

# LaTeX

## **Intro to LaTeX**

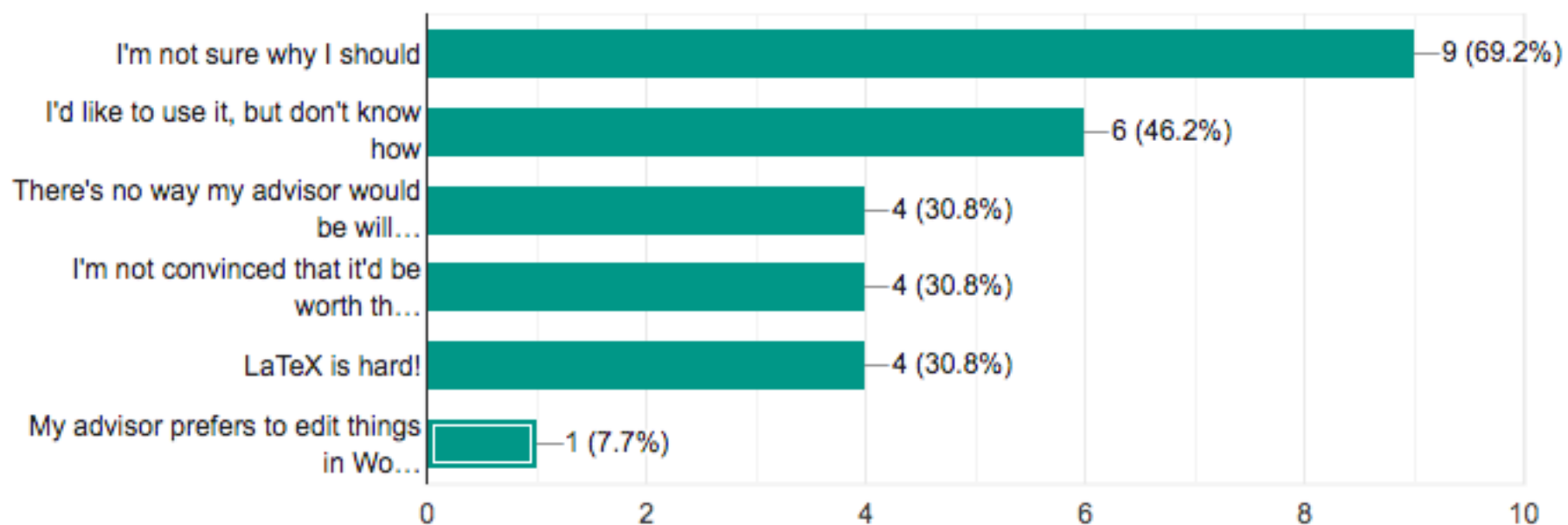
“Lah-tech” or “Lay-tech” *not* “Lay-Tex”

# Today's Workshop: Game Plan

- (1) Share the benefits of using LaTeX
- (2) Teach how to use LaTeX (the basics)
- (3) Give a little taste of advanced features

What current barriers exist to you using LaTeX for document creation (e.g. manuscript writing)?

13 responses



# What is LaTeX?

“*WYSIWYM*” – focus on the contents of your document, and the computer takes care of formatting

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Write in plain text, and then use a “style file” to format it  
Can be used to create written documents, posters, presentations, books, etc.

# Who uses LaTeX?



	LaTeX rate	SE	N	Guideline words count	SE	N
Mathematics	96.9	3.1	4	604.4	158.5	10
Statistics and Probability	89.1	4.0	6	1208.6	259.4	10
Physics	74.0	11.7	3	2912.1	970.3	10
Computer Sciences	45.8	40.9	2	1354.3	195.3	10
Astronomy and Astrophysics	35.1	21.4	5	3171.4	856.8	10
Engineering	1.0	1.0	2	1429.8	169.5	10
Geosciences	0.8	0.6	6	2284.6	439.0	10
Ecology	0.4	0.4	4	3212.4	1160.7	10
Chemistry	0.3	0.3	3	1739.2	222.1	10
Biology	0.0	0.0	4	1879.7	402.7	10
Medicine	0.0		1	2490.8	362.3	10
Psychology	0.0	0.0	7	1646.5	267.6	10
Sport Sciences	0.0	0.0	6	1663.7	509.4	10
Mean/Total	<b>26.8</b>	<b>5.6</b>	<b>53</b>	<b>1979.6</b>	<b>162.3</b>	<b>130</b>

Table 1. Summary statistics (mean  $\pm$  SE) of the use of LaTeX in science disciplines (% of submitted papers) and the number of words contained in the guidelines for authors. The red line indicates the separation between LaTeX-using and non-LaTeX-using disciplines.



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# Why Use LaTeX?

The content of the document is separate from the style

*It looks nice with very little effort from you*



**Fig. 1**

LaTeX, basically.

Source: <https://twitter.com/IvyDesert>

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## LaTeX Template/Overleaf [↗](#)

[Overleaf](#) and the [Genetics Society of America](#) have created a LaTeX template for authors submitting manuscripts to G3. The template allows authors to easily prepare and edit their manuscripts using [Overleaf](#). Authors can then submit manuscripts to G3 by using the PDF and source files generated from Overleaf.

The template is available [here](#) and contains guidelines for preparing your submission within the template itself. If you're new to [Overleaf](#) and LaTeX, help is available via their [free introductory course](#).

## Reference-quality genome sequences for two species of *Lates* endemic to Lake Tanganyika

Jessica A. Rick<sup>\*†,1</sup> and Catherine E. Wagner<sup>\*‡</sup>

<sup>\*</sup>Department of Botany, University of Wyoming, Laramie, WY 82071, <sup>†</sup>Program in Ecology, University of Wyoming, Laramie, WY 82071, <sup>‡</sup>Biodiversity Institute, University of Wyoming, Laramie, WY 82071

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**ABSTRACT** The abstract should be written for people who may not read the entire paper, so it must stand on its own. The impression it makes usually determines whether the reader will go on to read the article, so the abstract must be engaging, clear, and concise. In addition, the abstract may be the only part of the article that is indexed in databases, so it must accurately reflect the content of the article. A well-written abstract is the most effective way to reach intended readers, leading to more robust search, retrieval, and usage of the article. Please see [additional guidelines notes on preparing your abstract below](#).

### KEYWORDS

Keyword  
Keyword2  
Keyword3  
...

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This G3: Genes | Genomes | Genetics journal template is provided to help you write your work in the correct journal format. Instructions for use are provided below.

- be a single paragraph of less than 250 words;
- contain the full name of the organism studied;
- NOT contain citations or abbreviations.

# Why Use LaTeX?



Our instructions to authors should be followed carefully before submitting a manuscript. Manuscripts not conforming to the instructions will be returned to the author(s) for adjustments before the review process can begin. The text can be submitted as either a PDF file or a Word document. We prefer document files because reviewers may wish to make suggestions using Track Changes. If the manuscript was created in LaTeX, please convert to a PDF version for submission. The available LaTeX templates are listed below:

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- be a single page
- contain the full text
- NOT contain figures or tables

*Systematic Biology* (2020), 0, 0, pp. 1–36  
doi:10.1093/sysbio/output

## Reference genome choice and filtering pipeline jointly influence phylogenetic analyses

JESSICA A. RICK<sup>1,2\*</sup>, CHAD D. BROCK<sup>2</sup>, AND CATHERINE E. WAGNER<sup>2,3</sup>

<sup>1</sup> Program in Ecology, University of Wyoming, Laramie, WY, 82071, USA

<sup>2</sup> Department of Botany, University of Wyoming, Laramie, WY, 82071, USA

<sup>3</sup> Biodiversity Institute, University of Wyoming, Laramie, WY, 82071, USA

\*Corresponding author: JA Rick, 1000 E University Dr, Laramie, WY 82070; jrick@uwyo.edu

### ABSTRACT

Molecular phylogenies are a cornerstone of modern comparative biology, and are commonly employed to investigate a range of biological phenomena, such as macroevolutionary patterns, trait evolution, biogeography, and community assembly. Recent technological and computational advances have made it possible for researchers to commonly use genomic data for phylogenetic analyses in non-model organisms, providing an unprecedented amount of information for inferring phylogenetic history. However, well-assembled reference genomes remain relatively sparse, leaving researchers with dilemmas about what reference

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Dynamic documents!

Way better than anything else for mathematical formulas

How do I use LaTeX?

