

LaTeX tutorial

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Outline

L^AT_EX tutorial

I. Holmes

Why L^AT_EX?

Hello World

Makefiles

Styling

Mathematics

Marmosets

Figures

Bibliography

Advanced

1 Why L^AT_EX?

2 Hello World

3 Makefiles

4 Styling

5 Mathematics

6 Marmosets

7 Figures

8 Bibliography

9 Advanced

Key

LaTeX tutorial

I. Holmes

Why LaTeX?

Hello World

Makefiles

Styling

Mathematics

Marmosets

Figures

Bibliography

Advanced

1 Exercises in white on red

2 Shell commands in green type on black

3 URLs in blue: <http://tinyurl.com/texroll>

4 Source code in boxes

```
This is some LaTeX source code
```

Try the URL now!

- 1 It's free, portable, open source & extensible
- 2 Source files are plain text, revision control easier
- 3 Typesetting is *much* better, especially math
- 4 Style changes are easier
- 5 Easy to integrate with programmatic workflows
- 6 **Separation of form and content**

L^AT_EX criticism

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I. Holmes

Why L^AT_EX?

Hello World

Makefiles

Styling

Mathematics

Marmosets

Figures

Bibliography

Advanced

- 1 Possibly the worst programming language ever
- 2 Syntax is horrible
- 3 Compilation from source is almost impossible
- 4 Mostly trial and error, unless you're a guru
- 5 Some things you just can't do (unless, guru)
- 6 **Will mark you forever as a nerd pariah**

Text editor

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Why L^AT_EX?

Hello World

Makefiles

Styling

Mathematics

Marmosets

Figures

Bibliography

Advanced

Before you start, your life will be much easier with a text editor that has L^AT_EX syntax-coloring, such as `emacs` or `vim`.

You could also use a specialized L^AT_EX editor that gives you previews, such as TeXmaker, or even a WYSIWYG L^AT_EX editor such as LyX (free) or Texpad (OSX, \$\$\$).

Best of all is <https://www.overleaf.com/> — collaborative browser-based editor. Try it!

You still need to understand the L^AT_EX underneath. So...

helloworld.tex

LaTeX tutorial

I. Holmes

Why LaTeX?

Hello World

Makefiles

Styling

Mathematics

Marmosets

Figures

Bibliography

Advanced

```
\documentclass{article}
\title{Marmosets Are Great}
\author{Ian Holmes}
\begin{document}
\maketitle
\abstract{A short treatise on marmosets.}
\section{Introduction}
Marmosets ({\em Callitrichidae})
are {\bf New World Monkeys}.
\end{document}
```

Compile with `pdflatex helloworld.tex`

Try this.

<http://tinyurl.com/texhello>

documentclass options

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I. Holmes

Why L^AT_EX?

Hello World

Makefiles

Styling

Mathematics

Marmosets

Figures

Bibliography

Advanced

- `\documentclass[10pt]{article}`
- `\documentclass[twocolumn]{article}`
- `\documentclass[landscape]{article}`
- `\documentclass{letter}`
- `\documentclass{book}`
- `\documentclass{beamer}` — presentation

Further classes can be defined using a *class file*.

For example, the journal *Bioinformatics* provides a class file `bioinfo.cls` invoked with `\documentclass{bioinfo}`.

Section references

L^AT_EX tutorial

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Why L^AT_EX?

Hello World

Makefiles

Styling

Mathematics

Marmosets

Figures

Bibliography

Advanced

Can use `\label` and `\ref` as follows:

```
\section{Introduction}
\label{intro}
Marmosets are New World Monkeys.

\section{Geography}
Marmosets are found in the New World,
as mentioned in Section~\ref{intro}.
```

Note tilde ~ between Section and `\ref`: prevents linebreak.

Add a section or two, and recompile.

Makefiles

L^AT_EX tutorial

I. Holmes

Why L^AT_EX?

