# **Manuscript Title**

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Computationally derived predictions allow for diversity audits on a scale that would not be possible otherwise. Numerous tools exist to algorithmically infer gender, nationality, and ethnicity information using only the feature most likely to be non-missing in a relevant dataset: an individual's name. Most of these models are highly scalable, allowing auditors to define the scope of their target group and background population as broadly as needed.

Prediction models are not a panacea; several factors limit both their accuracy at recapitulating self-reported information and their ability to address the underlying motivating questions of diversity audits. For an example of the former, gender associations of a given name can vary by culture, potentially biasing gender predictions where additional information is not available [1]. For an example of the latter, most gender prediction models are trained on binary gender labels, which occludes assessing the representation of transgender, non-binary, and intersex individuals [2].

Proxy predictions of ethnicity via name origin are more difficult still; the choice of categories to probabilistically predict on is non-trivial and difficult to define. Furthermore, there is no one-to-one mapping between having a name from a linguistic group and belonging to a minoritized or underrepresented group. Colonialism, immigration, and structural racism have affected most groups' linguistic history and inclusion or exclusion from scientific communities in complex ways that are nearly impossible to parse from names alone. For instance, these classifiers are usually unable to distinguish if names of Hispanic origin come from the Iberian Peninsula or from Latin America [3]. If a target and background population had identical probabilistic proportions of Hispanic names, but the target group primarily consisted of individuals from Spain and Portugal, underrepresentation of Latin American scientists would then go unnoticed in an exclusively computational analysis.

Considering these things, we propose the following recommendations for best practices in auditing scientific systems:

This manuscript is a template (aka "rootstock") for <u>Manubot</u>, a tool for writing scholarly manuscripts. Use this template as a starting point for your manuscript.

The rest of this document is a full list of formatting elements/features supported by Manubot. Compare the input (.md files in the /content directory) to the output you see below.

# **Basic formatting**

### Centered text

Right-aligned text

Italic text

Combined italics and bold

### Strikethrough

- 1. Ordered list item
- 2. Ordered list item
  - a. Sub-item
  - b. Sub-item
    - i. Sub-sub-item
- 3. Ordered list item
  - a. Sub-item
- List item
- · List item
- · List item

subscript: H<sub>2</sub>O is a liquid

superscript: 2<sup>10</sup> is 1024.

unicode superscripts<sup>0123456789</sup>

### unicode subscripts<sub>0123456789</sub>

A long paragraph of text. Lorem ipsum dolor sit amet, consectetur adipiscing elit, sed do eiusmod tempor incididunt ut labore et dolore magna aliqua. Ut enim ad minim veniam, quis nostrud exercitation ullamco laboris nisi ut aliquip ex ea commodo consequat. Duis aute irure dolor in reprehenderit in voluptate velit esse cillum dolore eu fugiat nulla pariatur. Excepteur sint occaecat cupidatat non proident, sunt in culpa qui officia deserunt mollit anim id est laborum.

Putting each sentence on its own line has numerous benefits with regard to <u>editing</u> and <u>version</u> <u>control</u>.

Line break without starting a new paragraph by putting two spaces at end of line.

# **Document organization**

Document section headings:

# **Heading 1**

# **Heading 2**

**Heading 3** 

Heading 4

Heading 5

Heading 6



### Horizontal rule:

Heading 1's are recommended to be reserved for the title of the manuscript.

Heading 2's are recommended for broad sections such as Abstract, Methods, Conclusion, etc.

Heading 3's and Heading 4's are recommended for sub-sections.

### Links

Bare URL link: https://manubot.org

<u>Long link with lots of words and stuff and junk and bleep and blah and stuff and other stuff and more stuff yeah</u>

Link with text

Link with hover text

Link by reference

## **Citations**

Citation by DOI [4].

Citation by PubMed Central ID [5].

Citation by PubMed ID [6].

Citation by Wikidata ID [7].

Citation by ISBN [8].

Citation by URL [9].

Citation by alias [10].