# How do I use LaTeX?

Download editor program or use online editor

# How do I use LaTeX?

The screenshot displays the TeXstudio interface. The main editor window shows LaTeX source code for a document. The code includes the `\begin{document}` command followed by three paragraphs of text, each describing a different figure in the field of free software and open-source systems. The first paragraph describes Richard Matthew Stallman, the second describes Linus Benedict Torvalds, and the third describes Eric Steven Raymond. The code concludes with `\end{document}`. The status bar at the bottom of the editor indicates 'Line: 5 Column: 4 INSERT'. Below the editor, a 'Messages' panel is visible. To the right of the editor, a preview window shows the rendered PDF document, which contains the same three paragraphs of text as the source code, formatted in a standard serif font. The TeXstudio window title is 'untitled - TeXstudio'. The menu bar includes 'File', 'Edit', 'Idefix', 'Tools', 'LaTeX', 'Math', 'Wizards', 'Bibliography', 'Macros', 'View', 'Options', and 'Help'. The toolbar contains various icons for file operations, editing, and LaTeX-specific functions. The status bar at the bottom of the window shows 'Page 1 of 1 91%' and the system tray includes icons for 'en\_GB', 'UTF-8', 'Ready', 'Automatic', and a volume control icon.

```
\begin{document}

Richard Matthew Stallman (born March 16, 1953), often known by his initials, rms,[1] is an American software freedom activist and programmer. He campaigns for software to be distributed in a manner such that its users receive the freedoms to use, study, distribute and modify that software. Software that ensures these freedoms is termed free software. Stallman launched the GNU Project, founded the Free Software Foundation, developed the GNU Compiler Collection and GNU Emacs, and wrote the GNU General Public License.

Linus Benedict Torvalds (born December 28, 1969) is a Finnish-American software engineer who is the creator, and for a long time, principal developer of the Linux kernel, which became the kernel for operating systems such as the Linux operating system, Android, and Chrome OS. He also created the distributed revision control system Git and the diving logging and planning software Subsurface. He was honored, along with Shinya Yamanaka, with the 2012 Millennium Technology Prize by the Technology Academy Finland "in recognition of his creation of a new open source operating system for computers leading to the widely used Linux kernel". He is also the recipient of the 2014 IEEE Computer Society Computer Pioneer Award.

Eric Steven Raymond (born December 4, 1957), often referred to as ESR, is an American software developer, author of the widely cited 1997 essay and 1999 book The Cathedral and the Bazaar and other works, and open-source software advocate. He wrote a guidebook for the Roguelike game NetHack. In the 1990s, he edited and updated the Jargon File, currently in print as The New Hacker's Dictionary.

