Homework 3: Discriminant Analysis

S&DS 5360 | Multivariate Statistics

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Setup & Data Overview

We continue with our analysis of the 2024–2025 Healthy Minds Study (HMS) student survey, this time performing discriminant analysis. We will investigate whether we can use the same psychological health scores we defined in Homework 2 to determine whether a student belongs to one of the following GSM identities:

1. Cis-Heterosexual
2. Cis-LGBQ+ (lesbian, gay, bisexual, or queer, but not TGNC)
3. Transgender and Gender Nonconforming (TGNC), including those who also identify as LGBQ+

Per the grader's feedback, we omit the code necessary to load and preprocess the data. However, we provide summary Table 1 contextualize the subsequent analyses:

Table 1: Descriptive Statistics by Identity Group

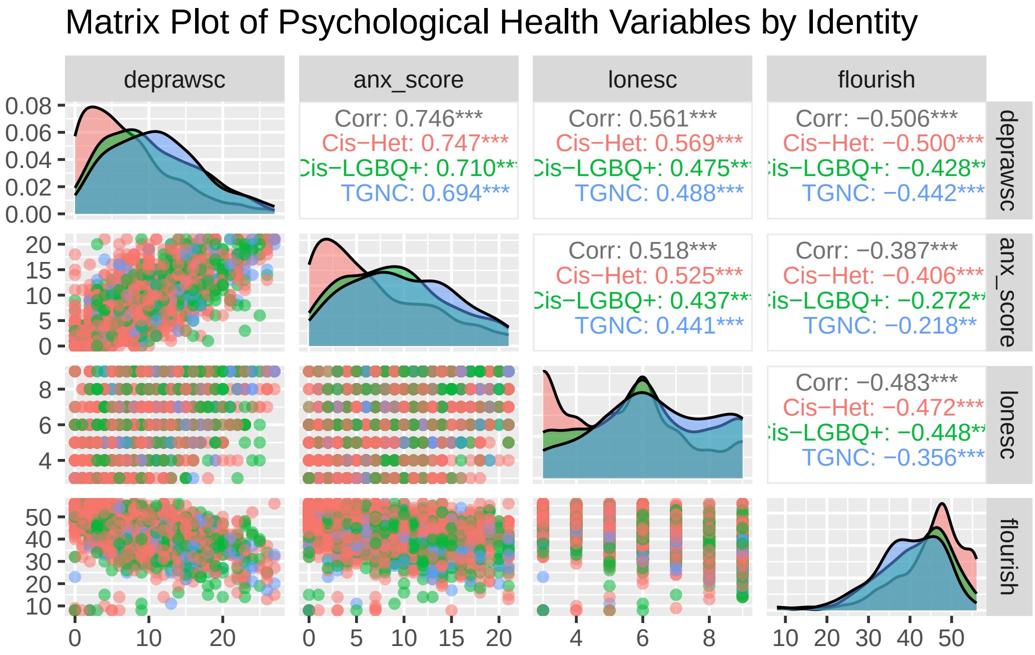
Statistic	Cis-Het	Cis-LGBQ+	TGNC
Sample Size			
n	44,791	16,387	5,155
Depression (PHQ-9)			
Depression Mean	7.26	9.93	12.06
Depression SD	5.80	6.16	6.42
Anxiety (GAD-7)			
Anxiety Mean	6.66	9.04	10.29
Anxiety SD	5.54	5.71	5.66
Loneliness (UCLA)			
Loneliness Mean	5.24	5.96	6.53
Loneliness SD	1.91	1.88	1.81
Flourishing			
Flourishing Mean	44.84	41.97	39.08
Flourishing SD	8.76	8.53	8.90

We visually observe a difference across psychological health score means for each group and note the significant sample size. We feel comfortable proceeding with our analysis.

Part 1 | Evaluating Assumptions

We begin by visualizing our data via a matrix (pairs) plot:

