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IPG

Plan

- **1)** Regulatory context
- 2) Statistical concepts and methods
- 3) QC concepts & important metrics
- 4) Practical application to molecular diagnostics



Institute for Pathology and Genetics (I.P.G.)

- Created 1958
- Located in the Brussels South BioPark in Gosselies (Biotech Hub)
- Our values:

Integrity – Equity – Respect – Communication – Professionnalism

Integrated diagnostic facility:

Pathology (>15 pathologists) Center for Human Genetics (12 clinical geneticists) Molecular Diagnostics (>20 PhDs)

- Revenues 2023: 50 Millions €
- ISO 15189:2012 accreditation BELAC 381-MED





Plan

- 1) Regulatory context
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- **3)** QC concepts & important metrics
- 4) Practical application to molecular diagnostics



Regulation and norms regarding validation

- ISO 15189: 2022
- IVD-R directive
- Practical directives for Pathology and Clinical biology
- Guidelines, reference articles
- Other regulations



ISO 15189:2022

- International norm
- ISO = International Organization for standardization
- Norm for Medical Laboratories, certainly non-specific
- Mandatory accreditation for most molecular tests in Belgium
- ISO 15189: 2022 mandatory starting Feb 2024 !



ISO 15189:2022, validation in general

7.3 Examination processes

7.3.1 General

a) The laboratory shall select and use examination methods which have been validated for their intended use to assure the clinical accuracy of the examination for patient testing.

NOTE Preferred methods are those specified in the instructions for use of in vitro diagnostic medical devices or those that have been published in established/authoritative textbooks, peer-reviewed texts, or journals, or in international and national consensus standards or guidelines, or national or regional regulations.

- b) The performance specifications for each examination method shall relate to the intended use of that examination and its impact on patient care.
- c) All procedures and supporting documentation, such as instructions, standards, manuals and reference data relevant to the laboratory activities, shall be kept up to date and be readily available to personnel (see <u>8.3</u>).
- d) Personnel shall follow established procedures and the identity of persons performing significant activities in examination processes be recorded, including POCT operators.
- e) Authorized personnel shall periodically evaluate the examination methods provided by the laboratory to ensure they are clinically appropriate for the requests received.



ISO 15189:2022, verification

7.3.2 Verification of examination methods

- a) The laboratory shall have a procedure to verify that it can properly perform examination methods before introducing into use, by ensuring that the required performance, as specified by the manufacturer or method, can be achieved.
- b) The performance specifications for the examination method confirmed during the verification process shall be those relevant to the intended use of the examination results.
- c) The laboratory shall ensure the extent of the verification of examination methods is sufficient to ensure the validity of results pertinent to clinical decision making.
- d) Personnel with the appropriate authorization and competence shall review the verification results and record whether the results meet the specified requirements.
- e) If a method is revised by the issuing body, the laboratory shall repeat verification to the extent necessary.
- f) The following records of verification shall be retained:
 - 1) performance specifications to be achieved,
 - 2) results obtained, and
 - 3) a statement of whether the performance specifications were achieved and if not, action taken.



ISO 15189:2022, validation

7.3.3 Validation of examination methods

- a) The laboratory shall validate examination methods derived from the following sources:
 - 1) laboratory designed or developed methods;
 - 2) methods used outside their originally intended scope (i.e. outside of the manufacturer's instructions for use, or original validated measurement range; third party reagents used on instruments other than intended instruments and where no validation data are available);



ISO 15189:2022, validation

- 3) validated methods subsequently modified.
- b) The validation shall be as extensive as is necessary and confirm, through the provision of objective evidence in the form of performance specifications, that the specific requirements for the intended use of the examination have been fulfilled. The laboratory shall ensure that the extent of validation of an examination method is sufficient to ensure the validity of results pertinent to clinical decision making.
- c) Personnel with the appropriate authorization and competence shall review the validation results and record whether the results meet the specified requirements.
- d) When changes are proposed to a validated examination method, the clinical impact shall be reviewed, and a decision made as to whether to implement the modified method.
- e) The following records of validation shall be retained:
 - 1) the validation procedure used;
 - 2) specific requirements for the intended use;
 - 3) determination of the performance specifications of the method;
 - 4) results obtained;
 - 5) a statement on the validity of the method, detailing its fitness for the intended use.



