glucose-monitoring-final

December 11, 2023

1 A Data Analysis on the Study "CGM Intervention in Teens and Young Adults with Type 1 Diabetes"

The aim of this notebook is to perform statistical anaylsis on the study "CGM Intervention in Teens and Young Adults with Type 1 Diabetes".

For the study the device that was implemented for the CGM patients was the Dexcom G5 which is a class II medical device. A class II medical device is an intermediate-risk device that must meet general controls as well and special controls.

Link to the clinical study: https://classic.clinicaltrials.gov/ProvidedDocs/32/NCT03240432/Prot_SAP_000.pdf

The Dexcom G5 transmits real time glucose readings every 5 minutes to a mobile medical app and will sound an alarm when a patient glucose level reaches too high or too low.

Type 1 diabetes is generally caused by the autoimmmune destruction of the insulin producing b-cells found in the pancreas. This leads the disease to manifest itself in the form of hyperglycaemia, which is high blood glucose level. This occurs due the insulin producing cells being destroyed, thus there is no insulin available to break down the blood glucose [1].

About 8% of people who have diabetes will be diagnosed with type 1. Along with this 90% of children and young adults with diabetes will have type 1. [2]

[ ]:
```
#Install packages
import warnings
warnings.filterwarnings("ignore")
import numpy as np
import pandas as pd
import io
import requests
import matplotlib.pyplot as plt
from tabulate import tabulate
import scipy.stats
import math
```

The necessary packages that are needed to complete the statistical anaylsis are installed.

For this analysis I will be looking at how CGM compares with that of blood glucose monitoring, through comparing the overall blood glucose level and glycemic variability. The hypothesis presented in this study are as follows:

1. Null hypothesis: There is no difference in blood glucose level at week 26 between those using BGM and CGM
2. Alternative hypothesis: There is a nonzero difference in blood glucose level at week 26 between those using BGM and CGM.

This will be calculated using a significance level of 0.05.

[ ]:
```
path="/content/drive/MyDrive/Python/roster2.csv"
from google.colab import data_table
data_table.enable_dataframe_formatter()
df1=pd.read_csv(path)
df1
```

[ ]:
```
     RecID  PtID  SiteID          EnrollDt            RandDt TrtGroup  \
0       10    70      11  29/01/2000 00:00  13/02/2000 14:28      CGM
1       43    47      11  01/03/2000 00:00  15/03/2000 09:41      BGM
2       44   136      11  02/03/2000 00:00  18/03/2000 15:06      BGM
3       48    39      11  08/03/2000 00:00  24/03/2000 11:38      CGM
4       62    91      11  23/03/2000 00:00  07/04/2000 14:56      CGM
..     …     …     …               …                 …      …
179    132   168       3  25/05/2000 00:00  14/07/2000 15:01      BGM
180    138    71       3  02/06/2000 00:00  17/06/2000 12:40      CGM
181    166    67       3  30/07/2000 00:00               NaN      NaN
182    173   130       3  20/08/2000 00:00  06/09/2000 15:39      CGM
183    177   184       3  31/08/2000 00:00  28/09/2000 16:34      BGM

     AgeAsOfEnrollDt         StudyPhase Phase1PtStatus Phase2PtStatus  \
0                 16  Observational Ext      Completed            NaN
1                 21      Extension RCT      Completed      Completed
2                 19      Extension RCT      Completed      Completed
3                 15  Observational Ext      Completed            NaN
4                 15  Observational Ext      Completed            NaN
..               …                …            …            …
179               14        Primary RCT        Dropped            NaN
180               15  Observational Ext      Completed            NaN
181               22        Primary RCT        Dropped            NaN
182               17  Observational Ext      Completed            NaN
183               14      Extension RCT      Completed      Completed

    Phase3PtStatus       Phase2RandDt      Phase2StartDt Phase2TrtGroup  \
0        Completed                NaN                NaN            NaN
1              NaN   16/09/2000 16:44   16/09/2000 00:00         Alarms
2              NaN   17/09/2000 15:18   17/09/2000 00:00      No Alarms
3        Completed                NaN                NaN            NaN
4        Completed                NaN                NaN            NaN
..             …                …                …            …
179            NaN                NaN                NaN            NaN
180      Completed                NaN                NaN            NaN
```

```
181            NaN                NaN                NaN              NaN
182      Completed                NaN                NaN              NaN
183            NaN   30/03/2001 16:12   30/03/2001 00:00           Alarms

     Phase3RandDt      Phase3StartDt  Phase3TrtGroup
0             NaN   13/08/2000 00:00             NaN
1             NaN                NaN             NaN
2             NaN                NaN             NaN
3             NaN   17/09/2000 00:00             NaN
4             NaN   07/10/2000 00:00             NaN
..            …               …              …
179           NaN                NaN             NaN
180           NaN   13/12/2000 00:00             NaN
181           NaN                NaN             NaN
182           NaN   10/03/2001 00:00             NaN
183           NaN                NaN             NaN

[184 rows x 17 columns]
```

A dataframe was created using the roster data collected during the trial. The roster dataframe provides us with information which included, the ages of the patients, the treatment group, if the patient completed each phase of the trial.

The trial was split into two main phases:

1. Phase 1: Randomized Trial
2. Phase 2: Extension Phase 2nd Randomization

Phase 1 involved screening, blinded CGM and baseline before randomization took place. If a pateint failed at any of the pre-trial testing such as ineligible HbA1c they were dropped from the trial. Once admitted onto the trial the participants were randomized into a CGM and BGM group. Both groups were monitored for 26 weeks, with in person and over the phone check ups. In this study the BGM group was the control group.

Phase 2 began after the 26 week visit from phase 1. Participants who were in the CGM group from phase one then got to choose if they would have the alarm on or off for their CGM device. Participents in the BGM group of phase 1 were now to recieve CGM. This time however they were randomised into 2 groups to deteremine whether their device would have alarms or not.

For this analysis I will only be considering Phase 1 of the trial

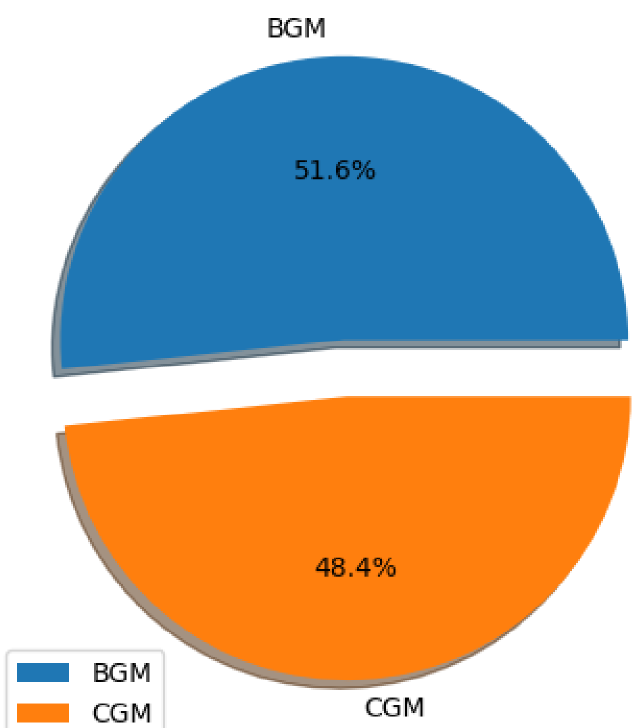
[ ]:
```
df1.groupby('TrtGroup').count()
```

[ ]:
```
          RecID  PtID  SiteID  EnrollDt  RandDt  AgeAsOfEnrollDt  StudyPhase  \
TrtGroup
BGM          79    79      79        79      79               79          79
CGM          74    74      74        74      74               74          74

          Phase1PtStatus  Phase2PtStatus  Phase3PtStatus  Phase2RandDt  \
TrtGroup
```

```
BGM                      79               32               38             32
CGM                      74                0               70              0

          Phase2StartDt  Phase2TrtGroup  Phase3RandDt  Phase3StartDt  \
TrtGroup
BGM                  32              32             0             38
CGM                   0               0             0             70

          Phase3TrtGroup
TrtGroup
BGM                    0
CGM                    0
```

The groupby function was used to group the treatment groups togther to show the number of patients in each section of the trial, BGM and CGM.