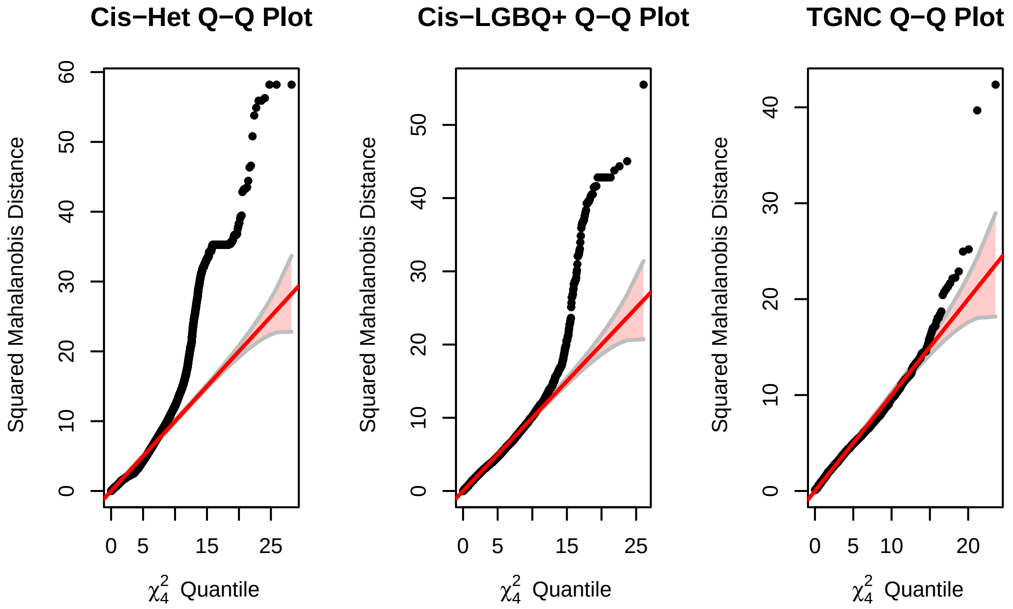
```r
set.seed(4747)
df_sample <- df %>% sample_n(2000)

ggpairs(
    df_sample,
    columns = c('deprawsc', 'anx_score', 'lonesc', 'flourish'),
    aes(color = identity_group, alpha = 0.5),
    upper = list(continuous = wrap('cor', size = 3)),
    title = 'Matrix Plot of Psychological Health Variables by Identity'
)
```



We see strong **separaton of means** for flourishing (`flourish`) and depression (`deprawsc`). In comparison, loneliness (`lonesc`) feataures a lot of overlap and likely will not be a strong predictor in our model.

Regarding **normality,** we first note a slight right skew for depression (`deprawsc`) and anxiety (`anx_score`), particularly for the Cis-Het group. The other groups appear more symmetrical. Loneliness (`lonesc`) is visibly multimodal, violating normality (likely due to the LIkert scale structure of the question), and potentially reducing the accuracy of the discriminant function. Finally, flourishing (`flourish`) is left-skewed. We formally analyze multivariate normality via chi-square quantile plots.

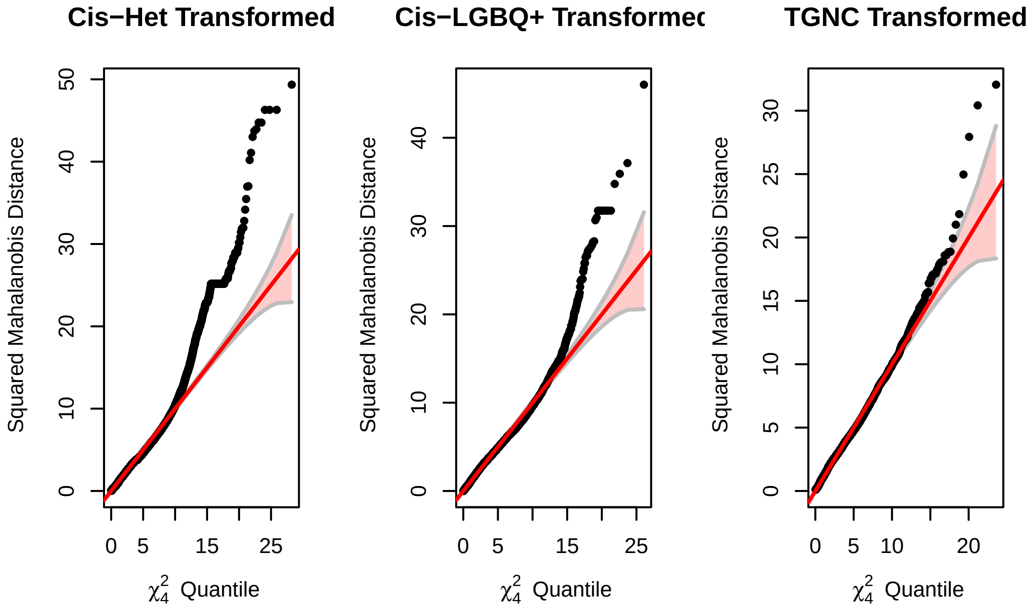
```
par(mfrow=c(1,3))
cqplot(df[df$identity_group == "Cis-Het",
    c("deprawsc", "anx_score", "lonesc", "flourish")], main = "Cis-Het Q-Q Plot")
cqplot(df[df$identity_group == "Cis-LGBQ+",
    c("deprawsc", "anx_score", "lonesc", "flourish")], main = "Cis-LGBQ+ Q-Q Plot")
cqplot(df[df$identity_group == "TGNC",
    c("deprawsc", "anx_score", "lonesc", "flourish")], main = "TGNC Q-Q Plot")
```



