F23B GenomicsCURE Assessment

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Assessing student outcomes of the fall 2022-B pilot genomics CURE

The pre- and post-asssement

The fall 2023-B pilot CURE required students to complete a pre- and post-examination to evaluate course outcomes. The pre-assessment acted as a baseline of individual student knowledge, and was divided into three learning submodules or topic areas: - (1) Biology - (2) Coding - (3) Professional development (research)

An additional section for self-reported student comfort and skill levels was included and evaluated independently: - (4) Personal feelings

The Weekly Progress Report

Students submitted weekly progress reports in open-repsonse format, and their organic feedback on challenges and how they addressed them (coping strategies), were also evaluated independently.

Based on these datasets, the following questions were asked to evaluate the impact of an asychrous online CURE on student ability to analyze and impact data: - (1) Q1: Can a remote CURE increase student ability to interpret and analyze data? (quantitative) - (2) Q2: How does a remote CURE affect student comfort levels in computational research? (quantitative) - (3) Q3: What self-reported coping strategies did students use to overcome asynchronous challenges? (qualitative)

Install and load packages

Input the data for the Fall 2022B pilot CURE

```r
overall_scores <- read.csv("C:/Users/splaisie/Dropbox (ASU)/GenomicsCURE/CCLE_Fall2023/analysis_grades/

deltas_overall <- read.csv("C:/Users/splaisie/Dropbox (ASU)/GenomicsCURE/CCLE_Fall2023/analysis_grades/

# Reduce the number of decimal places as a global option
options(digits = 4)

# Input the results of both treatments
combined_scores <- data.frame(deltas_overall)

prescore = data.frame(cbind(overall_scores$ID, overall_scores$Module.0..Pre.Test...4362118.))
colnames(prescore) = c("student", "score")
```

```
postscore = data.frame(cbind(overall_scores$ID, overall_scores$Module.7..Post.Test..4549646.))
colnames(postscore) = c("student", "score")

# remove students with 0 for pre or post test scores
# check_pre_zero =
# prescore_table$student[prescore_table$score == 0]
# check_post_zero =
# postscore_table$student[postscore_table$score == 0]
# students_with_zeros = c(check_pre_zero,check_post_zero)

# prescore = prescore_table %>% filter(!(student %in%
# students_with_zeros)) postscore = postscore_table %>%
# filter(!(student %in% students_with_zeros))

# summarize pre and post scores
summary(prescore)
```

```
##     student            score
##  Min.   :  58360   Min.   :51.5
##  1st Qu.: 550217   1st Qu.:59.8
##  Median : 763857   Median :62.0
##  Mean   : 707915   Mean   :61.6
##  3rd Qu.: 924273   3rd Qu.:64.3
##  Max.   :1029245   Max.   :72.3
```

```
summary(postscore)
```

```
##     student            score
##  Min.   :  58360   Min.   :56.0
##  1st Qu.: 550217   1st Qu.:61.2
##  Median : 763857   Median :66.0
##  Mean   : 707915   Mean   :65.2
##  3rd Qu.: 924273   3rd Qu.:69.0
##  Max.   :1029245   Max.   :72.2
```
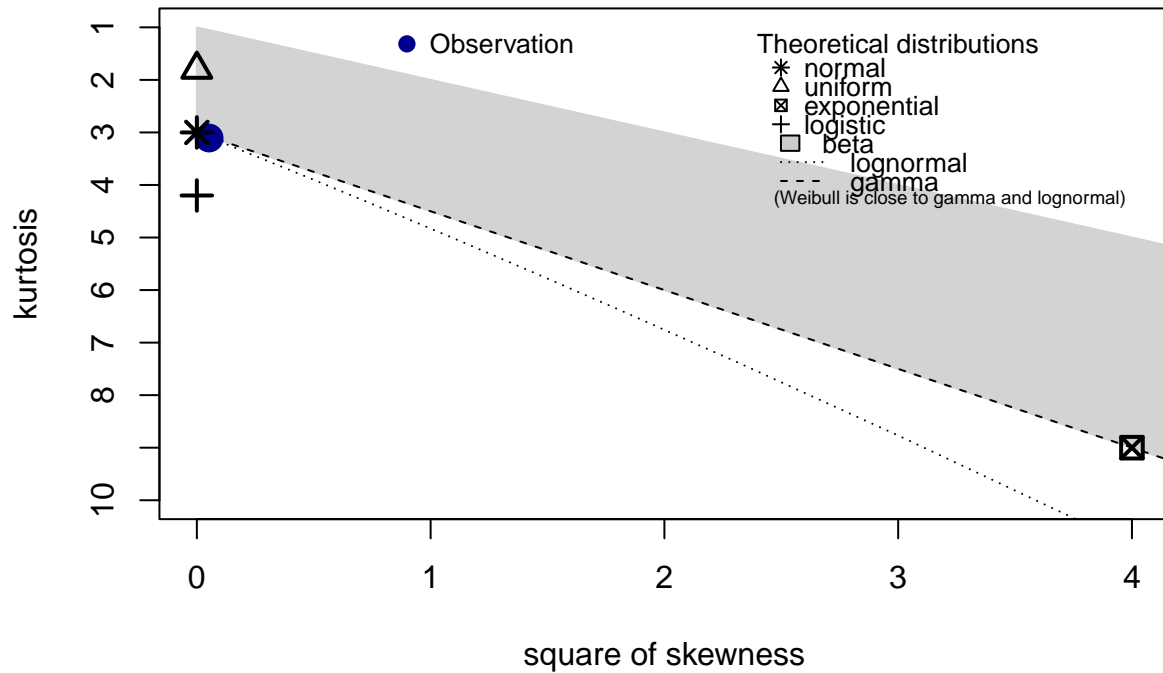
Section 1: Do exam scores differ significantly before and after the asychronous CURE?

```
# Fitting the data to a distribution
descdist(combined_scores$prescore, discrete = F)  #beta distributionn
```
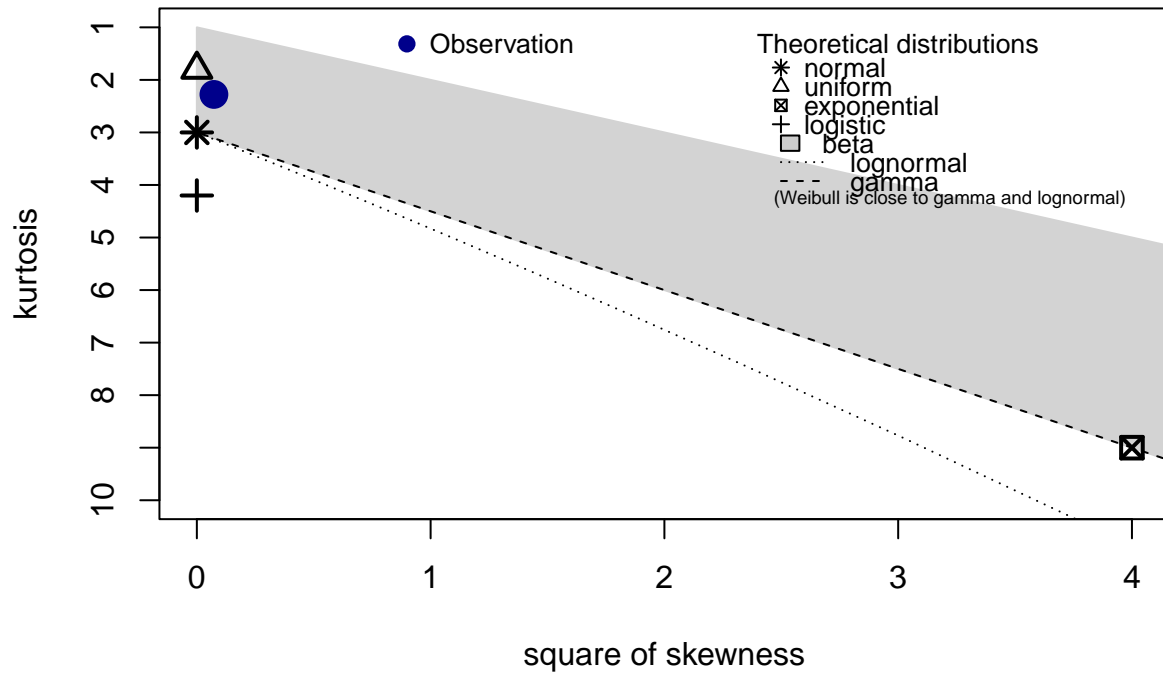
Cullen and Frey graph


```
## summary statistics
## ------
## min:  0.515    max:  0.7233
## median:  0.62
## mean:  0.6162
## estimated sd:  0.04509
## estimated skewness:  -0.2289
## estimated kurtosis:  3.106
```

```
descdist(combined_scores$postscore, discrete = F)   #beta distribution
```
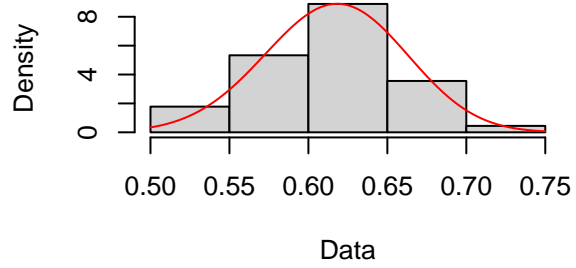
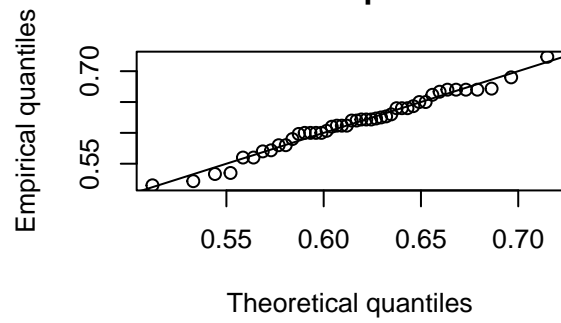# Cullen and Frey graph


```
## summary statistics
## ------
## min:  0.56    max:  0.7217
## median:  0.66
## mean:  0.6516
## estimated sd:  0.04125
## estimated skewness:  -0.2702
## estimated kurtosis:  2.277
```

```r
fit.beta_pre <- fitdist(combined_scores$prescore, "beta", method = "mme")
fit.beta_post <- fitdist(combined_scores$postscore, "beta", method = "mme")
plot(fit.beta_pre)
```
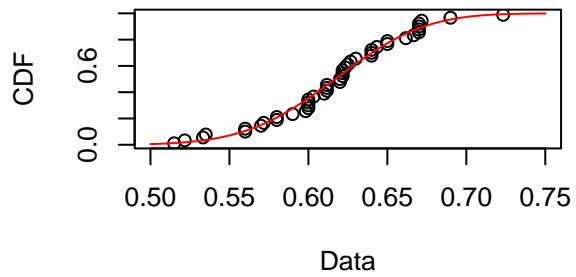
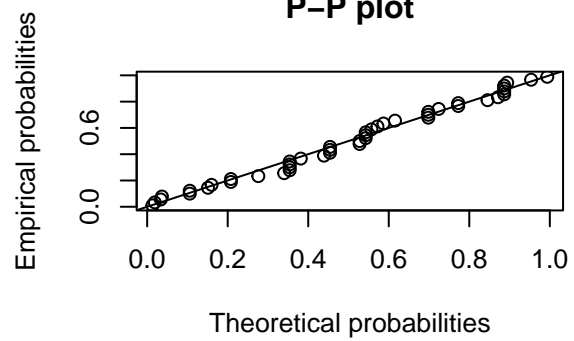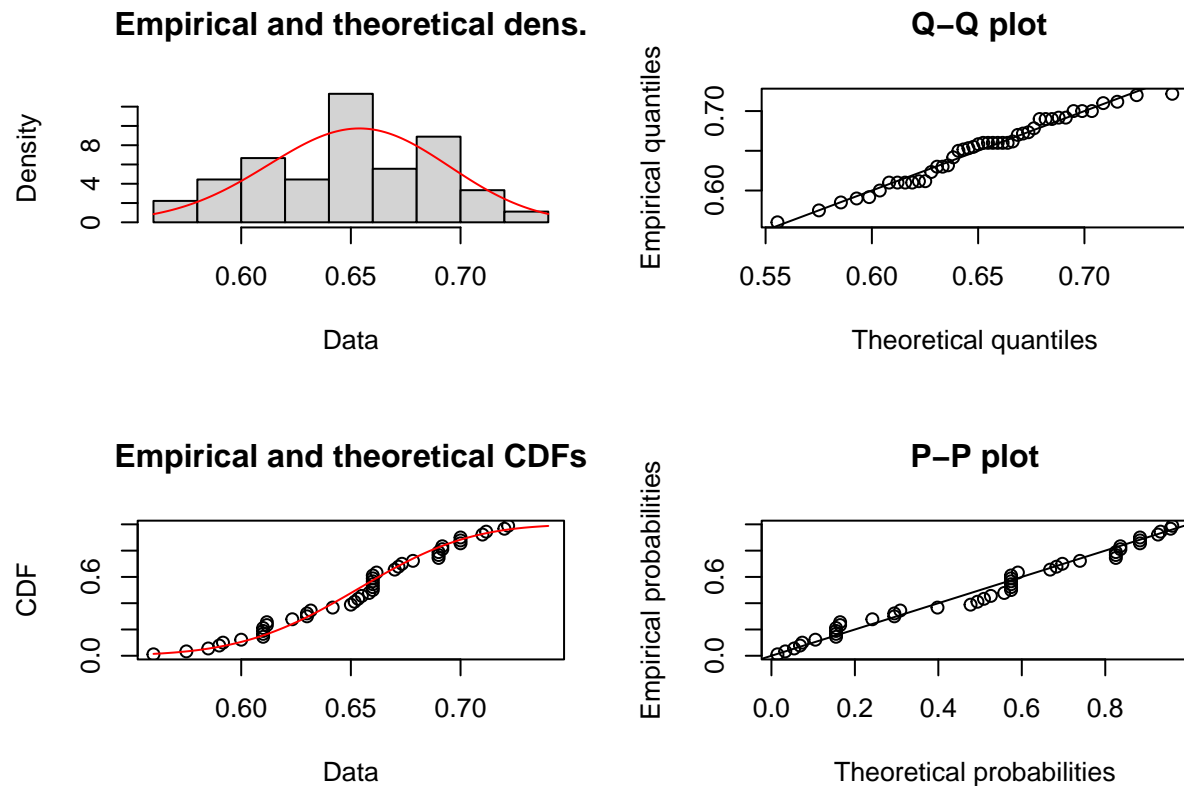**Empirical and theoretical dens.**

Q–Q plot

Empirical and theoretical CDFs

P–P plot

```
plot(fit.beta_post)
```

Empirical and theoretical dens.

