

Practising Scientific English

Focus su Risultati, Discussione e Conclusione



Roma, 25/03/21

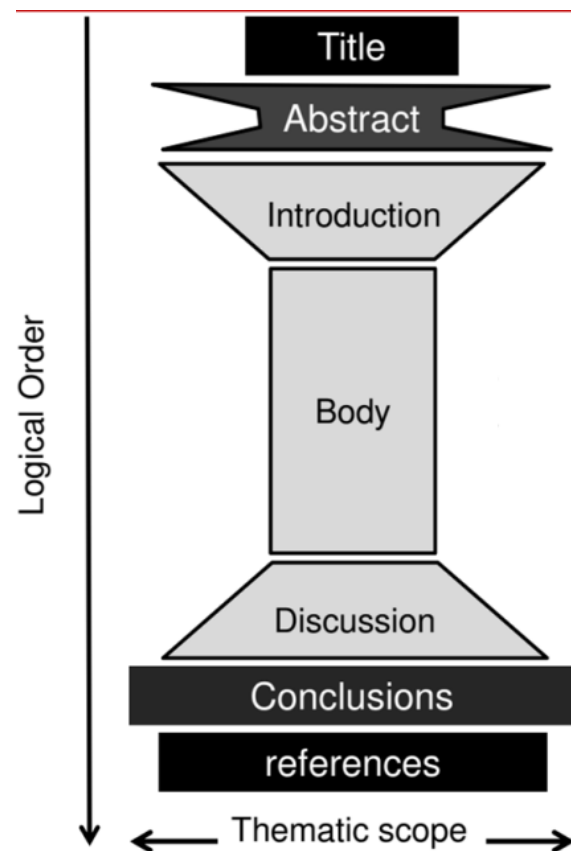


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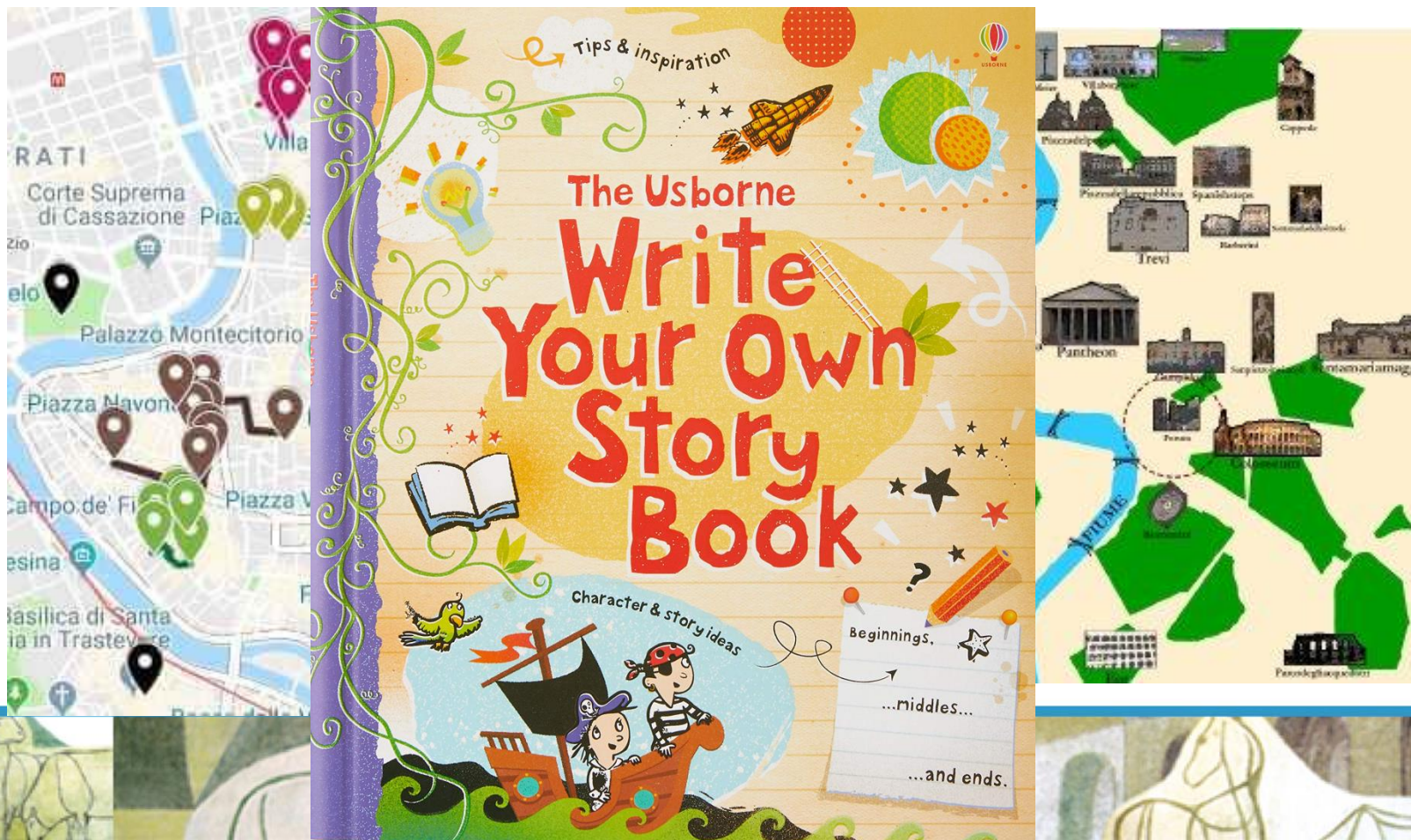