[ ]:
```
y = np.array([79, 74])
mylabels = ['BGM', 'CGM']
myexplode =([0.2,0])
plt.pie(y, labels=mylabels, explode = myexplode, shadow = True, autopct = '%1.
 ↪1f%%')
plt.legend()
plt.show()
```



The information that was presented in the above table due to the groupby function was then able to be processed and presented in the form of a pie chart.

```
[ ]: path="/content/drive/MyDrive/Python/Screening.csv"
     from google.colab import data_table
     data_table.enable_dataframe_formatter()
     df2=pd.read_csv(path)
     df2
```

```
Warning: Total number of columns (63) exceeds max_columns (20). Falling back to
pandas display.
```

```
[ ]:      RecID  PtID  ParentLoginVisitID  EligCritMet  ExclCritAbsent Sex  \
     0       12    70                  16            1               1   M
     1       41    47                  82            1               1   F
     2       42   136                  91            1               1   F
     3       45    39                 102            1               1   M
     4       69    91                 228            1               1   M
     ..     …     …                   …            …               …  ..
     166    128   180                 561            1               1   M
     167    131   168                 612            1               1   F
     168    132    71                 623            1               1   M
     169    159   130                 955            1               1   F
     170    164   184                1034            1               1   F

                    Ethnicity                             Race            DiagDt  \
     0         Hispanic or Latino         Black/African American  21/03/1989 00:00
     1     Not Hispanic or Latino                          White  11/09/1979 00:00
     2     Not Hispanic or Latino                          White  20/09/1989 00:00
     3     Not Hispanic or Latino                          White  11/07/1987 00:00
     4     Not Hispanic or Latino                          White  04/05/1996 00:00
     ..                       …                              …                 …
     166   Not Hispanic or Latino  American Indian/Alaskan Native               NaN
     167   Not Hispanic or Latino                          White               NaN
     168   Not Hispanic or Latino                          White  07/11/1998 00:00
     169   Not Hispanic or Latino                          White  20/06/1999 00:00
     170   Not Hispanic or Latino                          White               NaN

          DiagDtApprox  …  PreExistMedCond  PtCurrMed  SHNumEverB  SHMostRecentB  \
     0             NaN  …              Yes        Yes         NaN            NaN
     1             NaN  …              Yes        Yes         NaN            NaN
     2             1.0  …              Yes        Yes         NaN            NaN
     3             1.0  …              Yes        Yes         NaN            NaN
     4             NaN  …              Yes         No         NaN            NaN
     ..              …  …                …          …           …              …
     166           NaN  …              Yes        Yes         NaN            NaN
     167           NaN  …              Yes        Yes         NaN            NaN
     168           1.0  …               No         No         NaN            NaN
```

```
169           NaN  ...                No         No          NaN            NaN
170           NaN  ...                No        Yes          NaN            NaN

    SHLast12MonthsB  SHSeizComaNumB SHSeizComaLast12MonthsB  DKANumEverB  \
0               NaN             NaN                     NaN          NaN
1               NaN             NaN                     NaN          NaN
2               NaN             NaN                     NaN          NaN
3               NaN             NaN                     NaN          NaN
4               NaN             NaN                     NaN          NaN
..              ...             ...                     ...          ...
166             NaN             NaN                     NaN          NaN
167             NaN             NaN                     NaN          NaN
168             NaN             NaN                     NaN          NaN
169             NaN             NaN                     NaN          NaN
170             NaN             NaN                     NaN          NaN

    DKAMostRecentB  DKALast12MonthsB
0              NaN               NaN
1              NaN               NaN
2              NaN               NaN
3              NaN               NaN
4              NaN               NaN
..             ...               ...
166            NaN               NaN
167            NaN               NaN
168            NaN               NaN
169            NaN               NaN
170            NaN               NaN

[171 rows x 63 columns]
```

A new dataframe was created using the data from the intial screening, which provided the background information for potential participants of the trial.

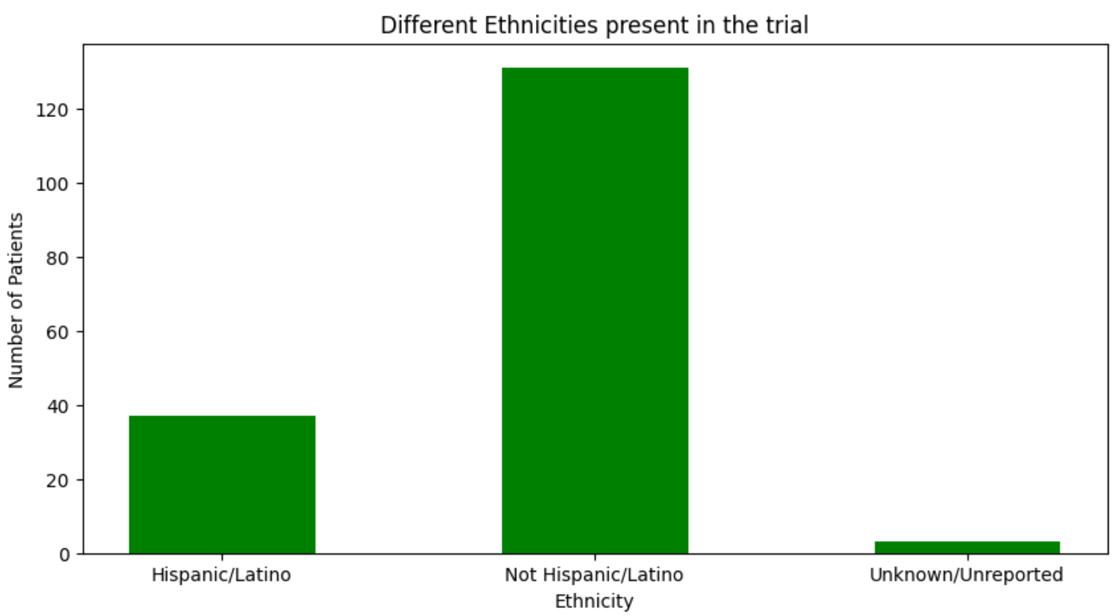
```
[ ]: df_crosstab = pd.crosstab(df2['Ethnicity'],
                               df2['Race'])
     print(df_crosstab)
```

```
Race                    American Indian/Alaskan Native  Asian  \
Ethnicity
Hispanic or Latino                                   0      0
Not Hispanic or Latino                               1      6
Unknown/not reported                                 0      0

Race                    Black/African American  More than one race  \
Ethnicity
Hispanic or Latino                           3                   4
Not Hispanic or Latino                      12                   6
```

```
Unknown/not reported                            0                    1

Race                    Unknown/not reported  White
Ethnicity
Hispanic or Latino                         9     21
Not Hispanic or Latino                     0    106
Unknown/not reported                       0      2
```

A contingency table was created to show the different ethnicities and races of the patients completing the study.

