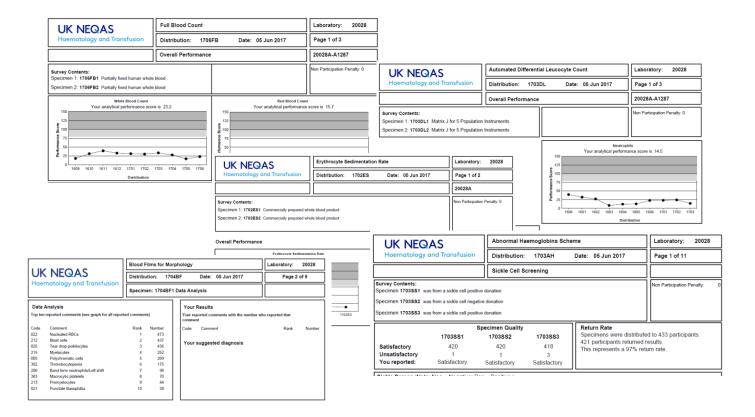
So my performance is satisfactory?

Barbara De la Salle





UK NEQAS Haematology reports



50 Years as World Leaders in EQA 1969–2019 UK NEQAS International Quality Expertise

Two types of scores

- UK NEQAS Haematology provides two scores for most programmes:
 - A participation score
 - An analytical performance score
- Analytical performance may be scored for:
 - Quantitative tests, e.g. FBC parametes
 - Qualitative tests, e.g. sickle cell screening
- Some reports are returned for information and education. Results are still reviewed and assessed even if no score is provided



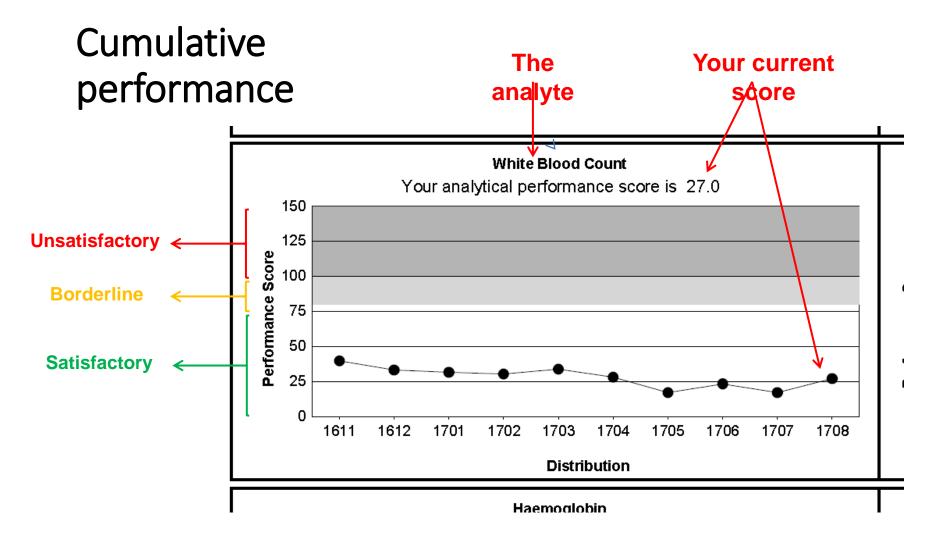


Definitions

- Satisfactory performance
- Unsatisfactory performance
- Poor performance
- Persistent unsatisfactory / poor performance
- Out of consensus performance
- Hazardous performance







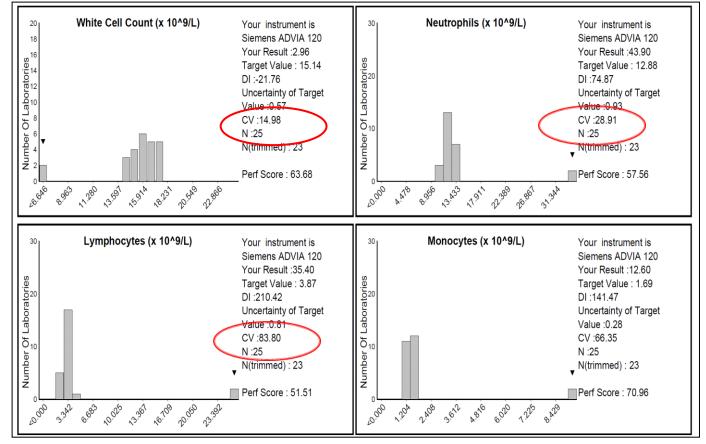
Target values

- A separate target value is determined for each analyte (measurand)
- The target value used in most UK NEQAS Haematology programmes are either:
 - The consensus result returned by participants. This is the most commonly used target
 - The expected result, e.g. for a haemoglobinopathy specimen
 - A model answer, defined by our expert advisors
- Data is trimmed to remove outliers
 - 10% symmetrical trimming
- The target value is shown to one decimal place more than the used to report the data but is calculated to many more decimal places than that





