```
In [1]: import warnings
        warnings.filterwarnings('ignore')
        import pandas as pd
        import numpy as np
        from plotnine import *
        from sklearn.tree import DecisionTreeClassifier # Decision Tree
        from sklearn.linear model import LogisticRegression # Logistic Regress
        ion Model
        from sklearn.naive bayes import GaussianNB, BernoulliNB, MultinomialNB
        , CategoricalNB # Decision Tree
        from sklearn.neighbors import KNeighborsClassifier
        from sklearn.model_selection import train test split
        from sklearn import metrics
        from sklearn.preprocessing import StandardScaler #Z-score variables
        from sklearn.model selection import train test split # simple TT split
        from sklearn.model selection import KFold # k-fold cv
        from sklearn.model selection import LeaveOneOut #LOO cv
        from sklearn.model_selection import cross val score # cross validation
        metrics
        from sklearn.model_selection import cross val predict # cross validati
        on metrics
        from sklearn.metrics import accuracy score, confusion matrix
        from sklearn.metrics import plot confusion matrix
        from sklearn.model selection import GridSearchCV
        %precision %.7g
        %matplotlib inline
```

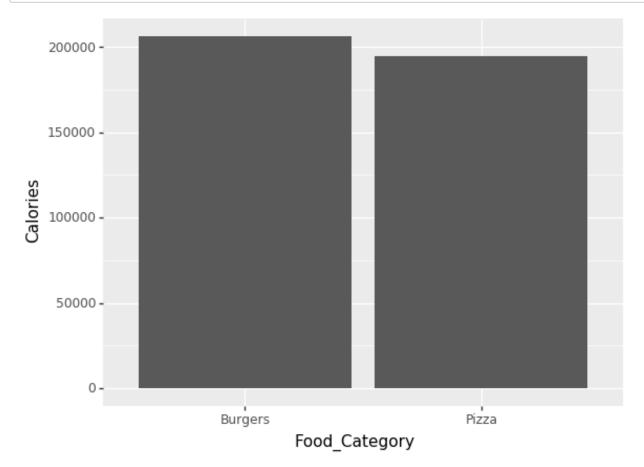
Part I

Out[2]:

	Item_Name	Item_Description	Food_Category	Calories	Total_Fat	Saturated_Fat	Trans_Fat
0	Chicken n Cheese Slider	Chicken n Cheese Slider on Mini Bun w/ Chicken	Burgers	290.0	12.0	3.5	0.0
1	Corned Beef n Cheese Slider	Corned Beef n Cheese Slider on Mini Bun w/ Cor	Burgers	220.0	9.0	3.5	0.0
2	Ham n Cheese Slider	Ham n Cheese Slider on Mini Bun w/ Roast Ham &	Burgers	230.0	9.0	3.5	0.0
3	Jalapeno Roast Beef n Cheese Slider	Jalapeno Roast Beef n Cheese Slider on Mini Bu	Burgers	240.0	11.0	4.5	0.0
4	Roast Beef n Cheese Slider	Roast Beef n Cheese Slider on Mini Bun w/ Roas	Burgers	240.0	11.0	4.5	0.0