- Results
- Discussion & Conclusions
- Bibliography



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!



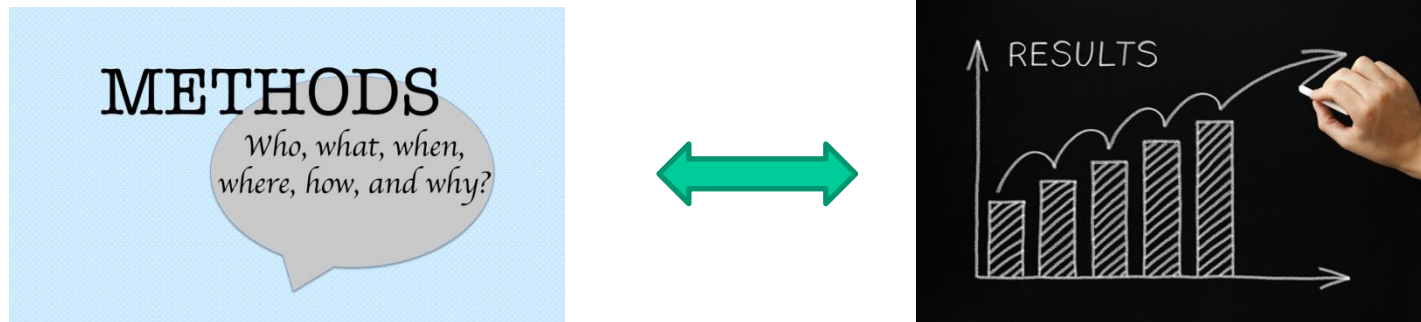


- *“The most relevant results are mentioned at the beginning of the section” True or not?*

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 midgets 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.

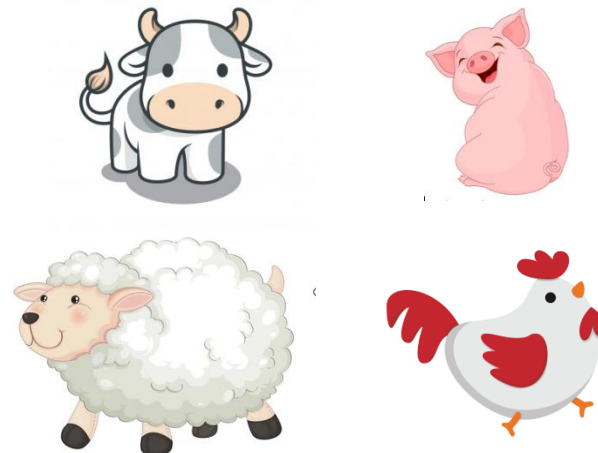
Estimation of transmission parameters

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

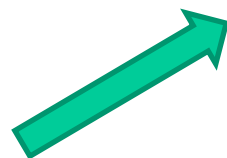
To verify if the miRNAs signature observed in cell lines was reproduced in tissues, we compared the miRNAs expression of BL tissues and reactive lymph nodes (LNs) as normal reference. BLs clustered separately from LNs and 56 miRNAs were differentially expressed: 34 upregulated and 21 downregulated in 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



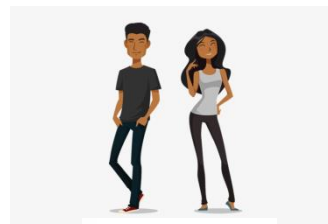
Results



By age?



