

✓ DANA 4800 Project 2 – Summer Semester 2025

Objective: Outline the purpose and the source of the data

The purpose of this analysis is to explore and understand the patterns and temporal dynamics of blood glucose levels in individuals with type 1 diabetes. By performing exploratory data analysis (EDA). The dataset used for this analysis comes from the BRIST1D competition hosted on Kaggle <https://www.kaggle.com/competitions/brist1d/data>

Methodology:# *• WH Questions: Identify the who, where and when

Objective:

The purpose of this dataset is to provide comprehensive information on several key health indicators. It includes data on:

- Blood glucose levels
 - Insulin levels
 - Heart rate readings
 - Carbohydrate intake
 - Step counts recorded at various times
 - Calorie burns during specific periods
 - Indicator of blood glucose level in future for train dataset Overall physical activity levels
- Additionally, the dataset aims to support the prediction of future blood glucose trends based on the combined analysis of these variables, the dataset does not specify clearly how to predict the blood glucose indicator, it's disposed to be used as a source to predict the indicator using the techniques of data analysis

Methodology

Who

The dataset contains information from nine young adults living with type 1 diabetes.

Where

The data was collected in the United Kingdom, although no specific city is mentioned.

When

The exact date of data collection is not specified. However, it can be reasonably assumed that the data originates from around the year 2024, based on the timing of the competition in which it was provided.

How

The dataset was collected as part of the BrisT1D Blood Glucose Prediction Competition, which ran from September to November 2024. It features real-world data from nine young adults in the UK living with type 1 diabetes. Participants wore continuous glucose monitors, used insulin pumps, and were provided with smartwatches to track physical activity. The goal of the study was to gather diverse, time-stamped health metrics to support the development of algorithms that predict blood glucose levels one hour into the future using the previous six hours of data. This data collection effort aimed to address the complexity of managing type 1 diabetes, where factors presumably like carbohydrates, physical activity in steps and heart rates, and levels of insulin. Although the dataset does not prescribe a specific modeling method, it was designed to encourage data scientists to explore predictive techniques using real-world conditions.

- How: Brief description of how the data set was drawn*
 - To answer these questions, the "train" dataset was taken, which is printed below.

```
#import libraries
import pandas as pd

train = pd.read_csv('train.csv', encoding='utf-8', sep=",", low_memory=False)
```

Identify the who: The p_num column indicates the patient number in this way:

```
train["p_num"].unique().tolist()
→ ['p01', 'p02', 'p03', 'p04', 'p05', 'p06', 'p10', 'p11', 'p12']
```

We identified that the dataset comprises information from 9 patients, patients 'p07', 'p08', 'p09' are not included.

Identify the where: According to the dataset description on Kaggle, the data was collected in the United Kingdom. It comes from a real-world study involving young adults with type 1 diabetes who used continuous glucose monitors, insulin pumps, and smartwatches to record their activity.

Identify the when: The dataset description text states that "The training set takes samples from the first three months of study data from nine of the participants..."

This indicates that the training data was collected during the first three months of the study, although the exact year and dates are not mentioned.

However, the time windows indicated in the time column and in the columns of the variables measured in the dataset are reviewed.

```
#Convert time to datetime.time format
train["time"] = pd.to_datetime(train["time"], format="%H:%M:%S")
#We will extract a new column, for example hour, from df["time"].
train["hour"] = train["time"].dt.hour
#minutes within each hour:
train["minute"] = train["time"].dt.minute

#Create the day_id column: We want to identify the day changes for each person (p_num)

# Convert the 'time' column to seconds since midnight (for easier comparison)
train["time_seconds"] = train["time"].dt.hour * 3600 + train["time"].dt.minute * 60 + tra
# Calculate the difference with the previous row (per person)
train["time_diff"] = train.groupby("p_num")["time_seconds"].diff()
# When the difference is negative, it means the clock has been reset (new day)
train["new_day"] = (train["time_diff"] < 0).astype(int)
# Accumulate the changes to obtain the day identifier per person
train["day_id"] = train.groupby("p_num")["new_day"].cumsum()

train["day_id"].unique()

→ array([ 0,  1,  2,  3,  4,  5,  6,  7,  8,  9, 10, 11, 12, 13, 14, 15, 16,
       17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33,
       34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50,
       51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67,
       68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84,
       85, 86, 87, 88, 89, 90, 91])
```

indicating that the time period is obtained by 90 days equivalent to 3 months, without knowing the exact date on which the measurement begins.

Additionally, you can review the window of each measurement for the variables.

```
column_counts = {
    "bg": len([c for c in train.columns if c.startswith("bg-")]),
    "insulin": len([c for c in train.columns if c.startswith("insulin-")]),
    "carbs": len([c for c in train.columns if c.startswith("carbs-")]),
    "hr": len([c for c in train.columns if c.startswith("hr-")]),
    "steps": len([c for c in train.columns if c.startswith("steps-")]),
    "cals": len([c for c in train.columns if c.startswith("cals-")]),
    "activity": len([c for c in train.columns if c.startswith("activity-")])}
```

```

}
#how many There are columns of each type
print("how many columns of each type are there")
print(column_counts)

→ how many columns of each type are there
{'bg': 72, 'insulin': 72, 'carbs': 72, 'hr': 72, 'steps': 72, 'cals': 72, 'activity': 72}

```

Indicating that there are 72 columns for each variable that represent a 5-minute interval, so 6 hours of measurement of said variables are observed.

Brief description of how the data set was drawn

The dataset was drawn from a clinical study of young adults in the UK living with type 1 diabetes. Participants wore three types of devices: a continuous glucose monitor (CGM), an insulin pump, and a smartwatch. These devices collected real-world data on blood glucose levels, insulin doses, carbohydrate intake, heart rate, physical activity (steps, calories, reported activity), and time of day. The raw data was preprocessed and aggregated in five-minute intervals to generate samples. Each sample included features representing the previous six hours of data. The training set was constructed with data from the first three months of nine participants. These samples are overlapped and ordered chronologically.

The continuous glucose monitor (CGM) measures glucose levels in real time using a sensor inserted under the skin.

The insulin pump delivers precise doses of insulin based on the user's needs.

The smartwatch records physical activity data such as heart rate, steps, calories burned, and user-reported activities.

▼ Data Description

What or Variables: Provide details of all variables (including the types of variables, the scale of measurements, and write out the units/list out all classes (if applicable)

For this we first perform an exploration of the shape of the dataset and the types of variables involved.

```

#Explore its general structure:
print(train.info())

→ <class 'pandas.core.frame.DataFrame'>
RangeIndex: 177024 entries, 0 to 177023
Columns: 514 entries, id to day_id
dtypes: datetime64[ns](1), float64(434), int32(3), int64(2), object(74)
memory usage: 692.2+ MB

```

None

types of variables: This DataFrame contains 176,526 rows and 514 columns, with a mix of data types including floats, integers, datetime, and object.

To know what type each of the columns or variables is:

```
#data type of each column:
# Dictionary to store data types by prefix
column_dtypes = {}

# List of prefixes
prefixes = ["bg", "insulin", "carbs", "hr", "steps", "cals", "activity"]

# Iterate over each prefix and get the unique dtypes
for prefix in prefixes:
    cols = [c for c in train.columns if c.startswith(f"{prefix}-")]
    dtypes = train[cols].dtypes.unique()
    column_dtypes[prefix] = dtypes

print("data types")
# Display results
for prefix, dtypes in column_dtypes.items():
    print(f"{prefix}: {dtypes}")
```

→ data types
 bg: [dtype('float64')]
 insulin: [dtype('float64')]
 carbs: [dtype('float64')]
 hr: [dtype('float64')]
 steps: [dtype('float64')]
 cals: [dtype('float64')]
 activity: [dtype('O')]

This output shows that the variables bg, insulin, carbs, hr, steps, and cals are all stored as float64, indicating numerical values with decimals, while activity is stored as object (dtype 'O'), typically representing categorical or string data.

The scale of measurements

The units of each variable as indicated in Kaggle

| Variable Prefix | Description | Unit |
|-----------------|--|------------------------|
| bg- / bg+ | Blood glucose levels (past and future) | mmol/L |
| insulin- | Insulin dose in last 5 minutes | Units |
| carbs- | Carbohydrates consumed in last 5 minutes | Grams |
| hr- | Mean heart rate in last 5 minutes | Beats per minute (bpm) |
| steps- | Total steps in last 5 minutes | Count (steps) |
| cals- | Total calories burned in last 5 minutes | Kilocalories (kcal) |

| Variable Prefix | Description | Unit |
|-----------------|--|----------------------|
| activity- | Type of activity performed in last 5 minutes | Categorical (string) |

the numerical scale on which each type of measurement operates:

```
for prefix in ["bg", "insulin", "carbs", "hr", "steps", "cals"]:
    cols = [c for c in train.columns if c.startswith(f"{prefix}-")]
    print(f"\n--- {prefix.upper()} ---")
    print("Min:", train[cols].min().min())
    print("Max:", train[cols].max().max())
    print("Mean:", train[cols].mean().mean())
```



```
--- BG ---
Min: 2.2
Max: 27.8
Mean: 8.234952989463247

--- INSULIN ---
Min: -0.3078
Max: 46.311
Mean: 0.20298837090086602

--- CARBS ---
Min: 1.0
Max: 852.0
Mean: 48.22758203886425

--- HR ---
Min: 37.6
Max: 185.3
Mean: 79.31482801424396

--- STEPS ---
Min: 0.0
Max: 1359.0
Mean: 53.09520599847842

--- CALS ---
Min: 0.03
Max: 116.1
Mean: 9.3614202728668
```

| Variable | Unit | Normal Range (approx.) | Notable |
|----------|-----------------|------------------------|--|
| BG | mmol/L | 4 – 8 | Values <4 (hypoglycemia) and >10 (hyperglycemia) observed, which is epsilon |
| Insulin | Units | 0 – ~15 (per interval) | Negative values are not physiologically valid. Very low mean suggests |
| Carbs | Grams | 0 – 60 per meal | Extreme values (>800 g) may be errors or inaccurate self-reports. Cons |
| HR | Beats/min (bpm) | 60 – 100 at rest | Ranges consistent with rest and exercise; extreme values (>180) expect |
| Steps | Step count | | Maximum suggests high physical activity, mean indicates generally low |
| Cals | Kilocalories | | |

Additionally we can analyze the categorical variable: Activity

```

activity_cols = [col for col in train.columns if col.startswith("activity-")]
train[activity_cols].astype(str)
# Unir todos los valores únicos en un solo conjunto
unique_activities = set()
for col in activity_cols:
    unique_activities.update(train[col].unique())
unique_activities

→ {'Aerobic Workout',
 'Bike',
 'Dancing',
 'HIIT',
 'Hike',
 'Indoor climbing',
 'Outdoor Bike',
 'Run',
 'Running',
 'Spinning',
 'Sport',
 'Stairclimber',
 'Strength training',
 'Swim',
 'Swimming',
 'Tennis',
 'Walk',
 'Walking',
 'Weights',
 'Workout',
 'Yoga',
 'Zumba',
 nan}

```

The activity labels show inconsistent naming, such as both "Walk" and "Walking", or "Swim" and "Swimming", which refer to the same activity. This inconsistency can lead to redundancy and misinterpretation during analysis or modeling. Therefore, replacement is performed as follows:

```

activity_mapping = {
    "Walk": "Walking",
    "Run": "Running",
    "Swim": "Swimming",
    "Bike": "Outdoor Bike"
}
train = train.replace(activity_mapping)
[col for col in train.columns if col.startswith("activity-")]
train[activity_cols].astype(str)
# Unir todos los valores únicos en un solo conjunto
unique_activities = set()
for col in activity_cols:
    unique_activities.update(train[col].unique())
unique_activities

→ {'Aerobic Workout',
 'Dancing',
 'HIIT',

```

```
'Hike',
'Indoor climbing',
'Outdoor Bike',
'Running',
'Spinning',
'Sport',
'Stairclimber',
'Strength training',
'Swimming',
'Tennis',
'Walking',
'Weights',
'Workout',
'Yoga',
'Zumba',
nan}
```

There are general tags like Workout, Sport that can be ambiguous

▼ Data Exploration

Accuracy: Cross-checking the source and see if the data set from Kaggle is the same as other sources like this one: <https://data.bris.ac.uk/data/dataset/33z5jc8fa6tob21ptrugzqog08>

First we describe the variables of our dataset, so we group the columns every six hours.

