



HPA Food and Water PT Schemes: A Guide to the Scoring Systems and Statistics Used for the HPA Proficiency Testing Schemes for Food and Water Microbiology



HPA Microbiology Services (Colindale)
Food and Environmental Proficiency Testing Unit (FEPTU)
61 Colindale Avenue
London
NW9 5EQ
Tel: +44 (0) 20 8327 7119
Fax: +44 (0) 20 8200 8264
Email: foodeqa@hpa.org.uk
Website : www.hpa.org.uk/eqa

Index

Section		Page
1.0	General introduction	3
1.1	HPA scores for on-going performance assessment	5
1.2	Z-scores	7
2.0	Standard Scheme	9
3.0	Extended Scheme	11
4.0	Food Law Scheme	15
5.0	Shellfish Scheme	17
6.0	Non-Pathogen Scheme	19
7.0	Legionella Isolation Scheme	20
8.0	Drinking Water Scheme	21
9.0	Surface Water Scheme	21

Website links for scheme-specific information

FOOD MICROBIOLOGY

Standard Scheme	www.hpa.org.uk/eqa/standard
Extended Scheme	www.hpa.org.uk/eqa/extended
Food Law Scheme	www.hpa.org.uk/eqa/foodlaw
Shellfish Scheme	www.hpa.org.uk/eqa/shellfish
Non-Pathogen Scheme	www.hpa.org.uk/eqa/nonpathogen
Pathogenic <i>Vibrio</i> Scheme	www.hpa.org.uk/eqa/vibrio
<i>Staphylococcus aureus</i> Enterotoxin Detection Scheme	www.hpa.org.uk/eqa/staphylococcus

WATER MICROBIOLOGY

<i>Legionella</i> Isolation Scheme	www.hpa.org.uk/eqa/legionella
Drinking Water Scheme	www.hpa.org.uk/eqa/drinkingwater
Surface Water Scheme	www.hpa.org.uk/eqa/surfacewater

1.0 General introduction

This guide is designed to help participants understand the scoring systems and statistics that are used to assist with assessing results reported for the HPA food and water microbiology proficiency testing (PT) schemes. The scoring systems were developed with input from participants and members of the Steering Group and are continually reviewed to ensure fitness-for-purpose. Scores are allocated to participants' results to help participants assess their performance not only with a single sample but also over a period of time. Scoring also helps the organisers to recognise those participants who experience problems with the samples and thus allows provision of additional help, advice and support.

The allocation of scores draws attention to differences between a participant's result and what has been designated as the 'assigned value'. Assigned values for qualitative (presence/absence) examinations are determined from the sample design and the results obtained in the FEPTU (Food and Environmental Proficiency Testing Unit) laboratory, although participants' results are also considered to help identify anomalies with the sample. Assigned values for enumerations are determined using robust statistics; the participants' median value is normally designated the assigned value, although the FEPTU quality control results are also considered. Differences of more than $0.5\log_{10}$ units between the participants' median and the FEPTU median are investigated.

Although scores may help participants to identify whether there is a problem with their testing, low or outlying scores do not always mean that this is the case. There will always be differences in laboratory practice; this means that the score allocated for the PT results may not be totally applicable to a particular laboratory situation. For example, a participant may report an outlying result for an enumeration because they use a method that results in a higher recovery than methods used in most other laboratories. In this situation the low score does not indicate a problem but this should be documented, indicating that no corrective actions are required.

Participants are advised that if they report outlying results for enumerations and are allocated low scores on single occasions only then they should not be unduly alarmed, although they should still assess the reason(s) for the outlying result. This is particularly important for samples that are likely to contain very low levels of micro-organisms, such as for the Drinking Water Scheme.

The allocation of scores is provided as a management tool to help assess performance; it cannot replace assessment of PT results in the context of the individual laboratory. Methods should never be amended for the sole purpose of achieving better scores with PT samples.

This document includes a summary of how scores are allocated for each scheme. Scoring systems are not used for the Pathogenic *Vibrio* Scheme and the Detection of *Staphylococcus aureus* Enterotoxin Scheme; these are single parameter schemes where it is very easy for participants to determine their performance without the aid of a scoring system.

Further guidance about the general use of the HPA PT schemes and advice for dealing with unsatisfactory results are available from the scheme guide: A Guide to the Use of the HPA Proficiency Testing Schemes for Food and Water Microbiology: www.hpa.org.uk/eqa/docs/