Our Chi-Square Quantile plots show heavy deviations from the diagonal in the upper tails for all groups, though less so for `TGNC`. This indicates that our data is not multivariate normal, likely due to the skew caused by Likert scale rankings. We consider the same transformations as in Homework 2:

- Square root of depression
- Square root of anxiety
- Square (quadratic) of flourish

However, these and similar transformations do not yield improved multivariate normality. We supporess the code for the ease of the grader but present the corresponding Q-Q plots for the transformed data:



While the Chi-Square Quantile plots indicate a violation of multivariate normality, we recall that discriminant analysis is traditionally robust to such violations in large samples like ours. The non-normality is an inherent feature of the floor effects of the Likert scale ratings, so while transformations were considered, we ultimately choose to proceed with the raw variables to preserve the interpretability of the results. The violation suggests that QDA could be tested as a potentially more flexible alternative to LDA, but ultimately, we feel comfortable proceeding with LDA.

Finally, we check for **equal covariance**. The matrix plot shows that anxiety versus depression maintains fairly equal correlation across all groups (0.747, 0.710, 0.694). This trend is reasonably consistent among other predictor pairs; however, flourishing versus depression, for example, features wider gaps in correlation $(0.472, 0.448, 0.356)$. These still feel reasoably equivalent, but for completeness, we formally test for equal covariance via Box's M-test.

```
boxM(df[, c("deprawsc", "anx_score", "lonesc", "flourish")], df$identity_group)
```

```
 Box's M-test for Homogeneity of Covariance Matrices

data:  df[, c("deprawsc", "anx_score", "lonesc", "flourish")] by df$identity_group
Chi-Sq (approx.) = 1198.817, df = 20, p-value = < 2.2e-16
```

As expected, given our large sample size of 66, 333 (aggregate count by group can be seen in Table 1), leads our Box's M test to reject the null hypothesis, indicating a difference in covariances across groups. We instead analyze the practical difference in covariance structures.

```r
vars <- c("deprawsc", "anx_score", "lonesc", "flourish")

get_ratio <- function(m1, m2) {
  r <- m1 / m2
  r[abs(r) < 1] <- 1 / r[abs(r) < 1]
  return(round(r, 1))
}

# Calculate Covariance Matrices
cov_cis  <- cov(df[df$identity_group == "Cis-Het", vars])
cov_lgbq <- cov(df[df$identity_group == "Cis-LGBQ+", vars])
cov_tgnc <- cov(df[df$identity_group == "TGNC", vars])

# Calculate Ratios
rat_tgnc_cis  <- get_ratio(cov_tgnc, cov_cis)
rat_lgbq_cis  <- get_ratio(cov_lgbq, cov_cis)
rat_tgnc_lgbq <- get_ratio(cov_tgnc, cov_lgbq)
```

Table 2: Ratio of Covariance Matrix Elements Between Groups

Metric	Depression	Anxiety	Loneliness	Flourishing
Comparison 1: TGNC vs. Cis-Het				
Depression	1.2	1.0	1.1	1.4
Anxiety	1.0	1.0	1.3	1.1
Loneliness	1.1	1.3	1.1	1.1
Flourishing	1.4	1.1	1.1	1.0
Comparison 2: Cis-LGBQ+ vs. Cis-Het				
Depression	1.1	1.0	1.1	1.2
Anxiety	1.0	1.1	1.2	1.0
Loneliness	1.1	1.2	1.0	1.0
Flourishing	1.2	1.0	1.0	1.1
Comparison 3: TGNC vs. Cis-LGBQ+				
Depression	1.1	1.0	1.1	1.2
Anxiety	1.0	1.0	1.1	1.1
Loneliness	1.1	1.1	1.1	1.1
Flourishing	1.2	1.1	1.1	1.1

Following the rule where if all ratios of covariance matrix elements between groups are less than four, the covariance matrices are similar enough, we feel comfortable proceeding with linear discriminant analysis, as all of our ratios fall between 1.0 and 1.4.