In this step, we calculate row-by-row summary statistics for each of the temporal variables in the dataset (bg, insulin, carbs, hr, steps, cals). For each sample, we group all columns corresponding to the same variable and calculate their mean, maximum, sum, and standard deviation. These values allow us to summarize the recent behavior of each variable within a six-hour window.

```
variables = ["bg", "insulin", "carbs", "hr", "steps", "cals"]
stats_df = pd.DataFrame() # This will store the final summary statistics

for var in variables:
    # Find all columns that start with var-
    cols = [col for col in train.columns if col.startswith(f"{var}-")]

    # Calculate statistics and add them to the new DataFrame
    stats_df[f"{var}_mean"] = train[cols].mean(axis=1)
    stats_df[f"{var}_max"] = train[cols].max(axis=1)
    stats_df[f"{var}_sum"] = train[cols].sum(axis=1)
    stats_df[f"{var}_std"] = train[cols].std(axis=1)

stats_df
```

| | bg_mean | bg_max | bg_sum | bg_std | insulin_mean | insulin_max | insulin_sum | i |
|--------|-----------|--------|--------|----------|--------------|-------------|-------------|-----|
| 0 | 13.341667 | 18.4 | 320.2 | 3.710492 | 0.025894 | 0.0583 | 1.8644 | |
| 1 | 13.541667 | 18.4 | 325.0 | 3.628500 | 0.027286 | 0.0583 | 1.9646 | |
| 2 | 13.716667 | 18.4 | 329.2 | 3.535247 | 0.028678 | 0.0583 | 2.0648 | |
| 3 | 13.908333 | 18.4 | 333.8 | 3.401907 | 0.030069 | 0.0583 | 2.1650 | |
| 4 | 14.104167 | 18.4 | 338.5 | 3.219435 | 0.031461 | 0.0583 | 2.2652 | |
| ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 177019 | 8.169444 | 10.4 | 588.2 | 1.043780 | 0.386319 | 13.0750 | 27.8150 | |
| 177020 | 8.190278 | 10.4 | 589.7 | 1.071153 | 0.397222 | 13.0750 | 28.6000 | |
| 177021 | 8.212500 | 10.7 | 591.3 | 1.106312 | 0.404306 | 13.0750 | 29.1100 | |
| 177022 | 8.237500 | 11.0 | 593.1 | 1.148476 | 0.403958 | 13.0750 | 29.0850 | |
| 177023 | 8.268056 | 11.6 | 595.3 | 1.207585 | 0.403264 | 13.0750 | 29.0350 | |

177024 rows × 24 columns

| Statistic | Description |
|-----------|--|
| mean | Average value of the variable over a 6-hour period (overall level) |
| max | Highest recorded value during the 6-hour window (peak) |
| sum | Total sum of all values over 6 hours (total quantity) |
| std | Standard deviation, indicating stability or variability over that period |

We observe this in a graph

```

import seaborn as sns
import matplotlib.pyplot as plt

#1. Filter only columns ending in "_mean"
mean_cols = [col for col in stats_df.columns if col.endswith('_mean')]

mean_long = stats_df[mean_cols].melt(var_name='Variable', value_name='Mean Value')
mean_long

```

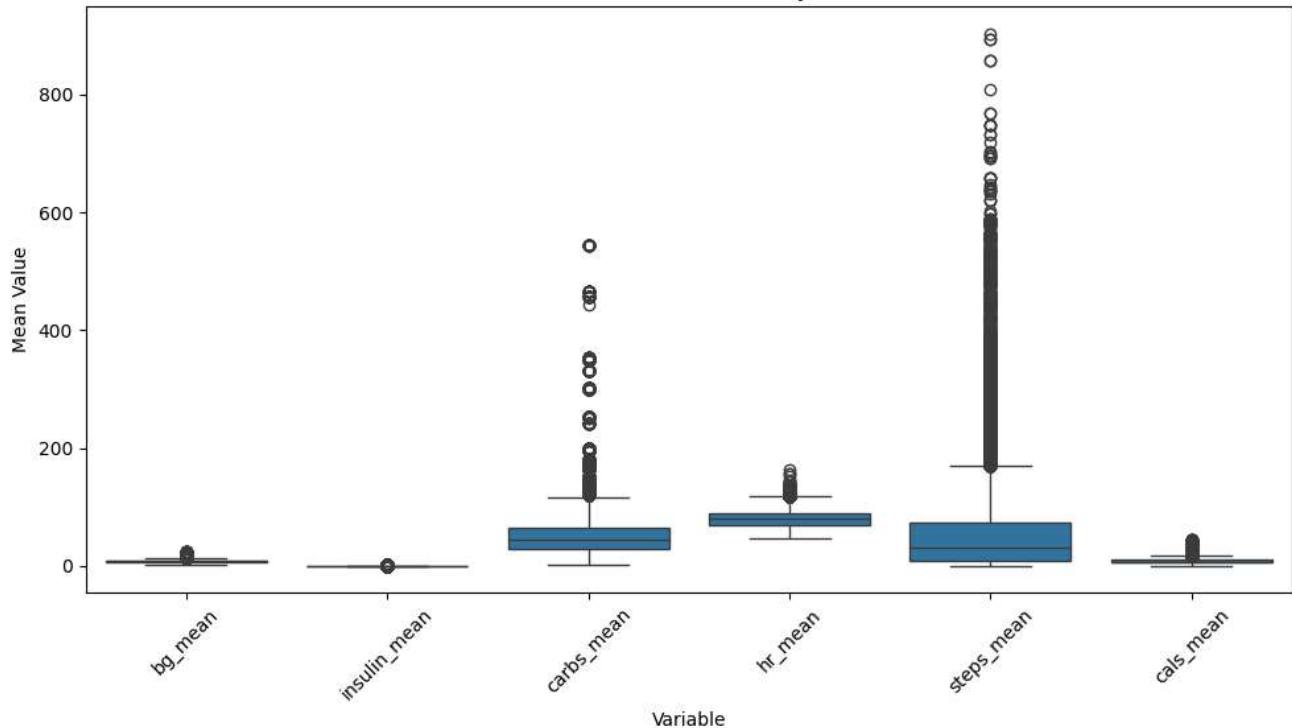
| | Variable | Mean Value |
|---------|-----------|------------|
| 0 | bg_mean | 13.341667 |
| 1 | bg_mean | 13.541667 |
| 2 | bg_mean | 13.716667 |
| 3 | bg_mean | 13.908333 |
| 4 | bg_mean | 14.104167 |
| ... | ... | ... |
| 1062139 | cals_mean | 6.750000 |
| 1062140 | cals_mean | 6.750000 |
| 1062141 | cals_mean | 6.750000 |
| 1062142 | cals_mean | 6.750000 |
| 1062143 | cals_mean | 6.750000 |

1062144 rows × 2 columns

```
plt.figure(figsize=(10, 6))
sns.boxplot(data=mean_long, x='Variable', y='Mean Value')
plt.title('Distribution of mean values by variable')
plt.xticks(rotation=45)
plt.tight_layout()
plt.show()
```



Distribution of mean values by variable



The variables bg_mean, insulin_mean, and cals_mean show more concentrated distributions with less variability in their mean values, generally in the low ranges.

hr_mean has a more centered distribution with fewer extreme outliers.

carbs_mean and steps_mean are the variables with the greatest dispersion and a significant number of high outliers, indicating greater variability in habits or measurements related to these variables. Steps_mean is particularly notable for the breadth of its distribution and the presence of numerous very high outliers.

```
import seaborn as sns
import matplotlib.pyplot as plt

# Variables únicas
variables = mean_long['Variable'].unique()

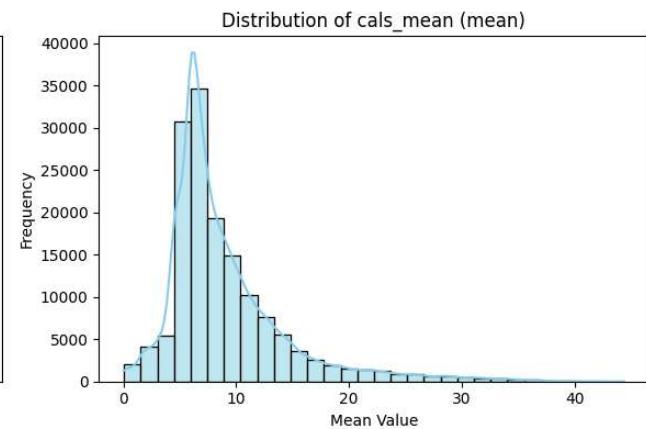
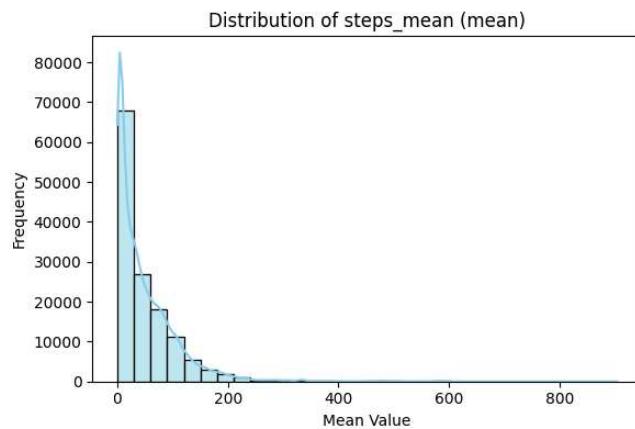
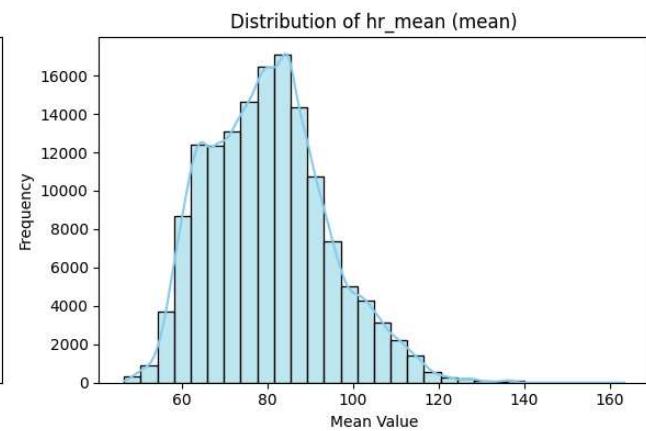
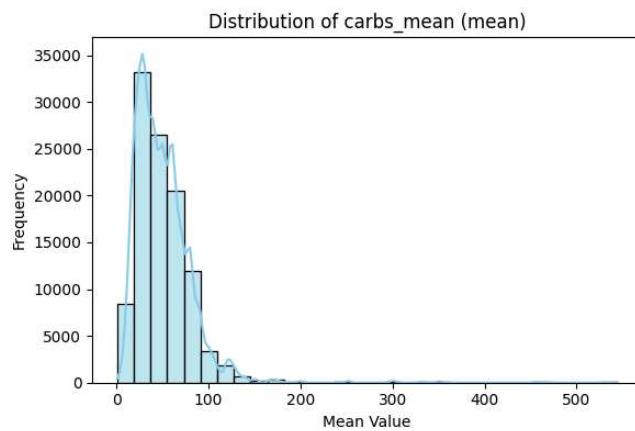
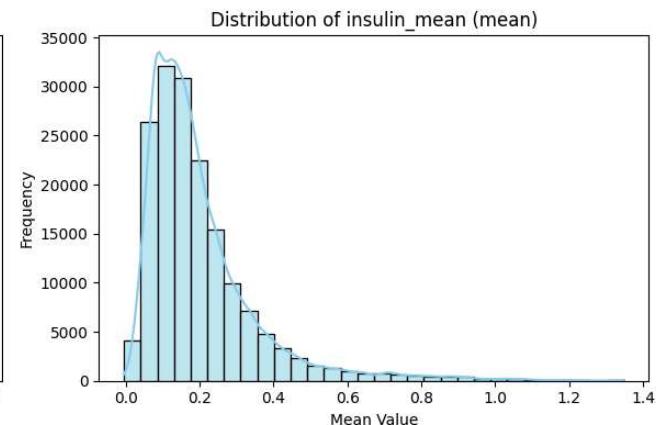
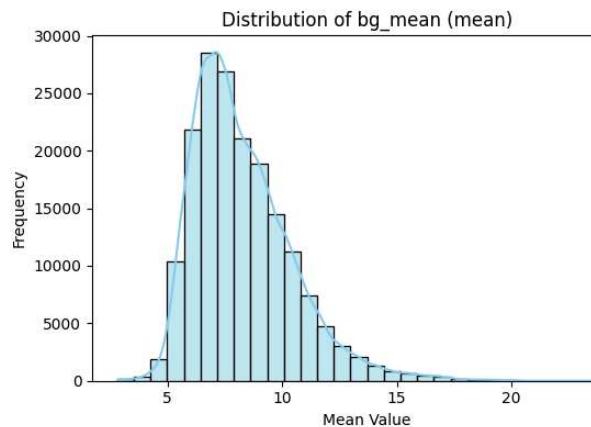
# Crear subplots: 2 columnas, filas según número de variables
n_cols = 2
n_rows = -(len(variables) // n_cols) # Redondeo hacia arriba
```

```
fig, axes = plt.subplots(n_rows, n_cols, figsize=(12, n_rows * 4))
axes = axes.flatten()

# Histograma por variable
for i, var in enumerate(variables):
    sns.histplot(
        data=mean_long[mean_long['Variable'] == var],
        x='Mean Value',
        ax=axes[i],
        kde=True,
        bins=30,
        color='skyblue'
    )
    axes[i].set_title(f'Distribution of {var} (mean)', fontsize=12)
    axes[i].set_xlabel('Mean Value')
    axes[i].set_ylabel('Frequency')

# Quitar ejes vacíos si hay
for j in range(i + 1, len(axes)):
    fig.delaxes(axes[j])

plt.tight_layout()
plt.show()
```



The steps_mean and cals_mean distributions are strongly positively skewed, meaning that most of the data are clustered at the lower end of their ranges.

steps_mean stands out for the high concentration of data in very low values and a very long tail with very high outliers, reflecting high variability in physical activity habits.

cals_mean is similar to bg_mean and insulin_mean in its strong bias toward low values, indicating that average caloric intakes are mostly low.