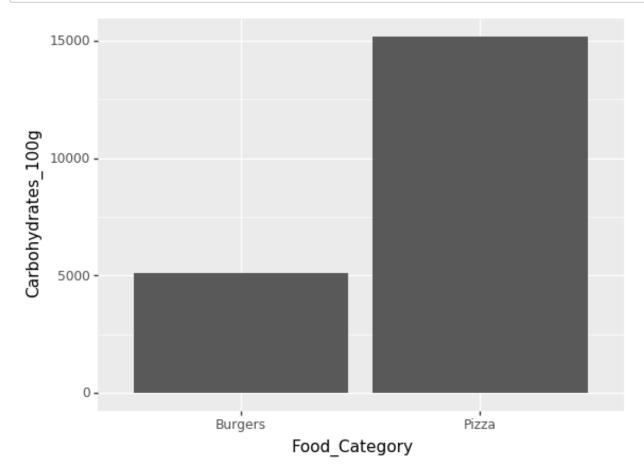
5 rows × 25 columns

1. Explore Data (with ggplot)



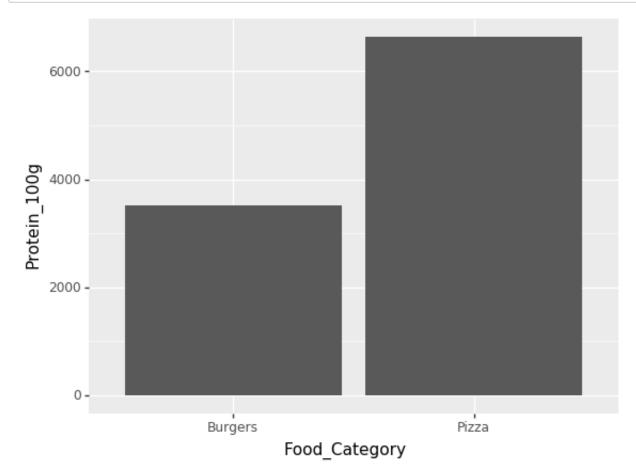
Out[27]: <ggplot: (307672741)>

```
In [28]: (ggplot(aye, aes(x = "Food_Category", y = "Carbohydrates_100g")) + geo
    m_bar(stat = "identity"))
```



Out[28]: <ggplot: (307202857)>

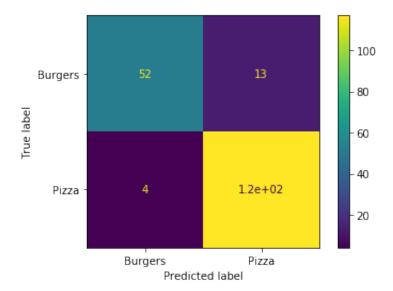
```
In [29]: (ggplot(aye, aes(x = "Food_Category", y = "Protein_100g")) + geom_bar(
    stat = "identity"))
```



Out[29]: <ggplot: (276454737)>

Model 1

```
predictors = ["Calories", "Carbohydrates 100g", "Protein 100g"]
In [33]:
         X = aye[predictors]
         y = aye["Food Category"]
         # split into training and test
         X train, X test, y train, y test = train test split(X,y, test size = 0
         .2)
         #standardize
         z = StandardScaler()
         X train = z.fit transform(X train)
         X test = z.transform(X test)
         # create model
         knn2 = KNeighborsClassifier()
         \# choose potential values of k
         ks = {"n neighbors": range(1,30)}
         # use grid search to find best parameters
         grid = GridSearchCV(knn2,ks, scoring = "accuracy", cv = 30)
         knnmod = grid.fit(X train, y train)
         plot confusion matrix(knnmod, X test, y test)
```



```
In [34]: knnmod.best_estimator_.get_params()["n_neighbors"]
Out[34]: 3
In [35]: knnmod.score(X_test,y_test)
Out[35]: 0.9086021505376344
```

2. Explain which variables you're using to predict the outcome

The variables I used to predict the outcome are calories, carbohydrates, and protein. I used these variables to predict the outcome because usually burgers tend to have more calories and protein compared to pizza. Whereas, a pizza would have more carbohydrates compared to a hamburger.

3. Explain which model validation technique you're using and why.

The model validation technique I used is hyper parameter grid searching. This helps me find the best parameter.

4. Explain why you did or did not choose to standardize your continuous variables.

I chose to standardize my continuous variable because if the variables are measured in different scales it can impact the way they're weighed when measuring variation.

5. Evaluate how the model performed. Explain.

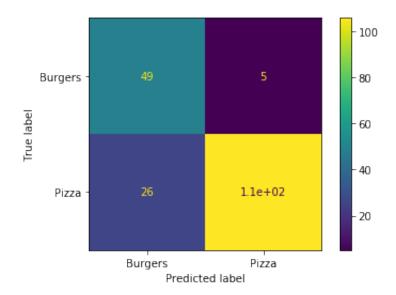
My model performed well and it shows a 90.86% accuracy score. Looking at the confusion matrix, the off-diagonal it was able to predict most of it correctly.