What is not in ISO 15189: 2022

- A specific template for validation and verification
- Statistical methods that need to be used
- The number of patients samples (classical question !), control materials, cell lines, ... that need to be run in a validation or verification file



IVD-R

- New European regulation for In Vitro Diagnostics
- Competent agency: FAGG AFMPS (additional inspections)
- IVD-R will make lab developed tests (LDT) more difficult to use



IVD-R – classification

<u>Class D</u>

High public health risk, high personal risk

Examples

- HIV 1/2,
- Hepatitis C virus
- Hepatitis B virus
- HTLV I/II
- Blood grouping ABO, Rhesus (including RHW1), Kell, Kidd and Duffy systems
- CHAGAS
- Syphilis (used to screen blood donations)

<u>Class C</u>

High personal risk, moderate to low public health risk

- Syphilis (diagnosis only)
- Neonatal screening for metabolic disorders e.g. PKU
- Rubella
- Cancer markers

Genetic tests

- Companion diagnostics
- Blood glucose meters/strips
- Blood gas analysers
- Self tests

Class B

Moderate to low personal risk, low public health risk

- Thyroid function
- Clinical chemistry
- Self-test devices listed as not Class C -> Pregnancy, Fertility, Cholesterol tests; and detection of glucose, erthrocytes, leucocytes and bacteria in urine

<u>Class A</u>

Low personal risk, low public health risk

- Accessories
- Wash buffers
- Specimen receptacles
- Instruments
- Culture media

Source BSI



IVD-R directive: timeline

26-05-2028

26-04-2024

ISO 15189 Public declaration of tests, IT In House Class C – D declaration

Respect of annex 1 Start FAGG-AFMPS inspections



Guidelines and reference articles



Figure 1 Workflow for the implementation of a NGS test

BELAC 2-405-NGS R3- 2021: guidelines for NGS validation





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What are statistics ? Why do we use statistics ?

- **Descriptive statistics** are used to characterize data
- Statistical analysis is used to distinguish between random and meaningful variations
- In the lab, we use statistics to verify method performance, interpret lab test results and assure quality of examinations procedures



Needed for validation

- Precision
- Accuracy
- Linearity measuring range limit of quantification
- Limit of detection (LOD) (analytical sensitivity)
- Analytical specificity
- Diagnostic performance (sensitivity, specificity, PPV, NPV, diagnostic efficiency)



Needed for verification

- Precision
- Accuracy
- Verification of LoD and LoQ have been frequently requested by BELAC auditors



Table 2: Performance characteristics.

	FDA/CE-IVD Peer review multicentre publications	Home brew Adapted FDA/CE-IVD Adapted peer review multicentre publications		
Precision (inter and intra run)	1 low positive sample, 1 high positive sample 3 replicates within 3 days. Preferentially from extraction.	1 low positive sample, 1 high positive sample 3 replicates within 7 days. Preferentially from extraction.		
Accuracy	3 low positive samples, 3 high positive samples, 3 negative samples. If applicable, when selecting the positive samples, the genetic diversity should be taken into account. Preferentially from extraction.	10 low positive samples, 10 high positive samples, 20 negative samples. If applicable, when selecting the positive samples, the genetic diversity should be taken into account. Preferentially from extraction.		
Linearity/ Measuring range/Limit of quantification	not necessary	Serial dilutions of min 5 log with 1 positive sample. 2 replicates in 2 runs. All log dilutions should be positive to be part of the measuring range.		
Limit of detection/analytical sensitivity	not necessary	Can be concluded from linearity/measuring range experiment, followed by 20 measurements for lowest concentration with a confidence interval of 95 % (19/20 samples are positive)		
Analytical specificity	not necessary	20 negative samples. If applicable: for microbiological tests, also analyse samples with microorganisms genetically related, unrelated but frequently detected in the same matrix, or presenting similar symptoms; for haematological tests, analyse samples from other haematological pathologies and healthy controls.		

