

Pubblicare un articolo scientifico

Struttura dell'articolo secondo il formato IMRAD: focus su materiali e metodi, risultati, conclusioni



Roma, 23/11/21



Roberto Condoleo – IZSLT
Osservatorio Epidemiologico



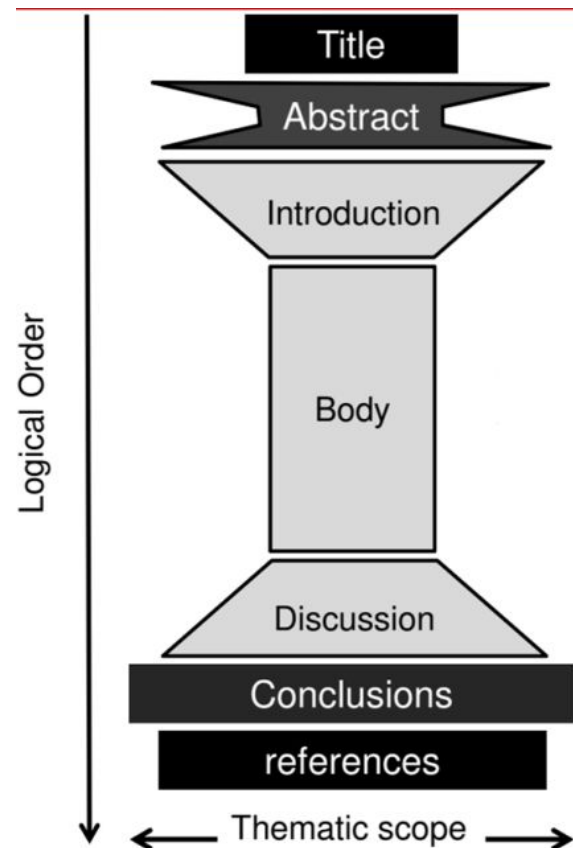


Istituto Zooprofilattico Sperimentale
del Lazio e della Toscana *M. Aleandri*

Agenda



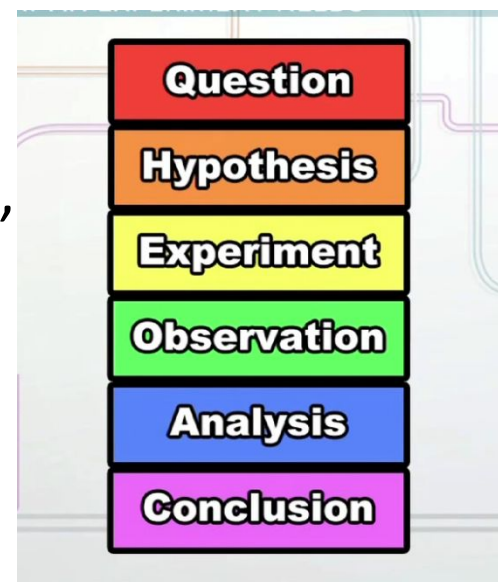
- Before we start...
- General recommendations
- Introduction
- Material and Methods
- Results
- Discussion & Conclusions
- Bibliography



Before we start...

Premise:

- We have already conducted a solid study (i.e. Original/innovative idea, strong/clear hypothesis, well-designed, reliable data sources...) *"A good manuscript starts with good Science"* Mary M. Christopher, DVM, PhD University of California-Davis
- We have done an extensive Bibliographic Review
- We have time! Writing a scientific paper is a demanding activity and it needs to be done without continuous interruptions
- We have decided the article type



Types of Articles

- Review/Mini-Review
- Original Articles (Full Articles/Short Communications)
- Clinical cases
- Opinions
- Technical Notes
- Letter to the Editor
- Point/Counterpoint



Types of Articles

- Review/Mini-Review
- **Original Articles (Full article/Short Communications)**
- Clinical cases
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- **Technical Notes**
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How do we choose a Journal?

- Quality of the research
- Topics of the journal
- Topics dealt by previous articles
- Look at your bibliography
- Bibliographic Indexes (i.e. IF)
- Open Access? (embark)
- Publication fee
- Recent Articles
- Journal Guidelines
- Revision and publication timing





Journal Citation Reports


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Select Journals 

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Journals By Rank **Categories By Rank**

All Journal Categories ranked by Number of Journals

Customize Indicators

	Category	Edition	#Journals	Total Cites	Median Impact Factor	Aggregate Impact Factor
29	COMPUTER SCIENCE, INFORMATION SYSTEMS	SCIE	156	543,628	2.468	3.297
31	LAW	SSCI	155	131,513	1.041	1.433
31	PHYSICS, APPLIED	SCIE	155	2,897,750	2.166	4.626
31	PSYCHIATRY	SCIE	155	925,489	2.500	3.640
34	BUSINESS	SSCI	152	708,481	2.509	3.534
35	SOCIOLOGY	SSCI	150	313,101	1.328	1.704
36	ENDOCRINOLOGY & METABOLISM	SCIE	143	1,085,816	3.235	4.316
36	ENGINEERING, CHEMICAL	SCIE	143	1,628,909	2.326	4.755
38	PSYCHIATRY	SSCI	142	667,994	1.941	3.206
39	VETERINARY SCIENCES	SCIE	141	357,943	1.135	1.478
40	FOOD SCIENCE & TECHNOLOGY	SCIE	139	1,051,204	2.095	3.279
40	MEDICINE, RESEARCH & EXPERIMENTAL	SCIE	139	1,041,927	3.139	3.380
42	CARDIAC & CARDIOVASCULAR	SCIE	138	1,051,808	2.375	4.361





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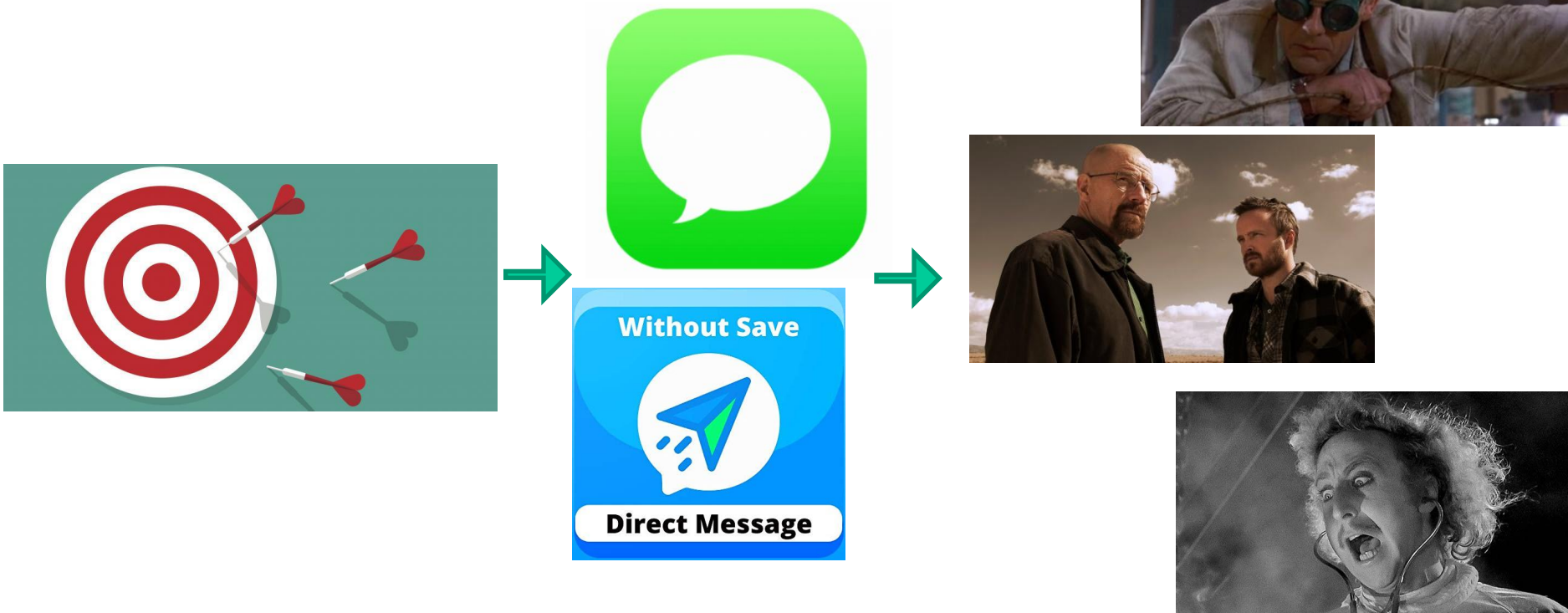
Before we start...

Journal Citation Reports

Journal Titles Ranked by Impact Factor

Compare Selected Journals		Add Journals to New or Existing List		Customize Indicators	
Select All		Full Journal Title	Total Cites	Journal Impact Factor ▼	Eigenfactor Score
<input type="checkbox"/>	1	LAB ANIMAL	732	9.600	0.00132
<input type="checkbox"/>	2	Annual Review of Animal Biosciences	955	6.091	0.00266
<input type="checkbox"/>	3	Animal Nutrition	1,214	4.492	0.00242
<input type="checkbox"/>	4	Transboundary and Emerging Diseases	4,477	4.188	0.00986
<input type="checkbox"/>	5	ANIMAL HEALTH RESEARCH REVIEWS	1,110	3.833	0.00090
<input type="checkbox"/>	6	VETERINARY RESEARCH	5,418	3.357	0.00707
<input type="checkbox"/>	7	VETERINARY MICROBIOLOGY	16,042	3.030	0.01569
<input type="checkbox"/>	8	MEDICAL MYCOLOGY	4,984	2.822	0.00540
<input type="checkbox"/>	9	EQUINE VETERINARY JOURNAL	7,200	2.477	0.00454
<input type="checkbox"/>	10	VETERINARY RECORD	9,896	2.442	0.00653

- Remember always the main goals of your study and the messages you want to deliver





Title

Firstname Lastname¹, Firstname Lastname² and Firstname Lastname^{2,*}

¹ Affiliation 1; e-mail@e-mail.com

² Affiliation 2; e-mail@e-mail.com

* Correspondence: e-mail@e-mail.com; Tel.: (optional; include country code; if there are multiple corresponding authors, add author initials) +xx-xxxx-xxx-xxxx (F.L.)

Received: date; Accepted: date; Published: date

Abstract: A single paragraph of about 200 words maximum.

Keywords: keyword 1; keyword 2; keyword 3 (List three to ten pertinent keywords specific to the article; yet reasonably common within the subject discipline.)