Multiple citations can be put inside the same set of brackets [4,8,10]. Manubot plugins provide easier, more convenient visualization of and navigation between citations [5,6,10,11].

Citation tags (i.e. aliases) can be defined in their own paragraphs using Markdown's reference link syntax:

# Referencing figures, tables, equations

Figure 1

Figure 2

```
Figure 3

Figure 4

Table 1

Equation 1

Equation 2
```

# **Quotes and code**

Quoted text

Quoted block of text

Two roads diverged in a wood, and I—I took the one less traveled by, And that has made all the difference.

Code in the middle of normal text, aka inline code.

Code block with Python syntax highlighting:

```
from manubot.cite.doi import expand_short_doi

def test_expand_short_doi():
    doi = expand_short_doi("10/c3bp")
    # a string too long to fit within page:
    assert doi == "10.25313/2524-2695-2018-3-vliyanie-enhansera-copia-i-
        insulyatora-gypsy-na-sintez-ernk-modifikatsii-hromatina-i-
        svyazyvanie-insulyatornyh-belkov-vtransfetsirovannyh-geneticheskih-
        konstruktsiyah"
```

Code block with no syntax highlighting:

```
Exporting HTML manuscript
Exporting DOCX manuscript
Exporting PDF manuscript
```

# **Figures**



**Figure 1:** A square image at actual size and with a bottom caption. Loaded from the latest version of image on GitHub.



**Figure 2:** An image too wide to fit within page at full size. Loaded from a specific (hashed) version of the image on GitHub.



Figure 3: A tall image with a specified height. Loaded from a specific (hashed) version of the image on GitHub.



**Figure 4:** A vector .svg image loaded from GitHub. The parameter sanitize=true is necessary to properly load SVGs hosted via GitHub URLs. White background specified to serve as a backdrop for transparent sections of the image.

# **Tables**

**Table 1:** A table with a top caption and specified relative column widths.

Bowling Scores	Jane	John	Alice	Bob
Game 1	150	187	210	105
Game 2	98	202	197	102
Game 3	123	180	238	134

**Table 2:** A table too wide to fit within page.

	Digits 1-33	Digits 34-66	Digits 67-99	Ref.
р	3.141592653589 8462643383279			I niday org
е	2.718281828459 5360287471352			nasa gov

 Table 3: A table with merged cells using the attributes plugin.

	Colors		
Size	Text Color	Background Color	
big	blue	orange	
small	black	white	

# **Equations**

A LaTeX equation:

$$\int_0^\infty e^{-x^2} dx = \frac{\sqrt{\pi}}{2} \tag{1}$$

An equation too long to fit within page:

$$x = a + b + c + d + e + f + g + h + i + j + k + l + m + n + o + p + q + r + s + t + u + v + w + x + y + z + 1 + 2 + 3 + 4 + 5 + 6 + 7 + 8 + 9$$
(2)

# **Special**

▲ WARNING The following features are only supported and intended for .html and .pdf exports. Journals are not likely to support them, and they may not display correctly when converted to other formats such as .docx.

LINK STYLED AS A BUTTON

Adding arbitrary HTML attributes to an element using Pandoc's attribute syntax:

Manubot Manubot Manubot Manubot Manubot. Manubot Manubot Manubot Manubot. Manubot. Manubot Manubot. Manubot. Manubot. Manubot. Manubot.

Adding arbitrary HTML attributes to an element with the Manubot attributes plugin (more flexible than Pandoc's method in terms of which elements you can add attributes to):

Manubot Manubot.