Density

Q–Q plot

Empirical quantiles

Data

Theoretical quantiles

Empirical and theoretical CDFs

CDF

P–P plot

Empirical probabilities

Data

Theoretical probabilities

Exploratory data analysis Using the parametric paired t-test, we assume that the data are normally distributed for our dataset.

```
# Create a dataframe of the pre- and post-scores
# histo_combined <- overall_scores


## ================================================

# density plots with histograms per treatment to show
# distribution
dp_pre <- ggplot(prescore, aes(x = score)) + geom_histogram(data = prescore,
    fill = "white", col = "darkgreen", alpha = 0.5, binwidth = 0.1,
    bins = 30, position = "identity") + labs(title = "Distribution of pre-test scores",
    y = "Number of students") + geom_density(data = prescore,
    fill = "darkolivegreen", alpha = 0.6) + scale_x_continuous(breaks = seq(0,
    1, 0.1))
dp_pre + ylim(0, 5)
```

Distribution of pre−test scores
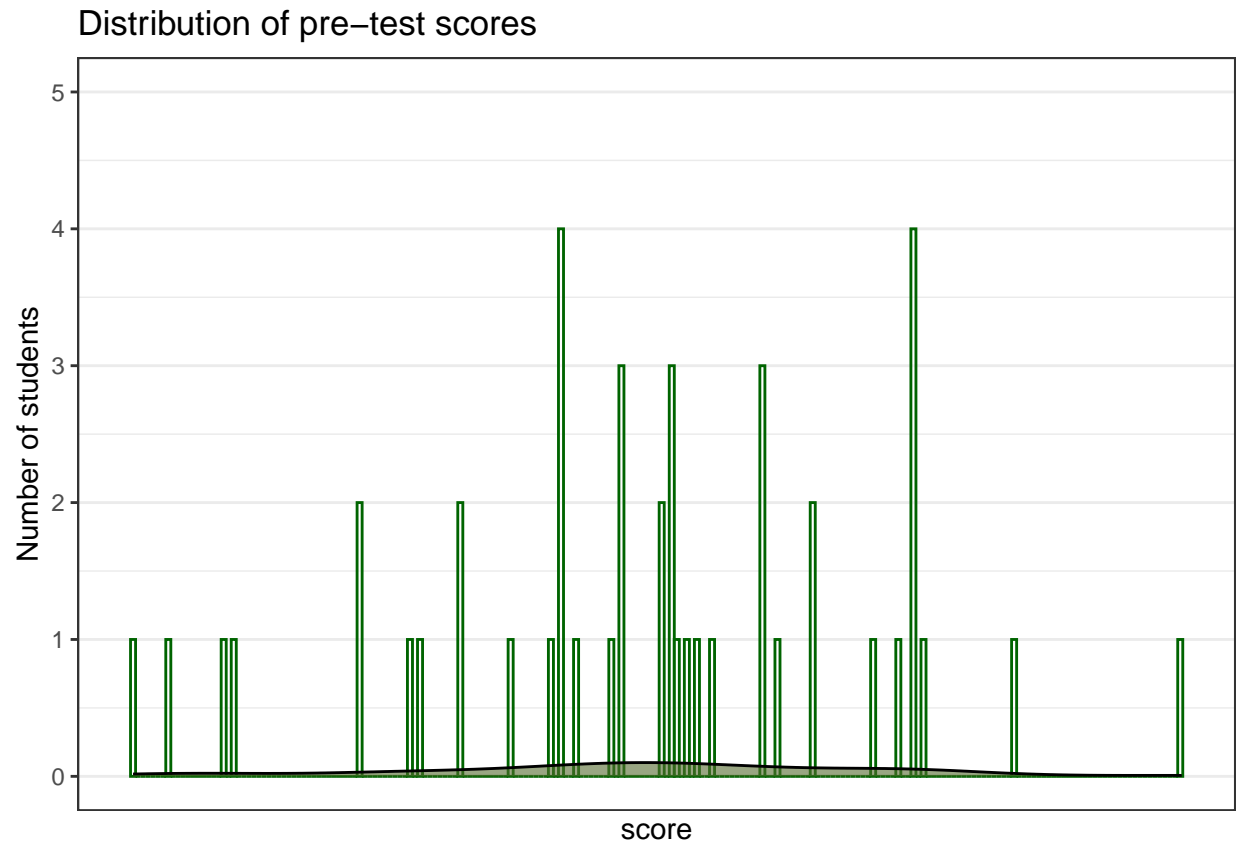

```
dp_post <- ggplot(postscore, aes(x = score)) + geom_histogram(data = postscore,
    fill = "white", alpha = 0.5, col = "darkorange2", binwidth = 0.1,
    bins = 30, position = "dodge") + labs(title = "Distribution of post-test scores",
    y = "Number of students") + geom_density(data = postscore,
    fill = "darkorange1", alpha = 0.6) + scale_x_continuous(breaks = seq(0,
    1, 0.1))
dp_post + ylim(0, 5)
```

```
## Warning: Removed 1 rows containing missing values (`geom_bar()`).
```

Distribution of post–test scores
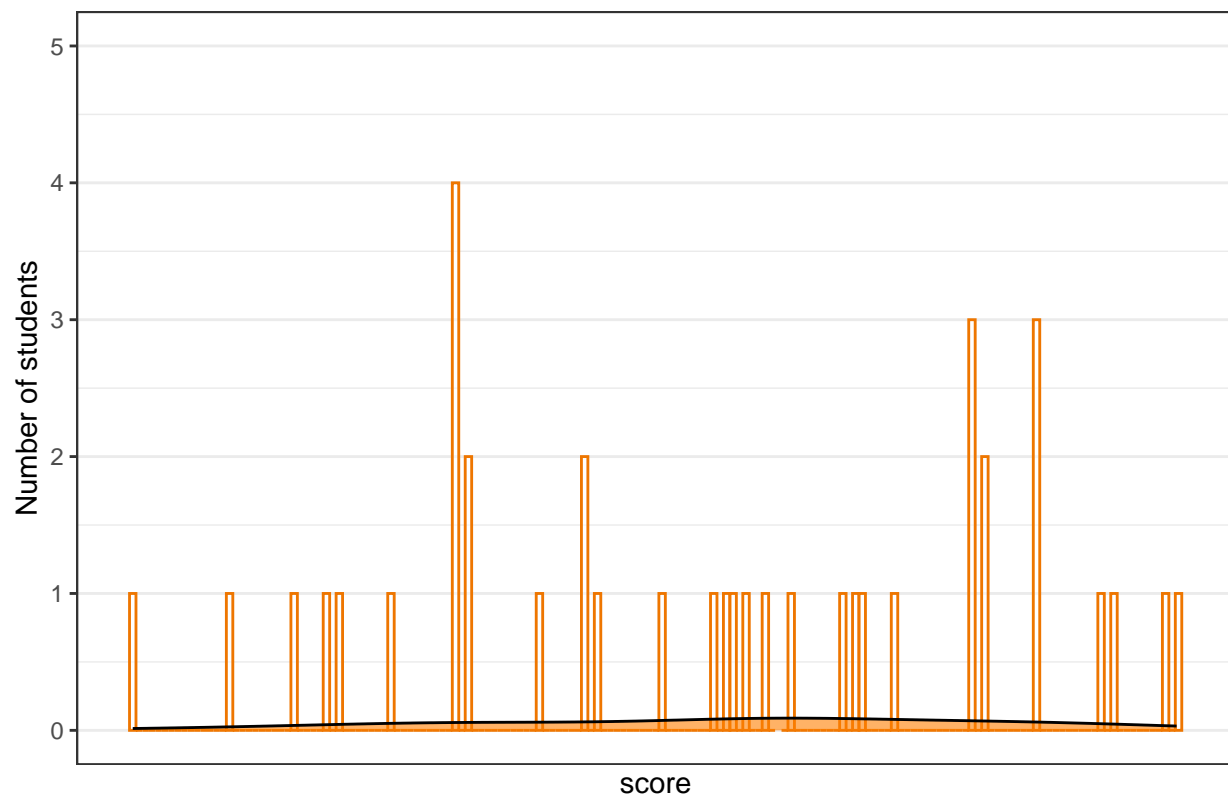

```
# The null hypothesis for the Wilk-Shapiro test of
# normality is that the data are normally distributed.
shapiro.test(prescore$score)
```

Test for normal distribution using ShapiroWilk

```
##
##   Shapiro-Wilk normality test
##
## data:  prescore$score
## W = 0.98, p-value = 0.6
```

```
## There is not enough evidence to reject the null
## hypothesis. Therefore, each group follows a normal
## distribution.

shapiro.test(postscore$score)
```

```
##
##   Shapiro-Wilk normality test
##
## data:  postscore$score
## W = 0.97, p-value = 0.2
```

```
## There is not enough evidence to reject the null
## hypothesis. Therefore, each group follows a normal
## distribution.
```

Visualize paired outcomes data using box plots

Use the boxplot to visualize differences in exam scores.

```r
# Create a dataframe that is separated by group, score, and
# student
my_data <- data.frame(group = rep(c("prescore", "postscore"),
    each = nrow(prescore)), score = c(prescore$score, postscore$score),
    student = c(prescore$student, postscore$student))

# Compute summary statistics by groups using dplyr:
summary_overall <- group_by(my_data, group) %>%
    dplyr::summarize(count = n(), mean = mean(score, na.rm = TRUE),
        sd = sd(score, na.rm = TRUE))
summary_overall
```

```
## # A tibble: 2 x 4
##   group     count  mean    sd
##   <chr>     <int> <dbl> <dbl>
## 1 postscore    45  65.2  4.13
## 2 prescore     45  61.6  4.51
```

Paired boxplots of average assessment scores pre vs post test

```r
pbp <- ggpaired(my_data, x = "group", y = "score", color = "group",
    line.color = "gray", line.size = 0.4, palette = "Dark2",
    xlab = "Assessment", ylab = "Overall score (%)") + theme(legend.position = "none")
pbp
```
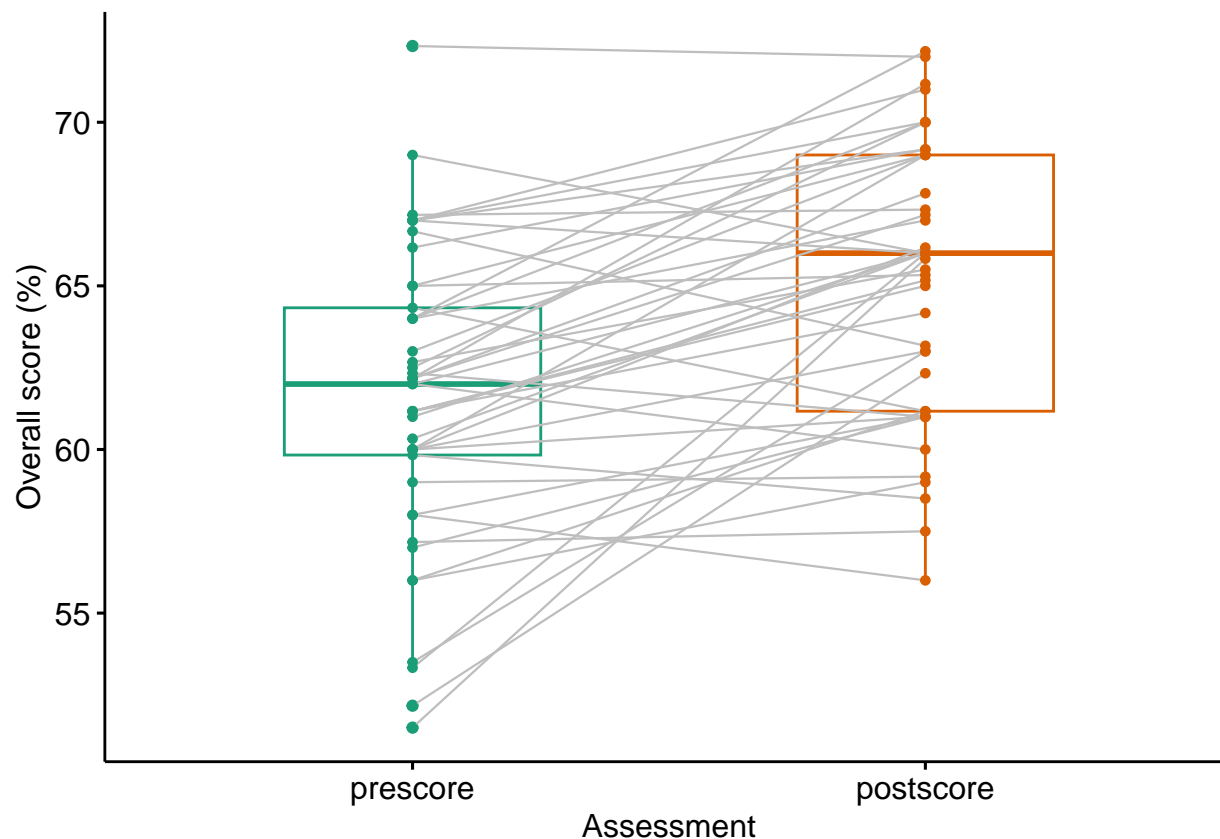
```
ggsave(filename = "overall_score.pdf", plot = pbp)
```

```
## Saving 6.5 x 4.5 in image
```

The change in scores is visually evident by the histograms and the boxplots, but is it significant?