The dataset was downloaded from the page:

<https://data.bris.ac.uk/data/dataset/33z5jc8fa6tob21ptrugzqog08> and the data from the device_data/processed_state folder was exported for the patients indicated in Kaggle

```
p01 = pd.read_csv("P01.csv")
p02 = pd.read_csv("P02.csv")
p03 = pd.read_csv("P03.csv")
p04 = pd.read_csv("P04.csv")
p05 = pd.read_csv("P05.csv")
p06 = pd.read_csv("P06.csv")
p10 = pd.read_csv("P10.csv")
p11 = pd.read_csv("P11.csv")
p12 = pd.read_csv("P12.csv")
```

p02

| | timestamp | bg | insulin | carbs | hr | dist | steps | cals | activity | device |
|-----|---------------------|-----|---------|-------|-----|------|-------|------|----------|------------------|
| 0 | 2023-06-01 00:01:00 | 9.3 | NaN | NaN | NaN | NaN | NaN | NaN | NaN | Dexcom G6 |
| 1 | 2023-06-01 00:05:00 | NaN | 0.1249 | NaN | NaN | NaN | NaN | NaN | NaN | Tandem t:slim X2 |
| 2 | 2023-06-01 00:06:00 | 9.5 | NaN | NaN | NaN | NaN | NaN | NaN | NaN | Dexcom G6 |
| 3 | 2023-06-01 00:10:00 | NaN | 0.0784 | NaN | NaN | NaN | NaN | NaN | NaN | Tandem t:slim X2 |
| 4 | 2023-06-01 00:11:00 | 9.6 | NaN | NaN | NaN | NaN | NaN | NaN | NaN | Dexcom G6 |
| ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| | 2023-12- | | | | | | | | | Apple |

more frequent time intervals:

```
# Convert the date column to datetime format
p01['timestamp'] = pd.to_datetime(p01['timestamp'])

# Sort by timestamp if it's not sorted
p01 = p01.sort_values('timestamp')

# Calculate the difference between consecutive timestamps
p01['delta'] = p01['timestamp'].diff()

# Display the most common time intervals
print(p01['delta'].value_counts().head(10))
```

→ delta

| | |
|-----------------|-------|
| 0 days 00:00:00 | 62038 |
| 0 days 00:05:00 | 42710 |
| 0 days 00:02:00 | 8034 |
| 0 days 00:03:00 | 7933 |
| 0 days 00:01:00 | 7876 |
| 0 days 00:04:00 | 7628 |

Name: count, dtype: int64

convert "timestamp" to datetime

```
# Suppose you already have the DataFrames loaded as p01, p02, ..., p12
```

```
# Dictionary that groups them
dfs = {
    'p01': p01,
    'p02': p02,
    'p03': p03,
    'p04': p04,
    'p05': p05,
    'p06': p06,
    'p10': p10,
    'p11': p11,
    'p12': p12,
}
```

```
# Converting to datetime
for name, df in dfs.items():
    df['timestamp'] = pd.to_datetime(df['timestamp'])
```

```
for name, df in dfs.items():
    df['day'] = df['timestamp'].dt.date # Extract only the date part (without time)
    unique_days = df['day'].nunique() # Count the unique days
    print(f"{name} tiene {unique_days} días únicos.")
```

→ p01 tiene 203 días únicos.
p02 tiene 210 días únicos.
p03 tiene 98 días únicos.
p04 tiene 219 días únicos.

```
p05 tiene 223 días únicos.
p06 tiene 201 días únicos.
p10 tiene 205 días únicos.
p11 tiene 222 días únicos.
p12 tiene 224 días únicos.
```

check if the data in each DataFrame is in chronological order

```
for name, df in dfs.items():
    is_sorted = df['timestamp'].is_monotonic_increasing
    print(f"{name} is in chronological order: {is_sorted}")
```

→ p01 is in chronological order: True
 p02 is in chronological order: True
 p03 is in chronological order: True
 p04 is in chronological order: True
 p05 is in chronological order: True
 p06 is in chronological order: True
 p10 is in chronological order: True
 p11 is in chronological order: True
 p12 is in chronological order: True

we extract only the first three months:

```
from datetime import timedelta

dfs_90days = {} # Nuevo diccionario para guardar los dataframes filtrados

for name, df in dfs.items():
    start_date = df['timestamp'].min()
    end_date = start_date + timedelta(days=90)
    df_90 = df[df['timestamp'] < end_date].copy()
    dfs_90days[name] = df_90
    print(f"{name}: {df_90['timestamp'].min().date()} → {df_90['timestamp'].max().date()}")
```

→ p01: 2023-06-01 → 2023-08-30 | Filas: 60179
 p02: 2023-06-01 → 2023-08-30 | Filas: 77124
 p03: 2023-06-01 → 2023-08-30 | Filas: 76182
 p04: 2023-06-06 → 2023-09-04 | Filas: 75933
 p05: 2023-06-01 → 2023-08-30 | Filas: 59559
 p06: 2023-06-01 → 2023-08-30 | Filas: 58798
 p10: 2023-06-01 → 2023-08-30 | Filas: 77022
 p11: 2023-06-01 → 2023-08-30 | Filas: 64601
 p12: 2023-06-01 → 2023-08-30 | Filas: 77120

resampling every 5 minutes:

```
for pid, df in dfs_90days.items():
    df = df.set_index("timestamp") # Set 'timestamp' as index
    df = df.sort_index() # Sort the DataFrame by timestamp
```

```
df_resampled = df.resample("5min").first() # Resample to 5-minute intervals, keeping
dfs_90days[pid] = df_resampled.reset_index() # Reset index and store back into the di
```

```
dfs_90days["p01"].head()
```

| | timestamp | bg | insulin | carbs | hr | dist | steps | cals | activity | device | del: |
|---|---------------------|-----|---------|-------|-----|------|-------|------|----------|------------------------|---------------|
| 0 | 2023-06-01 00:05:00 | 8.6 | 0.0083 | NaN | NaN | NaN | NaN | NaN | None | Medtronic MiniMed 640G | 0 da: 00:01:(|
| 1 | 2023-06-01 00:10:00 | NaN | 0.0083 | NaN | NaN | NaN | NaN | NaN | None | Medtronic MiniMed 640G | 0 da: 00:04:(|
| | 2023-06- | | | | | | | | | Medtronic | 0 da: |

```
# Add the 'p_num' column to each DataFrame
for pid, df in dfs_90days.items():
    p_num = pid.split("_")[0] # Extract the patient code, e.g. 'p01'
    df['p_num'] = p_num
    dfs_90days[pid] = df
dfs_90days["p01"].head()
```

| | timestamp | bg | insulin | carbs | hr | dist | steps | cals | activity | device | del: |
|---|---------------------|-----|---------|-------|-----|------|-------|------|----------|------------------------|---------------|
| 0 | 2023-06-01 00:05:00 | 8.6 | 0.0083 | NaN | NaN | NaN | NaN | NaN | None | Medtronic MiniMed 640G | 0 da: 00:01:(|
| 1 | 2023-06-01 00:10:00 | NaN | 0.0083 | NaN | NaN | NaN | NaN | NaN | None | Medtronic MiniMed 640G | 0 da: 00:04:(|
| | 2023-06- | | | | | | | | | Medtronic | 0 da: |

```
df_all = pd.concat(dfs_90days.values(), ignore_index=True)
```

```
df_all
```

| | timestamp | bg | insulin | carbs | hr | dist | steps | cals | activity | device |
|-----|---------------------|-----|---------|-------|-----|------|-------|------|----------|------------------------|
| 0 | 2023-06-01 00:05:00 | 8.6 | 0.0083 | NaN | NaN | NaN | NaN | NaN | None | Medtronic MiniMed 640G |
| 1 | 2023-06-01 00:10:00 | NaN | 0.0083 | NaN | NaN | NaN | NaN | NaN | None | Medtronic MiniMed 640G |
| 2 | 2023-06-01 00:15:00 | NaN | 0.0083 | NaN | NaN | NaN | NaN | NaN | None | Medtronic MiniMed 640G |
| 3 | 2023-06-01 00:20:00 | 9.6 | 0.0083 | NaN | NaN | NaN | NaN | NaN | None | Medtronic MiniMed 640G |
| 4 | 2023-06-01 00:25:00 | NaN | 0.0083 | NaN | NaN | NaN | NaN | NaN | None | Medtronic MiniMed 640G |
| ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... |

Due to the way in which the data are arranged, it is very cumbersome to process them to obtain the same df, therefore all the values of the variables will be averaged by patients and the data will be compared.

```
# List of columns to average
variables = ['bg', 'insulin', 'carbs', 'hr', 'steps', 'cals']

# Calculate averages ignoring NaNs
averages = df_all[variables].mean(skipna=True)

# Convert to DataFrame (optional)
averages_df = pd.Series(averages, name="mean").to_frame()
print(averages_df)
```

| | mean |
|---------|-----------|
| bg | 8.278703 |
| insulin | 0.193260 |
| carbs | 42.858234 |
| hr | 78.203309 |
| steps | 55.557082 |
| cals | 9.327919 |

```
# List of prefixes to average
prefixes = ["bg", "insulin", "carbs", "hr", "steps", "cals"]
# Dictionary to store the global average per variable
global_averages = {}

for prefix in prefixes:
```

```

columns = [col for col in train.columns if col.startswith(prefix)]
if columns:
    # Calculate the mean of all values across all columns with that prefix
    values = train[columns].values.flatten()
    mean_value = pd.Series(values).dropna().mean()
    global_averages[prefix] = mean_value

# Convert to DataFrame (optional)
df_averages = pd.Series(global_averages, name="mean").to_frame()
print(df_averages)

```

→ mean

| | |
|---------|-----------|
| bg | 8.236726 |
| insulin | 0.202988 |
| carbs | 48.227292 |
| hr | 79.314833 |
| steps | 53.095167 |
| cals | 9.361426 |

Compare the calculations of the averages

```

# First series (in DataFrame format)
mean1 = averages_df

# Second series (can come as a flat dict or Series)
mean2 = df_averages
common_vars = mean1.index.intersection(mean2.index)
common_vars

→ Index(['bg', 'insulin', 'carbs', 'hr', 'steps', 'cals'], dtype='object')

# Join both DataFrames by index
comparison = mean1.join(mean2, lsuffix='_1', rsuffix='_2', how='inner')

# Calculate absolute and relative difference
comparison["abs_diff"] = (comparison["mean_1"] - comparison["mean_2"]).abs()
comparison["rel_diff_%"] = comparison["abs_diff"] / (
    comparison["mean_1"] + comparison["mean_2"]) / 2
) * 100
comparison

```

| | mean_1 | mean_2 | abs_diff | rel_diff % |
|----------------|---------------|---------------|-----------------|-------------------|
| bg | 8.278703 | 8.236726 | 0.041976 | 0.508330 |
| insulin | 0.193260 | 0.202988 | 0.009728 | 4.910210 |
| carbs | 42.858234 | 48.227292 | 5.369057 | 11.789046 |
| hr | 78.203309 | 79.314833 | 1.111523 | 1.411296 |
| steps | 55.557082 | 53.095167 | 2.461916 | 4.531735 |
| cals | 9.327919 | 9.361426 | 0.033507 | 0.358570 |

There are differences between the two sets of averages, with the change in carbohydrates being the most notable, while calories and blood glucose show the greatest stability.

The data set has another format and when you try to configure it from the same structure as the train, it is a rather cumbersome process that would require more time, even as much as the same EDA.

Missing Data: Identify missing data, if any, and suggest how to manage it

```
# Count null values per column for each patient
nulls_per_patient = train.groupby("p_num").apply(lambda x: x.isna().sum())

→ /tmp/ipython-input-37-2378630639.py:2: DeprecationWarning: DataFrameGroupBy.apply ope
nulls_per_patient = train.groupby("p_num").apply(lambda x: x.isna().sum())

nulls_per_patient = nulls_per_patient.rename(columns={"p_num": "p_num_1"}).reset_index()
#sum of missing data for patient

prefixes = ["bg", "insulin", "carbs", "hr", "steps", "cals"]

# Select only columns that start with the specified prefixes
selected_columns = [col for col in nulls_per_patient.columns if any(col.startswith(prefix))

# Create a new DataFrame with only those columns
train_selected = nulls_per_patient[selected_columns]

nulls_per_patient["total_nulls"] = nulls_per_patient.drop(columns=["p_num"]).sum(axis=1)

nulls_per_patient_sorted = nulls_per_patient.sort_values(by="total_nulls", ascending=False)

nulls_per_patient_sorted[["p_num", "total_nulls"]]
```

| | p_num | total_nulls |
|---|-------|-------------|
| 1 | p02 | 8066185 |
| 7 | p11 | 6013668 |
| 3 | p04 | 5721124 |
| 6 | p10 | 5036419 |
| 2 | p03 | 4816879 |
| 8 | p12 | 4687348 |
| 4 | p05 | 2169869 |
| 5 | p06 | 1964052 |
| 0 | p01 | 1819259 |

The one with the most missing data (total_nulls) is the participant with p_num = p02, with a total of 8,066,185 null values.

Now null according to the variables

```
# Define the prefixes of interest
prefixes = ["bg", "insulin", "carbs", "hr", "steps", "cals", "activity"]

# Create a dictionary where nulls by prefix will be stored
nulls_by_prefix = {}

# Iterate through each prefix, filter the corresponding columns, calculate nulls by patient
for prefix in prefixes:
    cols = [c for c in train.columns if c.startswith(f"{prefix}-")]
    nulls_by_prefix[prefix] = train[cols].isna().groupby(train["p_num"]).sum().sum(axis=1)

# Combine everything into a single DataFrame
nulls_by_variable_and_patient = pd.DataFrame(nulls_by_prefix)

# Reset index so `p_num` is a normal column (optional)
nulls_by_variable_and_patient = nulls_by_variable_and_patient.reset_index()
nulls_by_variable_and_patient
```

| | p_num | bg | insulin | carbs | hr | steps | cals | activity |
|---|-------|--------|---------|---------|---------|---------|---------|----------|
| 0 | p01 | 409686 | 0 | 599148 | 32689 | 186405 | 6252 | 585078 |
| 1 | p02 | 22640 | 0 | 1839242 | 1464176 | 1566168 | 1328607 | 1845351 |
| 2 | p03 | 18863 | 0 | 1851652 | 196203 | 782364 | 101844 | 1865952 |
| 3 | p04 | 19507 | 0 | 1744331 | 879067 | 1117523 | 203292 | 1757403 |
| 4 | p05 | 407515 | 0 | 587155 | 99260 | 347281 | 139284 | 589373 |
| 5 | p06 | 407807 | 0 | 598281 | 118862 | 221574 | 29580 | 587947 |
| 6 | p10 | 21642 | 0 | 1807092 | 136835 | 855589 | 448524 | 1766736 |
| 7 | p11 | 28524 | 677556 | 1754561 | 668213 | 1047533 | 102636 | 1734644 |
| 8 | p12 | 35500 | 0 | 1780392 | 113789 | 742497 | 199188 | 1815981 |

Higher numbers = more missing data.