Hello World

Makefiles

Styling

Mathematics

Marmosets

Figures

Bibliography

Advanced

If you change the section numbers, you will have to re-run **pdflatex**. Consequently, it's common to run the program twice. Can do this with a Makefile:

```
helloworld.pdf: helloworld.tex
    pdflatex helloworld.tex
    pdflatex helloworld.tex
```

General form of Makefile stanza:

```
TARGET: DEPENDENCIES
    <TAB> COMMANDS
```

Make command-line usage

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Why L^AT_EX?

Hello World

Makefiles

Styling

Mathematics

Marmosets

Figures

Bibliography

Advanced

- General: `make helloworld.pdf`
- Force rebuild: `make -B helloworld.pdf`
- Dry run: `make -n helloworld.pdf`

By default, `make` just builds first target in Makefile.

Makefiles and replicability

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I. Holmes

Why LaTeX?

Hello World

Makefiles

Styling

Mathematics

Marmosets

Figures

Bibliography

Advanced

Titus Brown's checklist for paper replicability:

- a link to the paper itself, in preprint form, stored at arXiv;
- a tutorial for running the software on a Linux machine hosted in the Amazon cloud;
- a git repository for the software itself (hosted on github);
- a git repository for the LaTeX paper and analysis scripts, including an ipython notebook for generating the figures;
- instructions on how to start up an EC2 cloud instance, install the software and paper pipeline, and build most of the analyses and all of the figures from scratch;
- the data necessary to run the pipeline;
- some of the output data discussed in the paper.

<http://ivory.idyll.org/blog/replication-i.html>

Pseudotargets, pattern rules and variables

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I. Holmes

Why LaTeX?

Hello World

Makefiles

Styling

Mathematics

Marmosets

Figures

Bibliography

Advanced

```
MAIN = helloworld

all: $(MAIN).pdf

%.pdf: %.tex
    pdflatex $<
    pdflatex $<
    open $@

clean:

    rm *.toc *.log *.out *.pdf *.aux *~
```

Try this.

Use `make`, `make -n` and `make -B`.
If in doubt: `make clean`

Loading other files

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Why L^AT_EX?

Hello World

Makefiles

Styling

Mathematics

Marmosets

Figures

Bibliography

Advanced

L^AT_EX files can include other files via the `\input` command. This is particularly useful with Makefiles, because you can generate data-driven parts of your article automatically, and combine them with manually-written sections.

The `\include` command is like `\input` but does some extra book-keeping (such as adding a page break). Useful for e.g. separating a thesis into chapter files.

Comments, escapes, styling

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Why L^AT_EX?

Hello World

Makefiles

Styling

Mathematics

Marmosets

Figures

Bibliography

Advanced

% Comments

Actual percent sign: 100\%

Other escapes: _, \&

Tilde escape: \~{ }

‘ ‘Pretty quotation marks’ ’

Empty line signals new paragraph.

Space: \quad Explicit line \\ break

Can you get **bold**, *italic* & typewriter fonts?

Google these typefaces.

Typefaces

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I. Holmes

Why LaTeX?

Hello World

Makefiles

Styling

Mathematics

Marmosets

Figures

Bibliography

Advanced

<code>{\bf Bold}</code>	Bold
<code>{\em Italic}</code>	<i>Italic</i>
<code>{\tt Typewriter}</code>	Typewriter

Page numbering

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I. Holmes

Why LaTeX?

Hello World

Makefiles

Styling

Mathematics

Marmosets

Figures

Bibliography

Advanced

These go in the preamble:

- `\pagenumbering{arabic}` — default
- `\pagenumbering{roman}`
- `\pagenumbering{Roman}`
- `\pagenumbering{alph}`
- `\pagenumbering{Alph}`

To suppress page numbers altogether, use `\pagestyle{empty}`.

To add a table of contents: `\tableofcontents`

Lists

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Why L^AT_EX?

Hello World

Makefiles

Styling

Mathematics

Marmosets

Figures

Bibliography

Advanced

List of books about wizard school

```
\begin{itemize}
```

```
\item Earthsea
```

```
\item Harry Potter
```

```
\item The Magicians
```

```
\item The Once and Future King
```

```
\end{itemize}
```

Try this.