1.0.1 Introduction to the scoring systems

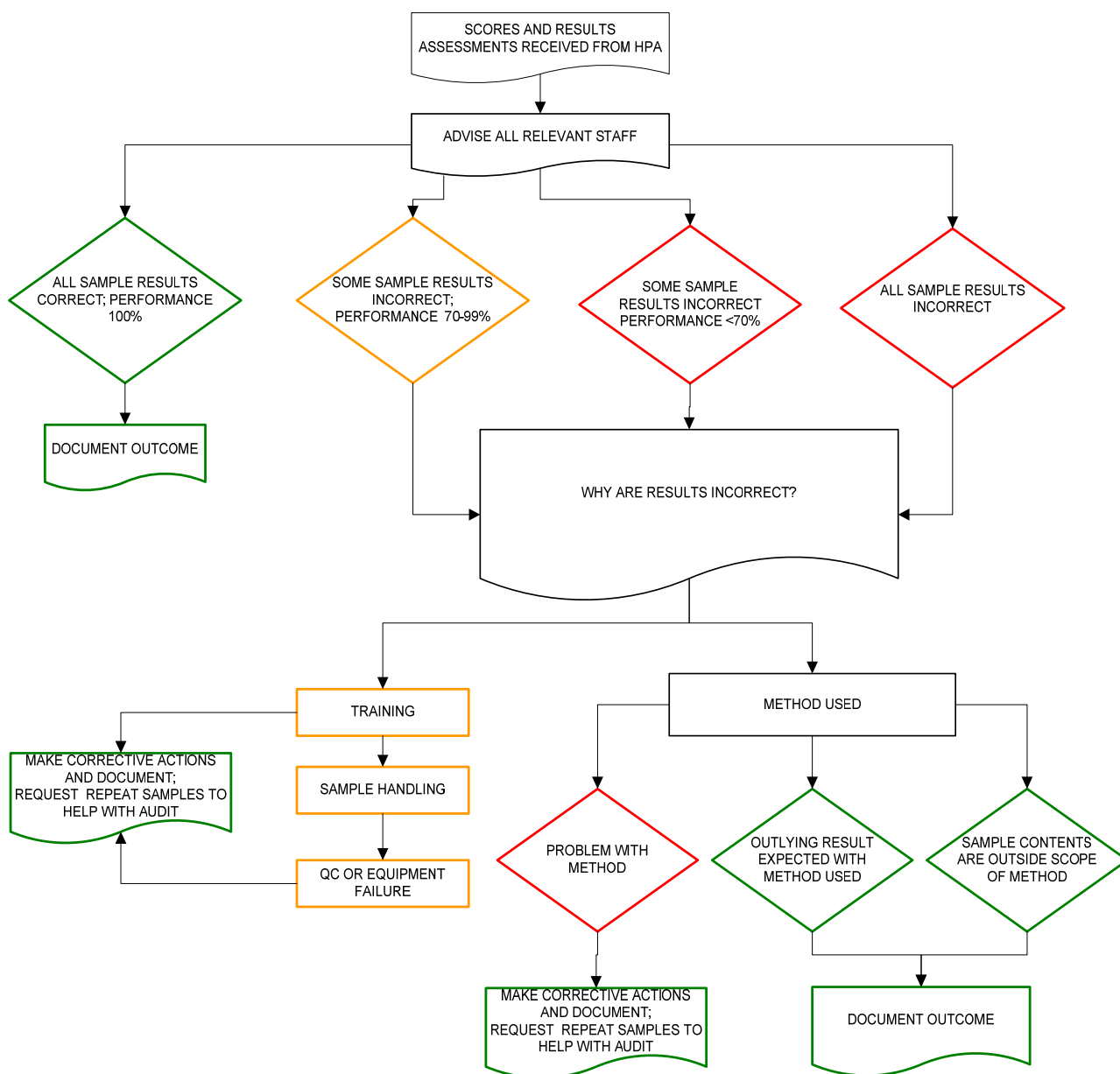
HPA scores are allocated for the Standard, Extended, Shellfish, Food Law, Non-Pathogen, Drinking Water, Surface Water and Legionella Isolation Schemes to assess performance with every sample and also to assess performance over a period of time. The HPA scoring systems are devised with microbiological outcome as a priority. They are specifically designed to make it easier to identify those laboratories that experience significant and on-going difficulties with their examinations, i.e. difficulties that may ultimately impact on peoples' health. Each HPA scoring system is tailored to the specific scheme, taking into account the sample designs and the examinations that are included for the scheme.

The HPA scoring systems recognise that, while every batch of HPA PT samples is fit-for-purpose, every participant will not receive a sample containing exactly the same number of micro-organisms. The samples are designed in such a way that participants are extremely unlikely to obtain an incorrect negative result for a presence/absence examination by chance. However, for enumeration tests there will be a range of acceptable results, and a laboratory may occasionally report an outlying result by chance. The HPA scoring system for on-going performance assessment is designed to take this into consideration so genuine

problems are always identified. **It is difficult to provide a meaningful assessment of performance over time using HPA scores if participants choose not to receive all the distributions provided for a particular scheme.**

Z-scores are determined routinely for the Standard, Non-Pathogen, Drinking Water, Surface Water and *Legionella* Isolation Schemes to assess performance with individual examinations. Z-scores provide a statistical means of assessing results but do not consider the microbiological impacts. However, they are used by many PT providers, and some participants find z-scores useful if they participate in schemes from different providers for comparing performance across the range of schemes. Z-scores are not used to assess on-going performance, although on-line tools are available to assist participants if they want to trend their results.

In most cases the HPA scores and the z-scores will provide compatible indications as to whether a result is likely to be satisfactory or not. However, it is ultimately the participant who must decide whether their PT results are acceptable and whether any actions are required. Guidance on the decision making process is provided below:



1.1 HPA scores for on-going performance assessment

HPA scores are allocated to results for the Standard, Extended, Shellfish, Food Law, Non-Pathogen, *Legionella* Isolation, Drinking Water and Surface Water Schemes. The mechanism for allocating HPA scores is dependent on a number of factors such as the expected number of laboratories participating in a distribution (round) of samples and the nature of the test.

HPA scores are allocated per examination for some of the schemes (Shellfish, Non-Pathogen, Drinking Water, Surface Water). For other schemes, a composite score may be allocated that takes a number of different factors into consideration:

For example, the laboratory's ability to isolate, enumerate, identify and determine the serogroup for a *Legionella* isolate are considered when the HPA score is allocated to the results for a sample from the *Legionella* Isolation Scheme.

