Medication recommendation analysis

The dataset was taken from kaggle and is designed to assist in predicting recommended medications for patients. It incorporates a mix of patient health data, environmental variables, and lifestyle choices to improve model accuracy and better simulate real-world scenarios. To get the data and check the source. Click on the Link.

In [1]:
```
#import needed packages
import pandas as pd
import matplotlib.pyplot as plt
import numpy as np
import seaborn as sns
from sklearn import preprocessing
from sklearn import metrics
```

In [2]:
```
# Load in Dataset
df = pd.read_csv("enhanced_fever_medicine_recommendation.csv")
```

In [3]:
```
# Look at Dataset
# 1000 Samples
# 19 features and 1 target column
df
```

Out[3]:

	Temperature	Fever_Severity	Age	Gender	BMI	Headache	Body_Ache	Fatigue	Chronic_Condit
0	36.1	Normal	89	Female	24.0	No	Yes	No	
1	37.5	Mild Fever	94	Male	26.6	No	No	No	
2	36.4	Normal	92	Male	27.8	No	No	No	
3	39.8	High Fever	66	Male	18.7	No	Yes	No	
4	39.3	High Fever	28	Male	21.0	No	Yes	No	
...	...	...	...	...	...	...	...	...	
995	39.9	High Fever	59	Male	22.1	Yes	Yes	Yes	
996	36.9	Normal	74	Female	18.1	Yes	Yes	Yes	
997	36.1	Normal	8	Female	29.6	Yes	Yes	No	
998	38.8	High Fever	87	Female	25.2	No	No	No	
999	38.2	High Fever	65	Female	26.0	No	Yes	No	

1000 rows × 20 columns

We can make a list of important features for our analysis

Describing Features:

1. Temperature (Celsius)
2. Age (1-100)
3. Gender (Male or Female)
4. BMI (Body Mass Index)
5. Headache (Yes or No)
6. Body_Ache (Yes or No)
7. Fatigue (Yes or No)
8. Chronic_Conditions (Yes or No)
9. Allergies (Yes or No)
10. Smoking_History (Yes or No)
11. Alcohol_Consumption (Yes or No)
12. Physical_Activity (Sedentary, Moderate, Active)
13. Diet_Type (Vegetarian, Non-Vegetarian, Vegan)
14. Heart_Rate (Resting Heart rate)
15. Blood_Pressure (Normal, High, Low)
16. Previous_Medication (Paracetamol, Ibuprofen, Aspirin, None)
17. Recommended_Medication (Paracetamol or Ibuprofen)
18. Humidity (Patient's area)
19. AQI (Air Quality Index)
20. Fever_Severity (Normal, Mild or High)

Most important ones:

1. Temperature
2. Age
3. Gender
4. Recommended_Medication
5. Previous_Medication
6. Fever_Severity

In [4]:
```
#If you need to get rid of categorized columns
from sklearn.preprocessing import LabelEncoder

le =LabelEncoder()

dfle = df

dfle.Fever_Severity = le.fit_transform(dfle.Fever_Severity)
dfle.Gender = le.fit_transform(dfle.Gender)
dfle.Headache = le.fit_transform(dfle.Headache)
dfle.Body_Ache = le.fit_transform(dfle.Body_Ache)
dfle.Fatigue = le.fit_transform(dfle.Fatigue)
dfle.Chronic_Conditions = le.fit_transform(dfle.Chronic_Conditions)
dfle.Allergies = le.fit_transform(dfle.Allergies)
dfle.Smoking_History = le.fit_transform(dfle.Smoking_History)
dfle.Alcohol_Consumption = le.fit_transform(dfle.Alcohol_Consumption)
dfle.Physical_Activity = le.fit_transform(dfle.Physical_Activity)
```

```
dfle.Diet_Type = le.fit_transform(dfle.Diet_Type)
dfle.Blood_Pressure = le.fit_transform(dfle.Blood_Pressure)
dfle.Previous_Medication = le.fit_transform(dfle.Previous_Medication)
dfle.Recommended_Medication = le.fit_transform(dfle.Recommended_Medication)

dfle
```

Out[4]:

	Temperature	Fever_Severity	Age	Gender	BMI	Headache	Body_Ache	Fatigue	Chronic_Condit
0	36.1	2	89	0	24.0	0	1	0	
1	37.5	1	94	1	26.6	0	0	0	
2	36.4	2	92	1	27.8	0	0	0	
3	39.8	0	66	1	18.7	0	1	0	
4	39.3	0	28	1	21.0	0	1	0	
...	...	...	...	...	...	...	...	...	
995	39.9	0	59	1	22.1	1	1	1	
996	36.9	2	74	0	18.1	1	1	1	
997	36.1	2	8	0	29.6	1	1	0	
998	38.8	0	87	0	25.2	0	0	0	
999	38.2	0	65	0	26.0	0	1	0	