Jon "maddog" Hall (born 7 August 1950) is the Executive Director of Linux International, a non-profit organization of computer professionals who wish to support and promote Linux-based operating systems.

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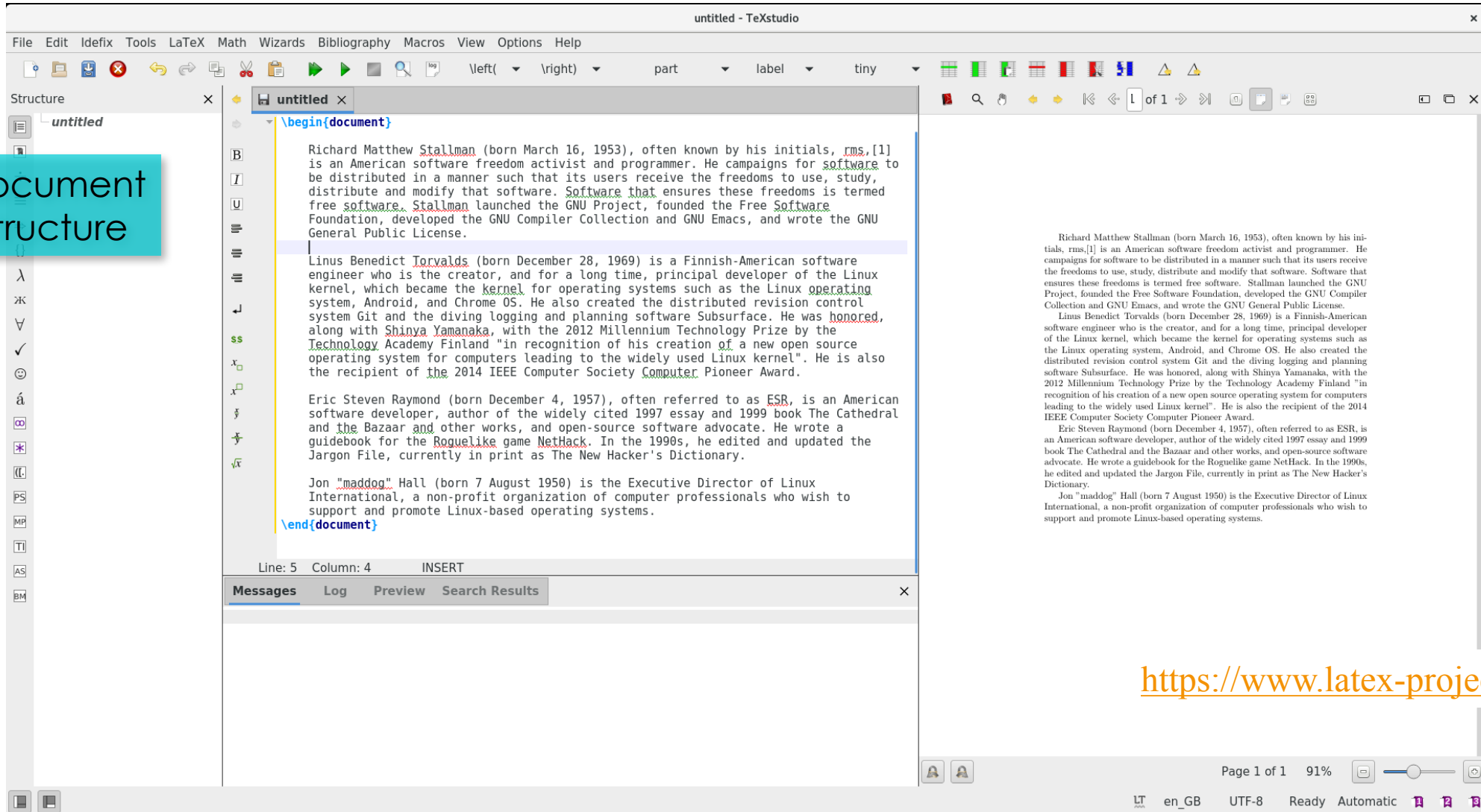
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<https://www.latex-project.org/get/>

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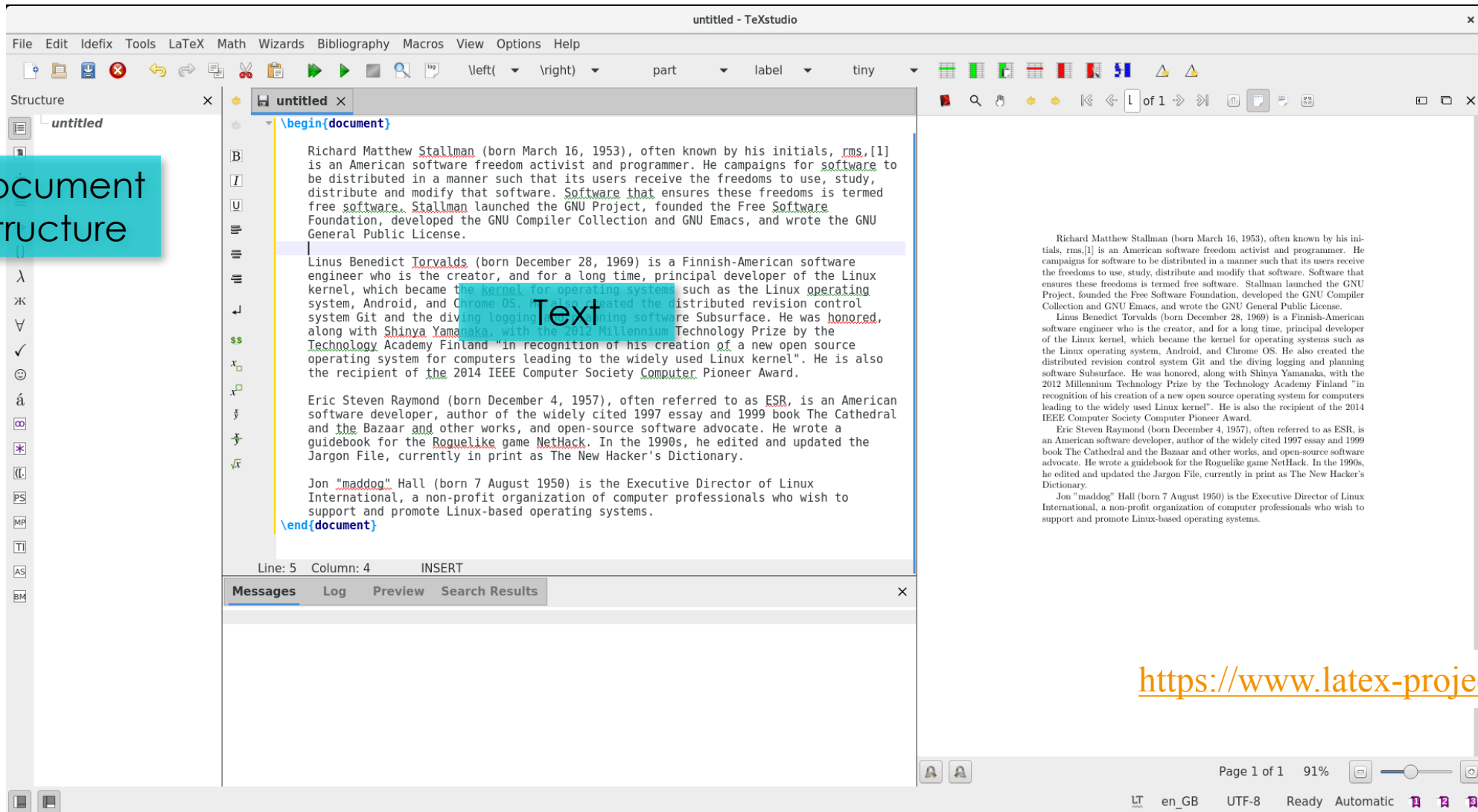
Document structure



<https://www.latex-project.org/get/>

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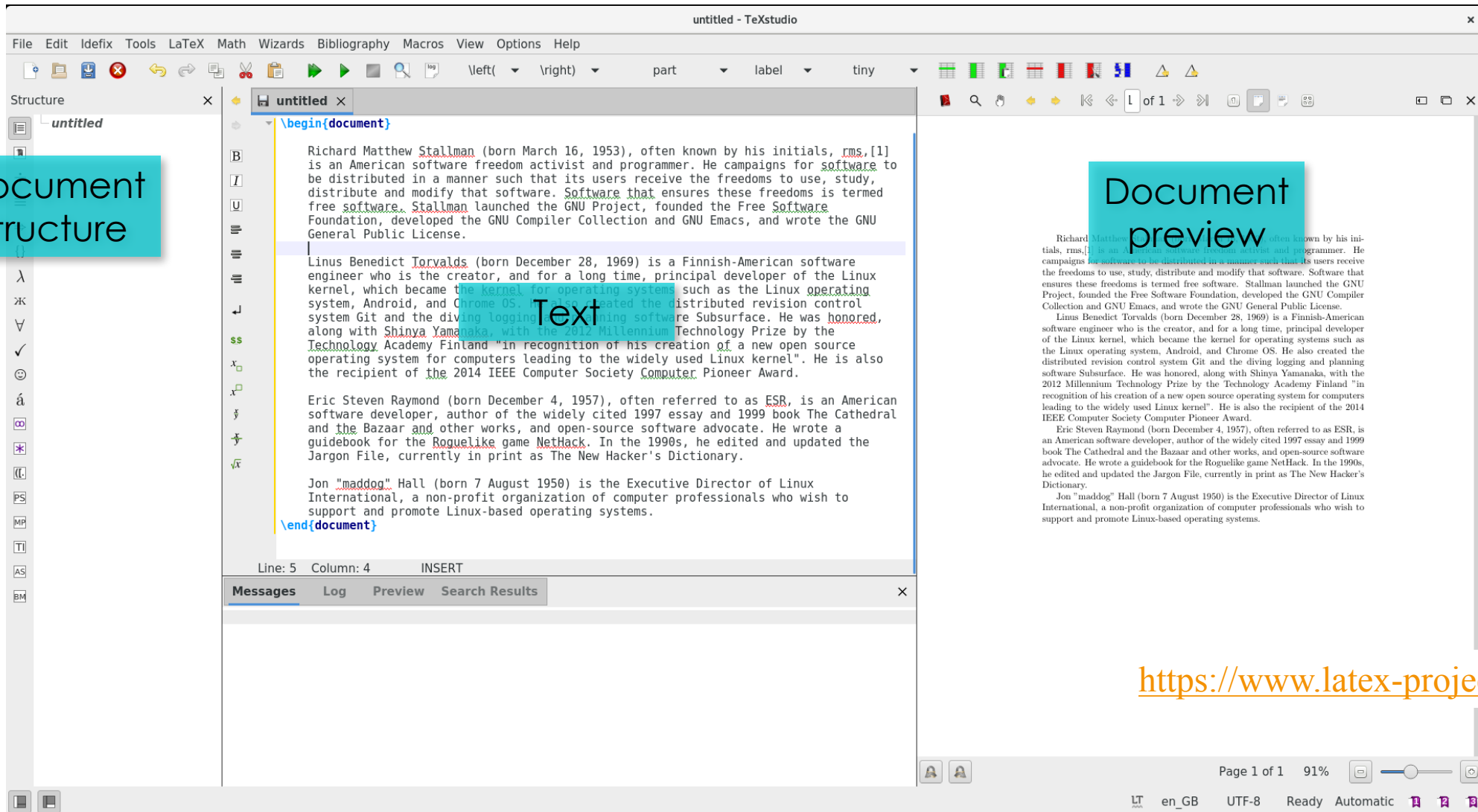
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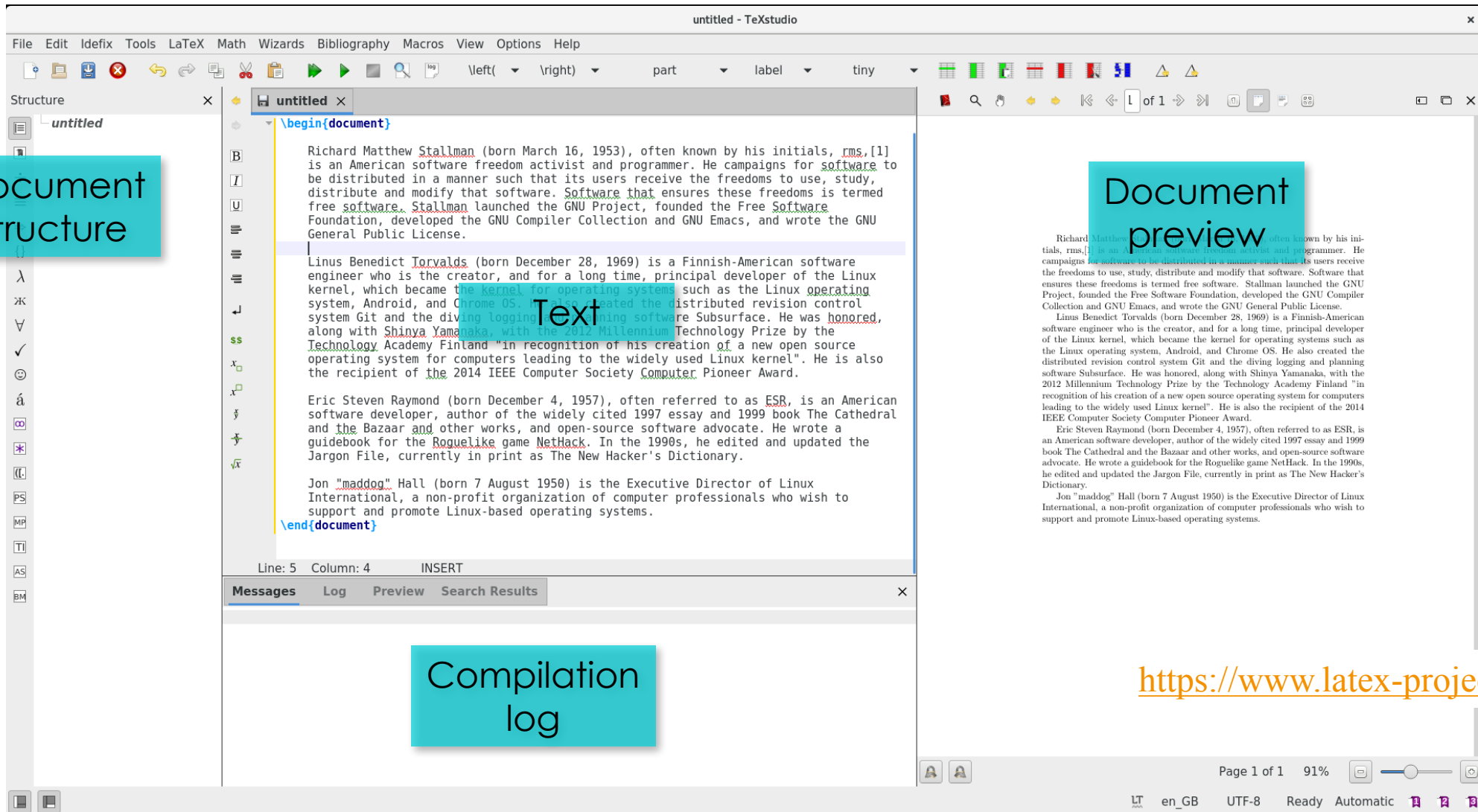
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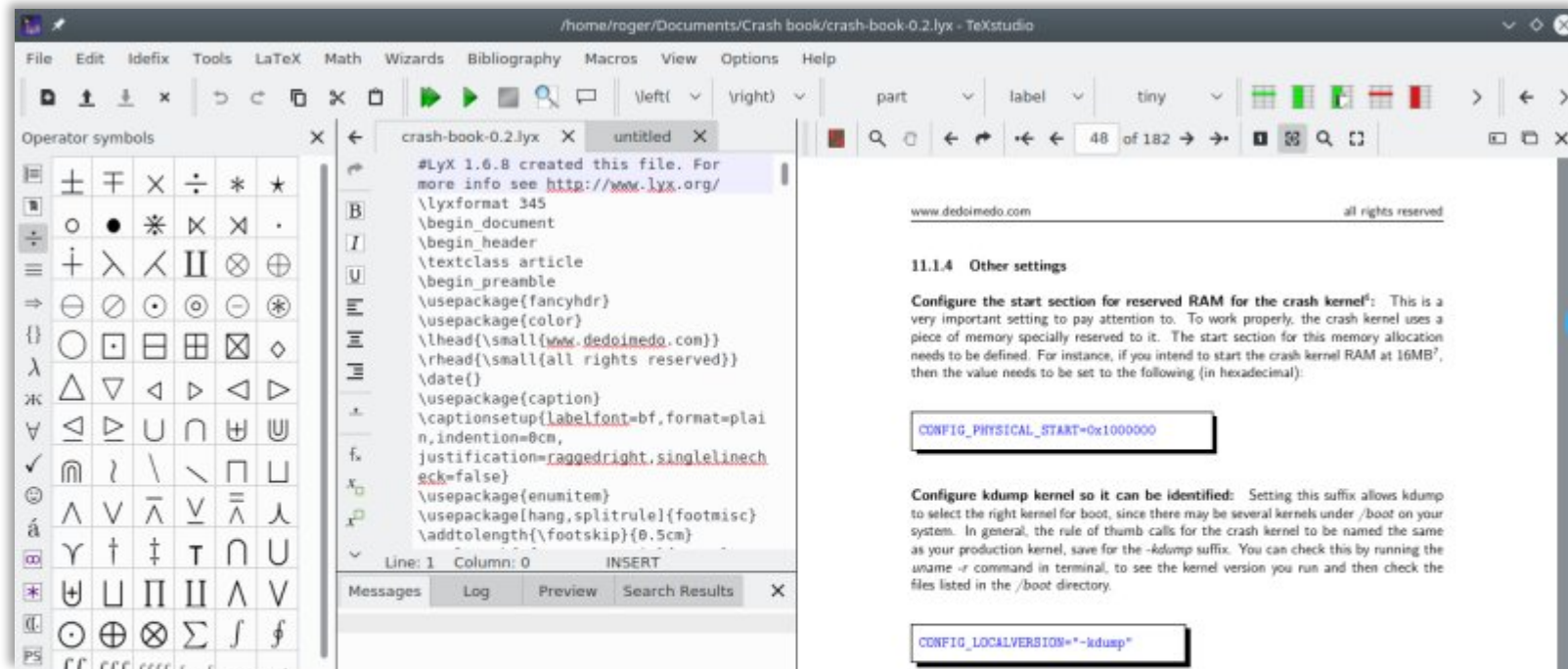
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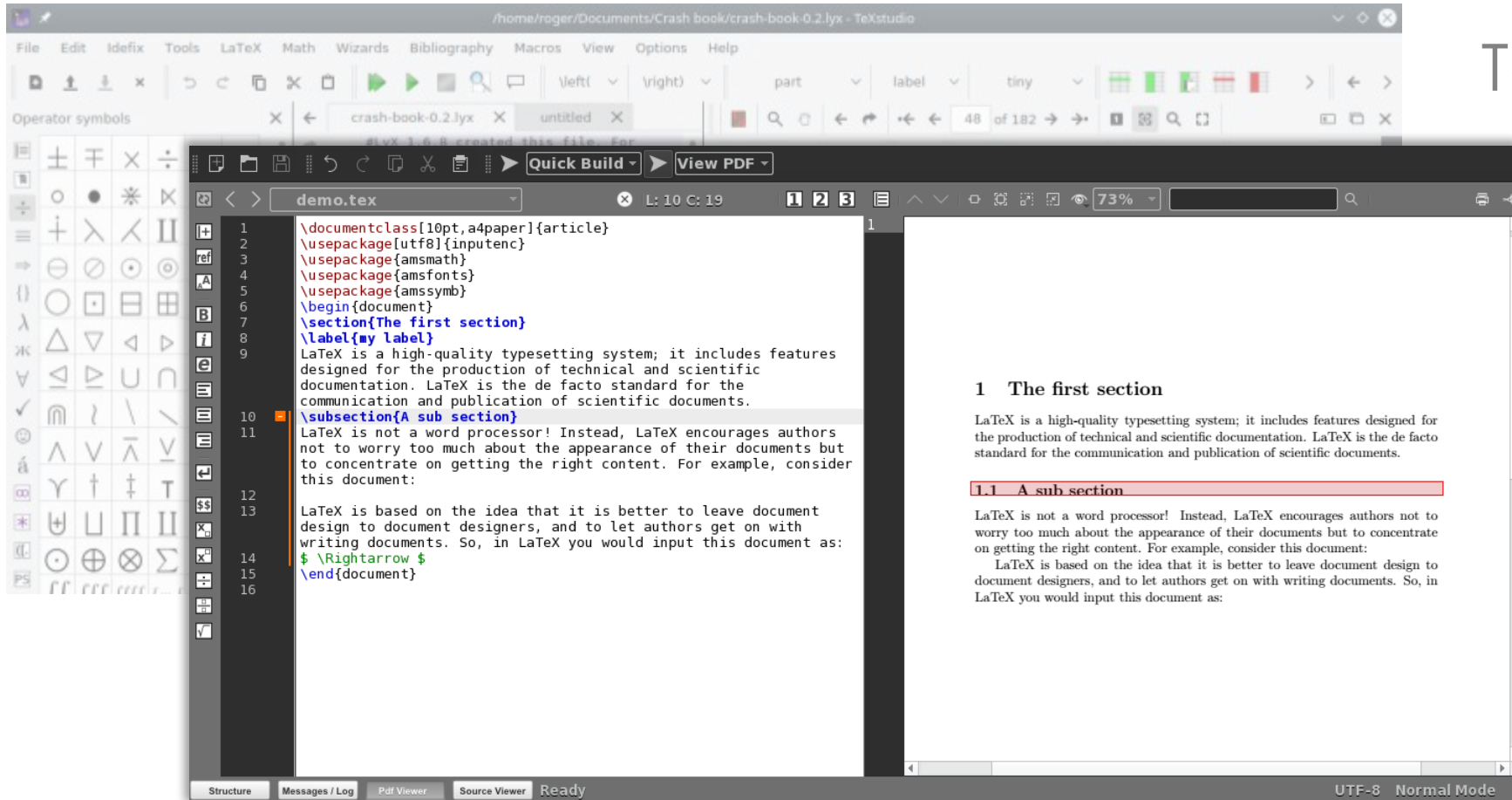


# How do I use LaTeX?



TeXstudio

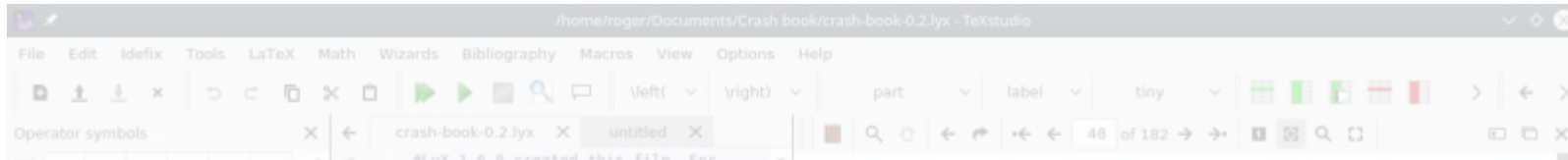
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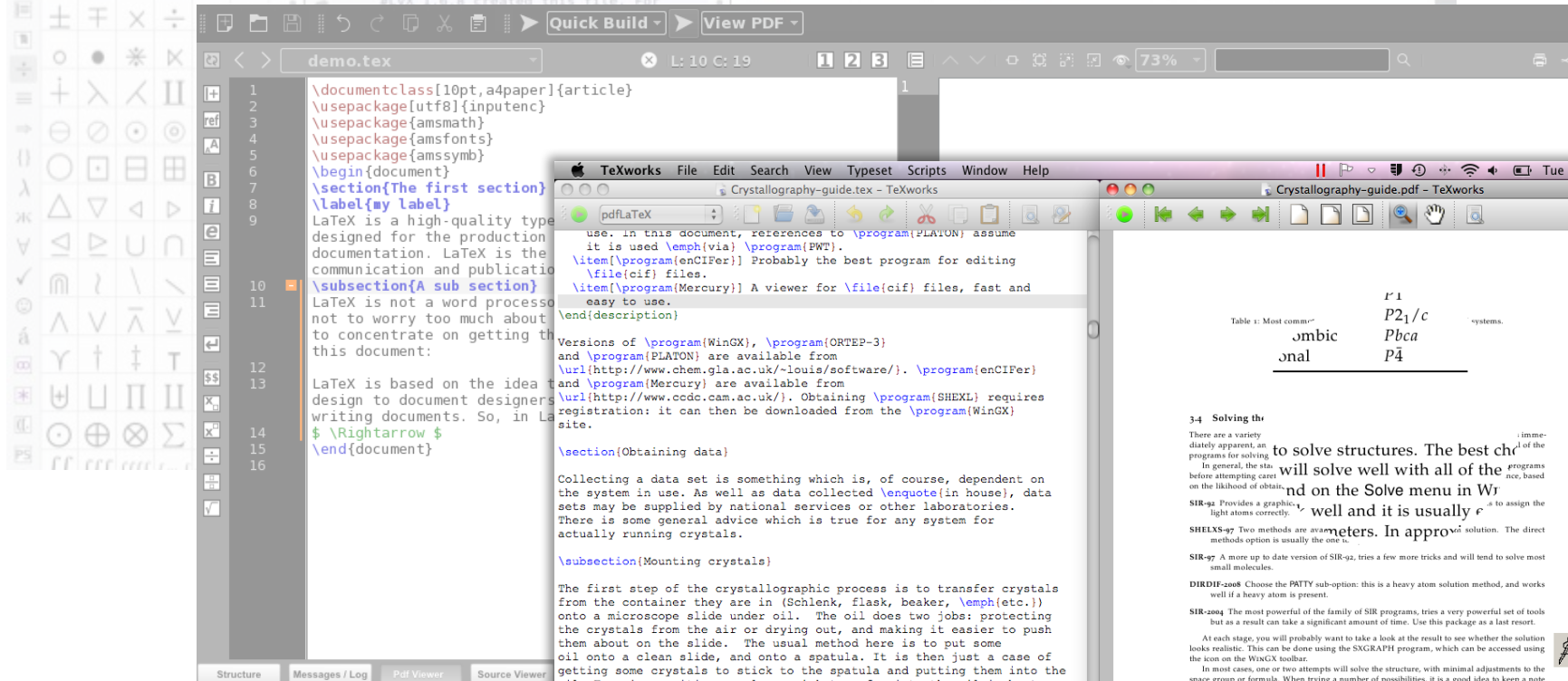
TeXstudio

TeXmaker

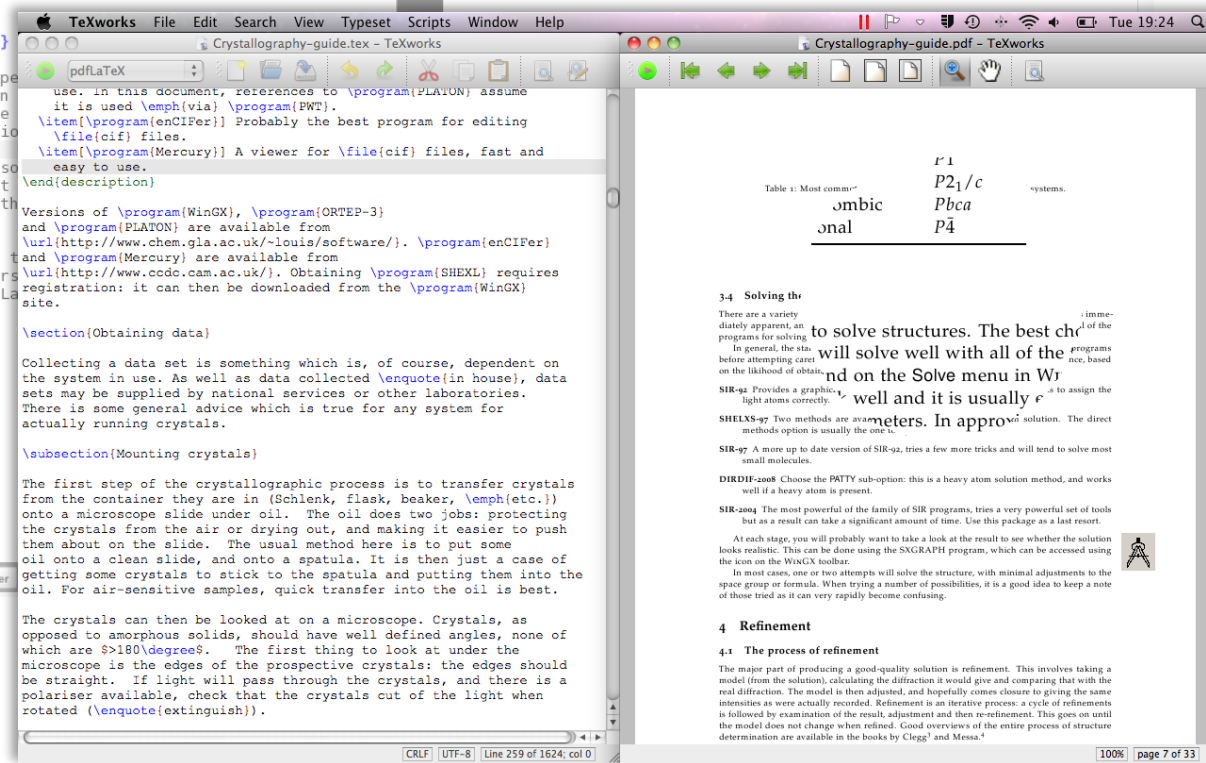
# How do I use LaTeX?



TeXstudio

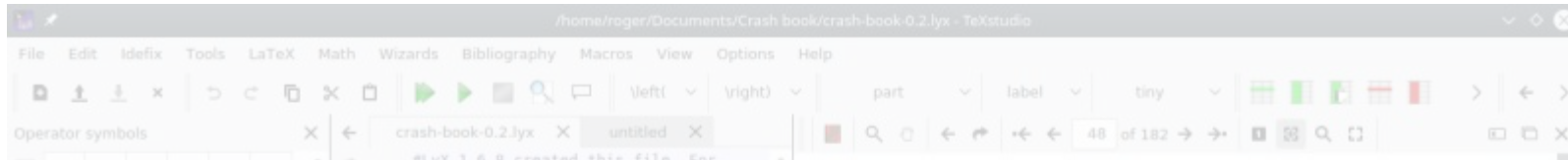


TeXmaker

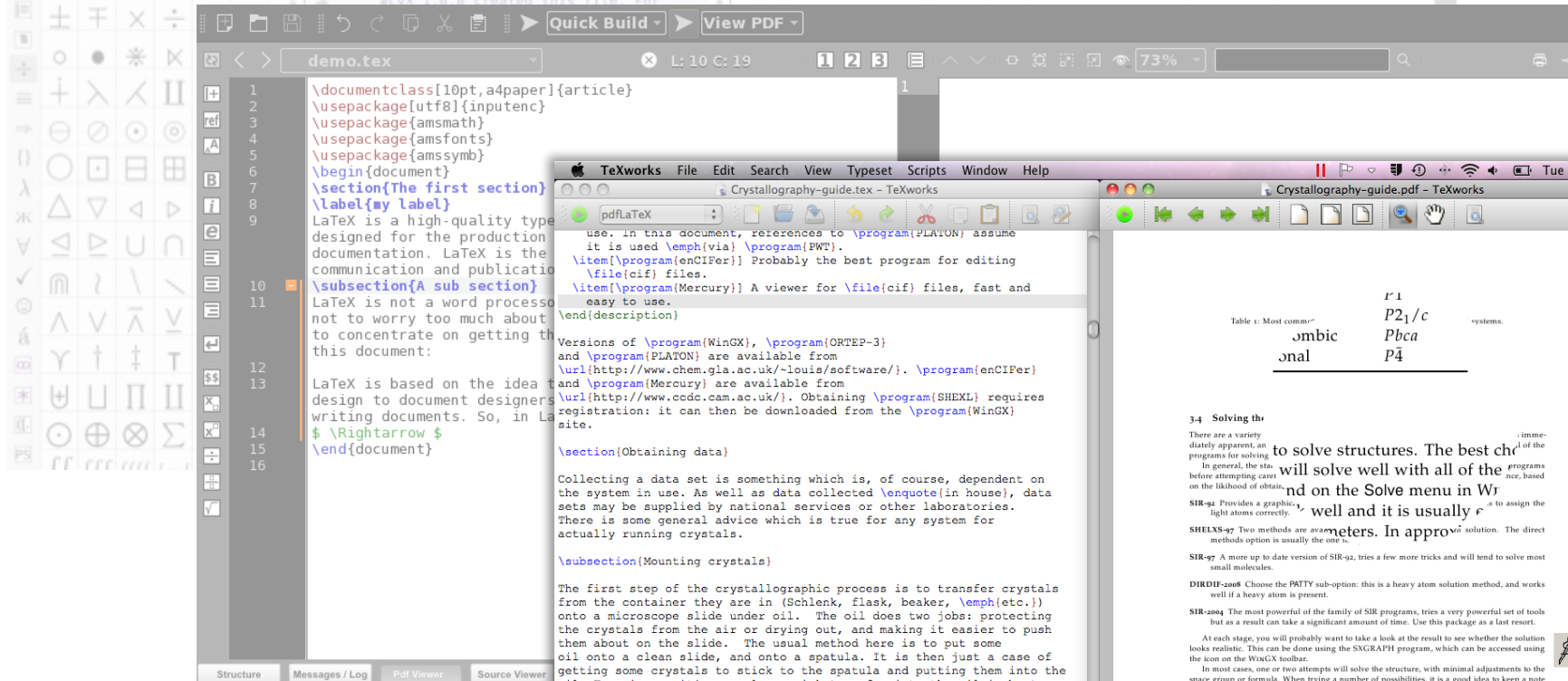


