

Module 1: Introduction

Module 1

(<https://canvas.asu.edu/courses/122165/files/50023766/download?wrap=1>)

Overview

Throughout the course, our learning objectives will focus on three specific areas: biology, coding, and professional development. In this module's Biology learning objectives, we will learn about the biology behind the placenta, the technologies used to evaluate gene expression, the preprocessing steps used on our dataset, and the research aims for this course. In this module's Coding learning objectives, we will help you with getting connected to the high-performance biocomputing cluster at ASU (Agave) and use it to access RStudio, navigate directories, and copy files. In this module's Professional Development learning objectives we will learn how to search for solutions to your coding challenges and get introduced to how to read a scientific paper.

We have provided reading and resources on the next few pages to help you to have the necessary background for attaining the skills presented in this course and help you to contextualize the research question we are tackling.

If you have questions about any of the content, please post in the course slack under the channel #module1; for assistance troubleshooting, please post in the #troubleshooting channel for class feedback. As a reminder, this is a judgment-free zone; the questions you have may very well be the same as another student so please feel free to post as needed. Any good workplace or research environment should have ways you can communicate with others to get support.

Please look at the assignments PRIOR to starting your work, so that you can accomplish the assignment your practice.

Learning Objectives

By the end of this module, you'll be able to:

1.1 Biology/Stats (3 hours)

1. Explain the research aims for this course
2. Describe the function of placenta and known sex differences in placental gene expression
3. Review mechanisms of gene expression and next-generation sequencing technologies, specifically RNAseq
4. Explain data preprocessing steps for RNAseq

1.2 Coding (30 min)

1. Navigate files and directories in a Unix shell environment

1.3 Research/Professional Development (30 min)

1. Use Google to search for useful R solutions to solve specific computational problems