Similarly, when the HPA scores are allocated for samples from the Food Law Scheme the process allows consideration of the microbiological results and also the interpretation of those results with regard to the correct part of the relevant EU legislation.

HPA scores are devised in such a way that they can be combined over a period of time; the cumulative results are summarised in the individualised distribution reports. Those laboratories with cumulative scores that are less than 70% of the maximum possible score are likely to have significant underlying problems with their examinations which should be addressed as a matter of urgency. Participants with cumulative scores of between 70% and 99% should also assess why they were allocated lower scores on one or more occasions. Note that the interpretations of HPA scores provided by FEPTU used to assess performance must be applied to the individual laboratory situation before a final conclusion is drawn. Charts are included in the individualised reports for the Standard, Extended, Food Law, Shellfish, *Legionella* Isolation and Drinking Water Schemes to summarise performance over time, with colour-coded bars to draw attention to those scores that indicate potential problems with the examination results.

Statistical models are not used to assess results for qualitative (presence/absence) tests when allocating HPA scores. However, statistical tests are undertaken to assess enumeration results before HPA scores are applied, as described below.

1.1.1 Percentiles

Percentiles are applicable to all the PT data sets, even when data does not show a normal distribution, provided there are more than 50 participants returning results (i.e. more than 50 data sets). Percentiles are used to identify outlying counts by ranking all participants' counts from lowest to highest and calculating the 5th, 10th, 90th and 95th percentiles. The results are initially interpreted as follows:

Results in 11 th to 89 th percentiles	satisfactory
Results in 6 th to 10 th or 90 th to 95 th percentiles	questionable
Results in 0 to 5 th or 96 th to 100 th percentiles	unsatisfactory

The $0.5\log_{10}$ rule is then applied before scores are allocated so that all counts within $0.5\log_{10}$ units of the consensus media are re-classified as satisfactory and allocated the maximum score. The value of the maximum score is scheme dependent. The interpretations suggested by HPA must be applied to the individual laboratory situation before a final conclusion is drawn. As a general rule, questionable and unsatisfactory results should be investigated.

1.1.2 The $0.5 \log_{10}$ rule

The $0.5 \log_{10}$ rule is adapted from a publication by Basil Jarvis (*Sampling for Microbiological Analysis in 'The Microbiological Safety and Quality of Food' Volume II, 2000, edited by Lund, Baird-Parker and Gould*). Although the $0.5\log_{10}$ rule is based on microbiological criteria, it is also statistically valid: for example, if the expected count on a plate is 10 colonies, and the organisms are randomly distributed, then 95% of results would be between 3 and 17 colonies. When the range is converted to a \log_{10} scale it would be between 0.47 and 1.23, with a median of 1.00, i.e. the lower and upper limits are within $0.5\log_{10}$ units. Therefore, it may be considered unreasonable to classify any result that is less than $\pm 0.5 \log_{10}$ units from the participants' consensus median as questionable or unsatisfactory. As a general rule, questionable and unsatisfactory results should be investigated.

1.1.3 The median absolute deviation from the median (MAD) values

The MAD method is used to identify outlying counts when there are less than 50 data sets, i.e. when less than 50 participants return results for an enumeration. The use of MAD values provides a statistically robust method for calculating the acceptable range using an analysis that requires calculation of the median difference from the median for every participant's result, which is then multiplied by a constant (1.4826) to obtain a robust estimate of the standard deviation (MAD value). The results are initially interpreted as follows:

Results in range of participants' median ± 2 MAD	satisfactory
Results between ± 2 MAD and ± 2.58 MAD	questionable
Results $> \pm 2.58$ MAD	unsatisfactory

If the data shows a normal distribution, approximately 5% of results will fall outside the ± 2 MAD values and 1% outside ± 2.58 MAD values.

The $0.5 \log_{10}$ rule is applied as previously described then scores can be allocated accordingly. The interpretations suggested by HPA must be applied to the individual laboratory situation before a final conclusion is drawn. As a general rule, questionable and unsatisfactory results should be investigated.

1.1.4 Assessing results for most probable number (MPN tests)

The method used to determine MPN results has greater inherent variability than colony count methods so statistical assessment of participants' results needs to take this into consideration. Analysing a number of sets of data has shown to inflate the variance (*Prior, Z., Andrews, N. and Russell J.E. 2005 41 334-340, Lett in Appl Microbiol*). Therefore, the limits of acceptability for participants' results for MPN determinations are raised beyond those of z-scores to ± 3 SD and ± 5 SD.

1.1.5 Summary of HPA scores

Sections 2.0 to 8.0 of this document summarise the specific details of how HPA scores are allocated for each of the schemes. The sections are colour coded to help identify the relevant information for the specific schemes. Participants are advised in advance, by email, of any changes to the scoring systems.

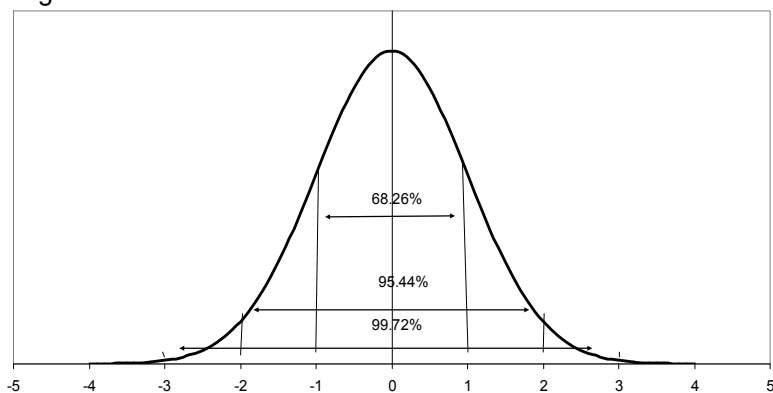
If a sample includes atypical micro-organisms then HPA scores may not be allocated. This decision is normally made in advance by the scheme organisers.