1000 rows × 20 columns

In [5]:
```
#Split the model for training
from sklearn.model_selection import train_test_split
X = dfle.drop('Fever_Severity', axis= 1)
y = dfle['Fever_Severity']

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=
```

In [6]:
```
#Try Various models
from sklearn.model_selection import KFold
from sklearn.linear_model import LinearRegression
from sklearn.metrics import mean_squared_error

kf= KFold(n_splits=5, shuffle=True, random_state=42)
```

In [7]:
```
# The error is low, which is good
for train_index, test_index in kf.split(X):
    X_train, X_test = X.iloc[train_index], X.iloc[test_index]
    y_train, y_test = y.iloc[train_index], y.iloc[test_index]

    model = LinearRegression()

    model.fit(X_train, y_train)

    y_pred= model.predict(X_test)
```

```
    mse= mean_squared_error(y_test, y_pred)
    print(f"Mean Squared Error: {mse}")
```

```
Mean Squared Error: 0.12491733943533895
Mean Squared Error: 0.14064663336470795
Mean Squared Error: 0.11463678723586966
Mean Squared Error: 0.12378715327803257
Mean Squared Error: 0.11266644806090119
```

In [8]:
```
# Try another model
from sklearn.ensemble import RandomForestClassifier

model = RandomForestClassifier()
model.fit(X_train, y_train)
```

Out[8]:
```
RandomForestClassifier
RandomForestClassifier()
```

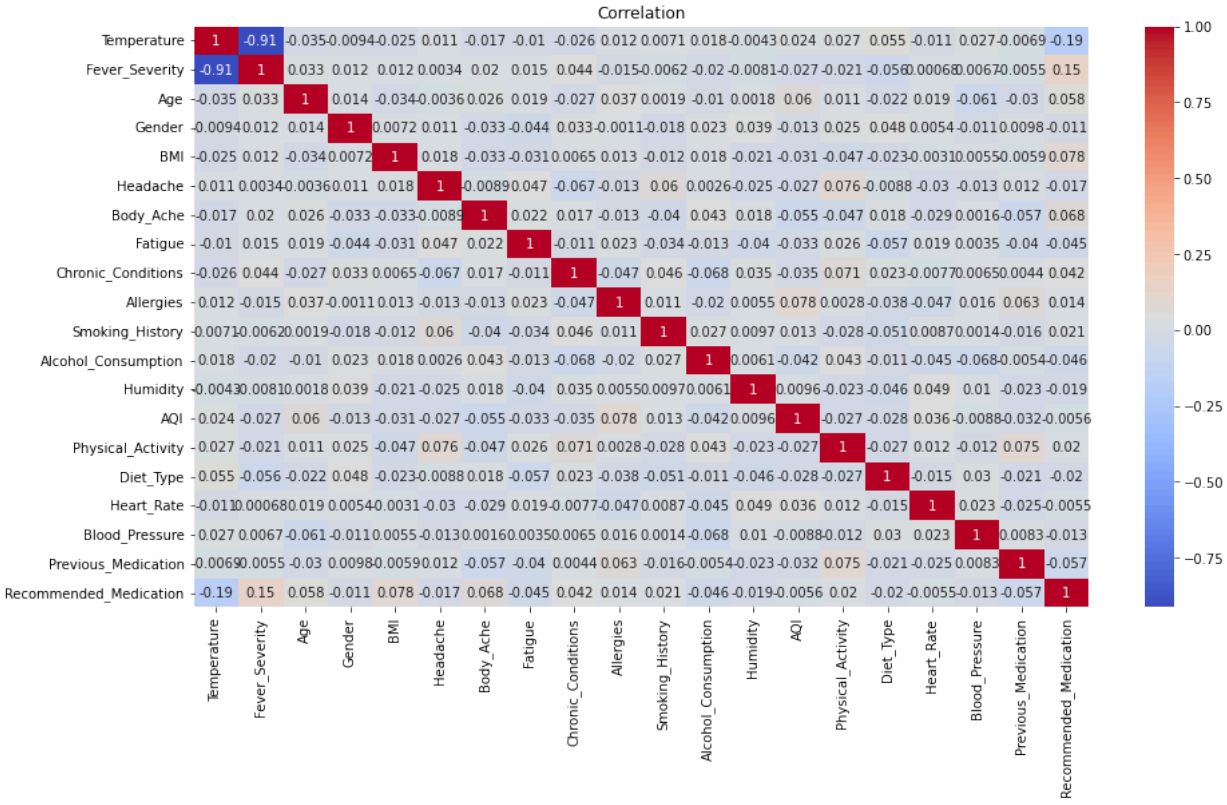
In [9]:
```
y_pred = model.predict(X_test)
```