Check for signficance

Paired t-test   Use the paired t-test on the dependent samples to test for significant differences in means between exam scores before and after the CURE

```
# Perform a paired samples t-test x,y: numeric vectors
# paired: a logical value specifying that we want to
# compute a paired t-test alternative: the alternative
# hypothesis. Allowed value is one of "two.sided"
# (default), "greater" or "less".

overall_ttest_all <- t.test(postscore$score, prescore$score,
    paired = TRUE, alternative = "two.sided")
overall_ttest_all
```

```
##
##  Paired t-test
##
```

```
## data:  postscore$score and prescore$score
## t = 5.8, df = 44, p-value = 8e-07
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  2.298 4.776
## sample estimates:
## mean difference
##           3.537
```

Check effect size using Cohen's d   Since the t-test calculated a p-value of 0.003, which is $< p = 0.05$, the overall score differences by individuals are significant. Next, effect size will express the magnitude of the significance to the population at large. - Small effect: 0.2 - Medium effect: 0.5 - Large effect: 0.8

```r
# Use the package effsize to determine the strength of the
# differences in scores
score_pre <- prescore$score
score_post <- postscore$score
effsize::cohen.d(score_post, score_pre)
```

```
##
## Cohen's d
##
## d estimate: 0.8185 (large)
## 95 percent confidence interval:
##  lower  upper
## 0.3823 1.2546
```

Scatter plot of overall scores and correlation

```r
# Scatter plot of overall scores
p1 <- ggplot(combined_scores, aes(x = prescore, y = postscore,
    color = student)) + geom_jitter() + geom_smooth(method = lm,
    color = "black", se = T) + theme(plot.title = element_text(size = 10)) +
    labs(title = "Assessment prescores versus postscores all students",
        x = "Pre-score", y = "Post-score")

p1
```

```
## `geom_smooth()` using formula = 'y ~ x'
```

Assessment prescores versus postscores all students
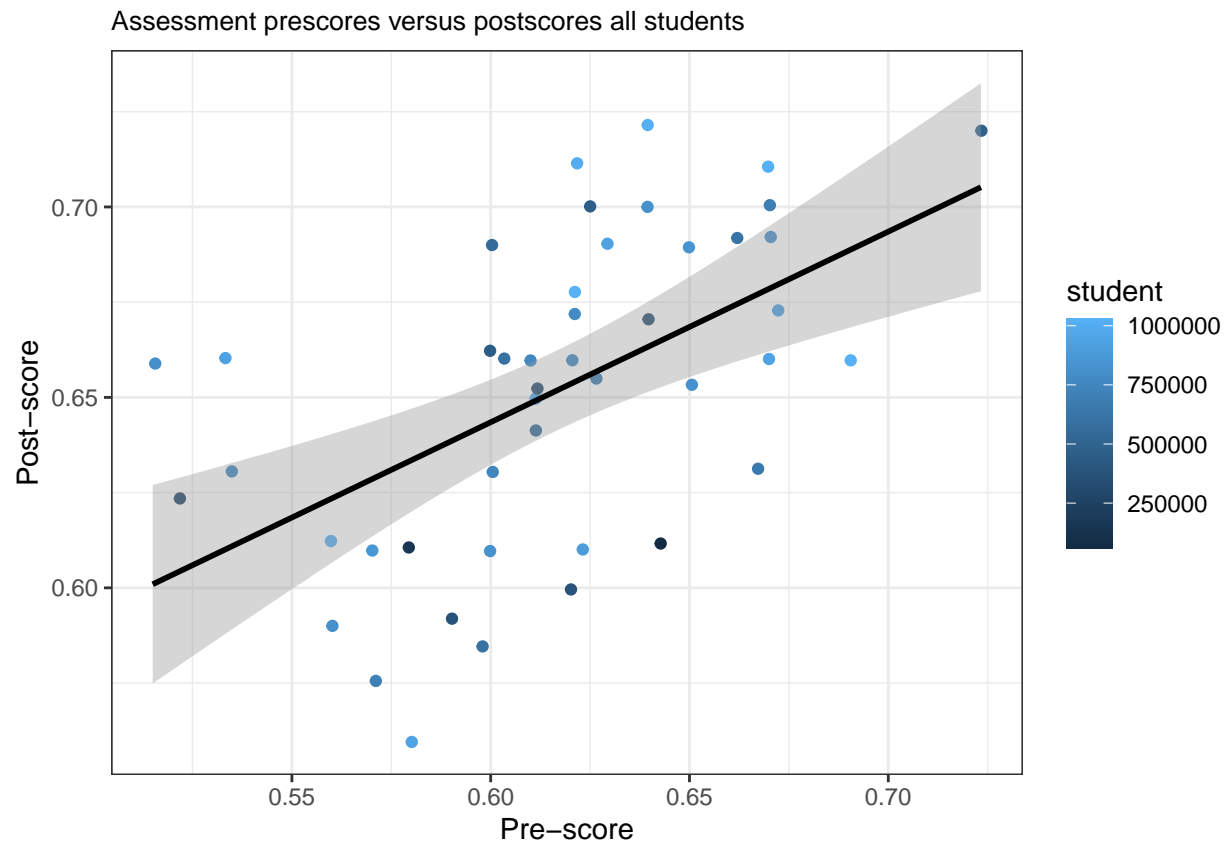
```
summary(combined_scores)
```

```
##     student          prescore        postscore          delta
##  Min.   :  58360   Min.   :0.515   Min.   :0.560   Min.   :-0.0350
##  1st Qu.: 550217   1st Qu.:0.598   1st Qu.:0.612   1st Qu.: 0.0033
##  Median : 763857   Median :0.620   Median :0.660   Median : 0.0300
##  Mean   : 707915   Mean   :0.616   Mean   :0.652   Mean   : 0.0354
##  3rd Qu.: 924273   3rd Qu.:0.643   3rd Qu.:0.690   3rd Qu.: 0.0567
##  Max.   :1029245   Max.   :0.723   Max.   :0.722   Max.   : 0.1433
```

```
# Check Pearson Correlation and test for significance
cor(combined_scores$prescore, combined_scores$postscore)
```

```
## [1] 0.5471
```

```
cor.test(combined_scores$prescore, combined_scores$postscore)
```

```
##
##  Pearson's product-moment correlation
##
## data:  combined_scores$prescore and combined_scores$postscore
## t = 4.3, df = 43, p-value = 1e-04
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
```

```
##  0.3021 0.7243
## sample estimates:
##    cor
## 0.5471
```

Do scores differ by question and topic?

Biology, coding, professional development

```r
# create the dataframes Import data for prescores by
# question
questions_pre <- read_csv("C:/Users/splaisie/Dropbox (ASU)/GenomicsCURE/CCLE_Fall2023/analysis_grades/p
```

```
## Rows: 2700 Columns: 6
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr (4): Topic, Subtopic, Question, Type
## dbl (2): Student, Score
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```r
# Import data for prescores by question
questions_post <- read_csv("C:/Users/splaisie/Dropbox (ASU)/GenomicsCURE/CCLE_Fall2023/analysis_grades/p
```

```
## Rows: 2700 Columns: 6
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr (4): Topic, Subtopic, Question, Type
## dbl (2): Student, Score
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```r
questions_all = rbind(questions_pre, questions_post)

# paired box plot by topic -- sum of scores by topic per
# student, pre vs pos questions_all_sum =
# aggregate(questions_all$Score, by =
# list(questions_all$Topic, questions_all$Type), FUN = sum)
questions_all_sum = aggregate(questions_all$Score, by = list(questions_all$Topic,
    questions_all$Type, questions_all$Student), FUN = sum)
colnames(questions_all_sum) = c("Topic", "Type", "Student", "SumScore")
write.csv(questions_all_sum, file = "SumCorrect_questions.csv")

questions_all_sum$Type <- factor(questions_all_sum$Type, levels = c("prescore",
    "postscore"))
pattern = c("darkcyan", "red3")

# ----- by topic ---------
sum_by_topic = ggplot(questions_all_sum, aes(x = Type, y = SumScore)) +
    geom_boxplot(aes(fill = Topic), alpha = 0.2, color = c("darkcyan",
```

```
        "red3", "darkcyan", "red3", "darkcyan", "red3"), fill = "white") +
    scale_x_discrete(labels = c(prescore = "pre", postscore = "post"),
        name = element_blank()) + geom_line(aes(group = Student),
    color = "gray", size = 0.4, position = "identity") + geom_point(size = 1) +
    facet_wrap(~Topic) + theme(panel.grid.major = element_blank(),
    panel.grid.minor = element_blank())
```

```
## Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
## i Please use `linewidth` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```

```
ggsave(filename = "C:/Users/splaisie/Dropbox (ASU)/GenomicsCURE/CCLE_Fall2023/analysis_grades/sum_score
    plot = sum_by_topic)
```

```
## Saving 6.5 x 4.5 in image
```

```
# cohen's score and ttest p-value by topic
score_post = questions_all_sum$SumScore[questions_all_sum$Type ==
    "postscore" & questions_all_sum$Topic == "Biology"]
score_pre = questions_all_sum$SumScore[questions_all_sum$Type ==
    "prescore" & questions_all_sum$Topic == "Biology"]
effsize::cohen.d(score_post, score_pre)
```

```
##
## Cohen's d
##
## d estimate: 0.9346 (large)
## 95 percent confidence interval:
##  lower  upper
## 0.4934 1.3758
```

```
t.test(score_post, score_pre, paired = TRUE, alternative = "two.sided")
```

```
##
##  Paired t-test
##
## data:  score_post and score_pre
## t = 5.8, df = 44, p-value = 6e-07
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  0.9015 1.8541
## sample estimates:
## mean difference
##           1.378
```

```
score_post = questions_all_sum$SumScore[questions_all_sum$Type ==
    "postscore" & questions_all_sum$Topic == "Coding"]
score_pre = questions_all_sum$SumScore[questions_all_sum$Type ==
    "prescore" & questions_all_sum$Topic == "Coding"]
effsize::cohen.d(score_post, score_pre)
```

```
##
## Cohen's d
##
## d estimate: 0.3726 (small)
## 95 percent confidence interval:
##   lower   upper
## -0.0500  0.7952
```

```
t.test(score_post, score_pre, paired = TRUE, alternative = "two.sided")
```

```
##
##  Paired t-test
##
## data:  score_post and score_pre
## t = 2.3, df = 44, p-value = 0.03
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  0.1289 1.9155
## sample estimates:
## mean difference
##           1.022
```

```
score_post = questions_all_sum$SumScore[questions_all_sum$Type ==
    "postscore" & questions_all_sum$Topic == "ProfDev"]
score_pre = questions_all_sum$SumScore[questions_all_sum$Type ==
    "prescore" & questions_all_sum$Topic == "ProfDev"]
effsize::cohen.d(score_post, score_pre)
```

```
##
## Cohen's d
##
## d estimate: 0.7328 (medium)
## 95 percent confidence interval:
## lower upper
## 0.300 1.166
```

```
t.test(score_post, score_pre, paired = TRUE, alternative = "two.sided")
```

```
##
##  Paired t-test
##
## data:  score_post and score_pre
## t = 4.7, df = 44, p-value = 2e-05
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  0.6892 1.7108
## sample estimates:
## mean difference
##             1.2
```

```r
# ----- by subtopic ---------
questions_all_sum = aggregate(questions_all$Score, by = list(questions_all$Subtopic,
    questions_all$Type, questions_all$Student), FUN = sum)
colnames(questions_all_sum) = c("Subtopic", "Type", "Student",
    "SumScore")

questions_all_sum$Type <- factor(questions_all_sum$Type, levels = c("prescore",
    "postscore"))

subtopic_order = unique(questions_all$Subtopic, fromLast = FALSE)
questions_all_sum$Subtopic <- factor(questions_all_sum$Subtopic,
    levels = subtopic_order)

pattern = c("darkcyan", "red3")

sum_by_subtopic = ggplot(questions_all_sum, aes(x = Type, y = SumScore)) +
    geom_violin(aes(fill = Subtopic), alpha = 0.2, fill = "white") +
    scale_x_discrete(labels = c(prescore = "pre", postscore = "post"),
        name = element_blank()) + geom_line(aes(group = Student),
    color = "gray", size = 0.4, position = "identity") + geom_point(size = 1) +
    facet_wrap(~Subtopic, ncol = 5) + theme(panel.grid.major = element_blank(),
    panel.grid.minor = element_blank(), strip.text = element_text(size = 7))

ggsave(filename = "C:/Users/splaisie/Dropbox (ASU)/GenomicsCURE/CCLE_Fall2023/analysis_grades/sum_score
    plot = sum_by_subtopic)
```

```
## Saving 6.5 x 4.5 in image
```

```r
for (subt in subtopic_order) {
    print(subt)
    score_post = questions_all_sum$SumScore[questions_all_sum$Type ==
        "postscore" & questions_all_sum$Subtopic == subt]
    score_pre = questions_all_sum$SumScore[questions_all_sum$Type ==
        "prescore" & questions_all_sum$Subtopic == subt]
    print(effsize::cohen.d(score_post, score_pre))
    print(t.test(score_post, score_pre, paired = TRUE, alternative = "two.sided"))
}
```

```
## [1] "Cancer_biology_cell_lines"
##
## Cohen's d
##
## d estimate: 0.1516 (negligible)
## 95 percent confidence interval:
##   lower   upper
## -0.2680  0.5711
##
##
##  Paired t-test
##
## data:  score_post and score_pre
## t = 0.77, df = 44, p-value = 0.4
## alternative hypothesis: true mean difference is not equal to 0
```

```
## 95 percent confidence interval:
##  -0.1076  0.2409
## sample estimates:
## mean difference
##        0.06667
##
## [1] "Sex_chromosomes"
##
## Cohen's d
##
## d estimate: 1.234 (large)
## 95 percent confidence interval:
## lower upper
## 0.777 1.691
##
##
##  Paired t-test
##
## data:  score_post and score_pre
## t = 5.9, df = 44, p-value = 6e-07
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  0.3934 0.8066
## sample estimates:
## mean difference
##             0.6
##
## [1] "RNA_RNAseq"
##
## Cohen's d
##
## d estimate: 0.1568 (negligible)
## 95 percent confidence interval:
##   lower   upper
## -0.2628  0.5764
##
##
##  Paired t-test
##
## data:  score_post and score_pre
## t = 0.73, df = 44, p-value = 0.5
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.1976  0.4198
## sample estimates:
## mean difference
##         0.1111
##
## [1] "Gene_expression"
##
## Cohen's d
##
## d estimate: 0.2284 (small)
## 95 percent confidence interval:
```

```
##    lower    upper
## -0.1920   0.6487
##
##
##  Paired t-test
##
## data:  score_post and score_pre
## t = 1.4, df = 44, p-value = 0.2
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.05451  0.32117
## sample estimates:
## mean difference
##         0.1333
##
## [1] "XCI"
##
## Cohen's d
##
## d estimate: 0.5705 (medium)
## 95 percent confidence interval:
##   lower  upper
## 0.1431 0.9979
##
##
##  Paired t-test
##
## data:  score_post and score_pre
## t = 2.7, df = 44, p-value = 0.01
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##   0.1182 0.8152
## sample estimates:
## mean difference
##         0.4667
##
## [1] "R_Rmd"
##
## Cohen's d
##
## d estimate: 0.5087 (medium)
## 95 percent confidence interval:
##    lower    upper
## 0.08307 0.93443
##
##
##  Paired t-test
##
## data:  score_post and score_pre
## t = 2.4, df = 44, p-value = 0.02
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##   0.03545 0.36455
## sample estimates:
```