Or...



geographically?

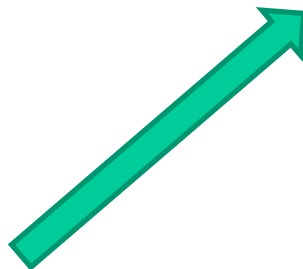


- Firstly describe/report results concerning the general population -> then repeat the same process for subgroups



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	



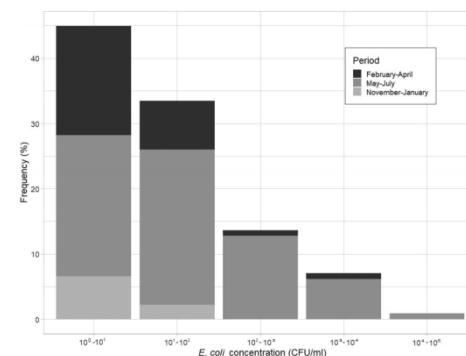
Recommendations

- 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

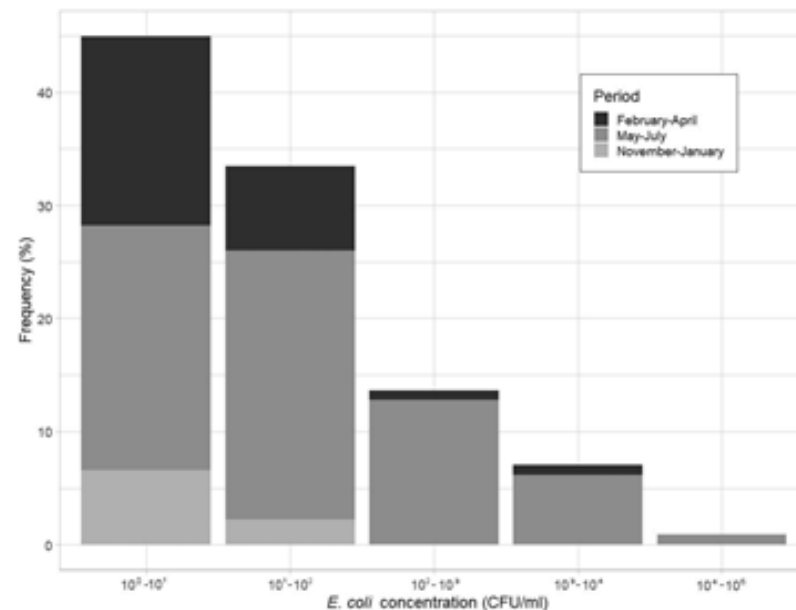


“It is more preferable to report your results through a figure than through a table” ... yes, but not always!



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

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).

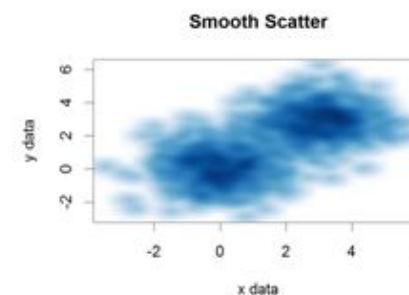
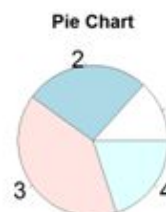
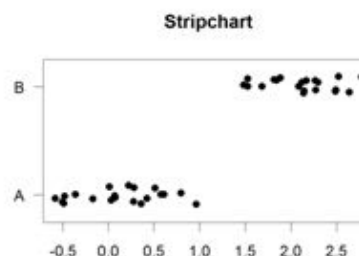
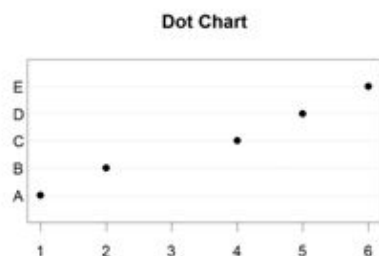
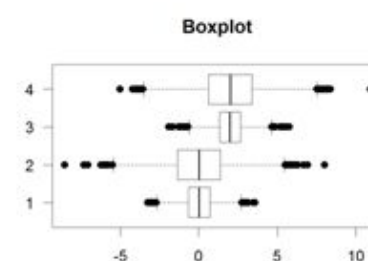
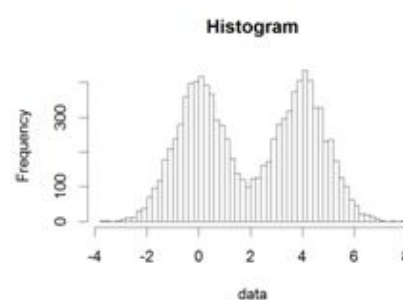
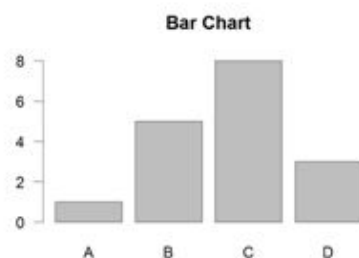
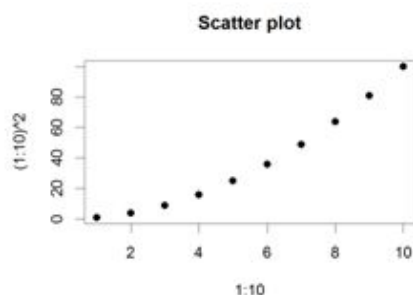
¶ RL was used when serotyping was done at a reference laboratory and was assumed to use the entire set of O-antisera present at the time of the study.

