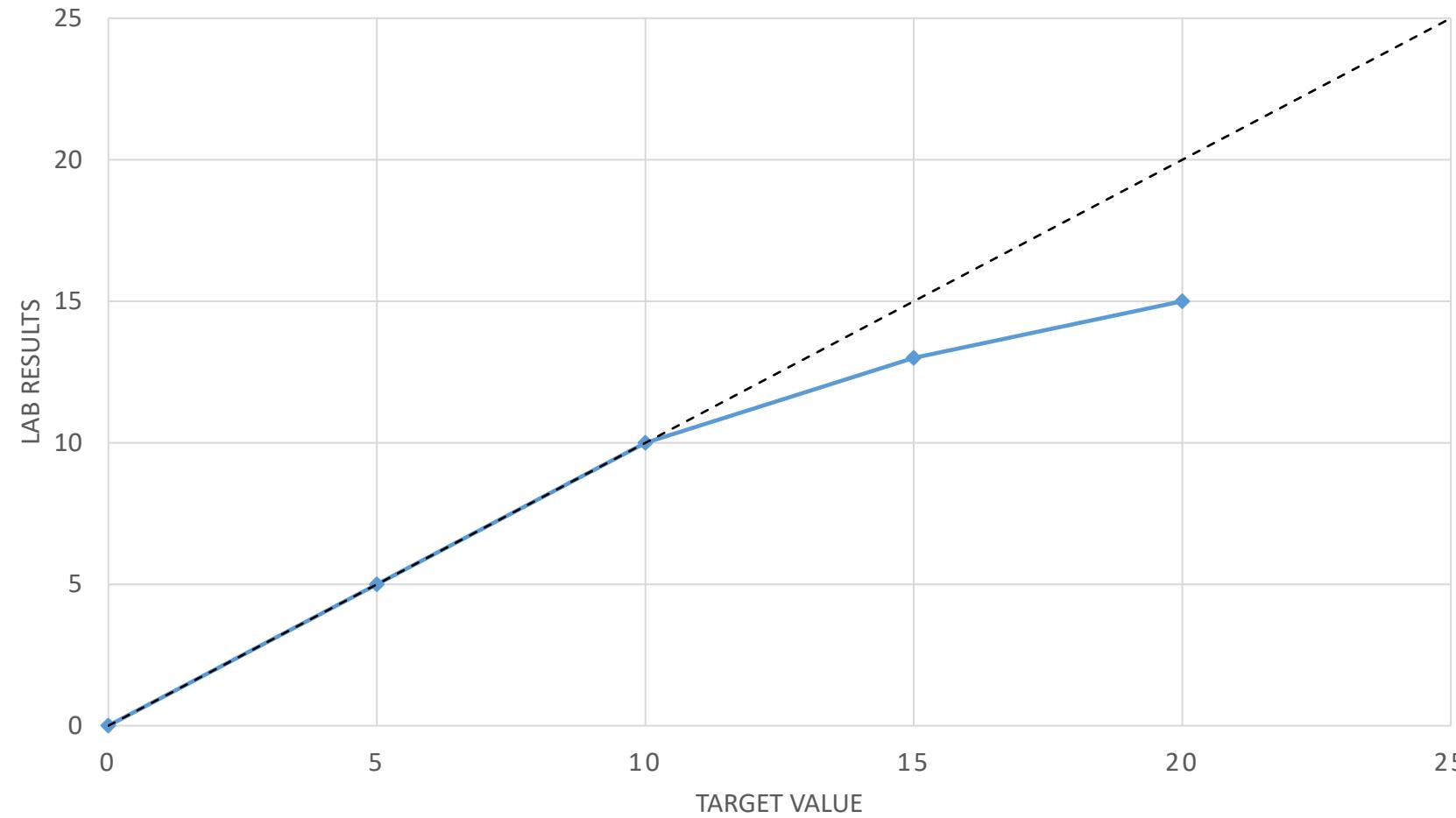
mixed (y=1.2x-2)

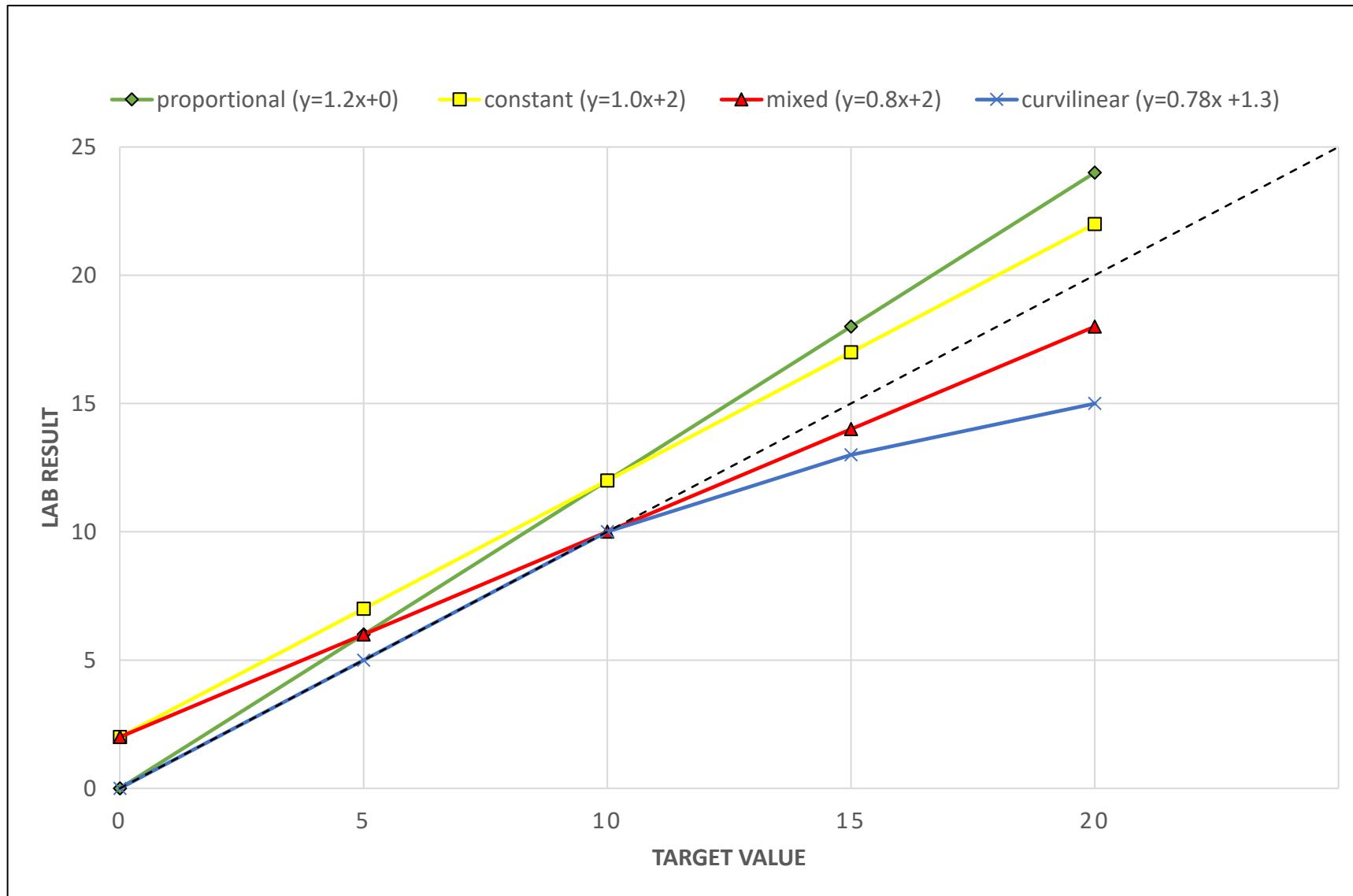


## ERRORS IN ACCURACY

### 7. CURVILINEAR

curvilinear ( $y=0.78x +1.3$ )





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## How do we set Analytical Performance Specifications (APS) and Target Values?

# The WeQas Report

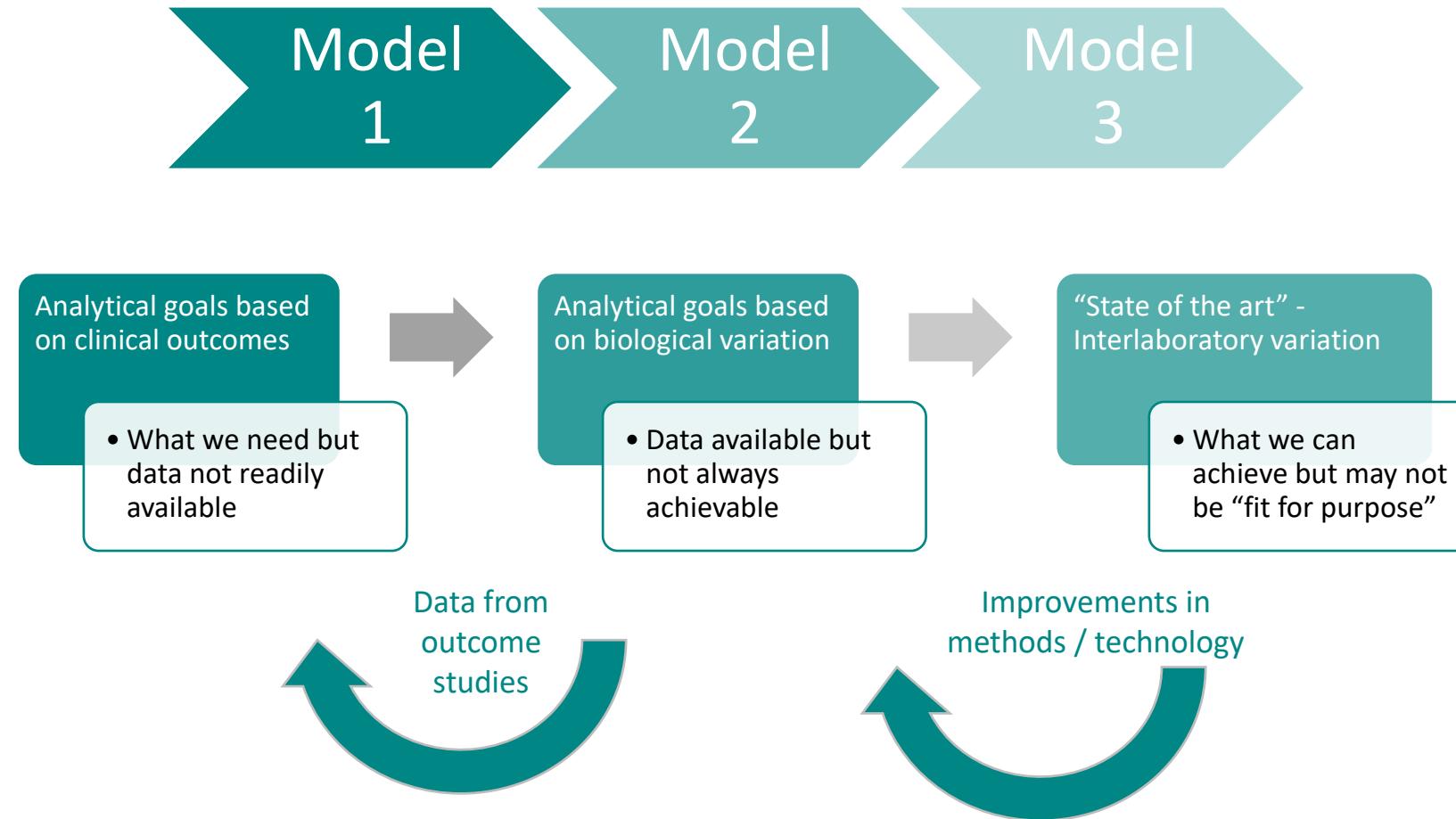
## Target values used in Statistical Analysis

Hierarchy



- Reference values – used for bias plot & SDI / PI calculation
- Method mean – used for SDI / PI calc if no ref value and  $n \geq 8$
- Overall mean – used for SDI / PI calc and bias plot if no ref value and  $n < 8$
- Instrument mean – on report for information only

# Hierarchy for setting APS



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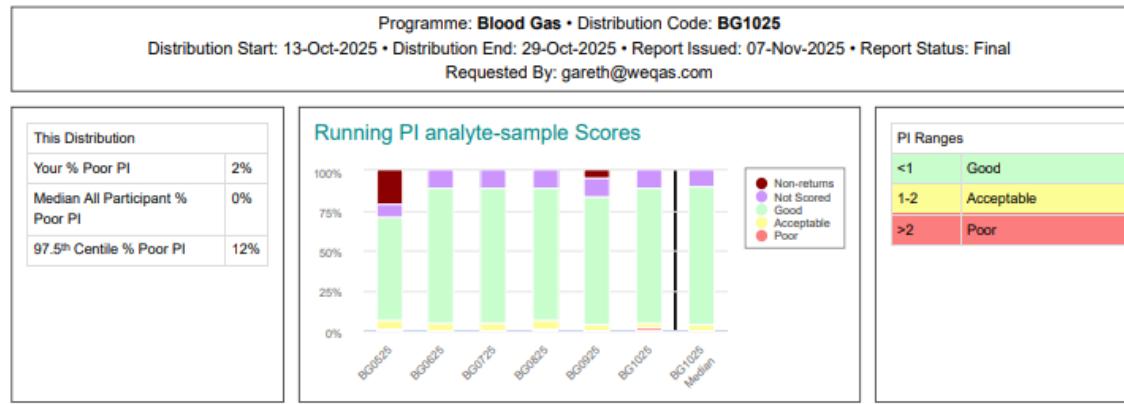
REFERENCE  
MEASUREMENT  
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## Weqas Connect Reports

# Standard Quantitative Report – Managers Summary



PI Scores				
Location	A&E	ITU	Labour Ward	SCBU
Instrument Name				
Instrument Serial #	13127048	13127045	13127050	11115017
pH	N/S	N/S	N/S	N/S
[H <sup>+</sup> ]	Good	Good	Good	Good
pCO <sub>2</sub>	Good	Good	Good	Good
pO <sub>2</sub>	Good	Good	Acceptable	Acceptable
Sodium	Good	Good	Good	Acceptable
Potassium	Good	Good	Good	Good
Chloride	Good	Good	N/A	Good
Ionized Calcium	Good	Good	N/A	Poor
Glucose	Good	Good	Good	Good
Lactate	Good	Good	Good	Good
<b>Overall % poor PI</b>	0%	0%	0%	7%
<b>Overall % Non-return</b>	0%	0%	0%	0%

PI Code	Meaning
N/A	Not enrolled for this analyte
NRR	Analyte enrolled but no results returned
N/S	This quantitative analyte not scored for this distribution

**\*\*\*\* Please note\*\*\*\*\***

The NQAAP expects 100% compliance on EQA returns. If you are enrolled for an analyte and have not returned a result (denoted by NRR in your PI table), this will be treated as a poor performance score. Please let us know as soon as possible if you are no longer providing this analyte as part of your diagnostic service.

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**Distribution Specific Comment**  
 There is no specific comment for this distribution.

No participant comments have been submitted for any instruments for this distribution.

Participant Code

WeQas

Participant Code: WQ00000

#####  
#####  
#####  
#####  
#####  
#####

Distribution details and report status.

WeQas

Unit 6, Parc Ty Glas  
Llanishen  
Cardiff  
United Kingdom  
CF14 5DU  
Tel: 02920 314750  
Email: office@weqas.com  
Programme Organiser: Mrs Annette Thomas

Your % Poor PI (Performance Index) across all samples for all instruments, the Median All Participants % Poor PI and the 97.5<sup>th</sup> Centile % Poor PI.

This Distribution	
Your % Poor PI	2%
Median All Participant % Poor PI	0%
97.5 <sup>th</sup> Centile % Poor PI	12%

Programme: Blood Gas • Distribution Code: BG1025  
Distribution Start: 13-Oct-2025 • Distribution End: 29-Oct-2025 • Report Issued: 07-Nov-2025 • Report Status: Final  
Requested By: gareth@weqas.com



PI Ranges	
<1	Good
1-2	Acceptable
>2	Poor

The running table shows the current distribution PI scores, and the previous 5 distribution PI scores for all analytes, for your Participant Code, plus all-Participant Median performance.

The PI Scores table shows performance for all analytes and all instruments.

