Rχiv-Maker: An Automated Template Engine for Streamlined Scientific Publications

Bruno M. Saraiva^{1,⊠}, Guillaume Jaguemet^{2,3,4,⊠}, and Ricardo Henrigues^{1,5,⊠}

¹ Instituto de Tecnologia Química e Biológica António Xavier, Universidade Nova de Lisboa, Oeiras, Portugal ² Faculty of Science and Engineering, Cell Biology, Åbo Akademi University, Turku, Finland ³ InFLAMES Research Flagship Center, University of Turku, Turku, Finland ⁴ Turku Bioscience Centre, University of Turku and Åbo Akademi University, Turku, Finland ⁵ UCL Laboratory for Molecular Cell Biology, University College London, London, United Kingdom

Modern scientific publishing has moved towards rapid dissemination through preprint servers, putting greater demands on researchers for preparing and quality-checking manuscripts. We introduce RXiv-Maker, a comprehensive system native to Github that simplifies scientific writing through markdownbased authoring with automated LaTeX conversion. It's specifically designed to help produce preprints for curation in arXiv, bioRxiv, and medRxiv. The system lets researchers write in the familiar and lightweight markdown syntax while generating publication-quality documents automatically. RXiv-Maker offers flexible compilation strategies, including cloudbased GitHub Actions, interactive Google Colab notebooks, and reproducible local builds via Docker containerisation, ensuring consistent environments and eliminating dependency conflicts. The framework inherently supports reproducible research by enabling programmatic figure generation using Python libraries and script-based diagramming with Mermaid.js. This selfdocumenting article, created entirely within the framework, shows how this markdown-centric workflow transforms scientific communication into an efficient, collaborative, and transparent process, empowering researchers to focus on content while upholding rigorous standards of quality and reproducibility.

article template | scientific publishing | preprints

Correspondence: (B. M. Saraiva) b.saraiva@itqb.unl.pt; (G. Jaquemet) guillaume.jacquemet@abo.fi; (R. Henriques) ricardo.henriques@itqb.unl.pt

Main

Today's scientific landscape is marked by the swift sharing of research findings, a trend largely driven by the exponential growth of preprint servers like arXiv, bioRxiv, and medRxiv (1-3). This shift, while accelerating scientific discovery and enhancing research transparency (4, 5), puts a significant new burden on researchers to produce polished manuscripts frequently and efficiently. Traditional tools and workflows for scientific writing, often reliant on proprietary word-processing software, are poorly suited to this new reality. They pose major challenges for version control, collaborative authoring, and ensuring the computational reproducibility of the final document (6, 7). To tackle these systemic issues, we've developed RXiv-Maker, a GitHub-native framework designed to streamline the entire scientific writing and publication pipeline. The system is built on the principle of using markdown, a simple and intuitive plain-text formatting syntax, as the primary authoring language. This approach fundamentally separates the scientific content from its

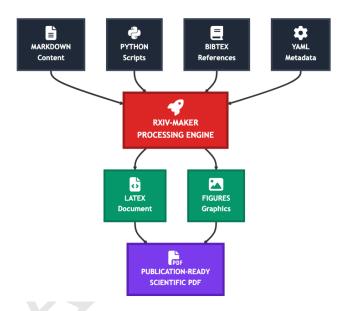


Fig. 1. The **RXiv-Maker Diagram.** The system integrates Markdown content, YAML metadata, Python scripts, and bibliography files through a processing engine. This engine leverages Docker, GitHub Actions, and LaTeX to produce a publication-ready scientific article, demonstrating a fully automated and reproducible pipeline.