10% may not be enough on some occasions



Draft results - not released!!



UK NEQAS

Calculating the analytical performance score

- The Deviation Index (DI) is calculated. This is analagous to a z-score and shows how far the laboratory's result is from the target
- The DI is calculated on the trimmed data and (in most cases) after log-transformation of the data
- The DI is used to calculate the cumulative analytical performance score, using the results of the last six specimens containing the analyte





The Deviation Index (DI)

• Calculating the DI:

$$DI = \frac{x_i - x_{pt}}{SD_{pt}}$$

Where

 x_i is the laboratory result

 x_{pt} is the consensus trimmed mean value or median value SD is either the HSD or the estimated SD

 SD_{pt} is either the HSD or the estimated SD

- Interpreting the DI:
 - Less than 1 is good
 - Between 1 and 2 is satisfactory
 - Between 2 and 3 is borderline
 - Greater than 3 may indicate a problem

	BS ISO 13528:2015
INTERNATIONAL	ISO
STANDARD	13528

Statistical methods for use in proficiency testing by interlaboratory comparison

Méthodes statistiques utilisées dans les essais d'aptitude par comparaison interlaboratoires



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Investigating a high DI value

Example:

- Participant Platelet count = 15 x 10^9/L
- "Target" Platelet count = 18.3 x 10^9/L
- Deviation Index > 3.0!

Consider:

- Normal statistical distribution of results
- The analyte concentration
- Are both samples affected?
- Has there been a trend in recent results?
- Is the cumulative score satisfactory?
- Are IQC and other performance indicators okay?





The analytical performance score: an example

• DI values are obtained for the most recent six specimens:

Survey	Specimen FB1	Specimen FB2
1	-0.64	+1.85
2	0.00	+1.13
3	-1.89	+0.64

- The score is calculated by ignoring the arithmetical sign, summing the DI values and applying a multiplication factor (in FBC this is 6)
- Score = (0.64+1.85+0.0+2.89+1.13+1.89+0.64) x 6 = 37 This is satisfactory performance, i.e. the score is less than 100
- A score of between 80 100 may be borderline
- A score of greater than 100 is unsatisfactory performance

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Avoiding unfair penalties

- A result may attract a very high DI because of a 'blunder', e.g. result transposition, therefore:
- All DI values are truncated to a maximum of 3.5 before calculating the performance score to avoid unfair penalties
- The multiplication factor varies according to the programme and the analyte, to make scores comparable





UK NEQAS FB Material: Clinically relevant ranges

UK NEQAS FB: Range of values distributed annually

	WBC (10 ⁹ /L)	RBC (10 ¹² /L)	Hb (g/L)	PCV (L/L)	MCV (fL)	PLT (10 ⁹ /L)
Minimum	1.1	2.52	75	0.237	88.6	13
Maximum	27.5	6.2	185	0.598	97.8	795

Monthly or bi-monthly distributions: all common analytes





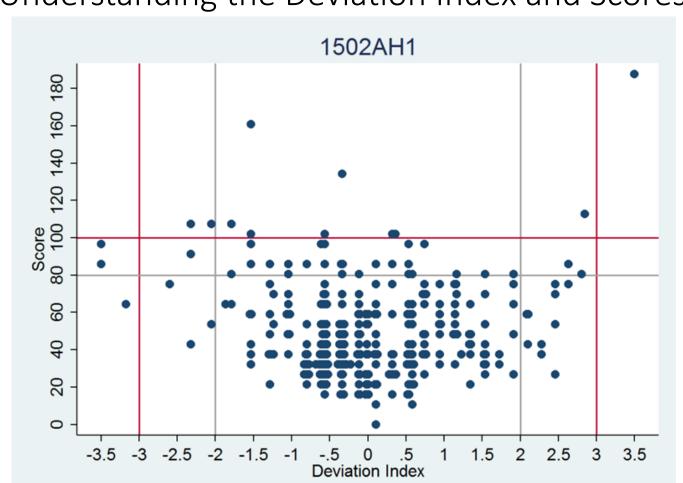
Robust statistics - Platelets

...