1. Introduction

2. Materials and Methods

2.1. *Study design Overview*

3. Results

4. Discussion

5. Conclusion

6. References

- If you can, start following the Author guidelines of the Journal or at least a generic layout





Bluetongue circulation in goats Lazio and Tuscany (Central Italy)

General recommendations

Outline the informations/
concepts / elements/
findings / reasonings you
want to include for each
section and guess a
«weight» -> logical
structure of the paper

Firstname Lastname ¹, Firstname Lastname ² and Firstname Lastname ^{2,*}

1. Introduction

- Describe briefly the Bluetongue (BT) disease
 - o Virus
 - Strains
 - characteristics
 - o competent, vectors
 - o mechanism of spread
 - o Factors of infections
- Bluetongue and goats
 - o Describe the pathogenesis
 - o Problems for farmers
 - economic loss (describe the reasons and quantify, search a paper)
 - husbandry problems (trade restrictions,
- Italian and European epidemiological situation
 - o Outbreaks in Italy (look the reference lab report)
 - o Outbreaks in Europe (look OIE reports)
- Problem: few studies regarding occurrence in goat and even less in Italy
 - o List studies for goats
 - o List Italian studies for goats
- Aim:
 - o Occurrence BT in goat in Italy
 - o Risk factor in goat
 - o Difference with ovine

2. Materials and Methods



- Share the job with the other Authors!



“You should spend the next week typing down names
of all co-authors on your paper.”



General recommendations

- Make your manuscript easy to follow for the reader! Make it attracting and catchy

“Making the simple complicated is commonplace; making the complicated simple, awesomely simple, that's creativity.” (Charles Mingus)

- Provide evidences to support your statements/concepts/facts -> you need to be objective

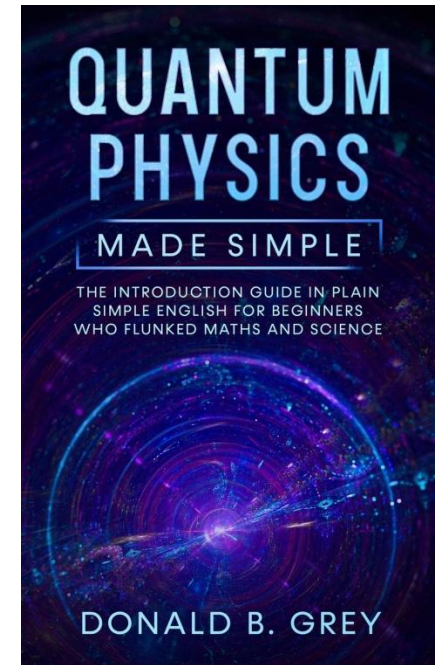




General recommendation

Some tips regarding the language

- **Use simple English!** clear form, no long and complex phrases
- **No contract forms** («It's», «We've studied»...)
- Paragraph organization is important in written English!
- Good/Clever usage of the linkers to express your concepts/thoughts («however», «anyway», «in contrast», «moreover», «as well as»...)

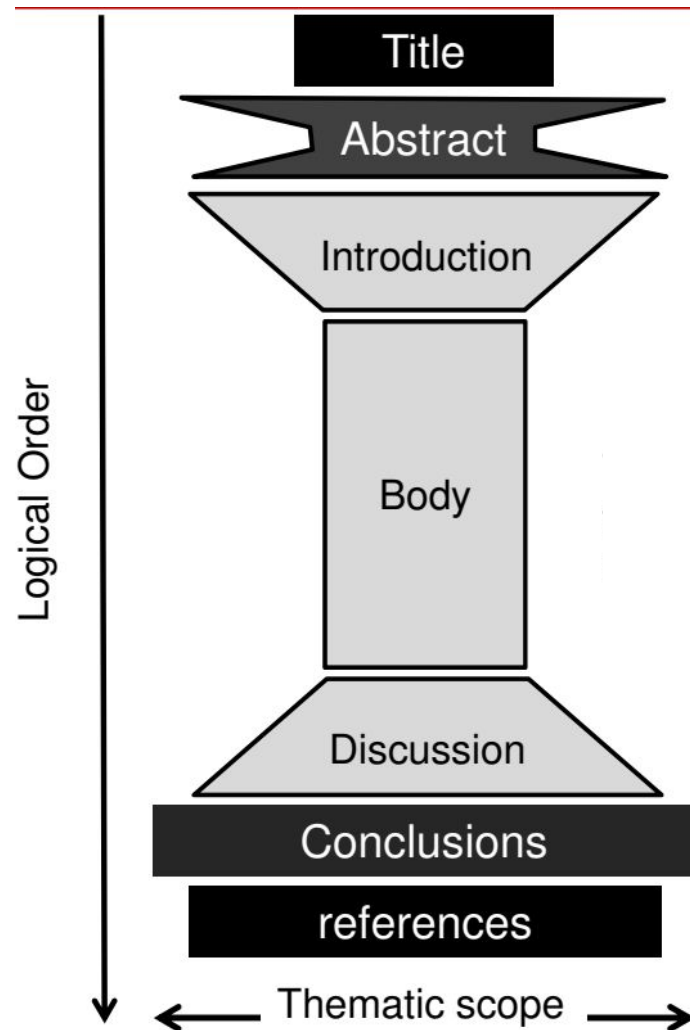


Some tips regarding the language

- Be cautious in your statements!! i.e. Strong expressions are rare because they are used for sure/certain beliefs.
 - Modal verbs are essential («might», «may», «could», «can», «must», «should», etc...)
 - Recurrent expressions in Academic English: «appear», «seems»...
- Tense use (past tense... but not only!)
- Be sure that your manuscript is revised by a mother language or proficient English Speaker before the submission

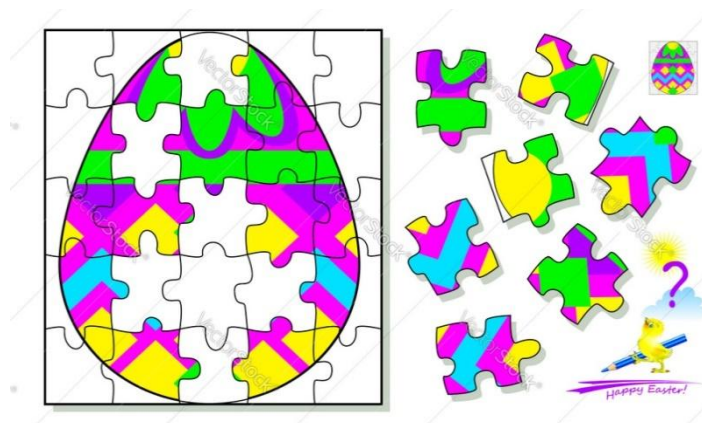
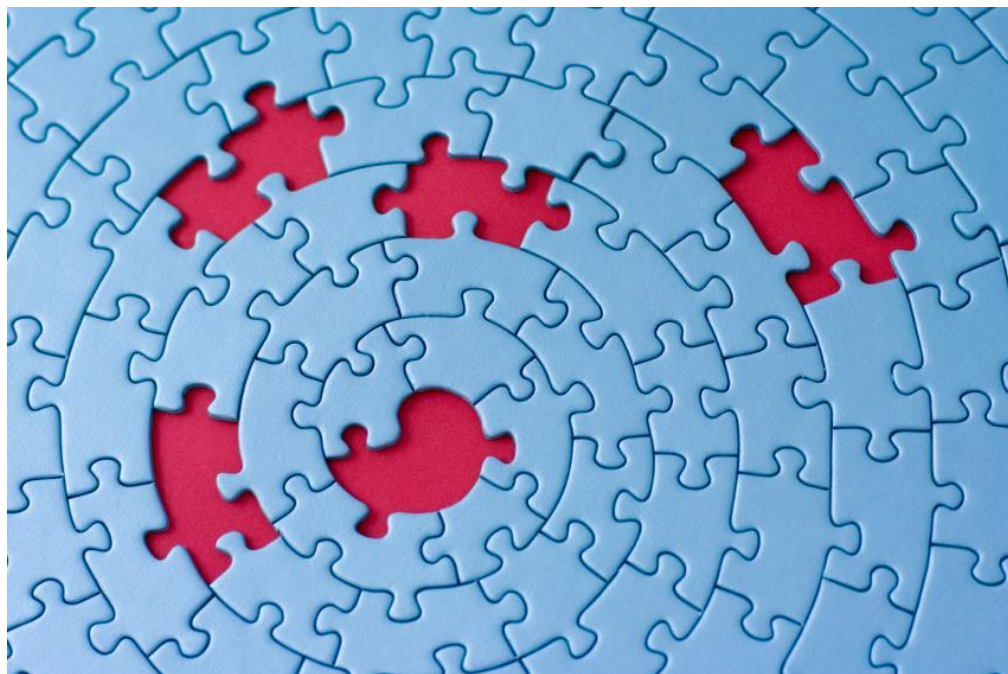


General recommendation



Introduction

Provides the reader with the Background/Context related to your research and includes the hypothesis/goals of your study



Good practices

- Try to be brief (2-3 typed pages)
- Focus on the main subject(s)
 - Cite the most recent literature (preferably from reliable/trusted sources)
 - State clearly the objective(s) of the study





Introduction

Good practice

- Try to be brief (2-3 typed pages)
- Focus on the main subject(s)
- Cite the most recent literature (preferably from reliable/trusted sources)
- State clearly the objective(s) of the study

Bad practices

- Long introduction
- Too wordy, too many subjects
- Extensive review of the topic
- The objective(s) are vague or not well described





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Introduction

Background

- Incipit*: Briefly describe the main characteristics of the object of your investigation
- What is known or believed about the topic?
- What is still unknown or problematic? (what's the problem?)
- Findings of relevant studies (past verb tense)
- Importance of the topic (support your study)



Goal(s) of the study

State clearly and concisely your hypothesis and the consequent objective(s) of the study at end of the introduction -> try to make your paper «appealing»

- Common expression

- *“To determine whether”*
- *«To this end, we investigated....»*
- *“The purpose/objective of this study was to”*
- *“This study tested the hypothesis that”*
- *“This study was undertaken to”*



Goal(s) of the study

Preventive Veterinary Medicine 181 (2020) 105074

Evaluation of intrinsic and extrinsic risk factors for dog visceral hemangiosarcoma: A retrospective case-control study register-based in Lazio region, Italy



The Risk of Infection by African Swine Fever Virus in European Swine Through Boar Movement and Legal Trade of Pigs and Pig Meat

Preventive Veterinary Medicine 149 (2018) 47–52

Monitoring for the possible introduction of Crimean-Congo haemorrhagic fever virus in Italy based on tick sampling on migratory birds and serological survey of sheep flocks

20 % of all malignant tumour cases detected at necropsy. The purpose of this study was to investigate the possible risk factors, both intrinsic and extrinsic, involved in visceral HSA development in dogs living in the Lazio region (Italy).

in that model to indicate which pathway was of greatest risk. In this study, we adapt a generic risk assessment framework (34) to assess quantitatively the risk of infection with ASFV in domestic pigs or wild boar across Europe at a fine spatial scale (100 km² cells) via multiple pathways, namely trade in live pigs, trade in pig meat products, and movement of wild boar. We create risk maps for 2019 of the probability of infection in pigs and boar for each pathway and for all pathways combined, in order to identify hotspots of ASFV incursions in the EU, and the pathways of most importance in each area.