final presentation, allowing researchers to focus on the substance of their work. The plain-text nature of markdown files makes them ideally suited for management with version control systems like Git. This integration provides an unparalleled level of transparency and traceability for the evolution of a manuscript. Every change, every contribution, and every revision can be precisely tracked, attributed, and, if necessary, reverted. Furthermore, it resolves the convoluted and error-prone process of merging changes from multiple collaborators, a common bottleneck in conventional workflows that often leads to duplicated effort and loss of information. At the heart of the RXiv-Maker philosophy is the pursuit of genuine reproducibility, a fundamental aspect of scientific integrity that extends beyond the experimental data to encompass the entire publication process (8-10). Our framework embodies this principle by enabling the programmatic generation of figures and tables, following best practices for computational research (11). Rather than manually inserting static image files, which obscures the connection between the data and its visualisation, our system promotes the use of scripting languages like Python, with its powerful data visualisation libraries such as Matplotlib (12) and Seaborn (13). Figures are generated directly from the source data and anal-

vsis scripts during the manuscript compilation process. This creates an unbreakable, auditable chain from raw data to the final figure. If the underlying data is updated or the analysis is refined, all affected figures are automatically regenerated, ensuring complete consistency and eliminating the possibility of outdated visuals persisting in the manuscript. This dynamic approach transforms figures from mere illustrations into reproducible scientific artefacts. The system also integrates Mermaid.js (14), a tool for generating complex diagrams and flowcharts from a simple, text-based syntax. This is particularly valuable for creating clear, version-controlled illustrations of experimental workflows, conceptual models, and algorithms, which are essential for communicating complex ideas in many scientific disciplines. RXiv-Maker, therefore, offers a holistic solution that treats the manuscript not as a static document but as the executable output of the research itself.

RXiv-Maker addresses these requirements through a markdown-centric authoring system that automatically translates familiar markdown syntax into professional LaTeX documents. Built upon the established HenriquesLab bioRxiv template (15), the system extends capabilities through automated processing pipelines, integrated figure generation, and flexible deployment strategies. The architecture, detailed in Fig. 1 and comprehensively illustrated in Sup. Fig. 1, provides automated figure generation for statistical visualisation, integrated Mermaid diagram creation, and robust build automation through containerised environments. The technical details of the figure generation system are described in B.

Using the RXiv-Maker framework results in a highly efficient and robust workflow for producing professional-quality scientific papers. The system's primary output is a fully type-set PDF document, as seen in the article you're currently reading, which was generated entirely using this process. The markdown source files are automatically converted into a structured LaTeX document, then compiled to produce a PDF with a clean, academic layout, proper pagination, and high-resolution figures. Bibliographic management is handled seamlessly through integration with a standard BibTeX file. The system automatically processes this file to generate correctly formatted in-text citations and a comprehensive bibliography section according to a specified citation style. This automation eliminates the tedious and error-prone task of manually formatting references.

Its utility is further highlighted by the system's flexible deployment options, which cater to a broad range of user preferences and technical environments. We have successfully validated three distinct compilation pathways. Firstly, the cloud-based GitHub Actions workflow offers a fully automated, hands-off experience. Every time code is pushed to the repository, the action is triggered, building a Docker container with all necessary dependencies, compiling the manuscript, and releasing the resulting PDF as a downloadable artefact. This continuous integration pipeline ensures a current, correctly compiled version of the manuscript is always available, serving as a top-notch quality control mechanism for

arXiv Preprint Growth (1991-2025)

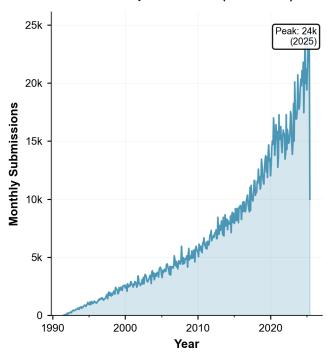


Fig. 2. The growth of preprint submissions on the arXiv server from 1991 to 2025. The data, sourced from arXiv's public statistics, is plotted using a Python script integrated into our RXiv-Maker pipeline. This demonstrates the system's capacity for reproducible, data-driven figure generation directly within the publication workflow.

collaborative projects. Secondly, for users who prefer an interactive, web-based environment, the system can be deployed in a Google Colab notebook. This method removes all local software requirements, allowing users to compile the manuscript simply by executing cells within the notebook, making the framework exceptionally accessible to those with limited command-line experience.

