

**Courseware**

Course Info

Discussion

Progress

Syllabus

R code

In the video we talk about phenotypes. Here we show some examples of what we mean by phenotypes, how they can be coded in R objects, and how we compute with them. Later in the course we will perform analyses that statistically connect these phenotypes to measured molecular outcomes. Here we explore the use of data frames to store phenotypes (columns) from several individuals (rows).

QUESTION 1.1.1 (1 point possible)

Install and attach the COPDSexualDimorphism.data package using biocLite. Use the commands

```
library(COPDSexualDimorphism.data)
data(lgrc.expr.meta)
```

to add the object expr.meta to your workspace. The variable pkys in the expr.meta data.frame represents pack years smoked. Other variables include gender (self-explanatory) and diagmaj (disease status).

What is the number of female participants in this study?:

☐**Answer:** 110**EXPLANATION**

Use table(expr.meta\$gender)

Hide Answer

*You have used 5 of 5 submissions***QUESTION 1.1.2** (1 point possible)

What is the median of the distribution of pack years smoked in this cohort (women and men)?

☐**Answer:** 40**EXPLANATION**

The answer can be read from:

summary(expr.meta\$pkys)

Hide Answer

You have used 5 of 5 submissions

Help

QUESTION 1.1.3 (1 point possible)

True or False: The distribution of pack-years smoked is well-approximated by a Gaussian (Normal) probability distribution.

Select one:

☐ TRUE

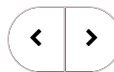
☒ FALSE 

EXPLANATION

Use qqnorm(expr.meta\$pkys). The substantial number of zero values renders a Gaussian model for pack years formally implausible.

Hide Answer

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