In [10]:
```
# If the accuracy is 1 it means the model may be overfitted, too clean or something we
from sklearn.metrics import accuracy_score

accuracy = accuracy_score(y_test, y_pred)
print("Accuracy:", accuracy)
```

```
Accuracy: 1.0
```

In [22]:
```
# We can see that the only feature with the best correlation is Fever_Severity with Te
corr_df = df.corr()
plt.figure(figsize=(15,8))
sns.heatmap(corr_df, annot=True, cmap='coolwarm')
plt.title('Correlation')
plt.show()
```



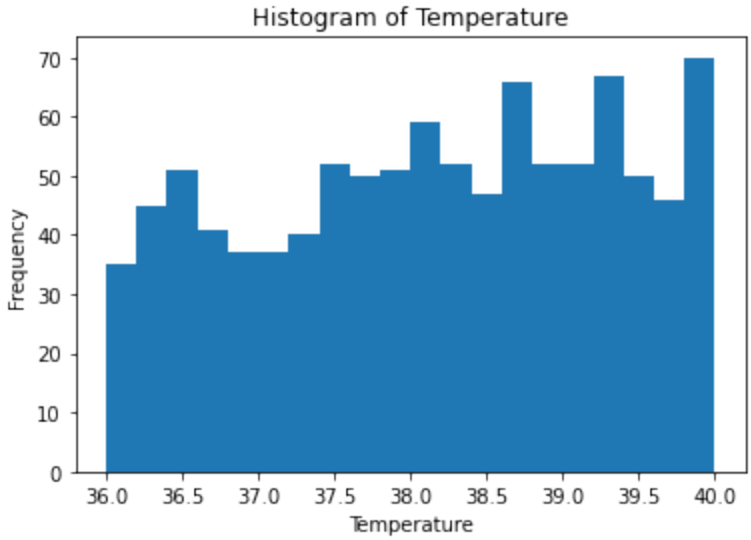
In [12]:
```
#Assesing data
# data is well distributed
df['Gender'].value_counts()
```

Out[12]:
```
0    512
1    488
Name: Gender, dtype: int64
```

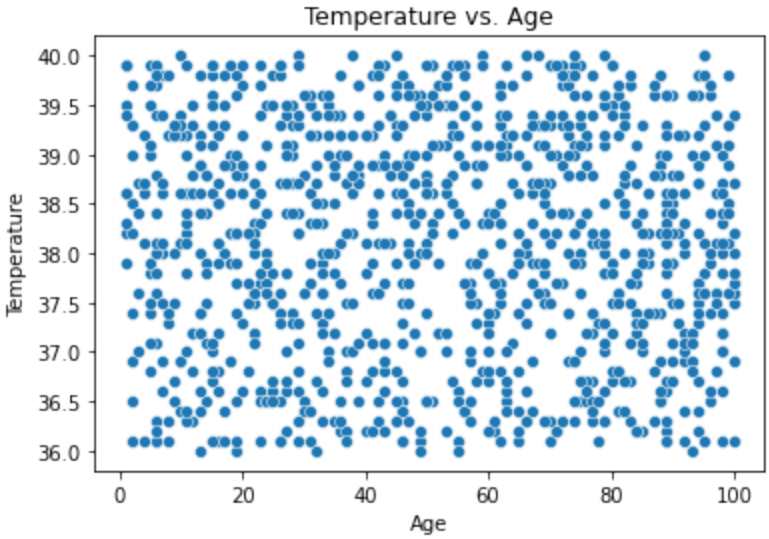
In [13]:
```
# We can reduce the size by selecting an Age group
# if we wanted to modify the data
df['Age'].describe()
```

Out[13]:
```
count    1000.000000
mean       51.152000
std        28.873354
min         1.000000
25%        26.000000
50%        51.000000
75%        76.000000
max       100.000000
Name: Age, dtype: float64
```