Also try `enumerate` instead of `itemize`, and try nesting lists inside other lists.

How many levels deep can you nest?

Tables

LaTeX tutorial

I. Holmes

Why LaTeX?

Hello World

Makefiles

Styling

Mathematics

Marmosets

Figures

Bibliography

Advanced

Right-justified	Centered	Left-justified
School vouchers	Science	Public education
Defense spending	Trade deals	Aid programs

```
\begin{tabular}{rcl}
Right-justified & Centered & Left-justified \\
\hline
School vouchers & Science & Public education \\
Defense spending & Trade deals & Aid programs
\end{tabular}
```

Time to add a table.

Make a table with some facts about marmosets. Or pick another vertebrate from hgdownload.cse.ucsc.edu and make a table about it.

Table captions and references

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Why LaTeX?

Hello World

Makefiles

Styling

Mathematics

Marmosets

Figures

Bibliography

Advanced

```
\begin{table}
\begin{tabular}
...
\end{tabular}
\caption{
  \label{MarmosetFacts}
  A table of marmoset facts.
}
\end{table}
```

For marmoset data, see Table~\ref{MarmosetFacts}.

Equations

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I. Holmes

Why L^AT_EX?

Hello World

Makefiles

Styling

Mathematics

Marmosets

Figures

Bibliography

Advanced

Inline: $a = 3$, $b = 5$

Non-numbered:

$$[$$

$$y = ax + b$$

$$]$$

Inline: $a = 3$, $b = 5$

Non-numbered:

$$y = ax + b$$

Equations

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Why L^AT_EX?

Hello World

Makefiles

Styling

Mathematics

Marmosets

Figures

Bibliography

Advanced

```
Numbered (Equation~\ref{Gaussian}):  
\begin{equation}  
x \sim {\cal N}(\mu,\sigma):  
\quad  
P(x' \leq x < x' + dx') =  
\frac{1}{\sqrt{2 \pi \sigma^2}}  
e^{-\frac{(x'-\mu)^2}{2\sigma^2}} dx'  
\label{Gaussian}  
\end{equation}
```

Numbered (Equation 1):

$$x \sim \mathcal{N}(\mu, \sigma) : \quad P(x' \leq x < x' + dx') = \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{(x'-\mu)^2}{2\sigma^2}} dx' \quad (1)$$

Equations

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I. Holmes

Why L^AT_EX?

Hello World

Makefiles

Styling

Mathematics

Marmosets

Figures

Bibliography

Advanced

```
Numbered (Equation~\ref{Gaussian}):  
\begin{equation}  
x \sim {\cal N}(\mu,\sigma):  
\quad  
P(x' \leq x < x' + dx') =  
\frac{1}{\sqrt{2 \pi \sigma^2}}  
e^{-\frac{(x'-\mu)^2}{2\sigma^2}} dx'  
\label{Gaussian}  
\end{equation}
```

Google “Latex math symbols”.

Write out another distribution e.g. Poisson.

Brackets, arrays

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Why L^AT_EX?

Hello World

Makefiles

Styling

Mathematics

Marmosets

Figures

Bibliography

Advanced

```
\[
\left(
  \begin{array}{c}
    n \\
    k
  \end{array}
\right)
= \frac{n \times (n-1) \times \dots \times (n-k+1)}{k \times (k-1) \times \dots \times 2 \times 1}
= \frac{n!}{k!(n-k)!}
\]
```

$$\binom{n}{k} = \frac{n \times (n-1) \times \dots \times (n-k+1)}{k \times (k-1) \times \dots \times 2 \times 1} = \frac{n!}{k!(n-k)!}$$

Macro commands

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I. Holmes

Why LaTeX?

Hello World

Makefiles

Styling

Mathematics

Marmosets

Figures

Bibliography

Advanced

```
\newcommand\MacroName[NumberOfArgs]{  
  Definition of macro  
  (Arg1 is #1, Arg2 is #2...)  
}
```

e.g.

```
\newcommand\isa[2]{  
  \fbox{ A {\em #1} is a type of {\em #2}. }  
}  
\isa{marmoset}{mammal}  
\isa{mammal}{vertebrate}
```

A *marmoset* is a type of *mammal*.

