

LaTeX tutorial

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Outline

L^AT_EX tutorial

I. Holmes

Why L^AT_EX?

Hello World

Makefiles

Styling

Mathematics

Marmosets

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Advanced

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3 Makefiles

4 Styling

5 Mathematics

6 Marmosets

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Key

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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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- 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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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

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```
\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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- `\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

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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

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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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- 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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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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```
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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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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% 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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<code>\bf</code>	Bold}	Bold
<code>\em</code>	Italic}	<i>Italic</i>
<code>\tt</code>	Typewriter}	Typewriter

Page numbering

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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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```
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

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

Non-numbered:

$$\left[$$

$$y = ax + b$$

$$\right]$$

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

Non-numbered:

$$y = ax + b$$

Equations

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

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

Macro commands

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

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

Equation arrays

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

$$F_1 = 1 \quad (2)$$

$$F_2 = 1 \quad (3)$$

$$F_{n+2} = F_n + F_{n+1} \quad (4)$$

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

Of course, you can get more elaborate...

Figure, with caption

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

Try adding a reference for your vertebrate of choice.

Commands

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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>

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```
\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*.

Packages

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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

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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