In this scenario, an innovative approach was adopted to monitor CCHFV introduction and circulation in Italy, targeting two epidemiological phases of the virus:

1) introduction: monitored by tick sampling on migratory birds to evaluate the arrival of potential CCHFV vectors in Italy from endemic areas of Africa and Eastern Europe. This would provide data

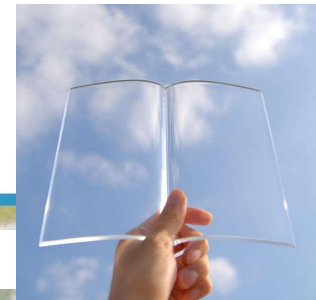


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Introduction

Recommendations

- From generic to specific: real/tangible problem -> literature -> your study
- Connect logically all elements: problem(s) -> potential reason(s) or solution(s) -> hypothesis -> type of study -> your study
- Select only important/pertinent studies
(and aggregate the results)
- Be honest and transparent!



Describes the materials and methodologies/techniques you used to conduct your investigation and provides such information with a level of detail that permits to repeat the study

- How did you study the problem?
Design of the study (including definition of time and space)
- What did you study and what did you use? (Materials)
Target/Study population (Animals? Foods?), Field and Lab materials, Tools (software, dataset...)
- How did you conduct the study? (Methods)
Explain (chronologically) the steps, the aims and what you did to accomplish it
Report the methodologies you applied (field, lab, statistical context)



Good practices

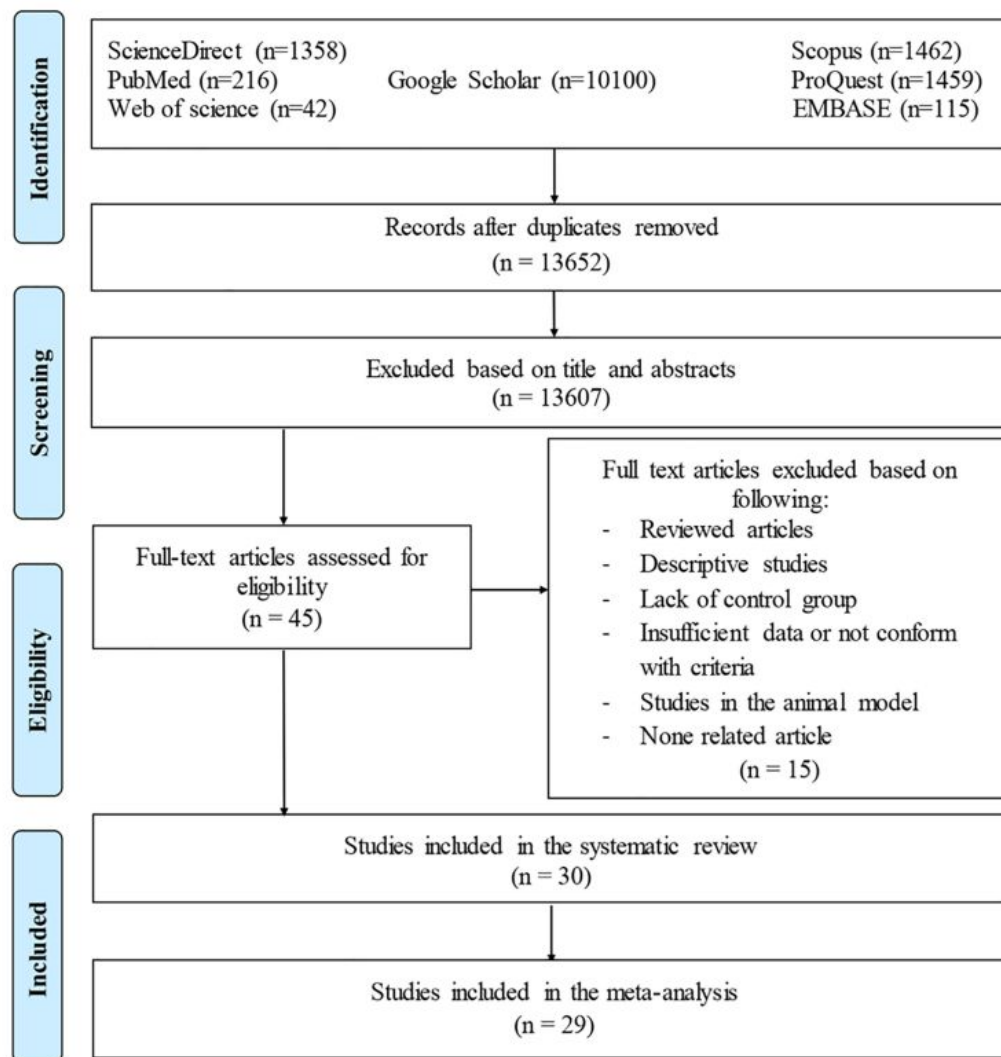
- Published method? Concise description and citation
- Unpublished or modified method? Detailed description
- Provide quantitative data (concentrations, measures, time, etc...) and material producers
- Statistical analysis is part of M&M!
- Subheadings make M&M more readable
- Too much data to report -> Appendix or Supplementary material

Bad practices

- Mix M&M with Results
- No clear description of some steps, data analysis in particular



- Diagrams / Schemes to better explain the methodology



Is there any association between *Toxoplasma gondii* infection and depression? A systematic review and meta-analysis

Fig 1. The PRISMA flow diagram of the search strategy, study selection, and data management procedure of *T. gondii* infection and depression.

- Diagrams / Schemes to better explain the methodology

Risk Assessment of Human Listeriosis from Semisoft Cheeses Made from Raw Sheep's Milk in Lazio and Tuscany (Italy)

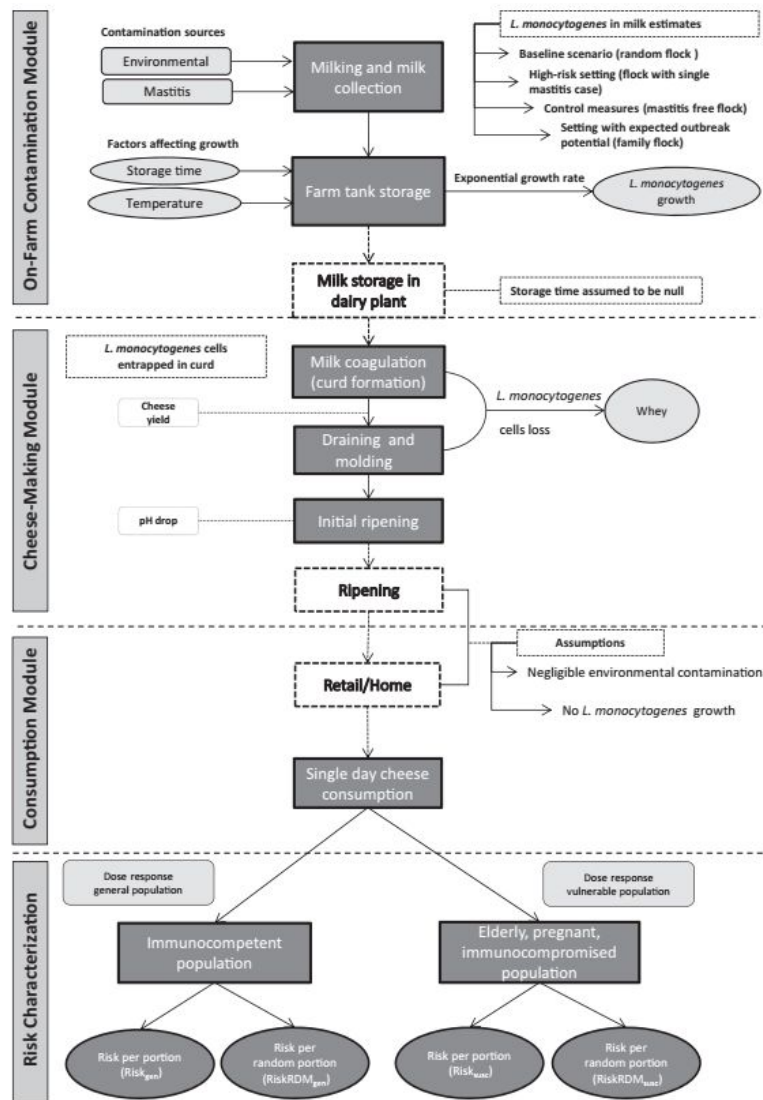


Fig. 1. Flow chart of the quantitative risk assessment model for *L. monocytogenes* in raw sheep's milk cheese.

- Figures/Maps

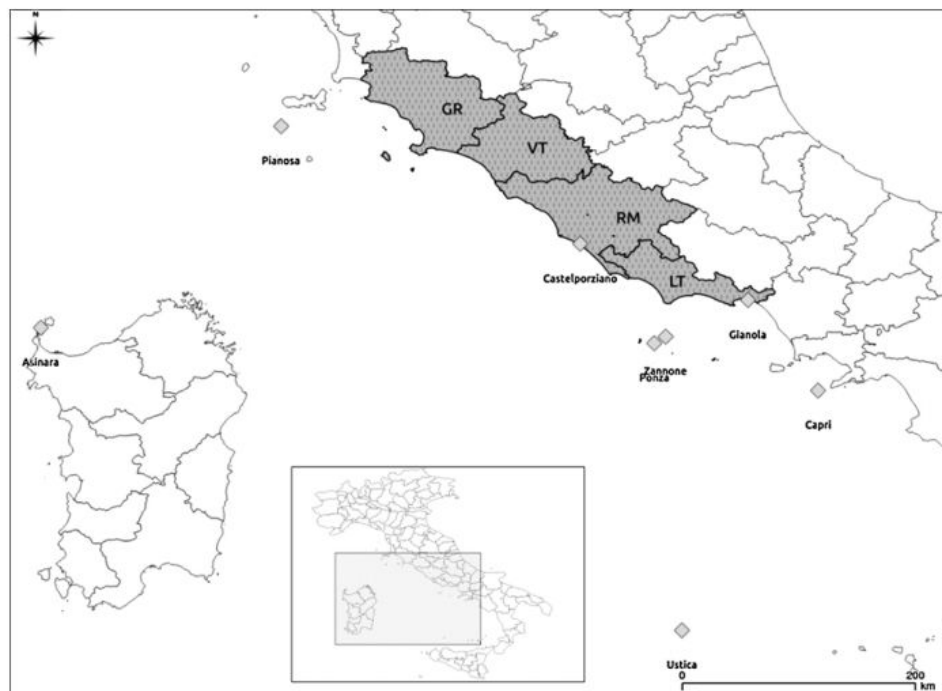


Fig. 1. Sampling area.

Legend

The dotted grey areas represent the provinces in which sheep were sampled (GR = Grosseto; LT = Latina; RM = Rome; VT = Viterbo). Grey diamonds indicate the ticks sampling sites (Castelporziano and Gianola are on the mainland, the remaining are islands). Localisation of the sampling area within Italy is displayed in the central box.