PI Scores				
Location	A&E	ITU	Labour Ward	SCBU
Instrument Name				
Instrument Serial #	13127048	13127045	13127050	11115017
pH	N/S	N/S	N/S	N/S
[H <sup>+</sup> ]	Good	Good	Good	Good
pCO <sub>2</sub>	Good	Good	Good	Good
pO <sub>2</sub>	Good	Good	Acceptable	Acceptable
Sodium	Good	Good	Good	Acceptable
Potassium	Good	Good	Good	Good
Chloride	Good	Good	N/A	Good
Ionized Calcium	Good	Good	N/A	Poor
Glucose	Good	Good	Good	Good
Lactate	Good	Good	Good	Good
Overall % poor PI	0%	0%	0%	7%
Overall % Non-return	0%	0%	0%	0%

PI Scores are converted into performance categories and colour coded.

Overall % Poor PI across all analytes for each instrument, and Overall % non return for each instrument.

PI Code	Meaning
N/A	Not enrolled for this analyte
NRR	Analyte enrolled but no results returned
N/S	This quantitative analyte not scored for this distribution

#### \*\*\*\*\* Please note\*\*\*\*\*

The NQAAP expects 100% compliance on EQA returns. If you are enrolled for an analyte and have not returned a result (denoted by NRR in your PI table), this will be treated as a poor performance score. Please let us know as soon as possible if you are no longer providing this analyte as part of your diagnostic service.

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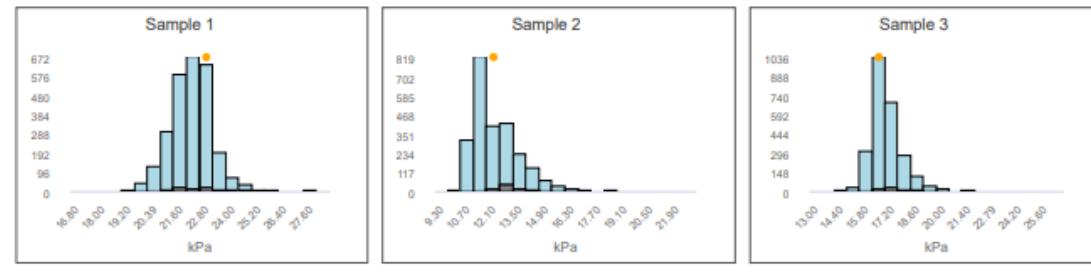
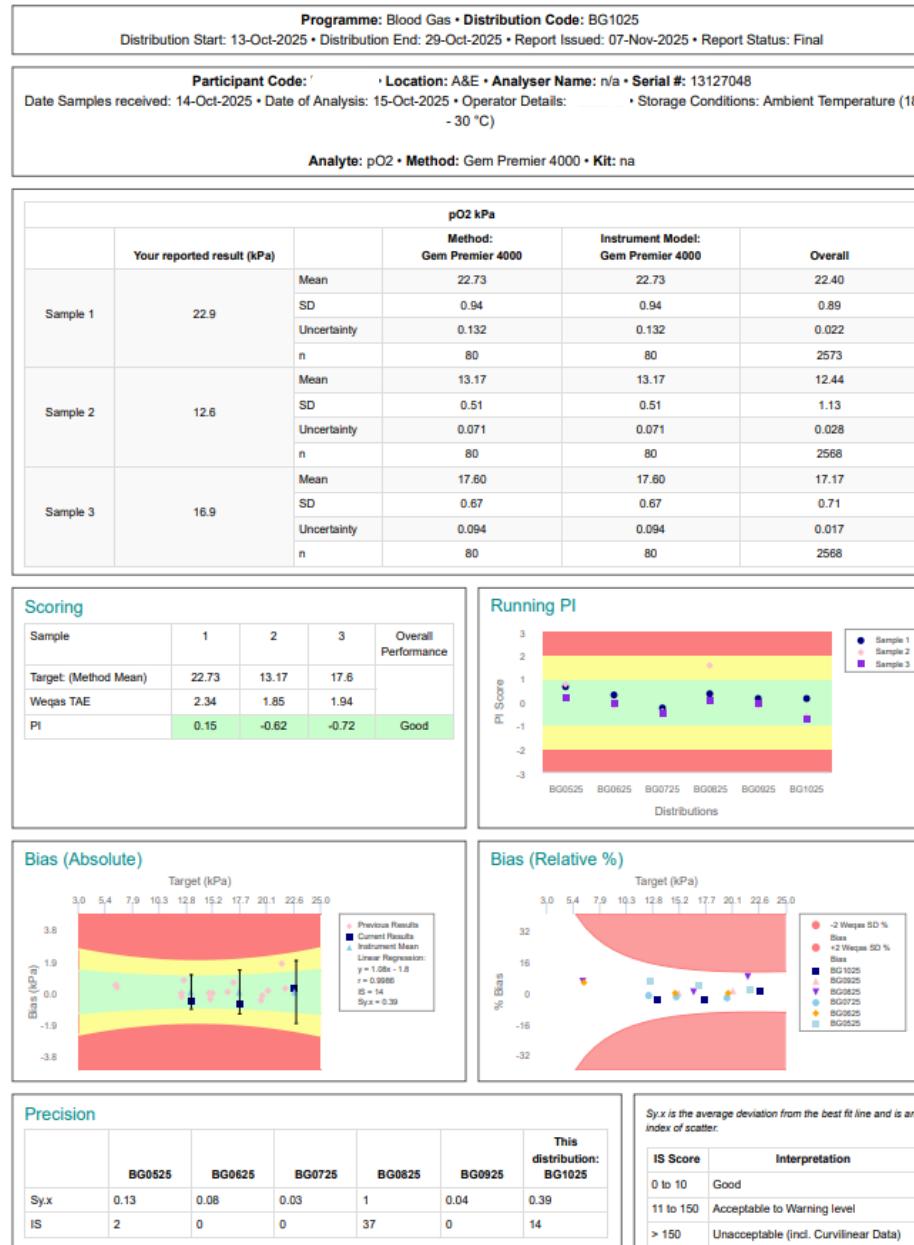
#### Distribution Specific Comment

There is no specific comment for this distribution.

Any WeQas comments or Participants comments are shown here

No participant comments have been submitted for any instruments for this distribution.

# Standard Quantitative Report – Analyte Page



**Method Summary**

BG1025		Sample 1		Sample 2		Sample 3	
Method Name	Mean	CV%	Mean	CV%	Mean	CV%	
ABL 800 Series (n=17)	22.74	2.6	13.56	1.6	17.81	2.3	
ABL 90 FLEX (n=1027)	22.81	2.6	11.54	2.8	17.02	2.8	
cobas b 123 (n=22)	22.48	4.2	11.89	3.8	16.72	3.8	
cobas b 221 (n=22)	22.83	2.6	15.44	1.6	18.35	1.7	
epoc (n=163)	23.02	4.4	13.65	9.2	18.23	5.5	
<b>Gem Premier 4000 (n=80)</b>	<b>22.73</b>	<b>4.1</b>	<b>13.17</b>	<b>3.9</b>	<b>17.60</b>	<b>3.8</b>	
Gem Premier 5000 (n=538)	21.68	3.4	12.18	5.0	16.82	3.6	
i-STAT (n=393)	22.11	4.5	14.25	6.0	17.95	5.0	
RAPIDLab 1200 System (n=6)	22.17	4.7	12.59	4.4	16.46	4.3	
Rapidpoint 500/500e (n=300)	22.06	3.2	12.90	2.6	16.89	2.4	

*There are no WeQas or Participant supplied comments for pO2 for this distribution.*

**Programme: Blood Gas • Distribution Code: BG1025**  
 Distribution Start: 13-Oct-2025 • Distribution End: 29-Oct-2025 • Report Issued: 07-Nov-2025 • Report Status: Final

**Participant Code:** • **Location:** A&E • **Analyser Name:** n/a • **Serial #:** 13127048  
 Date Samples received: 14-Oct-2025 • Date of Analysis: 15-Oct-2025 • Operator Details: • Storage Conditions: Ambient Temperature (18 - 30 °C)

**Analyte: pO2 • Method: Gem Premier 4000 • Kit: na**

**Your reported results for each sample**

**pO2 kPa**

			Method: Gem Premier 4000	Instrument Model: Gem Premier 4000	Overall
Sample 1	22.9	Mean	22.73	22.73	22.40
		SD	0.94	0.94	0.89
		Uncertainty	0.132	0.132	0.022
		n	80	80	2573
Sample 2	12.6	Mean	13.17	13.17	12.44
		SD	0.51	0.51	1.13
		Uncertainty	0.071	0.071	0.028
		n	80	80	2568
Sample 3	16.9	Mean	17.60	17.60	17.17
		SD	0.67	0.67	0.71
		Uncertainty	0.094	0.094	0.017
		n	80	80	2568

Method Mean,  
SD, uncertainty  
and n

Instrument  
Mean, SD,  
uncertainty  
and n

Overall Mean, SD,  
uncertainty and n

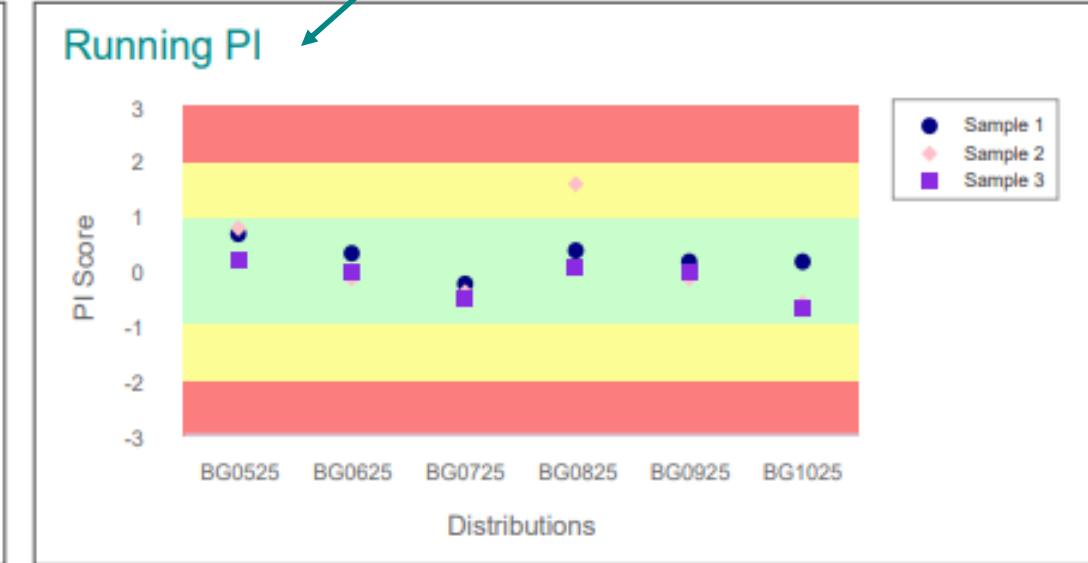
Target Value: This will show whether you have been scored against Reference value, method mean or overall mean

Overall Performance Category is assigned using an algorithm based on the individual sample PIs

Running PI chart shows the PI score for each sample for the current distribution and the last 5 distributions, with colour coding for each performance category

**Scoring**

Sample	1	2	3	Overall Performance
Target: (Method Mean)	22.73	13.17	17.6	
WeQas TAE	2.34	1.85	1.94	
PI	0.15	-0.62	-0.72	Good



WeQas Total Allowable Error (TAE) ( $2 * \text{WeQas SD}$ )

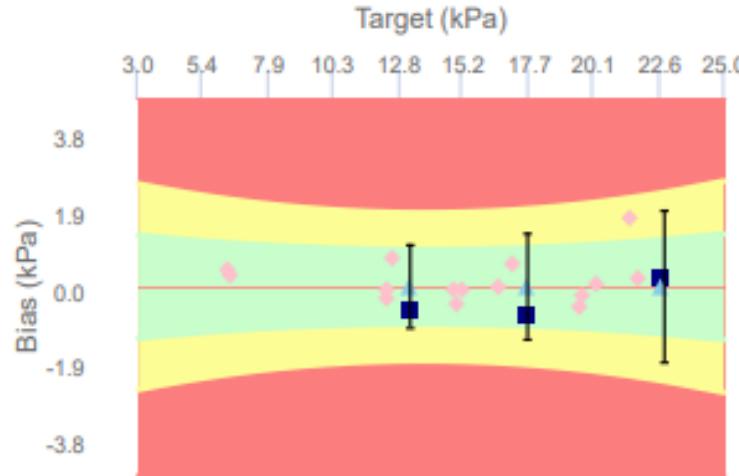
PI (Performance Index) score is shown for each sample

$$\text{PI} = \frac{(\text{Reported Result} - \text{Target Value})}{(\text{WeQas TAE} / 2)}$$

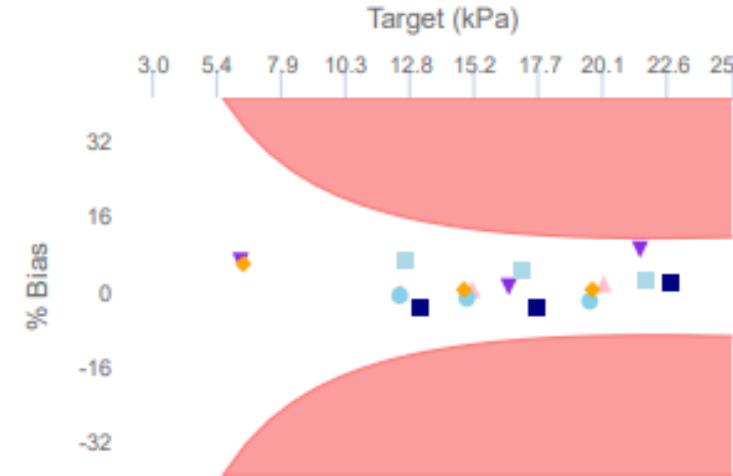
The bias (Absolute) plot shows absolute bias in WeQas standard units for each sample for the current distribution and 5 previous distributions

The bias (Relative) plot shows the relative (%) bias to the target value for the current results and the 5 previous distributions

**Bias (Absolute)**



**Bias (Relative %)**



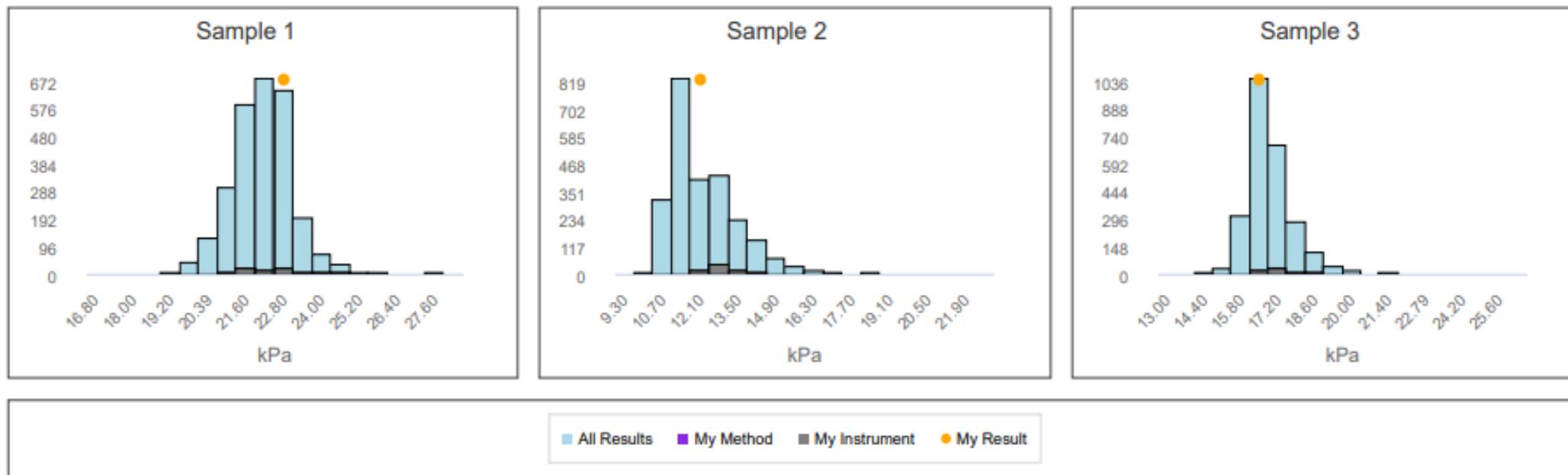
Linear regression analysis and indices of accuracy and precision are shown

### Precision

	BG0525	BG0625	BG0725	BG0825	BG0925	This distribution: BG1025
Sy.x	0.13	0.08	0.03	1	0.04	0.39
IS	2	0	0	37	0	14

*Sy.x is the average deviation from the best fit line and is an index of scatter.*