```
## mean difference
##             0.2
##
## [1] "R_data_frames"
##
## Cohen's d
##
## d estimate: 0.3282 (small)
## 95 percent confidence interval:
##    lower    upper
## -0.09356  0.74998
##
##
##  Paired t-test
##
## data:  score_post and score_pre
## t = 2, df = 44, p-value = 0.06
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.008954  0.586732
## sample estimates:
## mean difference
##          0.2889
##
## [1] "R_functions_loops"
##
## Cohen's d
##
## d estimate: 0.08156 (negligible)
## 95 percent confidence interval:
##   lower   upper
## -0.3376  0.5007
##
##
##  Paired t-test
##
## data:  score_post and score_pre
## t = 0.36, df = 44, p-value = 0.7
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.3035  0.4368
## sample estimates:
## mean difference
##         0.06667
##
## [1] "R_if_statements"
##
## Cohen's d
##
## d estimate: 0.128 (negligible)
## 95 percent confidence interval:
##   lower   upper
## -0.2914  0.5473
##
```

```
##
##  Paired t-test
##
## data:  score_post and score_pre
## t = 0.72, df = 44, p-value = 0.5
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.2380  0.5046
## sample estimates:
## mean difference
##          0.1333
##
## [1] "Linux_command_line"
##
## Cohen's d
##
## d estimate: 0.2781 (small)
## 95 percent confidence interval:
##    lower    upper
## -0.1428  0.6991
##
##
##  Paired t-test
##
## data:  score_post and score_pre
## t = 1.7, df = 44, p-value = 0.1
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.06151  0.72818
## sample estimates:
## mean difference
##          0.3333
##
## [1] "Authorship"
##
## Cohen's d
##
## d estimate: 0.7407 (medium)
## 95 percent confidence interval:
##   lower   upper
## 0.3076 1.1737
##
##
##  Paired t-test
##
## data:  score_post and score_pre
## t = 4.3, df = 44, p-value = 9e-05
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  0.2949 0.8162
## sample estimates:
## mean difference
##          0.5556
##
```

```
## [1] "Reading_papers"
##
## Cohen's d
##
## d estimate: 0.8808 (large)
## 95 percent confidence interval:
## lower upper
## 0.442 1.320
##
##
##  Paired t-test
##
## data:  score_post and score_pre
## t = 4.5, df = 44, p-value = 5e-05
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  0.2705 0.7073
## sample estimates:
## mean difference
##         0.4889
##
## [1] "Writing_paper"
##
## Cohen's d
##
## d estimate: -0.2037 (small)
## 95 percent confidence interval:
##   lower   upper
## -0.6238  0.2163
##
##
##  Paired t-test
##
## data:  score_post and score_pre
## t = -1.3, df = 44, p-value = 0.2
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.28325  0.06103
## sample estimates:
## mean difference
##        -0.1111
##
## [1] "Coding_solutions"
##
## Cohen's d
##
## d estimate: 0.1803 (negligible)
## 95 percent confidence interval:
##   lower   upper
## -0.2395  0.6002
##
##
##  Paired t-test
##
```

```
## data:  score_post and score_pre
## t = 0.94, df = 44, p-value = 0.4
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.1014  0.2791
## sample estimates:
## mean difference
##        0.08889
##
## [1] "Interpreting_plots"
##
## Cohen's d
##
## d estimate: 0.2523 (small)
## 95 percent confidence interval:
##   lower   upper
## -0.1683  0.6729
##
##
##  Paired t-test
##
## data:  score_post and score_pre
## t = 1.6, df = 44, p-value = 0.1
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.04676  0.40232
## sample estimates:
## mean difference
##        0.1778
```

```r
comfort_pre <- read_csv("C:/Users/splaisie/Dropbox (ASU)/GenomicsCURE/CCLE_Fall2023/analysis_grades/pre
```

```
## Rows: 225 Columns: 4
## -- Column specification ---------------------------------------------------------
## Delimiter: ","
## chr (2): Type, Question
## dbl (2): Student, Score
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```r
comfort_post <- read_csv("C:/Users/splaisie/Dropbox (ASU)/GenomicsCURE/CCLE_Fall2023/analysis_grades/pos
```

```
## Rows: 225 Columns: 4
## -- Column specification ---------------------------------------------------------
## Delimiter: ","
## chr (2): Type, Question
## dbl (2): Student, Score
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
comfort_all = rbind(comfort_pre, comfort_post)

comfort_all$Type <- factor(comfort_all$Type, levels = c("prescore",
    "postscore"))
pattern = c("darkcyan", "red3")
colors = rep(pattern, times = 5)

# by question
comfort_plot_by_question = ggplot(comfort_all, aes(x = Type,
    y = Score)) + geom_boxplot(aes(fill = Question), alpha = 0.2,
    color = colors, fill = "white") + scale_x_discrete(labels = c(prescore = "pre",
    postscore = "post"), name = element_blank()) + geom_line(aes(group = Student),
    color = "gray", size = 0.4, position = "identity") + geom_point(size = 1) +
    facet_wrap(~Question, ncol = 5) + ylim(-3.5, 3.5) + theme(panel.grid.major = element_blank(),
    panel.grid.minor = element_blank())

ggsave(filename = "C:/Users/splaisie/Dropbox (ASU)/GenomicsCURE/CCLE_Fall2023/analysis_grades/Likert_co
    plot = comfort_plot_by_question, width = 8, height = 4)

# overall
comfort_plot = ggplot(comfort_all, aes(x = Type, y = Score)) +
    geom_boxplot(aes(fill = Question), alpha = 0.2, color = pattern,
        fill = "white") + scale_x_discrete(labels = c(prescore = "pre",
    postscore = "post"), name = element_blank()) + geom_line(aes(group = Student),
    color = "gray", size = 0.4, position = "identity") + geom_point(size = 1) +
    ylim(-3.5, 3.5) + theme(panel.grid.major = element_blank(),
    panel.grid.minor = element_blank())

ggsave(filename = "C:/Users/splaisie/Dropbox (ASU)/GenomicsCURE/CCLE_Fall2023/analysis_grades/Likert_co
    plot = comfort_plot)
```

```
## Saving 6.5 x 4.5 in image
```

```
# cohen's score and ttest p-value by topic
comfort_post = comfort_all$Score[comfort_all$Type == "postscore"]
comfort_pre = comfort_all$Score[comfort_all$Type == "prescore"]
t.test(comfort_post, comfort_pre, paired = TRUE, alternative = "two.sided")
```

```
##
##  Paired t-test
##
## data:  comfort_post and comfort_pre
## t = 1.7, df = 224, p-value = 0.09
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.04126  0.55379
## sample estimates:
## mean difference
##          0.2563
```

```
summary(comfort_pre)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## -3.000  -1.000   1.000   0.776   2.000   3.000
```

```
summary(comfort_post)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## -3.00    0.66    1.50    1.03    2.00    3.00
```

```
comfort_post = comfort_all$Score[comfort_all$Type == "postscore" &
    comfort_all$Question == "CodingQuestion"]
comfort_pre = comfort_all$Score[comfort_all$Type == "prescore" &
    comfort_all$Question == "CodingQuestion"]
t.test(comfort_post, comfort_pre, paired = TRUE, alternative = "two.sided")
```

```
##
##  Paired t-test
##
## data:  comfort_post and comfort_pre
## t = -0.43, df = 44, p-value = 0.7
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.9466  0.6132
## sample estimates:
## mean difference
##         -0.1667
```

```
comfort_post = comfort_all$Score[comfort_all$Type == "postscore" &
    comfort_all$Question == "CommandLine_Linux"]
comfort_pre = comfort_all$Score[comfort_all$Type == "prescore" &
    comfort_all$Question == "CommandLine_Linux"]
t.test(comfort_post, comfort_pre, paired = TRUE, alternative = "two.sided")
```

```
##
##  Paired t-test
##
## data:  comfort_post and comfort_pre
## t = -0.55, df = 44, p-value = 0.6
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.7768  0.4435
## sample estimates:
## mean difference
##         -0.1667
```

```
comfort_post = comfort_all$Score[comfort_all$Type == "postscore" &
    comfort_all$Question == "ProgrammingR"]
comfort_pre = comfort_all$Score[comfort_all$Type == "prescore" &
    comfort_all$Question == "ProgrammingR"]
t.test(comfort_post, comfort_pre, paired = TRUE, alternative = "two.sided")
```

```
##
```

```
##  Paired t-test
##
## data:  comfort_post and comfort_pre
## t = 2.1, df = 44, p-value = 0.05
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##   0.01776 1.72268
## sample estimates:
## mean difference
##          0.8702
```

```
table(sign(comfort_pre))
```

```
##
## -1  0  1
## 26  1 18
```

```
table(sign(comfort_post))
```

```
##
## -1  0  1
## 16  1 28
```

```
comfort_post = comfort_all$Score[comfort_all$Type == "postscore" &
    comfort_all$Question == "ReadingPaper"]
comfort_pre = comfort_all$Score[comfort_all$Type == "prescore" &
    comfort_all$Question == "ReadingPaper"]
t.test(comfort_post, comfort_pre, paired = TRUE, alternative = "two.sided")
```

```
##
##  Paired t-test
##
## data:  comfort_post and comfort_pre
## t = 1.3, df = 44, p-value = 0.2
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##   -0.2132  0.9981
## sample estimates:
## mean difference
##          0.3924
```

```
comfort_post = comfort_all$Score[comfort_all$Type == "postscore" &
    comfort_all$Question == "WritingPaper"]
comfort_pre = comfort_all$Score[comfort_all$Type == "prescore" &
    comfort_all$Question == "WritingPaper"]
t.test(comfort_post, comfort_pre, paired = TRUE, alternative = "two.sided")
```

```
##
##  Paired t-test
##
## data:  comfort_post and comfort_pre
```

```
## t = 1.1, df = 44, p-value = 0.3
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.3081  1.0121
## sample estimates:
## mean difference
##           0.352
```

```
comfort_deltas <- read_csv("C:/Users/splaisie/Dropbox (ASU)/GenomicsCURE/CCLE_Fall2023/analysis_grades/
```

```
## Rows: 225 Columns: 6
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr (2): Question, Trend
## dbl (4): Student, prescore, postscore, delta
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
info = data.frame(table(comfort_deltas$Trend))
lbls = info$Var1
slices = info$Freq
pct = round(slices/sum(info$Freq) * 100)
lbls <- paste(lbls, pct)
lbls <- paste(lbls, "%", sep = "")  # ad % to labels
pie(info$Freq, labels = lbls)
title("All Likert Questions with All Students")
```

All Likert Questions with All Students
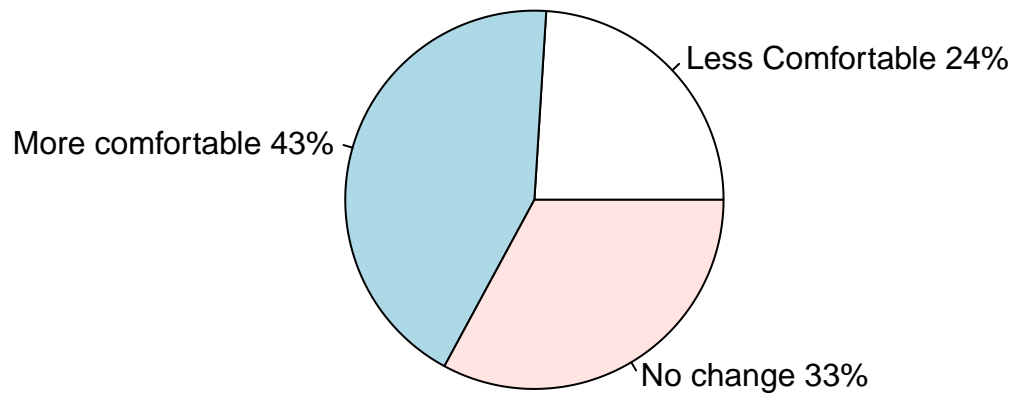


```r
pdf("piechart_comfort_delta_ProgrammingR.pdf", height = 3.5,
    width = 3)
filter_df = comfort_deltas %>%
    filter(Question == "ProgrammingR")
info = data.frame(table(filter_df$Trend))
lbls = info$Var1
slices = info$Freq
pct = round(slices/sum(info$Freq) * 100)
lbls <- paste(lbls, pct)
lbls <- paste(lbls, "%", sep = "")   # ad % to labels
pie(info$Freq, labels = lbls)
title("ProgrammingR with All Students")
dev.off()
```
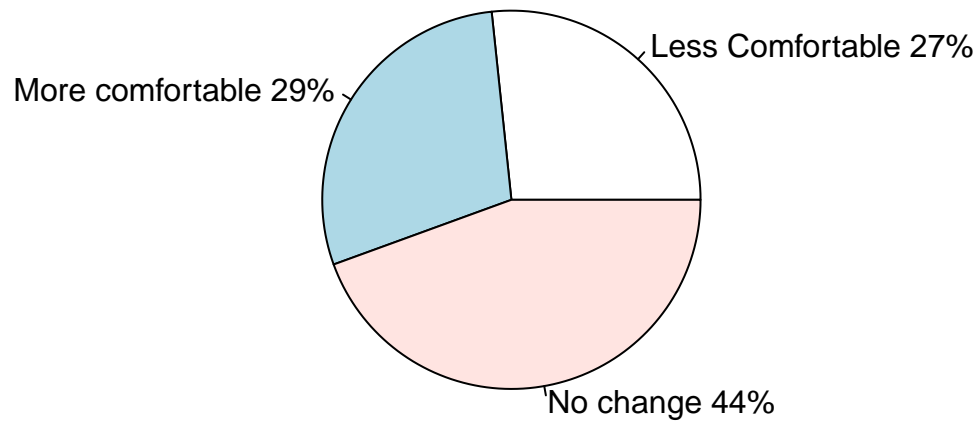
```
## pdf
##   2
```