Too much information to report -> Appendix or Supplementary material

Appendix I. Analytical methods used for microbial analysis

Bacterial analysis	Method identification number (date issued)	Title of method ^a (Brief description of the method)
<i>L. monocytogenes</i>	MFLP-28 (November 2011)	The Qualicon Bax® System Method for the Detection of <i>Listeria monocytogenes</i> in a Variety of Food (PCR-based screening method)
	MFHPB-30 (February 2011)	Isolation of <i>Listeria monocytogenes</i> and other <i>Listeria</i> spp. from foods and environmental samples (Culture-based isolation and identification method)
	MFLP-74 (February 2011)	Enumeration of <i>Listeria monocytogenes</i> in foods (Enumeration method)
<i>E. coli</i> O157:H7/NM	MFLP-30 (November 2012)	Detection of <i>Escherichia coli</i> O157:H7 in select foods using the BAX® System <i>E. coli</i> O157:H7 MP (PCR-based screening method)
	MFHPB-10 (October 2014)	Isolation of <i>Escherichia coli</i> O157:H7/NM from foods and environmental surface samples (Culture-based isolation and identification method)
<i>Salmonella</i> spp.	MFHPB-20 (March 2009)	Methods for the Isolation and Identification of <i>Salmonella</i> from Foods and Environmental Samples (Culture-based isolation and identification method)
<i>Shigella</i> spp.	MFLP-25 (March 2006)	Isolation and Identification of <i>Shigella</i> spp. from Foods (Culture-based isolation and identification method)
<i>Campylobacter</i> spp.	MFLP-46 (March 2002, modified ^{**})	Isolation of Thermophilic <i>Campylobacter</i> from Food (Culture-based isolation and identification method)
Generic <i>E. coli</i>	MFHPB-19 (April 2002)	Enumeration of Coliforms, Faecal Coliforms and <i>E. coli</i> in Foods (Most Probable Number (MPN) enumeration method)
	MFHPB-27 (September 1997)	Enumeration of <i>Escherichia coli</i> in Foods by the Direct Plating (DP) Method (Direct Plating enumeration method)
pH level	MFHPB-03 (July 2014)	Determination of the pH of Foods including Foods in Hermetically Sealed Containers
Water activity level	MFLP-66 (August 2014)	Determination of Water Activity Using the Decagon Aqualab

^a *Compendium of Analytical Methods* (Health Canada, 2018), the methods used were the published versions at the time of analysis.

^b MFLP-46 was performed as written with the following modifications: 25 g from each sample were added to a filtered stomacher bag and stomached with 50 mL of peptone water for 2 min at 200 RPM. 25 mL of supernatant were removed and added to 100 mL of Park and Sanders Enrichment Broth, which is comprised of 100 mL of brucella broth, 0.5 mL supplement A per 100 mL of broth, 0.5 mL supplement B per 100 mL of broth, 5 mL blood per 100 mL of broth. The sample was then incubated under microaerophilic atmosphere in a Tri-Gas incubator (5% O₂, 10% CO₂, 85% N₂) at 37 °C for 3 to 4 h and then transferred to a 42 °C incubator and incubated under microaerophilic atmosphere (as specified above) for 24 and 48 h. Following incubation, the enrichment broth was plated as described in Section 6.3

Microbiological safety of ready-to-eat fresh-cut fruits and vegetables sold on the Canadian retail market

Helen Zhang*, Etsuko Yamamoto, Johanna Murphy, Annie Locas

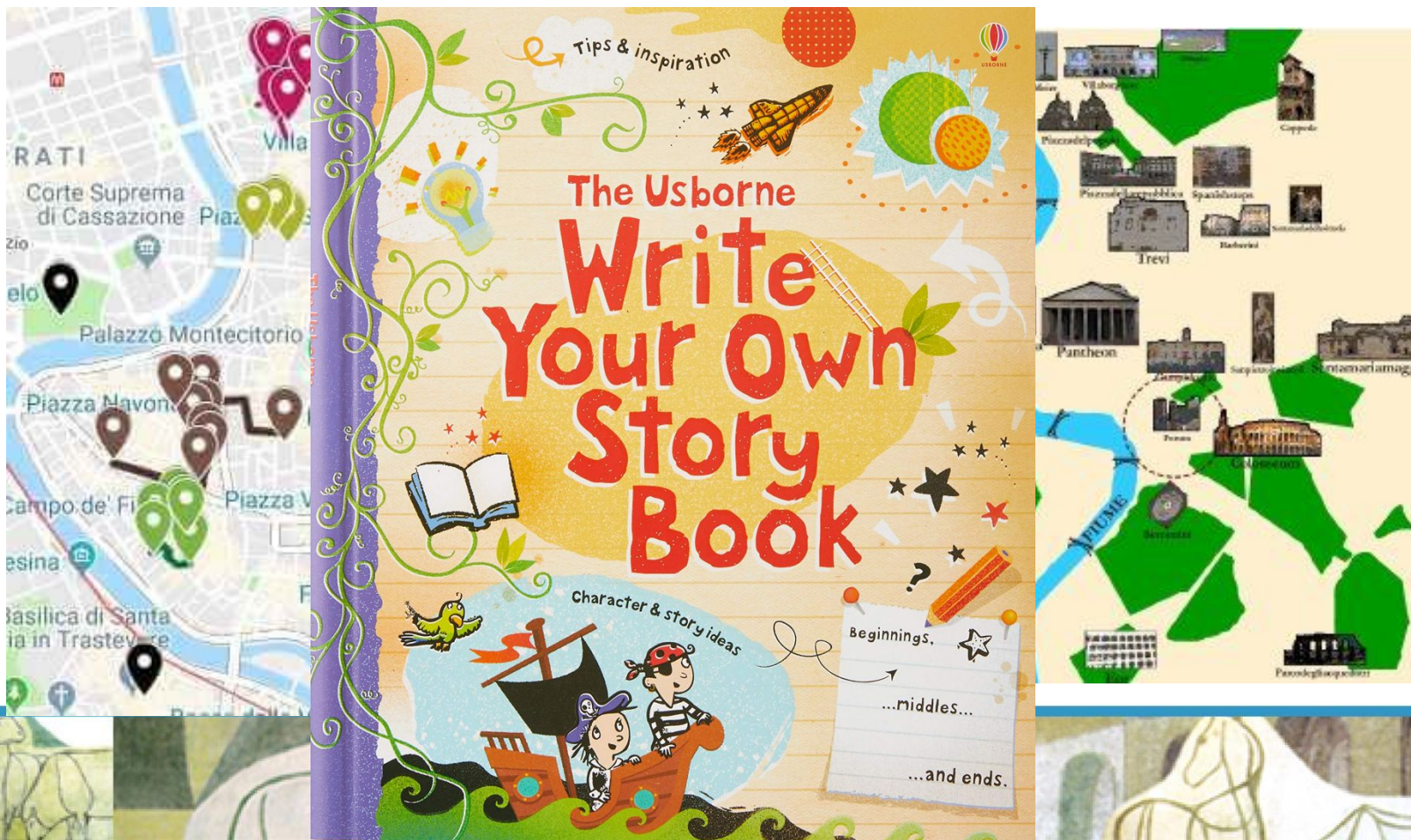
International Journal of Food Microbiology 335 (2020) 108855

Too much information to report -> Appendix or Supplementary material

APPENDIX: DESCRIPTION OF THE PARAMETERS AND STATISTICAL DISTRIBUTIONS USED IN THE QMRA MODEL FOR EACH PRODUCT (BASELINE SCENARIO)

Variable	Description	Value/Distribution	Source
Bradyzoites Concentration in the Portion			
Concentration of bradyzoites in muscle	Concentration of bradyzoites in muscle from an infected animal; data retrieved from a study that quantifies bradyzoites in muscle samples from infected goats using real-time polymerase chain reaction (PCR)	Lognormal distribution (μ, σ) ($\mu = 11.67, \sigma = 97.31$) truncated to (0.04; 41.3) (bradyzoites/g)	Juránková <i>et al.</i> ; ⁽⁵⁵⁾ Guo <i>et al.</i> ⁽²⁰⁾
Portion size	Size (in grams) of the portion for each food product in Italy prior to consumption	Cumulative distributions (Additional Supporting Information, Table SI) (in grams)	Food Consumption Survey INRAN-SCAI 2005–06; Leclercq <i>et al.</i> ⁽¹⁹⁾
Proportion of pork muscle tissue in the portion	Correction factors used to estimate the proportion of pork muscle tissue in each portion for every type of food	Several values and distributions (Additional Supporting Information, Table SII)	Several sources (see Table SII)
Weight loss	Correction factors used to quantify the loss of weight by muscle tissues in the portion after cooking or curing	Several values and distributions (Additional Supporting Information, Table SIII)	Several sources (see Table SIII)
Amount of raw pork muscle in the portion	Overall amount of raw pork muscle that was originally present in a portion considering the weight loss and the presence of other nonmuscle tissues	(Portion size \times Proportion of pork muscle tissue in the portion) + (Portion size \times Proportion of pork muscle tissue in the portion \times Weight loss) (grams)	Calculation
Number of bradyzoites in the contaminated portion	Number of bradyzoites originally present in the contaminated portion before the effect of cooking, curing, and freezing	Concentration of bradyzoites in the muscle \times Amount of raw pork muscle in the portion	Calculation
Treatment Models (Salting, Freezing, and Cooking)			
Probability of infection of a mouse for the salting model	Probability of infection of a mouse returned by the logistic model on the basis of the different salting parameters; the model was built using data regarding mice that were inoculated with an infected salted brain sample	$\frac{1}{1 + e^{-(22.349 - 0.412 \times \text{temperature} - 0.193 \times \text{treat. duration} - 3.316 \times \text{NaCl conc.} - 0.02 \times \text{temperature} \times \text{treat. duration})}}$	Opsteegh <i>et al.</i> ; ⁽¹⁷⁾ Table SIV (parameters for salting)
r_value for mouse dose response	Dose–response parameter that can be interpreted as the probability of one bradyzoite to successfully initiate an infection for mouse species	0.011	Opsteegh <i>et al.</i> ; ⁽¹⁷⁾ AFSSA ⁽⁶⁷⁾

Provides an overview of the main results originated from the study, it is a sort of «tour» that illustrates the most relevant findings to readers



- You have to answer the question:

What did you find through your investigation?



Select only the most important results!



Note: Appendix and Supplementary material can be used!