TeXworks

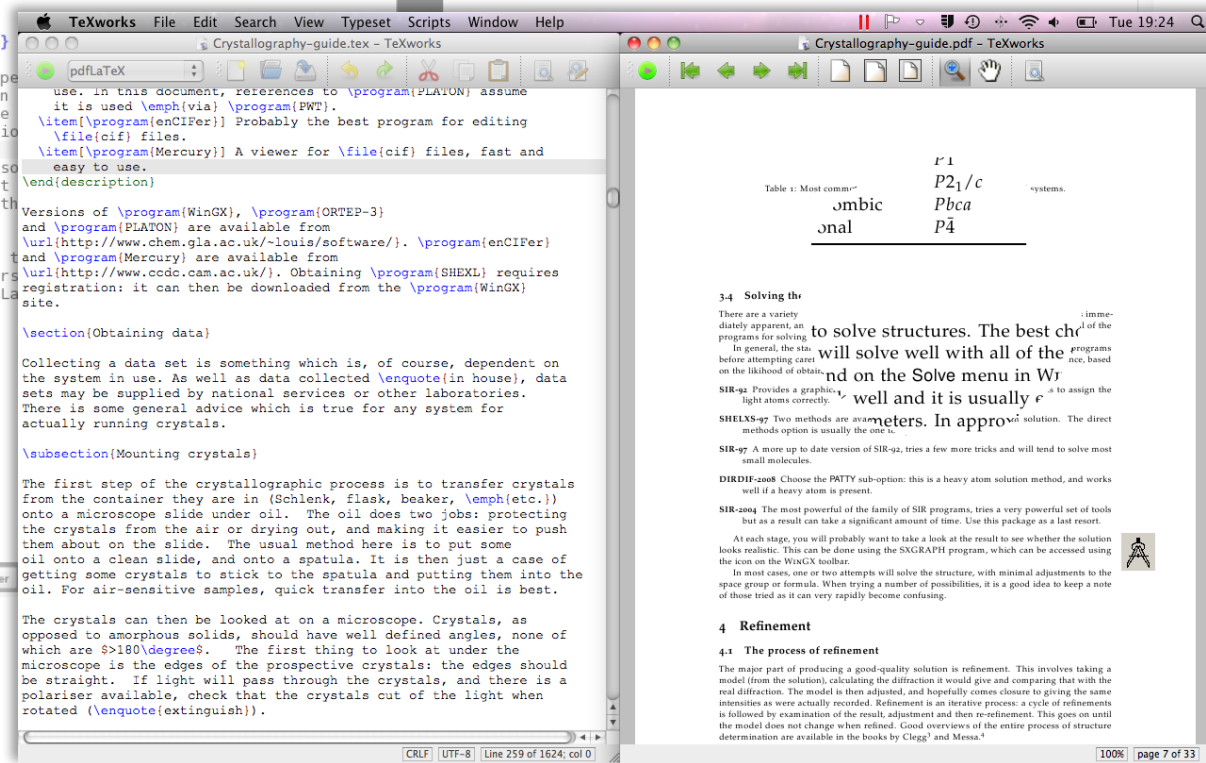
# How do I use LaTeX?



TeXstudio



TeXmaker



TeXworks

...and many others

# How do I use LaTeX?

The image shows the Overleaf web-based LaTeX editor interface. The top navigation bar includes 'Menu', 'Reference Bias in SNP-based Phylogenetics', 'Review', 'Share', 'Submit', 'History', and 'Chat'. Below the navigation bar, there are tabs for 'Source' and 'Rich Text', and a 'Recompile' button. The left sidebar shows a file explorer with folders like 'bibliography', 'figures', and 'sections', and files like '0-abstract.tex', '1-new\_introd...', '2-methods.tex', '3-results.tex', '4-discussion.tex', '5-acknowledgeme...', '5.5-figures.tex', '6-supplemental.tex', 'NA-introduction.tex', 'MAIN\_SB\_TEMPLA...', 'notes.tex', 'sb\_latex\_style.sty', 'SB\_LaTeX\_Template...', and 'sysbio.cls'. The main editor area shows the source code for a LaTeX document. The code includes a title 'Reference genome choice and filtering pipeline jointly influence phylogenetic analyses', authors 'JESSICA A. RICK<sup>1,2\*</sup>, CHAD D. BROCK<sup>2</sup>, AND CATHERINE E. WAGNER<sup>2,3</sup>', and an abstract. The rendered PDF preview on the right shows the title 'Overleaf', the journal information 'Systematic Biology (2020), 0, 0, pp. 1–36', the title 'Reference genome choice and filtering pipeline jointly influence phylogenetic analyses', the authors, and the abstract text.