IS Score	Interpretation
0 to 10	Good
11 to 150	Acceptable to Warning level
> 150	Unacceptable (incl. Curvilinear Data)



## Method Summary

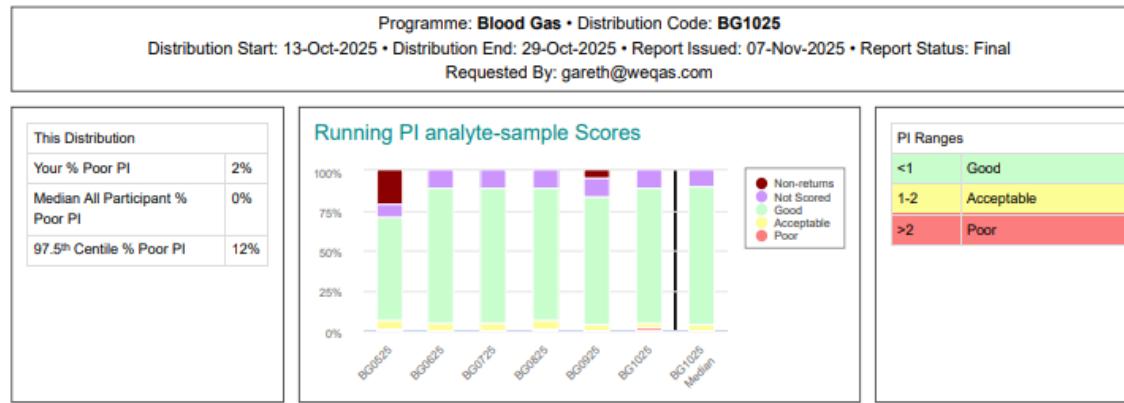
Method Name	BG1025		Sample 1		Sample 2		Sample 3	
	Mean	CV%	Mean	CV%	Mean	CV%	Mean	CV%
ABL 800 Series (n=17)	22.74	2.6	13.56	1.6	17.81	2.3		
ABL 90 FLEX (n=1027)	22.81	2.6	11.54	2.8	17.02	2.8		
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Gem Premier 5000 (n=538)	21.68	3.4	12.18	5.0	16.82	3.6		
i-STAT (n=393)	22.11	4.5	14.25	6.0	17.95	5.0		
RAPIDLab 1200 System (n=6)	22.17	4.7	12.59	4.4	16.46	4.3		
Rapidpoint 500/500e (n=300)	22.06	3.2	12.90	2.6	16.89	2.4		

*There are no WeQas or Participant supplied comments for pO2 for this distribution.*

# Overall Performance

Traffic light colour	Performance category	Description
Red	Non-Return	(Any number of samples in distribution) and (No results submitted for any samples)
	Poor	(Any number of sample in distribution) and (one or more $ PI  > 3$ )
		(number of samples in distribution = 1) and ( $2 <  PI  \leq 3$ )
		(number of samples in distribution > 1) and (2 or more $ PI  > 2$ ) ( <i>Westgard 2<sub>2s</sub></i> )
		(number of samples in distribution > 1) AND ( $\text{sign } x_i \neq \text{sign } x_j$ ) AND $ x_i  > 2$ AND $ x_j  > 2$ * for at least one pair of scores $x_i$ and $x_j$ where $x_n$ with $i \neq j$ are the individual sample-analyte scores for the instrument in question ( <i>Westgard R<sub>4s</sub></i> )
Orange	Warning	(number of samples in distribution > 1) and (single sample with $2 <  PI  \leq 3$ ) and (no sample with $ PI  > 3$ )
Yellow	Acceptable	(any number of samples in distribution) AND ( $1 < \text{Max }  PI  \leq 2$ )
Green	Good	$ PI  < 1$ for all samples Green is only assigned if all the individual samples are good.

# Simplified Report – Managers Summary



PI Scores				
Location	A&E	ITU	Labour Ward	SCBU
Instrument Name				
Instrument Serial #	13127048	13127045	13127050	11115017
pH	N/S	N/S	N/S	N/S
[H <sup>+</sup> ]	Good	Good	Good	Good
pCO <sub>2</sub>	Good	Good	Good	Good
pO <sub>2</sub>	Good	Good	Acceptable	Acceptable
Sodium	Good	Good	Good	Acceptable
Potassium	Good	Good	Good	Good
Chloride	Good	Good	N/A	Good
Ionized Calcium	Good	Good	N/A	Poor
Glucose	Good	Good	Good	Good
Lactate	Good	Good	Good	Good
<b>Overall % poor PI</b>	0%	0%	0%	7%
<b>Overall % Non-return</b>	0%	0%	0%	0%

PI Code	Meaning
N/A	Not enrolled for this analyte
NRR	Analyte enrolled but no results returned
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**\*\*\*\* Please note\*\*\*\*\***

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**Distribution Specific Comment**  
 There is no specific comment for this distribution.

No participant comments have been submitted for any instruments for this distribution.

Participant Code

WeQas

Participant Code: WQ00000

#####  
#####  
#####  
#####  
#####  
#####

Distribution details and report status.

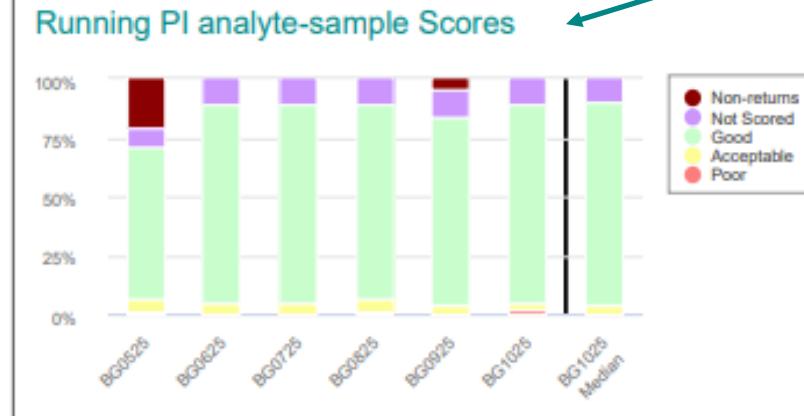
WeQas

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Tel: 02920 314750  
Email: office@weqas.com  
Programme Organiser: Mrs Annette Thomas

Your % Poor PI (Performance Index) across all samples for all instruments, the Median All Participants % Poor PI and the 97.5<sup>th</sup> Centile % Poor PI.

This Distribution	
Your % Poor PI	2%
Median All Participant % Poor PI	0%
97.5 <sup>th</sup> Centile % Poor PI	12%

Programme: Blood Gas • Distribution Code: BG1025  
Distribution Start: 13-Oct-2025 • Distribution End: 29-Oct-2025 • Report Issued: 07-Nov-2025 • Report Status: Final  
Requested By: gareth@weqas.com



PI Ranges	
<1	Good
1-2	Acceptable
>2	Poor

The running table shows the current distribution PI scores, and the previous 5 distribution PI scores for all analytes, for your Participant Code, plus all-Participant Median performance.

The PI Scores table shows performance for all analytes and all instruments.

PI Scores				
Location	A&E	ITU	Labour Ward	SCBU
Instrument Name				
Instrument Serial #	13127048	13127045	13127050	11115017
pH	N/S	N/S	N/S	N/S
[H <sup>+</sup> ]	Good	Good	Good	Good
pCO <sub>2</sub>	Good	Good	Good	Good
pO <sub>2</sub>	Good	Good	Acceptable	Acceptable
Sodium	Good	Good	Good	Acceptable
Potassium	Good	Good	Good	Good
Chloride	Good	Good	N/A	Good
Ionized Calcium	Good	Good	N/A	Poor
Glucose	Good	Good	Good	Good
Lactate	Good	Good	Good	Good
Overall % poor PI	0%	0%	0%	7%
Overall % Non-return	0%	0%	0%	0%

PI Scores are converted into performance categories and colour coded.

Overall % Poor PI across all analytes for each instrument, and Overall % non return for each instrument.

PI Code	Meaning
N/A	Not enrolled for this analyte
NRR	Analyte enrolled but no results returned
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#### \*\*\*\*\* Please note\*\*\*\*\*

The NQAAP expects 100% compliance on EQA returns. If you are enrolled for an analyte and have not returned a result (denoted by NRR in your PI table), this will be treated as a poor performance score. Please let us know as soon as possible if you are no longer providing this analyte as part of your diagnostic service.

WeQas are a UKAS ISO 17043 accredited EQA provider. Our accredited programmes are described on our UKAS schedule of accreditation which is available here: [WEQAS 17043 Schedule of Accreditation](#)

#### Distribution Specific Comment

There is no specific comment for this distribution.

Any WeQas comments or Participants comments are shown here

No participant comments have been submitted for any instruments for this distribution.

# Simplified Report – Analyte Page

Reports are very interactive.

You can hover over various parts of any of the graphical displays within the reports to focus in on the element you wish to see.

[Sign in - WeQas Connect](#)

Programme: Blood Gas • Distribution Code: BG1025  
 Distribution Start: 13-Oct-2025 • Distribution End: 29-Oct-2025 • Report Issued: 07-Nov-2025 • Report Status: Final

Participant Code: A&E • Location: A&E • Analyser Name: n/a • Serial #: 13127048  
 Date Samples received: 14-Oct-2025 • Date of Analysis: 15-Oct-2025 • Operator Details: • Storage Conditions: Ambient Temperature (18 - 30 °C)

Analyte: [H+] • Method: Gem Premier 4000 • Kit: na

[H+] (nmol/L)			
	Sample 1	Sample 2	Sample 3
Your reported result (nmol/L)	20.42	56.23	34.67
Your results are scored against: (Method Mean)	19.15	56.06	33.85

Good
Acceptable
Poor – discuss with POCT Coordinator

**Running Performance**

**Bias (Absolute)**

Your overall performance for this analyte is: **Good**

- There are no current performance alerts for this analyte

There are no WeQas or Participant supplied comments for [H+] for this distribution.

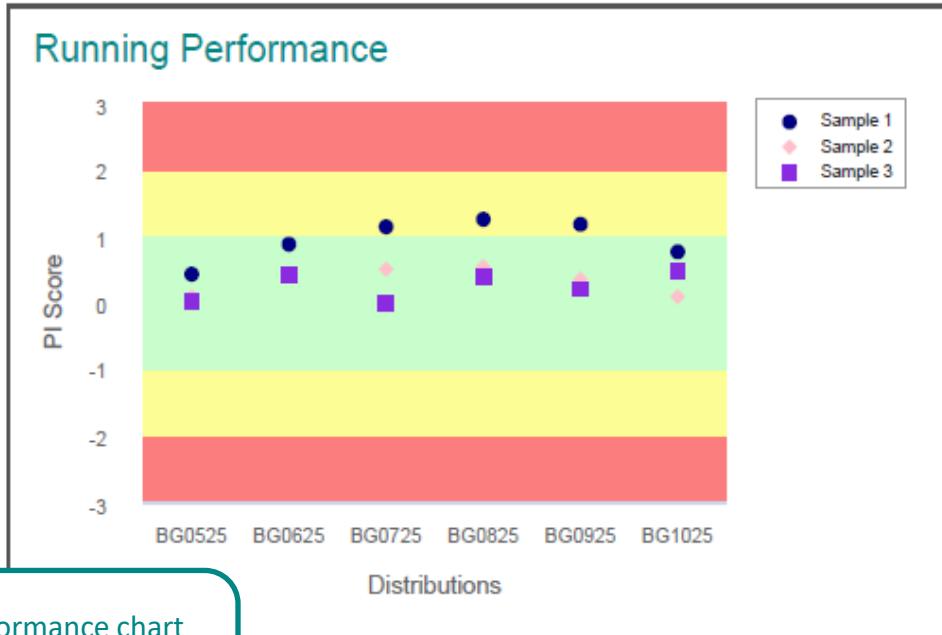
# Simplified Reports

‘Your reported result’ will be shown in the units entered, in the WeQas standard units (if units entered are different from the WeQas standard units), and method corrected result (if appropriate for the analyte).

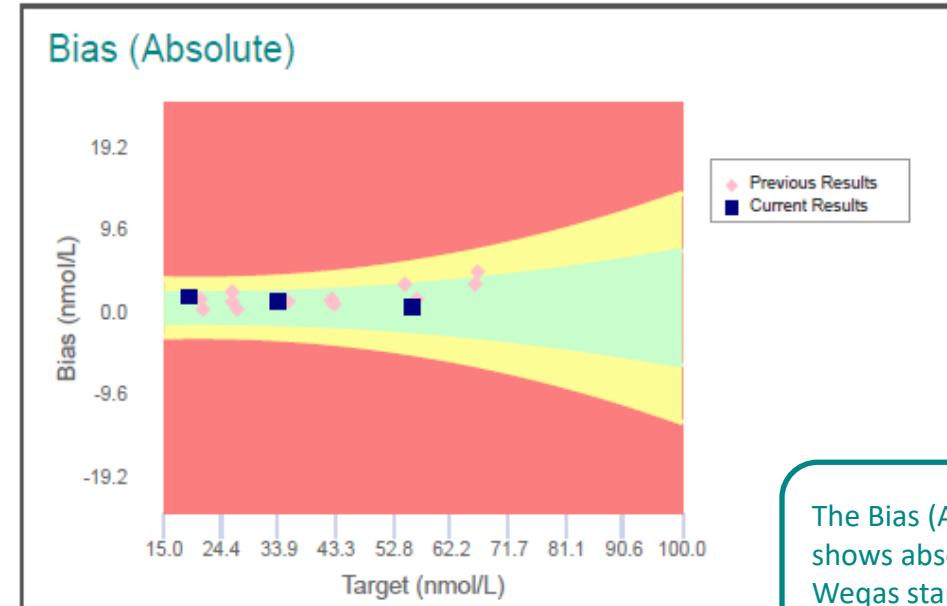
This will show whether you have been scored against Reference Value, Method Mean or Overall Mean and the actual target value will be shown here.

<b>Programme:</b> Blood Gas • <b>Distribution Code:</b> BG1025 <b>Distribution Start:</b> 13-Oct-2025 • <b>Distribution End:</b> 29-Oct-2025 • <b>Report Issued:</b> 07-Nov-2025 • <b>Report Status:</b> Final																					
<b>Participant Code:</b> . . . . . • <b>Location:</b> A&E • <b>Analyser Name:</b> n/a • <b>Serial #:</b> 13127048			<b>Date Samples received:</b> 14-Oct-2025 • <b>Date of Analysis:</b> 15-Oct-2025 • <b>Operator Details:</b> . . . . . • <b>Storage Conditions:</b> Ambient Temperature (18 - 30 °C)																		
<b>Analyte:</b> [H+] • <b>Method:</b> Gem Premier 4000 • <b>Kit:</b> na																					
<table border="1"><thead><tr><th colspan="4">[H+] (nmol/L)</th></tr><tr><th></th><th>Sample 1</th><th>Sample 2</th><th>Sample 3</th></tr></thead><tbody><tr><td>Your reported result (nmol/L)</td><td>20.42</td><td>56.23</td><td>34.67</td></tr><tr><td>Your results are scored against: (Method Mean)</td><td>19.15</td><td>56.06</td><td>33.85</td></tr></tbody></table>						[H+] (nmol/L)					Sample 1	Sample 2	Sample 3	Your reported result (nmol/L)	20.42	56.23	34.67	Your results are scored against: (Method Mean)	19.15	56.06	33.85
[H+] (nmol/L)																					
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Your reported result (nmol/L)	20.42	56.23	34.67																		
Your results are scored against: (Method Mean)	19.15	56.06	33.85																		
<table border="1"><tr><td>Good</td></tr><tr><td>Acceptable</td></tr><tr><td>Poor – discuss with POCT Coordinator</td></tr></table>						Good	Acceptable	Poor – discuss with POCT Coordinator													
Good																					
Acceptable																					
Poor – discuss with POCT Coordinator																					

# Simplified Reports



Running Performance chart shows the PI (Performance Index) score for each sample for the current distribution and the last 5 distributions, with colour coding for each performance category.



The Bias (Absolute) Plot shows absolute bias in WeQas standard units for each sample for the current distribution. The x-axis is the target value; if the target value is a Reference Value or the Overall Mean, your Method Means will be plotted.

# Simplified Reports

Overall Performance is shown as a 'Traffic light', with performance colour coded to easily identify the performance category.



Your overall performance for this analyte is: Good

- There are no current performance alerts for this analyte

Overall Performance is stated here along with a basic interpretation of your performance and potential error identified.

*There are no WeQas or Participant supplied comments for [H+] for this distribution.*

Analyte Specific Comments from WeQas or participant.