Model 2

```
In [21]:
         X = aye[["Calories","Carbohydrates 100g","Protein 100g"]]
         y = aye["Food Category"]
         X train, X_test, y_train, y_test = train_test_split(X,y, test_size = 0
         .2)
         zscore = StandardScaler()
         zscore.fit(X train)
         X train = zscore.transform(X train)
         X test = zscore.transform(X test)
         tree = DecisionTreeClassifier()
         tree.fit(X train, y train)
Out[21]: DecisionTreeClassifier(ccp alpha=0.0, class weight=None, criterion='
         gini',
                                max_depth=None, max_features=None, max_leaf_n
         odes=None,
                                min impurity decrease=0.0, min impurity split
         =None,
                                min samples leaf=1, min samples split=2,
                                 min weight fraction leaf=0.0, presort='deprec
         ated',
                                 random state=None, splitter='best')
In [22]: y pred = tree.predict(X test)
         accuracy_score(y_pred, y_test)
```

Out[22]: 0.83333333333333334

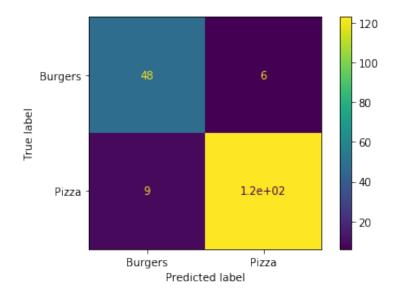
```
In [23]: plot_confusion_matrix(tree, X_test, y_test)
```



```
In [24]:
         tree.get depth()
Out[24]: 17
         tree.get n leaves()
In [25]:
Out[25]: 124
         tree = DecisionTreeClassifier(max depth = 5)
In [26]:
         tree.fit(X train, y train)
Out[26]: DecisionTreeClassifier(ccp alpha=0.0, class weight=None, criterion='
         gini',
                                 max depth=5, max features=None, max leaf node
         s=None,
                                 min_impurity_decrease=0.0, min impurity split
         =None,
                                 min samples leaf=1, min samples split=2,
                                 min weight fraction leaf=0.0, presort='deprec
         ated',
                                 random state=None, splitter='best')
In [27]:
         y pred = tree.predict(X test)
         accuracy score(y pred, y test)
```

Out[27]: 0.9193548387096774

```
In [28]: plot_confusion_matrix(tree, X_test, y_test)
```



2. Explain which variables you're using to predict the outcome.

The variables I used to predict the outcome are calories, carbohydrates, and protein. I used these variables to predict the outcome because usually burgers tend to have more calories and protein compared to pizza. Whereas, a pizza would have more carbohydrates compared to a hamburger.

3.Explain which model validation technique you're using and why.

The model validation technique I used is train split test. I used this technique because our data includes different nutrition facts of pizza and burgers. The train split test technique will help boost the algorithm performance. We will train the models, each time using one variable for testing and the other variables for training. Then, we will be able to evaluate better our algorithm and be able to build our model.

4. Explain why you did or did not choose to standardize your continuous variables.

I chose to standardize my continuous variable because if the variables are measured in different scales it can impact the way they're weighed when measuring variation.

5. Evaluate how the model performed. Explain

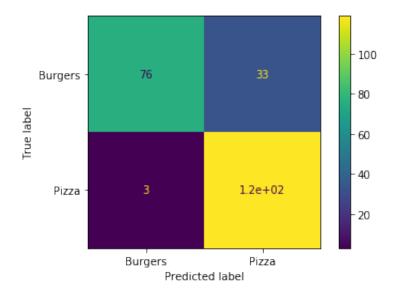
My model performed well and it shows a 91.94% accuracy score. Looking at the confusion matrix, the off-diagonal it was able to predict most of it correctly.