Definitions: Low positive sample= LOQ lowest concentration; High positive sample= LOQ highest concentration

Raymaekers M et al. Acta Clin Belg 2011; 66(1):33-41



A few definitions: Precision

Closeness of agreement between independent results of measurements obtained under stipulated conditions

Repeatability

- Closeness of agreement between independent results of measurements obtained under the same operating conditions
 - Same operator
 - Same instrument
 - Same day
 - Same reagent lot
 - • •



PRECISION: example- intra-run repeatability on 13 replicates

ABL

0	n Cq	1,13 %
0	n AQ	2,11 %
On A	Q / ABL	N/A



On Cq	0,21 %
On AQ	3,38 %
On AQ / ABL	4 %







BAALC

WT1

On Cq	0,37 %
On AQ	6,31 %
On QAQ/ ABL	6,48 %

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A few definitions:

Reproducibility

- Closeness of agreement between independent results of measurements obtained under changed conditions
 - Different operator
 - Different days
 - Different reagent lots
 - ...





Accurate and precise Low CV, low bias



Not accurate, but precise Low CV, high bias



Accurate, but not precise *High CV, low bias*



Not accurate and not precise *High CV, high bias*



Statistical concepts and methods

- **1.** Type of data
- **2.** Estimation of the centrality of data
- **3.** Estimation of the variation of data
- 4. Confidence intervals
- 5. Regression
- 6. Probits
- 7. Bayesian statistics



1. Type of data:

- Quantitative data
- Categorical data
 - Nominal data
 - Ordinal data (scale data)



1. Type of data – applied to molecular tests

	Description	Examples
A	Quantitative tests. The result can have any value between two limits (including decimals).	Determination of methylation load (%); characterization of a mosaic mutation; heteroplasmy of mitochondrial variants.
в	Categorical tests where the quantitative signal is placed into an ordinal series to give the final result.	Sizing a PCR product; determination of triplet repeat size (FRAXA, Huntington disease, etc.)
с	Categorical tests where the quantitative signal is placed into one of a limited series of predefined categories to give the final result.	Determination of copy number using PCR or MLPA.: exon deletion / duplication in BRCA1; PMP22 gene dosage in CMT and HNPP;
D	Qualitative tests where the true quantitative signal can have one of many possible values, but the required result can only have one of two possible values.	Mutation scanning for unknown mutations e.g. by sequencing or high resolution melt.
Е	Qualitative [binary] tests where the true quantitative signal can only have one of two possible values	Genotyping for a specific mutation e.g. CFTR Phe508del in cystic fibrosis or HFE Cys282Tyr in hemochromatosis.

2. Estimation of centrality of data:

- Mean(s)
- Mode
- Midrange
- Median



2. Estimation of the centrality of a dataset

• Arithmetical Mean

$$\overline{x} = \frac{1}{N} \sum_{i=1}^{N} x_i$$

Arithmetical mean use the sum of the values



2. Estimation of the centrality of a dataset

Geometrical mean

$$\overline{x}_g = \sqrt[N]{x_1 \cdot x_2 \cdot x_3 \cdots x_N} = \sqrt[N]{\prod_{i=1}^N x_i}$$

Geometrical mean use the product of the values



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2. Estimation of the centrality of a dataset

Harmonic mean



Harmonic mean is appropriate to estimate the average of rates



2. Estimation of the centrality of a dataset

Other means:

Root square mean

$$\overline{x}_{rms} = \sqrt{\frac{x_1^2 + x_2^2 + x_3^2 + \dots + x_N^2}{N}} = \sqrt{\frac{1}{N} \sum_{i=1}^N x_i^2}$$

• Weighted mean

$$x_w = \frac{\sum_{i=1}^N x_i \cdot w_i}{\sum_{i=1}^N w_i}$$



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2. Estimation of the centrality of a dataset- other than mean(s)

Mode:

• Mode is the value that occurs the most often

Midrange:

• Midrange is the mean of the highest and lowest values



Median

The median is the value for which half of the remaining values are above and half are below it.

