Reading Journal Articles in Science & Engineering

STUDENT LEARNING SUPPORT

Graduate Student Support

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Ryerson University sits on the Traditional Territory of the Mississauga's of New Credit First Nation. We are honoured to be a part of this community of our Indigenous colleagues and students.

- Chi Miigwetch

Most Science Research is Quantitative

	Quantitative	Qualitative
Results	Reported as numbers	Reported as words
Investigator	Concerned with objectivity	Concerned with subjectivity
Reality	Distinct from subjective states	Dependent on subjective states
Participants	Random sample	No sampling
Objects of research	Physical objects	Minds, meanings, understandings, beliefs, etc.

Main Types of Quantitative Research

Descriptive:
- Survey, Polling, Delphi Survey

Correlational:
- Predictive, Multiple Regression, Causal Modelling, Path Analysis, etc.

(Quasi-)Experimental:
- Causal Comparative, Repeated Measure Design, Randomized Block Design, etc.

Step 1: Read the Abstract

- The abstract appears above the introduction.
- A good abstract is a summary of the entire article.

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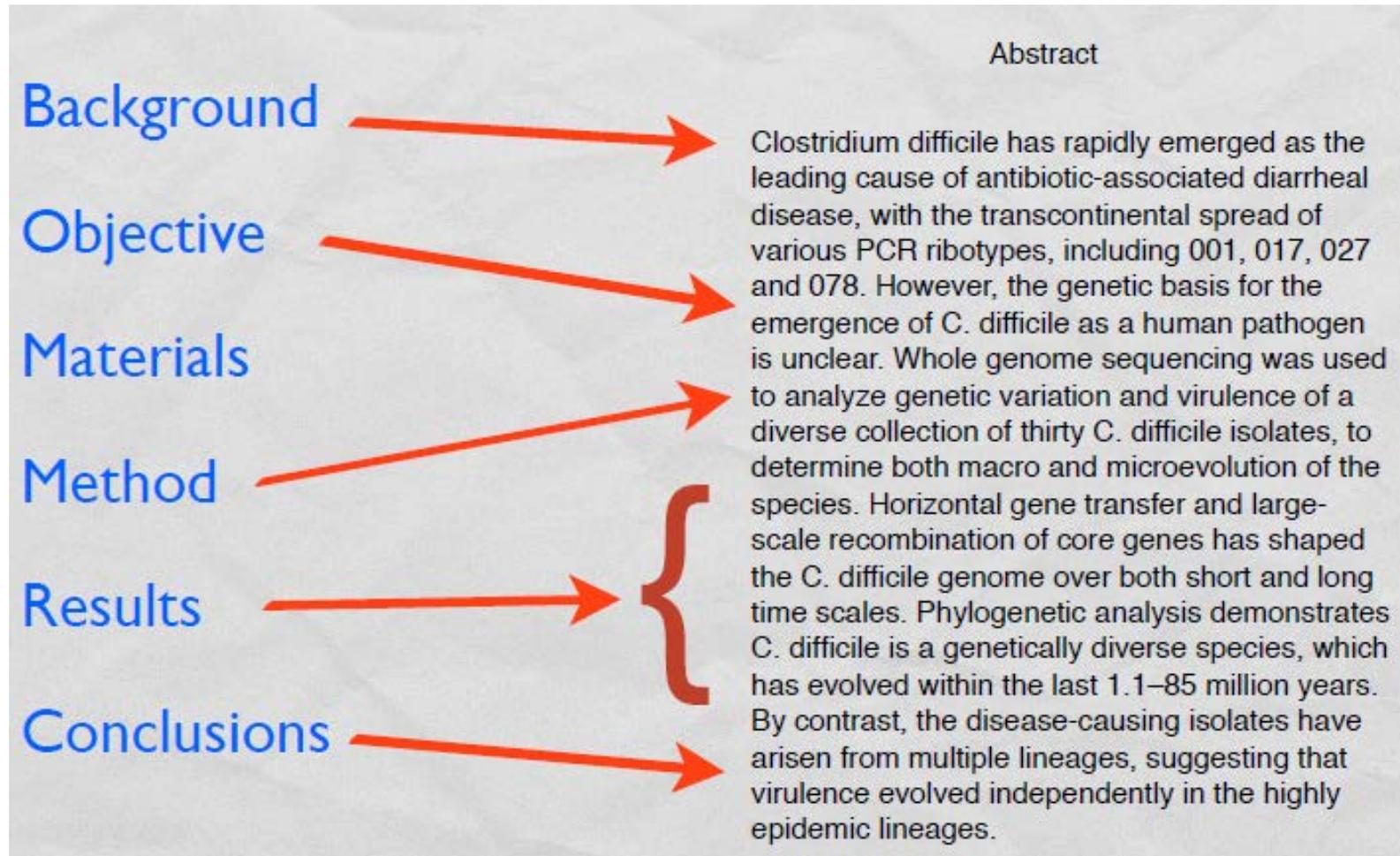UNIVERSITY

