Machine Learning of Biomedical Text for Gene Network Knowledge

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Machine Learning of Biomedical Text for Gene Network Knowledge

A project Report
Presented to
The Faculty of Computer Engineering Department
San Jose State University

In Partial Fulfillment
Of the Requirements for the Degree
Bachelor of Science in Software Engineering

By Tue Do Ausin Fong Thinh Huynh Mary Markart 02/2023

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Abstract{.page_break_before}

Machine Learning of Biomedical Text for Gene Network Knowledge By Tue Do, Austin Fong, Thinh Huynh, Mary Markart

Genetic research is the study of DNA to find out what genes and environmental factors contribute to diseases. There are multiple studies conducted on individuals or groups of genes and how they impact health and disease. Thus, there is no lack in the amount of data to draw conclusions from and researchers have the potential to make more connections from within the data.

An issue arises when it takes a long time to find and sift through biomedical research papers to find knowledge useful to researchers. There are already ideas present in literature, but also a lack of finding a connection between already present ideas. Researchers are constantly looking to find these connections; however, there is a limiting factor of time and can be overwhelming without the right tools.

Data from text mining biomedical texts was warehoused through the College of Engineering HPC or AWS DynamoDB and AWS Redshift. Data processing utilized BERT and GNormPlus models to categorize and normalize input. TigerGraph was used to represent the knowledge accumulated to visualize relationships. This project reduced the amount of time needed to search through biomedical research by making it easier to discover knowledge about various biological mechanisms using machine learning.

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

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 superscripts⁰¹²³⁴⁵⁶⁷⁸⁹

unicode subscripts₀₁₂₃₄₅₆₇₈₉

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

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-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. Note that if you want to export to Word (.docx), you need to download the image and reference it locally (e.g. content/images/vector.svg) instead of using a URL.

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.
pi	3.14159265358979323 846264338327950	28841971693993751 0582097494459230	78164062862089986 2803482534211706	piday.org
е	2.71828182845904523 536028747135266	24977572470936999 5957496696762772	40766303535475945 7138217852516642	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.

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 Manubo

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. 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) https://doi.org/ckcj

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

2. Reproducibility of computational workflows is automated using continuous analysis

Brett K Beaulieu-Jones, Casey S Greene

Nature biotechnology (2017-04) https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6103790/
DOI: 10.1038/nbt.3780 · PMID: 28288103 · PMCID: PMC6103790

3. **Bitcoin for the biological literature.**

Douglas Heaven

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

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

4. 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

5. **Open access**

Peter Suber *MIT Press* (2012)

ISBN: 9780262517638

6. 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/

7. 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) https://doi.org/gddkhn DOI: 10.1098/rsif.2017.0387 • PMID: 29618526 • PMCID: PMC5938574

8. 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) https://doi.org/c7np

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