- In an ordered array of 15 values, the 8th value is the median.
- If the array has 16 values, the median is the mean of the 8th and 9th values



2. Estimation of the centrality of a dataset

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- 3. Estimation of variability
 - Variance
 - SD
 - CV (RSD)


- **3. Estimation of variability**
 - Two sets of data may have similar means, but otherwise be very dissimilar
 - What is the Variance ?
 - "Variance is the mean of the squared differences between single data points and the mean of the array"
 - Variance has no units



- 3. Estimation of variability
 - Expression of variability= Variance

$$V = \frac{1}{N} \sum_{i=1}^{N} (x_i - \bar{x})^2$$



- 3. Estimation of variability
 - Standard deviation (SD or sigma)

$$\boldsymbol{\sigma} = \sqrt{V} = \sqrt{\frac{1}{N} \sum_{i=1}^{N} (x_i - \overline{x})^2}$$



- 3. Estimation of variability
 - Standard deviation (SD or sigma)
 - SD is the square root of the variance
 - SD has also no units



- **3. Estimation of variability**
 - Coefficient of variation (CV)
 - CV is the expression, in percentage, of the division of the standard deviation by the mean
 - Sometimes called the relative standard deviation (RSD)



- 3. Estimation of variability
 - Coefficient of variation (CV)

$$CV = \frac{\sigma}{x} \cdot 100$$



4. Confidence intervals

- A confidence interval is a margin of error that indicates how precise an estimate is
- Generally, 95 % confidence intervals are used
- We can define 95 % CI for means, proportions, and other estimates



- 4. Confidence intervals- for a mean
 - To compute CI for a mean, we need first to compute the standard error (SE) of the mean
 - SE of the mean = SD/ \sqrt{n}
 - As n increases, SE decreases and the precision is greater



- 4. Confidence intervals- for a mean
 - 95 % CI for a mean:

from – 1,96 x SE (mean) *to* + 1,96 x SE (mean)

- 95 % CIs are the most used
- For 90 % CI, use 1,64 instead of 1,96
- For 99 % Cl, use 2,58



5. Regression

- Will be useful for:
 - Evaluation of linearity
 - Estimation of the limit of quantification



5. Regression

 Linear regression analysis is a function that will generate an equation for a straight line: y = ax + b

Where *a* is the slope of the line and *b* is the value of *y* when *x*= 0 (the *y*-intercept).

• The equation will give the expected value of y for each value of x



Correlation versus linear regression

- Correlation using Pearson's correlation coefficient investigates the strength of a linear relationship between two continuous variables;
- It will give a correlation coefficient, noted r, and a p-value



Correlation versus linear regression

- Linear regression investigates the nature of the linear relationship between two continuous variables;
- It will give an equation in the form of y = ax + b



What is a P-value ?

- A P-value is a probability
- A P-value can take any value between 0 and 1
- P-value is the probability, given that the null hypothesis is true, of obtaining data as extreme or more extreme than the one that is observed
- Many statistical tests will give a P-value



Null hypothesis

Null hypothesis: there is no difference between two comparison groups

Interpretation of P-values

- P values < 0,05 are generally considered significant;
- P values > 0,05 are generally considered non significant.