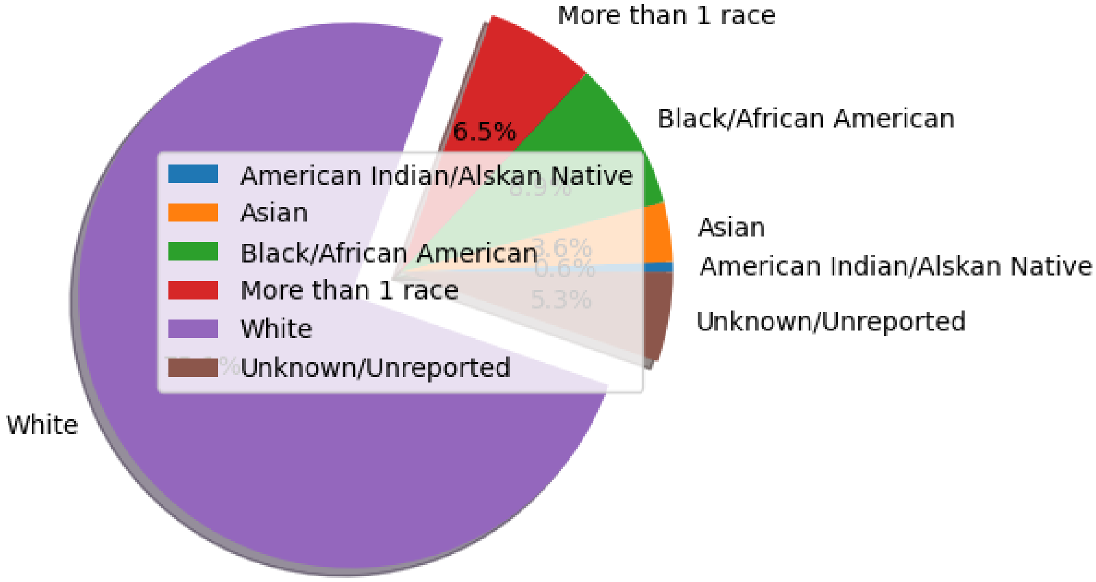
```
[ ]: data = {'Hispanic/Latino':37, 'Not Hispanic/Latino':131, 'Unknown/Unreported':3}
fig = plt.figure(figsize = (10,5))
Ethnicity = list(data.keys())
Values = list(data.values())
plt.bar(Ethnicity, Values, color = 'green', width = 0.5)
plt.xlabel('Ethnicity')
plt.ylabel('Number of Patients')
plt.title('Different Ethnicities present in the trial')
plt.show()
```



The data from the contingency table was used to create this bar chart showing the different ethnicities

```
[ ]: y = np.array([1, 6, 15, 11, 127, 9])
mylabels = ['American Indian/Alskan Native', 'Asian', 'Black/African American',␣
 ↪'More than 1 race', 'White', 'Unknown/Unreported']
myexplode =([0,0,0,0,0.2,0])
```

```
plt.pie(y, labels=mylabels, explode = myexplode, shadow = True, autopct = '%1.
  ↪1f%%')
plt.legend()
plt.show()
```



Following on a pie chart was created showing the different races.

[ ]:
```
path="/content/drive/MyDrive/Python/adverseevent.csv"
from google.colab import data_table
data_table.enable_dataframe_formatter()
df3=pd.read_csv(path)
df3
```

```
Warning: Total number of columns (47) exceeds max_columns (20). Falling back to
pandas display.
```

[ ]:
```
   RecID  PtID  ParentLoginVisitID        AENotifiedDt       MedicalCondition  \
0     20   154                 NaN  03/09/2000 00:00  Diabetic ketoacidosis
1     15   107                 NaN  04/08/2000 00:00           Hypoglycemia
2     30     1                 NaN  11/01/2001 00:00             Depression
3     34    52                 NaN  08/02/2001 00:00           Hypoglycemia
4     35    52                 NaN  11/08/2000 00:00  Diabetic ketoacidosis
5     23    87                 NaN  08/10/2000 00:00               Vomiting
6     40   106                 NaN  05/07/2001 00:00          Pyelonephritis
```

7	13	56	NaN	22/06/2000 00:00	Panic attack
8	21	144	NaN	17/08/2000 00:00	Syncope
9	25	144	NaN	06/11/2000 00:00	Fainting
10	24	183	NaN	03/09/2000 00:00	Hyperglycemia
11	17	148	NaN	14/09/2000 00:00	Suicidal ideation
12	41	95	NaN	22/08/2001 00:00	Hypoglycemia
13	42	95	NaN	22/08/2001 00:00	Hypoglycemia
14	39	131	NaN	25/04/2001 00:00	Diabetic ketoacidosis
15	6	72	NaN	24/04/2000 00:00	Allergic skin reaction
16	31	116	NaN	28/12/2000 00:00	Hyperglycemia
17	27	27	NaN	17/12/2000 00:00	Hyperglycemia
18	10	140	NaN	29/06/2000 00:00	Appendicitis
19	28	94	NaN	31/12/2000 00:00	Diabetic ketoacidosis
20	2	161	NaN	03/03/2000 00:00	Hyperglycemia
21	5	161	NaN	07/04/2000 00:00	Suicidal ideation
22	7	85	NaN	18/06/2000 00:00	Pregnancy
23	32	88	NaN	28/04/2001 00:00	Uterine fibroid
24	9	133	NaN	30/06/2000 00:00	Concussion
25	37	133	NaN	30/06/2000 00:00	Hypoglycemia
26	14	57	NaN	15/08/2000 00:00	Hyperglycemia
27	3	152	NaN	03/03/2000 00:00	Hypoglycaemic seizure
28	8	152	NaN	13/06/2000 00:00	Hypoglycemia
29	36	6	NaN	10/03/2001 00:00	Hypoglycemia
30	22	43	NaN	04/10/2000 00:00	Gastroenteritis
31	33	96	NaN	01/07/2000 00:00	Hypoglycemia
32	18	71	NaN	22/09/2000 00:00	Diabetic ketoacidosis

	MedicalConditionMM	AdverseEventType	AEOnsetDt	AEPrEnroll	\
0	Diabetic ketoacidosis	NaN	03/09/2000 00:00	No	
1	Hypoglycemia	NaN	04/08/2000 00:00	No	
2	Depression	NaN	04/01/2001 00:00	Yes	
3	Hypoglycemia	NaN	07/02/2001 00:00	No	
4	Diabetic ketoacidosis	NaN	05/07/2000 00:00	Yes	
5	Vomiting	NaN	08/10/2000 00:00	No	
6	Pyelonephritis	NaN	17/06/2001 00:00	No	
7	Panic attack	NaN	08/06/2000 00:00	No	
8	Syncope	NaN	13/08/2000 00:00	No	
9	Fainting	NaN	05/11/2000 00:00	No	
10	Hyperglycemia	NaN	02/09/2000 00:00	No	
11	Suicidal ideation	NaN	14/09/2000 00:00	Yes	
12	Hypoglycemia	NaN	20/07/2001 00:00	No	
13	Hypoglycemia	NaN	22/07/2001 00:00	No	
14	Diabetic ketoacidosis	NaN	24/04/2001 00:00	Yes	
15	Allergic skin reaction	NaN	24/04/2000 00:00	No	
16	Hyperglycemia	NaN	16/12/2000 00:00	No	
17	Hyperglycemia	NaN	17/12/2000 00:00	No	
18	Appendicitis	NaN	13/06/2000 00:00	No	

19	Diabetic ketoacidosis	NaN	12/12/2000 00:00	No
20	Hyperglycemia	NaN	28/02/2000 00:00	No
21	Suicidal ideation	NaN	27/03/2000 00:00	No
22	Pregnancy	NaN	06/05/2000 00:00	No
23	Uterine fibroid	NaN	22/12/2000 00:00	No
24	Concussion	NaN	26/05/2000 00:00	No
25	Hypoglycemia	NaN	26/05/2000 00:00	No
26	Hyperglycemia	NaN	15/08/2000 00:00	No
27	Hypoglycaemic seizure	NaN	27/02/2000 00:00	No
28	Hypoglycemia	NaN	13/06/2000 00:00	No
29	Hypoglycemia	NaN	04/03/2001 00:00	No
30	Gastroenteritis	NaN	04/10/2000 00:00	No
31	Hypoglycemia	NaN	01/07/2000 00:00	No
32	Diabetic ketoacidosis	NaN	21/09/2000 00:00	Yes