If the results for a sample are not as expected, either in the FEPTU laboratory or after analysis of the results submitted by participants, then the organisers may decide not to allocate HPA scores. This will be explained in the relevant distribution summary.

1.2 Z-scores

Z-scores provide a statistical means of standardising data points on a single scale so they can be compared. Each z-score corresponds to a point in a normal distribution, describing how far each data point deviates from the consensus median. Fig 1 below shows a normal distribution curve:

Fig 1



- Mean = 0
- 68.26% data points fall within 1 standard deviation of the mean
- 95.44% data points fall within 2 standard deviations of the mean
- 99.72% data points fall within 3 standard deviations of the mean

Participants' results are converted into z-scores, reflecting the difference between the participant's result and the assigned value (participants' median).

The advantages of z-scores are:

- They are relatively easy to calculate using a commonly-used standard formula
- They are commonly used by other proficiency testing scheme providers so participants are likely to be familiar with their interpretation

The disadvantages of z-scores are:

- They can easily be misinterpreted in the laboratory
- They use a statistical formula that does not take into consideration the limits of acceptability for specific microbiological examinations
- There will always be some participants who are allocated a z-score indicating unsatisfactory performance for an enumeration, even if their result is acceptable according to microbiological criteria
- For low counts, such as counts below 15 in drinking water samples, the z score may be more than ± 2 whereas the participant's result is within the 95% confidence interval of the expected result
- They are not particularly helpful for qualitative data (presence/absence tests)
- They are more difficult to apply to results that do not show a normal distribution
- They are not suitable for censored values (less than or greater than values, e.g. <1, >10)
- They can be used only with extreme caution to assess performance over time

1.2.1 Calculation of z-scores for enumerations

Participants' enumeration results are converted into z-scores using the following formula:

$$Z = \frac{(x-X)}{\sigma}$$

x = participants' result (expressed as a log₁₀ value)
X = assigned value (participants' consensus median (expressed as a log₁₀ value))
σ = the fixed standard deviation for the examination (calculated by FEPTU)

The σ-value expresses the acceptable difference between the individual participant's result and the participants' consensus median. The σ-values have been calculated by FEPTU staff using data from previous distributions. For most parameters the value of σ = 0.35, although for *Legionella* enumerations σ = 0.55.

1.2.2 Calculation of z-scores for qualitative (presence/absence) tests

The z-score formula is not used for allocating z-scores for qualitative tests.

Participants who report a correct result are allocated a z-score of 0.

Participants who report an incorrect result are allocated a z-score of 4.

1.2.3 Interpretation of z-scores

A z-score of zero implies a perfect result, i.e. a result that is exactly the same as the participants' median. However, any z-score between -2 and +2 may be considered satisfactory; 95.44% participants will be allocated a z-score between -2 and +2.

Z-scores outside the range of -3 to +3 are very unusual, i.e. will be allocated to only 0.28% participants; such results may be considered unsatisfactory.

Therefore, z-scores used in PT are usually interpreted as follows:

z = -1.99 to +1.99	satisfactory
z = -2 to -2.99 or +2 to +2.99	questionable
z = <-3.00 or >+3.00	unsatisfactory

It is usually recommended that z-scores exceeding ± 2.0 are investigated to establish the possible cause. As a general rule, HPA recommends that all questionable and unsatisfactory results are investigated.

Z-scores must not be considered in isolation when assessing laboratory results; the microbiological impact and subsequent outcome for the food or water source must also be considered together with the specific conditions such as the method used within the testing laboratory. The suggested interpretations must be applied to the individual laboratory situation before a final conclusion is drawn.

1.2.4 Z-scores for on-going performance assessment

Z-scores must be used with caution for assessing on-going performance with a number of PT samples over time. A z-score of 0.2 followed by a subsequent z-score of 1.6 does not indicate deterioration in performance. Similarly, if z-scores are used to assess the performance of individual staff members, then a person allocated a z-score of 0.1 for their results has not demonstrated better performance than a colleague who was allocated a z-score of -1.4.

The calculation of average z-scores over a period of time is not recommended because this may result in hiding one or more unsatisfactory results.

The HPA uses z-scores to help assess performance with individual examinations only; z-scores are not used by the HPA to assess participants' performance over a range of samples. However, HPA on-line tools are available for participants who want to trend their z-scores over a range of different samples, by parameter, or to compare the z-scores of different personnel. A z-score calculator is also available for participants who want to apply z-scores to other scheme results: www.hpa.org.uk/eqa/zscores

HPA scoring systems by scheme:

2.0 The Standard Scheme:

Scores are allocated to participants' results for every sample as follows:

- i. **pathogen examinations:** a combined score is allocated for each sample to assess the all results submitted for presence/absence examinations enumerations of pathogenic organisms. The scores for each sample are collated to provide an overall performance assessment for the results submitted for pathogenic micro-organisms over the past 12 months (six distributions, 12 samples).
- ii. **aerobic colony counts (ACCs):** a single score is allocated for each sample to assess the results for the ACCs; the scores are collated to provide an overall performance assessment over the past 12 months (six distributions, 12 samples).
- iii. **indicator organism enumerations:** a single score is allocated for each sample for the enumeration of the relevant indicator organism (coliforms, Enterobacteriaceae and *Escherichia coli*). The scores are combined to provide an overall performance assessment for the enumeration of indicator organisms over the past 12 months (six distributions, 12 samples).