Thirdly, for local development, the Docker-based approach provides a perfectly reproducible compilation environment on any host machine. By running a simple command, a user can start the build process within a self-contained Docker container that encapsulates the exact versions of LaTeX and all other required system libraries. This completely eliminates the 'works on my machine' problem, guaranteeing that the output is identical byte-for-byte regardless of the user's local operating system or software configuration (16). The integration of programmatic figure generation was also validated, supporting interactive computational environments like Jupyter notebooks (17). Python scripts placed within the designated directory were automatically executed during compilation. These scripts loaded data, performed analyses, and generated visualisations, which were then saved as image files and seamlessly included in the final PDF. Similarly, Mermaid.js diagrams embedded within the markdown source were correctly rendered into SVG images and incorporated into the document. This programmatic integration demonstrates a closed loop of reproducibility, where the final manuscript serves as a verifiable and self-contained record of the research findings and their presentation.

Our RXiv-Maker system marks a major step forward in how scientific manuscripts are prepared. By using plain-text markdown and robust open-source tools like Docker, we've created a workflow that boosts efficiency and promotes best practices for reproducibility and collaboration. The main benefit of our framework is that it removes technical complexity from the author's hands. Scientists can focus on the research content and narrative, using simple and widely understood markdown syntax, while the system handles the complex and often frustrating aspects of typesetting, reference management, and dependency control. This approach embraces literate programming principles (18), creating documents that seamlessly blend narrative text with executable code. This is a significant departure from traditional workflows, where researchers often have to act as amateur typesetters, spending hours wrestling with the formatting intricacies of word processors or raw Latex. The integration with Git provides a robust platform for collaborative writing (19, 20), far superior to the chaotic exchange of files via email. It enables transparent attribution, conflict-free merging of contributions, and a complete, auditable history of the manuscript's development.

Within the larger context of the open science movement, RXiv-Maker acts as a practical tool for turning principles into reality. By focusing on automated figure generation and a fully containerised, reproducible build process, the path from raw data to final publication becomes transparent and verifiable. This directly tackles the 'reproducibility crisis' by making it easy to create publications that are not just reports of research, but are themselves computationally reproducible artefacts. This aligns with a growing consensus that the publication itself should be accompanied by the code and data needed to reproduce its findings (8). Our framework makes this possible by design, treating the manuscript and the code to generate it as two sides of the same coin. While other platforms and tools for scientific writing exist, including sophisticated environments like DL4MicEverywhere (21), RXiv-Maker stands out through its simplicity, flexibility, and tight integration with the GitHub ecosystem, which is already the de facto standard for collaborative software development and is increasingly used for scientific projects.

Although Rxiv-Maker has its advantages, we acknowledge certain limitations and areas for future improvement. The current system is mainly designed to produce PDF outputs using Latex. While this is the standard for many scientific disciplines, future versions could support other output formats, such as HTML for web-native articles, potentially leveraging universal document converters like Pandoc (22). Additionally, concerns about reporting quality in preprints (23) suggest opportunities for integrating automated quality checks. Additionally, although the system is designed to be accessible, researchers new to Git and markdown may encounter an initial learning curve. To address this, we plan to develop more comprehensive documentation and tutorial materials. Future work will also focus on deeper integration with data analysis environments like Jupyter notebooks, allowing for a more seamless transition from exploratory analysis to manuscript-ready figures. We could also explore integrating automated tools for checking style, grammar, and scientific rigour, further enhancing the system's role as a comprehensive quality control platform. Ultimately, RXiv-Maker is a contribution to a more open, efficient, and reproducible future for scientific communication, providing a powerful and accessible tool for modern researchers.

MANUSCRIPT PREPARATION

This manuscript was prepared using RXiv-Maker version 1.11.0.