# Performance Comments

Your results for this distribution are acceptable

You have at least one sample in this distribution with a poor score:  $|score| > 2$

You have at least two samples in this distribution with a poor score:  $|score| > 2$

Your results show a consistent bias.

Please discuss your results with your EQA officer / POCT Co-ordinator

There are no current performance alerts for this analyte

Non-compliance: you have not reported results for this analyte

You have at least one sample in this distribution with a very poor score:  $|score| > 3$

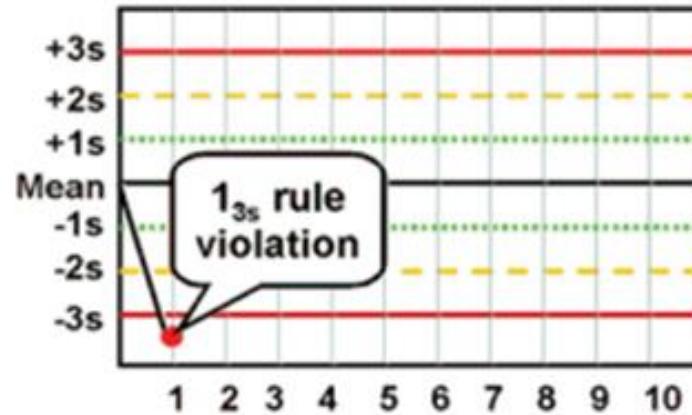
Your results suggest a potential bias

You have poor performance for this distribution due to a mixed positive and negative bias

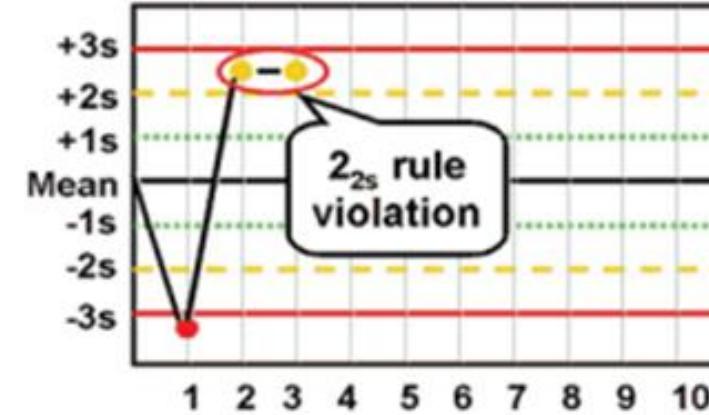
Scoring is currently unavailable for your reported results

You have a poor score for this distribution:  $|score| > 2$

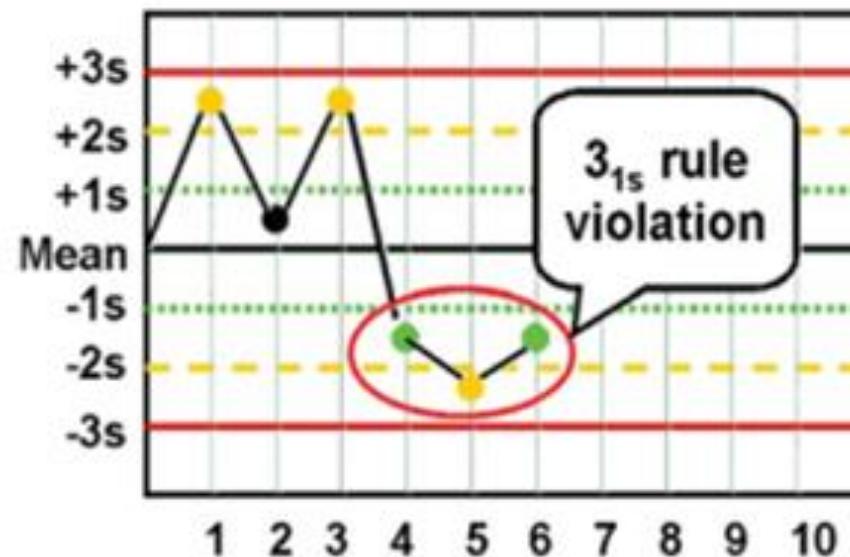
# Examples of rules used for the Performance Alert

**Comment:**

You have at least one sample in this distribution with a very poor score:  $|score| > 3$

**Comment:**

You have at least two samples in this distribution with a poor score:  $|score| > 2$



The rule is used when the distribution has a set of 3 or more samples.

If the PI (Performance Index) for all samples is  $>1$   
OR PI for all samples  $< -1$

The rule does not show whether the bias is positive or negative, but indicates that there is a bias to be investigated.

This example shows a negative bias.

**Comment:**  
Your results show a consistent bias.

# POCT Co-ordinators Report

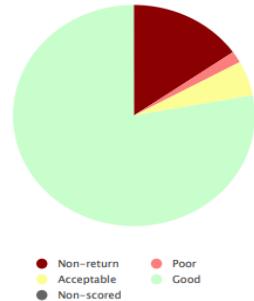
Reports are very interactive.

You can hover over various parts of any of the graphical displays within the reports to focus in on the element you wish to see.

[Sign in - WeQas Connect](#)

Participant Code: **POCT**  
Programme: **POCT Glucose and Ketones** • Distribution Code: **GK1025** • Analyte: **Glucose** • Units: **mmol/L**  
Distribution Start: 30-Sep-2025 • Distribution End: 21-Oct-2025 • Report Issued: 31-Oct-2025 • Report Status: Final

Overall

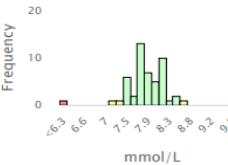


	Overall		Sample 1	
	n	%	n	%
Good	46	78	46	78
Acceptable	3	5.1	3	5.1
Poor	1	1.7	1	1.7
Non-Return	9	15.3	9	15.3
Non-scored	0	0	0	0
Total	59		59	

Hyperlinks on 'Poor' and 'Non Returns' to take you to further information.

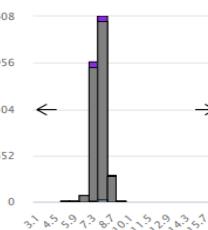
Sample 1 – My Results – Nova

StatStrip Connectivity



Method	Nova StatStrip Connectivity
Target Value Type	
Sample 1	
Target Value	8.05
My result(s)	Method
Mean	7.92
SD	0.41
Uncertainty	0.058
n	50
	5107

Sample 1



Method: Nova StatStrip Connectivity

Instrument: StatStrip Glucose/Ketone

Your results

WeQas supplied comment for Glucose:

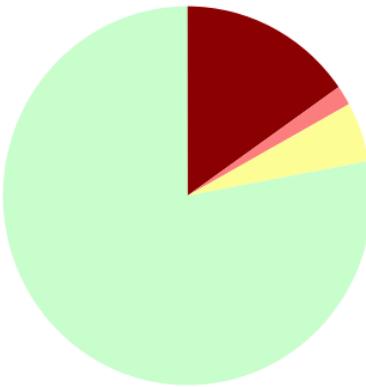
There is no comment for Glucose for this distribution

# POCT Co-ordinators Report

Participant Code,  
Distribution details and  
report status.

Participant Code:  
Programme: **POCT Glucose and Ketones** • Distribution Code: **GK1025** • Analyte: **Glucose** • Units: **mmol/L**  
Distribution Start: 30-Sep-2025 • Distribution End: 21-Oct-2025 • Report Issued: 31-Oct-2025 • Report Status: Final

Overall



Analyte specific  
breakdown of  
performance categories  
for all samples.

● Non-return      ● Poor  
● Acceptable      ● Good  
● Non-scored

	Overall		Sample 1	
	n	%	n	%
Good	46	78	46	78
Acceptable	3	5.1	3	5.1
Poor	1	1.7	1	1.7
Non-Return	9	15.3	9	15.3
Non-scored	0	0	0	0
Total	59		59	

Numerical analyte specific  
breakdown of performance  
categories for each sample  
and overall for your  
Participant, Group or Super  
Group dependent on access  
level and report chosen.

# Poor Performance report from Hyperlink

Participant Code:

Programme: **POCT Glucose and Ketones** • Distribution Code: **GK1025** • Analyte: **Glucose** • Units: **mmol/L**

Distribution Start: **30-Sep-2025** • Distribution End: **21-Oct-2025** • Report Issued: **31-Oct-2025** • Report Status: **Final**

Location	Serial #	Name	Sample 1 result	Sample 1 score	Overall performance
			6	-3.49	Poor

Request PDF of Simplified Analyte reports for all poor performing instruments for this analyte

[Request PDF](#)

PDF will be created only for the sites that have poor performance to allow full review of the individual reports.

## Non-Returns Report

Participant: **WQ00001**

Programme: **POCT INR** • Distribution Code: **IN0922** • Analyte: **INR**

Distribution start: **13-Sep-2022** • Distribution End: **11-Oct-2022** • Report Issued: **26-Oct-2022** • Report Status: **n/a**

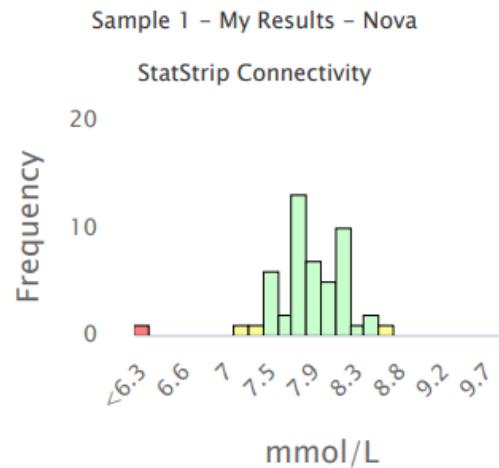
Participant Code	Location	Serial #	Name
WQ00001	POCT Lab		n/a
WQ00001	POCT Lab		n/a

# POCT Co-ordinators Report

Method specific data table showing:

- Target Value to which the submitted result is compared against and Target Value type e.g. Method Mean.
- Mean and SD of your submitted results for this method / instrument.
- Method data (all participants within this method) is also supplied in the right-hand column.

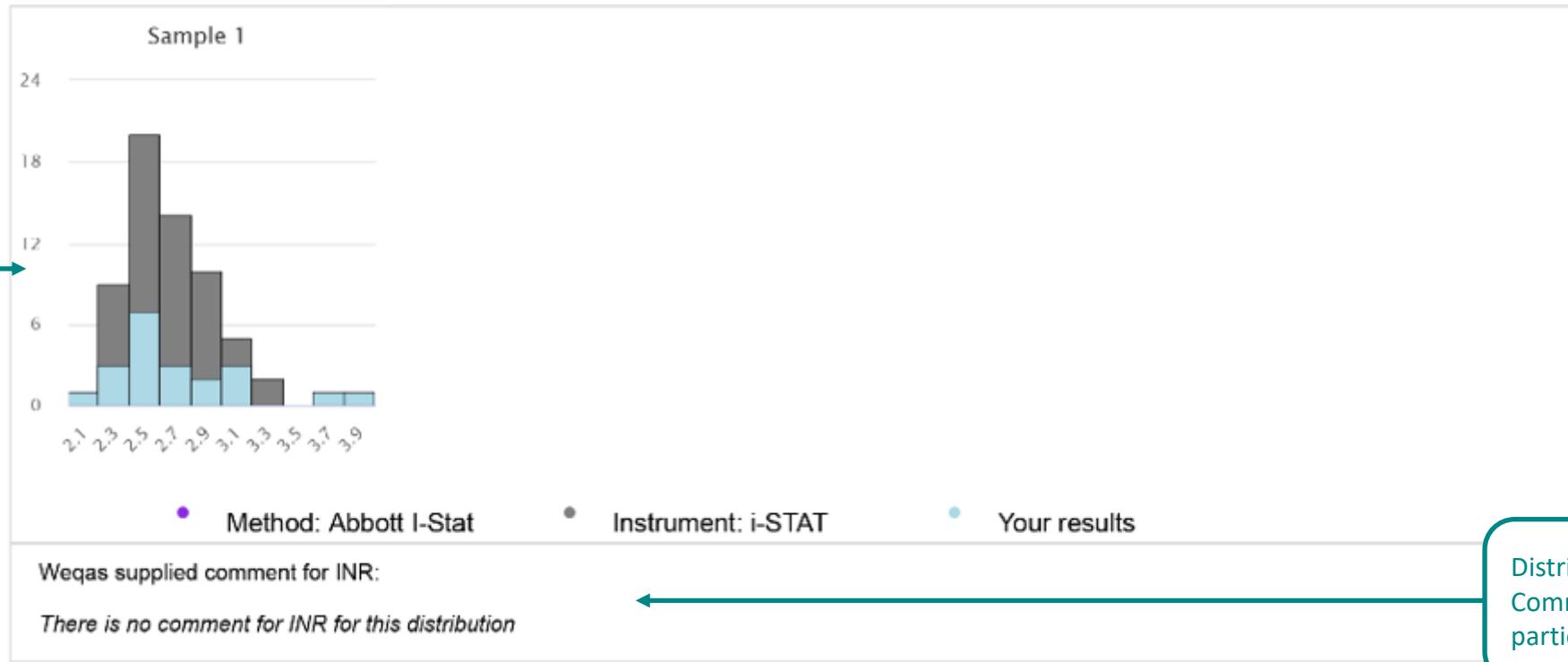
If you have more than one meter type, this data will be shown in a separate table.



Method	Nova StatStrip Connectivity	
Target Value Type	Method Mean	
	Sample 1	
Target Value	8.05	
	My result(s)	Method
Mean	7.92	8.05
SD	0.41	0.41
Uncertainty	0.058	0.007
n	50	5107

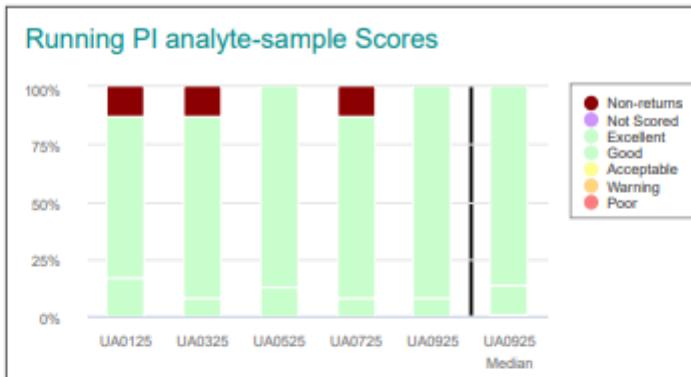
Histograms showing the spread of your results. Bars are colour coded to show performance categories across the range.

