Introduction to R 2024

June 11 - June 12 2024

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Introduction

Welcome to CBW's Introduction to R 2024 Workshop!

Before continuing, ensure to register, complete your pre-work (below) and ensure your zoom is functional.

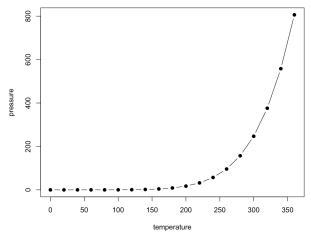
1.1 Pre-Workshop Materials

Click here for the pre-work. This includes programs to install.

Meet Your Faculty

Here's the team!

Frances Wong (she/her)

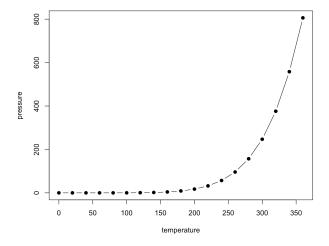


Assistant Professor, Teaching Stream, University of Toronto Missisauga

— frances.wong@utoronto.ca

Frances Wong is an assistant professor, teaching stream, at the University of Toronto Mississauga Department of Biology. She is interested in how dynamic cell populations make decisions (sometimes incorrectly!) during development. Frances used a systems biology approach to investigate human placenta development by isolating single cells at multiple time points during early development to computationally assemble a cell atlas of first trimester development. Currently, Frances incorporates computational literacy as a core course objective in biology courses she teaches to empower over 1000 students to analyze the data they collect each semester.

Andrés Melani (he/him)

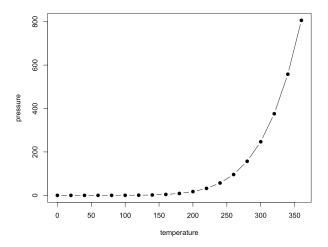


Ph.D. student, Courtot Lab University of Toronto | Ontario Institute for Cancer Research Toronto, ON, Canada

— amelanidelahoz@oicr.on.ca

Andres is a Software Engineer with a MSc in Business Information Technologies, who is currently pursuing his PhD in Medical Biophysics at the University of Toronto. Previously, Andres was a professor and project coordinator for programming courses at Universidad de Los Andes, Colombia. His main interests are Artificial Intelligence, software development, and data analytics. Currently, his PhD project applies AI, specifically Natural Language Processing, Large Language Models and Knowledge Representation and Reasoning, to healthcare scenarios.

Amin Noorani (he/him)

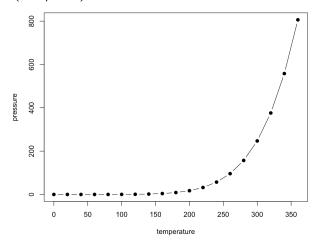


Master Student | Bioinformatician Toronto Metropolitan University (Olson Lab) Princess Margaret Genomic Centre (Epigenome Lab) Toronto, ON, Canada

— amin.noorani@uhn.ca

Amin is a bioinformatician at Princess Margaret Genomic Centre (PMGC) who is also pursuing his master's degree at Olson Lab at Toronto Metropolitan University (TMU). Prior to his current roles, he earned his bachelor's degree in Bioinformatics and started his current position at PMGC in 2022. His expertise includes analyzing various types of data, including epigenomics and genomics, from raw data to visualization. His master's project focuses on exploring gene expression data in ovarian cancer cell lines, as well as image classification to determine whether cell images have been treated with various compounds.

Zoe Klein (she/her)

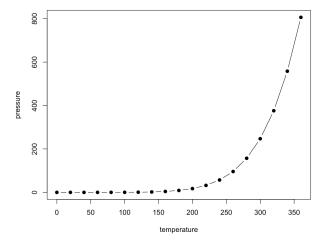


PhD Candidate, Reimand Lab University of Toronto

— z.klein@mail.utoronto.ca

Zoe Klein is a PhD candidate at the University of Toronto and the Ontario Institute for Cancer Research. She uses large-scale data analytics and machine learning to study the role of non-coding RNA transcripts in cancer.