DATA AVAILABILITY

Arxiv monthly submission data used in this article is available at https://arxiv.org/stats/monthly_submissions. The source code and data for the figures in this article are available at https://github.com/henriques/rxiv-maker.

CODE AVAILABILITY

The RXiv-Maker computational framework is available at https://github.com/henriques/rxiv-maker. All source code is under an MIT License.

AUTHOR CONTRIBUTIONS

Both Bruno M. Saraiva, Guillaume Jacquemet and Ricardo Henriques conceived the project and designed the framework. All authors contributed to writing and reviewing the manuscript.

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EXTENDED AUTHOR INFORMATION

- · Bruno M. Saraiva:
- © 0000-0002-9151-5477; **У** Bruno_MSaraiva; **in** bruno-saraiva
- · Guillaume Jaquemet:
- © 0000-0002-9286-920X; ♥ guijacquemet; ★ guijacquemet.bsky.social
- Ricardo Henriques:

Bibliography

- Jeremy M Berg, Narinder Bhalla, Philip E Bourne, M Cacchione, D Egnor, J Flombaum, E Ghanem, M Ginsburg, B Goldstein, L Gorodetski, et al. Preprint servers. Science, 352 (6288):899, 2016. doi: 10.1126/science.aaf9133.
- Richard J Abdill and Ran Blekhman. The growth of biorxiv preprints and the implications for preprint discovery. PLoS Biology, 17(4):e3000269, 2019. doi: 10.1371/journal.pbio.3000269.
- Nicholas Fraser, Fakhri Momeni, Philipp Mayr, and Isabella Peters. The relationship between biorxiv preprints, citations and altmetrics. *Quantitative Science Studies*, 2(2):618–638, 2021. doi: 10.1162/gss a 00043.
- Ronald D Vale. Accelerating scientific publication in biology. Proceedings of the National Academy of Sciences, 116(52):26222–26229, 2019. doi: 10.1073/pnas.1915668116.
- Jonathan P Tennant, François Waldner, Damien C Jacques, Paola Masuzzo, Lauren B Collister, and Chris HJ Hartgerink. The academic, economic and societal impacts of open access: an evidence-based review. F1000Research, 5:632, 2016. doi: 10.12688/ f1000research.8460.3.
- Vincent Lariviere, Cassidy R Sugimoto, Benoît Macaluso, Staša Milojević, and Blaise Cronin. arxiv. org and the dissemination of scholarly information: The case of computer science. *Journal of the Association for Information Science and Technology*, 65(4):844– 848, 2014. doi: 10.1002/asi.23081.
- Jerson L da Silva. The challenge of being a scientist in the 21st century. Anais da Academia Brasileira de Ciências, 94, 2022. doi: 10.1590/0001-3765202220211396.
- David L Donoho. An invitation to reproducible computational research. The American Statis tician, 64(1):1–2, 2010. doi: 10.1198/tast.2010.09132.