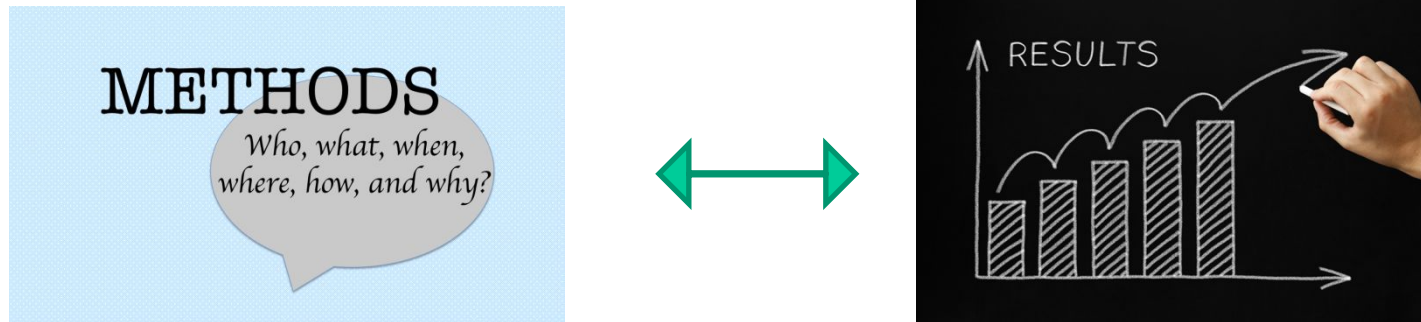


- *“The most relevant results are mentioned at the beginning of the section” True or not?*

Options for presentation order of results

1. Chronological order
2. Grouping by topic or experiment
3. General to specific
4. Most to least important

1. Chronological order



- M&M and Results section are developed “in parallel”
- Most used and straightforward approach
- Practical for the reader -> easy to link the two sections

1. Chronological order

Materials and methods

Description of prevalence patterns

We summarized the test results by listing the total number of animals tested, the numbers of animals found seropositive and the numbers of animals found (rRT)-PCR positive at each sampling time point. Taking PCR positivity as a proxy for being infectious, the latter numbers describe the pattern of apparent infection prevalence. As the time between samplings was several months, the numbers of animals born or moved off the farm between consecutive observations were non-negligible. For this reason we also listed the number of between-samplings status conversions amongst animals present at both consecutive samplings, e.g. the number of negatives turning positive and vice versa.

Estimation of transmission parameters

Leaving the role of the midges implicit, we adopted a simple SIR-type description of transmission during the vector season and use it to estimate a minimum value for the net between-ruminant basic reproduction number R_0 . A number of methods are available to estimate R_0 based on such an SIR description, although we should note that none of these methods was designed for a situation in which non-negligible numbers of animals are born or moved off the population between consecutive observations. Established methods for the case where temporal information on the infection status of all individuals in the population have been obtained, are the methods designed for analysing small-scale transmission experiments: the final-size method [22] and the 'generalized linear model' (GLM) analysis (see e.g. [23]). In our study however, it turned out that the population sizes were too large to apply the final-size method. Furthermore, as will become clear in the results, between the most interesting consecutive sampling points in our data, infection status changes occurred for a large proportion of the population, and this prevented meaningful application of the GLM analysis. We therefore used the simpler approach of applying the final-size equation [24] to the field data; in contrast to the final-size method this approach yields only point estimates and no confidence bounds. More specifically, we used the version of this equation that estimates the basic reproduction number for a fully susceptible population from data on an outbreak in a population with pre-existing immunity ($S_0 < N$) by correcting for this immunity using the standard SIR model assumption of homogeneous mixing. This equation reads as follows:

$$R_0 = -\frac{N}{Y} \ln \left(1 - \frac{Y}{S_0} \right)$$

Here N is the total number of hosts, S_0 the total number of susceptible hosts before the outbreak (i.e. discounting from N any immune hosts), and Y the total number of susceptible hosts that became infected during the outbreak. To apply this equation, we defined a reference time interval of virus spread by identifying both a sampling point during the 2007 vector season that serves as a 'before-outbreak' reference as well as a sampling point close to the end of the

Results

Description of prevalence patterns

In Tables 1 and 2, we give a by herd/flock overview of the sampling and test results through time. The observed patterns of both seroprevalence and infection prevalence were similar across most herds/flocks, and are displayed as percentages of test positive animals in Figs 1

and 2. In all five herds and all five flocks monitored, the seroprevalence increased significantly after the start of the 2007 vector season, consistent with vector-borne virus transmission occurring in all farms monitored. Highest seroprevalence was found at sampling moments between August 2007 and January 2008, i.e. in the second half of the vector season. Virus positive animals were almost exclusively found at sampling moments in this same period, i.e. between August and January, with prevalence peaking in August-December. In the cattle herds studied, seroprevalence values were already high before the 2007 vector season and increased further during that season. Fig 1 shows that the seroprevalence at around the start of the 2007 vector season ranged between 37% (Herd 1) and 78% (Herd 3) and the maximum seroprevalence attained at around the end of this vector season ranged between 82% (Herd 5) and 100% (Herd 3). In the sheep flocks studied, the seroprevalence values were still low before the 2007 vector season and tended to increase (even) more sharply during this season than in the cattle herds. Fig 2 shows that the seroprevalence in the sheep flocks at around the start of the 2007 vector season ranged between 0% (Flock 2 and 3) and 17% (Flock 1) and the maximum seroprevalence attained at around the end of this vector season ranged between 33% (Flock 5) and 100% (Flock 2). The prevalence patterns of PCR positivity compared with the seroprevalence patterns consistently with the expectation that the duration of PCR positivity is shorter than the duration of seropositivity, and thus PCR positivity is an indicator of having been infected relatively more recently. The prevalence range of PCR positivity at around the end of the 2007 vector season (second reference point) was higher in the sheep flocks (between 29% in Flock 3 and 95% in Flock 2) than in the cattle herds (between 7% in Herd 3 to 31% in Herd 4), in line with the observed more sharp increase of seropositivity in sheep during the vector season.

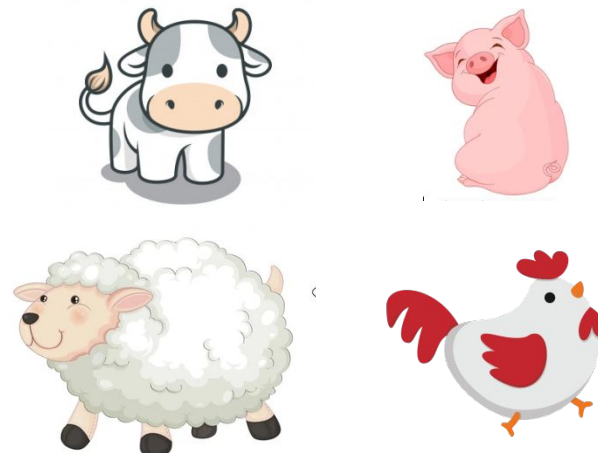
Estimation of transmission parameters

For the sampling intervals evidencing initial epidemic virus spread we estimated the net between-ruminant basic reproduction number R_0 . These estimates are listed in Table 3.

Table 3. Estimated minimum values for the within-farm basic reproduction number R_0 .

Herd/flock number	Reference interval	N	S_0	Y	Estimated R_0
Herd 1	(2,3)	103	74	67	3.6
Herd 2	(3,4)	71	30	28	6.9
Herd 4	(2,3)	29	20	16	2.9
Herd 5	(5,6)	101	54	36	3.1
Flock 1	(2,4)	90	84	66	2.1
Flock 2	(2,4)	21	21	20	3.2
Flock 3	(3,4)	14	14	8	1.5
Flock 4	(2,4)	78	73	49	1.8
Flock 5	(2,3)	432	431	164	1.3

2. Grouping by topic/study group/experiment/measured parameter



- Results are aggregated and shown on the basis of different
 - topics (i.e. different clinical manifestations)
 - study group (i.e. species, ages, matrix...)
 - experiment (multiple experiments with different conditions to verify the hypothesis)
 - measured parameter (i.e. milk production, milk yield, milk composition...)



RESULTS

Differences of miRNA signatures in non-Hodgkin's B-cell Lymphoma types

We investigated the miRNAs profile in different NHBCLs types having origin from follicular *naïve* or germinal center (GC) B-cells. We compared 76 NHBCL samples comprising 12 Burkitt's lymphoma (BL), 13 diffuse large B-cell lymphoma (DLBCL), 8 primary mediastinal B-cell lymphoma (PMBL), 17 mantle cell lymphoma (MCL) and 26 follicular lymphomas (FL) (Figures 1 and 2). According to the miRNA profiles, intratype heterogeneity was shown in each NHBCL type. Clusterization procedures split samples in two large clusters: a cluster included mainly BL, DLBCL and PMBL; the other cluster included mainly FL and MCL cases. A total of 110 miRNAs subdivided in three clusters were differentially expressed among the five NHBCL types at FDR 0.5%, fold change >1.5, (Figure 2). One miRNA cluster included miRNAs upregulated in MCL and FL. A second cluster included miRNAs upregulated in BL, DLBCL and PMBL. A third miRNA cluster encompassed mainly miRNAs of the *miR-17-92* cluster and paralogues. These miRNAs were expressed at a higher level in BL and in a minor portion of DLBCL, PMBL, MCL and FL cases. The polycistron *miR-17-92* cluster, *miR-29* family, *miR-150* and *miR-497* showed the highest power of discrimination of the five NHBCL types (Table 1).

Strong up-regulation of *miR-17-92* cluster and downregulation of *miR-221*, *miR-222*, *miR-223* and *miR-224* in BL and MCL cell lines compared to normal B-cells

We investigated whether the differences of miRNA profiles observed among NHBCL tissues were recapitulated in corresponding lymphoma cell lines. To capture the pathological signature in cell lines, we compared the miRNAs expression profile of six BL and two MCL cell lines (of these, one with known MYC overexpression) with normal B-cell populations at diverse differentiation stages, ranging from bone marrow CD34⁺

BL cell lines showed homogeneous profiles: only members of the *miR-181* family, *miR-9**, *miR-130a* and *miR-130b* were variably expressed. The miRNA profile of the MCL cell lines was more similar to that of BL cell lines than to that of *naïve* B-cells. The main differences of miRNA expression between MCL cell lines MAVER-1 (known to overexpress MYC due to translocation) and GRANTA-519 regarded *miR-181* family and *miR-17-92* cluster. In particular, MAVER-1 but not GRANTA-519 showed levels of *miR-17-92* cluster similar to those of BL cell lines.

MiRNA signature in Burkitt's lymphoma tissues

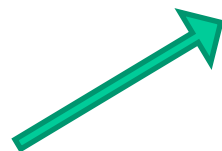
To verify if the miRNAs signature observed in cell lines was reproduced in tissues, we compared the miRNAs expression of BL tissues and reactive lymph nodes (LNs) as normal reference. BLs clustered separately from LNs and 56 miRNAs were differentially expressed: 34 upregulated and 21 downregulated in BL at FDR 2% and fold change >1.5 (Figure 4). Top upregulated miRNAs included *miR-17-92* cluster, *miR-499*, *miR-206*, *miR-9**. Top downregulated miRNAs were *miR-222*, *miR-221*, *miR-150*, *miR-29* family, *let-7* family, *miR-342*, *miR-155*, *miR-146a*, *miR-146b* and *miR-23a*.