Part 2 | Discriminant Analysis

With our assumptions somewhat satisfied in Part 1, we proceed with both Linear Discriminant Analysis and Quadratic Discriminant Analysis. We will compare their classification accuracy and proceed with analysis via the outperforming method.

```r
lda_cv <- lda(
    identity_group ~ deprawsc + anx_score + lonesc + flourish,
    data = df,
    prior = c(1/3, 1/3, 1/3),
    CV = TRUE)

qda_cv <- qda(
    identity_group ~ deprawsc + anx_score + lonesc + flourish,
    data = df,
    prior = c(1/3, 1/3, 1/3),
    CV = TRUE)

lda_cv_acc <- round(sum(diag(prop.table(table(df$identity_group, lda_cv$class)))), 4)
qda_cv_acc <- round(sum(diag(prop.table(table(df$identity_group, qda_cv$class)))), 4)

cat("LDA CV Accuracy:", lda_cv_acc, "\nQDA CV Accuracy:", qda_cv_acc)
```

```
LDA CV Accuracy: 0.5167
QDA CV Accuracy: 0.52
```

We see that the cross-validated accuracy of QDA is only 0.0033 higher than that of LDA. Therefore, to preserve interpretability (as discussed in Part 1) and to adhere with the principle of parsimony, we proceed with LDA on our raw (untransformed) variables.

Note that we compared LDA versus QDA as full models (inclusive of all discriminants). Now that we have elected to use LDA, we proceed with Stepwise Discriminant Analysis to determine whether there are any redundant discriminators we should drop. Note we proceed with 10-fold validation due to our large sample size.

```r
df_clean <- df %>% drop_na()

X <- df_clean[, c('deprawsc', 'anx_score', 'lonesc', 'flourish')]
y <- df_clean$identity_group

step_model <- stepclass(
    X,
    y,
    method = "lda",
    direction = "both",
    prior = c(1/3, 1/3, 1/3),
    improvement = 0.01,
    fold = 10,
    trace = FALSE)
```

```
 `stepwise classification', using 10-fold cross-validated correctness rate of method lda'.

66333 observations of 4 variables in 3 classes; direction: both


stop criterion: improvement less than 1%.


correctness rate: 0.51697;  in: "flourish";  variables (1): flourish

 hr.elapsed min.elapsed sec.elapsed
       0.00        0.00        4.99
```

```r
step_model
```

```

method      : lda
final model : y ~ flourish
<environment: 0x0000014f39563b68>

correctness rate = 0.517
```

With equal priors and a low improvement threshold, our Stepwise Discriminant Analysis proceeds with solely `deprawsc` as the discriminator, yielding essentially the same correctness rate as our full model (0.5172 versus 0.5167, respectively). This is unsurprising, as we saw that the discriminators themselves exhibit multicollinearity. Thus, one discriminator alone may already provide a bulk of the signal used to classify each individual. However, per the recommendation in the assignment text, we proceed with the full model (all four discriminators).

This will allow us to conduct a more granular deep dive into the multivariate psychological health profiles of each group in later analyses. The model summary is produced below:

```
lda_fit <- lda(identity_group ~ ., data = df, prior = c(1/3, 1/3, 1/3)); lda_fit
```

```
Call:
lda(identity_group ~ ., data = df, prior = c(1/3, 1/3, 1/3))

Prior probabilities of groups:
  Cis-Het Cis-LGBQ+      TGNC
0.3333333 0.3333333 0.3333333

Group means:
          deprawsc anx_score   lonesc flourish
Cis-Het    7.25590  6.662142 5.244625 44.84475
Cis-LGBQ+  9.93086  9.040459 5.959968 41.97223
TGNC      12.06324 10.293889 6.530747 39.08380

Coefficients of linear discriminants:
                  LD1          LD2
deprawsc  -0.08766862 -0.119020335
anx_score -0.01848018  0.238315655
lonesc    -0.16241115  0.009194239
flourish   0.03460451  0.054181217

Proportion of trace:
   LD1    LD2
0.9828 0.0172
```

Part 3 | Multivariate Group Means

To determine whether the multivariate group means are different, we perform the multivariate Wilks' Lambda Test:

```
df_manova <- manova(as.matrix(df[, vars]) ~ df$identity_group)
summary(df_manova, test = "Wilks")
```

```
                     Df  Wilks approx F num Df den Df    Pr(>F)
df$identity_group     2 0.9191   714.34      8 132654 < 2.2e-16 ***
Residuals         66330
```

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Our Wilks' Lambda is 0.9191, indicating that approximately 8.1% of the total variance in the combined mental health scores is explained solely by the student's identity group. With an extremely small *p*-value, we can reject the null hypothesis and conclude that mean vectors are not the same across groups.