A *mammal* is a type of *vertebrate*.

Macro commands

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I. Holmes

Why L^AT_EX?

Hello World

Makefiles

Styling

Mathematics

Marmosets

Figures

Bibliography

Advanced

```
\newcommand\binomial[2]{  
  \left(  
    \begin{array}{c}  
      #1 \\  
      #2  
    \end{array}  
  \right)  
}  
\[  
  \binomial{5}{2} = (5 \times 4) / 2 = 10  
\]
```

$$\binom{5}{2} = (5 \times 4) / 2 = 10$$

Try this.

More arrays; text in math environments

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Why LaTeX?

Hello World

Makefiles

Styling

Mathematics

Marmosets

Figures

Bibliography

Advanced

```
\[
H(x) = \left\{
\begin{array}{ll}
0 & \text{\mbox{for } $x < 0$} \\
1 & \text{\mbox{for } $x \geq 0$}
\end{array}
\right.
\]
```

$$H(x) = \begin{cases} 0 & \text{for } x < 0 \\ 1 & \text{for } x \geq 0 \end{cases}$$

Equation arrays

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Why L^AT_EX?

Hello World

Makefiles

Styling

Mathematics

Marmosets

Figures

Bibliography

Advanced

```
\begin{eqnarray}
F_1 & = & 1 \\
F_2 & = & 1 \\
F_{n+2} & = & F_n + F_{n+1}
\end{eqnarray}
```

$$F_1 = 1 \tag{2}$$

$$F_2 = 1 \tag{3}$$

$$F_{n+2} = F_n + F_{n+1} \tag{4}$$

Equation arrays (cleaner numbering)

```
\begin{eqnarray}
F_1 & = & 1 \ \nonumber \\
F_2 & = & 1 \ \nonumber \\
F_{n+2} & = & F_n + F_{n+1} \\
\label{Fibonacci} \\
\end{eqnarray}
Fibonacci numbers (\ref{Fibonacci})
arise naturally in phyllotaxis.
```

$$\begin{array}{rcl} F_1 & = & 1 \\ F_2 & = & 1 \\ F_{n+2} & = & F_n + F_{n+1} \end{array} \tag{5}$$

Fibonacci numbers (5) arise naturally in phyllotaxis.

Equation arrays (no numbering)

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Why L^AT_EX?

Hello World

Makefiles

Styling

Mathematics

Marmosets

Figures

Bibliography

Advanced

```
\begin{eqnarray*}
F_1 & = & 1 \\
F_2 & = & 1 \\
F_{n+2} & = & F_n + F_{n+1}
\end{eqnarray*}
```

$$\begin{array}{rcl} F_1 & = & 1 \\ F_2 & = & 1 \\ F_{n+2} & = & F_n + F_{n+1} \end{array}$$

Do the following:

- 1 Download a set of predicted gene annotations from UCSC for your vertebrate of choice. (I used the Augustus gene predictions for marmoset.)
- 2 Also download the description of that table. Find out which column in the table has the number of exons for each gene.
- 3 Using `perl`, `python`, `sed`, `cut`, or another such tool, extract the number of exons as a column of numbers.
- 4 Plot the frequency distribution in R (or otherwise).
- 5 Export as a PDF file, `exonFreqs.pdf`

Example R script

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Why LaTeX?

Hello World

Makefiles

Styling

Mathematics

Marmosets

Figures

Bibliography

Advanced

```
require("ggplot2")
exons <- read.csv("numExons.txt")
plot <- qplot(exons,geom="histogram",binwidth=1,
              main="Marmoset exon count distribution") +
  scale_y_continuous() +
  scale_x_continuous(limits=c(0,100)) +
  xlab("Number of exons")
ggsave ("exonFreqs.pdf", plot)
```

Save as plot.R

Example Makefile

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Why L^AT_EX?