	AENotedStdyVisExam	…	MMAESerious	MMUnexpected	AERelStdyDrugDevice	\
0	No	…	Yes	NaN	NaN	
1	No	…	Yes	NaN	NaN	
2	No	…	Yes	NaN	NaN	
3	No	…	Yes	NaN	NaN	
4	No	…	Yes	NaN	NaN	
5	No	…	No	No	NaN	
6	No	…	Yes	NaN	NaN	
7	No	…	No	NaN	NaN	
8	No	…	Yes	NaN	NaN	
9	No	…	Yes	NaN	NaN	
10	No	…	Yes	NaN	NaN	
11	No	…	Yes	NaN	NaN	
12	No	…	No	NaN	NaN	
13	No	…	No	NaN	NaN	
14	No	…	Yes	NaN	NaN	
15	No	…	No	No	NaN	
16	No	…	No	NaN	NaN	
17	No	…	No	NaN	NaN	
18	No	…	Yes	NaN	NaN	
19	No	…	No	NaN	NaN	
20	No	…	No	NaN	NaN	
21	No	…	Yes	NaN	NaN	
22	No	…	No	NaN	NaN	
23	No	…	Yes	NaN	NaN	
24	No	…	No	NaN	NaN	
25	No	…	Yes	NaN	NaN	
26	No	…	No	NaN	NaN	
27	No	…	Yes	NaN	NaN	
28	No	…	Yes	NaN	NaN	
29	No	…	Yes	NaN	NaN	
30	No	…	No	NaN	NaN	

```
31                 No  …          Yes          NaN                    NaN
32                 No  …          Yes          NaN                    NaN

   AERelStdyDrugDeviceUncertain MMHospDiscRptObtained  \
0                           NaN     No, Not Requested
1                           NaN     No, Not Requested
2                           NaN     No, Not Requested
3                           NaN     No, Not Requested
4                           NaN     No, Not Requested
5                           NaN     No, Not Requested
6                           NaN     No, Not Requested
7                           NaN     No, Not Requested
8                           NaN     No, Not Requested
9                           NaN     No, Not Requested
10                          NaN     No, Not Requested
11                          NaN     No, Not Requested
12                          NaN     No, Not Requested
13                          NaN     No, Not Requested
14                          NaN     No, Not Requested
15                          NaN     No, Not Requested
16                          NaN     No, Not Requested
17                          NaN     No, Not Requested
18                          NaN     No, Not Requested
19                          NaN     No, Not Requested
20                          NaN     No, Not Requested
21                          NaN     No, Not Requested
22                          NaN     No, Not Requested
23                          NaN     No, Not Requested
24                          NaN     No, Not Requested
25                          NaN     No, Not Requested
26                          NaN     No, Not Requested
27                          NaN     No, Not Requested
28                          NaN     No, Not Requested
29                          NaN     No, Not Requested
30                          NaN     No, Not Requested
31                          NaN     No, Not Requested
32                          NaN     No, Not Requested

         AERelStdyTrtHighLvl AERelStdyTrtWhich AERelStdyDrugDeviceHighLvl  \
0                        NaN               NaN                        NaN
1                        NaN               NaN                        NaN
2                        NaN               NaN                        NaN
3                        NaN               NaN                        NaN
4                        NaN               NaN                        NaN
5   Study diagnostic procedure             NaN                        NaN
6                        NaN               NaN                        NaN
7                        NaN               NaN                        NaN
```

8	NaN	NaN	NaN
9	NaN	NaN	NaN
10	NaN	NaN	NaN
11	NaN	NaN	NaN
12	NaN	NaN	NaN
13	NaN	NaN	NaN
14	NaN	NaN	NaN
15	NaN	NaN	NaN
16	NaN	NaN	NaN
17	NaN	NaN	NaN
18	NaN	NaN	NaN
19	NaN	NaN	NaN
20	NaN	NaN	NaN
21	NaN	NaN	NaN
22	NaN	NaN	NaN
23	NaN	NaN	NaN
24	NaN	NaN	NaN
25	NaN	NaN	NaN
26	NaN	NaN	NaN
27	NaN	NaN	NaN
28	NaN	NaN	NaN
29	NaN	NaN	NaN
30	NaN	NaN	NaN
31	NaN	NaN	NaN
32	NaN	NaN	NaN

	AERelStdyDrugDeviceWhich	MMAERelStdyTrtHighLvl
0	NaN	NaN
1	NaN	NaN
2	NaN	NaN
3	NaN	NaN
4	NaN	NaN
5	NaN	Study diagnostic procedure
6	NaN	NaN
7	NaN	NaN
8	NaN	NaN
9	NaN	NaN
10	NaN	NaN
11	NaN	NaN
12	NaN	NaN
13	NaN	NaN
14	NaN	NaN
15	NaN	NaN
16	NaN	NaN
17	NaN	NaN
18	NaN	NaN
19	NaN	NaN

```
20                      NaN                        NaN
21                      NaN                        NaN
22                      NaN                        NaN
23                      NaN                        NaN
24                      NaN                        NaN
25                      NaN                        NaN
26                      NaN                        NaN
27                      NaN                        NaN
28                      NaN                        NaN
29                      NaN                        NaN
30                      NaN                        NaN
31                      NaN                        NaN
32                      NaN                        NaN

[33 rows x 47 columns]
```

Another dataframe was created to show the data collected on adverse events that occured during the trial. An adverse event is "any untoward medical occurence in a study participant, irrespective of the relationship between the adverse event and the device(s) under investigation."

[ ]:
```
df3.groupby('AEIntensity').count()
```

```
Warning: Total number of columns (46) exceeds max_columns (20). Falling back to
pandas display.
```

[ ]:
```
             RecID  PtID  ParentLoginVisitID  AENotifiedDt  MedicalCondition  \
AEIntensity
Mild             4     4                   0             4                 4
Moderate        16    16                   0            16                16
Severe          13    13                   0            13                13

             MedicalConditionMM  AdverseEventType  AEOnsetDt  AEPrEnroll  \
AEIntensity
Mild                          4                 0          4           4
Moderate                     16                 0         16          16
Severe                       13                 0         13          13

             AENotedStdyVisExam  …  MMAESerious  MMUnexpected  \
AEIntensity                      …
Mild                          4  …            4             2
Moderate                     16  …           16             0
Severe                       13  …           13             0

             AERelStdyDrugDevice  AERelStdyDrugDeviceUncertain  \
AEIntensity
Mild                           0                             0
Moderate                       0                             0
```