Parts of Abstract

Can you identify the parts of this abstract?
- Background
- Objective
- Materials
- Method
- Results
- Conclusions

Abstract

Clostridium difficile has rapidly emerged as the leading cause of antibiotic-associated diarrheal disease, with the transcontinental spread of various PCR ribotypes, including 001, 017, 027 and 078. However, the genetic basis for the emergence of C. difficile as a human pathogen is unclear. Whole genome sequencing was used to analyze genetic variation and virulence of a diverse collection of thirty C. difficile isolates, to determine both macro and microevolution of the species. Horizontal gene transfer and large-scale recombination of core genes has shaped the C. difficile genome over both short and long time scales. Phylogenetic analysis demonstrates C. difficile is a genetically diverse species, which has evolved within the last 1.1–85 million years. By contrast, the disease-causing isolates have arisen from multiple lineages, suggesting that virulence evolved independently in the highly epidemic lineages.

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Abstract Parts Identified

Background
Objective
Materials
Method
Results
Conclusions

Abstract

Clostridium difficile has rapidly emerged as the leading cause of antibiotic-associated diarrheal disease, with the transcontinental spread of various PCR ribotypes, including 001, 017, 027 and 078. However, the genetic basis for the emergence of C. difficile as a human pathogen is unclear. Whole genome sequencing was used to analyze genetic variation and virulence of a diverse collection of thirty C. difficile isolates, to determine both macro and microevolution of the species. Horizontal gene transfer and large-scale recombination of core genes has shaped the C. difficile genome over both short and long time scales. Phylogenetic analysis demonstrates C. difficile is a genetically diverse species, which has evolved within the last 1.1–85 million years. By contrast, the disease-causing isolates have arisen from multiple lineages, suggesting that virulence evolved independently in the highly epidemic lineages.

Which Abstract is Better & Why?

1. Clostridium difficile has rapidly emerged as the leading cause of antibiotic-associated diarrheal disease, with the transcontinental spread of various PCR ribotypes, including 001, 017, 027 and 078. However, the genetic basis for the emergence of C. difficile as a human pathogen is unclear. Whole genome sequencing was used to analyze genetic variation and virulence of a diverse collection of thirty C. difficile isolates, to determine both macro and microevolution of the species. Horizontal gene transfer and large-scale recombination of core genes has shaped the C. difficile genome over both short and long time scales. Phylogenetic analysis demonstrates C. difficile is a genetically diverse species, which has evolved within the last 1.1-85 million years. By contrast, the disease-causing isolates have arisen from multiple lineages, suggesting that virulence evolved independently in the highly epidemic lineages.

2. In this paper we study the accuracy of photometric redshifts computed through a standard SED fitting procedure, where SEDs are obtained from broad-band photometry. We present our public code hyperz, which is presently available on the web. We introduce the method and we discuss the expected influence of the different observational conditions and theoretical assumptions. In particular, the set of templates used in the minimization procedure (age, metallicity, reddening, absorption in the Lyman forest, ...) is studied in detail, through both real and simulated data. The expected accuracy of photometric redshifts, as well as the fraction of catastrophic identifications and wrong detections, is given as a function of the redshift range, the set of filters considered, and the photometric accuracy. Special attention is paid to the results expected from real data.