Participants p02, p03, and p11 have large portions of missing values across most variables.

p01, p05, and p06 have the least missing data, especially for key variables like bg, carbs, and activity.

insulin is almost entirely missing, except for p11, who may have partial data. for which we could consider to avoid use the data of this patient

```
# Identify the day with the most data (fewest nulls)
```

```
#count number of nan per day
```

```
non_null_counts = train.groupby('day_id').apply(lambda x: x.notnull().sum().sum())
best_day = non_null_counts.idxmax()
max_values = non_null_counts.max()
best_day, max_values
```

```
→ /tmp/ipython-input-46-1600811343.py:5: DeprecationWarning: DataFrameGroupBy.apply ope
    non_null_counts = train.groupby('day_id').apply(lambda x: x.notnull().sum().sum())
(np.int64(59), 657522)
```

The day with the fewest null values is the day 59 with 657522 non-null values.

Look at the time interval with the most null values

```
cols_of_interest = [col for col in train.columns if any(col.startswith(prefix) for prefix
train['null_count'] = train[cols_of_interest].isnull().sum(axis=1)
nulls_by_time = train.groupby('time')['null_count'].sum().sort_values(ascending=False).re
```

nulls_by_time

| | time | null_count |
|-----|---------------------|------------|
| 0 | 1900-01-01 06:25:00 | 160241 |
| 1 | 1900-01-01 06:55:00 | 159903 |
| 2 | 1900-01-01 06:40:00 | 159896 |
| 3 | 1900-01-01 07:10:00 | 159542 |
| 4 | 1900-01-01 07:25:00 | 159383 |
| ... | ... | ... |
| 283 | 1900-01-01 17:55:00 | 124363 |
| 284 | 1900-01-01 18:50:00 | 124038 |
| 285 | 1900-01-01 18:05:00 | 124031 |
| 286 | 1900-01-01 18:35:00 | 124023 |
| 287 | 1900-01-01 18:20:00 | 124010 |

288 rows × 2 columns

```
nulls_by_time['hour'] = pd.to_datetime(nulls_by_time['time'], errors='coerce').dt.time
nulls_by_time
```

| | time | null_count | hour |
|-----|---------------------|------------|----------|
| 0 | 1900-01-01 06:25:00 | 160241 | 06:25:00 |
| 1 | 1900-01-01 06:55:00 | 159903 | 06:55:00 |
| 2 | 1900-01-01 06:40:00 | 159896 | 06:40:00 |
| 3 | 1900-01-01 07:10:00 | 159542 | 07:10:00 |
| 4 | 1900-01-01 07:25:00 | 159383 | 07:25:00 |
| ... | ... | ... | ... |
| 283 | 1900-01-01 17:55:00 | 124363 | 17:55:00 |
| 284 | 1900-01-01 18:50:00 | 124038 | 18:50:00 |
| 285 | 1900-01-01 18:05:00 | 124031 | 18:05:00 |
| 286 | 1900-01-01 18:35:00 | 124023 | 18:35:00 |
| 287 | 1900-01-01 18:20:00 | 124010 | 18:20:00 |

288 rows × 3 columns

It is suggested that patient p011 be eliminated, as it has the least data. Additionally, it is suggested that imputations be made according to time windows.

Duplicate Checking:# *Check for duplicates, if any, and decide what to

do with them*

Duplicates are not processed, as the dataset structure presents values by interval.

Only for the activity, the activity names are corrected, as mentioned in the code above.

Merging:# Explore if it is reasonable to merge the two datasets (train

and test) and briefly justify your decision.)

The merge is not performed because it is considered that there is enough data to perform initial model training. Including the test in the train or performing the merge implies greater complexity in an already complex dataset. It has too many null values and is difficult to process.

Graphs:# Provide visuals of all of your insights and discussions

```
#Look at one day
train_day = train.copy()
train_day["day_id"] = train['day_id']
train_day["time"] = train["time"]
train_day["hour"] = train["hour"]
#predicted variable
train_day["bg+1:00"] = train["bg+1:00"]

train_day
```

| | | id | p_num | time | bg- 5:55 | bg- 5:50 | bg- 5:45 | bg- 5:40 | bg- 5:35 | bg- 5:30 | bg- 5:25 | ... | acti |
|-----|--|-----------|--------------|---------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-----|-------------|
| 0 | | p01_0 | p01 | 1900-01-01 06:10:00 | NaN | NaN | 9.6 | NaN | NaN | 9.7 | NaN | ... | |
| 1 | | p01_1 | p01 | 1900-01-01 06:25:00 | NaN | NaN | 9.7 | NaN | NaN | 9.2 | NaN | ... | |
| 2 | | p01_2 | p01 | 1900-01-01 06:40:00 | NaN | NaN | 9.2 | NaN | NaN | 8.7 | NaN | ... | |
| 3 | | p01_3 | p01 | 1900-01-01 06:55:00 | NaN | NaN | 8.7 | NaN | NaN | 8.4 | NaN | ... | |
| 4 | | p01_4 | p01 | 1900-01-01 07:10:00 | NaN | NaN | 8.4 | NaN | NaN | 8.1 | NaN | ... | |
| ... | | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... |

```
#Graph the activity curves for each day for a patient
```

```
#1. Filter var- columns
```

```
import matplotlib.pyplot as plt
variables = ["bg-", "carbs-", "insulin-", "hr-", "steps-", "cals-"]
bg_cols = [col for col in train_day.columns if col.startswith("bg-")]
measurement_type = bg_cols[0].split("-")[0] if bg_cols else "?"
```

```
# 2. Choose the day you want to graph
```

```
selected_day = 59
```

```
# 3. Filter only the rows on the selected day
```

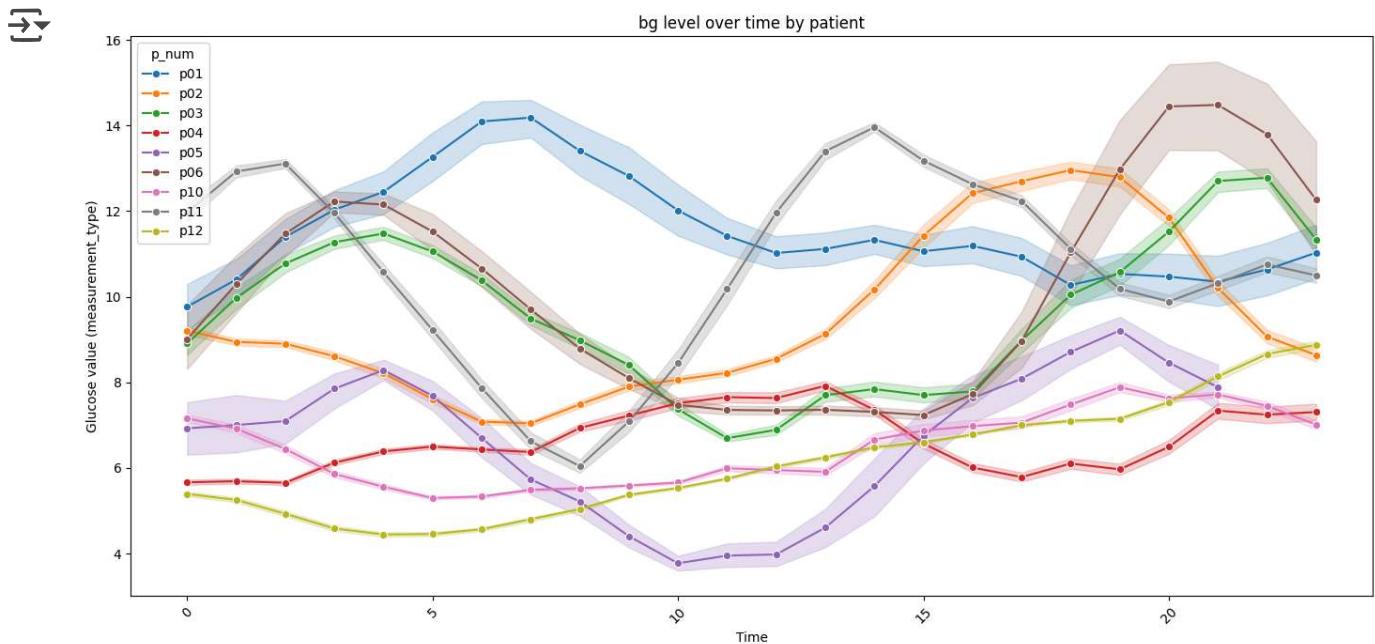
```
df_day = train_day[train_day["day_id"] == selected_day]
```

```
df_bg = df_day[["p_num", "day_id", "time", "hour"] + bg_cols].copy()
print(f"Datos disponibles para el día {selected_day}: {df_day.shape[0]} filas")
print(f"Columnas de glucosa (bg_cols): {bg_cols}")
# 2. Melt - pasamos de ancho a largo
df_melt = df_bg.melt(
```

```
    id_vars=["p_num", "day_id","hour", "time"],
    value_vars=bg_cols,
    var_name="bg_timepoint",
    value_name="bg_value"
)
```

→ Datos disponibles para el día 59: 2000 filas
Columnas de glucosa (bg_cols): ['bg-5:55', 'bg-5:50', 'bg-5:45', 'bg-5:40', 'bg-5:35']

```
plt.figure(figsize=(14, 7))
sns.lineplot(data=df_melt, x='hour', y='bg_value', hue='p_num', marker='o')
plt.title(f'{measurement_type} level over time by patient')
plt.xlabel('Time')
plt.ylabel(f'Glucose value ({measurement_type})')
plt.xticks(rotation=45)
plt.tight_layout()
plt.show()
```



```

import matplotlib.pyplot as plt
import seaborn as sns

# Variables de interés
variables = ["bg-", "carbs-", "insulin-", "hr-", "steps-", "cals-"]

# Día a graficar
selected_day = 59
df_day = train_day[train_day["day_id"] == selected_day].copy()

# Crear figura
fig, axes = plt.subplots(nrows=3, ncols=2, figsize=(18, 12), sharex=False)
axes = axes.flatten()

# Para cada variable
for i, prefix in enumerate(variables):

```

```
# Selecciona columnas con ese prefijo
cols = [col for col in train_day.columns if col.startswith(prefix)]
if not cols:
    continue

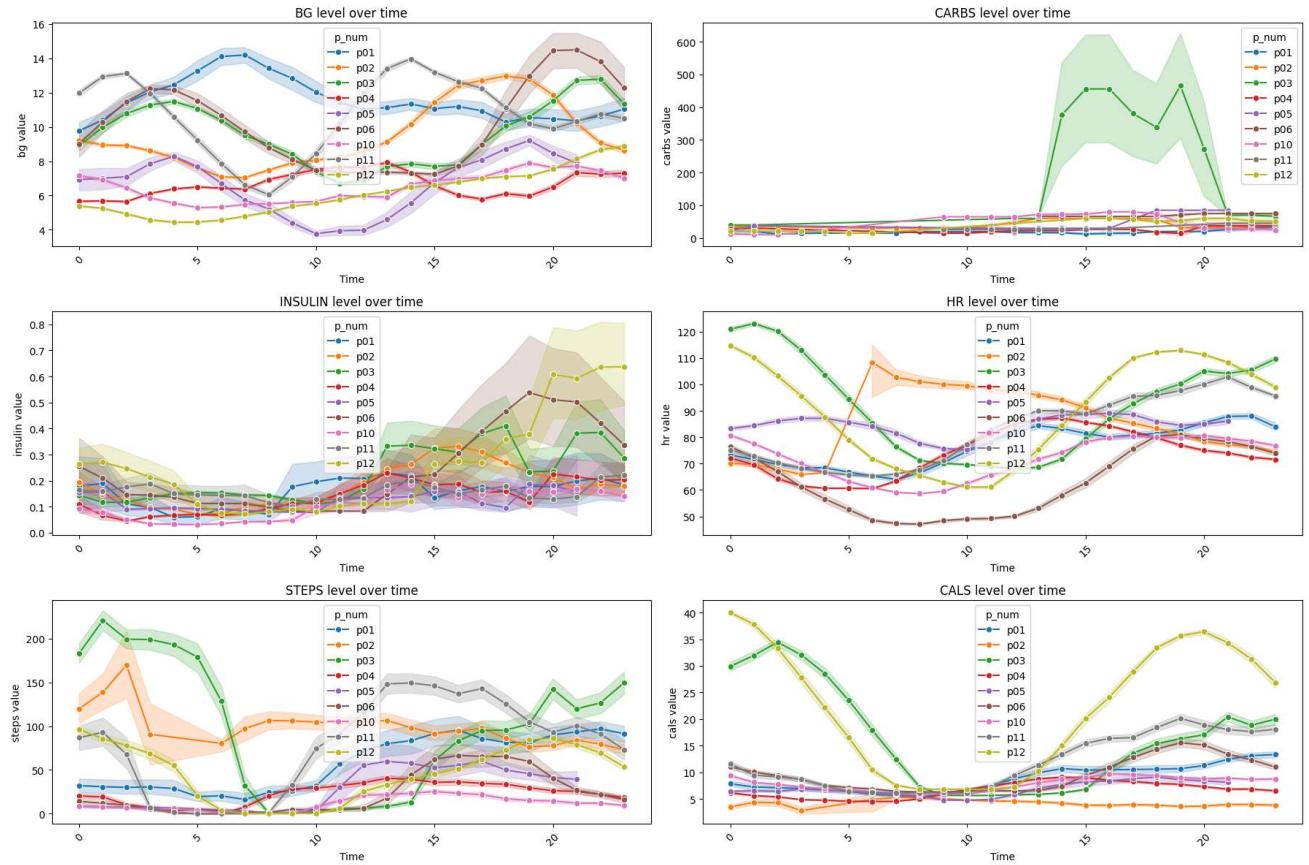
# Tipo de medición (ej. 'bg')
measurement_type = cols[0].split("-")[0] if cols else prefix[:-1]

# Seleccionar columnas para el día específico
df_var = df_day[["p_num", "day_id", "time", "hour"] + cols].copy()

# Melt para long format
df_melt = df_var.melt(
    id_vars=["p_num", "day_id", "hour", "time"],
    value_vars=cols,
    var_name=f"{measurement_type}_timepoint",
    value_name=f"{measurement_type}_value"
)

# Graficar
ax = axes[i]
sns.lineplot(
    data=df_melt,
    x='hour',
    y=f'{measurement_type}_value',
    hue='p_num',
    marker='o',
    ax=ax
)
ax.set_title(f'{measurement_type.upper()} level over time')
ax.set_xlabel("Time")
ax.set_ylabel(f'{measurement_type} value')
ax.tick_params(axis='x', rotation=45)

# Ajustar espacio
plt.tight_layout()
plt.show()
```