```r
pie(info$Freq, labels = lbls)
title("ProgrammingR with All Students")
```
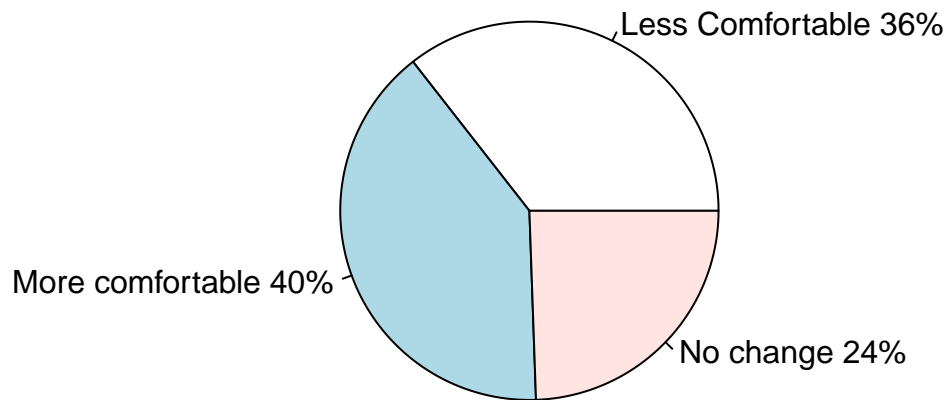
ProgrammingR with All Students
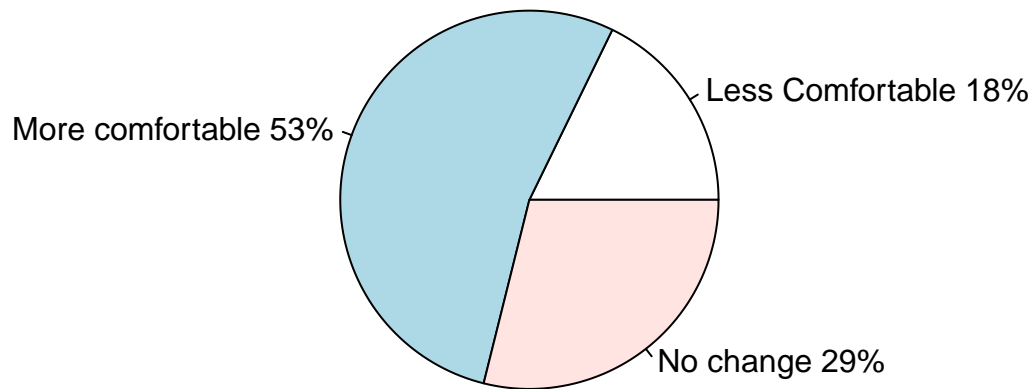

```
filter_df = comfort_deltas %>%
    filter(Question == "CodingQuestion")
info = data.frame(table(filter_df$Trend))
lbls = info$Var1
slices = info$Freq
pct = round(slices/sum(info$Freq) * 100)
lbls <- paste(lbls, pct)
lbls <- paste(lbls, "%", sep = "")  # ad % to labels
pie(info$Freq, labels = lbls)
title("CodingQuestion  with All Students")
```

CodingQuestion with All Students

More comfortable 29%

Less Comfortable 27%

No change 44%

```r
filter_df = comfort_deltas %>%
    filter(Question == "CommandLine_Linux")
info = data.frame(table(filter_df$Trend))
lbls = info$Var1
slices = info$Freq
pct = round(slices/sum(info$Freq) * 100)
lbls <- paste(lbls, pct)
lbls <- paste(lbls, "%", sep = "")   # ad % to labels
pie(info$Freq, labels = lbls)
title("CommandLine_Linux  with All Students")
```

CommandLine_Linux with All Students


```r
pdf("piechart_comfort_delta_ReadingPaper.pdf", height = 3.5,
    width = 3)
filter_df = comfort_deltas %>%
    filter(Question == "ReadingPaper")
info = data.frame(table(filter_df$Trend))
lbls = info$Var1
slices = info$Freq
pct = round(slices/sum(info$Freq) * 100)
lbls <- paste(lbls, pct)
lbls <- paste(lbls, "%", sep = "")  # ad % to labels
pie(info$Freq, labels = lbls)
title("ReadingPaper  with All Students")
dev.off()
```

```
## pdf
##   2
```

```r
pie(info$Freq, labels = lbls)
title("ReadingPaper  with All Students")
```
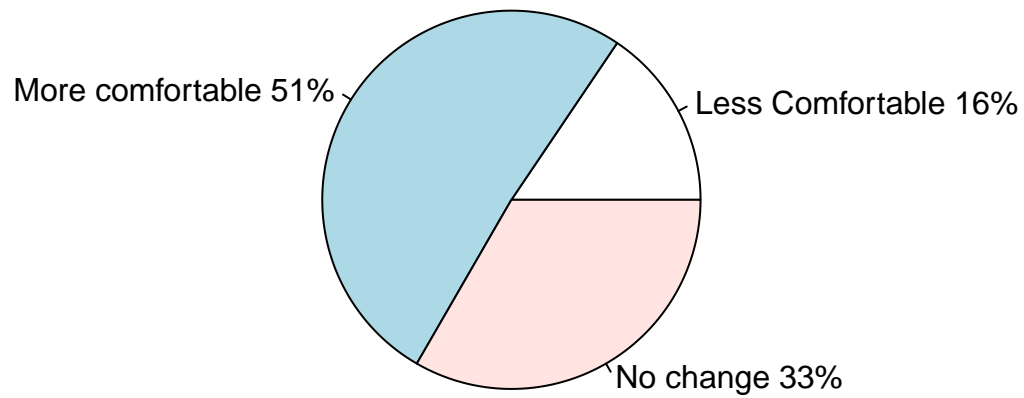
ReadingPaper with All Students


```
pdf("piechart_comfort_delta_WritingPaper.pdf", height = 3.5,
    width = 3)
filter_df = comfort_deltas %>%
    filter(Question == "WritingPaper")
info = data.frame(table(filter_df$Trend))
lbls = info$Var1
slices = info$Freq
pct = round(slices/sum(info$Freq) * 100)
lbls <- paste(lbls, pct)
lbls <- paste(lbls, "%", sep = "")  # ad % to labels
pie(info$Freq, labels = lbls)
title("WritingPaper  with All Students")
dev.off()
```

```
## pdf
##   2
```

```
pie(info$Freq, labels = lbls)
title("WritingPaper  with All Students")
```
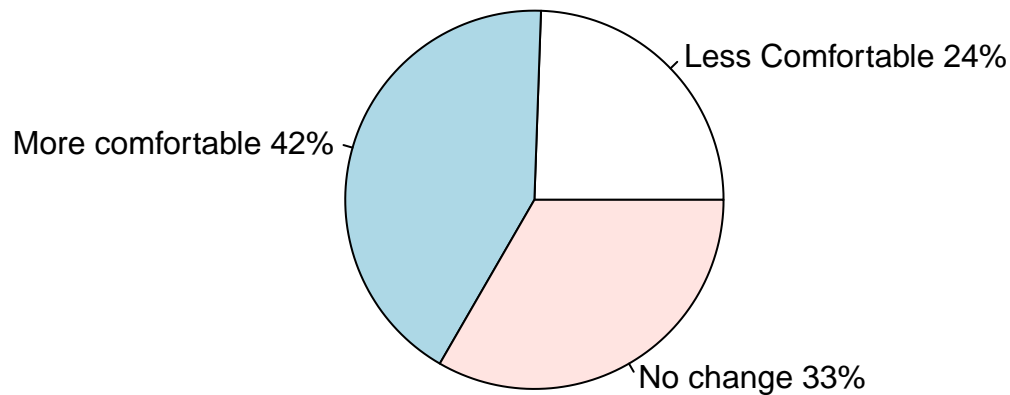
WritingPaper with All Students

Less Comfortable 24%

More comfortable 42%

No change 33%

```
qualsurvey_pre = read_csv("C:/Users/splaisie/Dropbox (ASU)/GenomicsCURE/Demographics/QualSurvey_pre.csv
```

```
## Rows: 68 Columns: 62
## -- Column specification ---------------------------------------------------------
## Delimiter: ","
## chr (51): Start Date, End Date, Response Type, IP Address, Recorded Date, Re...
## dbl  (5): Progress, Duration (in seconds), Iteration, Location Latitude, Loc...
## lgl  (6): Finished, Recipient Last Name, Recipient First Name, Recipient Ema...
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
qualsurvey_post = read_csv("C:/Users/splaisie/Dropbox (ASU)/GenomicsCURE/Demographics/QualSurvey_post.c
```

```
## Rows: 61 Columns: 96
## -- Column specification ---------------------------------------------------------
## Delimiter: ","
## chr (84): Start Date, End Date, Response Type, IP Address, Recorded Date, Re...
## dbl  (6): Progress, Duration (in seconds), Iteration, Location Latitude, Loc...
## lgl  (6): Finished, Recipient Last Name, Recipient First Name, Recipient Ema...
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
# do iteration 1 pre
pie_chart_directory = "C:/Users/splaisie/Dropbox (ASU)/GenomicsCURE/Demographics/pie_charts/iteration1/"

qualsurvey_pre_iteration1 = qualsurvey_pre[qualsurvey_pre$Iteration ==
    1, ]
colnames(qualsurvey_pre_iteration1)
```

```
##  [1] "Start Date"
##  [2] "End Date"
##  [3] "Response Type"
##  [4] "IP Address"
##  [5] "Progress"
##  [6] "Duration (in seconds)"
##  [7] "Finished"
##  [8] "Recorded Date"
##  [9] "Iteration"
## [10] "Response ID"
## [11] "Recipient Last Name"
## [12] "Recipient First Name"
## [13] "Recipient Email"
## [14] "External Data Reference"
## [15] "Location Latitude"
## [16] "Location Longitude"
## [17] "Distribution Channel"
## [18] "User Language"
## [19] "Q177_I am 18 years or older and I agree to participate in this study."
## [20] "Q176_1_Q176 - First name"
## [21] "Q176_2_Q176 - Last name"
## [22] "Q176_3_Q176 - Date"
## [23] "Q115_1_Please respond to each of the following statements. - Research makes me anxious."
## [24] "Q115_2_Please respond to each of the following statements. - I feel insecure concerning the ana
## [25] "Q115_3_Please respond to each of the following statements. - Research scares me."
## [26] "Q115_4_Please respond to each of the following statements. - Research is stressful."
## [27] "Q115_5_Please respond to each of the following statements. - Research makes me nervous."
## [28] "Q115_6_Please respond to each of the following statements. - Research is complicated."
## [29] "Q115_7_Please respond to each of the following statements. - Research is difficult."
## [30] "Q115_8_Please respond to each of the following statements. - Research is a complex subject."
## [31] "Q135_Please indicate how confident you are in your ability to use technical science skills (use
## [32] "Q137_Please indicate how confident you are in your ability to generate a research question to a
## [33] "Q139_Please indicate how confident you are in your ability to figure out what data/observations
## [34] "Q141_Please indicate how confident you are in your ability to create explanations for the resul
## [35] "Q143_Please indicate how confident you are in your ability to use scientific literature and/or
## [36] "Q145_Please indicate how confident you are in your ability to develop theories (integrate and
## [37] "Q161_A person who thinks it is valuable to conduct research that builds on the world's scientif
## [38] "Q163_A person who feels discovering something new in the sciences is thrilling"
## [39] "Q165_A person who thinks discussing new theories and ideas between scientists is important"
## [40] "Q167_A person who thinks that scientific research can solve many of today's world challenges"
## [41] "Q149_\"I have a strong sense of belonging to the community of scientists\""
## [42] "Q151_\"I derive great personal satisfaction from working on a team that is doing important rese
## [43] "Q153_\"I have come to think of myself as a scientist\""
## [44] "Q155_\"I feel like I belong in the field of science\""
## [45] "Q157_\"The daily work of a scientist is appealing to me\""
## [46] "Q48_To what extent do you intend to pursue a career in science, but not medicine?"
```

```
## [47] "Q52_To what extent do you intend to pursue a science-related research career?"
## [48] "Q123_I most closely identify as - Selected Choice"
## [49] "Q123_3_TEXT_I most closely identify as - a gender not listed, please describe - Text"
## [50] "Q125_I most closely identify as - Selected Choice"
## [51] "Q125_8_TEXT_I most closely identify as - Other, please describe - Text"
## [52] "Q127_What is your parents' or your guardians' highest completed level of education? If you hav
## [53] "Q129_1_Please write in your parent or guardian's occupation - Parent or guardian 1"
## [54] "Q129_2_Please write in your parent or guardian's occupation - Parent or guardian 2"
## [55] "Q126_What is your current GPA?"
## [56] "Q131_What is your major?"
## [57] "Q133_What year are you in college?"
## [58] "Q135_Have you participated in an undergraduate research experience? (e.g. doing research in a
## [59] "Q131_Please describe the main project that you worked on during your undergraduate research ex
## [60] "Q137_Do you plan to do research after you graduate?"
## [61] "Q157_7_Please fill in your first and last name to ensure you get credit for completing the sur
## [62] "Q157_8_Please fill in your first and last name to ensure you get credit for completing the sur
```

```r
for (i in 19:60) {
    info = data.frame(table(qualsurvey_pre_iteration1[i]))
    if (nrow(info) > 0) {
        pdf(paste0(pie_chart_directory, "pre", i, ".pdf"))
        lbls = info[, 1]
        slices = info$Freq
        if (length(slices) <= 10) {
            pct = round(slices/sum(info$Freq) * 100)
            lbls <- paste(lbls, pct)
            lbls <- paste(lbls, "%", sep = "")  # ad % to labels
            pie(info$Freq, labels = lbls)
            title(colnames(qualsurvey_pre_iteration1)[i], cex.main = 0.5)
        }
        dev.off()
    }
}


# do iteration 2 pre
pie_chart_directory = "C:/Users/splaisie/Dropbox (ASU)/GenomicsCURE/Demographics/pie_charts/iteration2/

qualsurvey_pre_iteration2 = qualsurvey_pre[qualsurvey_pre$Iteration ==
    2, ]
colnames(qualsurvey_pre_iteration2)
```

```
##  [1] "Start Date"
##  [2] "End Date"
##  [3] "Response Type"
##  [4] "IP Address"
##  [5] "Progress"
##  [6] "Duration (in seconds)"
##  [7] "Finished"
##  [8] "Recorded Date"
##  [9] "Iteration"
## [10] "Response ID"
## [11] "Recipient Last Name"
## [12] "Recipient First Name"
## [13] "Recipient Email"
```

