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

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Modern scientific publishing has shifted towards rapid dissemination through preprint servers, placing increased demands on researchers for manuscript preparation and quality control. We present RXiv-Maker, a comprehensive GitHub-native system that simplifies scientific writing through markdown-based authoring with automated LaTeX conversion. The system enables researchers to write in familiar markdown syntax whilst producing publication-quality documents with professional typesetting. RXiv-Maker offers flexible compilation strategies ranging from GitHub Actions and Google Colab to local compilation with minimal installation requirements using Docker containerisation. The framework supports diverse visualisation approaches, including programmatic figure generation through Python libraries such as Matplotlib and Seaborn, alongside integrated Mermaid diagram rendering for conceptual illustrations. This self-documenting article demonstrates the system's capabilities, showcasing how markdown-centric authoring transforms scientific communication into an efficient, collaborative, and reproducible process. RXiv-Maker serves as a foundational tool for research groups seeking streamlined publishing workflows, enabling scientists to focus on research content whilst maintaining rigorous technical standards.

article template | scientific publishing | preprints

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Main

Scientific publishing has undergone profound transformation over the past two decades, fundamentally altering how researchers communicate and disseminate findings (1). The emergence of preprint servers such as arXiv, bioRxiv, and medRxiv has enabled millions of manuscripts to bypass traditional peer-review bottlenecks, with exponential growth particularly evident during the COVID-19 pandemic (2, 3). This shift towards immediate publication reflects growing recognition that traditional publishing timelines are incompatible with the pace of modern scientific discovery.

Concurrent with this transformation, computational tools and automated workflows have become essential to contemporary research practice. Version control systems, particularly Git and GitHub, have evolved into platforms for scientific collaboration, enabling transparent manuscript development and reproducible analyses (4, 5). Containerisation technologies such as Docker have enhanced reproducibility by providing standardised computational environments (6, 7). Traditional manuscript preparation remains largely unchanged,

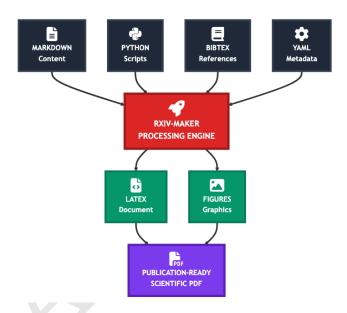


Fig. 1. The RXiv-Maker Diagram. The system integrates Markdown content, YAML metadata, Python scripts, and bibliography files through a processing engine. This engine leverages Docker, GitHub Actions, and LaTeX to produce a publication-ready scientific article, demonstrating a fully automated and reproducible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

relying on fragmented workflows that separate content creation, figure generation, and document compilation. This fragmentation introduces opportunities for error and version conflicts. Contemporary research demands sophisticated figure generation capabilities integrating statistical analysis and publication-quality visualisation. Whilst Python libraries such as Matplotlib and Seaborn provide foundational tools for scientific visualisation (8, 9), modern workflows also benefit from declarative diagram creation through Mermaid, enabling researchers to generate flowcharts and conceptual illustrations using text-based syntax.

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 Jacquemet and Henriques bioRxiv template (10), 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.

25k - 20k - 20k - 15k - 5k - 5k - 5k - 20k - 20k

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.

2010

Year

2020

2000

RXiv-Maker provides extensive capabilities for programmatic and reproducible figure generation directly from underlying data and source code, though researchers may choose traditional static figure inclusion based on their workflow preferences. When employed, this approach ensures that visualisations become dynamic artefacts, intrinsically linked to the research process and subject to the same rigorous version control as the manuscript text itself.

This figure is rendered automatically during the article's compilation by executing a version-controlled Python script (Figure_2.py) found in FIGURES/

Core Functionality Overview

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RXiv-Maker provides comprehensive manuscript authoring capabilities through its integrated toolchain. The system supports multiple input formats including standard markdown syntax, YAML-based metadata configuration, and BibTeX bibliography management. Figure generation encompasses both programmatic approaches through Python scripts and declarative diagram creation using Mermaid syntax, enabling researchers to maintain complete reproducibility whilst accommodating diverse visualisation requirements.

The compilation pipeline offers multiple deployment strategies to accommodate different research environments and computational preferences. Users can leverage GitHub Actions for automated cloud-based compilation, utilise Google Colab for interactive development and testing, or deploy locally using Docker containers with minimal system requirements. This flexibility ensures that RXiv-Maker

remains accessible across different computational environments and institutional constraints.

Comparative Analysis

Table* 1: presents a detailed comparison of RXiv-Maker against established manuscript preparation systems, highlighting key differentiators in workflow integration, reproducibility features, and deployment flexibility.