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The First One is Better.. The Second Has Missing Parts

Background →

Objective ?

Materials →

Method?

Results?

Conclusions?

Abstract

In this paper we study the accuracy of photometric redshifts computed through a standard SED fitting procedure, where SEDs are obtained from broad-band photometry. We present our public code hyperz, which is presently available on the web. We introduce the method and we discuss the expected influence of the different observational conditions and theoretical assumptions. In particular, the set of templates used in the minimization procedure (age, metallicity, reddening, absorption in the Lyman forest, ...) is studied in detail, through both real and simulated data. The expected accuracy of photometric redshifts, as well as the fraction of catastrophic identifications and wrong detections, is given as a function of the redshift range, the set of filters considered, and the photometric accuracy. Special attention is paid to the results expected from real data.

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Step 2: Pre-read the Article

- Glance quickly through the article to locate all the sections, visuals, and list of references.

- Check to see that each essential part is present.

- Check to see that each part does what it is supposed to do.

- Find the research question or hypothesis.

- Find the purpose of the research.

What Does A Journal Article Do?

- It provides an introduction

- It narrates a methodology

- It presents results

- It discusses the meaning of the results

What Does An Introduction Do?

- It identifies the topic.
- It reviews the existing studies in the field.
- It identifies an important area for research.
- It states the purpose of the study.

The Parts of an Introduction

The topic is usually identified in the first sentence or two of the Introduction.

SINCE the original demonstration by SATTIN & RALL (1970) that adenosine elevates the level of cyclic AMP in brain slices, several unusual regulatory properties of the nucleoside on the accumulation of cyclic AMP in brain tissue have been reported (for review see DALY, 1976).

The literature review follows the topic and usually comprises about half of the Introduction.

Evidence for a role of adenosine or closely related compounds in neuronal transmission was obtained from a number of studies (Kuroda & McIlwain, 1974), Kostopoulos et a., 1975, Kuroda et al., 1976; Schubert et al., 1976; Schofield, 1978; Stone & Taylor, 1978). However, the demonstration by Clark et al. (1974) that adenosine elevates.. the level of cyclic AMP in human astrocytoma cells points to . . . .

An important research area is identified.

Surprisingly, adenosine exerts a dual action on these normal glia-like cells: (a) it stimulates the accumulation of cyclic AMP (Giln & Schrier, 1972; Van Calker, 1977); (b) it inhibits the increase of the level of cyclic AMP caused by p-adrenoceptor stimulation (Van Calker, 1977; Van Calker et al., 1977).

The purpose of the study is announced.

Here we present evidence that these two effects of adenosine are mediated by two different types of receptors present on the outer surface of the cells.

Pre-read the Introduction

- Quickly skim through the introduction.
- Find the topic and mark it.
- Find the purpose and mark it.
- Stop skimming.

What Does a Methodology Section Do?

- It explains the materials used in the study
- It narrates the procedure used in the experiment or study
- It uses the past tense
- Also called: Design (or),Materials and Method

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Does This Fulfill Requirements of Methodology?

2.4 One-dimensional SDS polyacrylamide gel electrophoresis One-dimensional gel electrophoresis was carried out in vertical SDS-polyacrylamide gels (10 x 14 x 0.15 cm) containing 0.1 % SDS [91, with a 1.5 cm long 5 % stacking gel on top of an 8.5 cm long 11 % separating gel. All solutions and buffers were filtered through 0.45 pm nitrocellulose filters in order to avoid staining of dust particles. Protoplasts were lysed in sample buffer (50 mM Tris-HCl, pH 6.8, 2 % SDS, 10 % glycerol, 3 %, 2-mercaptoethanol), heated for 3 min at 95o C and subjected to electrophoresis. Gels were subsequently fixed overnight and silver stained.