Model 3

```
In [5]: pred = ["Calories", "Carbohydrates 100g", "Protein 100g"]
        X = aye[pred]
        y = aye["Food Category"]
        pizza = np.where(y == 'Pizza')[0]
        burger = np.where(y == 'Burgers')[0]
        pizzaDownSample = np.random.choice(pizza, size = len(burger), replace
        = False)
        downSampledData = np.concatenate([burger,pizzaDownSample])
        downSampledData
        X d = aye.iloc[downSampledData,][pred]
        y d = aye.iloc[downSampledData,]["Food Category"]
        X d.shape
        kf = KFold(n splits = 4)
        nb = GaussianNB()
        acc = []
        for train, test in kf.split(X,y):
            X train = X.iloc[train]
            X test = X.iloc[test]
            y train = y[train]
            y \text{ test} = y[\text{test}]
            nb.fit(X train,y train)
            acc.append(nb.score(X test,y test))
            plot confusion matrix(nb, X test,y test)
        print(acc)
        print(np.mean(acc))
```

[0.8189655172413793, 0.8620689655172413, 0.9353448275862069, 0.84415 58441558441] 0.8651337886251679





2. Explain which variables you're using to predict the outcome.

The variables I used to predict the outcome are calories, carbohydrates, and protein. I used these variables to predict the outcome because usually burgers tend to have more calories and protein compared to pizza. Whereas, a pizza would have more carbohydrates compared to a hamburger.

3. Explain which model validation technique you're using and why.

The model validation technique I used is K fold. This technique helps split the data and use performance metrics on test data to evaluate the model's performance. K fold cross validation is able to take all the performance metric and adds them together.

4. Explain why you did or did not choose to standardize your continuous variables.

I chose to not standardize my continuous variable because the code would throw me an error. When I didn't standardize my continuous variable the code worked and gave me a good accuracy score.

5. Evaluate how the model performed. Explain.

My model performed well with the average accuracy score being 86.51%. Looking at all of the confusion matrix,

the off-diagonal it was able to predict most of it correctly.

At the end

1. Compare the performance of the 3 models using the accuracy, and the confusion matrix

All 3 models performed well with high accuracy scores. The lowest accuracy score was Model 3, 86.51%. While the highest accuracy score was Model 2, 91.94%. Model 3 is will be the one that will most to make an error compared to the other models. All 3 confusion matrices's off-diagonal was able to predict most of it correctly.

Part II

```
In [1]: import warnings
warnings.filterwarnings('ignore')

import pandas as pd
import numpy as np
from plotnine import *

from sklearn.preprocessing import StandardScaler

from sklearn.cluster import AgglomerativeClustering

from sklearn.cluster import KMeans
from sklearn.mixture import GaussianMixture

from sklearn.metrics import silhouette_score

import scipy.cluster.hierarchy as sch
from matplotlib import pyplot as plt

%matplotlib inline
```

In [2]: ayenapapas = pd.read_csv("https://raw.githubusercontent.com/cmparlettp
elleriti/CPSC392ParlettPelleriti/master/Data/KrispyKreme.csv")
ayenapapas.head()

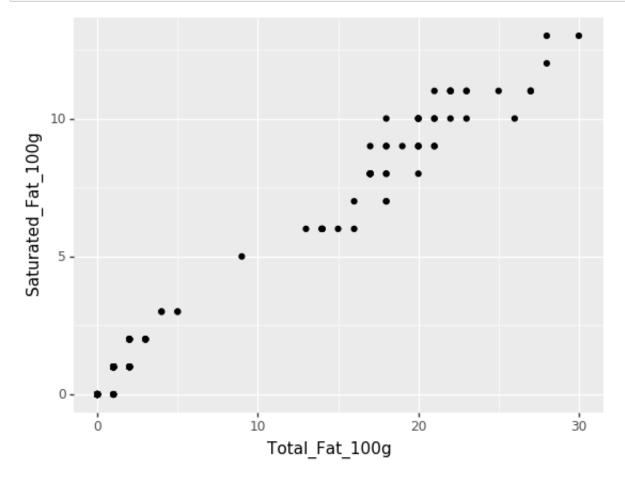
Out[2]:

