

Module 1

Taking epidemiology into account – what to sequence and how much?

SEQAFRICA



15 February 2021 (10:30 – 11:00)

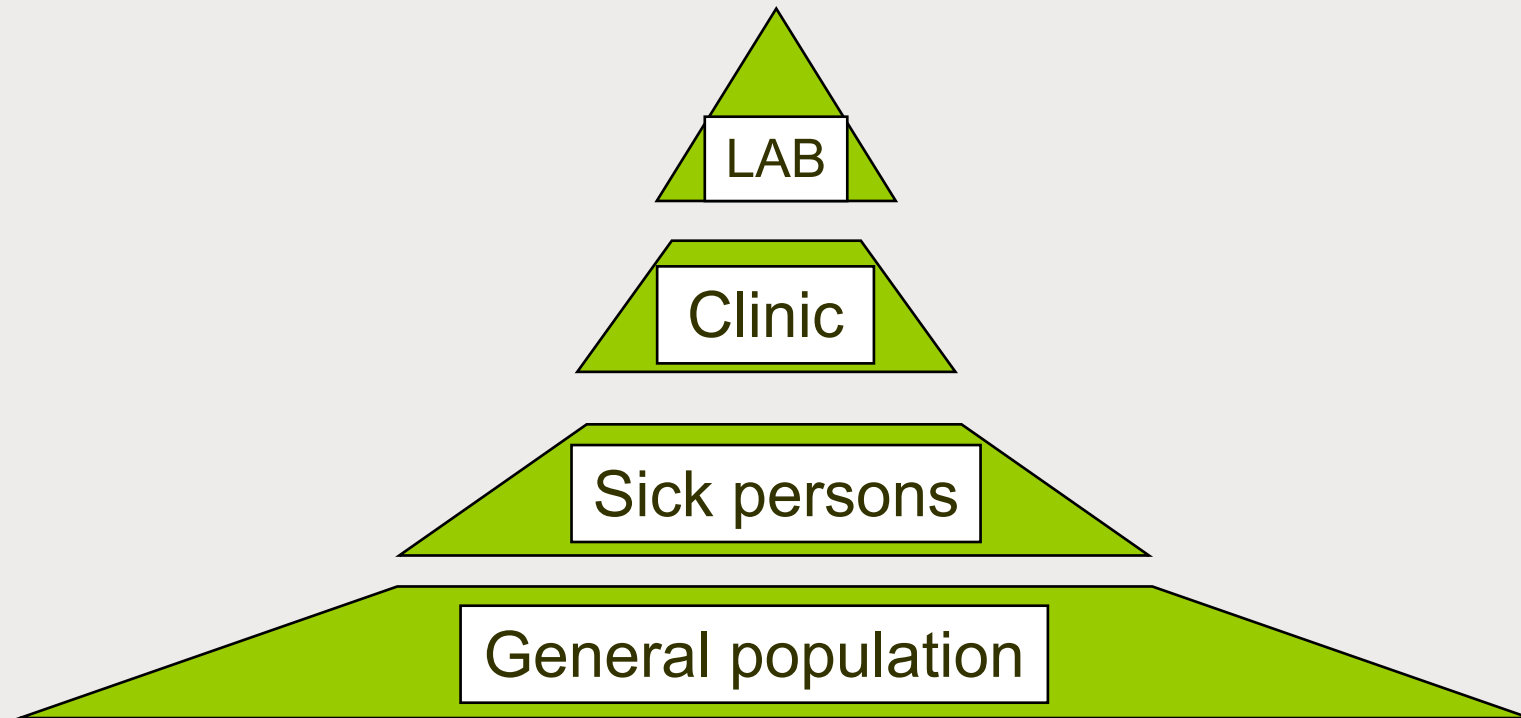
Dr. Alessandro Foddai (DVM, MSc, PhD, epidemiologist)

Aim of the lecture

- **Basic sampling design** to test stored specimens, while **keeping track of the main limitations**
- **Estimate confidence in absence or eventual prevalence** of pathogen **AMR “P1”** in a “population” of lab stored **specimens “Np”**

General principle behind the lecture....

NUMERATOR DATA (cases) pros and cons



What to test and how much?