```
1 ***** INTRODUCTION *****
2
3 % SUMMARY: In phylogenetics, biases introduced by the choice of reference genome for
4 sequence alignment when using reduced-representation or whole genome resequencing data
5 has received little attention. We are investigating the effects of the distance of
6 reference genome to the in-group taxa, whether the reference genome is an in- or
7 outgroup individual, and the manner in which this interacts with downstream filtering
8 choices made before analysis steps. %
9
10 Understanding the evolutionary relationships between taxa is an important foundation
11 for studies in fields across the natural sciences. In evolutionary biology, we are
12 often interested both in how organisms are related to one another and in what factors
13 have influenced those relationships throughout the history of the organisms. Molecular
14 phylogenies are a cornerstone of modern comparative biology, and are commonly employed
15 to investigate a range of biological phenomena, such as macroevolutionary patterns,
16 trait evolution, biogeography, and community assembly. Phylogenetic trees based on
17 large multilocus datasets have become crucial for resolving phylogenetic histories
18 (e.g. \citealt{Edwards2009}, other citations?), and our ability to resolve these trees
19 has greatly improved as a result of advances in high-throughput sequencing methods
20 (cite early phylogenomics papers here: e.g.
21 \citealt{Wagner2013Genome-wideRadiation,Rokas2003,Philippe2004,Prasad2008}).
22
23 However, inferring phylogenetic relationships between taxa is not trivial, even with
24 high-throughput sequencing data, and these large datasets present novel, and in some
25 cases, unexplored, challenges to phylogenetic analyses (e.g.
26 \citealt{Kumar2012,Jeffroy2006}; other citations). Phylogenetic trees are reconstructed
27 based on similarities and differences among DNA sequences for individuals belonging to
28 different taxa, and therefore are sensitive to sampling methods that alter which sites
29 are sequenced and retained in analyses. [examples; make the point that we still lack
30 information about all of these]
31
32 Following sequencing, short reads are typically aligned to either a reference genome or
33 a pseudo-reference created from short reads (often called "\textit{de novo} assembly").
34 [more] Recent advances in sequencing technologies and decreasing sequencing costs have
35 made it increasingly feasible to sequence and assemble reference genomes for non-model
36 species. This has led to an increase in the number of studies choosing to use a
37 reference genome of a focal study taxon for assembly rather than \textit{de novo}
38 assembly. Assembly of reads to a reference genome is based on sequence similarity
39 \citep{Catchen2011stacks}, and reads with higher mutation rates and lower diversity
40 will tend to have lower alignment scores \citep{Nielsen2011}. Therefore, choice of an
41 ingroup versus an outgroup reference genome with which to align reads may have
42 substantial impacts on downstream phylogenetic analyses. For example, there are likely
```

# How do I use LaTeX?

Reference Bias in SNP-based Phylogenetics

Menu ↑

Source Rich Text

Recompile

Ab Review Share Submit History Chat

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Overleaf

Systematic Biology (2020), 0, 0, pp. 1–36  
doi:10.1093/sysbio/utp004

Reference genome choice and filtering pipeline jointly influence phylogenetic analyses

JESSICA A. RICK<sup>1,2\*</sup>, CHAD D. BROCK<sup>2</sup>, AND CATHERINE E. WAGNER<sup>2,3</sup>  
<sup>1</sup> Program in Ecology, University of Wyoming, Laramie, WY, 82071, USA  
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<sup>3</sup> Biodiversity Institute, University of Wyoming, Laramie, WY, 82071, USA

\*Corresponding author: JA Rick, 1000 E University Dr, Laramie, WY 82070; jrnick@uwyo.edu

ABSTRACT

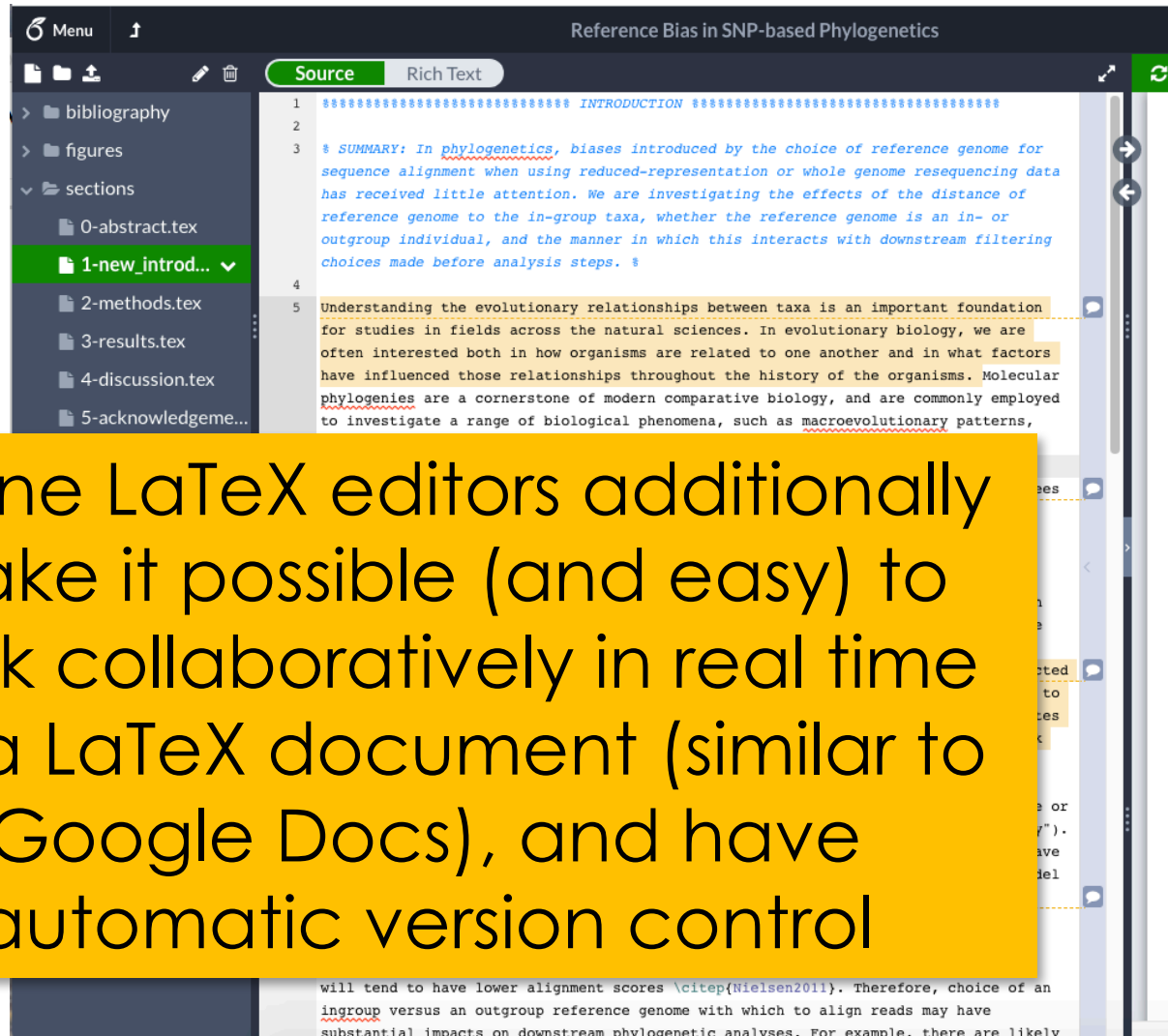
Molecular phylogenies are a cornerstone of modern comparative biology, and are commonly employed to investigate a range of biological phenomena, such as macroevolutionary patterns, trait evolution, biogeography, and community assembly. Recent technological and computational advances have made it possible for researchers to commonly use genomic data for phylogenetic analyses in non-model organisms, providing an unprecedented amount of information for inferring phylogenetic history. However, well-assembled reference genomes remain relatively sparse, leaving researchers with dilemmas about what reference genomes are optimal to work with for different phylogenetic datasets, and what impacts these decisions have on downstream analytical results. Next-generation sequencing (NGS) data require extensive processing (i.e. filtering for site quality, missing data, etc.), which may include the alignment to a reference genome, prior to conducting analyses. Recent work has demonstrated that significant biases may be introduced into downstream phylogenetic analyses from these processing pipelines. However, little attention has been paid to potential biases introduced through the choice of reference genome in sequence alignment and variant-calling pipelines when using reduced-representation or whole genome resequencing data. Here we investigate whether the choice of reference genome in

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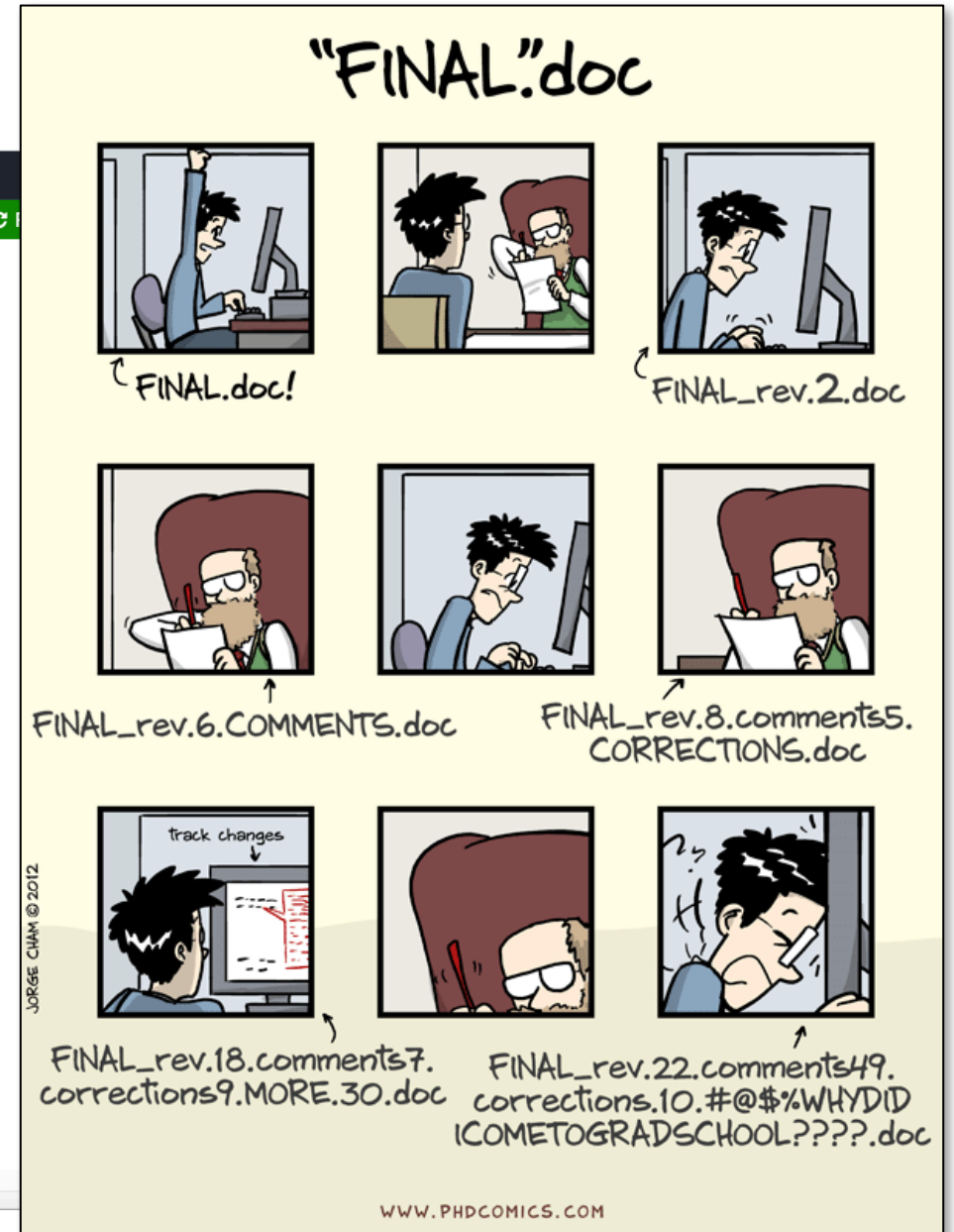
will tend to have lower alignment scores `\citep{Nielsen2011}`. Therefore, choice of an ingroup versus an outgroup reference genome with which to align reads may have substantial impacts on downstream phylogenetic analyses. For example, there are likely

Online LaTeX editors additionally make it possible (and easy) to work collaboratively in real time on a LaTeX document (similar to Google Docs), and have automatic version control

# How do I use LaTeX?



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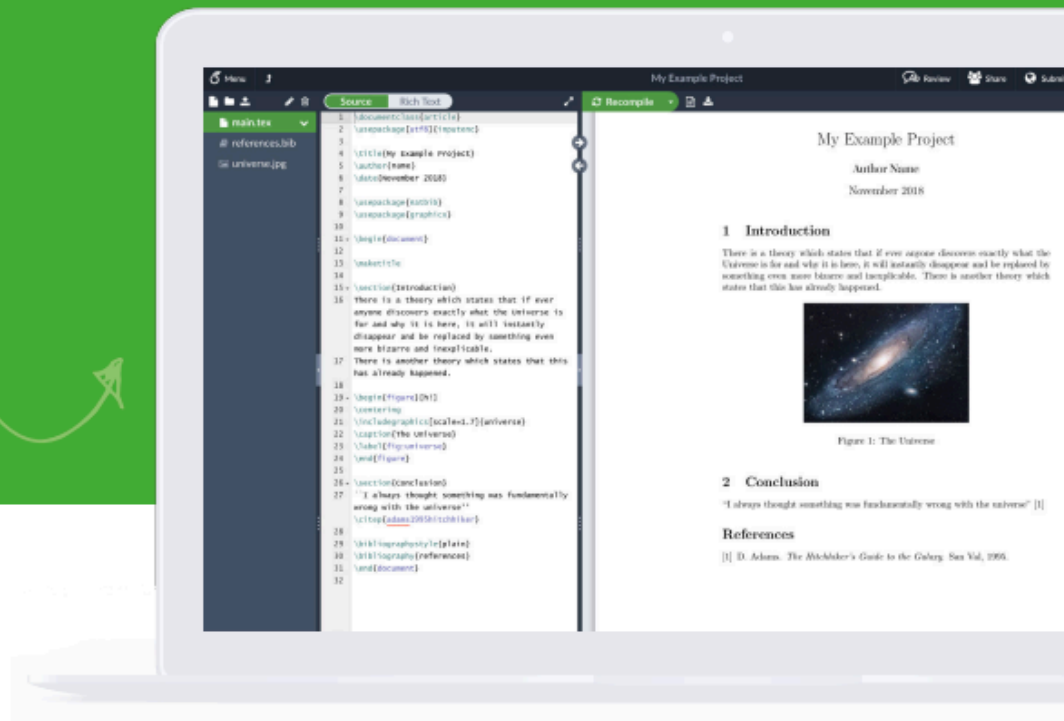


# LaTeX, Evolved

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Overleaf is a great online LaTeX editor for people not familiar/comfortable with LaTeX

**Disclaimer:** I am a part of the Overleaf Advisor Program, which means that I get a free Overleaf professional account in exchange for promoting Overleaf on campus – but also would be telling you about how awesome it is even without this perk!



# How do I use LaTeX?

Download editor program or use online editor

Start from a template, learn as you go

Remember, it's a new language

Easiest to learn by following someone else's LaTeX document

# How do I use LaTeX?

Filters: All / Templates / Examples / Articles

## Articles — Academic Journal

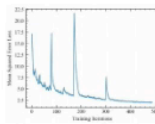
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Show all Articles

Here we provide a selection of academic journal templates for articles and papers which automatically format your manuscripts in the style required for submission to that journal. Thanks to the partnerships we're building within the publishing community, you can also now submit your paper directly to a number of journals and other editorial and review services via the publish menu in the editor.

### Adaptive Learning Rate Clipping Stabilizes Learning

Jeffrey M. Eld and Richard Scaife



**Abstract**—Artificial neural network training with stochastic gradient descent can be destabilized by “bad batches” with high loss. This is often problematic for training with small batch sizes. High order loss functions or carefully high learning rates. In practice, however, we have developed adaptive learning rate clipping (ALRC) in our background paper as a regularizer of gradient descent that has proved useful. ALRC is designed to complement existing learning algorithms. Our algorithm is computationally lightweight, can be applied to any loss function or batch size, is robust to hyperparameter changes, and does not affect high-order gradient clipping. We demonstrate with the MNIST handwritten digit task that ALRC decreases variance and stabilizes training. We also show that ALRC decreases training time compared to the standard training. Empirical results are provided in the appendix. Our source code is publicly available at <https://github.com/jeffreyeld/ALRC>.

**I. INTRODUCTION**

This paper addresses loss spikes, one of the most common sources for low performance in artificial neural networks trained with stochastic gradient descent (SGD). Gradient backpropagation from high losses can occasionally produce transient parameter distributions and destabilize learning. An example of loss spikes destabilizing learning is shown in Fig. 1. Loss spikes can occur for small batch sizes, high order loss functions and carefully high learning rates. Existing neural network training with vanilla SGD is a variable parameter. In each step  $t$ , we update  $\theta_t$  in step 1-1. The size of the update is given by the product of a learning rate,  $\alpha$ , and the backpropagated gradient of a loss function with respect to the trainable parameter