```
## [14] "External Data Reference"
## [15] "Location Latitude"
## [16] "Location Longitude"
## [17] "Distribution Channel"
## [18] "User Language"
## [19] "Q177_I am 18 years or older and I agree to participate in this study."
## [20] "Q176_1_Q176 - First name"
## [21] "Q176_2_Q176 - Last name"
## [22] "Q176_3_Q176 - Date"
## [23] "Q115_1_Please respond to each of the following statements. - Research makes me anxious."
## [24] "Q115_2_Please respond to each of the following statements. - I feel insecure concerning the ana
## [25] "Q115_3_Please respond to each of the following statements. - Research scares me."
## [26] "Q115_4_Please respond to each of the following statements. - Research is stressful."
## [27] "Q115_5_Please respond to each of the following statements. - Research makes me nervous."
## [28] "Q115_6_Please respond to each of the following statements. - Research is complicated."
## [29] "Q115_7_Please respond to each of the following statements. - Research is difficult."
## [30] "Q115_8_Please respond to each of the following statements. - Research is a complex subject."
## [31] "Q135_Please indicate how confident you are in your ability to use technical science skills (us
## [32] "Q137_Please indicate how confident you are in your ability to generate a research question to a
## [33] "Q139_Please indicate how confident you are in your ability to figure out what data/observations
## [34] "Q141_Please indicate how confident you are in your ability to create explanations for the resul
## [35] "Q143_Please indicate how confident you are in your ability to use scientific literature and/or
## [36] "Q145_Please indicate how confident you are in your ability to develop theories (integrate and c
## [37] "Q161_A person who thinks it is valuable to conduct research that builds on the world's scientif
## [38] "Q163_A person who feels discovering something new in the sciences is thrilling"
## [39] "Q165_A person who thinks discussing new theories and ideas between scientists is important"
## [40] "Q167_A person who thinks that scientific research can solve many of today's world challenges"
## [41] "Q149_\"I have a strong sense of belonging to the community of scientists\""
## [42] "Q151_\"I derive great personal satisfaction from working on a team that is doing important rese
## [43] "Q153_\"I have come to think of myself as a scientist\""
## [44] "Q155_\"I feel like I belong in the field of science\""
## [45] "Q157_\"The daily work of a scientist is appealing to me\""
## [46] "Q48_To what extent do you intend to pursue a career in science, but not medicine?"
## [47] "Q52_To what extent do you intend to pursue a science-related research career?"
## [48] "Q123_I most closely identify as - Selected Choice"
## [49] "Q123_3_TEXT_I most closely identify as - a gender not listed, please describe - Text"
## [50] "Q125_I most closely identify as - Selected Choice"
## [51] "Q125_8_TEXT_I most closely identify as - Other, please describe - Text"
## [52] "Q127_What is your parents' or your guardians' highest completed level of education? If you have
## [53] "Q129_1_Please write in your parent or guardian's occupation - Parent or guardian 1"
## [54] "Q129_2_Please write in your parent or guardian's occupation - Parent or guardian 2"
## [55] "Q126_What is your current GPA?"
## [56] "Q131_What is your major?"
## [57] "Q133_What year are you in college?"
## [58] "Q135_Have you participated in an undergraduate research experience? (e.g. doing research in a
## [59] "Q131_Please describe the main project that you worked on during your undergraduate research exp
## [60] "Q137_Do you plan to do research after you graduate?"
## [61] "Q157_7_Please fill in your first and last name to ensure you get credit for completing the surv
## [62] "Q157_8_Please fill in your first and last name to ensure you get credit for completing the surv

for (i in 19:60) {
    info = data.frame(table(qualsurvey_pre_iteration2[i]))
    if (nrow(info) > 0) {
        pdf(paste0(pie_chart_directory, "pre", i, ".pdf"))
```

```
        lbls = info[, 1]
        slices = info$Freq
        if (length(slices) <= 10) {
            pct = round(slices/sum(info$Freq) * 100)
            lbls <- paste(lbls, pct)
            lbls <- paste(lbls, "%", sep = "")  # ad % to labels
            pie(info$Freq, labels = lbls)
            title(colnames(qualsurvey_pre_iteration2)[i], cex.main = 0.5)
        }
        dev.off()
    }
}


# do iteration 1 post
pie_chart_directory = "C:/Users/splaisie/Dropbox (ASU)/GenomicsCURE/Demographics/pie_charts/iteration1/

qualsurvey_post_iteration1 = qualsurvey_post[qualsurvey_post$Iteration ==
    1, ]
colnames(qualsurvey_post_iteration1)
```

```
##  [1] "Start Date"
##  [2] "End Date"
##  [3] "Response Type"
##  [4] "IP Address"
##  [5] "Progress"
##  [6] "Duration (in seconds)"
##  [7] "Finished"
##  [8] "Recorded Date"
##  [9] "Iteration"
## [10] "Response ID"
## [11] "Recipient Last Name"
## [12] "Recipient First Name"
## [13] "Recipient Email"
## [14] "External Data Reference"
## [15] "Location Latitude"
## [16] "Location Longitude"
## [17] "Distribution Channel"
## [18] "User Language"
## [19] "Q16_In the Genomics CURE, I was encouraged to discuss elements of my investigation with classma
## [20] "Q18_In the Genomics CURE, I was encouraged to reflect on what I was learning."
## [21] "Q20_In the Genomics CURE, I was encouraged to contribute my ideas and suggestions during class
## [22] "Q22_In the Genomics CURE, I was encouraged to help other students collect or analyze data."
## [23] "Q24_In the Genomics CURE, I was encouraged to provide constructive criticism to classmates and
## [24] "Q26_In the Genomics CURE, I was encouraged to share the problems I encountered during my invest
## [25] "Q28_In the Genomics CURE, I was expected to generate novel results that are unknown to the inst
## [26] "Q30_In the Genomics CURE, I was expected to conduct an investigation to find something previous
## [27] "Q32_In the Genomics CURE, I was expected to formulate my own research question or hypothesis to
## [28] "Q34_In the Genomics CURE, I was expected to develop new arguments based on data."
## [29] "Q36_In the Genomics CURE, I was expected to explain how my work has resulted in new scientific
## [30] "Q38_In the Genomics CURE, I had time to revise or repeat work to account for errors or fix prob
## [31] "Q40_In the Genomics CURE, I had time to change the methods of the investigation if it was not w
## [32] "Q42_In the Genomics CURE, I had time to share and compare data with other students."
## [33] "Q44_In the Genomics CURE, I had time to collect and analyze additional data to address new ques
```

[34] "Q46_In the Genomics CURE, I had time to revise or repeat analyses based on feedback."
[35] "Q48_In the Genomics CURE, I had time to revise drafts of my research poster about my investiga
[36] "Q115_1_Please respond to each of the following statements considering your experience in the Ge
[37] "Q115_2_Please respond to each of the following statements considering your experience in the Ge
[38] "Q115_3_Please respond to each of the following statements considering your experience in the Ge
[39] "Q115_4_Please respond to each of the following statements considering your experience in the Ge
[40] "Q115_5_Please respond to each of the following statements considering your experience in the Ge
[41] "Q115_6_Please respond to each of the following statements considering your experience in the Ge
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[43] "Q115_8_Please respond to each of the following statements considering your experience in the Ge
[44] "Q33_Reflecting on your research experience, please describe any aspects of the Genomics CURE e
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[47] "Q52_My findings in the Genomics CURE were important to the scientific community."
[48] "Q54_I faced challenges that I managed to overcome in completing the work I did in the Genomics
[49] "Q56_I was responsible for the outcomes of the work I did in the Genomics CURE."
[50] "Q58_The findings of the work I did in the Genomics CURE gave me a sense of personal achievement
[51] "Q60_I had a personal reason for choosing what I worked on in the Genomics CURE course."
[52] "Q62_The work I did in the Genomics CURE was important to me."
[53] "Q64_In conducting the work I did in the Genomics CURE, I actively sought advice and assistance
[54] "Q66_The work I did in the Genomics CURE was interesting."
[55] "Q68_The work I did in the Genomics CURE was exciting."
[56] "Q70_To what extent does the word delighted describe your experience of the Genomics CURE?"
[57] "Q72_To what extent does the word happy describe your experience of the Genomics CURE?"
[58] "Q74_To what extent does the word joyful describe your experience of the Genomics CURE?"
[59] "Q76_To what extent does the word astonished describe your experience of the Genomics CURE?"
[60] "Q78_To what extent does the word surprised describe your experience of the Genomics CURE?"
[61] "Q80_To what extent does the word amazed describe your experience of the Genomics CURE?"
[62] "Q135_Please indicate how confident you are in your ability to use technical science skills (use
[63] "Q137_Please indicate how confident you are in your ability to generate a research question to a
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[70] "Q165_A person who thinks discussing new theories and ideas between scientists is important"
[71] "Q167_A person who thinks that scientific research can solve many of today's world challenges"
[72] "Q149_\"I have a strong sense of belonging to the community of scientists\""
[73] "Q151_\"I derive great personal satisfaction from working on a team that is doing important rese
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[75] "Q155_\"I feel like I belong in the field of science\""
[76] "Q157_\"The daily work of a scientist is appealing to me\""
[77] "Q48_To what extent do you intend to pursue a career in science, but not medicine?"
[78] "Q52_To what extent do you intend to pursue a science-related research career?"
[79] "Q123_I most closely identify as - Selected Choice"
[80] "Q123_3_TEXT_I most closely identify as - a gender not listed, please describe - Text"
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[82] "Q125_8_TEXT_I most closely identify as - Other, please describe - Text"
[83] "Q127_What is your parents' or your guardians' highest completed level of education? If you have
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[85] "Q129_2_Please write in your parent or guardian's occupation - Parent or guardian 2"
[86] "Q126_What is your current GPA?"
[87] "Q131_What is your major?"

```
## [88] "Q133_What year are you in college?"
## [89] "Q135_Have you participated in an undergraduate research experience? (e.g. doing research in a
## [90] "Q131_Please describe the main project that you worked on during your undergraduate research exp
## [91] "Q137_Do you plan to do research after you graduate?"
## [92] "Q157_7_Please fill in your first and last name to ensure you get credit for completing the surv
## [93] "Q157_8_Please fill in your first and last name to ensure you get credit for completing the surv
## [94] "Q176 - First name"
## [95] "Q176 - Last name"
## [96] "Q176 - Date"
```

```r
for (i in 19:60) {
    info = data.frame(table(qualsurvey_post_iteration1[i]))
    if (nrow(info) > 0) {
        pdf(paste0(pie_chart_directory, "post", i, ".pdf"))
        lbls = info[, 1]
        slices = info$Freq
        if (length(slices) <= 10) {
            pct = round(slices/sum(info$Freq) * 100)
            lbls <- paste(lbls, pct)
            lbls <- paste(lbls, "%", sep = "")  # ad % to labels
            pie(info$Freq, labels = lbls)
            title(colnames(qualsurvey_post_iteration1)[i], cex.main = 0.5)
        }
        dev.off()
    }
}

# do iteration 2 post
pie_chart_directory = "C:/Users/splaisie/Dropbox (ASU)/GenomicsCURE/Demographics/pie_charts/iteration2/"

qualsurvey_post_iteration2 = qualsurvey_post[qualsurvey_post$Iteration ==
    2, ]
colnames(qualsurvey_post_iteration2)
```