We further present the univariate analyses (equivalent to `summary.aov` output) to better understand the relevance of each discriminator in Table 3.

Table 3: MANOVA and Univariate ANOVA Results for Identity Groups

Analysis Level	Wilks' Lambda	F-Statistic	p-value
Multivariate Test			
Multivariate (Wilks)	0.9191	714.34	< 2.2e-16
Univariate Response Tests			
Depression (PHQ-9)	—	2342.80	< 2.2e-16
Anxiety (GAD-7)	—	1766.50	< 2.2e-16
Loneliness (UCLA)	—	1645.50	< 2.2e-16
Flourishing	—	1432.40	< 2.2e-16

We see that each predictor independently is a statistically significant discriminator of group differences. Given our sample size and earlier discussion on collinearity, this is unsurprising. However, note that the F- statistic for depression is much larger than the other discriminators. This confirms the stepwise decision earlier to retain only depression in the model.

Ultimately, we are satisfied with our Wilks' Lambda value of 0.9191. Explaining 8.1% of the total variance across groups is generally considered a medium effect in the social sciences.

Part 4 | Signifiance of Discriminant Functions

Recall the proportion of trace metrics we computed in Part 2:

```r
lda_fit
```

```
Call:
lda(identity_group ~ ., data = df, prior = c(1/3, 1/3, 1/3))

Prior probabilities of groups:
  Cis-Het Cis-LGBQ+      TGNC
```

```
0.3333333 0.3333333 0.3333333

Group means:
          deprawsc anx_score   lonesc flourish
Cis-Het    7.25590  6.662142 5.244625 44.84475
Cis-LGBQ+  9.93086  9.040459 5.959968 41.97223
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Coefficients of linear discriminants:
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anx_score -0.01848018  0.238315655
lonesc    -0.16241115  0.009194239
flourish   0.03460451  0.054181217

Proportion of trace:
   LD1    LD2
0.9828 0.0172
```

Since we have 3 groups, we have 2 discriminant functions. Our first discriminant function (`LD1`) accounts for 98.28% of the relative discriminating power—almost all of the necessary discriminatory signal in our predictor variables. `LD2`, on the other hand, captures only the remaining 1.72%, though it is statistically significant (likely due to sample size). This suggests that the psychological differences between each group are largely one-dimensional.

Part 5 | Classification

Recall that we performed both regular and 10-fold cross validation to determine whether to proceed with LDA or QDA in Part 2.

```r
lda_regular_acc <- round(sum(diag(prop.table(table(df$identity_group, predict(lda_fit)$class)
acc_comp <- data.frame(
  Type = c("Regular Accuracy", "Cross-Validated Accuracy"),
  Value = c(lda_regular_acc, lda_cv_acc)
)

acc_comp
```

```
                      Type  Value
1         Regular Accuracy 0.5168
2 Cross-Validated Accuracy 0.5167
```

Our regular accuracy and 10-fold cross-validated accuracy are nearly identical, with a difference of 0.0001. This indicates that our model is stable. Now, we are curious whether there are certain areas where the model does particularly well (or not). For this, we generate a confusion matrix and append recall (accuracy percentages):

```
conf_matrix <- table(Actual = df$identity_group, Predicted = lda_cv$class)
```

Table 4: Cross-Validated Confusion Matrix for Identity Groups

	Predicted Group Membership			
Actual Group	Pred: Cis-Het	Pred: Cis-LGBQ+	Pred: TGNC	Recall (%)
Cis-Het	28363	6331	44791	63.32
Cis-LGBQ+	7040	3106	16387	18.95
TGNC	1498	852	5155	54.41

Though our overall cross-validated accuracy is ≈ 52%, as illustrated in Table 4 the model is most effective at predicting `Cis-Het` and `TGNC`, with recalls of 63.3% and 54.4%, accordingly. However, the `Cis-LGBQ+` group has a low recall of 19.0%. Most of these students are misclassified as one of the other two groups, illustrating that their mental health data doesn't form a unique cluster.