Pathogen examinations: A maximum score of 12 points allocated as follows:

	Score
Return form	2
Pathogen 1	3
Pathogen 2	3
Pathogen 3	3
Bonus if all correct	1*
Total score	12

* Bonus point awarded if all results reported are correct.

Standard Scheme examples: Two pathogens present in the sample

	Pathogen 1 (cfu g ⁻¹)	Pathogen 2 (cfu g ⁻¹)	Pathogen 3	Total	Bonus	Return report	Total score	Max possible
Result reported	Present (in range)	Present (in range)	Not detected					
Score	3	3	3	9	1	2	12	12 (100%)

	Pathogen 1 (cfu g ⁻¹)	Pathogen 2 (cfu g ⁻¹)	Pathogen 3	Total	Bonus	Return report	Total score	Max possible
Result reported	Outlying results (1*)	Outlying results (2*)	Not detected					
Score	2	1	3	6	1	2	9	12 (75%)

* Bonus point awarded if all results reported are correct; also if all pathogens are detected even if the enumeration is out of range

	Pathogen 1 (cfu g ⁻¹)	Pathogen 2 (cfu g ⁻¹)	Pathogen 3	Total	Bonus	Return report	Total score	Max possible
Result reported	Not examined	Not detected	Present					
Score		0	0	0	0	2	2	9 (22%)

Enumerations: Results for pathogen enumerations are allocated a score up to a maximum of three points for each examination and the score is incorporated into the overall score for pathogens.

ACCs and indicator organisms enumerations are each allocated a score up to a maximum of two points. Counts are ranked from lowest to highest and the participants' median is calculated:

		Scores for pathogen enumeration	Scores for ACC and indicator organisms
Expected range	Median \pm 0.5 log ₁₀ units or counts within 11 th to 89 th percentiles	3	2
Outlying results (1)	Median \pm >0.5 log ₁₀ units and in 6 th to 10 th or 90 th to 95 th percentiles	2	1
Outlying results (2)	Median \pm >0.5 log ₁₀ units and in 0 th to 5 th or 96 th to 100 th percentiles	1	0

If a low censored value (< value) arises by chance because the target organism(s) or group is present at a low level then the maximum score is allocated; zero points are allocated to participants reporting high counts.

Participants who do not return report forms or return report forms after the specified return date (late results) are allocated an HPA score of zero for all tests.

3.0 The Extended Scheme:

Scores are allocated to participants' results for every sample as follows:

- i. **pathogen examinations:** a combined score is allocated for each sample to assess the all results submitted for presence/absence examinations enumerations of pathogenic organisms. The scores for each sample are collated to provide an overall performance assessment for the results submitted for pathogenic micro-organisms over the past 12 months (six distributions, 12 samples).
- ii. **aerobic colony counts (ACCs):** a single score is allocated for each sample to assess the results for the ACCs; the scores are collated to provide an overall performance assessment over the past 12 months (six distributions, 12 samples).
- iii. **indicator organism enumerations:** a single score is allocated for each sample for the enumeration of the relevant indicator organism (coliforms, Enterobacteriaceae and *Escherichia coli*). The scores are combined to provide an overall performance assessment for the enumeration of indicator organisms over the past 12 months (six distributions, 12 samples).

Pathogen examinations: A maximum score of 12 points allocated as follows:

	Score allocated when there is one target organism	Score allocated when there are two target organisms	Score allocated when there are three target organisms
Return form	1	1	1
Pathogen 1	10	5	3
Pathogen 2	N/A	5	3
Pathogen 3	N/A	N/A	3
Bonus if all correct	1	1	2
Total score	12	12	12

Points will be deducted if a species name is reported incorrectly. Some examples follow; the examples below do not cover every possible combination of results that may be reported by participants, but are provided as guidance.

Extended Scheme - Example 1: One target organism in the sample

Correct result: ***Campylobacter jejuni* present**

- *If two pathogens were reported as present, i.e. one incorrectly reported, then the allocation of points would be as described in example 2*

	Result reported				
	Maximum scores for one target organism	<i>C.jejuni</i> present	<i>Campylobacter</i> sp. present	<i>Campylobacter</i> sp. not detected	<i>Campylobacter</i> sp. present; <i>Salmonella</i> sp. present
Return form	1	1	1	1	1
Pathogen 1	10	10	10	0	5
Bonus if all correct	1	1	1	0	0
Total score	12	12	12	1	6

Extended Scheme - Example 2: Two target organisms

Correct result: ***Listeria monocytogenes* present; *Salmonella* sp. present**

- If a participant did not undertake an examination for one of the two target pathogens then the scoring system would be applied in accordance with example 1.
- If an unexpected pathogen was reported in addition to the correct results, the points allocated would be adapted accordingly as demonstrated in the table below.