Michelle Brazas, PhD (she/her)



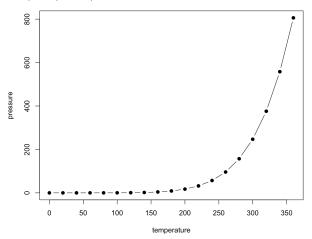
Scientific Director Canadian Bioinformatics Workshops (CBW) Toronto, ON, CA

— support@bioinformatics.ca

Dr. Michelle Brazas is the Associate Director for Adaptive Oncology at the

Ontario Institute for Cancer Research (OICR), and acting Scientific Director at Bioinformatics.ca. Previously, Dr. Brazas was the Program Manager for Bioinformatics.ca and a faculty member in Biotechnology at BCIT. Michelle co-founded and runs the Toronto Bioinformatics User Group (TorBUG) now in its 11th season, and plays an active role in the International Society of Computational Biology where she sits on the Board of Directors and Executive Board.

Nia Hughes (she/her)



Program Manager, Bioinformatics.ca Ontario Institute for Cancer Research Toronto, ON, Canada

— nia.hughes@oicr.on.ca

Nia is the Program Manager for Bioinformatics.ca, where she coordinates the Canadian Bioinformatics Workshop Series. Prior to starting at OICR, she completed her M.Sc. in Bioinformatics from the University of Guelph in 2020 before working there as a bioinformatician studying epigenetic and transcriptomic patterns across maize varieties.

Course Schedule

CBW's			
Introduction to R workshop (INR) 2024			
		Day	
		$2^{\tilde{}}$	
June 11		June	
		12	
Time (EDT)	Module	Time	Module
		(EDT)	
8:30	Arrivals & Check-in	8:30	Arrivals
9:00	Welcome (Nia	9:00	Review & Module 3:
	Hughes)		Loops and functions
			(Frances Wong)
9:30	Module 1: Getting to	10:00	Break (15min)
	Know R (Frances		
10:30	Wong)	10:15	Module 2. Leong and
10.30	Break (15min)	10:15	Module 3: Loops and functions (cont'd)
10:45	Module 1: Getting to	11:00	Break (15min)
10.40	Know R (cont'd)	11.00	Bleak (19mm)
11:15	Break (15min)	11:15	Module 3: Loops and
11.10	Dicak (10mm)	11.10	functions (cont'd)
11:30	Module 1: Getting to	12:00	Class Photo + Break
	Know R (cont'd)		(1h)
12:00	Break (1h)	13:00	Module 4: Linear
	,		regression (Frances
			Wong)

CBW's Introduction to R workshop (INR) 2024			
13:00	Module 2: Exploring your data in R (Frances Wong)	14:00	Break (15min)
14:00	Break (15min)	14:15	Module 4: Linear regression (cont'd)
14:15	Module 2: Exploring your data in R (cont'd)	15:15	Break (15min)
15:15	Break (15min)	15:30	Short Project
15:30	Review and Short project	17:00	Survey & Closing Remarks
17:30	Finished	17:30	Finished

Cross-references

calendar (cal_demo_data("week"), view = "week", default Date = Sys.Date()) %>% cal_week_options (startDayOfWeek = 1, workweek = TRUE) %>% cal_props (cal_demo_props())

Parts

You can add parts to organize one or more book chapters together. Parts can be inserted at the top of an .Rmd file, before the first-level chapter heading in that same file.

Add a numbered part: # (PART) Act one {-} (followed by # A chapter)

Add an unnumbered part: # (PART*) Act one {-} (followed by # A chapter)

Add an appendix as a special kind of un-numbered part: # (APPENDIX) Other stuff {-} (followed by # A chapter). Chapters in an appendix are prepended with letters instead of numbers.

Footnotes and citations

5.1 Footnotes

Footnotes are put inside the square brackets after a caret ^[]. Like this one ¹.

5.2 Citations

Reference items in your bibliography file(s) using @key.

