

Manuscript Title

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Abstract

This manuscript is a template (aka “rootstock”) for [Manubot](#), 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

Bold text

Semi-bold text

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: H₂O is a liquid

superscript: 2¹⁰ is 1024.

[unicode superscripts](#)⁰¹²³⁴⁵⁶⁷⁸⁹

[unicode subscripts](#)₀₁₂₃₄₅₆₇₈₉

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 [editing](#) and [version control](#).

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

A heading centered on its own printed page

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>

[Long link with lots of words and stuff and junk and bleep and blah and stuff and other stuff and more stuff yeah](#)

[Link with text](#)

[Link with hover text](#)

[Link by reference](#)

Citations

Citation by DOI [1].

Citation by PubMed Central ID [2].

Citation by PubMed ID [3].

Citation by Wikidata ID [4].

Citation by ISBN [5].

Citation by URL [6].

Citation by alias [7].

Multiple citations can be put inside the same set of brackets [1,5,7]. Manubot plugins provide easier, more convenient visualization of and navigation between citations [2,3,7,8].

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-geneticheskikh-
        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.

<i>Bowling Scores</i>	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.
pi	3.14159265358979323846264338327950	288419716939937510582097494459230	781640628620899862803482534211706	piday.org
e	2.71828182845904523536028747135266	249775724709369995957496696762772	407663035354759457138217852516642	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:

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

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.

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



Blue Banner

useful for *important information* - manubot.org



Light Red Banner

useful for *warnings* - manubot.org

Introduction

1. Biomedical language is constantly changing
 1. Scientists make new discoveries
 2. Old technologies are being revamped
 3. More reasons for language changes
2. Diachronic studies aims to capture these types of changes through time
 1. Insert papers for language changes in general
 1. doi:10.1007/s00799-019-00271-6
 2. doi:10.1142/9789811232701_0011
 3. arxiv:1605.09096
 4. arxiv:1806.03537
 5. arxiv:1606.02821
 6. doi:10.18653/v1/N18-1044
3. Gap in knowledge:
 1. work has focused majorly on non-biomedical text
 2. biomedical related work is only on abstract and titles
 3. Work has yet to focus on individual tokens and themes.
4. Goal is to examine longitudinal trends for biomedical term changes.

Don't forget in here your methodological contribution to estimate uncertainty with variable-size training datasets in each year by training multiple models and examining variability across them.

Methods

1. Pubtator Central
 1. breif description about the dataset
 2. talk about how it contains entities tagged
2. Word2vec Model
 1. training parameters
 2. Use 10 models for each year
 3. min cutoff is 10
3. Orthogonal Procrustes - to align models onto year 2021
 1. Allows for the models to be directly compared
4. Determining semantic change
 1. Cosine metric to determine difference between words
 2. Scaf ratio method to model temporal changes
 3. CUSUM to actually detect change throughout the years

5. Umap visualization
 1. Explain why aligned umap - preserves local and global structure
 2. mention parameters for aligned umap

Results

One potential results panel: comparing results with abstract and full text (since you say above full text is not so often used).

1. Figure 1 - Visual to show that alignment works along intra year variation (Procrustes Validation)
2. Umap panel for an individual year to show models are separated

I would start with the simplest possible way that you can show things, and only bring in more complexity like UMAP when necessary. I'm guessing that you would be able to show this with just PCA or similar, unless I'm not thinking correctly.
3. Umap panel to show the same year after models have been aligned
4. Umap panel to show across years (inter-year variation)
 1. might not have this as a figure given the aligned umap results, but we shall see
5. Figure 2 - CUSUM validation

I think you might want another figure here that shows how you can use the variability in distance to address the challenges of variable training set size / model uncertainty. Let's see how things shake out as you're writing.
6. Table of found timepoint changes using this algorithm
7. Highlight pandemic as positive control
8. Nearest Neighbors upset plot ^^
9. Might look into lung cancer or other form of cancer results
10. Figure 3 - Website walkthrough for the work done here
11. Website screenshots

The figures that make up the website might be nice to show/explain individually - not as screenshots but as actual figures (remember the PLOS situation where using a screenshot was an issue we had to work through).
12. Basically a walkthrough of the website and how a user can operate the web resource (similar to preprint similarity search)

Discussion and Conclusion

1. We provided a website resource to allow users to see token association changes
2. Word2vec is unstable and we implemented an approach to account for that variation
3. Constructs groundwork for future research into token changes
4. Will implement biorxiv and other preprint resources as a next step.

References

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