	Restaurant_Item_Name	restaurant	Restaurant_ID	Item_Name	Item_Description	Food_Cate
0	Krispy Kreme Apple Fritter	Krispy Kreme	49	Apple Fritter	Apple Fritter, Doughnuts	Baked Go
1	Krispy Kreme Chocolate Iced Cake Doughnut	Krispy Kreme	49	Chocolate Iced Cake Doughnut	Chocolate Iced Cake Doughnut, Doughnuts	Baked Go
2	Krispy Kreme Chocolate Iced Custard Filled Dou	Krispy Kreme	49	Chocolate Iced Custard Filled Doughnut	Chocolate Iced Custard Filled Doughnut, Doughnuts	Baked Go
3	Krispy Kreme Chocolate Iced Glazed Doughnut	Krispy Kreme	49	Chocolate Iced Glazed Doughnut	Chocolate Iced Glazed Doughnut, Doughnuts	Baked Go
4	Krispy Kreme Chocolate Iced Glazed Cruller Dou	Krispy Kreme	49	Chocolate Iced Glazed Cruller Doughnut	Chocolate Iced Glazed Cruller Doughnut, Doughnuts	Baked Go

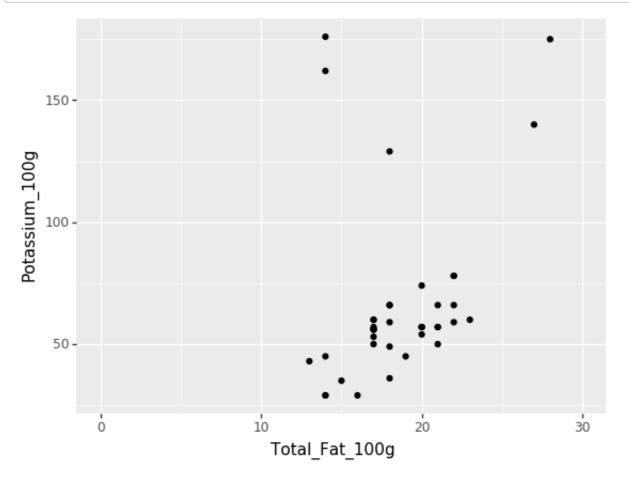
5 rows × 32 columns

1. Explore Data (with ggplot)

```
In [7]: (ggplot(ayenapapas, aes(x = "Total_Fat_100g", y = "Saturated_Fat_100g"
)) + geom_point())
```

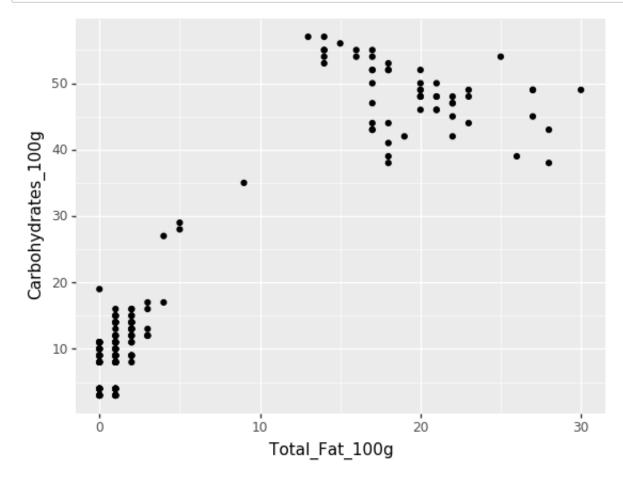


Out[7]: <ggplot: (304557621)>



Out[34]: <ggplot: (306564201)>

```
In [35]: (ggplot(ayenapapas, aes(x = "Total_Fat_100g", y = "Carbohydrates_100g"
)) + geom_point())
```