- Geir Kjetil Sandve, Anton Nekrutenko, James Taylor, and Eivind Hovig. Ten simple rules for reproducible computational research. *PLoS Computational Biology*, 9(10):e1003285, 2013. doi: 10.1371/journal.pcbi.1003285.
- Greg Wilson, Dhavide A Aruliah, C Titus Brown, Neil P Chue Hong, Matt Davis, Richard T Guy, Steven HD Haddock, Kathryn D Huff, Ian M Mitchell, Mark D Plumbley, et al. Best practices for scientific computing. *PLoS Biology*, 12(1):e1001745, 2014. doi: 10.1371/ journal.pbio.1001745.
- Dominik Scherer, Lars Bendix, Stephan Greiner, and Julian Lück. A survey on the state of research data reproducibility in computer science. In 2020 IEEE/ACM 42nd International Conference on Software Engineering Workshops (ICSEW), pages 310–317. IEEE, 2020. doi: 10.1109/ICSEWS0701.2020.00052.
- John D Hunter. Matplotlib: A 2d graphics environment. Computing in Science & Engineering, 9(3):90–95, 2007. doi: 10.1109/MCSE.2007.55.
- Michael L Waskom. seaborn: statistical data visualization. Journal of Open Source Software, 6(60):3021, 2021. doi: 10.21105/joss.03021.
- Mermaid Team. Mermaid: Generation of diagrams and flowcharts from text in a similar manner as markdown, 2023. Accessed: 2024-12-01.
- Ricardo Henriques. Henriques biorxiv template, 2015. Overleaf LaTeX template. Accessed: 2025-06-16
- Carl Boettiger. An introduction to docker for reproducible research. ACM SIGOPS Operating Systems Review, 49(1):71–79, 2015. doi: 10.1145/2723872.2723882.
- Thomas Kluyver, Benjamin Ragan-Kelley, Fernando Pérez, Brian E Granger, Matthias Bussonnier, Jonathan Frederic, Kyle Kelley, Jessica B Hamrick, Jason Grout, Sylvain Corlay, et al. Jupyter notebooks—a publishing format for reproducible computational workflows. In Positioning and Power in Academic Publishing: Players, Agents and Agendas, pages 87–90. IOS Press, 2016. doi: 10.3233/978-1-61499-649-1-87.
- Donald E Knuth. Literate programming. The Computer Journal, 27(2):97–111, 1984. doi: 10.1093/cominl/27.2.97.
- Karthik Ram. Git can facilitate greater reproducibility and increased transparency in science. Source Code for Biology and Medicine, 8(1):7, 2013. doi: 10.1186/1751-0473-8-7.
- Yasset Perez-Riverol, Laurent Gatto, Rui Wang, Timo Sachsenberg, Julian Uszkoreit, Felipe da Veiga Leprevost, Christian Fufezan, Tobias Ternent, Stephen J Eglen, Daniel S Katz, et al. Ten simple rules for taking advantage of git and github. PLoS Computational Biology, 12(7):e1004947, 2016. doi: 10.1371/journal.pcbi.1004947.
- Ivan Hidalgo-Cenalmor, Joanna W Pylvänäinen, Mariana G Ferreira, Craig T Russell, Alon Saguy, Ignacio Arganda-Carreras, Guillaume Jacquemet, and Ricardo Henriques. Dl4miceverywhere: deep learning for microscopy made flexible, shareable and reproducible. Nature Methods, 21(5):804–810, 2024. doi: 10.1038/s41592-024-02295-6.
- John MacFarlane. Pandoc: A universal document converter. Journal of Open Source Software, 7(76):4642, 2022. doi: 10.21105/joss.04642.
- Jamie J Kirkham, Christopher M Penfold, Fiona Murphy, and John PA loannidis. The quality of reporting in preprints. bioRxiv, page 451822, 2018. doi: 10.1101/451822.

Methods

The RXiv-Maker system is architected as a modular pipeline orchestrated by a central Makefile, which automates all stages of manuscript production from markdown source to a final PDF document. The core conversion from markdown to LaTeX is handled by custom scripts, leveraging the versatility of Python to accommodate specialised scientific formatting requirements not natively supported in standard markdown. For bibliographic management, the system integrates seamlessly with BibTeX, utilising .bib files to manage references. These are automatically processed to generate formatted citations and a complete bibliography within the final document. The project structure is standardised to ensure clarity and ease of use. All manuscript text is located in markdown files within a designated src/ directory. Figures can be either static images placed in src/figures/ or generated programmatically by scripts in the scripts/ directory. A YAML file, metadata/metadata.yaml, centrally stores all manuscript metadata, such as title, authors, affiliations, and abstract, separating content from presentation. This separation is critical for programmatic access and modification of document properties without altering the narrative text.