Result reported					
	Maximum scores for two target organisms	<i>L.monocytogenes</i> present; <i>Salmonella</i> present	<i>L.innocua</i> present; <i>Salmonella</i> present	<i>L. monocytogenes</i> present; <i>Salmonella</i> not detected	<i>L.monocytogenes</i> present; <i>Salmonella</i> present; <i>Campylobacter</i> present
Return form	1	1	1	1	1
Pathogen 1	5	5	3	5	3
Pathogen 2	5	5	5	0	3
Bonus if all correct	1	1	0	0	0
Total score	12	12	9	6	7

Extended Scheme - Example 3: Three target pathogens.

Correct result: ***Salmonella* sp. present, *Campylobacter* sp. present; *Y.enterocolitica* present**

Result reported					
	Maximum scores for target organisms	<i>Salmonella</i> present; <i>Campylobacter</i> sp. present; <i>Y.enterocolitica</i> present	<i>Salmonella</i> present; <i>Campylobacter</i> not detected; <i>Y.enterocolitica</i> present	<i>Salmonella</i> present; <i>Campylobacter</i> sp. not detected; <i>Y.enterocolitica</i> not detected	<i>Salmonella</i> present; <i>Campylobacter</i> sp. present; <i>Y.enterocolitica</i> present; <i>S.aureus</i> present (at any level)
Return form	1	1	1	1	1
Pathogen 1	3	3	3	3	2
Pathogen 2	3	3	0	0	2
Pathogen 3	3	3	3	0	2
Bonus if all correct	2	2	0	0	0
Total score	12	12	7	4	7

Enumeration of pathogens: Scores are allocated for results reported for samples containing pathogens that require enumerations. Participants must report the organism name correctly and the reported count must be within the expected range in order to be allocated the maximum 12 points. The expected range for the results reported is calculated using the median absolute deviation from the median (MAD) values which are determined from the median result reported by participants' and take into account the following criteria:

- (1) median \pm 2 MAD
- (2) median \pm 3 MAD
- (3) median \pm 0.5 log₁₀ units

If the ranges in (1) and/or (2) are less than the value of the median \pm 0.5 log₁₀ units then the expected range is extended as described in (3).

		Score
Expected range	within the range according to criteria (1)	Maximum score allocated
Outlying results (1)	within the range of criteria (2) but not within criteria (1)	Half of maximum score allocated (rounded up if maximum points available is an odd number)
Outlying results (2)	outside the range of criteria (2)	0

Extended Scheme - Example 4: One target organism

Correct result: ***B.cereus* 1.0x10⁴ - 1.0x10⁵ cfu g⁻¹**

	Maximum scores for one target organism enumeration	Result reported			
		<i>B.cereus</i> 1.0x10 ⁴ to 1.0x10 ⁵ cfu g ⁻¹ (result is in range)	<i>B.cereus</i> 6.9x10 ⁶ cfu g ⁻¹ (result is outside the median \pm 0.5 log ₁₀ units / \pm 2SD values but within median \pm 3SD values)	<i>B.cereus</i> 7.5x10 ³ cfu g ⁻¹ (result is outside median \pm 3 SD values)	<i>B.cereus</i> 1.0x10 ⁴ to 1.0x10 ⁵ cfu g ⁻¹ ; <i>S.aureus</i> reported (any level)
Return form	1	1	1	1	1
Pathogen 1	10	10	5	0	5
Bonus if all correct	1	1	0	0	0
Total score	12	12	6	1	6

Extended Scheme - Example 5: Two target pathogens, one requiring presence/absence examination and one requiring enumeration

Correct result: **Salmonella present; S.aureus $1.0 \times 10^5 - 1.0 \times 10^6$ cfu g⁻¹**

	Results reported				
	Maximum scores for two target organisms	<i>Salmonella</i> present; <i>S.aureus</i> within range	<i>Salmonella</i> present; <i>S.aureus</i> out of range	<i>Salmonella</i> not detected; <i>S.aureus</i> out of range	<i>Salmonella</i> present; <i>S.aureus</i> within range <i>Campylobacter</i> present
Return form	1	1	1	1	1
Pathogen 1	5	5	5	0	3
Pathogen 2	5	5	3 or 0	3 or 0	3
Bonus if all correct	1	1	0	0	0
Total score	12	12	9 or 7	4 or 1	7

Scores for other enumerations: ACCs and indicator organisms (Enterobacteriaceae and *E.coli*) enumerations are each allocated a score to a maximum of two points. Counts are ranked from lowest to highest and the participants' median is calculated. The scores are allocated as follows:

		Scores for ACC and indicator organisms
Expected range	Median $\pm 2 \times$ MAD	2
Outlying results (1)	Median $\pm 3 \times$ MAD	1
Outlying results (2)	Median $\pm >0.5 \log_{10}$ units	0

If a low censored value (< value) arises by chance because the target organism(s) or group is present at a low level then the maximum score is allocated; zero points are allocated to participants reporting high counts.

Participants who do not return report forms or return report forms after the specified return date (late results) are allocated an HPA score of zero for all tests.

4.0 The Food Law Scheme:

A separate score is allocated for the results for each examination undertaken on a sample. The scores are allocated for the microbiological results and the conclusion about the batch. All the scores are collated to provide an overall performance assessment for the results submitted over the past 12 months (four distributions, 12 samples).