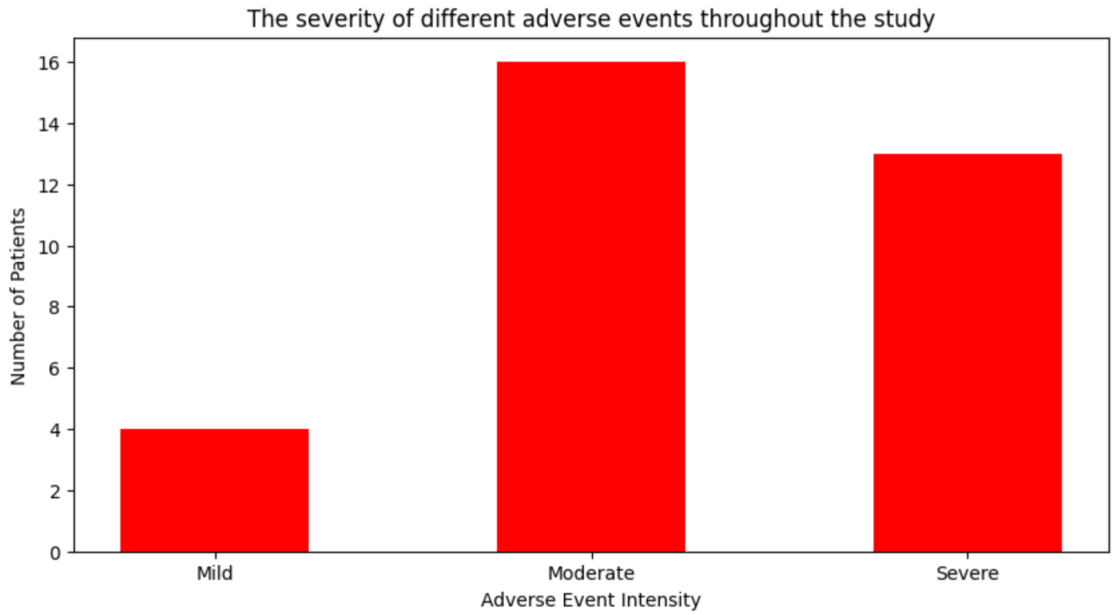
```
Severe                              0                               0

             MMHospDiscRptObtained  AERelStdyTrtHighLvl  AERelStdyTrtWhich  \
AEIntensity
Mild                            4                    1                  0
Moderate                       16                    0                  0
Severe                         13                    0                  0

             AERelStdyDrugDeviceHighLvl  AERelStdyDrugDeviceWhich  \
AEIntensity
Mild                                  0                         0
Moderate                              0                         0
Severe                                0                         0

             MMAERelStdyTrtHighLvl
AEIntensity
Mild                            1
Moderate                        0
Severe                          0

[3 rows x 46 columns]
```

Groupby was used to group the events based on their severity. For the study an adverse event was rated on a three point scale as either mild, moderate or severe. As this is just a measures of intensity a severe event may not be that serious. How the intensity rating was decided is seen below.

1. Mild: Usually transient, requires no special treatment, and does not interfere with the participant's daily activities
2. Moderate: Usually causes a low level of inconvience or concern to the participant and may interfere with daily activities, but is usually ameliorated by simple therapeutic measures
3. Severe: Interrupts a participants's usual daily activities and generally requires systemic drug therapy or other treatment.

Whether or not the adverse event was caused due to the study will be decided by the study investigator.

[ ]:
```
data = {'Mild':4, 'Moderate':16, 'Severe':13}
fig = plt.figure(figsize = (10,5))
Adverse_event_intensity = list(data.keys())
Values = list(data.values())
plt.bar(Adverse_event_intensity, Values, color = 'red', width = 0.5)
plt.xlabel('Adverse Event Intensity')
plt.ylabel('Number of Patients')
plt.title('The severity of different adverse events throughout the study')
plt.show()
```



This data was then visualised in the bar chart.

[ ]:
```
path="/content/drive/MyDrive/Python/Adverse event.csv"
from google.colab import data_table
data_table.enable_dataframe_formatter()
df4=pd.read_csv(path)
df4
```

```
Warning: Total number of columns (31) exceeds max_columns (20). Falling back to
pandas display.
```

[ ]:
```
   RecID  PtID  ParentLoginVisitID        DKAOccurDt  DKAOccurDtApprox  \
0      4   154                 NaN  03/09/2000 00:00               NaN
1     12    52                 NaN  05/07/2000 00:00               NaN
2      7   183                 NaN  02/09/2000 00:00               NaN
3     13   131                 NaN  24/04/2001 00:00               NaN
4     10   116                 NaN  16/12/2000 00:00               NaN
5      9    27                 NaN  17/12/2000 00:00               NaN
6     11    94                 NaN  12/12/2000 00:00               NaN
7      2   161                 NaN  28/02/2000 00:00               NaN
8      3    57                 NaN  15/08/2000 00:00               NaN
9      6    71                 NaN  21/09/2000 00:00               NaN

   DKAOccurDtUnk DKAMetCriteria  GlucLevel GlucLevelUnits  GlucLevelUnk  …  \
0            NaN     Cant deter      288.0          mg/dL           NaN  …
1            NaN     Definitely      600.0          mg/dL           NaN  …
2            NaN             No      328.0          mg/dL           NaN  …
```

```
3            NaN    Definitely      587.0          mg/dL            NaN  …
4            NaN            No      516.0          mg/dL            NaN  …
5            NaN            No      331.0          mg/dL            NaN  …
6            NaN    Definitely      617.0          mg/dL            NaN  …
7            NaN    Cant deter        NaN            NaN            1.0  …
8            NaN            No      532.0          mg/dL            NaN  …
9            NaN    Definitely      478.0          mg/dL            NaN  …

  CerebEdema  EventCauseStdyDev EventCauseNonStdy       DKAOutcome  \
0         No                 No               Yes            Other
1         No                 No               Yes  Fully recovered
2         No                 No                No  Fully recovered
3         No                 No               Yes  Fully recovered
4         No                 No               Yes  Fully recovered
5         No                 No               Yes  Fully recovered
6         No                Yes                No  Fully recovered
7    Unknown                 No                No  Fully recovered
8    Unknown                 No               Yes  Fully recovered
9    Unknown                Yes               Yes            Other

  SensorWear  SensorGluc  SensorGlucUnits SensorGlucUnk  AutoInsDelivWear  \
0        Yes         NaN              NaN           1.0                No
1    Unknown         NaN              NaN           NaN                No
2        Yes         NaN              NaN           1.0                No
3         No         NaN              NaN           NaN                No
4         No         NaN              NaN           NaN                No
5        Yes         NaN              NaN           1.0                No
6         No         NaN              NaN           NaN                No
7         No         NaN              NaN           NaN                No
8         No         NaN              NaN           NaN                No
9        Yes         NaN              NaN           1.0                No

  AutoInsDelivMode
0              NaN
1              NaN
2              NaN
3              NaN
4              NaN
5              NaN
6              NaN
7              NaN
8              NaN
9              NaN

[10 rows x 31 columns]
```

A dataframe was created on the data related to Diabetic Ketoacidosis, which involves symptoms such as polyuria, nausea or vomitting, serum ketones>1.5mmol/L or large/moderate keytones; either arterial blood pH<7.30 or venous pH<7.24 or serum biocarbonate<1.5; and treatment provided in a healthcare facility.

Diabetic ketoacidosis is a serious condition that can occur as a result of diabetes. The lack of insulin means the body cannot use sugar for energy so instead uses fat. However the breakdown of fat releases chemicals known as ketones. Ketones are acidic, and if let unchecked to build up can make the blood acidic.

Although it can affect people with type 2 diabetes it mainly occurs in people with type 1.

[ ]:
```
a = df4[['GlucLevel']].mean()
b = df4[['GlucLevel']].std()
print(a)
print(b)
```

```
GlucLevel    475.222222
dtype: float64
GlucLevel    127.762258
dtype: float64
```

From the calculations above we can see that when diabetic ketoacidosis occurs the average blood glucose is much higher than what it should be, highlighting how dangerous it can.

Along with this the standard deviation is also larger indication a high glycemic variability.

[ ]:
```
df_crosstab = pd.crosstab(df4['DKAMetCriteria'],
                          df4['DKAOutcome'])
print(df_crosstab)
```

```
DKAOutcome      Fully recovered  Other
DKAMetCriteria
Cant deter                    1      1
Definitely                    3      1
No                            4      0
```

A simply contingency table was created to show the outcome and if the event met the criteria for it to have thought to be caused by the trial itself.

