Callout Test Page

Faculty: INSTRUCTOR AND TA NAMES

DATES

Contents

Part I

Introduction

Chapter 1

Workshop Info

Welcome to the YEAR WORKSHOP Canadian Bioinformatics Workshop webpage!

1.1 Schedule

YOUR SCHEDULE HERE

1.2 Pre-work

You can find your pre-work here.

In this tutorial, you can choose between using:

16S dataset from wild blueberry, *Vaccinium angustifolium* (soil microbiome) - Variation in Bacterial and Eukaryotic Communities Associated with Natural and Managed Wild Blueberry Habitats - Metagenomic Functional Shifts to Plant Induced Environmental Changes

18S dataset from plastics incubated in a coastal marine environment (plastisphere) - Microbial pioneers of plastic colonisation in coastal seawaters

ITS2 dataset from stool samples from pregnant women (gut microbiome) - Landscape of the gut mycobiome dynamics during pregnancy and its relationship with host metabolism and pregnancy health

This is a subtle blue tip with a custom lightbulb icon and a left-aligned title. The main content can have **bold** and *italic* text as usual.

Your process completed successfully. All data has been saved.

test text

Chapter 2

Meet Your Faculty

2.0.0.1 NAME

JOB TITLE INSTITUTION LOCATION

— CONTACT INFO, IF PROVIDED

BIO GOES HERE

2.0.0.2 Michelle Brazas, PhD

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

— director@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.

2.0.0.3 Nia Hughes (she/her)

Platform Training Manager, Canadian Bioinformatics Hub Ontario Institute for Cancer Research Toronto, ON, Canada

— training@bioinformatics.ca

Nia is the Platform Training Manager for the Canadian Bioinformatics Hub, 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.

Chapter 3

Data and Compute Setup

3.0.0.1 Course data downloads

Coming soon!

3.0.0.2 Compute setup

Coming soon!

Part II

Modules

Chapter 4

Module 1

4.1 Lecture

Here is an example of a pdf embedded:

Sample PDF

This is a simple PDF file. Fun fun fun.

Lorem ipsum dolor sit amet, consectetuer adipiscing elit. Phasellus facilisis odio sed mi. Curabitur suscipit. Nullam vel nisi. Etiam semper ipsum ut lectus. Proin aliquam, erat eget pharetra commodo, eros mi condimentum quam, sed commodo justo quam ut velit. Integer a erat. Cras laoreet ligula cursus enim. Aenean scelerisque velit et tellus. Vestibulum dictum aliquet sem. Nulla facilisi. Vestibulum accumsan ante vitae elit. Nulla erat dolor, blandit in, rutrum quis, semper pulvinar, enim. Nullam varius congue risus. Vivamus sollicitudin, metus ut interdum eleifend, nisi tellus pellentesque elit, tristique accumsan eros quam et risus. Suspendisse libero odio, mattis sit amet, aliquet eget, hendrerit vel, nulla. Sed vitae augue. Aliquam erat volutpat. Aliquam feugiat vulputate nisl. Suspendisse quis nulla pretium ante pretium mollis. Proin velit ligula, sagittis at, egestas a, pulvinar quis, nisl.

Pellentesque sit amet lectus. Praesent pulvinar, nunc quis iaculis sagittis, justo quam lobortis tortor, sed vestibulum dui metus venenatis est. Nunc cursus ligula. Nulla facilisi. Phasellus ullamcorper consectetuer ante. Duis tincidunt, urna id condimentum luctus, nibh ante vulputate sapien, id sagittis massa orci ut enim. Pellentesque vestibulum convallis sem. Nulla consequat quam ut nisl. Nullam est. Curabitur tincidunt dapibus lorem. Proin velit turpis, scelerisque sit amet, iaculis nec, rhoncus ac, ipsum. Phasellus lorem arcu, feugiat eu, gravida eu, consequat molestie, ipsum. Nullam vel est ut ipsum volutpat feugiat. Aenean pellentesque.

In mauris. Pellentesque dui nisi, iaculis eu, rhoncus in, venenatis ac, ante. Ut odio justo, scelerisque vel, facilisis non, commodo a, pede. Cras nec massa sit amet tortor volutpat varius. Donec lacinia, neque a luctus aliquet, pede massa imperdiet ante, at varius lorem pede sed sapien. Fusce erat nibh, aliquet in, eleifend eget, commodo eget, erat. Fusce consectetuer. Cras risus tortor, porttitor nec, tristique sed, convallis semper, eros. Fusce vulputate ipsum a mauris. Phasellus mollis. Curabitur sed urna. Aliquam nec sapien non nibh pulvinar convallis. Vivamus facilisis augue quis quam. Proin cursus aliquet metus. Suspendisse lacinia. Nulla at tellus ac turpis eleifend scelerisque. Maecenas a pede vitae enim commodo interdum. Donec odio. Sed sollicitudin dui vitae justo.

Morbi elit nunc, facilisis a, mollis a, molestie at, lectus. Suspendisse eget mauris eu tellus molestie cursus. Duis ut magna at justo dignissim condimentum. Cum sociis natoque penatibus et magnis dis parturient montes, nascetur ridiculus mus. Vivamus varius. Ut sit amet diam suscipit mauris ornare aliquam. Sed varius. Duis arcu. Etiam tristique massa eget dui. Phasellus congue. Aenean est erat, tincidunt eget, venenatis quis, commodo at, quam.

Here is an example of a YouTube video embedded:

4.1.1 Downloads

[insert your downloads for this module here (ex. datasets)]

4.2 Lab

[Your lab here]

```
# Your R code here

# For example:
x <- 42
x
```

```
## [1] 42
```

```
# Your python code here

# For example:
print("hello world")
```

```
## hello world
```

```
# Your bash code here

# For example:
#pwd
```

Try running these code "chunks" by pressing the green (left-pointing) triangle next to your code chunks.

You will see the code run in the console and the output provided below the code chunk.

The output of the code will also be produced under the code chunk on your website page.

Chapter 5

Callout Tests

This page tests the static and dropdown callout blocks.

5.1 Regular Callouts

5.1.1 Red Regular

Static:

This is a regular red static callout. It can contain `inline code` and also:

```
# R code block
print("Hello from static red!")
x <- 1 + 1
```

More text after the code block.

Dropdown:

This is the content of a regular red dropdown. It can contain `inline code` and also:

```
# R code block
print("Hello from dropdown red!")
y <- 2 * 2
```

More text after the code block.

5.1.2 Blue Regular

Static:

This blue static callout uses a specific icon.

Dropdown:

Details for the blue dropdown.

5.1.3 Green Regular (No Icon)

Static:

This green static callout has no icon.

Dropdown:

Content for the green dropdown without an icon.

5.2 Important Callouts

5.2.1 Red Important

Static:

This is an important red static callout.

Dropdown:

Content of the important red dropdown.

5.2.2 Yellow Important

Static:

This is an important yellow static callout.

Dropdown:

Content of the important yellow dropdown.

5.3 Subtle Callouts

5.3.1 Purple Subtle

Static:

A subtle purple idea, presented statically.

Dropdown:

Details of the subtle purple idea in a dropdown.

5.3.2 Gray Subtle (No Title)

Static:

This is a subtle gray static callout with no explicit title. The icon should still align with the first line of text.

Dropdown:

This is a subtle gray dropdown with no explicit title (will default to “Details”). The icon should align with the “Details” text in the summary. Content is here.