Other important general statistical concept one tailed and two-tailed tests

- = an option in many statistical tests
- *Two-tailed* or *two-sided* tests:
 - to be used when we cannot predict the direction of the difference between comparison groups
 - To be used in most of the cases
- One sided test:
 - to be used when we can predict the direction of the difference



Linearity

• Example of linearity evaluation





6. Probits

- **Probits = probability units**
- Interesting statistical concept to estimate Limit Of Detection (LOD) at a little cost



LOD: methodology A

- Serial dilutions from a reference material (WHO or other)
- Estimation base on hit rate (proportion of positives)
 - 20 replicates located close to the estimated LOD
 - The dilution being tested 19 times positive on 20 is the LOD
 - Problem: Hard and costly



LOD: methodology B

• Estimation based on Probits (Probability units)



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6. Probits

- Probits : "Probability units"
- Probit= Regression model
- Useful to estimate LOD when method gives a binomial answer
 - Binomial= detected or not detected
- Useful when the number of replicates is low
- Less costly



6. Probits

- Make serial dilutions
- Test these dilutions several times (from 3 to 8 to...)
- Calculate hit rate per dilution
- "Hit rate" = H_i= Npos_i/Ntot_i
- Put the data on a graph: positivity on Y and concentration on X



Probit approach uses IDF mathematical model :

Inverse Cumulative Distribution function

Probit





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LOD/ Probit



Abbreviation: LoD, limit of detection.

Figure 3. Probit Analysis. These plots illustrate hypothetical experimental results (left hand plot) and regression analysis to determine the LoD for a molecular measurement procedure by the probit approach (right hand plot).

CLSI EP17-A2 reference document



LOD/Probit

- Probit analysis transforms the concentration/response curve into a straight line
- Probit= computed with statistical softwares (XLSTAT,...)





PG

LOD/Probit examples

Three HBV Viral Load Assay Formats

TABLE 1 Limits of detection									
	CAP/CTM			HP			TNAI		
IU/ml	No. detected	No. not detected	% Detected	No. detected	No. not detected	% Detected	No. detected	No. not detected	% Detected
0	0	14	0	0	14	0	0	14	0
2.5	8	6	57	10	3	77	11	3	79
5	10	4	71	13	1	93	14	0	100
10	13	1	93	14	0	100	14	0	100
15	14	0	100	14	0	100	14	0	100
20	14	0	100	14	0	100	14	0	100
25	14	0	100	13	0	100	14	0	100

TABLE 1 Limits of detection^a

^a Probit results (95% confidence interval) were as follows: CAP/CTM, 10.2 IU/ml (6.8 to 27.8); HP and TNAI, not available.

The limits of detection of the assays were evaluated using dilutions of the WHO standard material as shown in Table 1. Probit analysis predicts a limit of detection of 10.2 IU/ml (95% confidence interval = 6.8 to 27.8 IU/ml) for CAP/CTM. The same concentrations of diluted standard had inadequate resolution for probit analysis for HP and TNAI. However, 100% of the samples were detected at \geq 10 IU//ml in the HP assay, and 100% of the samples were detected at \geq 5 IU/ml in the TNAI assay.



- **7. Bayesian statistics**
 - Evaluation of the diagnostic accuracy
 - Based on the exploitation of a contingency table



Evaluation of the clinical performance of a test

- The *sensitivity* of a test indicates the likelihood that the test will be positive when disease is present
- The *specificity* of a test indicates the likelihood that the test will be negative when disease is absent
- The *predictive value* of a test indicates the probability that the test result correctly classifies a patient



Diagnostic sensitivity and specificity= Bayesian statistics

	Gold Sta		
	Disease present Disease absent		
Positive test	True Positive (TP)	False Positive (FP)	TP + FP
NegativeFalse Negative (FN)test		True Negative (TN)	FN + TN
	TP + FN	FP + TN	



Bayesian statistics: sensitivity

	Gold Sta		
	Disease present	Disease absent	
Positive test	True Positive (TP)	False Positive (FP)	TP + FP
Negative test	False Negative (FN)	True Negative (TN)	FN + TN
	TP + FN	FP + TN	

Sensitivity= sick patients who show a positive test

Sensitivity= TP/ (TP+FN)