- **Not always possible** to use the **most sophisticated test** on big populations. Consider:
 - Testing capacity
 - Feasibility
 - Logistics
 - Limitations

Test/s performance:

- **Sensitivity (Se):** % of “truly positive” units correctly identified pos
- **Specificity (Sp):** % of “truly negative” units correctly identified neg

Testing strategy:

Parallel testing to increase sensitivity (but can ↑ false +ves)

Serial testing to increase specificity (but can ↑ false -ves)

Surveillance type combines:

Objective, way of sampling, test performance, testing strategy e.g:

- **Passive surveillance**
 - Observer/patient initiated, could be part of early warning or monitoring
- **Active surveillance**
 - specific questions about a defined disease/pathogen
 - investigator initiated and defined

The context of the lecture

- **Samples collected from passive surveillance** available at the labs
- **Investigating** some of them with special test (e.g WGS for AMR)
- **WGS on all available samples** could be **time consuming and expensive**
- **Results and limitations of the study** are both important....

Practical example of the lecture for a basic protocol

Background

- Authorities of country “C” know that pathogen “P” is endemic
- Wondering if AMR subtype “P1” is present in a region
- 3/100 “P1” cases (travel related) detected in a previous study
- This is our “Prior” knowledge available (before our study is made)

Example context

- **Authorities do not exclude a random survey later on** in the resident population
- But before.. a **pilot study** is commissioned for addressing two research questions (“a” and “b”), **using samples** already available (**≈ 3000 specimens stored at regional lab**).

Example context

- **Specimens uniquely indentified** e.g. by: patient passport, name, etc
- Suppose the **WGS** used to detect P1 has **Se 98%** and **Sp 100%**

Research questions from authorities

- a) Is P1 absent? Confidence in freedom?
- b) If P1 is present, what is the prevalence?

Aim

From all available specimens we would like to test “enough” for:

Detecting P1 with 95% confidence IF PRESENT in the population of stored specimens, at the expected prior design prevalence 3%

IF NOT FOUND → reach confidence in freedom $P_{Free} \geq 95\%$

IF DETECTED → estimate its “true” prevalence TP with 95% confidence and precision 2%, considering “prior” prevalence 3%

How many to test randomly between those stored?

Two steps:

- 1) Calculate sample sizes "n1" and "n2" to address "a" and "b"
- 2) **Randomize** list of stored specimens from which sampling "n1" & "n2"

1) Calculate "n1" to estimate "PFree"

<https://epitools.ausvet.com.au/freedomssthree>

1-Stage Freedom analysis

Sample size required to achieve target confidence of freedom

Test (or cluster) sensitivity	<input type="text" value="0.98"/>
Prior confidence of freedom	<input type="text" value="0.5"/>
Probability of introduction during period	<input type="text" value="0.00"/>
Required confidence of freedom	<input type="text" value="0.95"/>
Population size (leave blank or 0 if not known)	<input type="text" value="3000"/>
Design prevalence (proportion or units)	<input type="text" value="0.03"/>

Submit

1) Calculated "n1"

Results

Adjusted prior	0.5
Population sensitivity required	0.947
Sample size required	99 units

1) Calculate "n2" to estimate "TP"

<https://epitools.ausvet.com.au/prevalences>

Estimating prevalence

Results pending ■■■

Sample size to estimate a true prevalence with an imperfect test

Assumed true prevalence

Assumed sensitivity)

Assumed specificity)

Desired precision

Confidence level

Submit

1) Calculated "n2"

<https://epitools.ausvet.com.au/prevalences>

Results

Sample size required for specified inputs

Sample size	286
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Sample sizes for varying prevalence and precision values

Samples sizes required for sensitivity = 0.98, specificity = 1 and a range of true prevalence and precision values are shown below:

	TP = 0.01	TP = 0.02	TP = 0.05	TP = 0.1	TP = 0.2	TP = 0.5
Precision = 0.01	389	769	1864	3536	6304	9996
Precision = 0.02	98	193	466	884	1576	2499
Precision = 0.05	16	31	75	142	253	400
Precision = 0.1	4	8	19	36	64	100
Precision = 0.2	1	2	5	9	16	25

2) Randomize list of all stored specimens

Can be made in different programs: excel, R, SAS etc.

e.g. in excel: <https://www.youtube.com/watch?v=CxSwNyVT1C8>

Test the first 286 of the **randomized list**, for both aims (“a” and “b”)

Discussion on advantages

The obtained PFree or TP will be corrected for:

1. The error of the test (Se e Sp)
2. The **assumptions** on PriorTP or PriorPFree
3. The **sample size**
4. The **number of stored specimens**