$$\theta_{t+1} = \theta_t - \alpha \nabla_{\theta} \mathcal{L}(\theta_t)$$

Without modification, variable parameter perturbations are proportional to the size of the loss function. This means that a low order loss will cause a large perturbation to the learned parameter distribution. Learning will then be destabilized when the perturbation updates trainable parameters back to their original distribution. This is often observed when clipping gradients to a multiple of their global norm. For large batch sizes, this can limit perturbations by two orders of magnitude, which will be larger than other gradients in the batch. However, global norm clipping alters the distribution of gradients backpropagated from high losses and is unable to preserve backpropagated gradient distributions. Like gradient clipping, it also has the capability to stabilize low learning and neural network architectures.

Rather than allowing loss spikes to destabilize learning,

Adaptive Learning Rate Clipping Stabilizes Lear...  
Adaptive learning rate clipping (ALRC) stabilizes...

### An Approach Based on Bayesian Networks for Query Selectivity Estimation

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**Abstract**—The efficiency of a query execution plan depends on the accuracy of the selectivity estimation given to the query optimizer by the user model. The user model uses simplifying approximations to order to produce valid estimates in a timely manner. These approximations lead to selective estimation errors that have dramatic effects on the quality of the resulting query execution plans. A common approximation that is ubiquitous among current user models is to assume that attributes are independent with each other. However, it ignores potential correlations that exist between attributes. In this paper, we propose a novel approach based on a particular type of Bayesian network to model correlations in approximate estimation. This approach allows us to model correlations between attributes in a more accurate way than other approaches while maintaining reasonable efficiency in terms of time and space.

**Keywords**—Query optimization; Cost Model; Selectivity Estimation; Bayesian networks.

**1. INTRODUCTION**

During query processing, each query goes through an optimization phase followed by an execution phase. The objective of the optimization phase is to produce an efficient query execution plan. In order to do this, the query optimizer needs to estimate the selectivity of each subquery. The user model provides the selectivity estimates for each subquery. The user model is a simplification of the actual data distribution. The user model is used to estimate the selectivity of each subquery. The user model is used to estimate the selectivity of each subquery. The user model is used to estimate the selectivity of each subquery.

An Approach Based on Bayesian Networks for Q...  
The efficiency of a query execution plan depends...

### Heat transport mechanisms for an end-heated aluminum rod

R. M. Scaife

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**Abstract**—The contributions from conduction, convection, and radiation for an end-heated aluminum rod were compared with experimental measurements in detail. Multiple experiments were carried out to measure various physical properties of the system and the aluminum rod. By applying heat loss from these measurements, and modeling convection, the specific heat capacity, conductivity, emissivity, and thermal expansion coefficient of the system, and thermal contact resistance between the joints were also determined.

**Heat transport mechanisms** describe the transfer of thermal energy between physical systems as a function of temperature and pressure. The fundamental modes of heat transfer are conduction, convection, and radiation which occur at the boundary between systems. For each of the fundamental modes, there is an associated physical property for an arbitrary material. In the application of materials to science and engineering, it is imperative that these physical properties are known. However, the determination of the fundamental modes of heat transfer within and across a rod is a difficult task. This is due to the complexity of the system and the difficulty of measuring the properties of the system. In this paper, we describe the contributions from conduction, convection, and radiation, as characterized by physical properties of the aluminum rod and heat transport parameters  $\alpha$ ,  $\beta$ , and  $\gamma$ , respectively. When  $\alpha$  is the thermal conductivity,  $\beta$  is the convective coefficient of the system, and  $\gamma$  is the emissivity. The thermal contact resistance between the end heat source,  $R_c$ , and the specific heat capacity,  $c_p$  is also discussed.

**A. Conduction**

Heat conduction is the transfer of energy through a material. It is the most common mode of heat transfer in solids. It is characterized by the thermal conductivity,  $\alpha$ . The thermal conductivity is a material property that is dependent on the material and the temperature. The thermal conductivity is a function of the material and the temperature. The thermal conductivity is a function of the material and the temperature. The thermal conductivity is a function of the material and the temperature.

Heat transport mechanisms for an end-heated al...  
The contributions from conduction, convection, ...

# How

The screenshot shows a GitHub repository page for 'jessicarick / resources'. The repository has 2 unwatchers, 3 stars, and 0 forks. The main content is the README file, which is titled 'Resources for Others'. The README text describes the repository's purpose and lists four templates: 'Template for Writing', 'Proposal Template', 'Research Log Template', and 'Academic CV Template'. Each template includes a brief description and a link to either download the source files or clone the Overleaf project.

jessicarick / resources

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README.md

## Resources for Others

This repository contains a smattering of tutorials and example documents that I've created to make others' lives a bit easier than mine was in trying to learn LaTeX and other things.

### LaTeX Templates

- 1. Template for Writing** - A general template for writing a manuscript, etc. You can either download the .zip file included [here](#), or clone the Overleaf project at: <https://www.overleaf.com/read/fqsfnqxsqbx>.
- 2. Proposal Template** - A generic template for writing a thesis or dissertation proposal. You can either download the .zip file [here](#), or clone the Overleaf project at: <https://www.overleaf.com/read/btddnrrztkgz>.
- 3. Research Log Template** - A template for keeping track of bioinformatics work (or any kind of research). Keeping a "lab notebook" for computer-based analyses is crucial for open and reproducible science, and has made a HUGE difference for me in streamlining my analyses (no matter how many times I have to re-do them). Different people have different things that work for them, but this is what has worked for me for integrating code, figures, and commentary across different types of analysis (i.e. some cluster computing, some R analysis, some GUI program work, etc). You can either download the .zip file [here](#), or clone the Overleaf project at: <https://www.overleaf.com/read/wkxxnwvfbdxn>.
- 4. Academic CV Template** - This is a general template for a CV, geared toward the style of CV used in academia in the (biological) sciences. Everyone has different opinions on how CVs should look, but this is what I've come up with for myself (you can see what my CV using this template looks like here: <http://www.jessicarick.com/aboutme>). You can either download the source files [here](#), or copy the Overleaf project at: <https://www.overleaf.com/read/qsjjdhkypkgv>.

# How do I use LaTeX?

Download editor program or use online editor

Start from a template, learn as you go

Remember, it's a new language

Easiest to learn by following someone else's LaTeX document

Lots of packages and customizations

# How do I use LaTeX?

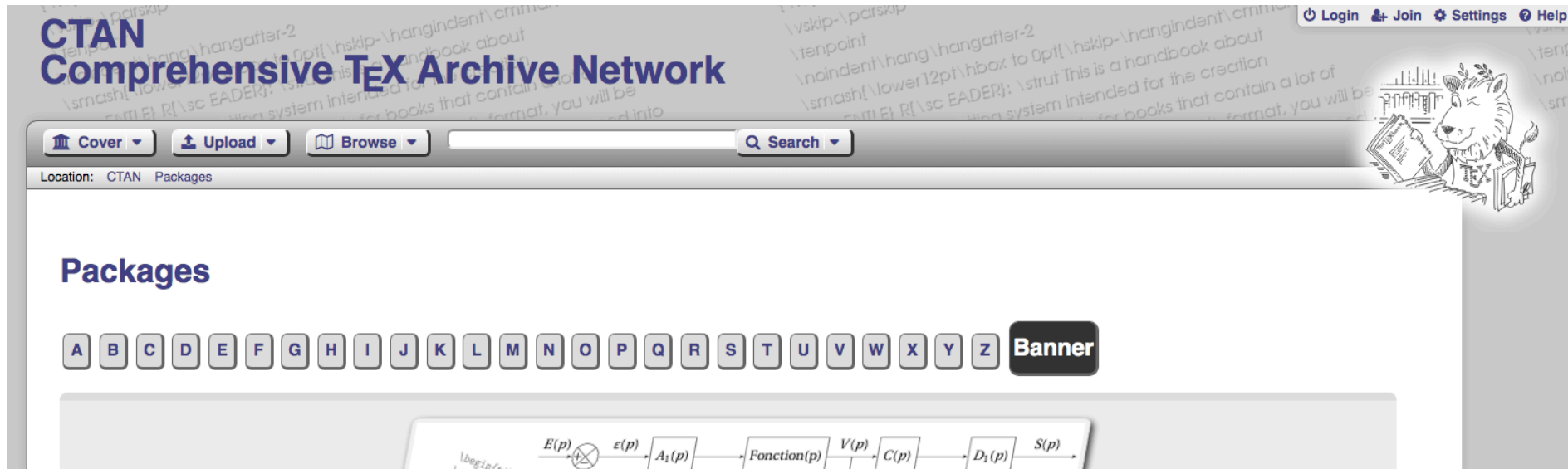
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$$\begin{array}{c} E(p) \otimes \epsilon(p) \rightarrow A_1(p) \rightarrow \text{Fonction}(p) \rightarrow V(p) \rightarrow C(p) \rightarrow D_1(p) \rightarrow S(p) \end{array}$$

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Source Rich Text Recompile

data.txt latex.png main.Rtex references.bib universe.jpg