[ ]:
```
path="/content/drive/MyDrive/Python/Device CGM.csv"
from google.colab import data_table
data_table.enable_dataframe_formatter()
df5=pd.read_csv(path)
df5
```

```
Warning: total number of rows (1048575) exceeds max_rows (20000). Falling back
to pandas display.
```

[ ]:
```
           RecID  PtID  ParentCITYDeviceUploadsID        DeviceDtTm  \
0        1539485    39                        651  21/04/2000 04:31
1        1539486    39                        651  21/04/2000 04:36
```

```
2        1539487    39                              651   21/04/2000 04:41
3        1539488    39                              651   21/04/2000 04:46
4        1539489    39                              651   21/04/2000 04:51
…             …    …                          …                …
1048570  2932875   152                              872   18/02/2000 14:44
1048571  2932876   152                              872   18/02/2000 14:49
1048572  2932877   152                              872   18/02/2000 14:54
1048573  2932878   182                              873   09/03/2000 13:34
1048574  2932879   182                              873   09/03/2000 13:34

          RecordType  Value  Units  SortOrd
0                CGM    135  mg/dL     7880
1                CGM    133  mg/dL     7881
2                CGM    133  mg/dL     7882
3                CGM    133  mg/dL     7883
4                CGM    134  mg/dL     7884
…                  …      …     …        …
1048570          CGM    233  mg/dL     3276
1048571          CGM    230  mg/dL     3277
1048572          CGM    229  mg/dL     3278
1048573  Calibration    215  mg/dL        1
1048574  Calibration    211  mg/dL        2

[1048575 rows x 8 columns]
```

This dataframe contains the readings obtained from the CGM device for the CGM group. As can be seen from the dataframe glucose values were taken every 5 seconds.

[ ]:
```
df5_1 = df5[['RecordType', 'Value',]]
df5_1.groupby(['RecordType', 'Value']).count()
```

[ ]:
```
Empty DataFrame
Columns: []
Index: [(CGM, 39), (CGM, 40), (CGM, 41), (CGM, 42), (CGM, 43), (CGM, 44), (CGM,
45), (CGM, 46), (CGM, 47), (CGM, 48), (CGM, 49), (CGM, 50), (CGM, 51), (CGM,
52), (CGM, 53), (CGM, 54), (CGM, 55), (CGM, 56), (CGM, 57), (CGM, 58), (CGM,
59), (CGM, 60), (CGM, 61), (CGM, 62), (CGM, 63), (CGM, 64), (CGM, 65), (CGM,
66), (CGM, 67), (CGM, 68), (CGM, 69), (CGM, 70), (CGM, 71), (CGM, 72), (CGM,
73), (CGM, 74), (CGM, 75), (CGM, 76), (CGM, 77), (CGM, 78), (CGM, 79), (CGM,
80), (CGM, 81), (CGM, 82), (CGM, 83), (CGM, 84), (CGM, 85), (CGM, 86), (CGM,
87), (CGM, 88), (CGM, 89), (CGM, 90), (CGM, 91), (CGM, 92), (CGM, 93), (CGM,
94), (CGM, 95), (CGM, 96), (CGM, 97), (CGM, 98), (CGM, 99), (CGM, 100), (CGM,
101), (CGM, 102), (CGM, 103), (CGM, 104), (CGM, 105), (CGM, 106), (CGM, 107),
(CGM, 108), (CGM, 109), (CGM, 110), (CGM, 111), (CGM, 112), (CGM, 113), (CGM,
114), (CGM, 115), (CGM, 116), (CGM, 117), (CGM, 118), (CGM, 119), (CGM, 120),
(CGM, 121), (CGM, 122), (CGM, 123), (CGM, 124), (CGM, 125), (CGM, 126), (CGM,
127), (CGM, 128), (CGM, 129), (CGM, 130), (CGM, 131), (CGM, 132), (CGM, 133),
```

```
(CGM, 134), (CGM, 135), (CGM, 136), (CGM, 137), (CGM, 138), …]

[838 rows x 0 columns]
```

The data was grouped togther by value and record type to show which values were actually taken from the CGM device and which were obtained for callibration of the device.

```
[ ]: CGM_glucose_value_total = df5['Value'].count()
     print(CGM_glucose_value_total)
```

```
1048575
```

The total number of glucose readings was calculated using the count function. This value is used in later calculations.

```
[ ]: CGM_glucose_values_in_sections = df5_1.groupby(pd.cut(df5_1['Value'], [0, 80,␣
      ↪180, 600 ])).count()
     print(CGM_glucose_values_in_sections)
```

```
            RecordType   Value
Value
(0, 80]          67806   67806
(80, 180]       409535  409535
(180, 600]      571234  571234
```

Using the groupby and cut functions the values were separted into three different range groups:

1. 0 - 80
2. 80 - 180
3. 180 - 600

These values were chosen as for a diabetic the normal blood glucose value range is between 80 and 180 mg/dL. Although they can vary due to different confounding factors such as if the person has ate recently, usually if the value goes below or above this range it can be considered hypoglycemia or hyperglycemia respectfully.

As stated earlier for a type 1 diabetic it is far more common fro them to experience hyperglycemia.

*Value 600 was chosen as no value went above this number.

```
[ ]: less_than_70 = (67806/CGM_glucose_value_total)*100
     between_70_150 = (409535/CGM_glucose_value_total)*100
     greater_than_150 = (571234/CGM_glucose_value_total)*100
     print(less_than_70)
     print(between_70_150)
     print(greater_than_150)
```

```
6.466490236749875
39.05633836397015
54.477171399279975
```

The values that were found above were then divided by the CGM_glucose_value_total, which was found earlier, and multiplied by to give the percentage of values in each group.

This was displayed in the table below.

[ ]:
```
myCGMdata = [
    ['<80', '6.46'],
    ['80<GL<180', '39.06'],
    ['>180', '54.48'],
]

head = ['CGM Glucose Value', 'Percentage of Values in that Range']
print(tabulate(myCGMdata, headers=head, tablefmt = 'grid'))
```

```
+---------------------+--------------------------------------+
| CGM Glucose Value   |   Percentage of Values in that Range |
+=====================+======================================+
| <80                 |                                 6.46 |
+---------------------+--------------------------------------+
| 80<GL<180           |                                39.06 |
+---------------------+--------------------------------------+
| >180                |                                54.48 |
+---------------------+--------------------------------------+
```

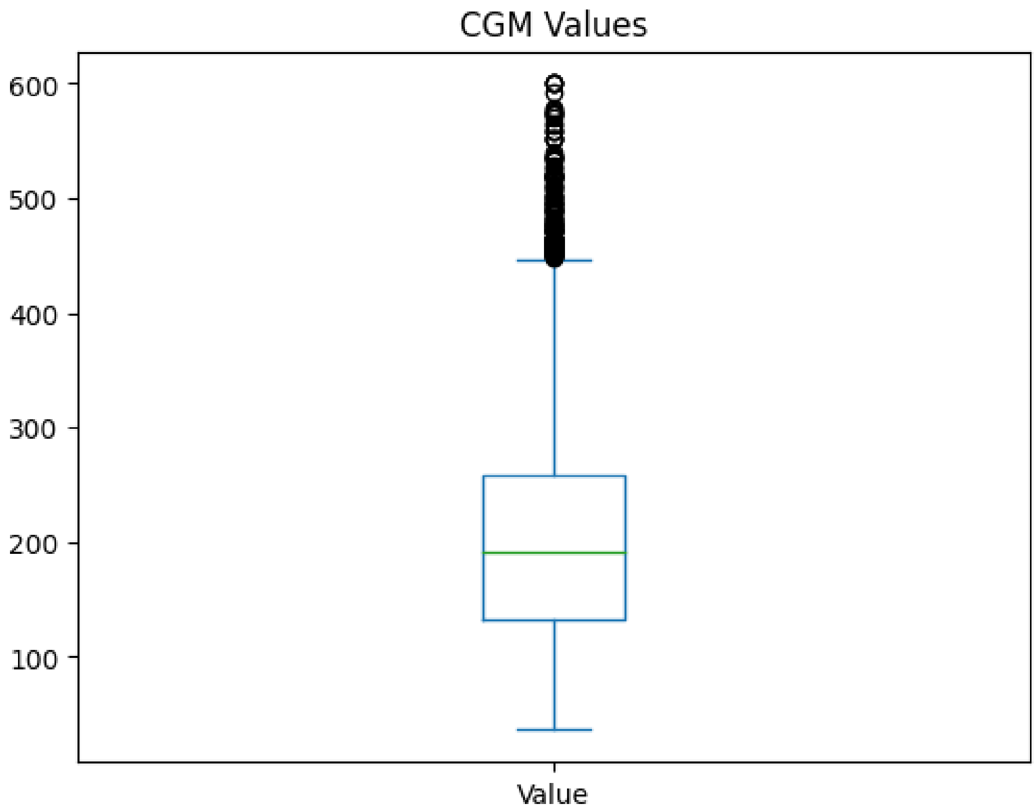
From the table it can be seen that the group that has the highest percentage is the greater than 180 group. This suggests that from the glucose values measured alot of the participants may have been verging on becoming hyperglycemic, however this table does not give an indicator of how far over the 180 mg/dL each value was.