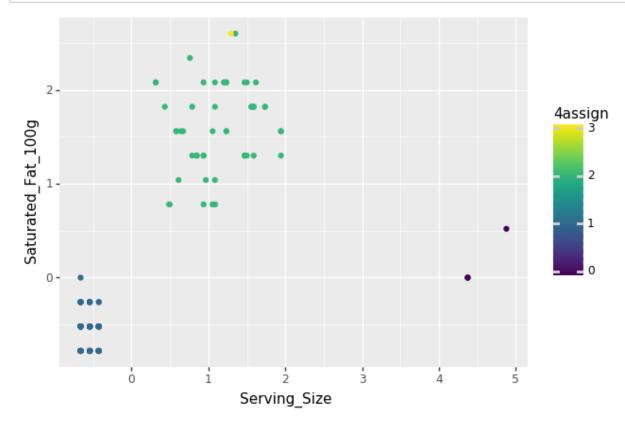


Out[35]: <ggplot: (305353501)>

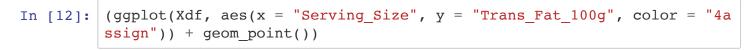
K-Means Model

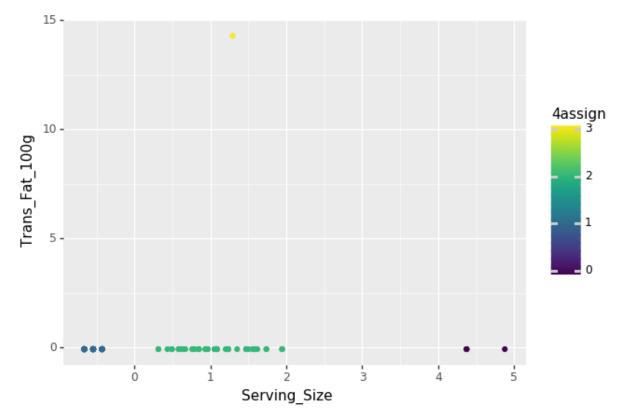
```
In [8]: features = ["Serving Size", "Total Fat 100g", "Saturated Fat 100g", "T
        rans Fat 100g", "Carbohydrates 100g"]
        X = ayenapapas[features]
        Xdf = X
        #standardize only the "total"
        z = StandardScaler()
        z.fit(X[features])
        X[features] = z.fit transform(X[features])
        n_{clusters} = [2,3,4,5]
        sil = []
        for n in n clusters:
            KM = KMeans(n clusters = n)
            KM.fit(X)
            membership = KM.predict(X)
            sil.append(silhouette score(X, membership))
            colName = str(n) + "assign"
            Xdf[colName] = membership
        print(sil)
```

[0.8179886477427847, 0.8345835290228476, 0.8579736121542978, 0.75392 59397471559]



Out[10]: <ggplot: (309496893)>





Out[12]: <ggplot: (310877585)>

2. Explain which variables you're using to predict the outcome.

The variables I am using to predict the outcome is total fat 100g, saturated fat 100g, trans fat 100g, and carbohydrates 100g. I am using these variables to predict the outcome because usually all of these variables are very unhealthy to the human body. Trans fat and saturated fat create LDL cholesterol that can lead to coronary artery disease. With too much carbohydrates can lead to high blood sugar levels that can result in more fat to build for the human body and possibly lead to diabetes and other health issues.

3. Evaluate how the model performed using silhoutte scores. Look at different numbers of clusters (like k = 3, 5). Which number of clusters is the best fit?

The fourth cluster is the best fit because it has the highest percentage, 85.80%, compared to the rest of the clusters.

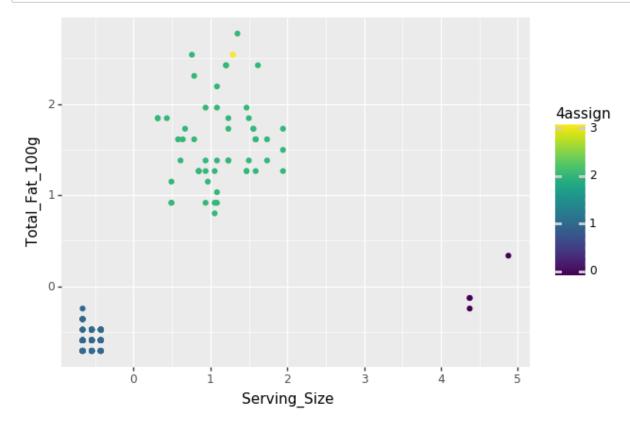
4. Describe the clusters

Looking at the graph saturated fat 100g, the blue colored points show that with no servings the value of the saturated fat would be 0g or below 0g. The green and yellow colored points is in the range for 0.5-2 servings. This group has the highest amount of saturated fat. Surprisingly, the purple points that have more than 4 servings have a lower saturated fat than serving size of 1 and 2 (green and yellow points). Looking at the graph for trans fat, most of the points (color blue, green, purple) have a trans fat of 0g. The yellow point is the only one to have a value higher than 0g. We can assume that this is an outlier.