For example, we are using the **bookdown** package [Xie, 2024] (check out the last code chunk in index.Rmd to see how this citation key was added) in this sample book, which was built on top of R Markdown and **knitr** [Xie, 2015] (this citation was added manually in an external file book.bib). Note that the .bib files need to be listed in the index.Rmd with the YAML bibliography key.

The RStudio Visual Markdown Editor can also make it easier to insert citations: https://rstudio.github.io/visual-markdown-editing/#/citations

¹This is a footnote.

Blocks

6.1 Equations

Here is an equation.

$$f(k) = \binom{n}{k} p^k \left(1 - p\right)^{n-k} \tag{6.1}$$

You may refer to using \@ref(eq:binom), like see Equation (6.1).

6.2 Theorems and proofs

Labeled theorems can be referenced in text using \@ref(thm:tri), for example, check out this smart theorem 6.1.

Theorem 6.1. For a right triangle, if c denotes the length of the hypotenuse and a and b denote the lengths of the **other** two sides, we have

$$a^2 + b^2 = c^2$$

 $Read\ more\ here\ https://bookdown.org/yihui/bookdown/markdown-extensions-by-bookdown.html.$

6.3 Callout blocks

The R Markdown Cookbook provides more help on how to use custom blocks to design your own callouts: https://bookdown.org/yihui/rmarkdown-cookbook/custom-blocks.html

Sharing your book

7.1 Publishing

HTML books can be published online, see: https://bookdown.org/yihui/bookdown/publishing.html

7.2 404 pages

By default, users will be directed to a 404 page if they try to access a webpage that cannot be found. If you'd like to customize your 404 page instead of using the default, you may add either a _404.Rmd or _404.md file to your project root and use code and/or Markdown syntax.

7.3 Metadata for sharing

Bookdown HTML books will provide HTML metadata for social sharing on platforms like Twitter, Facebook, and LinkedIn, using information you provide in the index.Rmd YAML. To setup, set the url for your book and the path to your cover-image file. Your book's title and description are also used.

This gitbook uses the same social sharing data across all chapters in your bookall links shared will look the same.

Specify your book's source repository on GitHub using the edit key under the configuration options in the _output.yml file, which allows users to suggest an edit by linking to a chapter's source file.

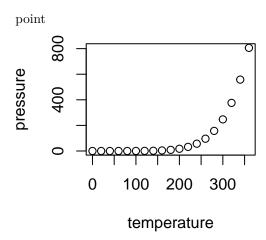
Read more about the features of this output format here:

https://pkgs.rstudio.com/bookdown/reference/gitbook.html

Or use:

?bookdown::gitbook

R Markdown



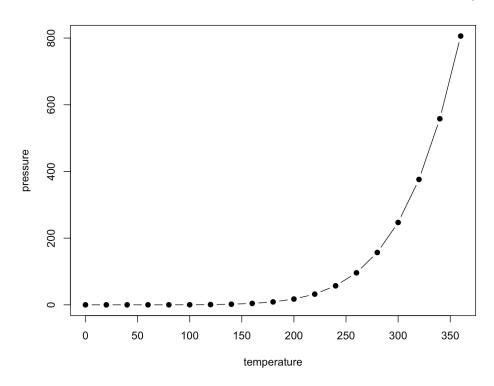
This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see http://rmarkdown.rstudio.com.

When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

Note that the echo = FALSE parameter was added to the code chunk to prevent printing of the R code that generated the plot.

```
cat("just as it *is*")
just as it is
library(knitr)
kable(cars)
```

speed	dist
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$\frac{21}{24}$	92
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$\frac{24}{24}$	120
$\frac{24}{25}$	85



Bibliography

Yihui Xie. Dynamic Documents with R and knitr. Chapman and Hall/CRC, Boca Raton, Florida, 2nd edition, 2015. URL http://yihui.org/knitr/. ISBN 978-1498716963.

Yihui Xie. bookdown: Authoring Books and Technical Documents with R Markdown, 2024. URL https://github.com/rstudio/bookdown. R package version 0.40.