MiRNAs deregulated in both cell lines and BL tissues were members of *miR-17-92* cluster, *miR-222*, *miR-221*, *miR-150*, *let-7* family members.

Validation of miRNA expression in NHBCLs and LNs by quantitative RT-PCR

Expression of 9 miRNAs was validated by quantitative RT-PCR in BL, DLBCL, PMBL, MCL, FL and LN (Supplementary Figure 1). The 9 miRNAs showed significant differences in at least one NHBCL type with respect to LN ($P < 0.05$): *let-7a* in DLBCL, PMBL and BL; *miR-9** in FL, MCL, DLBCL, PMBL and BL; *miR-10a* in DLBCL and PMBL BL; *miR-20b* in MCL and BL; *miR-21* in FL, MCL, DLBCL, PMBL and BL; *miR-29a* in FL, MCL and BL; *miR-150* in DLBCL, PMBL and BL; *miR-155* in FL, MCL, DLBCL, PMBL and BL; *miR-222* in FL, DLBCL, PMBL and BL.

3. From General to Specific



Results

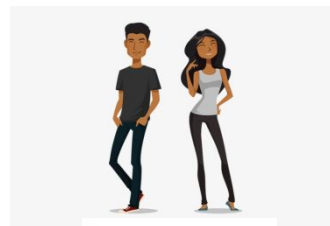


By age?

geographically?



Or...

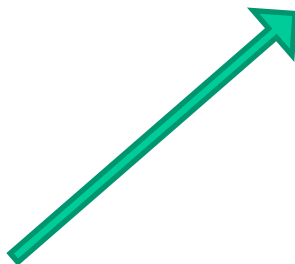


- Firstly describe/report results concerning the general population -> then repeat the same process for subgroups



Results

4. Most to least important



- This approach emphasizes the most important results



Recommendations

- “Negative” results must be reported!



- “Missing” results must be reported!



Recommendations

- Choose immediately tables/figures (photographs, drawings, graphs, flow diagrams) that you want to include in your manuscript -> most relevant data!
- Organize your text on the basis of your Tables and Graphs sequence (don't forget including the reference in the text!)

Table 2. Descriptive, univariable and multivariable logistic analysis of characteristics associated with dogs registered in the

	Dog Registry		
	No/Do not know (N = 182)(%)	Yes (N = 130)(%)	Univariable analysis OR (95% CI)
Sex			
Male	78 (60)	86 (47)	-
Female	54 (40)	96 (53)	1.6 (1.0–2.6)*
Missing	1	0	
Age (years)			
≤2	36 (29)	43 (24)	-
2.1–8	52 (42)	99 (56)	1.5 (0.9–2.7)
>8	37 (30)	34 (19)	0.7 (0.4–1.4)
Missing	6	6	



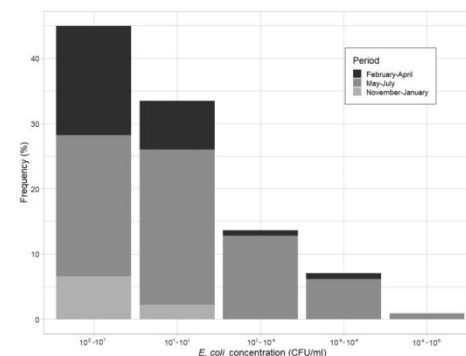
Recommendations

- Avoid absolutely repetitions of results!
 - Text or Table/Figures
 - Table or Figure

Overall, we analyzed 372 milk samples. No *L. monocytogenes* or other potentially pathogenic species, such as *L. ivanovii*, were detected (maximum possible prevalence 0.8%, CL 95%), but one milk sample was positive for *L. innocua*. In contrast, *E. coli* was detected in 227 samples (61.0%, CL 95% [56.1 to 66.0%]) from 80 farms. The distribution of the positive samples according to

Table 2. Range of concentrations of Verotoxigenic *Escherchia coli* O157:H7 in sheep at slaughter, Italy

VTEC O 157 (CFU g ⁻¹)	Number of sheep
<10 ²	24
10 ² –10 ³	3
10 ³ –10 ⁴	8
10 ⁴ –10 ⁵	1
10 ⁵ –10 ⁶	2

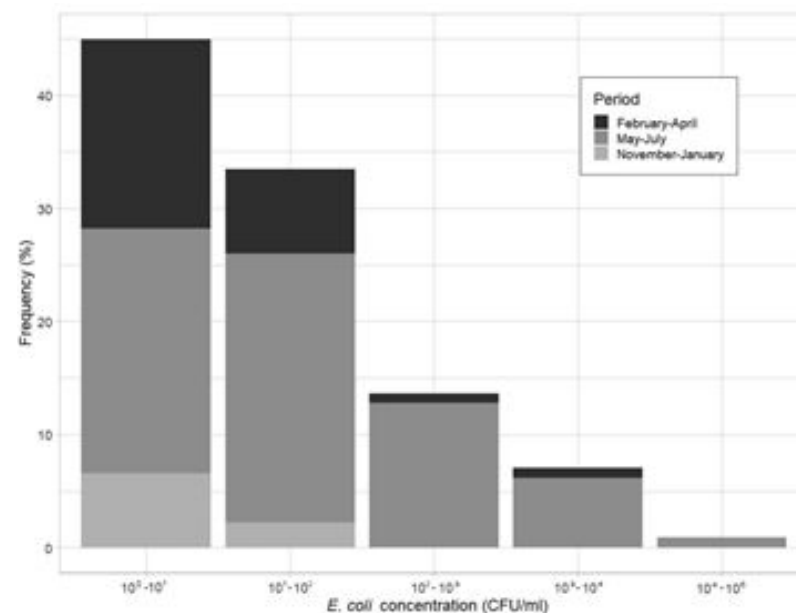


“It is more preferable to report your results through a figure than through a table” ... yes, but not always!



Why should I use a figure?

- We want to give an overview of my data (i.e. temporal/spatial trends, comparison between groups, etc...)
- We need to highlight/make more evident some aspects -> greater impact on the reader!
- Great deal of data -> it's more appropriate to summarize



Why should I use a table?

- We want to provide data in detail
- Great deal of data -> it's necessary to provide descriptive statistics

Results

Table 3

Virulence genes in the *Escherichia coli* O157 strains isolated from raw milk in Greece.

Strain	Origin ^a	Shiga-toxinogenic ^b	<i>fliC_{H7}</i> gene ^{c,d,e}	Virulence genes ^{d,e}			
				<i>stx₁</i>	<i>stx₂</i>	<i>eae</i>	<i>ehxA</i>
LFH1	O	+	+	+	+	+	+
LFH2	O	+	+	+	+	+	+
LFH3	O	+	+	—	+	+	+
LFH4	C	+	+	+	+	+	+
LFH5	C	+	+	—	+	+	+
LFH6	B	+	+	—	+	+	+
LFH7	B	+	+	—	+	+	+
LFH8	B	+	+	—	+	+	+
LFH9	B	+	+	—	+	+	+
LFH10	B	+	+	+	+	+	+
LFH11	B	+	+	+	+	+	+
LFH12	B	+	+	+	—	+	+
LFH13	O	—	—	—	—	—	—
LFH14	O	—	—	—	—	—	—
LFH15	C	—	—	—	—	+	+
LFH16	B	—	—	—	—	—	—

Table III. Estimated Risk per Portion (Contaminated or Random) and Annual Number of New Infections Associated with the Consumption of Pork Products in Italy (Baseline Scenario)

Category	Product	Risk per Contaminated Portion, Mean (5th, 95th, 99th Percentiles)	Risk per Random Portion, Mean (5th, 95th, 99th Percentiles)	New Infections per Year—Adults, Mean (5th, 95th, 99th Percentiles)	New Infections per Year—Pregnant Women, Mean (5th, 95th, 99th Percentiles)
Fresh meat	Fresh pork meat (generic)	5.5×10^{-5} (0, 9.4×10^{-5} , 1.4×10^{-3})	7.2×10^{-6} (0, 1.2×10^{-5} , 1.8×10^{-4})	5,737 (0, 9,848, 146,149)	42 (0, 73, 956)
	Fresh pork meat (steak)	4.7×10^{-5} (0, 8.2×10^{-5} , 1.2×10^{-3})	6.1×10^{-6} (0, 1.1×10^{-5} , 1.5×10^{-4})	2,354 (0, 4,138, 59,347)	17 (0, 30, 321)
	Fresh pork meat (leg)	5.5×10^{-5} (0, 9.4×10^{-5} , 1.4×10^{-3})	7.2×10^{-6} (0, 1.2×10^{-5} , 1.8×10^{-4})	641 (0, 1,097, 11,874)	5 (0, 8, 87)
	Fresh wild boar meat	5.5×10^{-5} (0, 9.5×10^{-5} , 1.4×10^{-3})	7.7×10^{-6} (0, 1.3×10^{-5} , 1.9×10^{-4})	75 (0, 128, 1,393)	1 (0, 1, 10)
	Fresh sausages	4.5×10^{-5} (0, 8.8×10^{-5} , 6.3×10^{-3})	5.9×10^{-6} (0, 1.2×10^{-5} , 1.5×10^{-4})	3,692 (0, 7,208, 92,545)	27 (0, 53, 680)

Table 2. Reported serogroups of *Escherichia coli* causing human extraintestinal infections: non-outbreak studies