```
##  [1] "Start Date"
##  [2] "End Date"
##  [3] "Response Type"
##  [4] "IP Address"
##  [5] "Progress"
##  [6] "Duration (in seconds)"
##  [7] "Finished"
##  [8] "Recorded Date"
##  [9] "Iteration"
## [10] "Response ID"
## [11] "Recipient Last Name"
## [12] "Recipient First Name"
## [13] "Recipient Email"
## [14] "External Data Reference"
## [15] "Location Latitude"
## [16] "Location Longitude"
## [17] "Distribution Channel"
## [18] "User Language"
## [19] "Q16_In the Genomics CURE, I was encouraged to discuss elements of my investigation with classma
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```

```
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## [22] "Q22_In the Genomics CURE, I was encouraged to help other students collect or analyze data."
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## [28] "Q34_In the Genomics CURE, I was expected to develop new arguments based on data."
## [29] "Q36_In the Genomics CURE, I was expected to explain how my work has resulted in new scientific
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## [39] "Q115_4_Please respond to each of the following statements considering your experience in the Ge
## [40] "Q115_5_Please respond to each of the following statements considering your experience in the Ge
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## [50] "Q58_The findings of the work I did in the Genomics CURE gave me a sense of personal achievement
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## [53] "Q64_In conducting the work I did in the Genomics CURE, I actively sought advice and assistance
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## [56] "Q70_To what extent does the word delighted describe your experience of the Genomics CURE?"
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## [65] "Q141_Please indicate how confident you are in your ability to create explanations for the resul
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## [67] "Q145_Please indicate how confident you are in your ability to develop theories (integrate and e
## [68] "Q161_A person who thinks it is valuable to conduct research that builds on the world's scienti
## [69] "Q163_A person who feels discovering something new in the sciences is thrilling"
## [70] "Q165_A person who thinks discussing new theories and ideas between scientists is important"
## [71] "Q167_A person who thinks that scientific research can solve many of today's world challenges"
## [72] "Q149_\"I have a strong sense of belonging to the community of scientists\""
## [73] "Q151_\"I derive great personal satisfaction from working on a team that is doing important rese
## [74] "Q153_\"I have come to think of myself as a scientist\""
```

```
## [75] "Q155_\"I feel like I belong in the field of science\""
## [76] "Q157_\"The daily work of a scientist is appealing to me\""
## [77] "Q48_To what extent do you intend to pursue a career in science, but not medicine?"
## [78] "Q52_To what extent do you intend to pursue a science-related research career?"
## [79] "Q123_I most closely identify as - Selected Choice"
## [80] "Q123_3_TEXT_I most closely identify as - a gender not listed, please describe - Text"
## [81] "Q125_I most closely identify as - Selected Choice"
## [82] "Q125_8_TEXT_I most closely identify as - Other, please describe - Text"
## [83] "Q127_What is your parents' or your guardians' highest completed level of education? If you have
## [84] "Q129_1_Please write in your parent or guardian's occupation - Parent or guardian 1"
## [85] "Q129_2_Please write in your parent or guardian's occupation - Parent or guardian 2"
## [86] "Q126_What is your current GPA?"
## [87] "Q131_What is your major?"
## [88] "Q133_What year are you in college?"
## [89] "Q135_Have you participated in an undergraduate research experience? (e.g. doing research in a
## [90] "Q131_Please describe the main project that you worked on during your undergraduate research ex
## [91] "Q137_Do you plan to do research after you graduate?"
## [92] "Q157_7_Please fill in your first and last name to ensure you get credit for completing the sur
## [93] "Q157_8_Please fill in your first and last name to ensure you get credit for completing the sur
## [94] "Q176 - First name"
## [95] "Q176 - Last name"
## [96] "Q176 - Date"
```

```r
for (i in 19:60) {
    info = data.frame(table(qualsurvey_post_iteration2[i]))
    if (nrow(info) > 0) {
        pdf(paste0(pie_chart_directory, "post", i, ".pdf"))
        lbls = info[, 1]
        slices = info$Freq
        if (length(slices) <= 10) {
            pct = round(slices/sum(info$Freq) * 100)
            lbls <- paste(lbls, pct)
            lbls <- paste(lbls, "%", sep = "")  # ad % to labels
            pie(info$Freq, labels = lbls)
            title(colnames(qualsurvey_post_iteration2)[i], cex.main = 0.5)
        }
        dev.off()
    }
}
```

```r
class_makeup_data = read.csv("C:/Users/splaisie/Dropbox (ASU)/GenomicsCURE/Demographics/QualSurvey_class
    check.names = FALSE)

class_makeup_df = data.frame(class_makeup_data)

library(grid)
library(gridExtra)

pdf("C:/Users/splaisie/Dropbox (ASU)/GenomicsCURE/Demographics/table_class_makeup.pdf",
    height = 8, width = 12)
tt2 <- ttheme_default(core = list(fg_params = list(hjust = 1)),
    rowhead = list(fg_params = list(hjust = 1)), colhead = list(fg_params = list(hjust = 1,
        fontsize = 12, fontface = "bold")))
class_makeup_table = tableGrob(class_makeup_df, theme = tt2)
```

```
class_makeup_table$gp = gpar(fontsize = 12)
grid.draw(class_makeup_table)

dev.off()
```

```
## pdf
##   2
```

```
questions_mean_pre = aggregate(questions_pre$Score, by = list(questions_pre$Type,
    questions_pre$Question), FUN = mean)
colnames(questions_mean_pre) = c("Type", "Question", "MeanScore")

questions_mean_post = aggregate(questions_post$Score, by = list(questions_post$Type,
    questions_post$Question), FUN = mean)
colnames(questions_mean_post) = c("Type", "Question", "MeanScore")

questions_mean_pre$Question == questions_mean_post$Question
```

```
##  [1] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [16] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [31] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [46] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
```

```
question_mean = data.frame(rbind(questions_mean_pre, questions_mean_post))

question_mean_diff = data.frame(questions_mean_pre$Question,
    questions_mean_post$MeanScore - questions_mean_pre$MeanScore)
colnames(question_mean_diff) = c("Question", "DiffMeanScore")

barplot(question_mean_diff$DiffMeanScore)
```
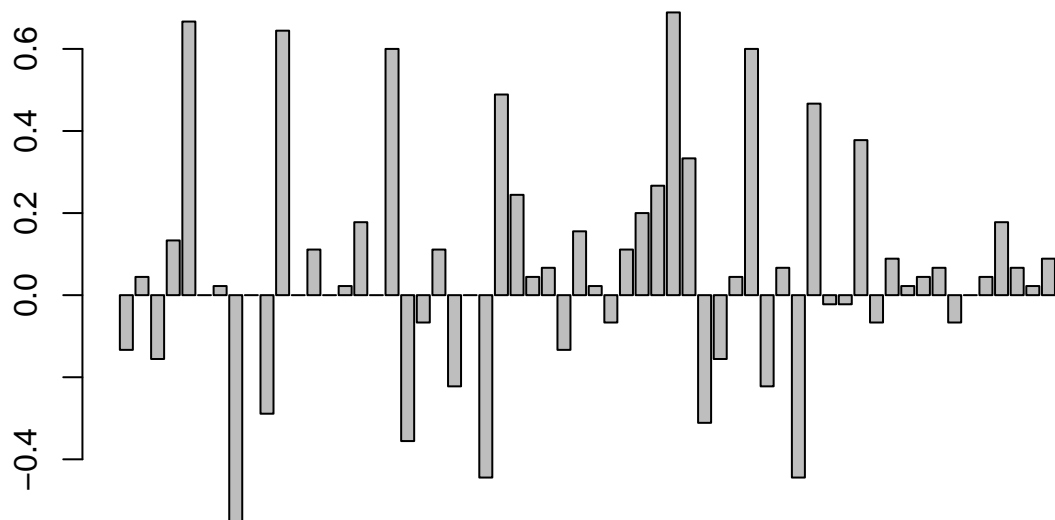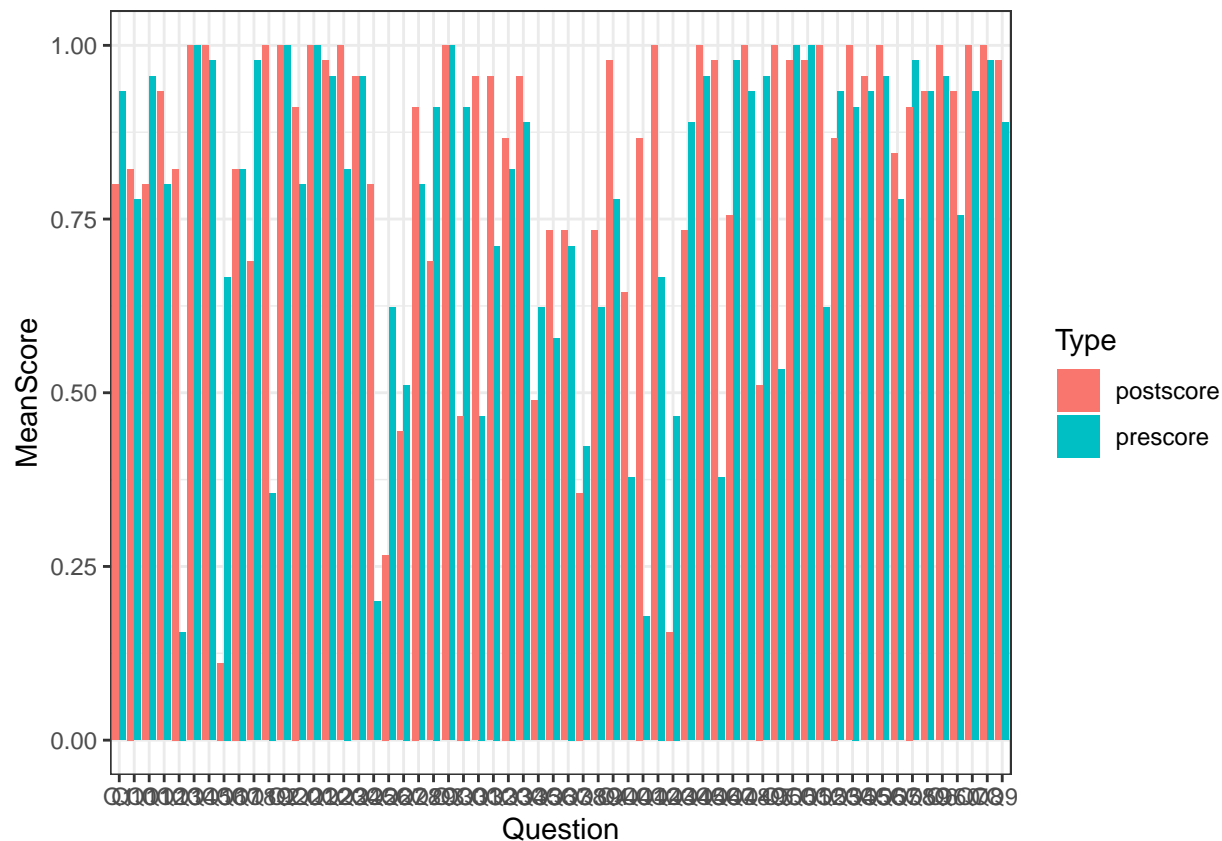
```
ggplot(question_mean, aes(x = Question, y = MeanScore, fill = Type)) +
    geom_bar(stat = "identity", position = position_dodge())
```

```
#+ facet_wrap(~ Topic)

question_mean_2 = data.frame(questions_mean_pre$Question, questions_mean_pre$MeanScore,
    questions_mean_post$MeanScore)
colnames(question_mean_2) = c("Question", "MeanScore_pre", "MeanScore_post")

question_mean_2$NLG = (question_mean_2$MeanScore_post - question_mean_2$MeanScore_pre)/(100 -
    question_mean_2$MeanScore_pre)

# get the correct order of questions
number_range = c(1:60)
number_range = as.character(number_range)
q_range = rep("Q", 60)
q_num_range = paste0(q_range, number_range)

question_mean_2$Question <- factor(question_mean_2$Question,
    levels = q_num_range)

ggplot(question_mean_2, aes(x = Question, y = NLG)) + geom_bar(stat = "identity") +
    theme(axis.text.x = element_text(angle = 90, vjust = 0.5,
        hjust = 1))
```
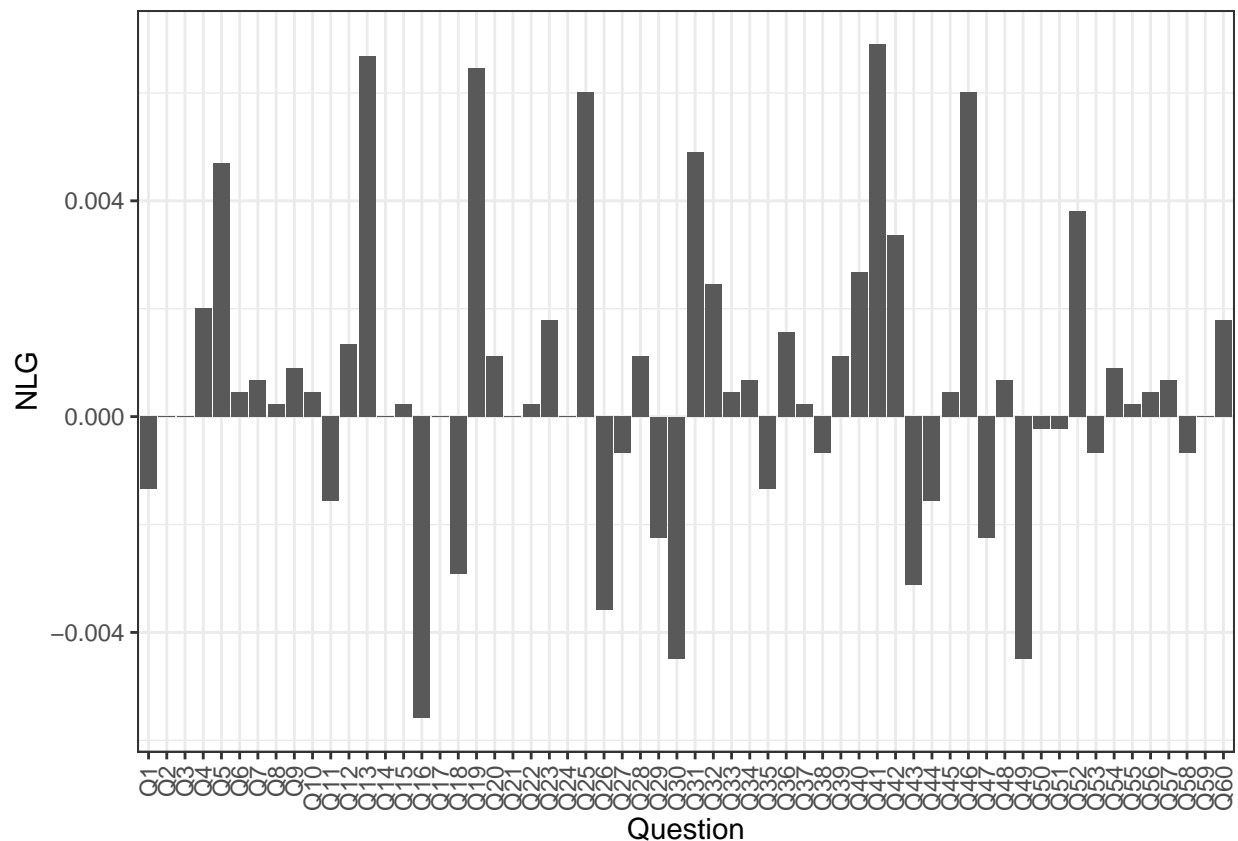
```
nrow(question_mean_diff)
```

```
## [1] 60
```

```
nrow(question_mean_diff[question_mean_diff$DiffMeanScore > 0,
    ])
```

```
## [1] 35
```

```
nrow(question_mean_diff[question_mean_diff$DiffMeanScore <= 0,
    ])
```

```
## [1] 25
```

```
#---------

# how many students got the right answer pre-test
questions_sum_pre = aggregate(questions_pre$Score, by = list(questions_pre$Type,
    questions_pre$Question), FUN = sum)
colnames(questions_sum_pre) = c("Type", "Question", "SumScore")

# how many students got the right answer post-test
questions_sum_post = aggregate(questions_post$Score, by = list(questions_post$Type,
```

```
    questions_post$Question), FUN = sum)
colnames(questions_sum_post) = c("Type", "Question", "SumScore")

question_sum_prepost = data.frame(questions_sum_pre$Question,
    questions_sum_pre$SumScore, questions_sum_post$SumScore)
colnames(question_sum_prepost) = c("Question", "SumScore_pre",
    "SumScore_post")

question_sum_prepost$NLG = (question_sum_prepost$SumScore_post -
    question_sum_prepost$SumScore_pre)/(100 - question_sum_prepost$SumScore_pre)

