

Authors' guidelines for CIBB short papers

First Author¹, Second Author², and Third Author^{*,3,4}

¹ First author's department, institute, city, country. Email, ORCID code

² Second author's department, institute, city, country. Email, ORCID code

³ Third author's primary affiliation department, institute, city, country. Email, ORCID code

⁴ Third author's secondary affiliation department, institute, city, country.

*corresponding author

Keywords: keyword1, keyword2, keyword3, keyword4, keyword5.

Abstract. In this document there are the main guidelines for preparing your contribution for the electronic proceedings of CIBB meeting. This document will help you to produce the PDF file of your paper. The paper length must be from 4 to 6 pages.

1 Introduction

In this document there are the guidelines for your contribution for the electronic proceedings of the Computational Intelligence Methods for Bioinformatics and Biostatistics (CIBB) meetings. In this section the authors need to write the Scientific Background or the Introduction.

2 Data and Methods

This document is the printed version of the cibb-sample-2023.pdf file, and is formatted following the guidelines here described. On the CIBB website you can download the zipped archive from the CIBB conference website.

Please note that only PDF versions of papers can be accepted, as the proceedings of CIBB will be produced starting from them.

3 Results

The paper must be formatted single column, 12 pt, on standard A4 paper, and its side edges should be 2.5 cm above, down, left, and right, as shown by this document. The maximum length of the paper is 6 pages.

The references should be cited in this way [1, 2], or also [3, 4, 5].

Software code commands should be written this way:

```
x <- 0.5
y <- 0.8
z <- x + y
print(z)
```

3.1 Tables and Figures

Tables and figures must be placed in the paper close where they are cited. The caption heading for a table should be placed at the top of the table, as shown in Table 1. The caption heading for a figure should be placed below the figure, as shown in Figure 1.

3.2 Equations

Equations should be centered and numbered consecutively, in this way:

method	result	interpretation
aaa	0.7	ccc
ddd	0.2	zzz
jjj	0.4	ppp
ggg	0.5	qqq

Table 1: **Recap of the results.** Example table containing results. Please alternate the background colors for each row, to facilitate a clearer interpretation

$$\mathbf{y}_j = \frac{\sum_{k=1}^n (u_{jk})^m \mathbf{x}_k}{\sum_{k=1}^n (u_{jk})^m} \quad \forall j, \quad (1)$$

and

$$u_{jk} = \begin{cases} \left(\sum_{l=1}^c \left(\frac{E_j(\mathbf{x}_k)}{E_l(\mathbf{x}_k)} \right)^{\frac{2}{m-1}} \right)^{-1} & \text{if } E_j(\mathbf{x}_k) > 0 \quad \forall j, k \\ 1 & \text{if } E_j(\mathbf{x}_k) = 0 \quad (u_{lk} = 0 \quad \forall l \neq j) \end{cases} \quad (2)$$

and referred as: Equation 1 and Equation 2.

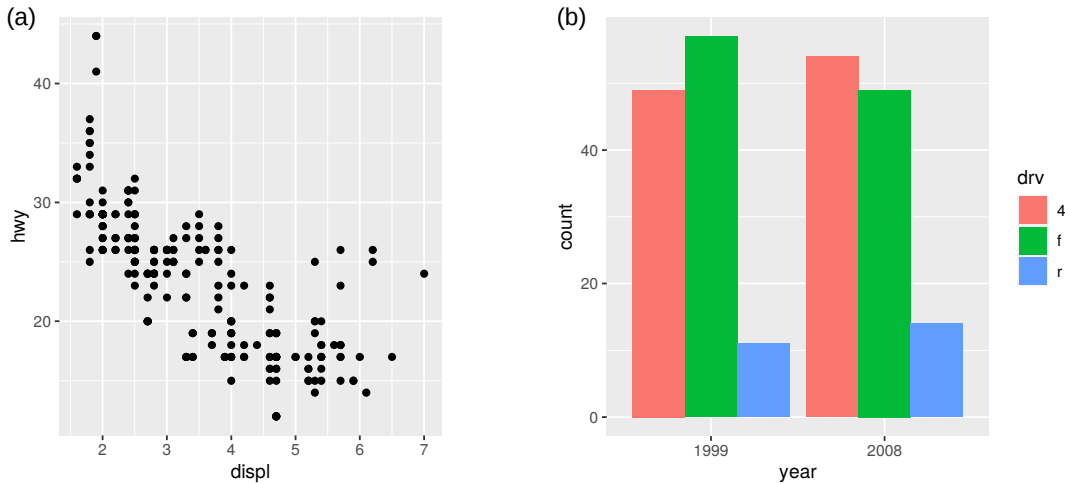


Figure 1: **Example figure.** Please generate your figure images as PDF files and include them here in the article within the text. We suggest you to generate your figures with the ggplot2 package in R or with Matplotlib in Python. Regarding colors, please make sure you use a colorblind palette. This image was generated with ggplot2 and then edited with LibreOffice Draw.

4 Conclusion

In this section the authors write the conclusion of the paper. Since this is a short paper, please do not include more than 10 references in the bibliography.

Conflict of interests

The authors should declare here any potential conflicts of interests.

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Availability of data and software code (optional)

Our software code is available at the following URL: XXX.

Our dataset is available at the following URL: XXX.

References

- [1] Pedro Domingos. A few useful things to know about machine learning. *Communications of the ACM*, 55(10):78–87, 2012.
- [2] Michael Powell, Mahan Hosseini, John Collins, Chloe Callahan-Flintoft, William Jones, Howard Bowman, and Brad Wyble. I tried a bunch of things: the dangers of unexpected overfitting in classification. *bioRxiv*, 078816, 2020.
- [3] Jelena Čuklina, Patrick GA Pedrioli, and Ruedi Aebersold. Review of batch effects prevention, diagnostics, and correction approaches. In *Mass Spectrometry Data Analysis in Proteomics*, pages 373–387. Springer, 2020.
- [4] Charles D Hansen, Min Chen, Christopher R Johnson, Arie E Kaufman, and Hans Hagen. *Scientific Visualization*. Springer, 2014.
- [5] The Gene Ontology Consortium. The Gene Ontology Resource. <http://www.geneontology.org/> URL visited on 21st April 2022.