Feature	RXiv-Maker	O
Input Format	Markdown + YAML	La
Learning Curve	Low	M
Version Control	Native Git	Li
Reproducible Figures	Python + Mermaid	M
Collaboration	GitHub-native	W
Deployment Options	GitHub Actions, Colab, Local Docker	W
Template System	Automated conversion	M
Citation Management	BibTeX integration	Bi
Containerisation	Docker-native	N/
Continuous Integration	GitHub Actions	N/

RXiv-Maker responds directly to evolving demands of modern scientific communication. The programmatic generation of Figure 2 within this document validates our framework, demonstrating how figures become reproducible and verifiable components of the scientific record rather than static images. This approach mitigates common errors whilst the integration of Git, Docker, and GitHub Actions establishes a research environment where transparency and collaboration are structurally embedded. RXiv-Maker provides a foundational tool for research groups adopting structured, automated publishing approaches, enabling scientists to focus on research content whilst ensuring efficient and robust dissemination processes.

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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Bibliography

- 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.
- 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/qss_a_00043.
- 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.
- 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.
- Carl Boettiger. An introduction to docker for reproducible research. ACM SIGOPS Operating Systems Review, 49(1):71–79, 2015. doi: 10.1145/2723872.2723882.
- Ivan Hidalgo-Cenalmor, Joanna W Pylvănăinen, 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 D Hunter. Matplotlib: A 2d graphics environment. Computing in Science & Engineer ing, 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.
- Jacquemet and Henriques Labs. Jacquemet and henriques biorxiv template, 2015. Overleaf LaTeX template. Accessed: 2025-06-16.

Methods

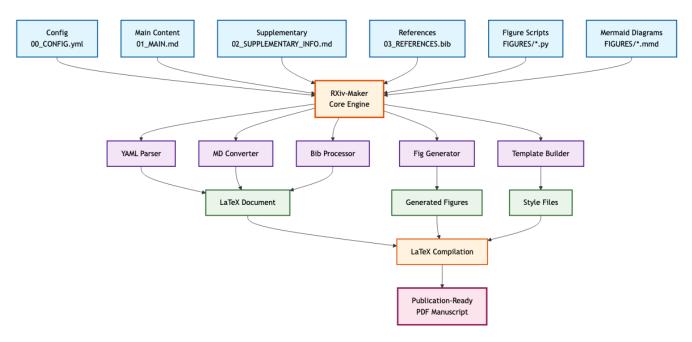
The RXiv-Maker framework orchestrates a series of computational tools to achieve a fully automated publication pipeline. The process begins with manuscript content authored in Markdown (01_MAIN.md) and metadata defined in a separate YAML configuration file (00_CONFIG.yml). Bibliographic information is managed in a standard BibTeX file (03_REFERENCES.bib). The core of the system is a set of Python scripts located in src/py/ which parse the Markdown and YAML to dynamically generate a main LaTeX file (MANUSCRIPT.tex) from a template (src/tex/template.tex). Figure generation is a key automated step. diagrams (.mmd) and Python scripts (.py) placed in the FIGURES/ directory are executed to produce visual content. For instance, Figure 2 was generated by executing FIGURES/Figure 2.py, which pro-FIGURES/DATA/Figure 2/ cesses data from arxiv monthly submissions.csv. build process is managed by a Makefile and can be encapsulated within a Docker container defined by the Dockerfile, ensuring a consistent and reproducible compilation environment. Continuous integration and deployment are handled by GitHub Actions, which automates the compilation of the PDF upon every commit, making the latest version of the manuscript perpetually available.

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Note 1: Supplementary Information

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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 Figures.

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- B. Supplementary Tables.
- B.1. RXiv-Maker Markdown Syntax Overview.

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- C. Supplementary Notes.
- C.1. File Structure and Organisation. Blablabla
- C.2. Figures and tables. Blablabla
- C.3. Comparison with similar systems.
- **C.4.** Supplementary Note 2: 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: "Åbo 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.svg) { #fig:1}
Statistical analysis demonstrates significant improvements [@reference2023].
## Methods
The RXiv-Maker framework orchestrates computational tools...
BibTeX Reference Format (03_REFERENCES.bib)
@article{Tennant2016 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\},
```

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```
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}
}
```

C.5. Supplementary Note 3: 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.

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Markdown Element	LaTeX Equivalent	Description
bold text	<pre>\{}textbf{bold text}</pre>	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
[cite1;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	<pre>\{}begin{itemize}\{}item\{}end{itemize}</pre>	Unordered list
1. list item	\{\}begin{enumerate}\{\}item\{\}end{enumerate}	Ordered list
<pre>[link text] (url)</pre>	\{}href{url}{link text}	Hyperlink with custom text
https://example.com	\{}url{https://example.com}	Bare URL
- comment -	% comment	Comments (converted to LaTeX style)
Markdown table	\{}begin{table}\{}end{table}	Table with automatic formatting

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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