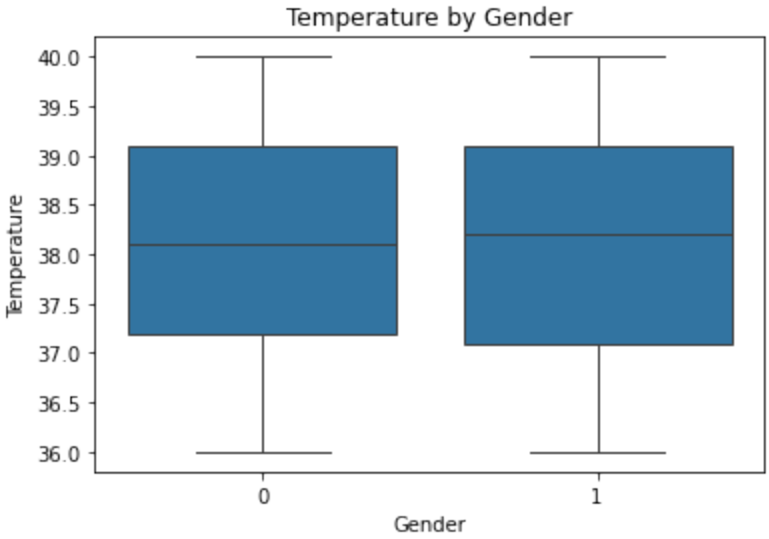
In [14]:
```
plt.hist(dfle['Temperature'], bins=20)
plt.xlabel('Temperature')
plt.ylabel('Frequency')
plt.title('Histogram of Temperature')
plt.show()
```



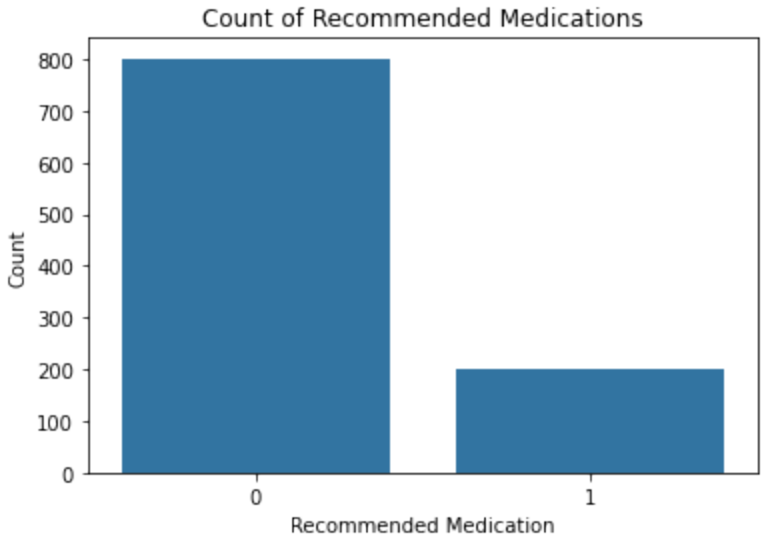
In [15]:
```
# A scatterplot it's not usefull in this case, there is no trend to work with
sns.scatterplot(x='Age', y='Temperature', data=dfle)
plt.xlabel('Age')
plt.ylabel('Temperature')
plt.title('Temperature vs. Age')
plt.show()
```



In [16]:
```
sns.boxplot(x='Gender', y='Temperature', data=df)
plt.xlabel('Gender')
plt.ylabel('Temperature')
plt.title('Temperature by Gender')
plt.show()
```



In [17]:
```
# Ibuprofen is recommended more than Paracetamol
sns.countplot(x='Recommended_Medication', data=df)
plt.xlabel('Recommended Medication')
plt.ylabel('Count')
plt.title('Count of Recommended Medications')
plt.show()
```



In [18]:
```
# This way you could work with the data separately and try to find differences.
male_data = df[df['Gender'] == 1]
female_data = df[df['Gender'] == 0]
male_data
```

Out[18]:

	Temperature	Fever_Severity	Age	Gender	BMI	Headache	Body_Ache	Fatigue	Chronic_Condit
1	37.5	1	94	1	26.6	0	0	0	
2	36.4	2	92	1	27.8	0	0	0	
3	39.8	0	66	1	18.7	0	1	0	
4	39.3	0	28	1	21.0	0	1	0	
6	39.1	0	63	1	18.5	1	0	0	
...	...	...	...	...	...	...	...	...	
984	36.1	2	29	1	34.4	1	0	0	
989	37.4	1	86	1	26.8	1	1	0	
990	39.8	0	74	1	32.1	1	0	1	
992	36.4	2	31	1	26.7	0	0	0	
995	39.9	0	59	1	22.1	1	1	1	