PFree and/or TP become **MORE** comparable between laboratories

Discussion on assumptions and limitations

- Calculation of **n2 assumed** $n2/Np < 10\%$
- The **surveillance unit** was at **individual level**
- **PriorPFree** set at **50%** conservatively → large n1
- **Initial passive collection bias of the 3,000 specimens/lab** remains

Discussion on limitations

- The example **is a basic approach**
- **Improvements possible** (e.g stratified random sampling for age cat.)
- **If 2 tests (1 & 2)** serially on each chosen unit, consider **serial Se & Sp**

Appendix: for two tests in series or parallel

<https://epitools.ausvet.com.au/twoteststwo>

Diagnostic test evaluation and comparison

Sensitivity and specificity of two tests used in parallel or series

Test sensitivities and specificities

Test Number	Test Name	Sensitivity (Se)	Specificity (Sp)
1	<input type="text" value="Test1"/>	<input type="text" value="0.80"/>	<input type="text" value="1"/>
2	<input type="text" value="Test2"/>	<input type="text" value="0.98"/>	<input type="text" value="1"/>

Submit

Appendix: for two tests in series or parallel

Sensitivity and specificity for two tests interpreted in parallel or series


Analysed: Tue Feb 09, 2021 @ 11:37 UTC

Results

The table below summarises the sensitivities and specificities of two tests used in parallel or series. These results assume that the two tests are independent, conditional on disease status.

	Test1	Test2	Series	Parallel
Sensitivity	0.8	0.98	0.784	0.996
Specificity	1	1	1	1

Example references:



Contents lists available at [ScienceDirect](#)

One Health

journal homepage: www.elsevier.com/locate/oneht

Editorial Commentary

Surveillance to improve evidence for community control decisions during the COVID-19 pandemic – Opening the animal epidemic toolbox for Public Health

Alessandro Foddai^{a,*}, Ann Lindberg^b, Juan Lubroth^{c,1},
Johanne Ellis-Iversen^{a,*}



Contents lists available at [ScienceDirect](#)

One Health

journal homepage: www.elsevier.com/locate/oneht

Base protocol for real time active random surveillance of coronavirus disease (COVID-19) – Adapting veterinary methodology to public health

Alessandro Foddai^{a,*}, Juan Lubroth^b, Johanne Ellis-Iversen^a

Example references:



Available online at www.sciencedirect.com



Preventive Veterinary Medicine 79 (2007) 71–97

www.elsevier.com/locate/prevetmed

**PREVENTIVE
VETERINARY
MEDICINE**

Demonstrating freedom from disease using
multiple complex data sources
1: A new methodology based
on scenario trees

P.A.J. Martin ^{a,c,*}, A.R. Cameron ^{b,c}, M. Greiner ^{c,1}



ELSEVIER

Available online at www.sciencedirect.com



Preventive Veterinary Medicine 79 (2007) 98–115


www.elsevier.com/locate/prevetmed

**PREVENTIVE
VETERINARY
MEDICINE**

Demonstrating freedom from disease using
multiple complex data sources
2: Case study—Classical swine fever in Denmark

P.A.J. Martin ^{a,e,*}, A.R. Cameron ^{c,e}, K. Barfod ^{b,1},
E.S.G. Sergeant ^d, M. Greiner ^{e,2}

Example references:



Corrected: Author correction

ARTICLE

DOI: [10.1038/s41467-018-06657-5](https://doi.org/10.1038/s41467-018-06657-5) OPEN



Substantiating freedom from parasitic infection by combining transmission model predictions with disease surveys

Edwin Michael¹, Morgan E. Smith¹, Moses N. Katarawa², Edson Byamukama³, Emily Griswold², Peace Habomugisha³, Thomson Lakwo⁴, Edridah Tukahebwa⁴, Emmanuel S. Miri⁵, Abel Eigege⁵, Evelyn Ngige⁶, Thomas R. Unnasch⁷ & Frank O. Richards²