write.csv(question_sum_prepost, file = "Questions_Sum_prepost.csv")

question_sum_prepost$Question <- factor(question_sum_prepost$Question,
    levels = q_num_range)


ggplot(question_sum_prepost, aes(x = Question, y = NLG)) + geom_bar(stat = "identity") +
    theme(axis.text.x = element_text(angle = 90, vjust = 0.5,
        hjust = 1))
```
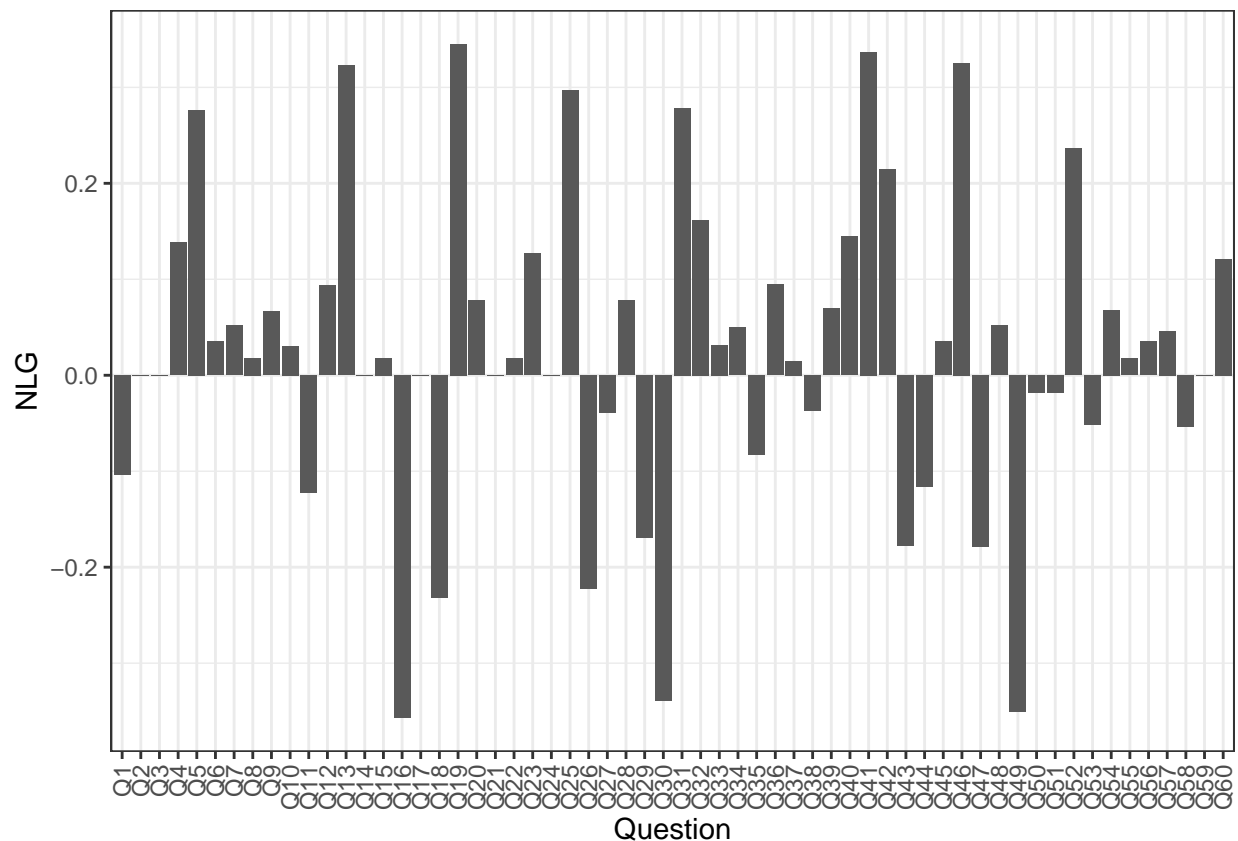


```
nrow(question_sum_prepost)
```

```
## [1] 60
```

```r
nrow(question_sum_prepost[question_sum_prepost$NLG > 0, ])
```

```
## [1] 35
```

```r
nrow(question_sum_prepost[question_sum_prepost$NLG == 0, ])
```

```
## [1] 7
```

```r
nrow(question_sum_prepost[question_sum_prepost$NLG < 0, ])
```

```
## [1] 18
```

```r
session_info()
```

```
## - Session info ---------------------------------------------------------------
##  setting  value
##  version  R version 4.2.1 (2022-06-23 ucrt)
##  os       Windows 10 x64 (build 19044)
##  system   x86_64, mingw32
##  ui       RTerm
##  language (EN)
##  collate  English_United States.utf8
##  ctype    English_United States.utf8
##  tz       America/Phoenix
##  date     2024-04-12
##  pandoc   2.17.1.1 @ C:/Program Files/RStudio/bin/quarto/bin/ (via rmarkdown)
##
## - Packages -------------------------------------------------------------------
##  package      * version   date (UTC) lib source
##  abind          1.4-5     2016-07-21 [1] CRAN (R 4.2.0)
##  backports      1.4.1     2021-12-13 [1] CRAN (R 4.2.0)
##  betareg      * 3.1-4     2021-02-09 [1] CRAN (R 4.2.3)
##  bit            4.0.5     2022-11-15 [1] CRAN (R 4.2.2)
##  bit64          4.0.5     2020-08-30 [1] CRAN (R 4.2.0)
##  broom          1.0.5     2023-06-09 [1] CRAN (R 4.2.3)
##  cachem         1.0.8     2023-05-01 [1] CRAN (R 4.2.3)
##  car            3.1-2     2023-03-30 [1] CRAN (R 4.2.3)
##  carData        3.0-5     2022-01-06 [1] CRAN (R 4.2.0)
##  class          7.3-22    2023-05-03 [1] CRAN (R 4.2.3)
##  cli            3.6.1     2023-03-23 [1] CRAN (R 4.2.3)
##  colorspace     2.1-0     2023-01-23 [1] CRAN (R 4.2.2)
##  crayon         1.5.2     2022-09-29 [1] CRAN (R 4.2.1)
##  curl           5.2.0     2023-12-08 [1] CRAN (R 4.2.3)
##  data.table   * 1.14.10   2023-12-08 [1] CRAN (R 4.2.3)
##  devtools     * 2.4.5     2022-10-11 [1] CRAN (R 4.2.3)
##  digest         0.6.33    2023-07-07 [1] CRAN (R 4.2.3)
##  dplyr        * 1.1.4     2023-11-17 [1] CRAN (R 4.2.3)
##  e1071          1.7-14    2023-12-06 [1] CRAN (R 4.2.3)
##  effsize      * 0.8.1     2020-10-05 [1] CRAN (R 4.2.3)
##  ellipsis       0.3.2     2021-04-29 [1] CRAN (R 4.2.0)
##  evaluate       0.23      2023-11-01 [1] CRAN (R 4.2.3)
```

```
## fansi          1.0.6      2023-12-08 [1] CRAN (R 4.2.3)
## farver         2.1.1      2022-07-06 [1] CRAN (R 4.2.1)
## fastmap        1.1.1      2023-02-24 [1] CRAN (R 4.2.3)
## fitdistrplus * 1.1-11     2023-04-25 [1] CRAN (R 4.2.3)
## flexmix        2.3-19     2023-03-16 [1] CRAN (R 4.2.3)
## forcats      * 1.0.0      2023-01-29 [1] CRAN (R 4.2.2)
## formatR        1.14       2023-01-17 [1] CRAN (R 4.2.2)
## Formula        1.2-5      2023-02-24 [1] CRAN (R 4.2.2)
## fs             1.6.3      2023-07-20 [1] CRAN (R 4.2.3)
## generics       0.1.3      2022-07-05 [1] CRAN (R 4.2.1)
## ggplot2      * 3.4.4      2023-10-12 [1] CRAN (R 4.2.3)
## ggpmisc      * 0.5.5      2023-11-15 [1] CRAN (R 4.2.3)
## ggpp         * 0.5.6      2024-01-09 [1] CRAN (R 4.2.3)
## ggpubr       * 0.6.0.999  2024-02-10 [1] Github (kassambara/ggpubr@6aeb4f7)
## ggrepel      * 0.9.5      2024-01-10 [1] CRAN (R 4.2.1)
## ggsignif       0.6.4      2022-10-13 [1] CRAN (R 4.2.1)
## gld          * 2.6.6      2022-10-23 [1] CRAN (R 4.2.3)
## glue           1.6.2      2022-02-24 [1] CRAN (R 4.2.0)
## gridExtra    * 2.3        2017-09-09 [1] CRAN (R 4.2.0)
## gtable         0.3.4      2023-08-21 [1] CRAN (R 4.2.3)
## highr          0.10       2022-12-22 [1] CRAN (R 4.2.2)
## hms            1.1.3      2023-03-21 [1] CRAN (R 4.2.3)
## htmltools      0.5.7      2023-11-03 [1] CRAN (R 4.2.3)
## htmlwidgets    1.6.4      2023-12-06 [1] CRAN (R 4.2.3)
## httpuv         1.6.14     2024-01-26 [1] CRAN (R 4.2.3)
## knitr        * 1.45       2023-10-30 [1] CRAN (R 4.2.3)
## labeling       0.4.3      2023-08-29 [1] CRAN (R 4.2.3)
## later          1.3.2      2023-12-06 [1] CRAN (R 4.2.3)
## lattice      * 0.22-5     2023-10-24 [1] CRAN (R 4.2.3)
## lifecycle      1.0.4      2023-11-07 [1] CRAN (R 4.2.3)
## likert       * 1.3.5      2016-12-31 [1] CRAN (R 4.2.3)
## lmom           3.0        2023-08-29 [1] CRAN (R 4.2.3)
## lmtest         0.9-40     2022-03-21 [1] CRAN (R 4.2.2)
## logspline    * 2.1.21     2023-10-26 [1] CRAN (R 4.2.3)
## lubridate    * 1.9.3      2023-09-27 [1] CRAN (R 4.2.3)
## magrittr       2.0.3      2022-03-30 [1] CRAN (R 4.2.0)
## MASS         * 7.3-60     2023-05-04 [1] CRAN (R 4.2.3)
## Matrix         1.6-4      2023-11-30 [1] CRAN (R 4.2.3)
## MatrixModels   0.5-3      2023-11-06 [1] CRAN (R 4.2.3)
## matrixTests  * 0.2.3      2023-10-05 [1] CRAN (R 4.2.1)
## memoise        2.0.1      2021-11-26 [1] CRAN (R 4.2.0)
## mgcv           1.9-1      2023-12-21 [1] CRAN (R 4.2.3)
## mime           0.12       2021-09-28 [1] CRAN (R 4.2.0)
## miniUI         0.1.1.1    2018-05-18 [1] CRAN (R 4.2.2)
## mnormt         2.1.1      2022-09-26 [1] CRAN (R 4.2.1)
## modeltools     0.2-23     2020-03-05 [1] CRAN (R 4.2.0)
## munsell        0.5.0      2018-06-12 [1] CRAN (R 4.2.0)
## mvtnorm      * 1.2-4      2023-11-27 [1] CRAN (R 4.2.3)
## nlme           3.1-164    2023-11-27 [1] CRAN (R 4.2.3)
## nnet           7.3-19     2023-05-03 [1] CRAN (R 4.2.3)
## PairedData   * 1.1.1      2018-06-02 [1] CRAN (R 4.2.3)
## pillar         1.9.0      2023-03-22 [1] CRAN (R 4.2.3)
## pkgbuild       1.4.3      2023-12-10 [1] CRAN (R 4.2.3)
## pkgconfig      2.0.3      2019-09-22 [1] CRAN (R 4.2.0)
```

```
## pkgload        1.3.4    2024-01-16 [1] CRAN (R 4.2.3)
## plyr         * 1.8.9    2023-10-02 [1] CRAN (R 4.2.3)
## polynom        1.4-1    2022-04-11 [1] CRAN (R 4.2.0)
## profvis        0.3.8    2023-05-02 [1] CRAN (R 4.2.3)
## promises       1.2.1    2023-08-10 [1] CRAN (R 4.2.3)
## proxy          0.4-27   2022-06-09 [1] CRAN (R 4.2.1)
## psych        * 2.4.1    2024-01-18 [1] CRAN (R 4.2.3)
## purrr        * 1.0.2    2023-08-10 [1] CRAN (R 4.2.3)
## quantreg       5.97     2023-08-19 [1] CRAN (R 4.2.3)
## R6             2.5.1    2021-08-19 [1] CRAN (R 4.2.0)
## ragg           1.2.7    2023-12-11 [1] CRAN (R 4.2.3)
## RColorBrewer * 1.1-3    2022-04-03 [1] CRAN (R 4.2.0)
## Rcpp           1.0.11   2023-07-06 [1] CRAN (R 4.2.3)
## readr        * 2.1.5    2024-01-10 [1] CRAN (R 4.2.1)
## remotes        2.4.2.1  2023-07-18 [1] CRAN (R 4.2.3)
## reshape2       1.4.4    2020-04-09 [1] CRAN (R 4.2.2)
## rlang          1.1.1    2023-04-28 [1] CRAN (R 4.2.3)
## rmarkdown      2.25     2023-09-18 [1] CRAN (R 4.2.3)
## rstatix        0.7.2    2023-02-01 [1] CRAN (R 4.2.2)
## rstudioapi     0.15.0   2023-07-07 [1] CRAN (R 4.2.3)
## sandwich       3.1-0    2023-12-11 [1] CRAN (R 4.2.3)
## scales         1.3.0    2023-11-28 [1] CRAN (R 4.2.3)
## sessioninfo    1.2.2    2021-12-06 [1] CRAN (R 4.2.3)
## shiny          1.8.0    2023-11-17 [1] CRAN (R 4.2.3)
## SparseM        1.81     2021-02-18 [1] CRAN (R 4.2.0)
## stringi        1.8.3    2023-12-11 [1] CRAN (R 4.2.3)
## stringr      * 1.5.1    2023-11-14 [1] CRAN (R 4.2.3)
## survival     * 3.5-7    2023-08-14 [1] CRAN (R 4.2.3)
## systemfonts    1.0.5    2023-10-09 [1] CRAN (R 4.2.3)
## textshaping    0.3.7    2023-10-09 [1] CRAN (R 4.2.3)
## tibble       * 3.2.1    2023-03-20 [1] CRAN (R 4.2.3)
## tidyr        * 1.3.0    2023-01-24 [1] CRAN (R 4.2.3)
## tidyselect     1.2.0    2022-10-10 [1] CRAN (R 4.2.3)
## tidyverse    * 2.0.0    2023-02-22 [1] CRAN (R 4.2.3)
## timechange     0.2.0    2023-01-11 [1] CRAN (R 4.2.2)
## tinytex      * 0.49     2023-11-22 [1] CRAN (R 4.2.3)
## tzdb           0.4.0    2023-05-12 [1] CRAN (R 4.2.3)
## urlchecker     1.0.1    2021-11-30 [1] CRAN (R 4.2.3)
## usethis      * 2.2.2    2023-07-06 [1] CRAN (R 4.2.3)
## utf8           1.2.4    2023-10-22 [1] CRAN (R 4.2.3)
## vctrs          0.6.5    2023-12-01 [1] CRAN (R 4.2.3)
## vroom          1.6.5    2023-12-05 [1] CRAN (R 4.2.3)
## withr          3.0.0    2024-01-16 [1] CRAN (R 4.2.3)
## xfun           0.40     2023-08-09 [1] CRAN (R 4.2.3)
## xtable       * 1.8-4    2019-04-21 [1] CRAN (R 4.2.0)
## yaml           2.3.7    2023-01-23 [1] CRAN (R 4.2.3)
## zoo            1.8-12   2023-04-13 [1] CRAN (R 4.2.3)
##
## [1] C:/Users/splaisie/AppData/Local/R/win-library/4.2
## [2] C:/Program Files/R/R-4.2.1/library
##
## --------------------------------------------------------------------------------
```