# POCT Co-ordinators Report



# POCT Urinalysis Report – Managers Summary

This Distribution	
Your % Poor PI	0%
Median All Participant % Poor PI	0%
97.5 <sup>th</sup> Centile % Poor PI	3%



PI Ranges	
0	Excellent
1	Good
2	Acceptable
3	Warning
4	Poor

PI Scores		
Location	POCT Lab	
Instrument Name	Clinitek	Urilyzer
Instrument Serial #	200124	6100072
Glucose	Excellent	Excellent
Ketones	Excellent	Excellent
Protein	Excellent	Excellent
Blood	Excellent	Excellent
Specific Gravity	Excellent	Good
pH	Good	Excellent
Bilirubin	Excellent	Excellent
Urobilinogen	Excellent	Excellent
Leucocytes	Excellent	Excellent
Nitrites	Excellent	Excellent
Albumin / Creatinine	Excellent	N/A
Urine Albumin (Microalbumin)	Excellent	N/A
Creatinine	Excellent	N/A
Ascorbic Acid	N/A	Excellent
Overall % poor PI	0%	0%
Overall % Non-return	0%	0%

# POCT Urinalysis – Instrument / Strip Report

\* indicates your selected response

Thick border indicates correct response(s)

Analyte	Kit	Responses						PI Score	Performance category	
Glucose	10SG - 03536597 (2300)	100% (2143) neg *	0% (5) Trace (5.5 mmol/L)	0% (2) 1+ (14 mmol/L)	0% (1) 2+ (28 mmol/L)	0% (0) 3+ (55 mmol/L)	0% (0) 4+ ( $\geq 111$ mmol/L)	0	Excellent	
Bilirubin	10SG - 03536597 (2300)	99% (601) neg *	0% (2) 1+	0% (3) 2+	0% (1) 3+			0	Excellent	
Ketones	10SG - 03536597 (2300)	17% (361) neg	61% (1313) Trace (0.5 mmol/L) *	21% (458) 1+ (1.5 mmol/L)	1% (16) 2+ (4 mmol/L)	0% (1) 3+ (8 mmol/L)	0% (2) 4+ ( $\geq 16$ mmol/L)	0	Excellent	
Specific Gravity	10SG - 03536597 (2300)	0% (2) 1	1% (22) 1.005	29% (526) 1.01	59% (1075) 1.015	9% (170) 1.02	1% (18) 1.025	0% (6) 1.03	0	Excellent

# Instrument Report – instrument / kit selection

WeQas

## Instrument Report

Distribution Code: **CR1023**

Distribution Date: **09-Oct-2023**

Analyte: **Creatinine (µmol/L)**

Method: **i-STAT**

Manufacturer: **Abbott**

Instrument Model: **i-STAT**

Kit: **Abbott 03P84-25 i-STAT CREA**

### Creatinine

Key

red	Outside Expected Range
*	Method Transformed

Participant Code	1	2	3
WQ00074	380	1064	691
WQ00074	361	1118	673
WQ00074	362	1147	680
WQ00074	369	1068	682
WQ00074	378	1085	695
WQ00074	375	1054	689
WQ00074	354	1063	658
WQ00241	382	1114	674
WQ00291	346 *	1011 *	654
WQ00291	377	1138	663
WQ00295	344 *	1032 *	640
WQ00295	343 *	1050	627 *

Overall	1	2	3
Mean	243.7	702.8	432.3

SD	44.4	101.3	63.3
Uncertainty	4.32	9.86	6.19
Number	165	165	163
Reference Value			
Nonscoring Reference Value			

Method	Instrument	Kit	1	2	3
i-STAT		Mean	367.4	1096.4	672.1
		SD	12.2	40.2	23.2
		Uncertainty	1.64	5.38	3.15
		Number	87	87	85
Abbott i-STAT		Mean	368	1090.2	669.3
		SD	12.7	50.2	25.5
		Uncertainty	2.86	11.47	5.81
		Number	31	30	30
Abbott i-STAT CREA 03P84-25		Mean	368	1090.2	669.3
		SD	12.7	50.2	25.5
		Uncertainty	2.86	11.47	5.81
		Number	31	30	30

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Email: contact@weqas.com

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EXTERNAL  
QUALITY  
ASSESSMENT



INTERNAL  
QUALITY  
CONTROL



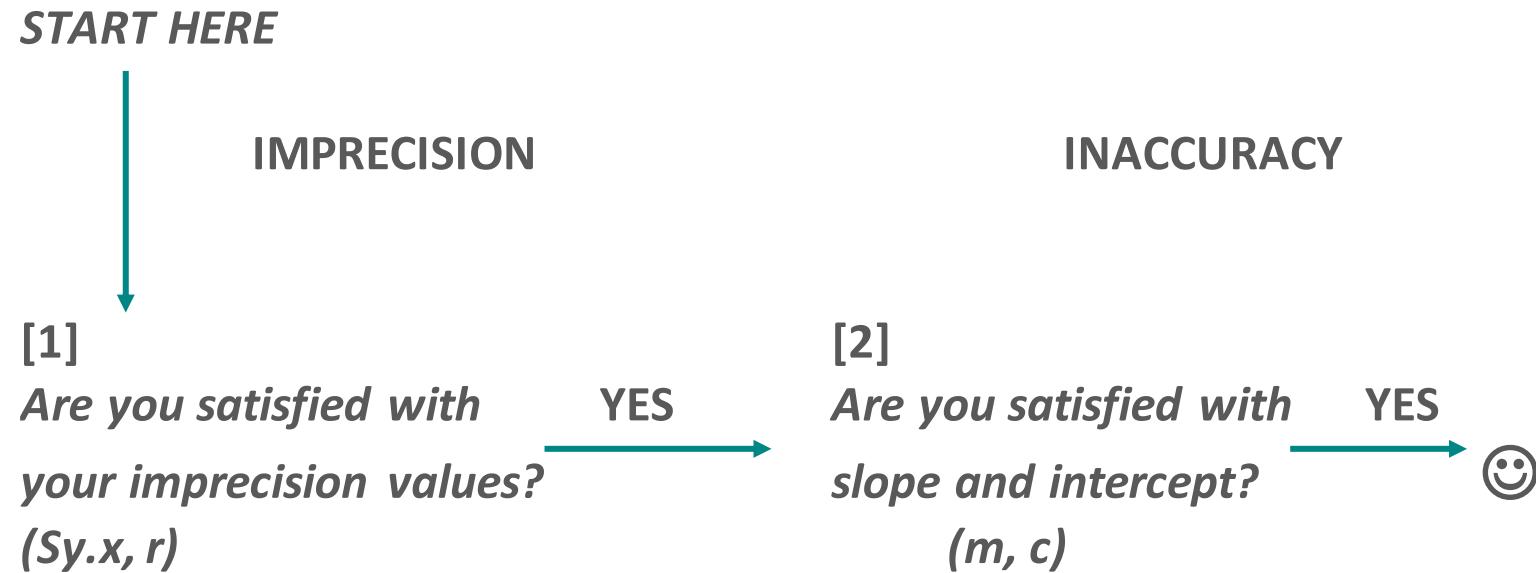
REFERENCE  
MEASUREMENT  
SERVICES

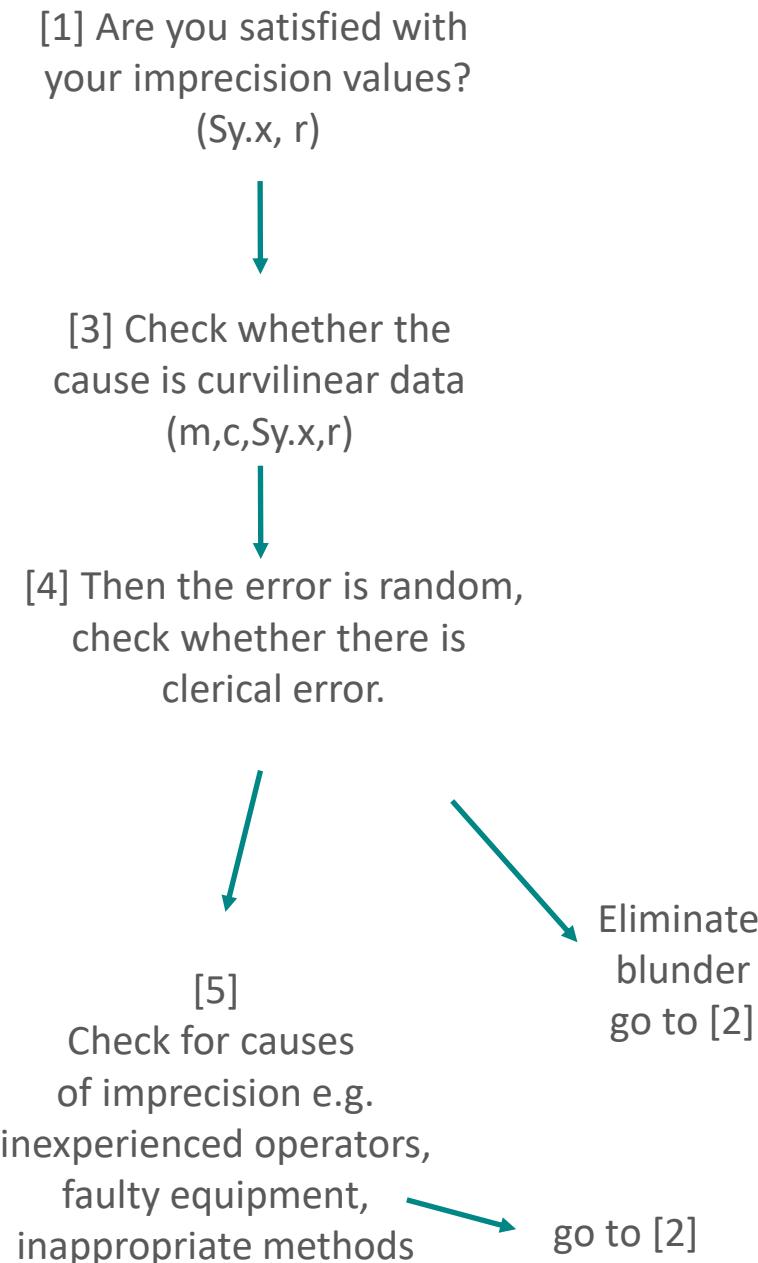


EDUCATION &  
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## Problem Solving and Cases

# Problem Solving Flow Chart

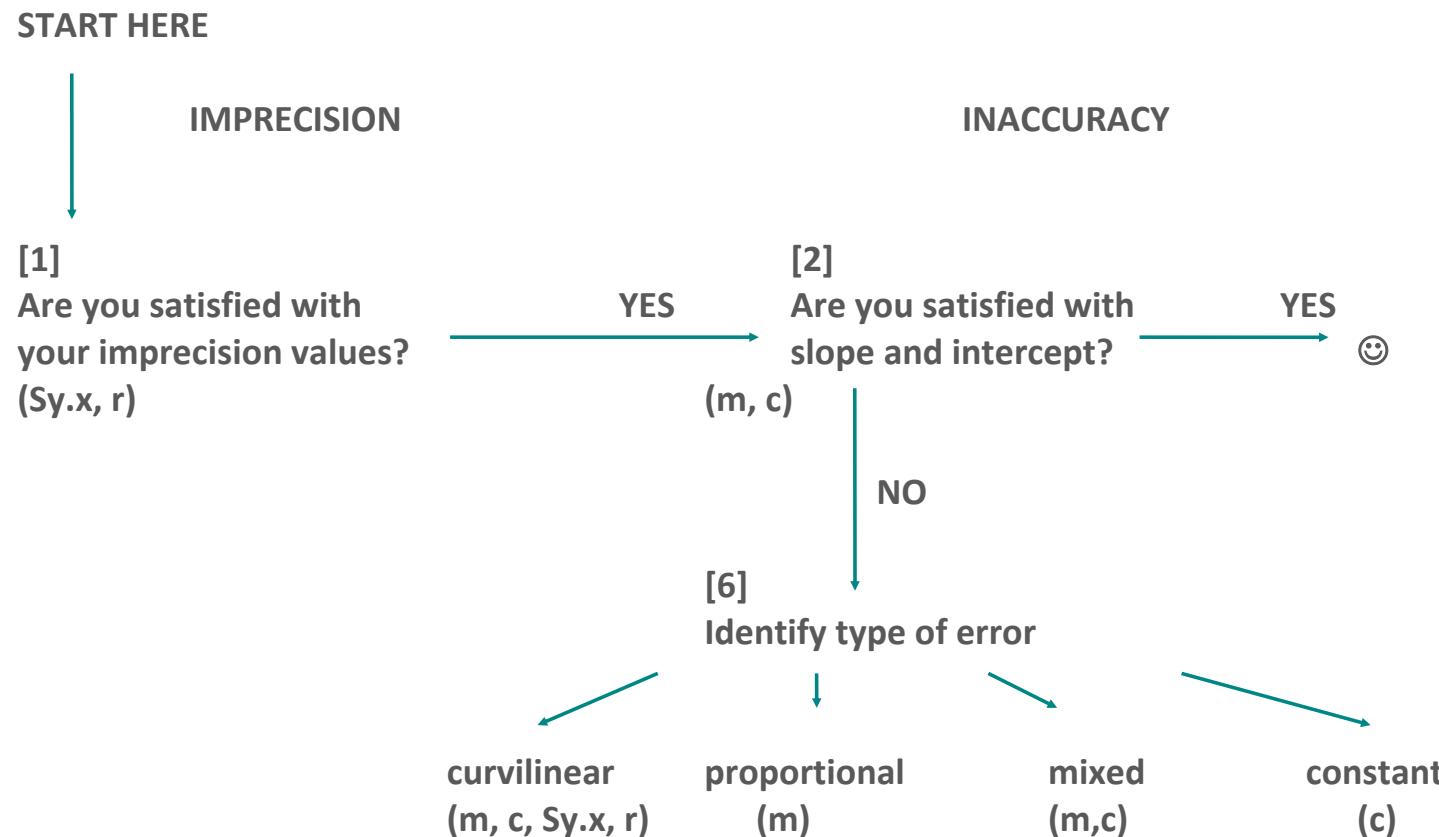




## Problem Solving Flow Chart

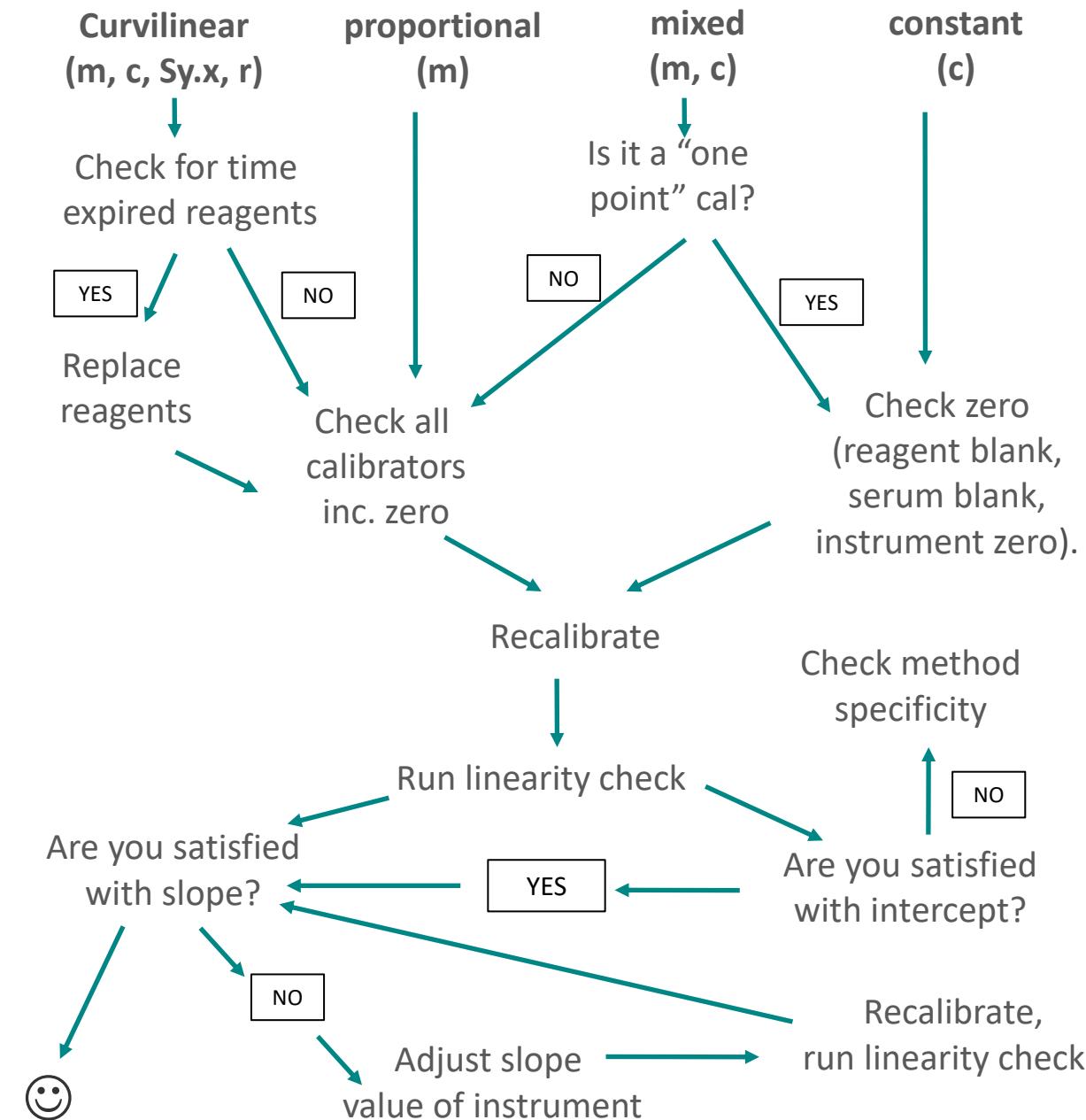
### IMPRECISION

# Problem Solving Flow Chart



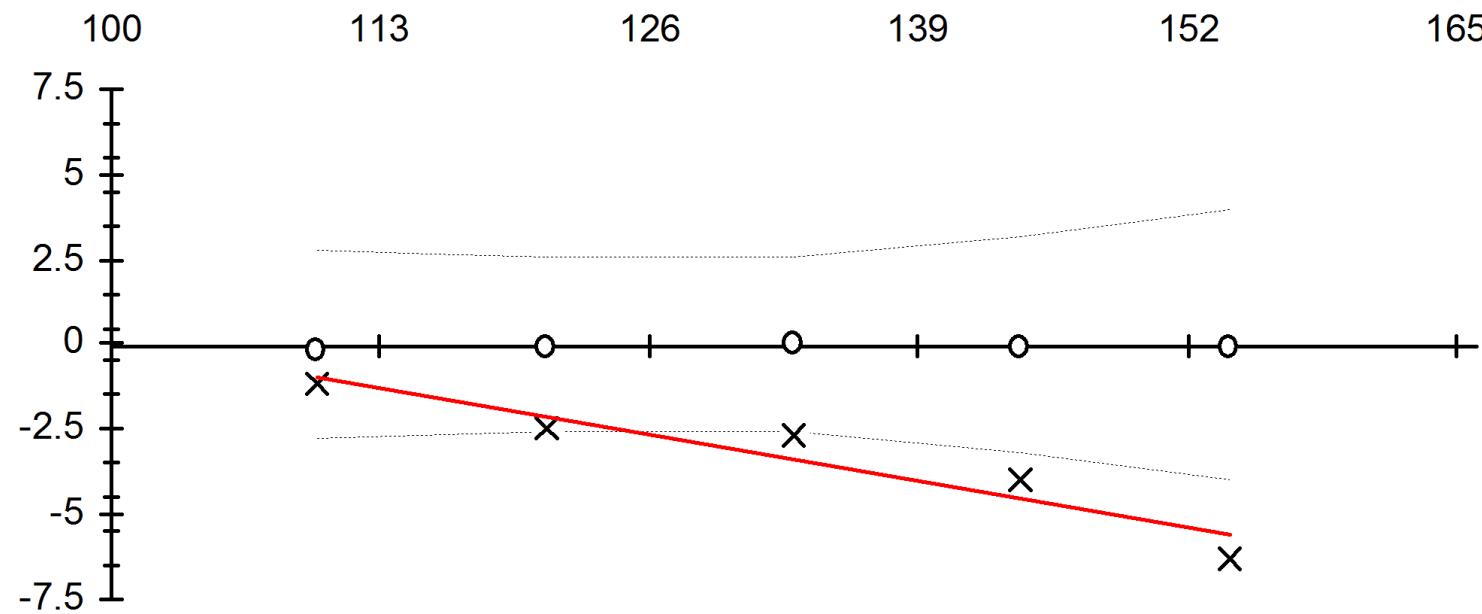
# Problem Solving Flow Chart

## INACCURACY



# Bias plot (1)

Sodium (mmol/l)