Available background colors for text, images, code, banners, etc:

white lightgrey grey darkgrey black lightred lightyellow lightgreen lightblue lightpurple red orange yellow green blue purple

Using the Font Awesome icon set:



Light Grey Banner
useful for general information - manubot.org

# **1** Blue Banner

useful for important information - manubot.org

**♦ Light Red Banner** useful for *warnings* - <u>manubot.org</u>

## References

# 1. A Data-driven Approach to Studying Given Names and their Gender and Ethnicity Associations

Shervin Malmasi

Proceedings of the Australasian Language Technology Association Workshop 2014 (2014-11) <a href="https://aclanthology.org/U14-1021">https://aclanthology.org/U14-1021</a>

# 2. Racial and ethnic imbalance in neuroscience reference lists and intersections with gender

Maxwell A Bertolero, Jordan D Dworkin, Sophia U David, Claudia López Lloreda, Pragya Srivastava, Jennifer Stiso, Dale Zhou, Kafui Dzirasa, Damien A Fair, Antonia N Kaczkurkin, ... Danielle S Bassett

Cold Spring Harbor Laboratory (2020-10-12) <a href="https://doi.org/gj7mdc">https://doi.org/gj7mdc</a>

DOI: 10.1101/2020.10.12.336230

### 3. Analysis of scientific society honors reveals disparities

Trang T Le, Daniel S Himmelstein, Ariel A Hippen, Matthew R Gazzara, Casey S Greene *Cell Systems* (2021-09) <a href="https://doi.org/gmhq49">https://doi.org/gmhq49</a>

DOI: <u>10.1016/j.cels.2021.07.007</u> · PMID: <u>34555325</u>

### 4. Sci-Hub provides access to nearly all scholarly literature

Daniel S Himmelstein, Ariel Rodriguez Romero, Jacob G Levernier, Thomas Anthony Munro, Stephen Reid McLaughlin, Bastian Greshake Tzovaras, Casey S Greene *eLife* (2018-03-01) <a href="https://doi.org/ckcj">https://doi.org/ckcj</a>

DOI: 10.7554/elife.32822 · PMID: 29424689 · PMCID: PMC5832410

# 5. Reproducibility of computational workflows is automated using continuous analysis

Brett K Beaulieu-Jones, Casey S Greene

Nature biotechnology (2017-04) <a href="https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6103790/">https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6103790/</a> DOI:  $10.1038/nbt.3780 \cdot PMID$ :  $28288103 \cdot PMCID$ : PMC6103790

### 6. **Bitcoin for the biological literature.**

Douglas Heaven

Nature (2019-02) https://www.ncbi.nlm.nih.gov/pubmed/30718888

DOI: <u>10.1038/d41586-019-00447-9</u> · PMID: <u>30718888</u>

# 7. Plan S: Accelerating the transition to full and immediate Open Access to scientific publications

cOAlition S

(2018-09-04) https://www.wikidata.org/wiki/Q56458321

### 8. **Open access**

Peter Suber MIT Press (2012)

ISBN: 9780262517638

### 9. **Open collaborative writing with Manubot**

Daniel S Himmelstein, Vincent Rubinetti, David R Slochower, Dongbo Hu, Venkat S Malladi, Casey S Greene, Anthony Gitter

Manubot (2020-05-25) https://greenelab.github.io/meta-review/

### 10. Opportunities and obstacles for deep learning in biology and medicine

Travers Ching, Daniel S Himmelstein, Brett K Beaulieu-Jones, Alexandr A Kalinin, Brian T Do, Gregory P Way, Enrico Ferrero, Paul-Michael Agapow, Michael Zietz, Michael M Hoffman, ... Casey S Greene

Journal of The Royal Society Interface (2018-04-04) <a href="https://doi.org/gddkhn">https://doi.org/gddkhn</a>
DOI: <a href="https://doi.org/gddkhn">10.1098/rsif.2017.0387</a> · PMID: <a href="https://doi.org/gddkhn">29618526</a> · PMCID: <a href="https://doi.org/gddkhn">PMC5938574</a>

### 11. Open collaborative writing with Manubot

Daniel S Himmelstein, Vincent Rubinetti, David R Slochower, Dongbo Hu, Venkat S Malladi, Casey S Greene, Anthony Gitter

PLOS Computational Biology (2019-06-24) <a href="https://doi.org/c7np">https://doi.org/c7np</a>

DOI: <u>10.1371/journal.pcbi.1007128</u> · PMID: <u>31233491</u> · PMCID: <u>PMC6611653</u>