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).

Mathematical 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")



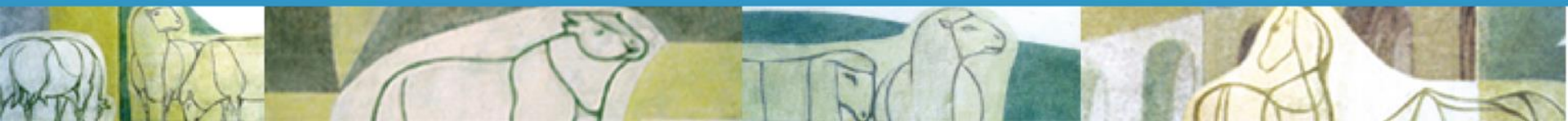
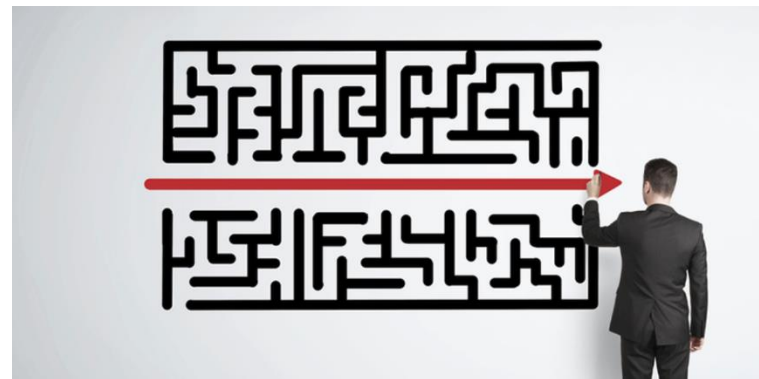
Most common mistakes

- Do not include 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



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

Looprofilattico 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.

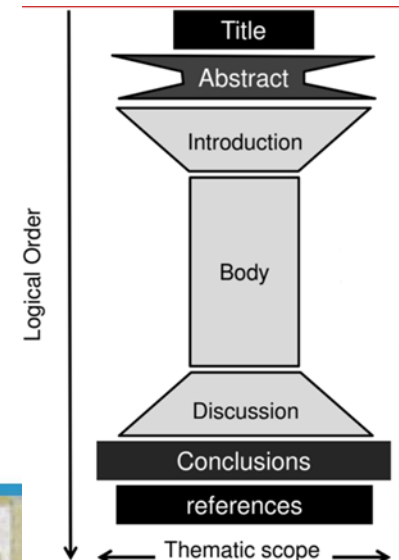
To our knowledge, the data presented here is the first report on sequence heterogeneity of *T. equi* and *B. caballi* detected in Italian horses, following the lead of previous studies, to verify if their conclusions are also valid for the Italian phylogenetic analysis results.