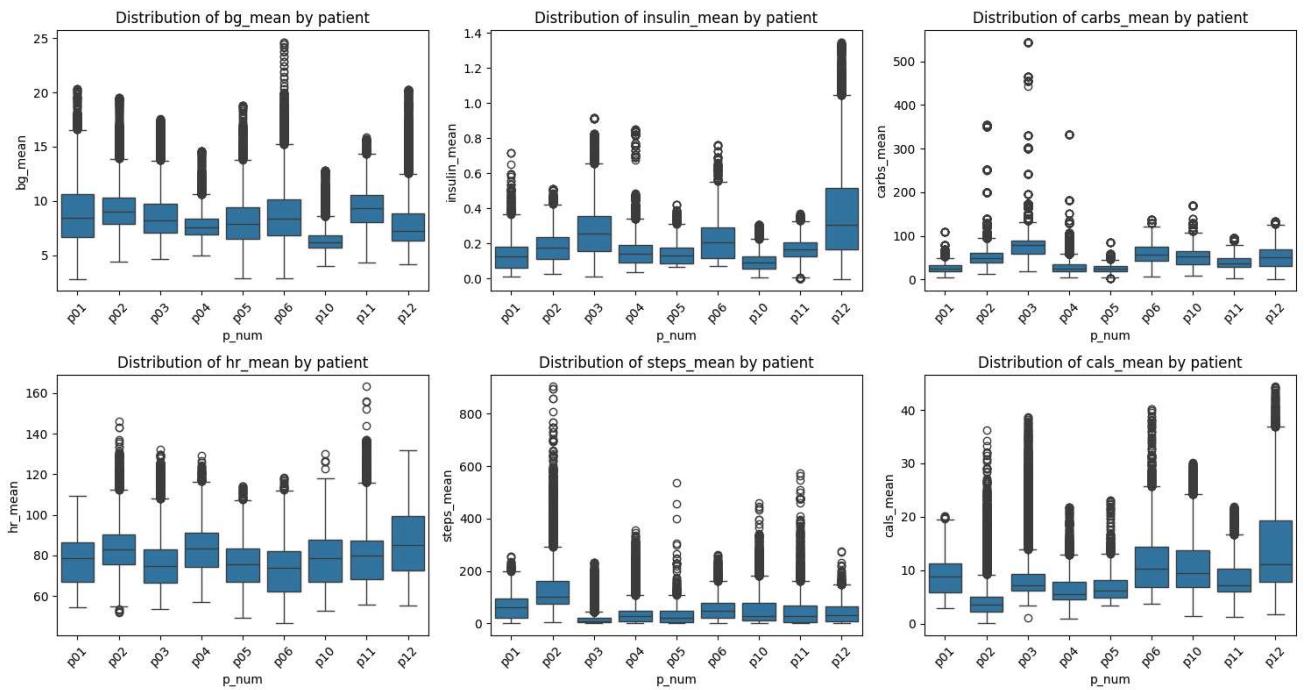


These graphs illustrate diurnal patterns of the monitored variables across different individuals. Some individuals show extreme spikes in variables such as carbohydrates and steps, while others maintain more stable profiles.

p03 stands out for having an extremely high peak carbohydrate intake around 3 p.m., far exceeding all other participants, and also exhibiting enormous variability at that time. In addition, is one of the participants with the highest step activity in the morning, reaching a significant peak.

p12 stands out for being the participant with the highest calorie levels overall.

```
stats_df["p_num"] = train_day["p_num"]
stats_df["time"] = train_day["time"]
# Only derived numeric columns
numeric_cols = [col for col in stats_df.columns if any(col.startswith(v) for v in ["bg",
                                                                 "calories", "steps", "carbohydrates", "protein", "fat", "sugar"])]  
  
import matplotlib.pyplot as plt
import seaborn as sns
import math  
  
# Filter columns ending with '_mean'
mean_cols = [col for col in numeric_cols if col.endswith('_mean')]  
  
# Number of plots per row in the grid
cols_per_row = 3  
  
# Total number of plots
n = len(mean_cols)  
  
# Calculate the number of rows needed
rows = math.ceil(n / cols_per_row)  
  
# Create figure and axes
fig, axes = plt.subplots(rows, cols_per_row, figsize=(cols_per_row*5, rows*4))
axes = axes.flatten()  
  
# Generate boxplots in each subplot
for i, col in enumerate(mean_cols):
    sns.boxplot(data=stats_df, x="p_num", y=col, ax=axes[i])
    axes[i].set_title(f"Distribution of {col} by patient")
    axes[i].tick_params(axis='x', rotation=45)  
  
# Remove empty axes if any
for j in range(i + 1, len(axes)):
    fig.delaxes(axes[j])  
  
plt.tight_layout()
plt.show()
```



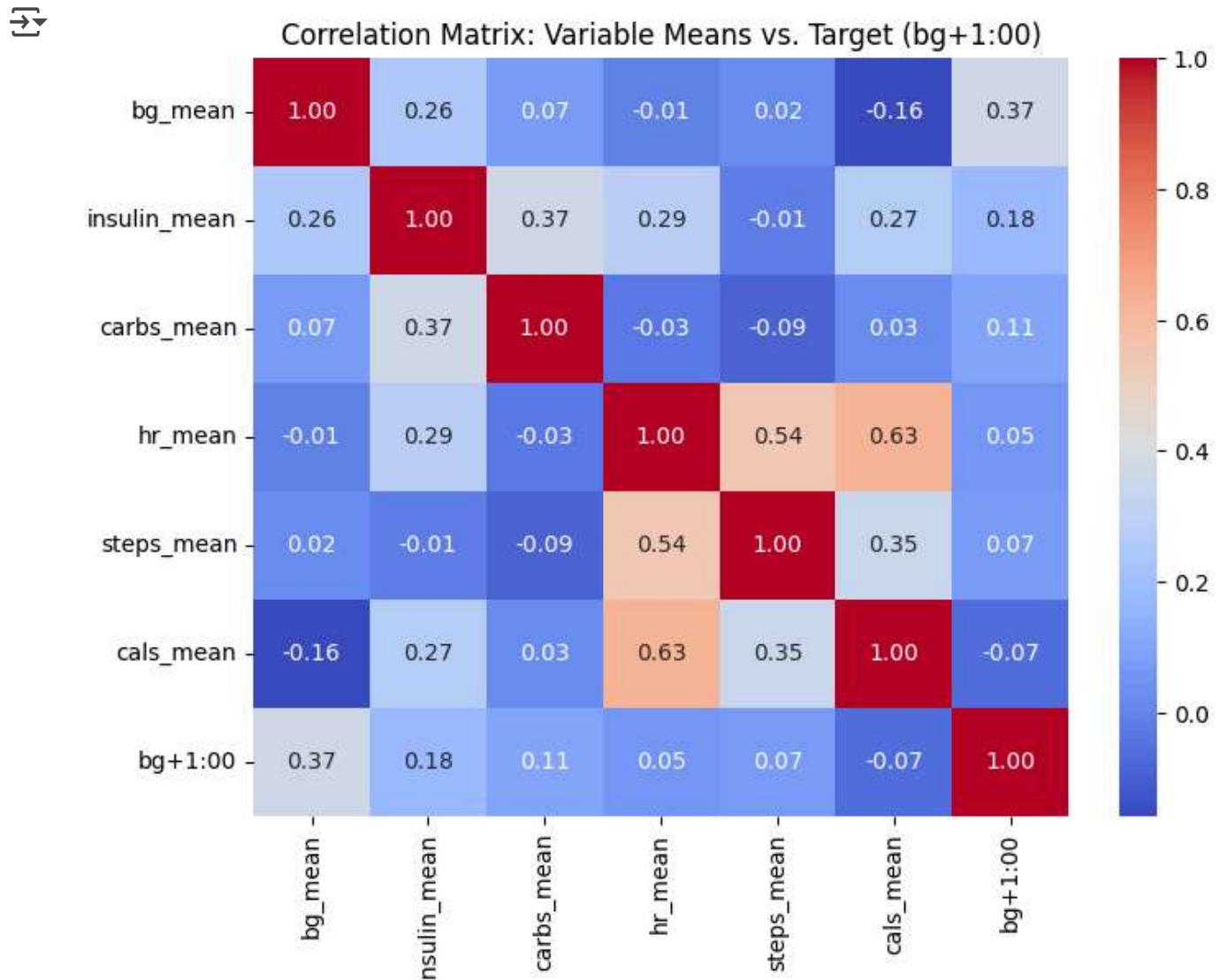
The boxplots per patient reveal high individual variability in mean glucose (bg_mean), insulin (insulin_mean), and carbohydrate (carbs_mean) values. Although most patients had similar central ranges, numerous outliers indicating extreme events were observed. P03 stands out for its highly variable carbohydrate intake and extremely high peaks, P12 for its consistently high mean insulin levels, and P05 and P06 for showing abnormally high glucose values.

Patient p06 consistently shows a significantly lower average heart rate, setting them apart from the rest, while p02 exhibits the highest and most consistent step activity, suggesting a more active lifestyle. Meanwhile, p12 stands out with the highest average caloric intake and variability,

Correlation between statistics and future glucose

```
mean_cols = [col for col in stats_df.columns if col.endswith("_mean")]
stats_df_with_target = stats_df[mean_cols].copy()
stats_df_with_target["bg+1:00"] = train_day["bg+1:00"]
corr_matrix = stats_df_with_target.corr()
```

```
plt.figure(figsize=(8, 6))
sns.heatmap(corr_matrix, annot=True, cmap="coolwarm", fmt=".2f")
plt.title("Correlation Matrix: Variable Means vs. Target (bg+1:00)")
plt.show()
```



hr_mean (heart rate) and cals_mean (calories) (0.63) have Strong positive correlation, a higher average heart rate is strongly associated with a higher average calorie intake.

hr_mean (heart rate) and steps_mean (steps) (0.54): Moderate to strong positive correlation. This is logical: the greater the activity (more steps), the higher the heart rate.