Ν					
trimmed	Mean	SD	HSD	CV	HCV
650	162.79	0.06	0.11	6.01	12.03
650	633.49	0.05	0.11	4.80	12.03
644	248.49	0.05	0.11	4.79	12.02
644	200.91	0.08	0.11	<mark>8.26</mark>	12.02
632	234.49	0.05	0.10	4.96	10.33
632	7.51	0.29	0.10	33.04	10.33
644	24.50	0.11	0.09	11.78	9.77
644	112.58	0.05	0.09	4.80	9.77
614	261.57	0.04	0.10	4.36	10.33
614	238.13	0.04	0.10	3.87	10.33
598	11.16	0.20	0.08	22.66	8.45
	650 650 644 644 632 632 644 644 614 614	trimmedMean650162.79650633.49644248.49644200.91632234.496327.5164424.50644112.58614261.57614238.13	trimmedMeanSD650162.790.06650633.490.05644248.490.05644200.910.08632234.490.056327.510.2964424.500.11644112.580.05614261.570.04614238.130.04	trimmedMeanSDHSD650162.790.060.11650633.490.050.11644248.490.050.11644200.910.080.11632234.490.050.106327.510.290.1064424.500.110.09644112.580.050.09614261.570.040.10614238.130.040.10	trimmedMeanSDHSDCV650162.790.060.116.01650633.490.050.114.80644248.490.050.114.79644200.910.080.118.26632234.490.050.104.966327.510.290.1033.0464424.500.110.0911.78644112.580.050.094.80614261.570.040.104.36614238.130.040.103.87

Robust statistics – Red cells $_{\rm N}$

SampleNo	trimmed	Mean	SD	HSD	CV	HCV
1908FB2	651	3.10	0.01	0.01	1.33	1.28
1908FB1	651	3.36	0.01	0.01	1.27	1.28
1907FB2	646	4.83	0.01	0.01	1.18	1.29
1907FB1	646	4.01	0.03	0.01	2.84	1.29
1906FB2	633	6.07	0.01	0.01	1.19	1.34
1906FB1	633	3.71	0.01	0.01	1.21	1.34
1905FB2	646	2.10	0.02	0.01	1.61	1.32
1905FB1	646	3.98	0.01	0.01	1.28	1.32
1904FB2	615	6.14	0.01	0.01	1.25	1.32
1904FB1	615	3.80	0.01	0.01	1.22	1.32
1903FB2	599	3.83	0.01	0.01	1.16	1.33

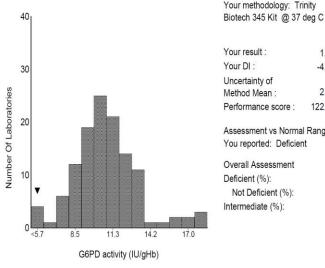


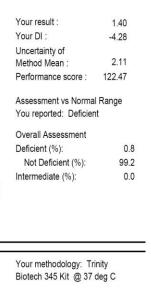
Understanding the Deviation Index and Scores

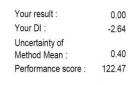
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Unsatisfactory performance – G6PD

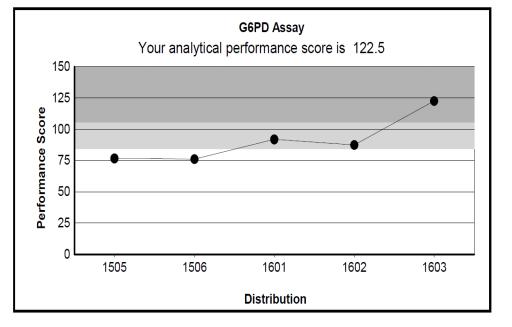






Assessment vs Normal Range You reported: Deficient

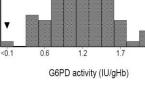
96.4
1.8
1.8



- Error in Hb units -> results 10x too low
- 62 patients affected
- 43 incorrectly diagnosed as G6PD deficient

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2.3

40

30

20

Number Of Laboratories

Thank you for your attention!