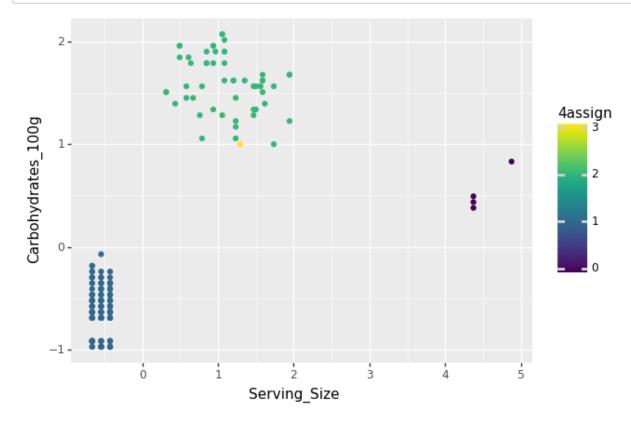
Gaussian Mixture Model

```
features = ["Serving Size", "Total Fat 100g", "Saturated Fat 100g", "T
In [36]:
         rans Fat 100g", "Carbohydrates 100g"]
         X = ayenapapas[features]
         Xdf = X
         z = StandardScaler()
         z.fit(X[features])
         X[features] = z.fit_transform(X[features])
         n components = [2,3,4,5]
         sil = []
         for n in n components:
             gmm = GaussianMixture(n components = n)
             qmm.fit(X)
             clusters = gmm.predict(X)
             sil.append(silhouette score(X, clusters))
             colName = str(n) + "assign"
             Xdf[colName] = clusters
         print(sil)
```

[0.8179886477427847, 0.8345835290228476, 0.8579736121542978, 0.76853 36362576782]



Out[15]: <ggplot: (311303013)>



Out[17]: <ggplot: (311303109)>

2. Explain which variables you're using to predict the outcome.

The variables I am using to predict the outcome is total fat 100g, saturated fat 100g, trans fat 100g, and carbohydrates 100g. I am using these variables to predict the outcome because usually all of these variables are very unhealthy to the human body. Trans fat and saturated fat create LDL cholesterol that can lead to coronary artery disease. With too much carbohydrates can lead to high blood sugar levels that can result in more fat to build for the human body and possibly lead to diabetes and other health issues.

3. Evaluate how the model performed using silhoutte scores. Look at different numbers of clusters (like k = 3, 5). Which number of clusters of clusters is the best fit?

The fourth cluster is the best fit because it has the highest percentage, 85.80%, compared to the rest of the

clusters.

4. Describe the clusters

Looking at the graph total fat, the blue colored points show that with no servings the value of the total fat would be 0g or below 0g. The green and yellow colored points is in the range for 0.5-2 servings. This group has the highest amount of total fat. Surprisingly, the purple points that have more than 4 servings have a lower total fat than serving size of 0.5-2 (green and yellow points). Looking at the graph carbohydrates, the blue colored points show that with no servings the value of the carbohydrates would be 0g or below 0g. The green and yellow colored points is in the range for 0.5-2 servings. This group has the highest amount of carbohydrates. Surprisingly, the purple points that have more than 4 servings have a lower total fat than serving size of 0.5-2 (green and yellow points).

At the end:

1. Compare the clusters obtained by the two models. Overall are they similar? or really different?

The clusters by the two models are very similar. Both models had the same high percentage of 85.80%. Both clusters also indicate that with a serving size or 0.5-2 would result in a lot of total fat, trans fat, saturated fat, and carbohydrates.