Compilation can be initiated through several mechanisms. The make command compiles the document locally, provided the necessary dependencies like a LaTeX distribution are installed. To eliminate the need for manual installation of dependencies, we provide a Dockerfile that defines

the complete software environment. Building this Dockerfile creates a container image from which a user can compile the manuscript with a single Docker command, ensuring perfect reproducibility of the environment. The build script (build.sh) automates the creation of this Docker image, supporting multi-architecture builds for both amd64 and arm64 platforms to ensure broad compatibility. For continuous integration and cloud-based compilation, a GitHub Actions workflow file, .github/workflows/main.yml, is included. This workflow automates the entire process of building the Docker container, compiling the manuscript, and releasing the resulting PDF as a downloadable artefact on every push to the repository, thereby providing a robust, automated pipeline for manuscript generation. This automated workflow serves as a powerful tool for quality control and immediate dissemination.

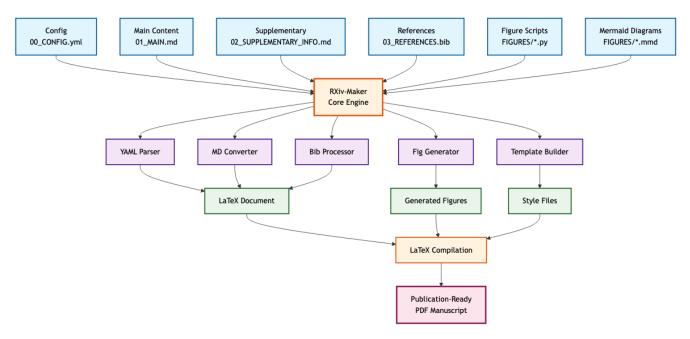
Supplementary Information

$R\chi$ iv-Maker: An Automated Template Engine for Streamlined Scientific Publications

Supplementary Information

RXiv-Maker: An Automated Template Engine for Streamlined Scientific Publications

This supplementary information provides additional technical details, implementation examples, and extended documentation for the RXiv-Maker framework. The content is organised into supplementary figures that illustrate system architecture and functionality, followed by supplementary notes that detail technical implementation aspects and provide practical examples of the auto-translation system.



Sup. Fig. 1. RXiv-Maker Workflow Details. This figure provides a comprehensive overview of the RXiv-Maker system architecture, showing how the simplified file naming convention (00_CONFIG.yml, 01_MAIN.md, 02_SUPPLEMENTARY_INFO.md, 03_REFERENCES.bib) integrates with the processing engine to generate publication-ready documents. The system demonstrates the complete automation pipeline from markdown input to PDF output.

A. Supplementary Notes.

- A.1. File Structure and Organisation. Blablabla
- **B. Supplementary Note 1: Figure Generation System.** The figure generation system is implemented in src/py/commands/generate_figures.py and provides automated processing of figure source files from the FIGURES/ directory. The system supports two primary figure types:

Mermaid Diagrams (.mmd files):

- Processed using the Mermaid CLI (mmdc) through the generate_mermaid_figure() method
- Automatically generates multiple output formats (SVG, PNG, and optionally PDF/EPS)
- Uses format-specific options:
- PNG files at 1200×800 resolution
- · SVG files maintain vector format
- PDF files use transparent backgrounds
- · Provides comprehensive error handling and status reporting

Python-Generated Figures (.py files):

- Python scripts are executed in the output directory context through the <code>generate_python_figure()</code> method
- · System features:
- Executes Python scripts using subprocess.run() with the current Python interpreter
- Changes the working directory to the output folder before execution
- Automatically detects generated figure files by scanning for common image formats (PNG, PDF, SVG, EPS)
- Matches output files to source scripts using filename patterns

The figure generation process includes automatic detection of available dependencies (matplotlib, seaborn, numpy, pandas) and provides fallback behavior when libraries are unavailable.