$$y = 0.9x + 9.6$$

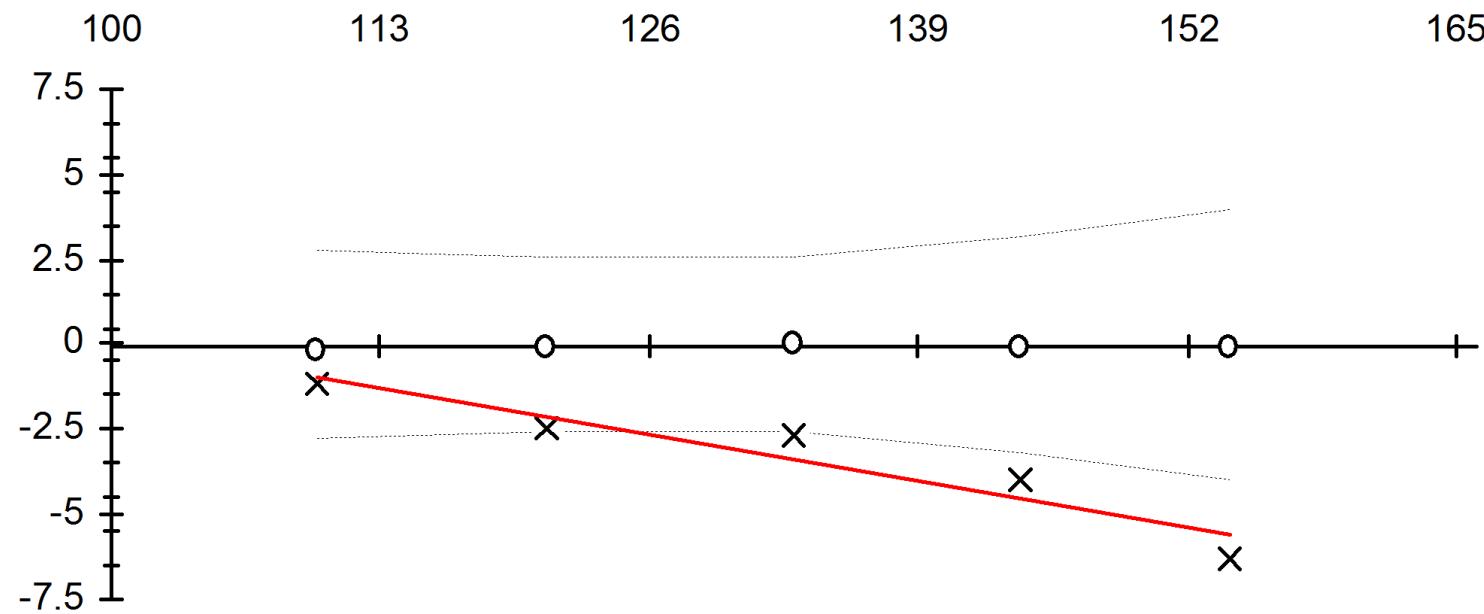
$$r = 0.9995$$

$$IS = 5$$

$$Sy.x = 0.63$$

# Bias plot (1)

Sodium (mmol/l)

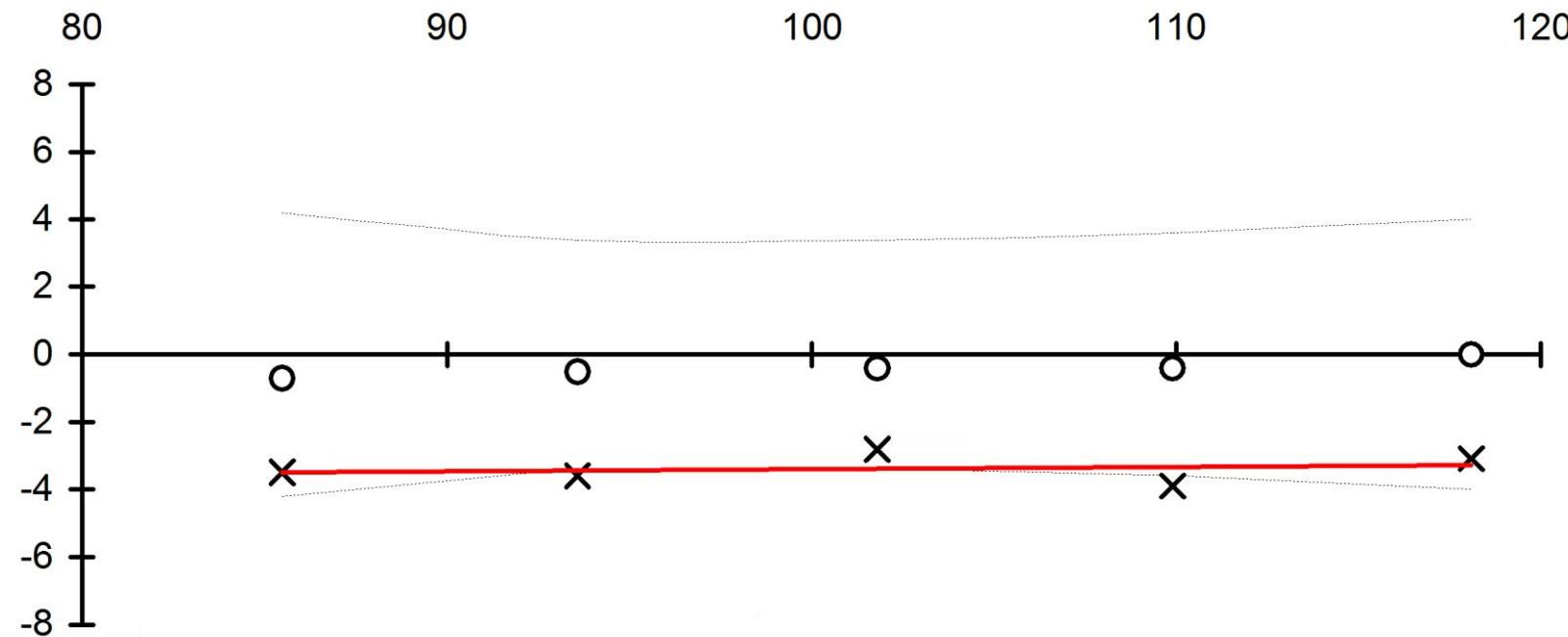


$y = 0.9x + 9.6$   
 $r = 0.9995$   
IS = 5  
 $S_{y,x} = 0.63$

Imprecision – satisfactory  
Inaccuracy – identify error  
 $m = 0.9, c = +9.6 \text{ mmol/L}$  – OK at 100 mmol/L  
2.5% negative bias at 130 mmol/L, 4% negative bias at 160 mmol/L  
Error – mixed. Two points calibration at 110 and 160 mmol/L  
**Cause – incorrect values for 160 mmol/L calibration**

# Bias plot (2)

Chloride (mmol/l)



$$y = 1.01x - 4.01$$

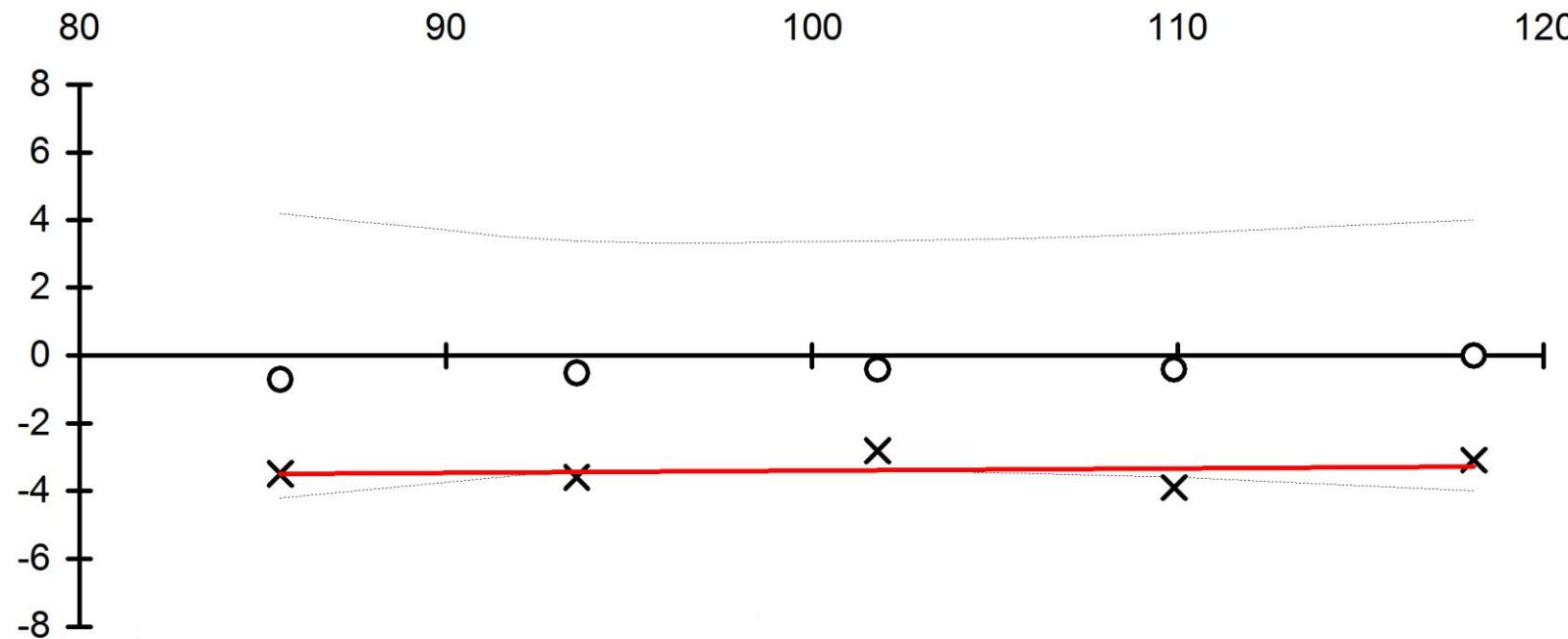
$$r = 0.9995$$

$$IS = 5$$

$$Sy.x = 0.49$$

# Bias plot (2)

Chloride (mmol/l)

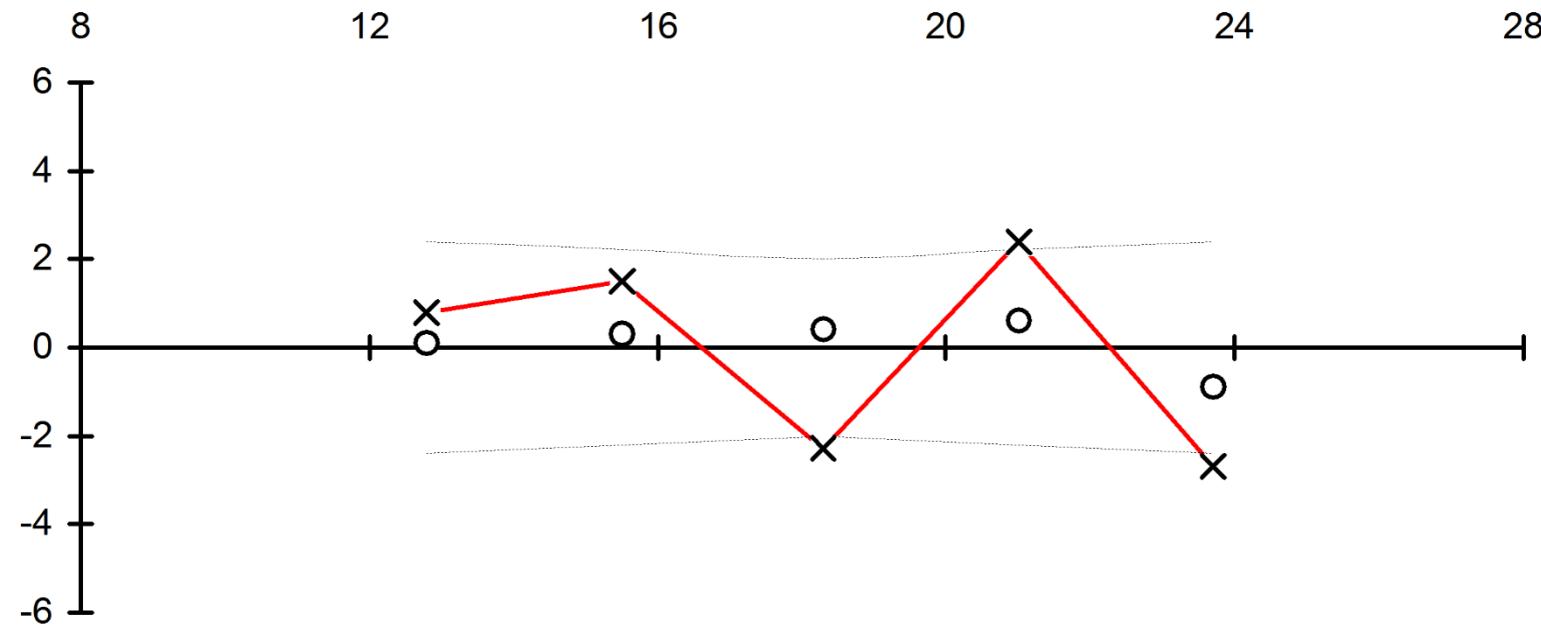


$y = 1.01x - 4.01$   
 $r = 0.9995$   
 $IS = 5$   
 $S_{y,x} = 0.49$

Imprecision – satisfactory  
Inaccuracy – identify error  
 $c = -4.0 \text{ mmol/L}$   
Error – systematic absolute. Results low by 4.0 mmol/L over whole range  
**Cause – incorrect serum blank compensation**