Pre-read the Methods Section

- Quickly skim through the Methods section. It may be divided into several parts. The section and subsection titles may relate to the topic.

- The word "Method" may be missing.

- This section may also be called "Materials and Method", "Procedure", "Methodology", or none of these.

- Find the materials that are used in the study.

- Find the procedure that is used in the study.

What Does a Results/Findings Section Do?

- It presents all the results of the experiment or study and summarizes the most important ones

- It includes negative results, if any

- It avoids discussing or explaining the results

- It uses tables, graphs, etc.

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A good example of Results (excerpt)

The values obtained for the skinfold thicknesses at the four separate sites are given in Table 2. Table 3 shows the values for the total of the four skinfolds, the density, and the fat content of the body expressed as a percentage of body-weight.

The correlation coefficients for sums of two and more skinfolds (in the logarithmic transformation) and body density varied from about - 0.7 to - 0.9 for the different age-groups of both the men and the women.

Table 4 shows the standard errors of the estimate of density using the logarithm of each of the four separate skinfolds, the logarithm of combinations of two and more skinfolds, and the logarithm of the sum of the four skinfolds in the respective linear regression equations. The SES for the logarithmic form are slightly lower than those for the raw measurement in the men whereas there is no consistent difference in the women. The SE of the estimate is considerably greater in both sexes for the combined age-group 17 years and over than for the selected smaller age-ranges.

Pre-read the Results Section

- Quickly skim through the Results section. It may be called "Findings" or something else.

- Sometimes Results and Discussion are combined. If so, focus only on the results for now.

- Look for tables, graphs, charts, or any other visuals that contain the results of the study.

- Look for a mention of the most important results.

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What Does the Discussion Section Do?

- It interprets the data from the Results section

- It answers the research question of the study or proves the hypothesis of the study.

A good example of Discussion (excerpt)

In this study, we showed that iPS cells can be generated from adult HDF and other somatic cells by retroviral transduction of the same four transcription factors with mouse iPS cells, namely Oct3/4, Sox2, Klf4, and c-Myc. The established human iPS cells are similar to hES cells in many aspects, including morphology, proliferation, feeder dependence, surface markers, gene expression, promoter activities, telomerase activities, in vitro differentiation, and teratoma formation. The four retroviruses are strongly silenced in human iPS cells, indicating that these cells are efficiently reprogrammed and do not depend on continuous expression of the transgenes for self renewal.

hES cells are different from mouse counterparts in many respects (Rao, 2004). hES cell colonies are flatter and do not override each other. hES cells depend on bFGF for self renewal (Amit et al., 2000), whereas mouse ES cells depend on the LIF/Stat3 pathway (Matsuda et al., 1999 and Niwa et al., 1998). BMP induces differentiation in hES cells (Xu et al., 2005) but is involved in self renewal of mouse ES cells (Ying et al., 2003). Despite these differences, our data show that the same four transcription factors induce iPS cells in both human and mouse. The four factors, however, could not induce human iPS cells when fibroblasts were kept under the culture condition for mouse ES cells after retroviral transduction (data not shown). These data suggest that the fundamental transcriptional network governing pluripotency is common in human and mice, but extrinsic factors and signals maintaining pluripotency are unique for each species.

Results or Discussion?

1. Experimental points (Arn, Ah) of tryptophan fluorescence for various native proteins in neutral aqueous solutions at room temperature are presented in Table 1 and in Fig. 1

2. However, NIR could also function to specifically inhibit target genes such as p21 that are known to suppress apoptosis, and thereby support an apoptopic response if necessary.

3. When considering more elaborated cluster-finding algorithms, such as the one produced by Kepner et al. (1999), Olsen et al. (1999), Scodeggio et al. (1999)..., these results could be regarded as the relative improvement due to photometric redshifts.

4. The phylogenetic tree reveals that the broad genetic diversity of C. difficile is predominantly reflected in the ribotyping scheme.