	Expected result	Score allocated
Name of examination	Correct examination	1
Stipulated method	Not scored	
Amount of sample examined	Not scored	
No. of samples from a batch required for compliance	Correct value	1
Expected range	Correct presence/absence or within range* <i>Outlying results</i>	3 2 or 0
Limits for compliance	Not scored	
Conclusion about the batch from result	Correct conclusion	2
	Partial conclusion e.g. about sample not batch	1
	No conclusion or misleading conclusion	0
Return of results form		1
Maximum possible score		8

*Refer to enumerations below

Enumerations: (Aerobic colony count, *Bacillus cereus*, *Cronobacter*, coagulase-positive staphylococci, Enterobacteriaceae, *Escherichia coli*, *Listeria* spp.)

The expected range for the results reported is calculated using the median absolute deviation from the median (MAD) values which are determined from the median result reported by participants' and take into account the following criteria:

- (1) median \pm 2 MAD
- (2) median \pm 3 MAD
- (3) median \pm 0.5 log₁₀ units

If the ranges in (1) and/or (2) are less than the value of the median \pm 0.5 log₁₀ units then the expected range is extended as described in (3).

		Score
Expected range	within the range according to criteria (1)	3
Outlying results (1)	within the range of criteria (2) but not within criteria (1)	2*
Outlying results (2)	outside the range of criteria (2)	0*

*If interpretation of an outlying result affects the outcome for the product in relation to the Directive standards/guidelines then the lower score indicated is allocated.

If a low censored value (< value) arises by chance because the target organism(s) or group is present at a low level then the maximum score of **three** points is allocated. Zero points are allocated to participants reporting high counts.

Scoring of MPN values:

The expected ranges for Enterobacteriaceae and *E.coli* MPN results are determined from the median result reported by participants ± 3 standard deviations (SD). Outlying results are defined as follows:

		Score
Expected range	median ± 3 SD	3
Outlying results (1)	median $\pm > 3 \pm \leq 5$ SD	2*
Outlying results (2)	median $\pm > 5$ SD	0*

*If interpretation of an outlying result affects the outcome for the product in relation to the Directive standards/guidelines then the lower score indicated is allocated.

If an incorrect dilution or incorrect MPN (due to misreading of the MPN table) is reported then only **one** point is allocated.

If the sample contains a low level of Enterobacteriaceae and Escherichia coli, the limits for low outlying counts may fall below the limit of detection for the test, e.g. <3 or 0.3 per g. Therefore, the limits for low outlying counts cannot be applied, i.e. <3 SD or <5 SD.

Scoring of results for presence/absence tests: (*L.monocytogenes*, *Salmonella* spp. and *Cronobacter sakazakii*)

	Score
Fully correct result	3
Incorrect species/serogroup identification	2
False positive or false negative result	0

Participants who do not return report forms or return report forms after the specified return date (late results) are allocated an HPA score of zero for all tests.

5.0 The Shellfish Scheme:

Separate scores are allocated for the results for each sample for the results for *E.coli* most probable numbers (MPN's) and *Salmonella* examinations. They are collated to provide an overall performance assessment for each of those examinations over the past 12 months (three distributions, nine samples).

A range of statistical analyses is performed on the results submitted for *E.coli* enumerations using the five or three tube MPN method. Each participant's reported MPN value is compared with the participants' median MPN.

Three initial analyses performed on participants' results as follows:

- I. **Within replicate variation**
To determine whether each tube combination reported by each participant is statistically acceptable.
- II. **Comparison with the participants' median MPN**
To determine the participants' median and compare each participant's MPN value, as calculated from the MPN value reported, with the median ± 3 and ± 5 standard deviation (SD) values.
- III. **Between sample variation**
When the two samples in the distribution are from the same batch, to determine whether there is a significant difference between the results reported for the two samples.

Participants' MPN results for both *E.coli* replicates are allocated a score up to a maximum of 12 points as follows:

Result	Score
Return of report	2
Both replicate MPN results reported are within the expected range	10
Total score	12

Scores are allocated as follows when both the MPN replicate results are reported:

Result	Replicate 1 Score allocated	Replicate 2 Score allocated	Return of report score	Total Score allocated
Both replicate MPN results reported are within the expected range	5	5	2	12
One replicate MPN result reported is outside the expected range and falls between the median ± 3 SD and median ± 5 SD values	2	5	2	9
Both replicate MPN results are outside the expected range and fall between the median ± 3 SD and median ± 5 SD values	2	2	2	6
One replicate MPN result reported is outside the median ± 5 SD values	0	5	2	7
Both replicate MPN results reported are outside the median ± 5 SD values	0	0	2	2
One replicate MPN result reported is outside the expected range and falls between the median ± 3 SD and median ± 5 SD values and One replicate MPN result reported is outside the median ± 5 SD values	2	0	2	4

Participants' MPN results for single *E.coli* replicate are allocated a score up to a maximum of 7 points as follows:

Result	Score
Return of report	2
Both replicate MPN results reported are within the expected range	5
Total score	7

Scores are allocated as follows when only a single MPN is result is reported:

Result	Single Replicate Score allocated	Return of report score	Total Score allocated
Single replicate MPN result reported is within the expected range	5	2	7
Single replicate MPN result reported is outside the expected range and falls between the median \pm 3SD and median \pm 5SD values	2	2	4
Single replicate MPN result reported is outside the median \pm 5SD values	0	2	2

Additionally the following scores are deducted if:

Any tube combinations are inconsistent with MPNs reported	2
Sample not examined or results returned late – no explanation received	12
High censored result (e.g. MPN = >16000 per 100g)	Depends on sample contents

Salmonella examinations: Participants' results for examinations for *Salmonella* spp. are allocated scores up to a maximum of two points as follows:

Result	Score
Fully correct result	2
Result partially misleading (e.g. incorrect serotype designation)	1
Grossly misleading result (false positive or false negative result)	0

Participants who do not return report forms or return report forms after the specified return date (late results) are allocated an HPA score of zero for all tests.