# Bias plot (3)

Bicarbonate (mmol/l)



y = slope not calculated

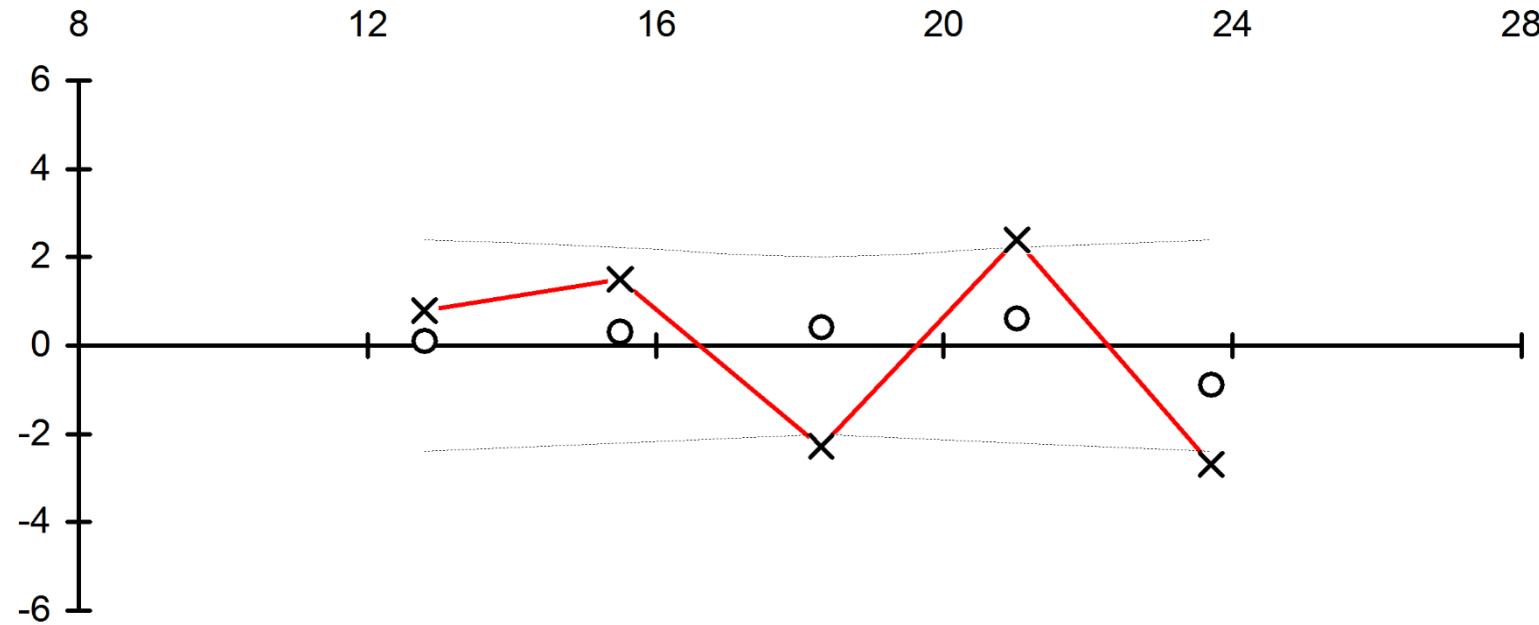
r = 0.8484

IS = 1516

Sy.x = 2.41

# Bias plot (3)

Bicarbonate (mmol/l)



y = slope not calculated

r = 0.8484

IS = 1516

Sy.x = 2.41

Imprecision – unsatisfactory,  $r = 0.8484$ ,  $Sy.x = 2.4$  mmol/L

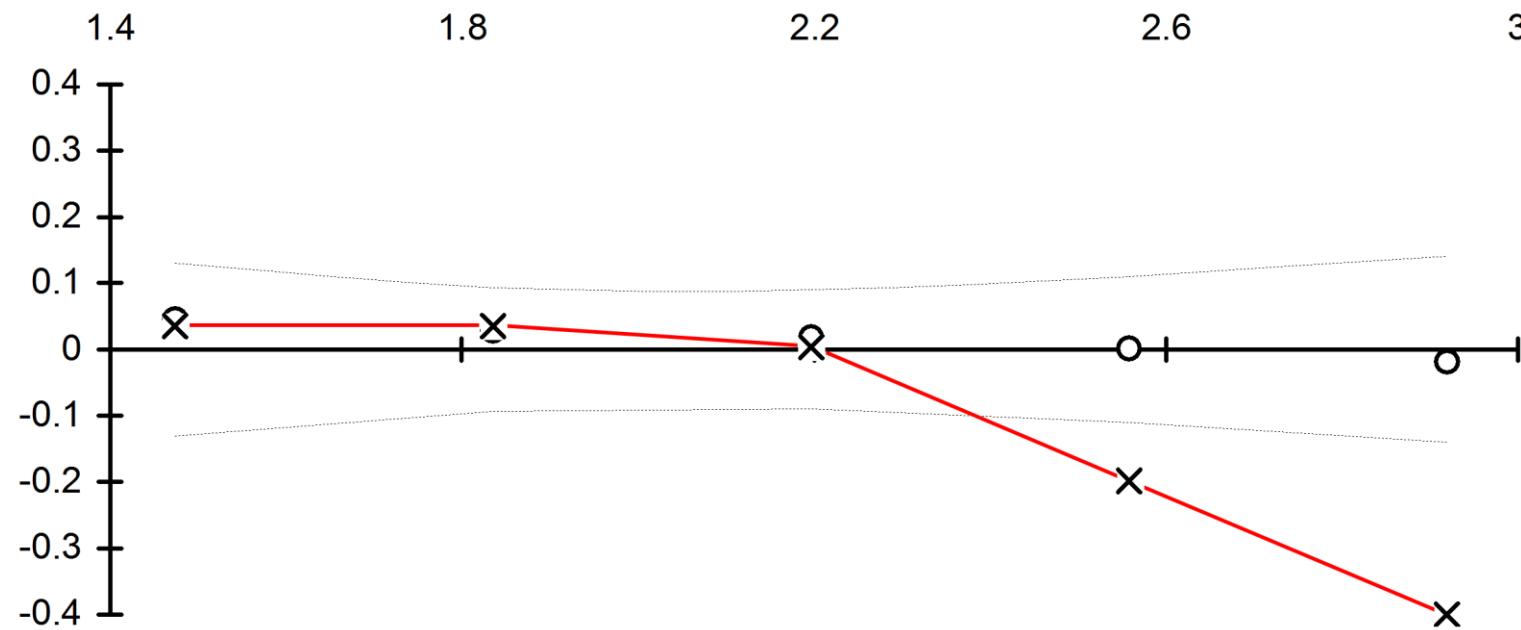
Not curvilinear

Error – random

**Cause – faulty syringe on instrument**

# Bias plot (4)

Calcium (mmol/l)



y = slope not calculated

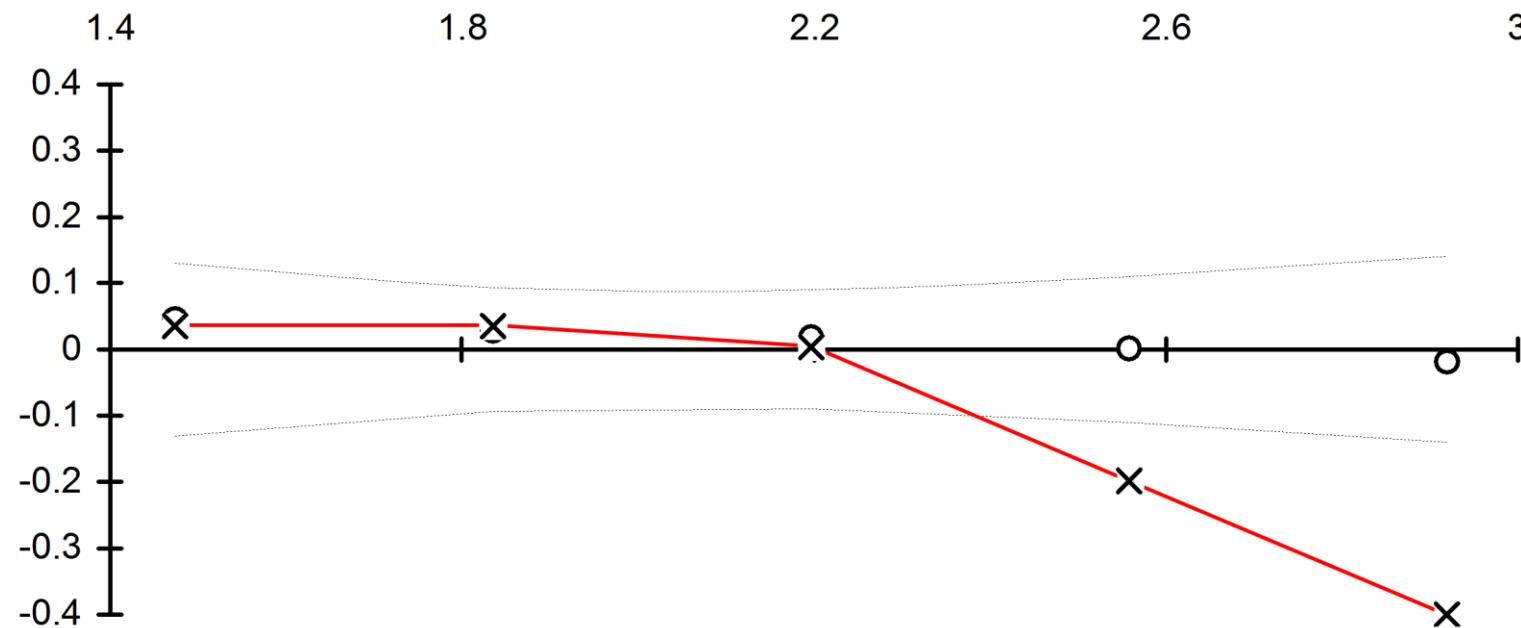
r = 0.9810

IS = 190

Sy.x = 0.09

# Bias plot (4)

Calcium (mmol/l)



y = slope not calculated

r = 0.9810

IS = 190

Sy.x = 0.09

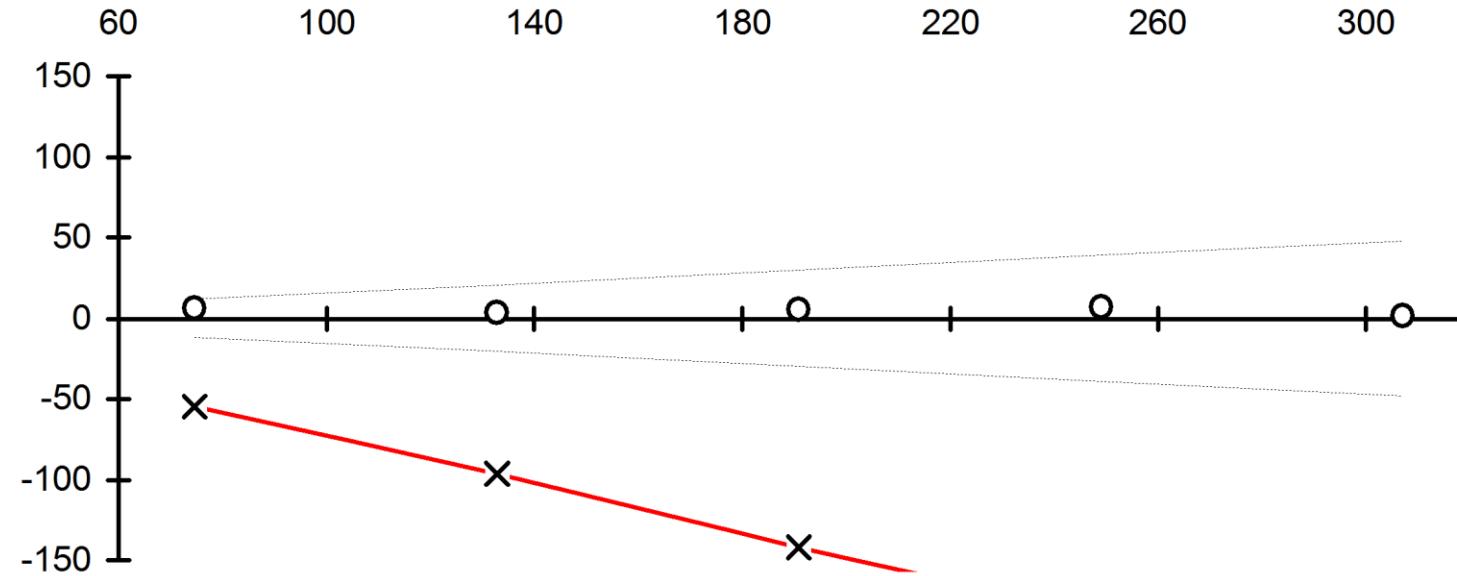
Imprecision – unsatisfactory, r = 0.9810, Sy.x = 0.09 mmol/L

Error – curvilinear data

Cause – time expired reagents

# Bias plot (5)

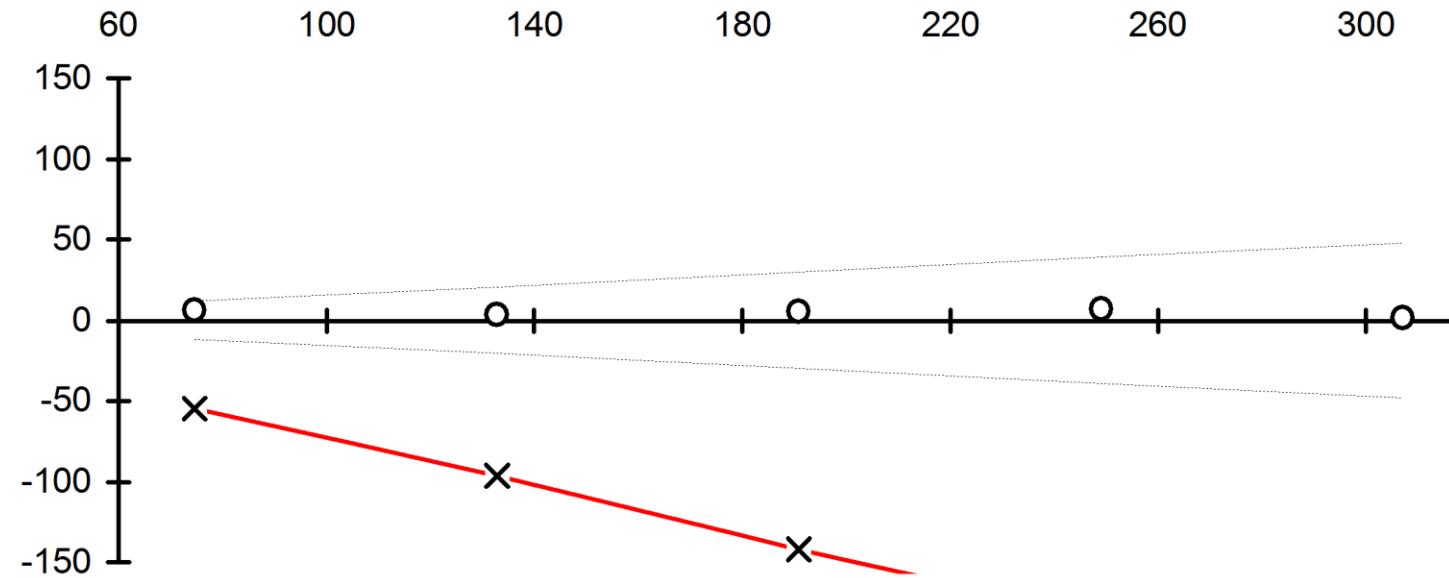
ALP (IU/L)



$y = 0.50x + 1.16$   
 $r = 0.9999$   
 $IS = 1$   
 $S_{y,x} = 1.30$

# Bias plot (5)

ALP (IU/L)



$y = 0.50x + 1.16$   
 $r = 0.9999$   
 $IS = 1$   
 $S_{y,x} = 1.30$

Imprecision – satisfactory  
Inaccuracy – identify error  
 $m = 0.57$   
Error – systematic proportional error. Results low by 41% over the whole range  
**Cause – incorrect method group classification. The lab was using AMP not DEA buffer**

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Unit 6, Parc Tŷ Glas  
Llanishen, Cardiff, CF14 5DU

Tel: 02920 314750  
Email: contact@weqas.com

# WeQas

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EXTERNAL  
QUALITY  
ASSESSMENT



INTERNAL  
QUALITY  
CONTROL



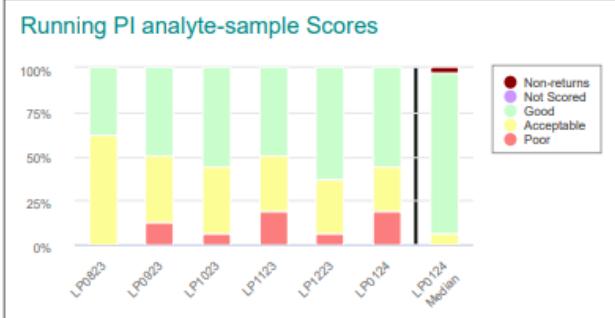
REFERENCE  
MEASUREMENT  
SERVICES



EDUCATION &  
TRAINING

## Case Study - example

This Distribution	
Your % Poor PI	19%
Median All Participant % Poor PI	0%
97.5 <sup>th</sup> Centile % Poor PI	51%



PI Ranges	
<1	Good
1-2	Acceptable
>2	Poor

PI Scores	
Location	The Path Lab
Instrument Name	Cobas C 311
Instrument Serial #	2039-05
Cholesterol	Acceptable
Triglyceride	Acceptable
HDL Cholesterol	Poor
LDL Cholesterol	Good
Overall % poor PI	19%
Overall % Non-return	0%

PI Code	Meaning
N/A	Not enrolled for this analyte
NRR	Analyte enrolled but no results returned
N/S	This quantitative analyte not scored for this distribution

\*\*\*\*\* Please note\*\*\*\*\*

The NQAAP expects 100% compliance on EQA returns. If you are enrolled for an analyte and have not returned a result (denoted by NRR in your PI table), this will be treated as a poor performance score. Please let us know as soon as possible if you are no longer providing this analyte as part of your diagnostic service.