488 rows × 20 columns

In [19]:

```
# This is one way to compare if stats are different by gender

output_string = ""

output_string += "male_mean_temperature: " + str(male_data['Temperature'].mean()) + "\
output_string += "female_mean_temperature: " + str(female_data['Temperature'].mean())
# 0= No 1 =Yes
output_string += "male_headache_count: " + str(male_data['Headache'].value_counts()) +
output_string += "female_headache_count: " + str(female_data['Headache'].value_counts(
# Previous_Medication : 1 None, 2 Ibuprofen, 3 Paracetamol, 0, Aspirin
output_string += "male_previous_medication_count: " + str(male_data['Previous_Medicati
output_string += "female_previous_medication_count: " + str(female_data['Previous_Medi
print(output_string)


#print("male_mean_temperature: " + str(male_data['Temperature'].mean()) + ", female_me
```

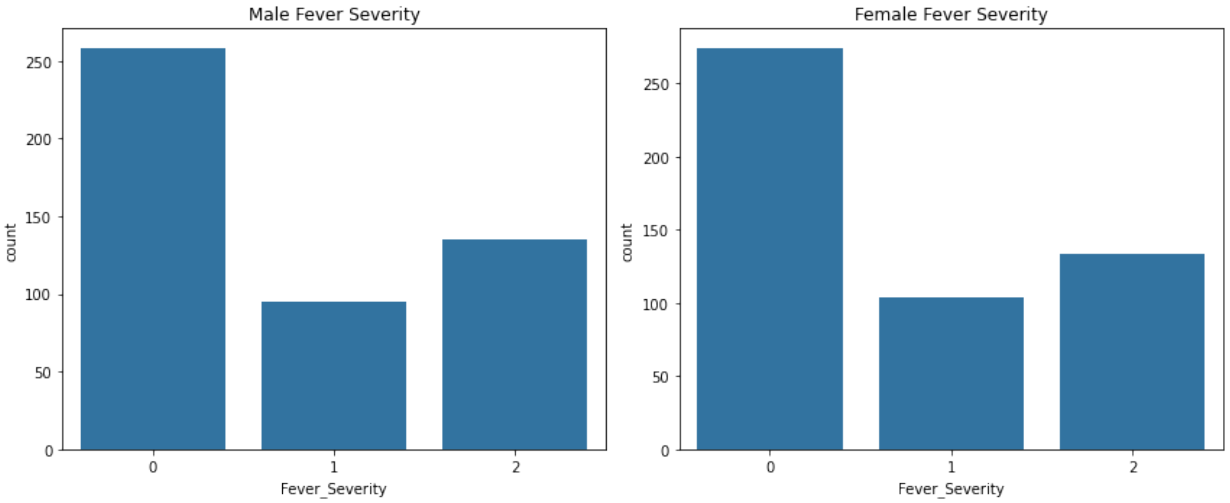
```
male_mean_temperature: 38.08790983606558
female_mean_temperature: 38.109375
male_headache_count: 1    254
0    234
Name: Headache, dtype: int64
female_headache_count: 1    261
0    251
Name: Headache, dtype: int64
male_previous_medication_count: 1    136
3    132
0    117
2    103
Name: Previous_Medication, dtype: int64
female_previous_medication_count: 2    134
0    131
3    124
1    123
Name: Previous_Medication, dtype: int64
```

In [20]:
```
# 0 High, 1 Mild, 2 Normal
fig, axes = plt.subplots(1, 2, figsize=(12, 5))

# Plot for male_data
sns.countplot(x='Fever_Severity', data=male_data, ax=axes[0])
axes[0].set_title('Male Fever Severity')

# Plot for female_data
sns.countplot(x='Fever_Severity', data=female_data, ax=axes[1])
axes[1].set_title('Female Fever Severity')

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



In [21]:
```
df.describe()
```

Out[21]:

	Temperature	Fever_Severity	Age	Gender	BMI	Headache	Body_Ache
count	1000.00000	1000.000000	1000.000000	1000.000000	1000.00000	1000.000000	1000.000000
mean	38.09890	0.737000	51.152000	0.488000	26.44320	0.515000	0.515000
std	1.13887	0.855899	28.873354	0.500106	4.90115	0.500025	0.500025
min	36.00000	0.000000	1.000000	0.000000	18.00000	0.000000	0.000000
25%	37.20000	0.000000	26.000000	0.000000	22.40000	0.000000	0.000000
50%	38.20000	0.000000	51.000000	0.000000	26.50000	1.000000	1.000000
75%	39.10000	2.000000	76.000000	1.000000	30.52500	1.000000	1.000000
max	40.00000	2.000000	100.000000	1.000000	35.00000	1.000000	1.000000

In order to get a clearer analysis one could work with the various features in this dataset and try to find a relation. In my case i find the data to be too similar. There is much that can be worked on or improved, my recommendation would be to add even more data from other sources. If it's not only a classifying data problem one could work with more complex models.