This can be further investigated by comparing this data with dataframe 3, which holds the information about adverse events. This dataframe shows that 5 hyperglyemic events occurred throughout the study.

For this study however hyperglycemia was only classed as an adverse event if it met one of the following criteria:

1. The event involved DKA or;
2. In the absence of DKA if evaluation or treatmment was obtained at a healthcare provider facility

[ ]:
```
df5['Value'].plot(kind='box', title = 'CGM Values')
plt.show()
```



The data can also be displayed in a box plot showing the different values the CGM takes on throughout the study.

The box plot helps to visualise where most of the values fall which supports the calculations performed above.

[ ]:
```
path="/content/drive/MyDrive/Python/CGM RCT.csv"
from google.colab import data_table
data_table.enable_dataframe_formatter()
df6=pd.read_csv(path)
df6
```

```
Warning: total number of rows (1048575) exceeds max_rows (20000). Falling back
to pandas display.
```

[ ]:
```
        PtID              DeviceDtTm  Value TrtGroup  nightFlg  \
0         70  29JAN2000:16:11:21.000     93      CGM         0
1         70  29JAN2000:16:16:21.000     92      CGM         0
2         70  29JAN2000:16:21:21.000     96      CGM         0
3         70  29JAN2000:16:26:22.000    101      CGM         0
4         70  29JAN2000:16:31:21.000    107      CGM         0
…        …                       …     …      …         …
```

```
1048570    44  15JUL2000:17:54:09.000    186      BGM          0
1048571    44  15JUL2000:17:59:09.000    186      BGM          0
1048572    44  15JUL2000:18:04:09.000    193      BGM          0
1048573    44  15JUL2000:18:09:09.000    216      BGM          0
1048574    44  15JUL2000:18:14:09.000    227      BGM          0

                  visit                  period
0        Randomization           1) Baseline
1        Randomization           1) Baseline
2        Randomization           1) Baseline
3        Randomization           1) Baseline
4        Randomization           1) Baseline
…                  …                      …
1048570  13 week visit  2) Follow-up (Phase 1)
1048571  13 week visit  2) Follow-up (Phase 1)
1048572  13 week visit  2) Follow-up (Phase 1)
1048573  13 week visit  2) Follow-up (Phase 1)
1048574  13 week visit  2) Follow-up (Phase 1)

[1048575 rows x 7 columns]
```

[ ]:
```python
df6_1 = pd.DataFrame()
df6_1['DateTime'] = df6['DeviceDtTm']
df6_1['Glucose Value'] = df6['Value']
df6_1['Patient ID'] = df6['PtID']
df6_1['DateTime'] = pd.to_datetime(df6_1['DateTime'], format = '%d%b%Y:%H:%M:%S.
↪%f')
df6_1
```

```
Warning: total number of rows (1048575) exceeds max_rows (20000). Falling back
to pandas display.
```

[ ]:
```
                   DateTime  Glucose Value  Patient ID
0       2000-01-29 16:11:21             93          70
1       2000-01-29 16:16:21             92          70
2       2000-01-29 16:21:21             96          70
3       2000-01-29 16:26:22            101          70
4       2000-01-29 16:31:21            107          70
…                       …              …           …
1048570 2000-07-15 17:54:09            186          44
1048571 2000-07-15 17:59:09            186          44
1048572 2000-07-15 18:04:09            193          44
1048573 2000-07-15 18:09:09            216          44
1048574 2000-07-15 18:14:09            227          44

[1048575 rows x 3 columns]
```

From df6 a new dataframe named df6_1 was created to only show the DateTime, Glucose Value and Patient ID columns. Along with this the format of the DateTime column was adjusted so that it was able to represent the date and time in a more clear format.

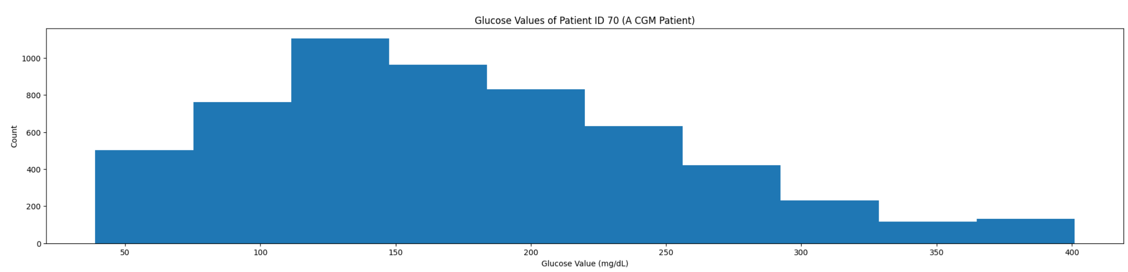
```
[ ]: df6_2 = df6_1[df6_1['Patient ID']==70]
     df6_2
```

```
[ ]:                   DateTime  Glucose Value  Patient ID
     0    2000-01-29 16:11:21             93          70
     1    2000-01-29 16:16:21             92          70
     2    2000-01-29 16:21:21             96          70
     3    2000-01-29 16:26:22            101          70
     4    2000-01-29 16:31:21            107          70
     …                   …              …           …
     5693 2000-08-05 15:30:03            315          70
     5694 2000-08-05 15:35:03            289          70
     5695 2000-08-05 15:40:03            309          70
     5696 2000-08-05 15:45:03            306          70
     5697 2000-08-05 15:50:03            293          70

     [5698 rows x 3 columns]
```

df_2 was created to only show the glucose values of Patient ID 70

```
[ ]: plt.figure(figsize=(25,5))
     plt.hist(df6_2['Glucose Value'] )
     plt.xlabel('Glucose Value (mg/dL)')
     plt.ylabel('Count')
     plt.title('Glucose Values of Patient ID 70 (A CGM Patient)')
```

```
[ ]: Text(0.5, 1.0, 'Glucose Values of Patient ID 70 (A CGM Patient)')
```



From df6_2 a histogram showing Patient ID 70's glucose values can be created.

```
[ ]: df6_2_1 = df6_1[df6_1['Patient ID']==44]
     df6_2_1
```