Bayesian statistics: Specificity

	Gold St		
	Disease present Disease absent		
Positive test	True Positive (TP)	False Positive (FP)	TP + FP
Negative test	False Negative (FN)	True Negative (TN)	FN + TN
	TP + FN	FP + TN	

Specificity= healthy people that show a negative test

Specificity = TN/ (FP+TN)



Bayesian statistics: Positive Predictive Value (PPV)

	Gold St		
	Disease present	Disease absent	
Positive test	True Positive (TP)	False Positive (FP)	TP + FP
Negative test	False Negative (FN)	True Negative (TN)	FN + TN
	TP + FN	FP + TN	

PPV= If the test is positive, what is the chance for the patient to have the disease ?

PPV = TP/TP+FP

Bayesian statistics: Negative Predictive Value (NPV)

	Gold St		
	Disease present Disease absent		
Positive test	True Positive (TP)	False Positive (FP)	TP + FP
Negative test	False Negative (FN)	True Negative (TN)	FN + TN
	TP + FN	FP + TN	

NPV= If the test is negative, what is the chance for the patient to really not have the disease?

NPV = TN/FN+TN

Bayesian statistics: Diagnostic accuracy

Diagnostic accuracy = the percentage of patients that are correctly categorized by the test

DA= (TP+TN) / (TP+FP+FN+TN)



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Bayesian statistics example: NGS validation

Conventional Methods Result					
Gene	Mutation/Fusion Detected	Not Detected	Parameter	Agreement	
EGFR-NGS Result					
Mutation Detected	13	0	PPA	92.9%	
Not Detected	1	86	NPA	100%	
			OA	99.0%	
KRAS-NGS Result					
Mutation Detected	74	5	PPA	97.4%	
Not Detected	2	50	NPA	90.9%	
			OA	94.7%	
NRAS-NGS Result					
Mutation Detected	3	0	PPA	100%	
Not Detected	0	54	NPA	100%	
			OA	100%	
BRAF-NGS Result					
Mutation Detected	9	2	PPA	100%	
Not Detected	0	45	NPA	95.8%	
			OA	96.4%	
ALK Fusions-NGS Result					
Fusion Detected	4	1	PPA	100%	
Not Detected	0	95	NPA	99.0%	
			OA	99.0%	
ROS1 Fusions-NGS Result					
Fusion Detected	1	0	PPA	100%	
Not Detected	0	99	NPA	100%	
			OA	100%	

Table 1. Comparison of NGS results with conventional methods.

NGS—Next Generation Sequencing; PPA—Positive percent agreement; NPA—Negative percent agreement; OA—Overall agreement.



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2. Statistical concepts and methods

Statistical packages

- Statistical packages are softwares that allow to compute statistical tests in a very fast way
- These include SAS, SPSS and Stata; they may be expensive, but there are student licences (for students)
- There are also add-ons for Microsoft Excel, such as XIstat and Analyze – IT



Statistical methods in validation reports and QC

Plan

- **1)** Regulatory context
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QC concepts

- Statistical Quality Control (QC) has long been used in clinical laboratories (clinical chemistry, immunoassays, ...)
- Theory is dating from 1970's- 1980's (seminal papers from JO Westgard)
- A "lifting" was applied to these concepts in 2005 with the publication of JO Westgard book "Six Sigma- quality control and design"



QC concepts

- In 2022, statistical QC (statistical treatment of QC data) is not a common practice in molecular diagnostics
- When applied, molecular statistical QC is sometimes limited to a Levey-Jennings graph with +-3 Cq limits !