I applies unsupervised clustering with KMeans to group patients based on their numerical characteristics from the summary_by_patient data frame. First, it standardizes the data so that all variables have the same scale (using StandardScaler), then runs KMeans with two groups (clusters) and assigns each patient their respective cluster. Finally, it prints the number of patients in each group and lists the patient IDs belonging to each group.

```
from sklearn.cluster import KMeans
from sklearn.preprocessing import StandardScaler

stats_by_patient = stats_df.copy()
stats_by_patient["p_num"] = train["p_num"]

summary_by_patient = stats_by_patient.groupby("p_num").mean()

summary_by_patient = stats_by_patient.groupby("p_num").mean()
X = summary_by_patient.copy()
X = X.drop(columns=["time"]) # ✅ this line fixes the error
scaler = StandardScaler()
X_scaled = scaler.fit_transform(X)

stats_df["p_num"].unique()

→ array(['p01', 'p02', 'p03', 'p04', 'p05', 'p06', 'p10', 'p11', 'p12'],
       dtype=object)

stats_by_patient["p_num"].unique()

→ array(['p01', 'p02', 'p03', 'p04', 'p05', 'p06', 'p10', 'p11', 'p12'],
       dtype=object)

summary_by_patient
```

| p_num | bg_mean | bg_max | bg_sum | bg_std | insulin_mean | insulin_max | insulin_st |
|-------|----------|-----------|------------|----------|--------------|-------------|------------|
| p01 | 8.929537 | 13.596678 | 210.284963 | 2.680693 | 0.133160 | 4.342846 | 9.58752 |
| p02 | 9.303589 | 12.959017 | 663.300286 | 1.960194 | 0.179241 | 4.212392 | 12.90534 |
| p03 | 8.599940 | 12.520286 | 611.805018 | 2.158641 | 0.269989 | 7.013686 | 19.43921 |
| p04 | 7.758556 | 11.121283 | 552.464235 | 1.746264 | 0.151264 | 3.783117 | 10.89098 |
| p05 | 8.127290 | 11.301243 | 185.189165 | 1.786217 | 0.142788 | 3.139265 | 10.28073 |
| p06 | 8.927207 | 12.498115 | 208.971359 | 2.064823 | 0.217821 | 5.837179 | 15.68312 |
| p10 | 6.375537 | 8.829367 | 453.147384 | 1.161909 | 0.096136 | 2.334856 | 6.92176 |
| p11 | 9.368038 | 13.053492 | 664.341894 | 2.009815 | 0.166653 | 3.443663 | 7.41193 |
| p12 | 7.861239 | 10.613665 | 555.036472 | 1.479968 | 0.376073 | 10.096783 | 27.07724 |

9 rows × 25 columns

```
kmeans = KMeans(n_clusters=2, random_state=42)
clusters = kmeans.fit_predict(X_scaled)
summary_by_patient["cluster"] = clusters
print(summary_by_patient["cluster"].value_counts())
```

```
cluster
0    7
1    2
Name: count, dtype: int64
```

```
# Patients from cluster 0
patients_cluster_0 = summary_by_patient[summary_by_patient["cluster"] == 0].index.tolist()
patients_cluster_0
```

```
['p01', 'p02', 'p04', 'p05', 'p06', 'p10', 'p11']
```

```
# Cluster 1 patients
patients_cluster_1 = summary_by_patient[summary_by_patient["cluster"] == 1].index.tolist()
patients_cluster_1
```

```
['p03', 'p12']
```

As observed in the KNN analysis, the patients' clusters that the model classifies are patients_cluster_0 ['p01', 'p02', 'p04', 'p05', 'p06', 'p10', 'p11'] and patients_cluster_1 ['p03', 'p12']

```
import seaborn as sns
import matplotlib.pyplot as plt

# Definir los grupos de pacientes manualmente
pacientes_cluster_0 = ['p01', 'p02', 'p04', 'p05', 'p06', 'p10', 'p11']
pacientes_cluster_1 = ['p03', 'p12']

# Añadir los identificadores de paciente al DataFrame de estadísticos
stats_df_with_target = stats_df.copy()
stats_df_with_target["p_num"] = train["p_num"]
stats_df_with_target["bg+1:00"] = train_day["bg+1:00"]

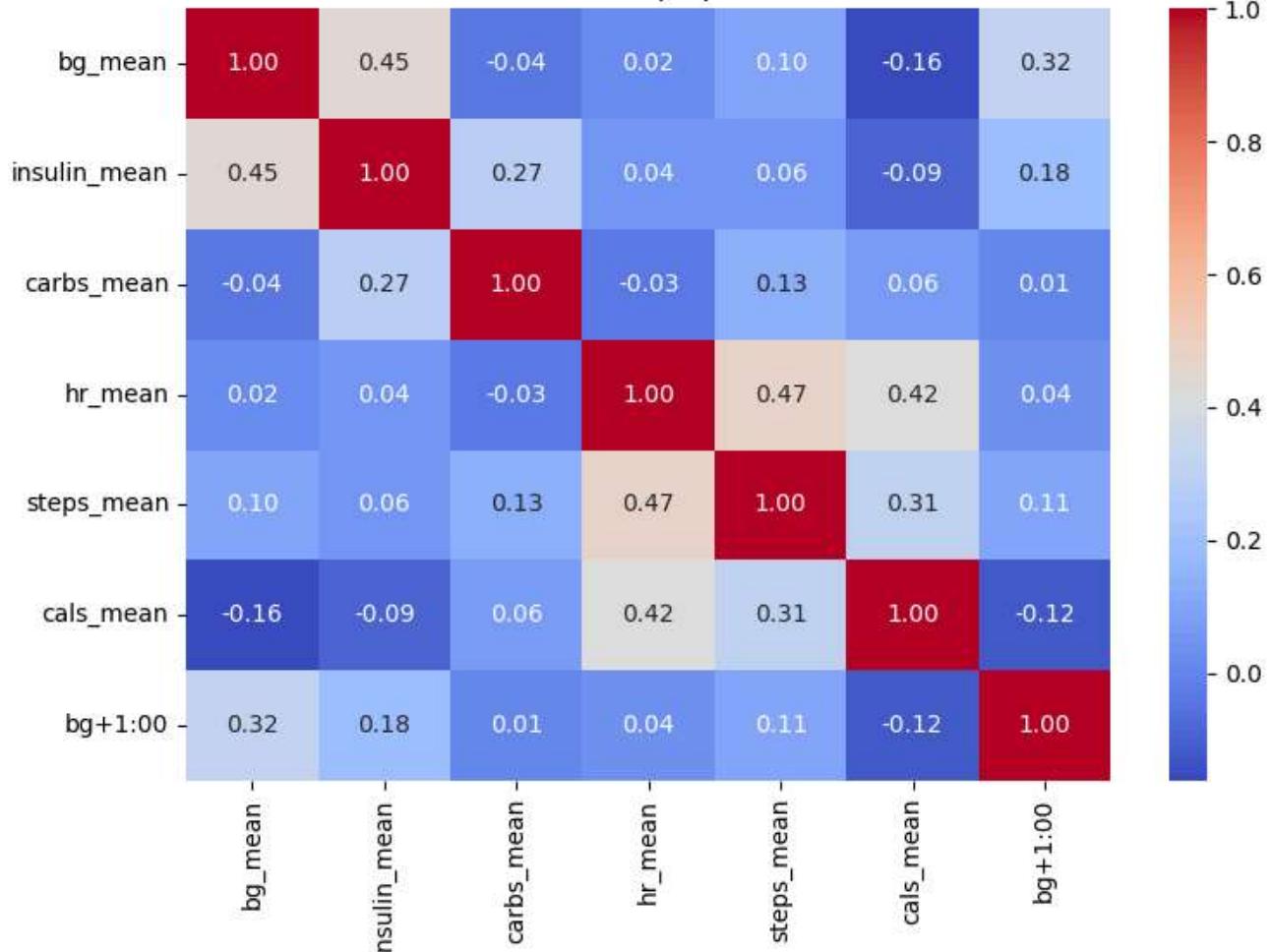
# Filtrar solo las columnas que terminan en "_mean"
mean_cols = [col for col in stats_df.columns if col.endswith("_mean")]

# Función para graficar el heatmap por grupo
def plot_corr_for_group(pacientes, cluster_name):
    subset = stats_df_with_target[stats_df_with_target["p_num"].isin(pacientes)]
    data = subset[mean_cols + ["bg+1:00"]].dropna()

    # Verificar que haya datos suficientes
    if data.shape[1] > 1 and not data.empty:
        corr_matrix = data.corr()
        plt.figure(figsize=(8, 6))
        sns.heatmap(corr_matrix, annot=True, cmap="coolwarm", fmt=".2f")
        plt.title(f"Correlation Matrix - Grupo pacientes {cluster_name}")
        plt.tight_layout()
        #plt.show()
    else:
        print(f"No hay suficientes datos para graficar el grupo {cluster_name}.")  
plot_corr_for_group(pacientes_cluster_0, "Cluster 0")
```



Correlation Matrix - Grupo pacientes Cluster 0

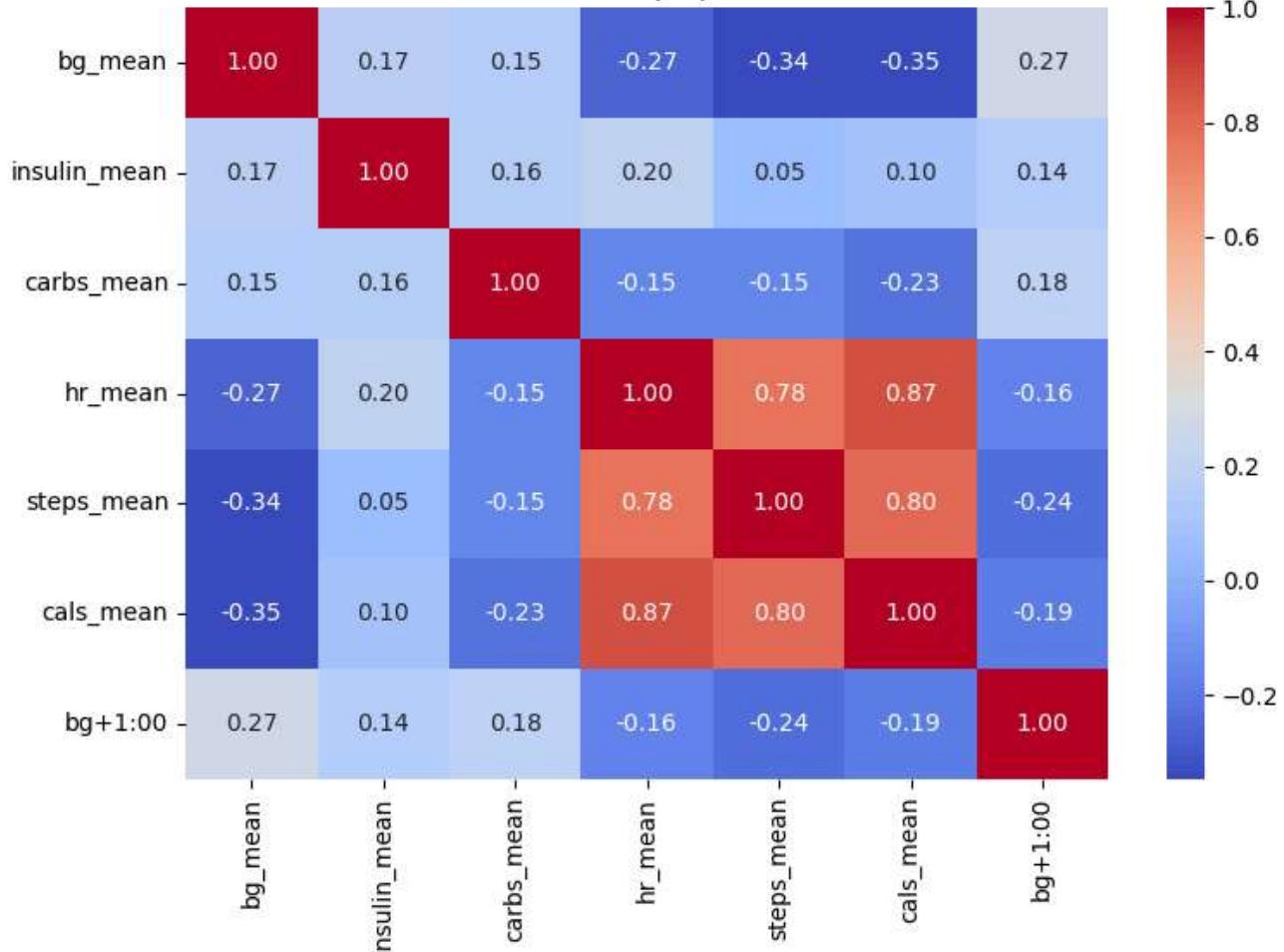


This correlation matrix visualizes the relationships between different variables for "Patient Group Cluster 0." The values in each cell indicate the correlation coefficient between the corresponding variables, with warmer colors (red) representing strong positive correlations and cooler colors (blue) indicating strong negative correlations. For example, a moderate positive correlation is observed between "hr_mean" and "steps_mean" (0.47), suggesting that as one increases, the other tends to do so.

```
plot_corr_for_group(pacientes_cluster_1, "Cluster 1")
```



Correlation Matrix - Grupo pacientes Cluster 1



This correlation matrix corresponds to "Patient Group Cluster 1". It highlights a strong positive correlation between "hr_mean", "steps_mean" and "cals_mean", with values ranging from 0.78 to 0.87, suggesting a close relationship between heart rate, steps and calories burned in this group. On the other hand, variables such as "bg_mean" and "insulin_mean" show generally weak correlations with most of the other variables in this cluster.

```
#Review distribution of activities
activity_cols = [col for col in train.columns if col.startswith("activity-")]
train_activity = train[activity_cols].astype(str) # Asegurarse que son string

train_activity
```

→

| | activity-5:55 | activity-5:50 | activity-5:45 | activity-5:40 | activity-5:35 | activity-5:30 | activity-5:25 |
|--------|---------------|---------------|---------------|---------------|---------------|---------------|---------------|
| 0 | nan |
| 1 | nan |
| 2 | nan |
| 3 | nan |
| 4 | nan |
| ... | ... | ... | ... | ... | ... | ... | ... |
| 177019 | nan |
| 177020 | nan |
| 177021 | nan |
| 177022 | nan |
| 177023 | nan |

177024 rows × 72 columns

```
# This counts how many times each activity appears in each row
activity_summary = train_activity[activity_cols].apply(lambda row: row.value_counts(), axis=1)
# Join with the p_num column to group by patient
activity_summary["p_num"] = train["p_num"]
```

```
activity_summary["Walking"].unique()
```

→ array([0., 2., 4., 1., 5., 8., 3., 6., 7., 11., 10., 13., 9.,
 12., 16., 19., 21., 20., 18., 15., 17., 22., 24., 27., 30., 31.,
 14., 23., 26., 29., 28., 25., 32., 33., 34., 35., 36., 37., 38.,
 39., 40., 41., 42., 43., 44., 45., 46., 49., 52., 55., 57., 53.,
 50., 47.])

```
activity_by_patient = activity_summary.groupby("p_num").sum(numeric_only=True)
activity_by_patient = activity_by_patient.drop(columns=["nan"])
activity_by_patient
```