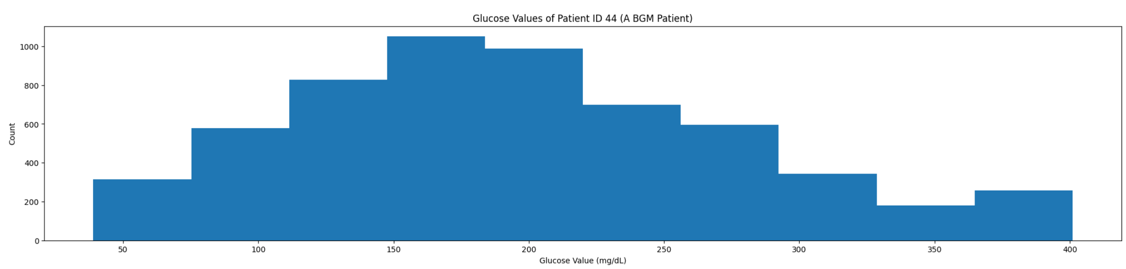
```
[ ]:                      DateTime  Glucose Value  Patient ID
     1042741 2000-03-25 18:48:32            107          44
```

```
1042742 2000-03-25 18:53:31           107           44
1042743 2000-03-25 18:58:31           106           44
1042744 2000-03-25 19:03:31           100           44
1042745 2000-03-25 19:08:31           103           44
…                      …            …         …
1048570 2000-07-15 17:54:09           186           44
1048571 2000-07-15 17:59:09           186           44
1048572 2000-07-15 18:04:09           193           44
1048573 2000-07-15 18:09:09           216           44
1048574 2000-07-15 18:14:09           227           44

[5834 rows x 3 columns]
```

df6_2_1 was created in the same way as df6_2 but this time it was to extract the glucose values of Patient Id 44.

```
[ ]: plt.figure(figsize=(25,5))
     plt.hist(df6_2_1['Glucose Value'] )
     plt.xlabel('Glucose Value (mg/dL)')
     plt.ylabel('Count')
     plt.title('Glucose Values of Patient ID 44 (A BGM Patient)')
```

```
[ ]: Text(0.5, 1.0, 'Glucose Values of Patient ID 44 (A BGM Patient)')
```



Again a histogram was created using the glucose values of Patient ID 44.

Patient ID 70 and 44's glucose values were extracted as 70 belongs to the CGM group whereas 44 belongs to the BGM. The histograms show that both patients blood glucose values follow a nealry normal distribution, which is important for later calculations.

A new dataframe was created using the data collected from the the randomised control trial, also known as Phase 1 of the study. This included information such as the glucose value, treatment group and which visit it was recorded at.

```
[ ]: df6_3 = df6[['TrtGroup', 'Value', 'visit']]
     print(df6_3)
```

```
        TrtGroup  Value          visit
0            CGM     93  Randomization
```

```
1             CGM     92  Randomization
2             CGM     96  Randomization
3             CGM    101  Randomization
4             CGM    107  Randomization
…               …    …            …
1048570       BGM    186  13 week visit
1048571       BGM    186  13 week visit
1048572       BGM    193  13 week visit
1048573       BGM    216  13 week visit
1048574       BGM    227  13 week visit

[1048575 rows x 3 columns]
```

[ ]:
```
x = df6_3.groupby(['TrtGroup', 'visit']).mean()
print(x)
y = df6_3.groupby(['TrtGroup', 'visit']).std()
print(y)
```

```
                            Value
TrtGroup visit
BGM      13 week visit  207.815593
         26 week visit  222.780212
         Randomization  209.203342
CGM      13 week visit  202.397047
         26 week visit  199.408356
         Randomization  211.729527
                           Value
TrtGroup visit
BGM      13 week visit  96.215428
         26 week visit  97.894132
         Randomization  96.755793
CGM      13 week visit  84.315317
         26 week visit  85.696603
         Randomization  94.019137
```

The groupby function was used to group the data togther by treatment group and visit. The mean and standard deviation functions were then applied to find the mean glucose value and the standard deviations at randomization (week 0 of the trial), week 13 and week 26 visits for the different treatment groups.

[ ]:
```
CGM_CV_randomization = (94.019/211.729)*100
CGM_CV_week26 = (85.697/199.408)*100
BGM_CV_randomization = (96.756/209.203)*100
BGM_CV_week26 = (97.894/222.780)*100
print(CGM_CV_randomization)
print(CGM_CV_week26)
print(BGM_CV_randomization)
print(BGM_CV_week26)
```

```
44.405348346235044
42.97570809596406
46.24981477321071
43.942005566029266
```

From the standard deviations I was able to calculate the coefficient of variation (CV). The CV summarizes the variation as a proportion of the mean value. This can be used instead of standard devaition as someone with a higher mean glucose level will also have a higher standard deviation. By using CV this helps to normalize glucose variability. [3]

Ideally most experts want to see a CV of 33% or lower. From the results above we can see that none of the the CV values meet this goal. However, we can also see that both the CV of the CGM and BGM did fall over the course of the size weeks. While BGM did have a bigger improvement, the CGM still has the lowest CV value meaning it has the least glucose variability.

[ ]:
```
J_CGM_rand = 0.001*(211.729 + 94.019)**2
J_CGM_26 = 0.001*(199.408 + 85.697)**2
J_BGM_rand = 0.001*(222.78 + 98.756)**2
J_BGM_26 = 0.001*(209.203 + 97.894)**2
print(J_CGM_rand)
print(J_CGM_26)
print(J_BGM_rand)
print(J_BGM_26)
```

```
93.48183950400004
81.28486102500001
103.385399296
94.30856740899998
```

Above the J-index has also been calculated for the CGM and BGM values at randomization and week 26. The J-index is similar to the CV value as it is also a parameter for measuring the average blood glucose level and its variability over time. [4]

From above again we can see that that both groups showed an improvement in variability from randomization to week 26. Along with this although BGM had the biggest difference CGM still had the lowest variability.

The J-index is still a relativitely new parameter for calculating glucose variability and has not yet been widely adopted by health-care proffesionals. CV is the more common parameter.

[ ]:
```
SE = math.sqrt(((8.31**2)/74) + ((1.135**2)/79))
T = (12.32 - 13.57)/(SE)
scipy.stats.t.sf(abs(T), df=73)
```

[ ]:
```
0.10180795365833413
```

As it can be seen from the 2 histograms created using the glucose values from Patient Id's 70 and 44, the glucose values follow a nearly normal distribution, meaning a T-test can be performed to find the p-value for the hypothesis test. As this was to compare the difference from randomization and week 26 for the CGM and BGM, the differences for CGM and BGM between the 2 weeks was calculated, and it was these values that were used in the calculation.

From this we got a p-value that is equal to 0.102. As this is bigger than the signficance level of 0.05, we fail to reject the null hypothesis, that was stated at the beginning of this notebook. This means that from the data provided there is currently not enough evidence to suggest that CGM leads to lower glucose variability compared to that of BGM.

References

[1] E. Hackett, A. Gallagher, N. Jacques (2013 March) "Type 1 diabetes: pathophysiology and diagnosis" *the Pharaceutical Journal* [online] https://pharmaceutical-journal.com/article/ld/type-1-diabetes-pathophysiology-and-diagnosis

[2] National Insititute for Health and Care Excellence (2023 July) "Diabetes - type 1: How common is it?" [online] https://cks.nice.org.uk/topics/diabetes-type-1/background-information/incidence-prevalence/#:~:text=About%208%25%20of%20people%20with%20diabetes%20have%20type,type%201%20diabet

[3]A. Brown, D. Gopisetty (2018 October) "Understanding Average Glucose, Standard Deviation, CV, and Blood Sugar Variability" *diaTribe Learn* [online] https://diatribe.org/understanding-average-glucose-standard-deviation-cv-and-blood-sugar-variability

[4]F.J. Service (2013 April) "Glucose Variability" *American Diabetes Association* [online] vol. 62 issue. 5 https://diabetesjournals.org/diabetes/article/62/5/1398/42890/Glucose-Variability