QC concepts: Ped and Pfr

Ped= probability of a QC rule to detect significant errors

Goal for a statistical QC procedure: *Ped>0,9 or > 90 %*

•Pfr= probability of falsely rejecting results when there is no significant out-of-control condition

Goal for a statistical QC procedure: *Pfr<0,05 or <5 %*



QC rules (Westgard rules)



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QC rules (Westgard rules)





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QC charts (Levey Jennings charts)

Plot of Cq value of positive control (CT and NG)





QC charts (Levey Jennings charts) Violation of QC rules (CT/NG)



PG

- Traditional QC principles *are applicable* to molecular diagnostics:
- Minimal condition is to have a continuous numerical value:
 - Cq value
 - Copies number
 - An independent QC (from DNA extraction) is preferabl



Statistical methods in validation reports and QC

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qPCR: example of a verification file

Œ	Qualité des résultats	IPG-VAL-347
T I P G	SARS-CoV-2- Perkin Elmer	Version nº: 001

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qPCR verification: repeatability

1. Répétabilité (+ calcul d'incertitude de mesure si justifié)

Fidélité mesurée aves des résultats d'essai indépendants obtenus par la même méthode, sur les mêmes échantillons, dans le même laboratoire, avec le même opérateur et les mêmes équipements utilisés en même temps ou durant une courte période de temps.

Objectif. Concordance des résultats intra-run.

Méthodologie et échantillons. 2 échantillons positifs pour SARS-CoV-2 et un échantillon négatif pour SARS-CoV-2 ont été analysés en triplicat au cours d'un même run d'extraction sur Chemagic (30M035) et de RT-PCR sur LightCycler (30M543). (20210107 BV RUN2 21GM000806)

Résultats.

FAM	21GM000467	21GM0005178	21GM00052		
Cq 1	22,61	15,83	Négatif		
Cq2	22,37	17,06	Négatif		
Cq3	22,07	16,39	Négatif		
Moyenne	22,35	16,42666667	/		
Ecart Type	0,270554985	0,615819238	/		
cv	0,012105368	0,037488996	1		

HEX	21GM000467	21GM0005178	21GM0005202
Cq 1	21,11	14,73	Négatif
Cq2	21,16	15,90	Négatif
Cq3	22,53	14,80	Négatif
Moyenne	21,6	15,14333333	1
Ecart Type	0,805791536	0,656226587	1
cv	0,037305164	0,043334355	1

Cys	21GM000467	21GM0005178	21GM0005202	
Cq 1	22,72	21,21	28,65	
Cq2	22,60	21,57	29,00	
Cq3	22,45	20,64	28,35	
Moyenne	Moyenne 22,59		28,66666667	
Ecart Type	0,135277493	0,468934964	0,325320355	
cv	0,005988379	0,022182354	0,011348384	



qPCR verification: reproductibility

Méthodologie et échantillons. 6 échantillons positifs pour SARS-CoV-2 et 3 échantillons négatifs pour SARS-CoV ont été analysés en simplicat au cours d'un run extraction Chemagic et 3 runs de RT-PCR : jour, TL, LightCycler480 différents.

Résultats.

FAM	21GM000408	21GM000281	21GM000443	21GM000282	21GM000394	21GM000407	21GM000508	21GM000509	21GM000510
Jour 1	16,55	15,46	19,67	28,37	27,67	28,77	Négatif	Négatif	Négatif
Jour 2	16,56	15,06	19,84	28,57	27,90	28,73	Négatif	Négatif	Négatif
Jour 3	16,08	14,96	19,60	28,41	27,93	28,16	Négatif	Négatif	Négatif
Moyenne	16,39666667	15,16	19,70333333	28,45	27,83333333	28,55333333	/	/	/
Ecart Type	0,274286954	0,264575131	0,123423391	0,105830052	0,142243922	0,34122329	/	/	/
cv	0,016728214	0,017452185	0,006264087	0,003719861	0,00511056	0,011950384	/	/	