Ref.	Pop. Type*	Observation period	Location†	Sex‡	Infection§	Isolates	No. O-antisera¶	Common serogroups (%)								Epidemic serogroups (%)							
								O1	O2	O6	O7	O8	O16	O75	O4	O11	O15	O17	O18	O25	O73	O77	O78
[47]	1	1960–1981	USA	F	UTI, PY, ABU	614	131	2	0.3	22	5	2		10	10	0.7	0.8	1	4	5	0.8	0.8	
[53]	2			U, UTI, PY	156	129	5	4	19	3	2		14	13			0.6	2	0.6			0.6	
[7]	1	1965–1967		UK	UTI	395	147	5	6	16	6	0.8	0.3	13	6	2	0.3	1	5	1	0.3		
[48]	1	1966–1970	DK	F	PY, B	367	150		14	8			10	8									
[54]	2		AU	B	UTI	1008	143	2		20	4	0.7	0.3	11	5	0.9	0.6	1	2	4	0.4	0.5	
[55]	3	1972–1973	SA		U	222	±150	2	5	30	3			7	18	1		15					
[56]	2	1969–1976	CH		UTI	427	164	4	8	5	1	3			7		2		2	3			
[57]	2	1969–1987	UK	B	B	861	RL	6	10	13				5	6		7		5				
[58]	3		USA		B	149	71	5	7	13	5	3	5	3	8	0.7	4	0.7	6	4		0.7	
[59]	1	1973–1981	NZ	F	UTI	101	164	3	6	13	3	5		16	2			2	1				
[60]	1	1979	NE	F	UTI	30		7	17	17		7		10					3		10		
[61]	1	1980–1983	SW	F	UTI, PY	84	165	11	5	6	5		13	6	6				4				
[62]	1	1980–1983	SW	F	PY, B	75	165	15	7	5	7		16	5	8		4		3				
[63]	3		NE & UK		UTI, PY, ABU	119	181	6	4	14		5		10				3	4			4.2	
[64]	1	1983–1992	SW	M	UTI, PY	88	171	1	7	26	1	2	5	7	7		9		5				
[65]	2	1986–1990	DK		B	172	171	6	7	12	3	5		8	2		6		5				
[66]	2	1987–1988	IN	B	U	56	RL	2	4	4	2				5		4						
[67]	2	1988–1991	USA & KE	B	B	187	173	5	8	19	1	2	2	4	5				6	3			
[68]	2	1989–1992	SP	B	UTI, PY, ABU	252	101	3	8	13	3	3		4	8	2	3	2	15	2	2		
[69]	1	1992–1993	IR	B	UTI	87	68	1	2	24	8	3			13		2	9	1				
[70]	3	1993–1996	SW	M	UTI	70		3	16	23		1		7	19				3	4			
[71]	1	1994–1999	USA	F	UTI, PY	329	RL	5	19	10	2		3	7				5					
[72]	1		SP	F	UTI, P	90	170	2	11	29	6	3		3	10								
[73]	3		JA	M	PR	107		4	16	11			3	5	9	0.9	0.9		14	5			
[73]	3		JA	F	UTI, PY	270		12	11	9		2	11	9	3		2		17	4		0.4	
[74]	3			F	UTI	74	RL	7	5	19				4	4				6				
[75]	3		DK	B	B	247	171	7	8	11	3	6		6		6			7	3			
[12]	3	1997–1997	IN		UTI	100	RL		2	5		2			12			1	2		2		
[76]	3	1998–2001	BR	B	B	60		3	13	10	3		2	5	2	3		12		3		2	
Weighted average								4	7	15	3	2	1	8	6	1	1	1	5	2	0.2	0.3	0.1

* Population type: 1, community-acquired infections; 2, community- and hospital-acquired infections; 3, patient population type not reported.

† AU, Australia; CH, China; UK, England; DK, Denmark; SP, Spain; NE, The Netherlands; SW, Sweden; JA, Japan; FN, Finland; CR, Croatia; CA, Canada; PR, Portugal; IN, India; BR, Brazil; KE, Kenya; IR, Iran; SA, South Africa; NZ, New Zealand.

‡ M, male; F, female; B, both male and female.

§ B, Isolates recovered from blood samples, bacteraemia cases or sepsis cases; U, isolates recovered from urine samples; UTI, isolates recovered from cases of cystitis or UTIs; PY, isolates recovered from pyelonephritis cases; PR, isolates recovered from prostatitis cases; ABU, isolates recovered from asymptomatic bacteriuria cases.

|| The denominator used for calculations may differ from the number of isolates tested. For Vosti [47], the denominator is 614 due to missing information from 291 patients; for Grandsen *et al.* [57], the denominator is 861 which is the number of patients studied; for Sandberg *et al.* [61], the denominator is 84 (only non-pregnant PY and UTI patients included); for Otto *et al.* [62] the denominator is 75 (92 minus complicated cases, including diabetic patients).

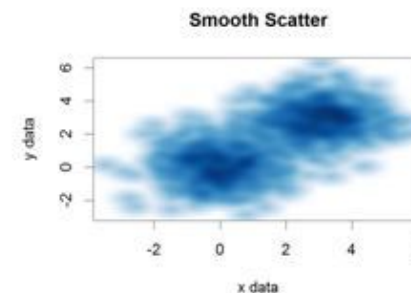
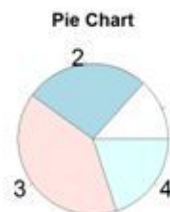
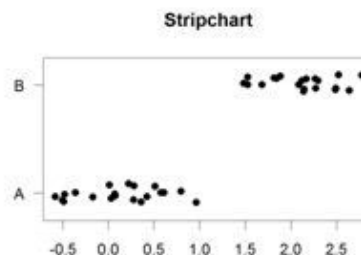
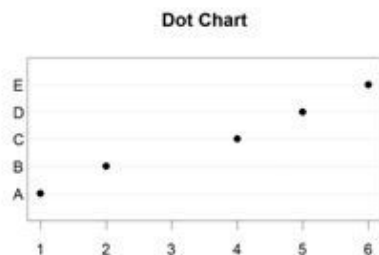
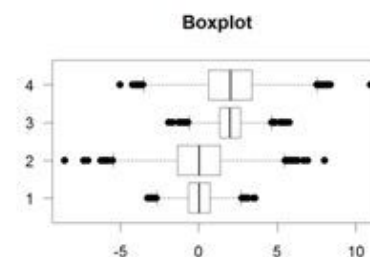
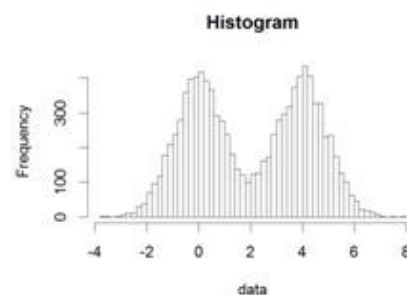
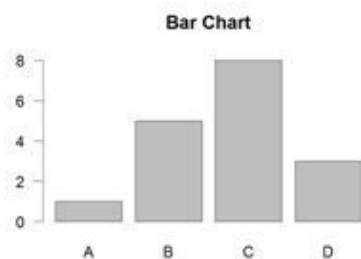
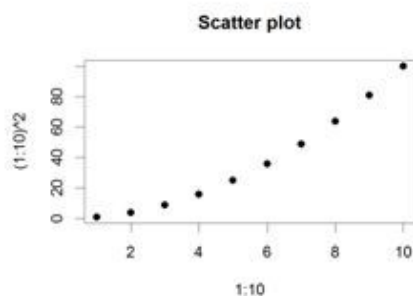
¶ RL was used when serotyping was done at a reference laboratory and was assumed to use the entire set of O-antisera present at the time of the study.

TABLE 2. *Microbiological results for 419 lettuce samples collected from July 2008 to March 2009*

Count (CFU/g)	No. of samples	
	APC results	Coliform results
$<10^1$	0	3
10^1-10^2	0	36
10^2-10^3	0	209
10^3-10^4	0	149
10^4-10^5	99	21
10^5-10^6	285	1
10^6-10^7	35	0
$>10^7$	0	0



Core Graph Types



Recommendations for table and figures

- Tables and figures must be easy to understand even “alone” (even if the reader has not read the main text). To this aim:
 - Include a concise but comprehensive caption
 - Define clear column/raw (for tables) or axis (for graphs) titles
 - A simple layout/graphic helps a lot the reader
 - Consider to include an explanation or footnotes or a legend



Recommendations for data reporting

- Check carefully the Author Guidelines!

Units

Follow internationally accepted rules and conventions: use the international system of units (SI). If other units are mentioned, please give their equivalent in SI.

Math formulae

Please submit math equations as editable text and not as images. Present simple formulae in line with normal text where possible and use the solidus (/) instead of a horizontal line for small fractional terms, e.g., X/Y. In principle, variables are to be presented in italics. Powers of e are often more conveniently denoted by exp. Number consecutively any equations that have to be displayed separately from the text (if referred to explicitly in the text).

Matematical and technical settings

Use the appropriate number of significant figures to express your data - they should be justifiable and reflect the necessary level of accuracy of the method. A normal maximum should be 3 - e.g. 37.1, 2.53). Detailed mathematical discussion should be placed in an appendix. Equations and formulae should be typewritten. Equations should be numbered consecutively with Arabic numerals in parentheses on the right hand side of the page. Special symbols should be identified in the margin, and the meaning of all symbols should be explained in the text where they first occur. If you use several symbols, a list of definitions (not necessarily for publication) will help the editor. Type mathematical equations exactly as they should appear in print. Journal style for letter symbols is as follows: italic (indicated by underlining); constants, roman type; matrices and vectors, bold type (indicated by wavy underlining).



Recommendations for data reporting

- Round data appropriately (15.306% -> NO!)
- Decimals -> use dot (".") not comma (",")

15.3%

2,300

- Missing data in your table? Use Dash "-" or (...) or NA (specify: "Not Applicable?", "Not Available"; "Not Analysed")



Most common mistakes

- Do not include to include too many results!
- Do not repeat your data!
- Do not comment/discuss your data
-> be objective!

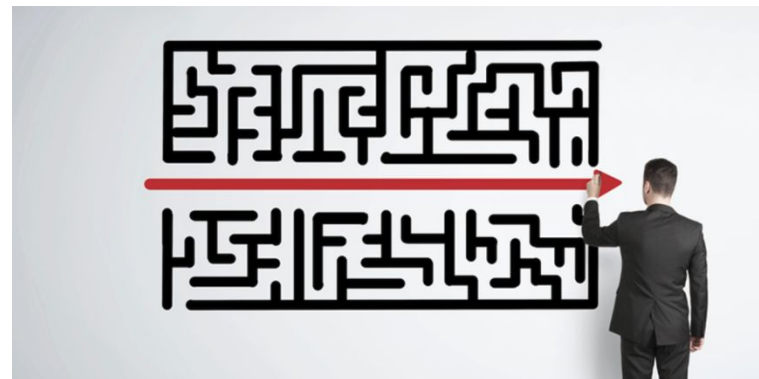


Most common mistakes

- Use a simple language
- Only one idea/concept in a sentence
- Keep short: <20 words
- Long sentences: greater risk of grammatical errors

⇒ Secret of writing is re-writing

⇒ Secret of rewriting is re-thinking





Istituto Zooprofilattico Sperimentale
del Lazio e della Toscana *M. Aleandri*

Discussion

Provides an explanation about the meaning of your findings and illustrates the contribution and implication of your research in relation to the current knowledge



General considerations

- It's the most important, interesting and crucial part of the “show”



- It must be transparent, fair and balanced



Typical structure – The initial part

- State immediately what's the most important achievement(s)/finding(s) of your study
- Keep in your mind the objective(s) of your study



Discussion

Zooprofilattico Sperimentale

Typical structure – The initial part

Occurrence of *Listeria monocytogenes* and *Escherichia coli* in Raw Sheep's Milk from Farm Bulk Tanks in Central Italy

The present study reduces the knowledge gaps concerning the presence and concentration of *L. monocytogenes* and *E. coli* in raw sheep's milk at the bulk tank level. Our findings suggest that the prevalence of *L. monocytogenes* in sheep's bulk milk should be considered sporadic or, at least, as a low probability event, as reported by other authors. Although such bacteria are regularly

Report of the human body louse (*Pediculus humanus*) from clothes sold in a market in central Italy

The exceptionality of the described case lies not only in the report of *P. humanus* from a developed country (Italy) where it had not been reported for decades, but also in its report from second-hand clothes for sale in a market, constituting a potential source of infection for people buying such goods and thus possibly spreading this parasite out of the typical host range where it is presently found in developed countries, homeless people and refugees [3, 4].