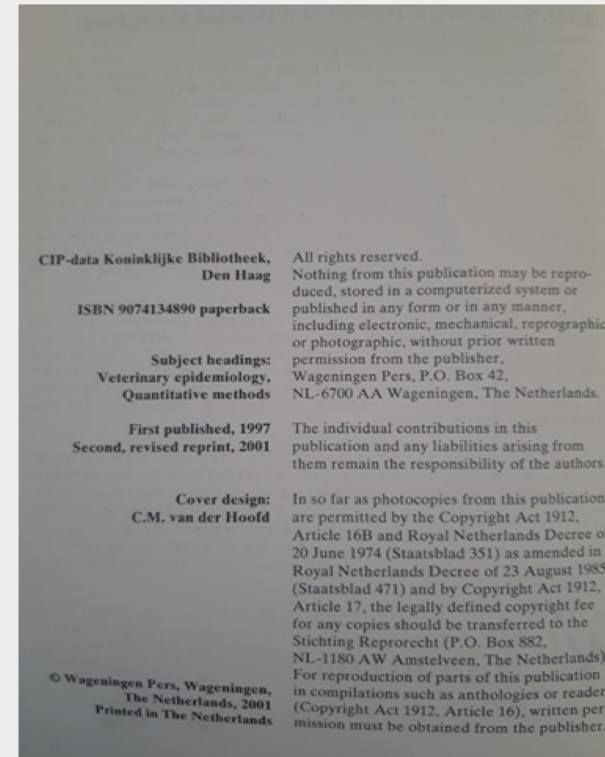
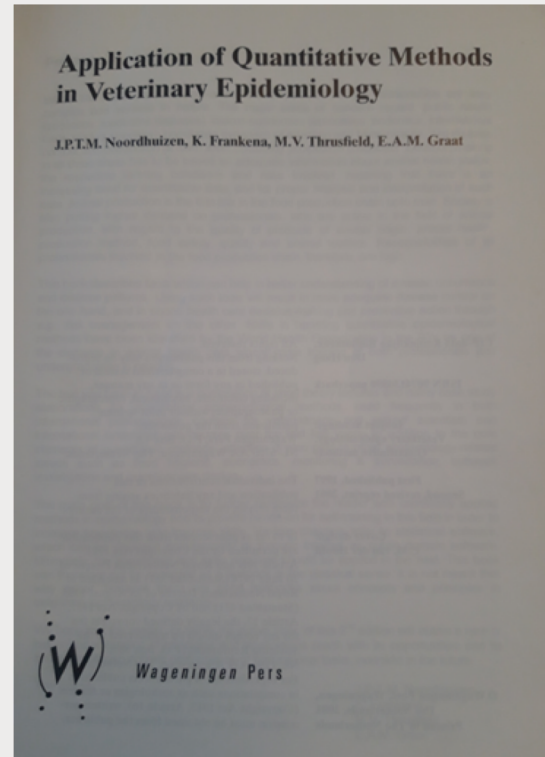
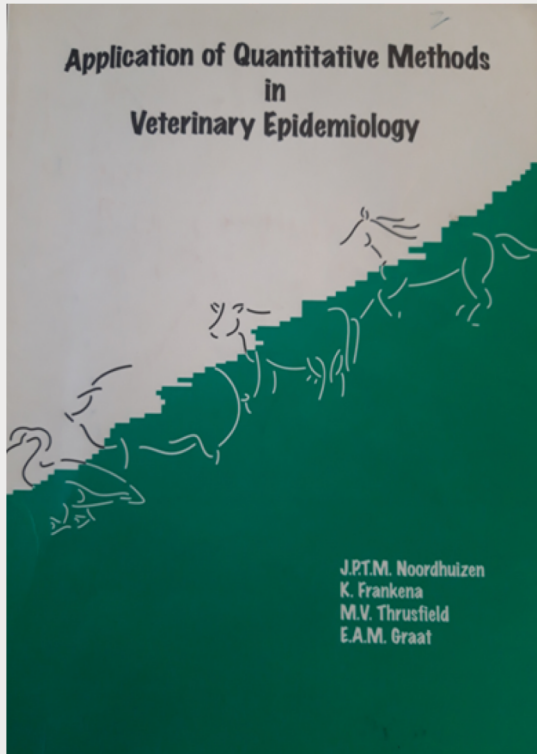
Global HIV Strategic Information Working Group

Biobehavioural Survey Guidelines

For Populations At Risk For HIV



Example references:



Useful links

- <https://epitools.ausvet.com.au/freedomssthree>
- <https://epitools.ausvet.com.au/prevalencess>
- <https://epitools.ausvet.com.au/twoteststwo>
- <https://epitools.ausvet.com.au/>
- <https://www.who.int/ncds/surveillance/steps/resources/EpiInfo/en/>
- <https://www.surveysystem.com/sscalc.htm>
- <https://epitools.fp7-risk-sur.eu/tools/index?toolId=46>

Thank you



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This programme is being funded by the UK Department of Health and Social Care.
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