Hello World

Makefiles

Styling

Mathematics

Marmosets

Figures

Bibliography

Advanced

```
PREFIX := hgdownload.cse.ucsc.edu/goldenPath
SPECIES := calJac3
URL := http://$(PREFIX)/$(SPECIES)/database

augustusGene.sql augustusGene.txt.gz:
    curl -O $(URL)/$@

%.txt: %.txt.gz
    gunzip --keep $<

numExons.txt: augustusGene.txt
    cat $< | cut -f 9 >$@

exonFreqs.pdf: numExons.txt plot.R
    R -f plot.R
```

Figure

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Why LaTeX?

Hello World

Makefiles

Styling

Mathematics

Marmosets

Figures

Bibliography

Advanced

```
\includegraphics{numExons.pdf}
```

Of course, you can get more elaborate...

Figure, with caption

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Why LaTeX?

Hello World

Makefiles

Styling

Mathematics

Marmosets

Figures

Bibliography

Advanced

```
\begin{figure}
\includegraphics[width=\textwidth]{numExons.pdf}
\caption{
  \label{ExonDistribution}
  Distribution of exon frequencies in marmosets.
}
\end{figure}
```

```
Marmosets are highly social \cite{Marx2016}.
```

```
...
```

```
\bibliographystyle{natbib} % or plain, unsrt, ...  
\bibliography{references}
```

Implies the existence of a file `references.bib`

```
@Article{Marx2016,  
  Author="Marx, V.",  
  Title="{N}eurobiology: learning from marmosets",  
  Journal="Nat. Methods",  
  Year="2016",  
  Volume="13",  
  Number="11"  
}
```

Running BibTeX

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Why LaTeX?

Hello World

Makefiles

Styling

Mathematics

Marmosets

Figures

Bibliography

Advanced

Typically you need to run `pdflatex`, then `bibtex`, then `pdflatex` again *twice* to ensure all numbering is correct.

In your Makefile:

```
%.pdf: %.tex references.bib
    pdflatex $<
    bibtex $<
    pdflatex $<
    pdflatex $<
```

Yes: this is really messed-up

TeXMed

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Why LaTeX?

Hello World

Makefiles

Styling

Mathematics

Marmosets

Figures

Bibliography

Advanced

<http://www.bioinformatics.org/texmed/>
BibTeX wrapper for PubMed.

Try adding a reference for your vertebrate of choice.

Commands

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Why LaTeX?

Hello World

Makefiles

Styling

Mathematics

Marmosets

Figures

Bibliography

Advanced

Command	Purpose
<code>\hspace</code>	Fill horizontal space
<code>\fbox</code>	Box with frame
<code>\parbox</code>	Box with line breaks
<code>\newcounter</code>	Create a new counter
<code>\stepcounter</code>	Increment counter
<code>\color</code>	Change text color
<code>\colorbox</code>	Change background color

See e.g. <https://en.wikibooks.org/wiki/LaTeX>

Packages

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Why LaTeX?

Hello World

Makefiles

Styling

Mathematics

Marmosets

Figures

Bibliography

Advanced

Loaded with `\usepackage`, e.g. `\usepackage{amsmath}`

Package	Purpose
<code>algorithm2e</code>	Writing out algorithms
<code>beamer</code>	Presentations (like this one)
<code>amsmath</code>	Better math formatting
<code>geometry</code>	Page formatting (e.g. margins)
<code>biblatex</code>	Better bibliographies
<code>chemfig</code>	Chemical structures

Try a few of these out...

CTAN (ctan.org): Comprehensive TeX Archive Network

These slides at <https://github.com/ihh/latex-tutorial>

Homework

L^AT_EX tutorial

I. Holmes

Why L^AT_EX?

Hello World

Makefiles

Styling

Mathematics

Marmosets

Figures

Bibliography

Advanced

Make a short report on a vertebrate in the UCSC genome database that is *not* a marmoset. Include:

- 1 Title, author, abstract
- 2 Two-column layout
- 3 Introduction, Results, References sections
- 4 A figure showing the distribution of exon counts (or other data from UCSC)
- 5 A mathematical formula (e.g. a fit to the histogram)
- 6 At least one table
- 7 At least one reference