6.0 The Non-Pathogen Scheme:

Separate scores are allocated for the results for every enumeration requested for each sample. The results are collated to provide an overall performance assessment (from distribution NP042) for each parameter over the past 12 months (4 distributions, 12 samples).

Enumerations: The expected range for the results reported is calculated using the median absolute deviation from the median (MAD*) values which are determined from the median result reported by participants' and take into account the following criteria: (1) median \pm 2 MAD (2) median \pm 3 MAD and (3) median \pm 0.5 log₁₀ units. If the ranges in (1) and/or (2) are less than the median \pm 0.5 log₁₀ units then the expected range is extended as described in (3).

*The median absolute deviation from the median value is a robust estimate of the standard deviation (SD). It is only possible to calculate a precise estimate of the SD if more than 20 participants report enumeration results.

		Points
Expected range	within the range according to criteria (1)	2
Outlying results (1)	within the range of criteria (2) but not within criteria (1)	1
Outlying results (2)	outside the range of criteria (2)	0

If a low censored value (< value) arises by chance because the target organism(s) or group is present at a low level then the maximum of **two** points are allocated. **Zero** points are allocated for participants reporting high counts. Presumptive results are taken into account when results are assessed.

Participants who do not return report forms or return report forms after the specified return date (late results) are allocated an HPA score of zero for all tests.

7.0 The Legionella Isolation Scheme:

Single scores are allocated for performance with each sample for the isolation, identification and enumeration of legionellae, and those scores are collated to provide an overall performance assessment for all the examinations undertaken over the past 12 months (four distributions, 12 samples). Note that the 0.5₁₀ rule is expanded to 0.75₁₀ for the enumeration of legionellae to reflect the greater variation inherent in the standard method.

Scores are allocated to participants' results submitted for every sample as follows:

	Score
Return of Report	1
Correct Result	11
Total Score	12

Samples containing *Legionella* sp.

Result	Breakdown of score	Score
Return of report	1	1
Isolation of a Legionellae	2	2
Correct identification of <i>L.pneumophila</i>	2	4
Correct serogroup	2	
Or		
Correct identification of <i>Legionella</i> sp. (not <i>L.pneumophila</i>)	4	
Enumeration within the expected range	5	5
Or		
Outlying result (1)*	4	
Or		
Outlying result (2)*	3	
Total maximum score		12

Enumerations:

Expected range	Median ± 0.75 log ₁₀ unit or counts within 11 th to 89 th percentiles
*Outlying results (1)	Median ± >0.75 log ₁₀ units and in 6 th to 10 th or 90 th to 95 th percentiles
*Outlying results (2)	Median ± >0.75 log ₁₀ units and in 0 th to 5 th or 96 th to 100 th percentiles

Dealing with Censored Values (< or > Values): It is difficult to assess enumeration results when participants report censored values, so criteria is applied depending on the sample contents. The results form indicates the dilutions required to help participants obtain a definitive enumeration result, thus avoiding reporting censored values where possible.

Scoring of other Legionella results:

	Score
Examination not performed (NE)	No score allocated
<i>Legionella</i> sp. reported incorrectly as present (i.e. false positive result)	1
<i>Legionella</i> sp. reported incorrectly as not detected (i.e. false negative result)	1
Negative result reported correctly for <i>Legionella</i> sp.	12

Participants who do not return report forms or return report forms after the specified return date (late results) are allocated an HPA score of zero for all tests.

8.0 The Drinking Water Scheme:

Separate scores are allocated for the results for every enumeration requested for each sample. The results are collated to provide an overall performance assessment for each parameter over the past 12 months (six distributions, 18 samples).

		Score
Expected range	Antilog of median $\pm 0.5 \log_{10}$ units or counts within 11 th to 89 th percentiles	2
Outlying results (1)	Antilog of median $\pm >0.5 \log_{10}$ units and in 6 th to 10 th or 90 th to 95 th percentiles	1
Outlying results (2)	Antilog of median $\pm >0.5 \log_{10}$ units and in 0 th to 5 th or 96 th to 100 th percentiles	0

Participants who do not return report forms or return report forms after the specified return date (late results) are allocated an HPA score of zero for all tests.

9.0 The Recreational and Surface Water Scheme:

Separate scores are allocated for the results for each parameter including examinations for *Salmonella*. The process for providing an overall performance assessment for examinations over the past 12 months will be introduced after the scheme, in its current format, has been in operation for 12 months.

Enumerations:

		Score
Expected range	Median $\pm 0.5 \log_{10}$ units or counts within 11 th to 89 th percentiles	2
Outlying results (1)	Median $\pm >0.5 \log_{10}$ units and in 6 th to 10 th or 90 th to 95 th percentiles	1
Outlying results (2)	Median $\pm >0.5 \log_{10}$ units and in 0 th to 5 th or 96 th to 100 th percentiles	0

Salmonella examinations: Participants' results for examinations for *Salmonella* spp. are allocated scores up to a maximum of two points as follows:

Result	Score
Fully correct result	2
Result partially misleading (e.g. incorrect serotype designation)	1
Grossly misleading result (false positive or false negative result)	0

Participants who do not return report forms or return report forms after the specified return date (late results) are allocated an HPA score of zero for all tests.