C. Supplementary Note 2: Markdown-to-LaTeX Conversion Architecture. The conversion system consists of specialized processors for different content types, implemented across multiple modules:

Figure Processing (src/py/converters/figure_processor.py):

The figure conversion system processes three markdown figure syntaxes:

- 1. New format: ! [] (path) followed by attributes **Caption** on the next line
- 2. Attributed format: !captionattributes
- 3. Simple format: !caption

The core conversion function convert_figures_to_latex() implements a multi-pass approach:

- 1. **Code protection**: Inline code (backticks) and fenced code blocks are temporarily replaced with placeholders to prevent interference with figure syntax parsing
- 2. Format processing: Each figure format is processed by dedicated functions
- 3. Code restoration: Protected code blocks are restored after figure processing

The create_latex_figure_environment () function generates complete LaTeX figure environments with:

- Path conversion (FIGURES/ → Figures/ and .svg → .png for LaTeX compatibility)
- Caption processing (markdown formatting converted to LaTeX equivalents)
- Attribute handling (position, width, and ID attributes are parsed and applied)
- Label generation (figure IDs are automatically converted to LaTeX commands)

The system provides user control over page breaks through <newpage> and <clearpage> markdown syntax, which are converted to LaTeX

and

Markdown Element	LaTeX Equivalent	Description
bold text	\{}textbf{bold text}	Bold formatting for emphasis
italic text	\{}textit{italic text}	Italic formatting for emphasis
# Header 1	\{}section{Header 1}	Top-level section heading
## Header 2	\{}subsection{Header 2}	Second-level section heading
### Header 3	\{}subsubsection{Header 3}	Third-level section heading
citation	\{}cite{citation}	Single citation reference
[citel;cite2]	\{}cite{cite1,cite2}	Multiple citation references
fig:label	\{}ref{fig:label}	Figure cross-reference
Image with attributes	\{}begin{figure}\{}end{figure}	Figure with attributes (old format)
Image with caption	\{}begin{figure}\{}end{figure}	Figure with separate caption (new format)
- list item	\{}begin{itemize}\{}item\{}end{itemize}	Unordered list
1. list item	\{}begin{enumerate}\{}item\{}enumerate}	Ordered list
[link text] (url)	\{}href{url}{link text}	Hyperlink with custom text
https://example.com	<pre>\\{\}url{\https://example.com}</pre>	Bare URL
- comment -	% comment	Comments (converted to LaTeX style)
Markdown table	\{}begin{table}\{}end{table}	Table with automatic formatting
<newpage></newpage>	\{}newpage	Manual page break control
<clearpage></clearpage>	\{}clearpage	Page break with float clearing

Sup. Table 1. RXiv-Maker Markdown Syntax Overview. Comprehensive overview of RXiv-Maker's markdown to LaTeX conversion capabilities, demonstrating the automated translation system that enables researchers to write in familiar markdown syntax while producing professional LaTeX output.

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commands respectively. The <newpage> command creates a simple page break, while <clearpage> forces a page break and flushes all pending floats (figures/tables). This allows precise control over document layout without automatic page breaks for figures and tables.

Table Processing (src/py/converters/table_processor.py):

Table conversion handles GitHub Flavored Markdown tables with additional LaTeX-specific features. The system supports two caption formats:

- 1. Legacy format: Table X: Caption (preceding the table)
- 2. New format: **Table X: Caption** #table:id (following the table)

Caption parsing includes:

- Width detection (Table* indicates double-column tables)
- ID extraction (attribute blocks are parsed for table labels)
- Rotation support (rotation angles can be specified in attribute blocks)

The _format_table_cell() function implements context-aware cell formatting with:

- Markdown syntax preservation (special handling for tables containing markdown syntax examples)
- LaTeX escaping (special characters are properly escaped)
- Code formatting (backtick-enclosed content is converted to commands)
- Emphasis conversion (**bold** and *italic* are converted to LaTeX equivalents)

Reference Processing:

Both figures and tables support automatic reference conversion:

- Figure references: @fig:id → ??
- Supplementary figure references: $@sfig:id \rightarrow ??$
- Table references: Similar pattern for @table:id and @stable:id

This reference system is implemented using regex-based substitution.