Distribution Specific Comment	
There is no specific comment for this distribution.	

No participant comments have been submitted for any instruments for this distribution.
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Programme: Lipids • Distribution Code: LP0124

Distribution Start: 22-Jan-2024 • Distribution End: 05-Feb-2024 • Report Issued: • Report Status: n/a

Participant Code: WQ00942 • Location: The Path Lab • Analyser Name: Cobas C 311 • Serial #: 2039-05

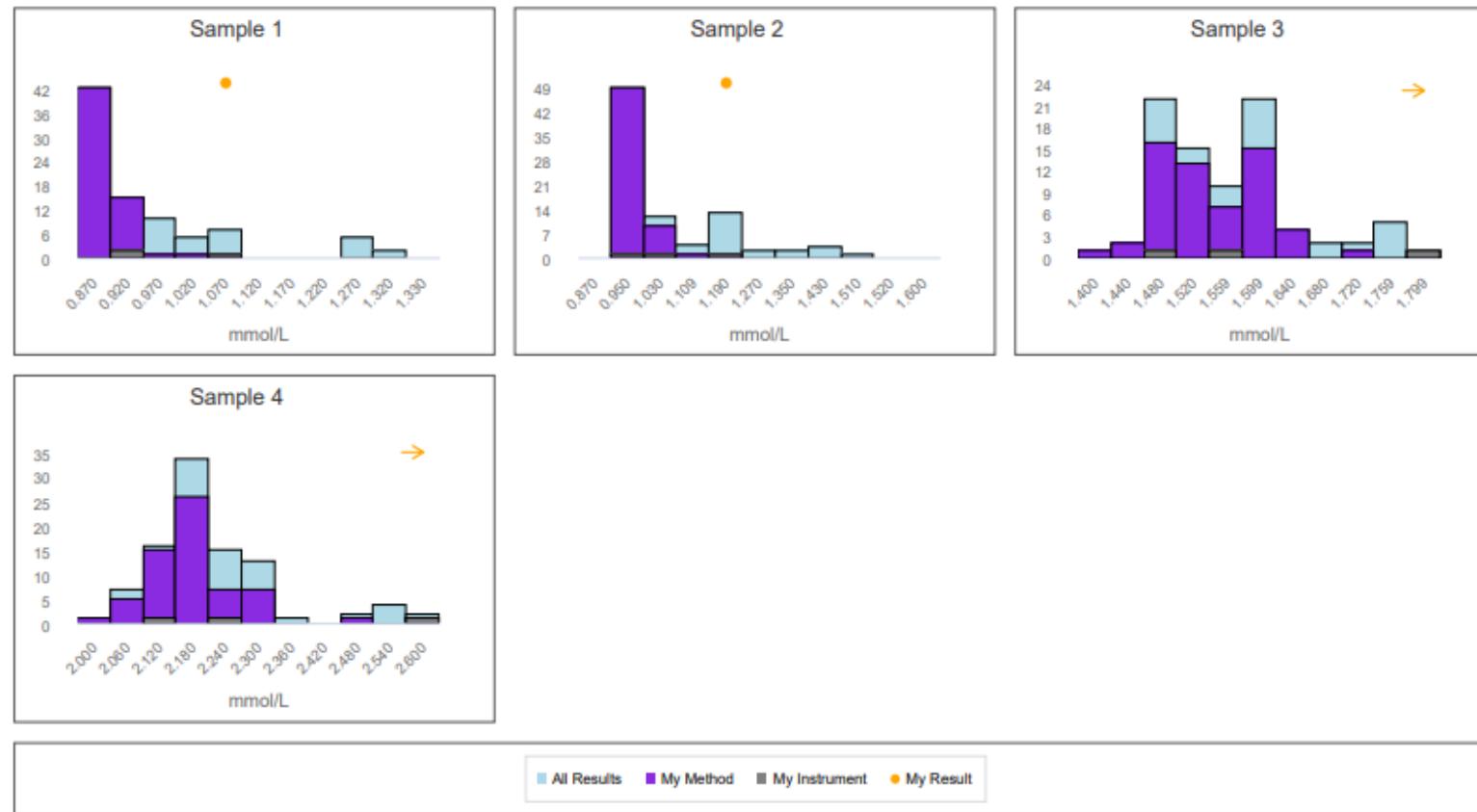
Date Samples received: 23-Jan-2024 • Date of Analysis: 23-Jan-2024 • Operator Details: YW • Storage Conditions: Ambient Temperature (18 - 30 °C)

Analyte: HDL Cholesterol • Method: Roche HDLC4 • Kit: HDLC4 (07528566 190)

## HDL Cholesterol mmol/L

	Your reported result (mmol/L)		Method: Roche HDLC4	Instrument Model: cobas c 311	Overall	Non-Scoring Reference Value
Sample 1	1.1	Mean	0.911	0.990	0.950	1
		SD	0.024	0.109	0.070	
		Uncertainty	0.0039	0.0789	0.0094	n/a
		n	60	3	86	
Sample 2	1.2	Mean	1.000	1.087	1.065	1.12
		SD	0.008	0.116	0.106	
		Uncertainty	0.0013	0.0840	0.0143	n/a
		n	60	3	86	
Sample 3	1.8	Mean	1.553	1.630	1.565	1.61
		SD	0.059	0.172	0.069	
		Uncertainty	0.0096	0.1238	0.0093	n/a
		n	60	3	86	
Sample 4	2.6	Mean	2.197	2.333	2.217	2.29
		SD	0.068	0.268	0.083	
		Uncertainty	0.0110	0.1934	0.0112	n/a
		n	60	3	86	





### Method Summary

LP0124	Sample 1		Sample 2		Sample 3		Sample 4	
Method Name	Mean	CV%	Mean	CV%	Mean	CV%	Mean	CV%
Elimination (n=8)	1.225	13.0	1.381	10.9	1.754	1.5	2.475	7.8
Enzymatic Immuno inhibition (n=14)	1.046	4.8	1.193	4.3	1.564	3.7	2.217	3.4
NMR Spectroscopy (n=1)	1.280	0.0	1.290	0.0	1.590	0.0	2.280	0.0
<b>Roche HDLC4 (n=60)</b>	<b>0.911</b>	<b>2.6</b>	<b>1.000</b>	<b>0.8</b>	<b>1.553</b>	<b>3.8</b>	<b>2.197</b>	<b>3.1</b>
Vitros (n=3)	1.033	6.3	1.200	0.0	1.633	4.0	2.333	2.8

There are no WeQas or Participant supplied comments for HDL Cholesterol for this distribution.

## Summary Report

Analyte: HDL

Overall Performance Category: Poor

Running PI analyte –sample scores: >50% good, some acceptable some poor. More poor and less good than median

## Standard Report

**Analyte results table:** your results higher than method mean, higher than instrument mean but n only 3. Non scoring ref value

**Scoring Table:** 3 samples poor PI, 1 sample acceptable but PI 1.99.

**Running PI scores:** LP0823 acceptable, since them got worse, mostly poor for LP0124

**Bias Chart (Absolute):** longstanding positive bias, this dist worse than previous, instrument mean close to method mean,  $y = 1.16*x + 0.03$ , 16% positive proportional bias. Instrument SDs wide but n = 3

**Bias Chart (Relative):** longstanding positive bias

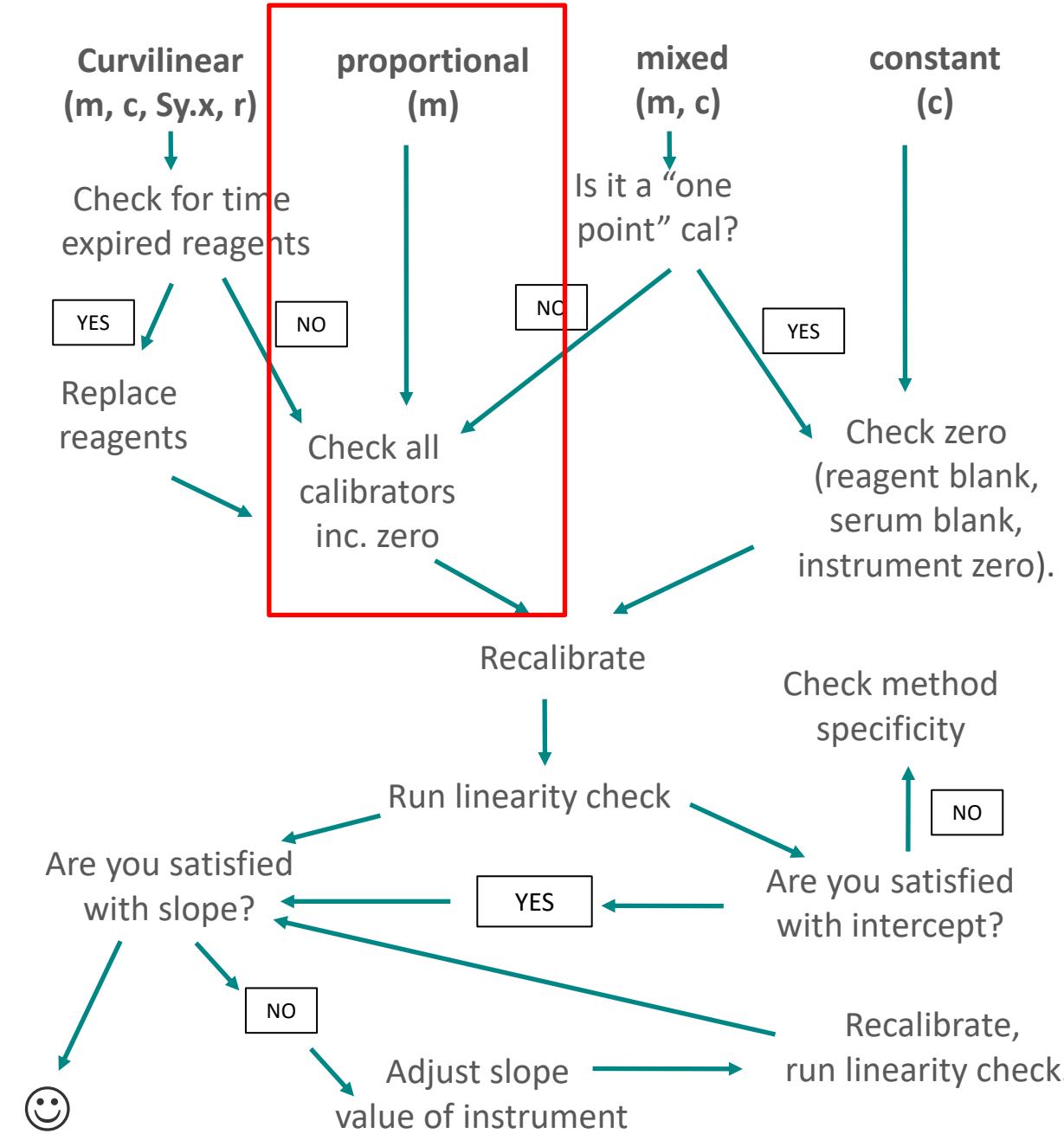
**Precision Scores:** precision good, previously good or acceptable

**Sample Histograms:** samples 3 and 4 off the scale, samples 1 and 2 non gaussian distributions but your result to the right of majority

**Method Summary Data:** Roche method negative bias to other methods

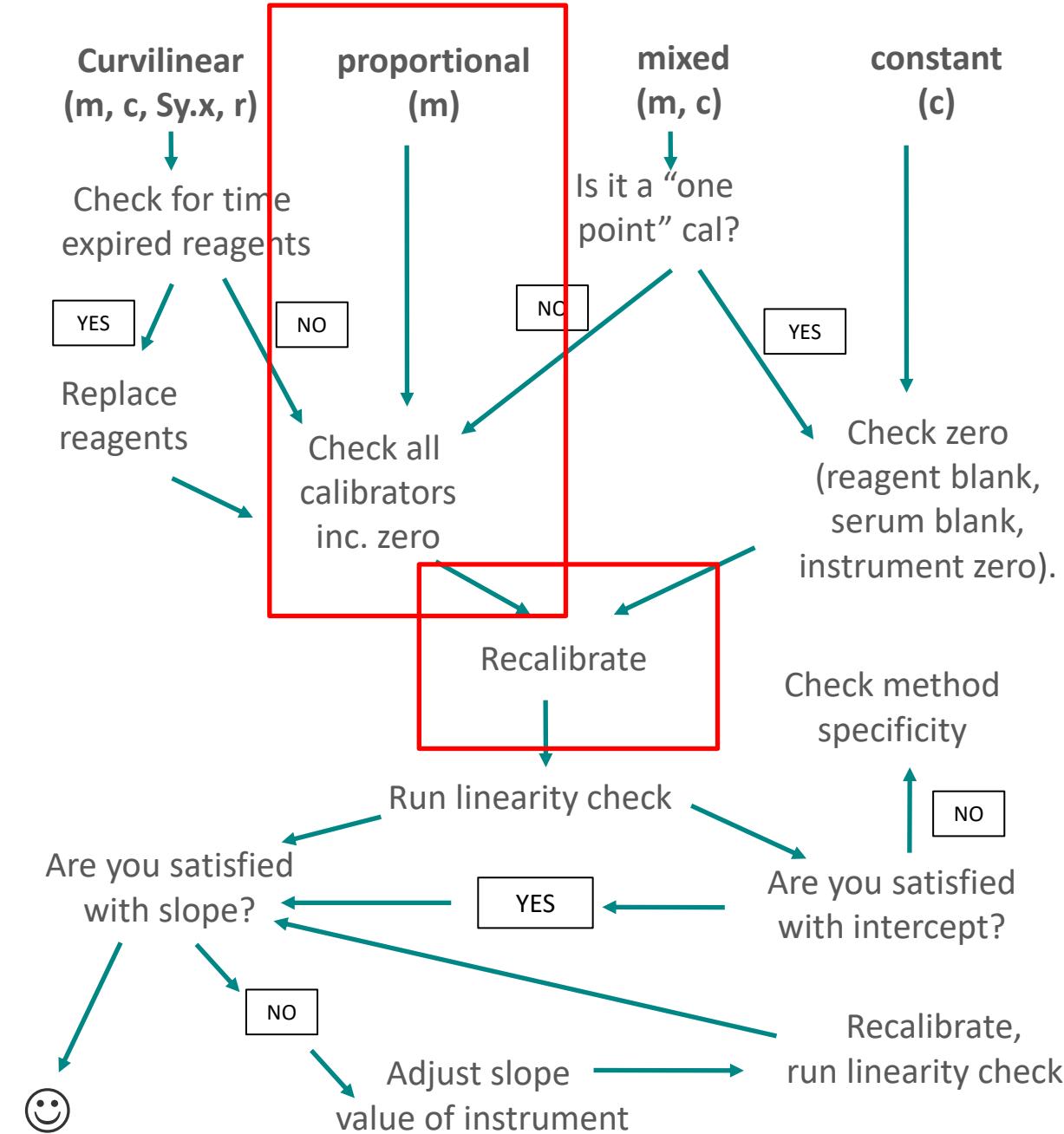
# Problem Solving Flow Chart

## INACCURACY



# Problem Solving Flow Chart

## INACCURACY



# Cases study Session

- 40 minutes workshop: each table has 3 cases to review
  - ✓ Comment on results and any points to note from the report
  - ✓ Identify the error
  - ✓ Discuss potential cause and resolution
- 20 minutes participant commentary and discussion