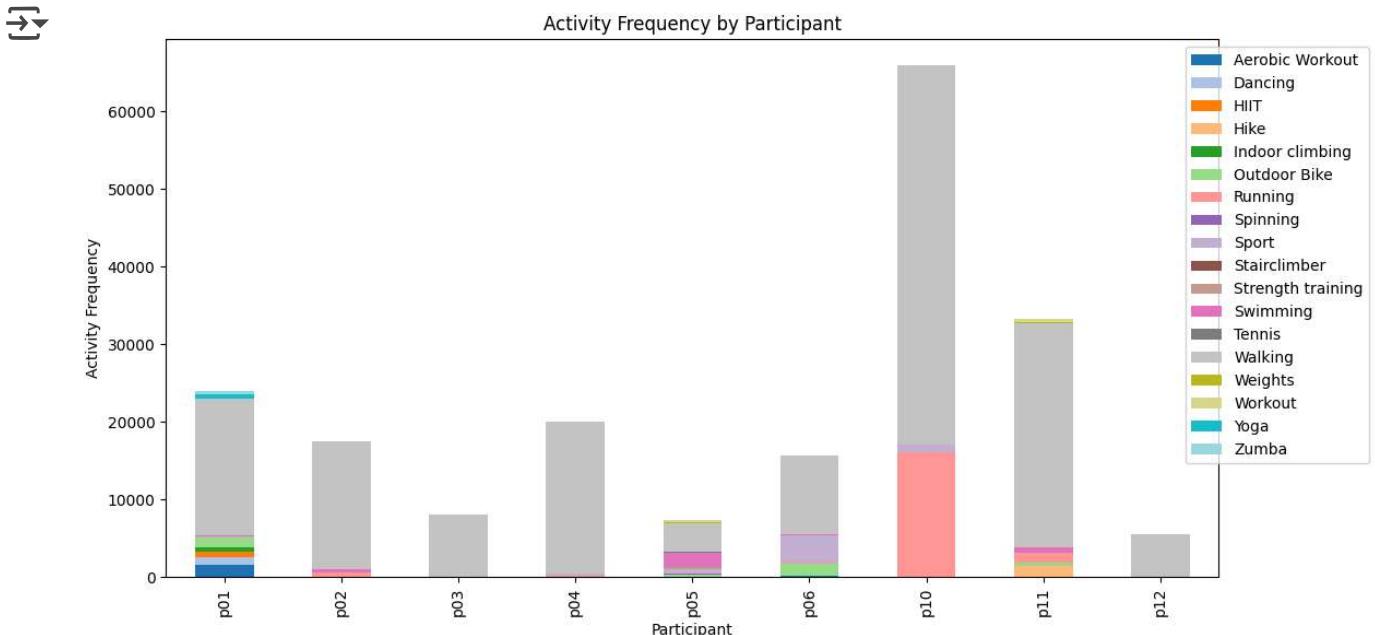


| | Aerobic Workout | Dancing | HIIT | Hike | Indoor climbing | Outdoor Bike | Running | Spinning | Sport | S |
|-------|-----------------|---------|-------|--------|-----------------|--------------|---------|----------|--------|-----|
| p_num | | | | | | | | | | |
| p01 | 1543.0 | 1025.0 | 738.0 | 0.0 | 520.0 | 1228.0 | 0.0 | 0.0 | 119.0 | |
| p02 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 600.0 | 0.0 | 0.0 | 0.0 |
| p03 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| p04 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 216.0 | 0.0 | 288.0 | |
| p05 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 281.0 | 0.0 | 144.0 | 594.0 | |
| p06 | 120.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1583.0 | 72.0 | 0.0 | 3541.0 | |
| p10 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 16050.0 | 0.0 | 1062.0 | |
| p11 | 0.0 | 0.0 | 0.0 | 1440.0 | 0.0 | 432.0 | 1224.0 | 0.0 | 0.0 | 0.0 |
| 12 | ^ ^ | ^ ^ | ^ ^ | ^ ^ | ^ ^ | ^ ^ | ^ ^ | ^ ^ | ^ ^ | ^ ^ |

```
#Display how many times (frequency) each type of activity appears per participant.
df_plot = activity_by_patient
```

```
df_plot.plot(kind='bar', stacked=True, figsize=(12, 6), colormap='tab20')

plt.title('Activity Frequency by Participant')
plt.xlabel('Participant')
plt.ylabel('Activity Frequency')
plt.legend(loc='upper right', bbox_to_anchor=(1.15, 1)) # adjust the legend if it gets in
plt.tight_layout()
plt.show()
```



The stacked bar chart shows the frequency of different types of physical activity per participant. Most participants primarily engaged in "Workout," which was the most common activity, followed by "Running". Participant p10 stands out with significantly higher activity levels than the rest, especially in "Workout" and "Running." Other participants such as p01, p04, and p11 also exhibit high levels of activity. In contrast, p03 and p12 have the lowest frequency.

This contrasts with the results obtained for patients p3 and p12, which showed a high correlation with calories burned, heart rate, and steps taken.

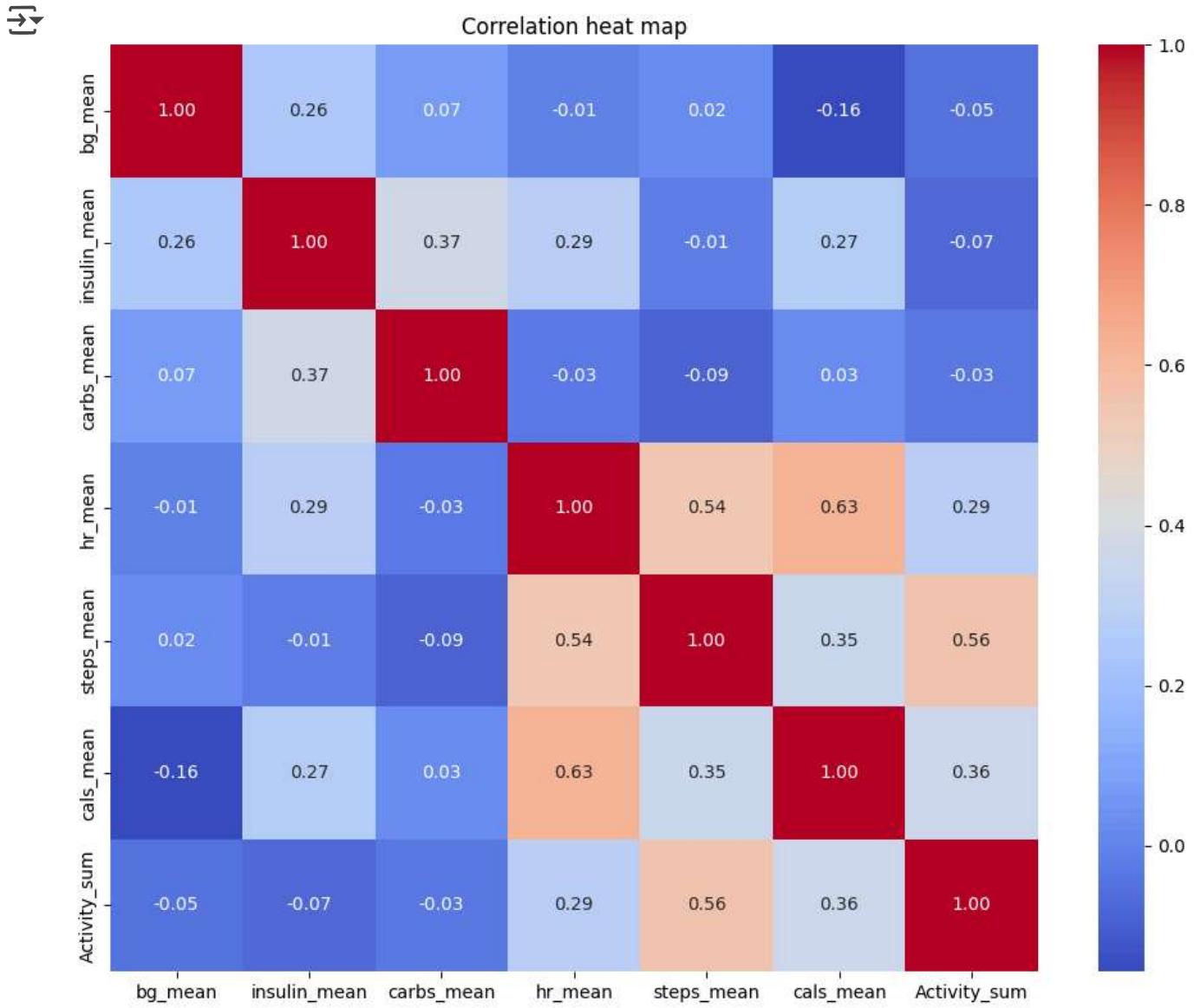
The number of times any activity appears is added together and the column sum of activities is created

```
# List of activity columns to sum
activity_columns = [
    "Indoor climbing", "Running", "Strength training", "Swimming", "Dancing",
    "Stairclimber", "Spinning", "HIIT", "Outdoor Bike", "Walking",
    "Aerobic Workout", "Tennis", "Workout", "Hike", "Zumba", "Sport",
    "Yoga", "Weights"]
```

```
# Sum the values row-wise and store the result in a new column
stats_by_patient["Activity_sum"] = activity_summary[activity_columns].sum(axis=1)

#plot a heatmap of correlations between all columns ending in '_mean' and the Activity_su
cols_interes = [col for col in stats_by_patient.columns if col.endswith('_mean')]
cols_interes.append('Activity_sum')
df_corr = stats_by_patient[cols_interes]

plt.figure(figsize=(10, 8))
sns.heatmap(df_corr.corr(), annot=True, cmap='coolwarm', fmt=".2f", square=True)
plt.title("Correlation heat map")
plt.tight_layout()
plt.show()
```



The heatmap shows that the sum of activities is correlated with the variables "Steps."

```
import seaborn as sns
import matplotlib.pyplot as plt

# define clusters
pacientes_cluster_0 = ['p01', 'p02', 'p04', 'p05', 'p06', 'p10', 'p11']
pacientes_cluster_1 = ['p03', 'p12']
```

```
stats_df_with_target = stats_by_patient.copy()
stats_df_with_target
```

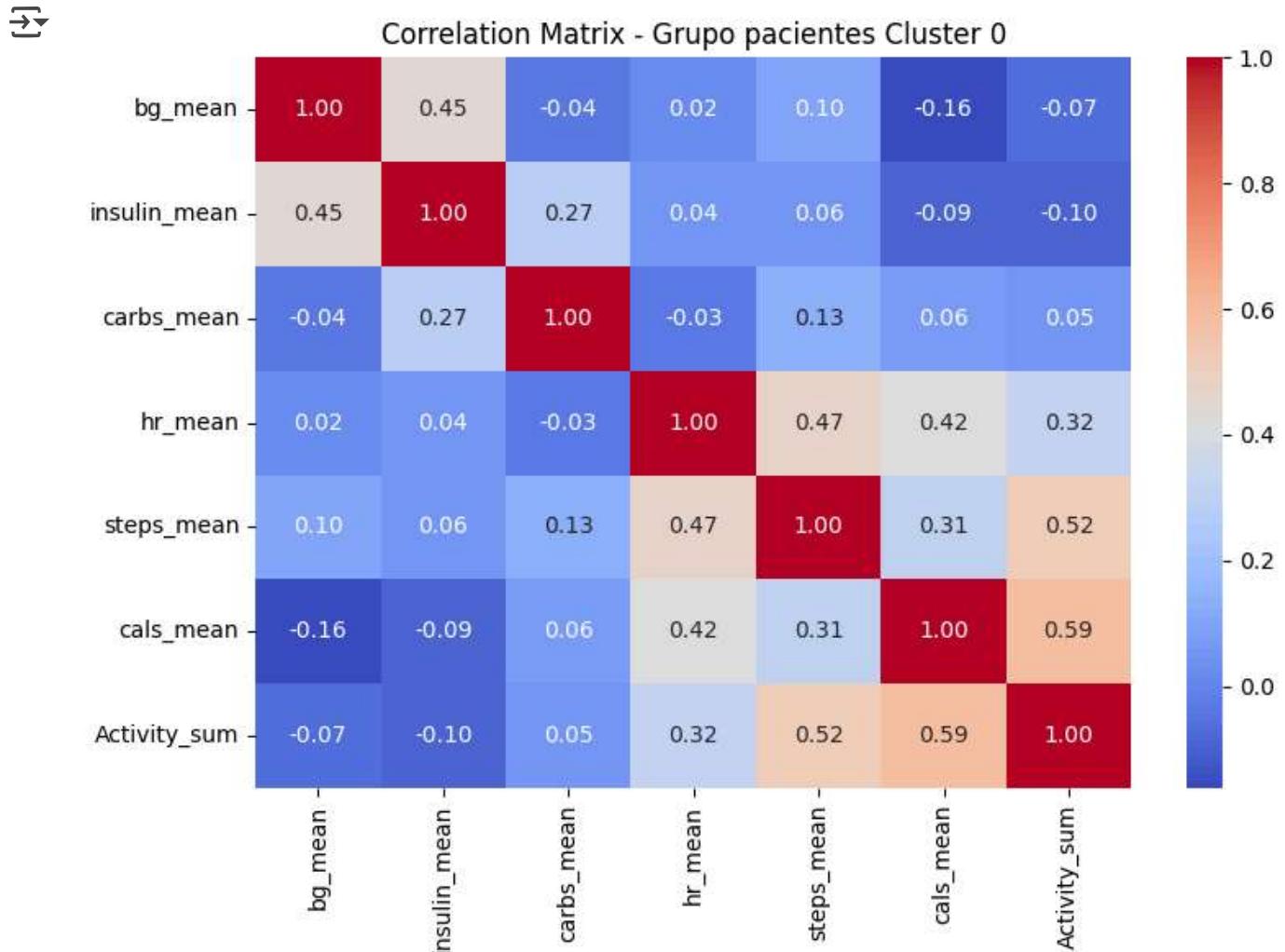
| | bg_mean | bg_max | bg_sum | bg_std | insulin_mean | insulin_max | insulin_sum | i |
|---------------|-----------|--------|--------|----------|--------------|-------------|-------------|-----|
| 0 | 13.341667 | 18.4 | 320.2 | 3.710492 | 0.025894 | 0.0583 | 1.8644 | |
| 1 | 13.541667 | 18.4 | 325.0 | 3.628500 | 0.027286 | 0.0583 | 1.9646 | |
| 2 | 13.716667 | 18.4 | 329.2 | 3.535247 | 0.028678 | 0.0583 | 2.0648 | |
| 3 | 13.908333 | 18.4 | 333.8 | 3.401907 | 0.030069 | 0.0583 | 2.1650 | |
| 4 | 14.104167 | 18.4 | 338.5 | 3.219435 | 0.031461 | 0.0583 | 2.2652 | |
| ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 177019 | 8.169444 | 10.4 | 588.2 | 1.043780 | 0.386319 | 13.0750 | 27.8150 | |
| 177020 | 8.190278 | 10.4 | 589.7 | 1.071153 | 0.397222 | 13.0750 | 28.6000 | |
| 177021 | 8.212500 | 10.7 | 591.3 | 1.106312 | 0.404306 | 13.0750 | 29.1100 | |
| 177022 | 8.237500 | 11.0 | 593.1 | 1.148476 | 0.403958 | 13.0750 | 29.0850 | |
| 177023 | 8.268056 | 11.6 | 595.3 | 1.207585 | 0.403264 | 13.0750 | 29.0350 | |