Integration Pipeline:

The figure and table processors are integrated into the main markdown-to-LaTeX conversion pipeline (src/py/converters/md2tex.py) through the convert_markdown_to_latex() function, which orchestrates:

- Content protection
- · Header conversion
- Figure processing
- Table processing
- · Reference resolution
- · Content restoration

This architecture ensures robust conversion while maintaining the semantic structure and formatting requirements of academic publications, demonstrating:

- Separation of concerns
- Extensibility
- Robustness through comprehensive error handling
- · Testability through modular design

- D. Supplementary Note 3: Comparison with similar systems.
- **E. Supplementary Note 4: Auto-Translation System Examples.** The RXiv-Maker auto-translation system processes structured input files to generate professional LaTeX output. The following examples demonstrate the system's capabilities across different file types.

YAML Configuration Example (00_CONFIG.yml)

```
title: "RXiv-Maker: An Automated Template Engine for Streamlined Scientific Publications"
short_title: "RXiv-Maker"
authors:
  - name: "Bruno M. Saraiva"
    affiliation: [1, 2]
    email: "bruno.saraiva@example.com"
    orcid: "0000-0000-0000-0000"
  - name: "Guillaume Jaquemet"
    affiliation: [3]
    email: "guillaume.jaquemet@example.com"
    orcid: "0000-0000-0000-0000"
  - name: "Ricardo Henriques"
    affiliation: [1, 2]
    email: "ricardo.henriques@example.com"
    orcid: "0000-0000-0000-0000"
    corresponding: true
affiliations:
  1: "Instituto Gulbenkian de Ciência, Oeiras, Portugal"
  2: "University College London, London, United Kingdom"
  3: "Abo Akademi University, Turku, Finland"
abstract: "Modern scientific publishing requires..."
keywords: ["scientific publishing", "reproducibility", "automation"]
Markdown Content Structure (01_MAIN.md)
## Abstract
Modern scientific publishing has shifted towards rapid dissemination...
## Main
Scientific publishing has undergone profound transformation...
![Figure caption with cross-reference] (FIGURES/Figure_1.svq) { #fig:1}
Statistical analysis demonstrates significant improvements [@reference2023].
## Methods
The RXiv-Maker framework orchestrates computational tools...
BibTeX Reference Format (03_REFERENCES.bib)
@article { Tennant 2016_academic_publishing,
  title={The academic, economic and societal impacts of Open Access},
  author={Tennant, Jonathan P and Waldner, Fran{\c{c}}ois and Jacques, Damien C},
  journal={PLoS Biology},
 volume={14},
 number=\{7\},
  pages = \{e1002510\},
  year = \{2016\},\
  publisher={Public Library of Science}
}
```

```
@article{Fraser2021_preprint_growth,
  title={The relationship between bioRxiv preprints and citations},
  author={Fraser, Nicholas and Momeni, Fakhri and Mayr, Philipp and Peters, Isabella},
  journal={Quantitative Science Studies},
  volume={2},
  number={2},
  pages={618--638},
  year={2021}
}
```

- **F.** Supplementary Note 5: Technical Implementation Pipeline. The system processes these files through a sophisticated conversion pipeline:
 - 1. **Configuration Parsing**: Extracts metadata from YAML configuration file, including author information, affiliations, and document settings
 - 2. **Content Conversion**: Transforms markdown syntax into LaTeX formatting, preserving cross-references, citations, and figure placements
 - 3. Figure Generation: Executes Python scripts and processes Mermaid diagrams automatically during compilation
 - 4. Document Assembly: Combines all components into a cohesive LaTeX document using the template system
 - 5. Citation Processing: Integrates BibTeX references with proper formatting and cross-referencing
 - 6. Output Compilation: Produces publication-ready PDF with professional typesetting and formatting

This approach ensures reproducibility, version control compatibility, and automated processing whilst maintaining the flexibility needed for academic publishing. The system automatically handles complex LaTeX formatting requirements, enabling researchers to focus on content creation rather than technical implementation details.