HEX	21GM000408	21GM000281	21GM000443	21GM000282	21GM000394	21GM000407	21GM000508	21GM000509	21GM000510
Jour 1	16,25	14,97	20,27	27,97	26,36	29,24	Négatif	Négatif	Négatif
Jour 2	16,25	14,01	19,87	27,99	26,32	28,79	Négatif	Négatif	Négatif
Jour 3	16,12	14	19,95	27,97	26,48	28,27	Négatif	Négatif	Négatif
Moyenne	16,20565667	14,32666667	20,03	27,97666667	26,38666667	28,76666667	/	1	/
Ecart Type	0,075055535	0,557165445	0,211660105	0,011547005	0,08326664	0,48542078	1	1	/
cv	0,004631152	0,038890096	0,010567155	0,000412737	0,003155633	0,016874419	/	/	

Cy5	21GM000408	21GM000281	21GM000443	21GM000282	21GM000394	21GM000407	21GM000508	21GM000509	21GM000510
Jour 1	22,83	25,28	23,78	22,67	24,58	25,01	21,68	25,66	26,39
Jour 2	22,99	24,89	23,8	22,96	25,54	24,96	21,54	28,19	27,89
Jour 3	22,74	24,57	23,51	22,82	25,2	24,61	19,06	25,62	27,68
Moyenne	22,85333333	24,91333333	23,69666667	22,81666667	25,10666667	24,86	20,76	26,49	27,32
Ecart Type	0,126622799	0,355574652	0,161967075	0,145028733	0,486757982	0,217944947	1,473906374	1,472379027	0,812219182
cv	0,005540671	0,014272464	0,006835015	0,006356263	0,019387599	0,008766892	0,070997417	0,055582447	0,029729838

Conclusion. 100% de concordance dans les résultats inter-run.



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qPCR verification: accuracy

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3. Justesse / exactitude (+ calcul d'incertitude de mesure si justifié)

Est mesurée par le biais entre la moyenne d'un nombre infini de valeurs mesurées répétées et la valeur de référence (µ).

Biais = moyenne des résultats (M) - valeur de référence (µ)

Exactitude (erreur totale) = Justesse (erreur systématique) + fidélité (Erreur aléatoire)

Objectif. Confirmation de la présence de SARS-CoV-2 via un QC externe QCMD.

Méthodologie et échantillons. 15 QC SARS-CoV-2 ont été extraits et analysés. Les résultats ont été envoyés à l'organisme organisateur.

Biais + Ecart-Type



qPCR verification: accuracy

Individual QCMD 2020 SARS-CoV-2 EQA Programme				QA		
Catalogue Code:	Ref Code:	Challenge:	Analysis Type:	Dataset:	Report UID: 1197/401539/3130	Laboratory
QAV204215	SCV2_20	C2	Qualitative	401539		BE034

Core Panel Members Results

Sample Code	Qualitative Results		Your Quantitative Data (for Information only) [3]			
	Percentage Correct (AII) [4]	Your Result	Detection Score	Reported Value	Unitage	Cycle Threshold
SCV2_101C2-01	97.8	Negative	0		N/A	a
SCV2_101C2-02	98.7	Positive			N/A	32.79
SCV2_101C2-03	93.1	Positive	٠		N/A	35.98
SCV2_101C2-04	93.6	Positive	۵		N/A	35.65
SCV2_101C2-05	99.1	Negative	0		N/A	



qPCR verification: linearity

N ^{bre}	log	CalEAM	Caller
Copies	LUE	cqrAin	cqnex
5,37E+07	7,73	16,91	14,96
5,37E+06	6,73	20,63	18,91
5,37E+05	5,73	23,46	21,7
5,37E+04	4,73	27,51	25,33
5,37E+03	3,73	30,26	28,17
5,37E+02	2,73	32,95	30,85
5,37E+01	1,73	36,06	33,79
5,37E+00	0,73		







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qPCR verification: linearity





Statistical methods in validation reports and QC

Important messages

- Impact of IVD-R and new ISO 15189:2022 version
- Validation vs Verification
- Statistics are important for validation/verification
- Statistical QC can be applied to molecular diagnostics



Thanks for your participation !

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Thanks for your attention !

HIM

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Statistical methods in validation reports and QC

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