Results or Discussion? Answers

1. **Experimental points** (Arn, Ah) of tryptophan fluorescence for various native proteins in neutral aqueous solutions at room temperature **are presented in Table 1 and in Fig. 1**

Results

2. However, NIR **could** also function to specifically inhibit target genes such as p21 that are known to suppress apoptosis, and thereby support an apoptopic response if necessary.

Discussion

3. When considering more elaborated cluster-finding algorithms, such as the one produced by Kepner et al. (1999), Olsen et al. (1999), Scodeggio et al. (1999)…, these results **could** be regarded as the relative improvement due to photometric redshifts.

Discussion

4. The phylogenetic tree **reveals** that the broad genetic diversity of C. difficile is predominantly reflected in the ribotyping scheme.

Results

Pre-read Discussion Section

- Quickly skim through the Discussion section. If it is combined with the Results section, look for discussion statements only.

- Find the answer(s) to the research questions(s).

Step 3: Read for Main Ideas

- You should now have a general overview of the article. Decide what parts you need to read in detail.

- It is rarely necessary to read an entire article. Often, reading the results and discussion is sufficient.

- Once you have the information you need to contribute to your own research, put the article aside.

Step 4: Re-read for Details

- If you have decided that the article is useful for your studies, you may want to read certain sections of it again to understand difficult concepts.

- If you are looking for other related research, you may want to examine the literature review section of the article (Mostly in the introduction).

Step 5: Validity Check

If you plan on using information from the article, you should do a validity check:

- It has internal validity if it deals with what it claims to study.
- It has external validity if it can be generalized to other situations, materials, etc.

Step 6: Reliability Check

- Is the author respected in the field?

- Is the journal respected in the field?

- Was the research funded by a reputable agency?

- Are the data reliable?

Reliability Challenges

- A weak methodology (e.g. small or non-representative sample)
- Not enough information given to enable replication
- The author has a conflict of interest (e.g. researches oil exploration, but the study is funded by an oil company)
- Careless with information; incomplete research

Summary

- A quantitative study contains an Abstract, an Introduction, a Methods section, a Results section, and a Discussion section. Occasionally, it ends with a Conclusions section, summing up the main outcomes of the study.

- Some sections may be combined or have other names.

- Step 1: Read the Abstract. If the article is not on topic, you may save yourself the trouble of reading further. But beware that some abstracts are poorly written.

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Summary (continued)

- Step 2: Pre-read the article. Dismiss the article if it is not on the topic.
- Step 3: Read for main ideas. Read only the relevant sections, usually Results and Discussion.
- Step 4: Re-read for details. Focus only on what is relevant to your own research.
- Step 5: Check for validity.
- Step 6. Check for reliability

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Sources

Slide	Source
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2, 3, 4, 5	He et al. (2010). Evolutionary dynamics of Clostridium difficile over short and long time scales. PNAS, 107(16), 7527-7532.
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12	Han, M., Özyilmaz, B., Zhang, Y., and Kim, P. (2007). Energy Band Gap Engineering of Graphene Nanoribbons. Physical Review Letters, 98, 206805.
13	Sentence 1: Burstein, E., Vedenkina, S. and Ivkova, M. (1973). Fluorescence and the location of tryptophan residues in protein molecules. Photochemistry and Photobiology. 18, 263-279. Sentence 2.: Heyne, K., Willnecker, V., Schneider, J., Conrad, M., Raulf, N., Roland Schüle, R. and Roemer, K. (2010). NIR, an inhibitor of histone acetyltransferases, regulates transcription factor TAp63 and is controlled by the cell cycle. Nucleic Acids Research, 38 (10), 3159–3171. Sentence 3: Micol Bolzonella, M., Joan-Marc Miralles, J.-M., Roser Pellö, R. (2008). Photometric Redshifts based on standard SED fitting procedures. Astronomy and Astrophysics, 1 (2). Sentence 4: Miao Hea et al. (2010). Evolutionary dynamics of Clostridium difficile over short and long time scales. PNAS, 107 (16), 7527-7532.
30	Locke, L., Silverman, S., & Spirduso, W. (2010). Reading and Understanding Research (3rd. ed.) p. 94. Los Angeles, Sage.

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