177024 rows × 27 columns

```
mean_cols = [col for col in stats_df.columns if col.endswith("_mean")]
# Función para graficar el heatmap por grupo
def plot_corr_for_group(pacientes, cluster_name):
    subset = stats_df_with_target[stats_df_with_target["p_num"].isin(pacientes)]
    data = subset[mean_cols + ["Activity_sum"]].dropna()
    # Verificar que haya datos suficientes
    if data.shape[1] > 1 and not data.empty:
        corr_matrix = data.corr()
        plt.figure(figsize=(8, 6))
```

```
sns.heatmap(corr_matrix, annot=True, cmap="coolwarm", fmt=".2f")
plt.title(f"Correlation Matrix - Grupo pacientes {cluster_name}")
plt.tight_layout()
#plt.show()
else:
    print(f"No hay suficientes datos para graficar el grupo {cluster_name}.")
```

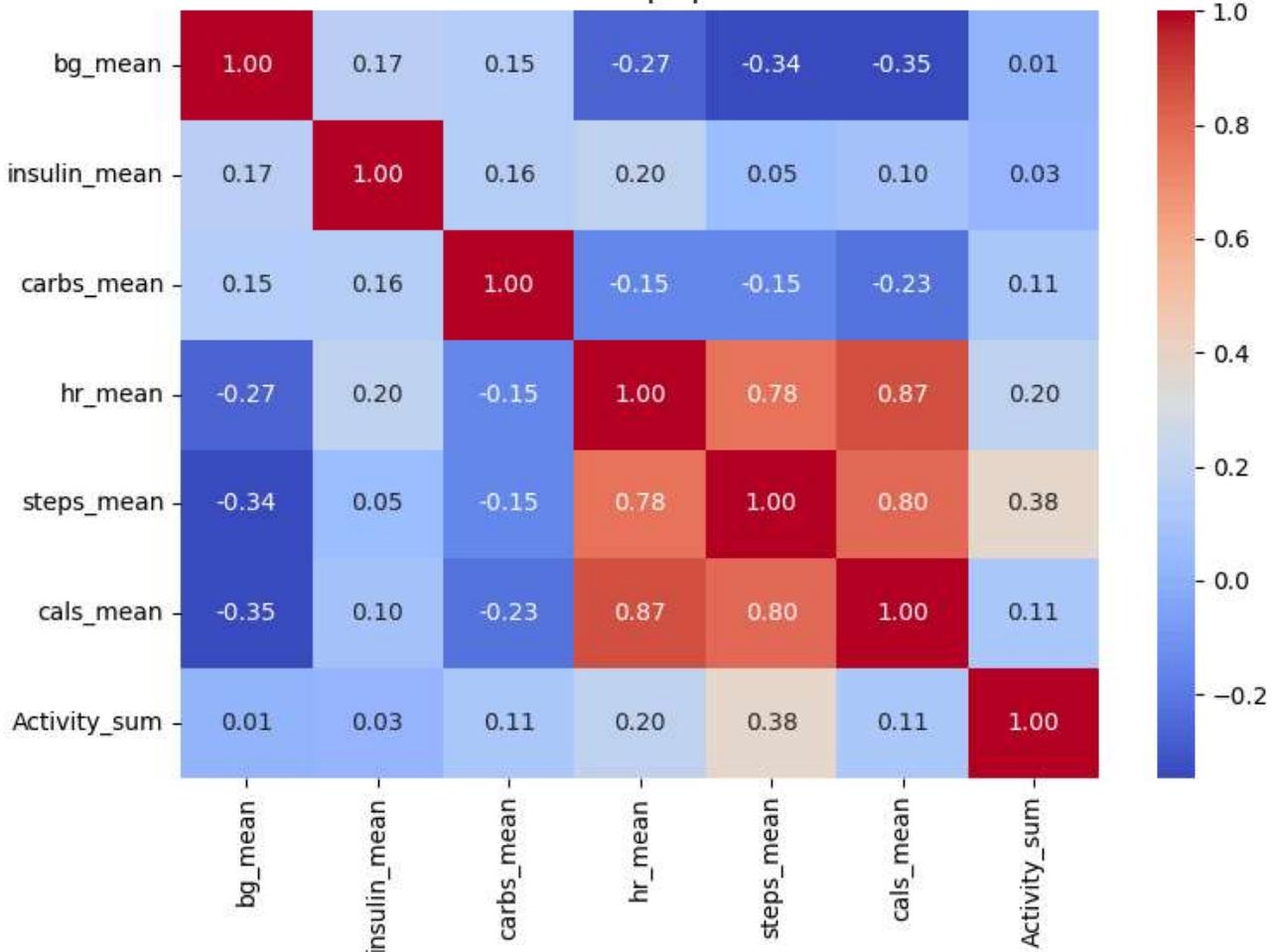
```
plot_corr_for_group(pacientes_cluster_0, "Cluster 0")
```



```
plot_corr_for_group(pacientes_cluster_1, "Cluster 1")
```



Correlation Matrix - Grupo pacientes Cluster 1



In these graphs a stronger relationship is observed for patients in cluster 0 'p01', 'p02', 'p04', 'p05', 'p06', 'p10', 'p11' and patients in cluster 1: p03', 'p12'. It is observed how a different behavior continues to exist for these two patients in cluster one, in the association of steps, heart rate, and calorie burning. Questions that may arise from data collection.

```
#Once we have analyzed the variables without processing the data, we will analyze the tim
#Group each 72 columns into blocks of 3
# (i.e., 24 blocks of 15 minutes), and then calculate the average per block.
```

```
variables = ["bg", "insulin", "carbs", "hr", "steps", "cals"]
```

```
for var in variables:
    var_cols = [col for col in train.columns if col.startswith(f"{var}-")]
```

```
for i in range(24):
    cols_3 = var_cols[i*3:(i+1)*3]
    train[f"{var}_avg_{i}"] = train[cols_3].mean(axis=1)
```

```
avg_cols = [col for col in train.columns if "_avg_" in col]
```

```
df_clean = train[["p_num", "time"] + avg_cols].copy()
```

→ Mostrar salida oculta

```
# Add the target variable bg+1:00
df_clean["target"] = train["bg+1:00"]
```

```
#bg+1:00 missing values:
print(df_clean["target"].isna().sum())
```

→ 0

This data frame has the columns averaged every three columns to be able to have the same range of the "time" column

```
df_clean
```

| | p_num | time | bg_avg_0 | bg_avg_1 | bg_avg_2 | bg_avg_3 | bg_avg_4 | bg_avg_5 |
|--------|-------|---------------------|-----------|-----------|-----------|----------|-----------|-----------|
| 0 | p01 | 1900-01-01 06:10:00 | 9.600000 | 9.700000 | 9.200000 | 8.700000 | 8.400000 | 8.100000 |
| 1 | p01 | 1900-01-01 06:25:00 | 9.700000 | 9.200000 | 8.700000 | 8.400000 | 8.100000 | 8.300000 |
| 2 | p01 | 1900-01-01 06:40:00 | 9.200000 | 8.700000 | 8.400000 | 8.100000 | 8.300000 | 9.600000 |
| 3 | p01 | 1900-01-01 06:55:00 | 8.700000 | 8.400000 | 8.100000 | 8.300000 | 9.600000 | 11.100000 |
| 4 | p01 | 1900-01-01 07:10:00 | 8.400000 | 8.100000 | 8.300000 | 9.600000 | 11.100000 | 11.800000 |
| ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 177019 | p12 | 1900-01-01 23:35:00 | 9.033333 | 9.800000 | 10.266667 | 9.766667 | 9.033333 | 8.266667 |
| 177020 | p12 | 1900-01-01 23:40:00 | 9.233333 | 10.133333 | 10.133333 | 9.500000 | 8.866667 | 7.900000 |
| 177021 | p12 | 1900-01-01 23:45:00 | 9.466667 | 10.300000 | 9.966667 | 9.233333 | 8.633333 | 7.666667 |
| 177022 | p12 | 1900-01-01 23:50:00 | 9.800000 | 10.266667 | 9.766667 | 9.033333 | 8.266667 | 7.633333 |
| 177023 | p12 | 1900-01-01 23:55:00 | 10.133333 | 10.133333 | 9.500000 | 8.866667 | 7.900000 | 7.666667 |

177024 rows × 147 columns

```
#create periods of the day
def get_day_period(hour):
    if 0 <= hour < 6:
        return "night"
    elif 6 <= hour < 12:
        return "morning"
    elif 12 <= hour < 18:
        return "afternoon"
    else:
        return "evening"
```

```
df_clean["period"] = train["hour"].apply(get_day_period)
df_clean
```

| | p_num | time | bg_avg_0 | bg_avg_1 | bg_avg_2 | bg_avg_3 | bg_avg_4 | bg_avg_5 |
|--------|-------|---------------------|-----------|-----------|-----------|----------|-----------|-----------|
| 0 | p01 | 1900-01-01 06:10:00 | 9.600000 | 9.700000 | 9.200000 | 8.700000 | 8.400000 | 8.100000 |
| 1 | p01 | 1900-01-01 06:25:00 | 9.700000 | 9.200000 | 8.700000 | 8.400000 | 8.100000 | 8.300000 |
| 2 | p01 | 1900-01-01 06:40:00 | 9.200000 | 8.700000 | 8.400000 | 8.100000 | 8.300000 | 9.600000 |
| 3 | p01 | 1900-01-01 06:55:00 | 8.700000 | 8.400000 | 8.100000 | 8.300000 | 9.600000 | 11.100000 |
| 4 | p01 | 1900-01-01 07:10:00 | 8.400000 | 8.100000 | 8.300000 | 9.600000 | 11.100000 | 11.800000 |
| ... | ... | ... | ... | ... | ... | ... | ... | ... |
| 177019 | p12 | 1900-01-01 23:35:00 | 9.033333 | 9.800000 | 10.266667 | 9.766667 | 9.033333 | 8.266667 |
| 177020 | p12 | 1900-01-01 23:40:00 | 9.233333 | 10.133333 | 10.133333 | 9.500000 | 8.866667 | 7.900000 |
| 177021 | p12 | 1900-01-01 23:45:00 | 9.466667 | 10.300000 | 9.966667 | 9.233333 | 8.633333 | 7.666667 |
| 177022 | p12 | 1900-01-01 23:50:00 | 9.800000 | 10.266667 | 9.766667 | 9.033333 | 8.266667 | 7.633333 |
| 177023 | p12 | 1900-01-01 23:55:00 | 10.133333 | 10.133333 | 9.500000 | 8.866667 | 7.900000 | 7.666667 |

177024 rows × 148 columns

We can graph the time vs. the period for each of the variables

```
import matplotlib.pyplot as plt
import seaborn as sns
import pandas as pd
import math

# Orden correcto del periodo
period_order = ["morning", "afternoon", "evening", "night"]
```

```
# Asegurar que 'period' tenga orden categórico
df_clean["period"] = pd.Categorical(df_clean["period"], categories=period_order, ordered=True)

prefixes = ["bg", "insulin", "carbs", "hr", "steps", "cals"]
melted_dfs = []

# Melt por variable
for prefix in prefixes:
    cols = [col for col in df_clean.columns if col.startswith(f"{prefix}_avg_")]
    if not cols:
        continue
    temp = df_clean[cols].copy()
    temp["period"] = df_clean["period"]
    melted = temp.melt(id_vars="period",
                        var_name="timepoint",
                        value_name="value")
    melted["variable"] = prefix
    melted_dfs.append(melted)

# Combinar todos los derretidos
df_all_melted = pd.concat(melted_dfs, ignore_index=True)

# Agrupar por period y variable para promediar
avg_df = df_all_melted.groupby(["variable", "period"], observed=True)[["value"]].mean().reset_index()

# Crear grilla de gráficos
n_vars = len(prefixes)
cols_per_row = 2
rows = math.ceil(n_vars / cols_per_row)

fig, axes = plt.subplots(rows, cols_per_row, figsize=(cols_per_row * 7, rows * 5))
axes = axes.flatten()
```