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

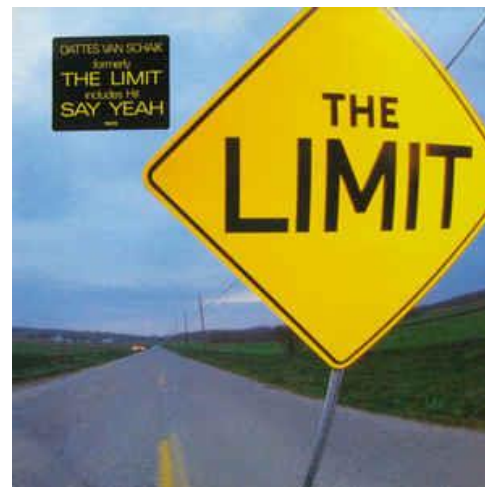
Follow the results section and comment the most important findings.

- 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?)



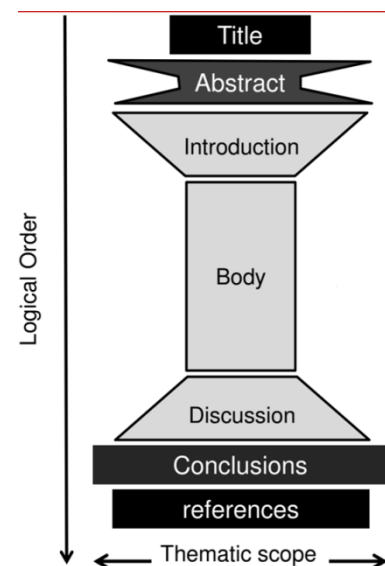
Typical structure – Limits & Strengths

- 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

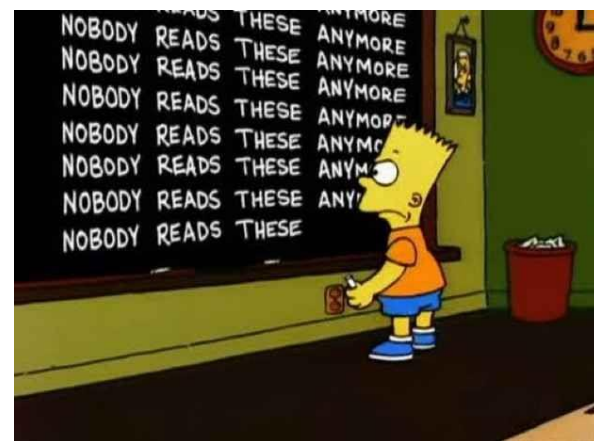
- Take home messages -> what do you want the reader remember about your study? (just few sentences or 1-2 paragraphs)
 - Concisely summarize the most important outcomes of your study but avoid repetitions -> elaborate them
 - Answer the question: «so what?» -> larger implication of your study
 - Prospective?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



Discussion

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!

- Refwork
- Endnote
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Accesso a RefWorks, il Software Web-Based adottato da BiblioSan per LA GESTIONE PERSONALE DELLE BIBLIOGRAFIE

- [RefWorks: il primo gestore di bibliografie con interfaccia web](#), che permette di organizzare e creare un proprio archivio personale di record bibliografici e generare automaticamente bibliografie in vari formati.
Per utilizzare il prodotto è necessario registrarsi usando il [Group Code di BiblioSan](#), da richiedere al responsabile della Biblioteca del proprio Ente (o referente BiblioSan).



Good practices

Put in relation....

the goal of your study

the results

the discussion

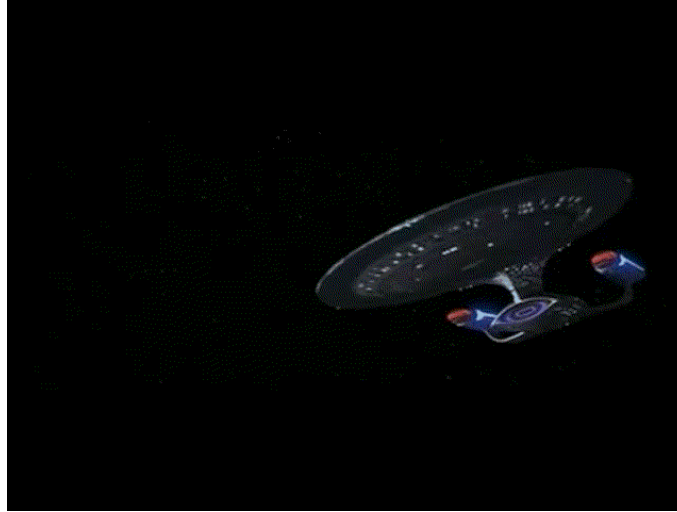
The key



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



BUONA RICERCA A TUTTI!



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