The following question therefore arises: how did adults and nits of *P. humanus* infest a garment for sale on a market stall in a country where it had not been

Prevalence and Concentration of Verotoxigenic *Escherichia coli* O157:H7 in Adult Sheep at Slaughter from Italy

This is the first reported study conducted in Italy with the aim of estimating prevalence and concentration of VTEC O157:H7 in adult sheep. The study also contributes to the demonstration that adult sheep represent a relevant reservoir for VTEC O157 with virulence profiles that are known to be harmful to humans, with a high proportion (nearly 30%) of positive animals that can be considered active shedders, and 8% of animals that can be considered high shedders ($>1 \times 10^4$ CFU g⁻¹ faeces), and harbouring more than 96% total VTEC O157 bacteria cultured by all animals tested. Such isolates possessed the

Genetic diversity of *Theileria equi* and *Babesia caballi* infecting horses of Central-Southern Italy and preliminary results of its correlation with clinical and serological status

The taxonomy of *Piroplasmorida* is in continuous evolution and revision as a result of the different studies conducted on their phylogenesis and for this, recent data obtained by Schreeg et al. (2016) proposes that *T. equi* should be allocated in a separate group from the other *Theileria* spp. The hypervariable regions of the 18S rRNA gene are the most suitable for phylogenetic studies of *Apicomplexa*, and also for *Piroplasmids* (Lack et al., 2012; Morrison, 2009), although some authors (Chae et al., 1999; Eickbush and Eickbush, 2007; Salim et al., 2010) disagree on the suitability of this gene for evolutionary studies, while others (Schreeg et al., 2016) propose to use it together with the mitochondrial genome.

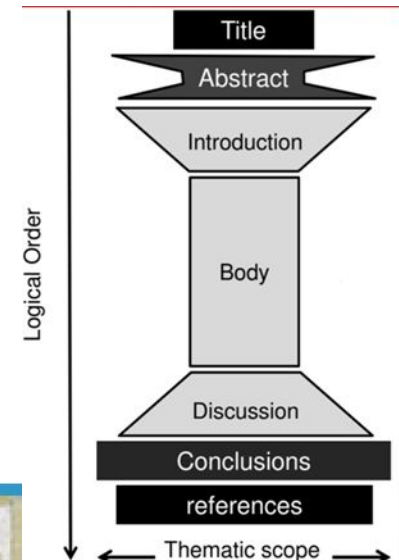
To our knowledge, the data presented here is the first report on sequence heterogeneity of *T. equi* and *B. caballi* detected in Italian horses, following the lead of previous studies, to verify if their conclusions are also valid for the Italian phylogenetic analysis results.

In brief, the present study identified three genotypes for the V4 hypervariable region of 18S rRNA gene of both *T. equi* (A, B and C) and *B. caballi* (A, B1 and B2), in line with the results of other authors (Bhoora et al., 2009). Moreover, the phylogenetic tree for EMA-1 gene

Typical structure – Central part

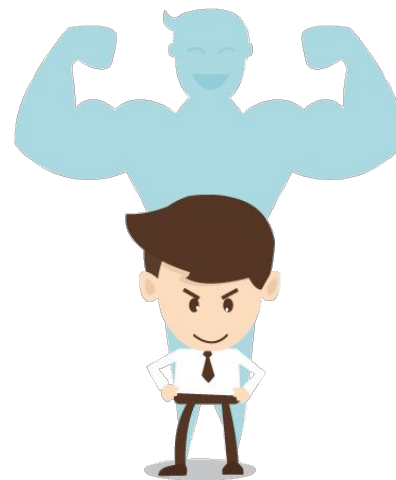
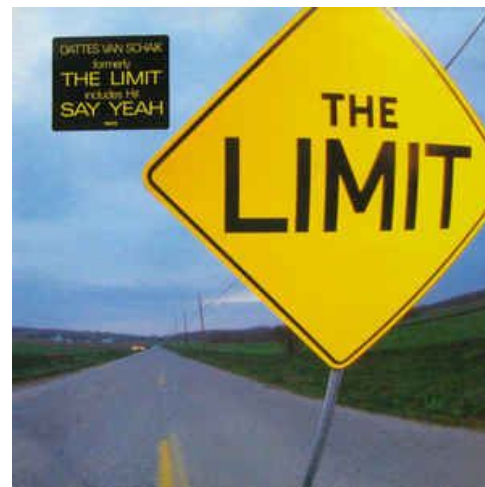
Follow the results section and comment the most important findings.

- What your result means?
- What other Authors founded?
- Compare/correlate your result with those from other similar/pertinent studies (studies you cited in your introduction can be useful and further discussed)
 - Are your data consistent with them? There are differences? Possible causes?
 - Can other studies integrate your findings?
- What's the implication of these new results?
 - Deduction & Speculation (New hypothesis?)



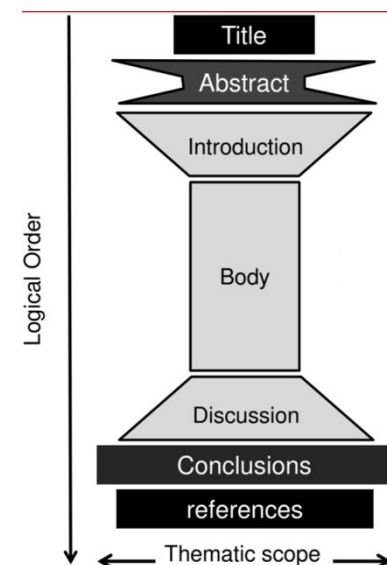
Typical structure – Limits & Strengths

- Limits & weaknesses
 - Design of the study?
 - Sample size?
 - Analytic methods?
 - ...
- Strengths (also comparing other studies)
 - First study?
 - Sample size?
 - New methodology?
 - ..



Typical structure – Final part

- Take home messages -> what do you want the reader remember about your study? (just few sentences or 1-2 paragraphs)
 - Concisely summarize the most important outcomes of your study but avoid repetitions -> elaborate them
 - Answer the question: «so what?» -> larger implication of your study
 - Prospective? What's about the future? What are the remaining (remarkable) gaps of knowledge?



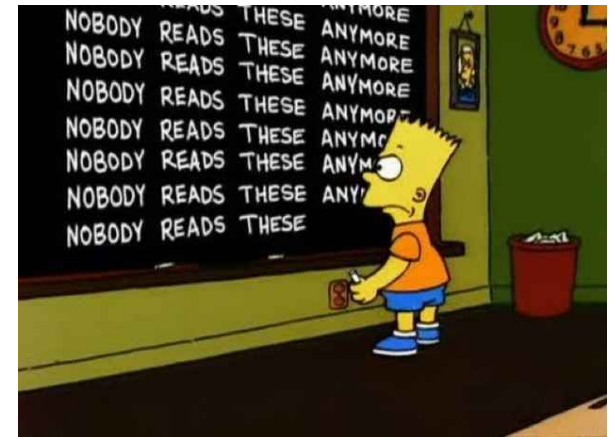
Common mistakes

- Do not select only studies that support your results or speculations



- Cite/mention properly parts of other studies -> plagiarism risk!

- Be aware regarding repeating the same information/concepts many times



Common mistakes

- Be careful when you comment your statistical analysis... (i.e. statistical significance is not evidence of causality)

«La **statistica** non può, come talvolta tendono a credere "i più inesperti", dare un significato a dati che non ne hanno o consistenza ad una realtà inesistente.»



Source: Prof.ssa Martina Montagnana –FAD Training Course «Come si scrive un contributo scientifico

Managing the bibliography can be very challenging....Many software can help you!

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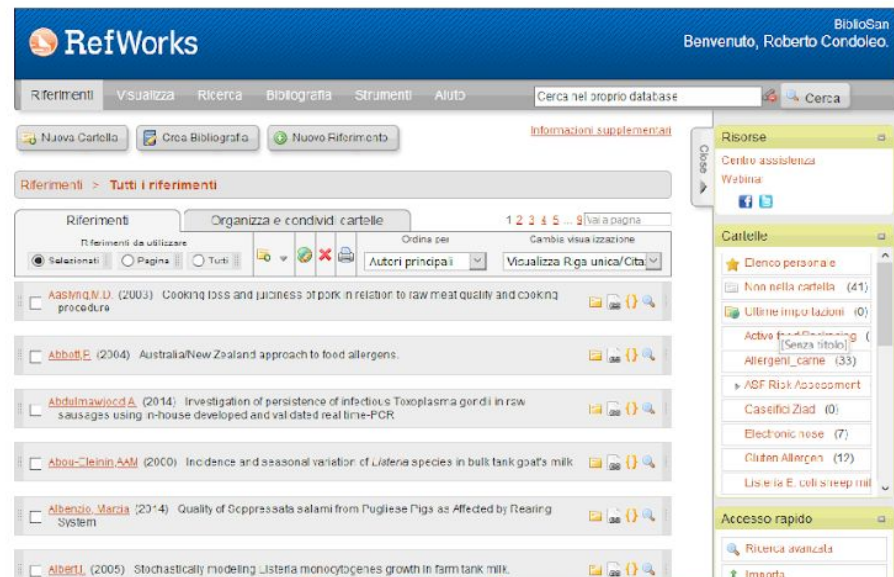
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•Refwork

•Endnote

•Medley



The key

Good practices

Put in relation....

the goal of your study

the results

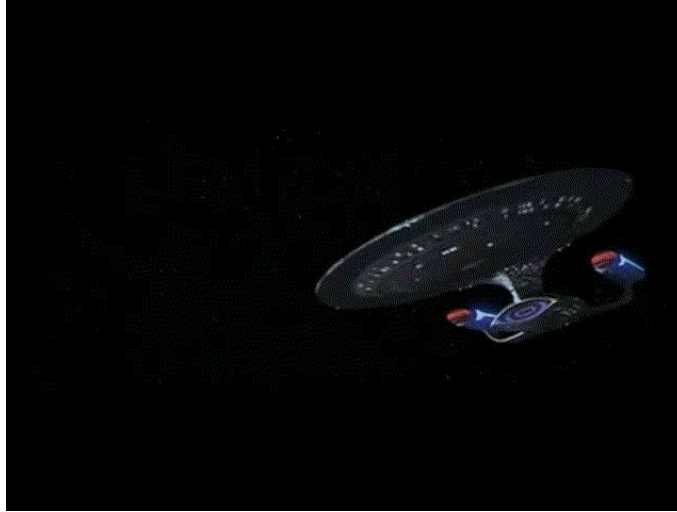
the discussion



It's not easy!
Perfect article does not exist!



BUONA RICERCA A TUTTI!



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