```

1 \documentclass{article}
2 \usepackage[utf8]{inputenc}
3
4 \title{PiE LaTeX Workshop}
5 \author{Notes and Tutorials}
6 \date{May 2020}
7
8 \usepackage{natbib}
9 \usepackage{graphicx}
10 \usepackage[letterpaper, margin=1in]{geometry}
11 \usepackage{wrapfig}
12 \usepackage[colorlinks=TRUE,urlcolor=blue]{hyperref}
13
14 \begin{document}
15
16 \maketitle

```

PiE LaTeX Workshop  
Notes and Tutorials  
May 2020

### 1 Introduction

This is a tutorial to go along with the workshop on  $\LaTeX$  hosted by the Program in Ecology. The goal of this workshop is three-fold:

1. Convince you why you should use  $\LaTeX$
2. Teach how to use  $\LaTeX$  (the basics)
3. Give you a little taste of advanced features

<https://www.overleaf.com/read/hczdvtccfcdf>

```

20 \begin{enumerate}
21   \item Convince you why you should use LaTeX
22   \item Teach how to use LaTeX (the basics)
23   \item Give you a little taste of advanced features
24 \end{enumerate}
25
26 This document will complement the material covered in the Zoom
27 workshop, and hopefully will serve as a reference that you can refer
28 back to in the future.
29
30 -----
31 \begin{figure}[bht]
32 \centering
33 \includegraphics[width=0.24\textwidth]{latex.png}
34 \caption{A comic about how easy it is to produce nice-looking
35 documents from \LaTeX.}\label{fig:latex}
36 \end{figure}
37 -----
38
39 \section{Why should you use \LaTeX?}
40 \begin{itemize}
41 \item The content of the document is separate from the style

```

Figure 1: A comic about how easy it is to produce nice-looking documents from  $\LaTeX$ .

### 2 Why should you use $\LaTeX$ ?

- The content of the document is separate from the style
  - This means that it looks nice with very little effort from you
  - It is easy to quickly and (relatively) painlessly switch the appearance
  - This point is SUPER useful for submitting manuscripts to journals!
  - Many journals have templates for formatting, so you can just place your manuscript within this framework.
- You can easily generate bibliographies, especially if you already use a reference manager (e.g. Zotero, Mendeley)

1

# Tasks

- Change document margins to 1"
  - Add an abstract
  - Add a section (with and without numbers)
  - Create a list of items
  - Change image to other figure
  - Add a bibliography (two ways) & cite sources (show three different ways)
  - Refer to the figure in-text
  - Add a link
  - Change citation format
  - Make a table (using latex table generator)
- 
- *Invite a collaborator*
  - *Track changes / make comments on a document*