

```
In [ ]: !pip install PyPDF2 pdf2image opencv-python pytesseract pillow
```

```
Collecting PyPDF2
  Downloading pypdf2-3.0.1-py3-none-any.whl (232 kB)
    ━━━━━━━━━━━━━━━━ 232.6/232.6 kB 2.0 MB/s et
a 0:00:00
Collecting pdf2image
  Downloading pdf2image-1.16.3-py3-none-any.whl (11 kB)
Requirement already satisfied: opencv-python in /usr/local/lib/python3.10/dist-packages (4.7.0.72)
Collecting pytesseract
  Downloading pytesseract-0.3.10-py3-none-any.whl (14 kB)
Requirement already satisfied: pillow in /usr/local/lib/python3.10/dist-packages (9.4.0)
Requirement already satisfied: numpy>=1.21.2 in /usr/local/lib/python3.10/dist-packages (from opencv-python) (1.25.2)
Requirement already satisfied: packaging>=21.3 in /usr/local/lib/python3.10/dist-packages (from pytesseract) (23.1)
Installing collected packages: pytesseract, PyPDF2, pdf2image
Successfully installed PyPDF2-3.0.1 pdf2image-1.16.3 pytesseract-0.3.10
```

```
In [ ]: !apt-get install -y poppler-utils
```

```
Reading package lists... Done
Building dependency tree... Done
Reading state information... Done
The following NEW packages will be installed:
  poppler-utils
0 upgraded, 1 newly installed, 0 to remove and 15 not upgraded.
Need to get 186 kB of archives.
After this operation, 696 kB of additional disk space will be used.
Get:1 http://archive.ubuntu.com/ubuntu (http://archive.ubuntu.com/ubuntu) jammy-updates/main amd64 poppler-utils amd64 22.02.0-2ubuntu0.1 [186 kB]
Fetched 186 kB in 0s (482 kB/s)
Selecting previously unselected package poppler-utils.
(Reading database ... 120500 files and directories currently installed.)
Preparing to unpack .../poppler-utils_22.02.0-2ubuntu0.1_amd64.deb ...
Unpacking poppler-utils (22.02.0-2ubuntu0.1) ...
Setting up poppler-utils (22.02.0-2ubuntu0.1) ...
Processing triggers for man-db (2.10.2-1) ...
```

```
In [ ]: !apt-get install -y tesseract-ocr
```

```
Reading package lists... Done
Building dependency tree... Done
Reading state information... Done
The following additional packages will be installed:
  tesseract-ocr-eng tesseract-ocr-osd
The following NEW packages will be installed:
  tesseract-ocr tesseract-ocr-eng tesseract-ocr-osd
0 upgraded, 3 newly installed, 0 to remove and 15 not upgraded.
Need to get 4,816 kB of archives.
After this operation, 15.6 MB of additional disk space will be used.
Get:1 http://archive.ubuntu.com/ubuntu (http://archive.ubuntu.com/ubuntu)
  jammy/universe amd64 tesseract-ocr-eng all 1:4.00~git30-7274cfa-1.1
  [1,591 kB]
Get:2 http://archive.ubuntu.com/ubuntu (http://archive.ubuntu.com/ubuntu)
  jammy/universe amd64 tesseract-ocr-osd all 1:4.00~git30-7274cfa-1.1
  [2,990 kB]
Get:3 http://archive.ubuntu.com/ubuntu (http://archive.ubuntu.com/ubuntu)
  jammy/universe amd64 tesseract-ocr amd64 4.1.1-2.1build1 [236 kB]
Fetched 4,816 kB in 1s (9,518 kB/s)
Selecting previously unselected package tesseract-ocr-eng.
(Reading database ... 120530 files and directories currently installed.)
Preparing to unpack .../tesseract-ocr-eng_1%3a4.00~git30-7274cfa-1.1_all.deb ...
Unpacking tesseract-ocr-eng (1:4.00~git30-7274cfa-1.1) ...
Selecting previously unselected package tesseract-ocr-osd.
Preparing to unpack .../tesseract-ocr-osd_1%3a4.00~git30-7274cfa-1.1_all.deb ...
Unpacking tesseract-ocr-osd (1:4.00~git30-7274cfa-1.1) ...
Selecting previously unselected package tesseract-ocr.
Preparing to unpack .../tesseract-ocr_4.1.1-2.1build1_amd64.deb ...
Unpacking tesseract-ocr (4.1.1-2.1build1) ...
Setting up tesseract-ocr-eng (1:4.00~git30-7274cfa-1.1) ...
Setting up tesseract-ocr-osd (1:4.00~git30-7274cfa-1.1) ...
Setting up tesseract-ocr (4.1.1-2.1build1) ...
Processing triggers for man-db (2.10.2-1) ...
```

```
In [ ]: from pdf2image import convert_from_path
from pytesseract import image_to_string
from PIL import Image
```

```
In [ ]: path_to_pdf = '/content/BP2023062630268.pdf'
```

```
In [ ]: def convert_pdf_to_img(pdf_file):
    return convert_from_path(pdf_file)

def convert_image_to_text(file):
    text = image_to_string(file)
    return(text)

def get_text_from_any_pdf(pdf_file):
    images = convert_pdf_to_img(pdf_file)
    final_text = ""
    for pg, img in enumerate(images):

        final_text += convert_image_to_text(img)
        print("Page n{}".format(pg))
        print(convert_image_to_text(img))

    return final_text
```

```
In [ ]: data = get_text_from_any_pdf(path_to_pdf)
```

Page n0
KONKISA, SUJATHA

303/35 WALDRON RD, SEFTON. 2162

Phone: 99115858

Birthdate: 01/12/1955 Sex: F Medicare Number: 2734521624
Your Reference: 00120677 Lab Reference: 884122152-E-Thyroid
Function

Laboratory: Douglass Hanly Moir Pathology eOrder

Addressee: DR GEETA TADIMALLA Referred by: DR GEETA TADIMALLA
Name of Test: Thyroid Function

Requested: 09/10/2022 Collected: 10/10/2022 Reported: 10/10/2022
19:42

ONLINE MEDICAL HEALTH CHECK UP

Exporting all the extracted data to CSV

```
In [ ]: import csv
import pandas as pd

def extract_values(text):
    values = []
    lines = text.split("\n")
    for line in lines:
        if line.strip(): # Check if the line is not empty after removing
            values.append(line.split())
    return values

def save_to_csv(values, filename):
    with open(filename, 'w', newline='') as csvfile:
        writer = csv.writer(csvfile)
        for row in values:
            if any(row): # Exclude empty rows
                writer.writerow(row)
```

```
In [ ]: values=extract_values(data)
save_to_csv(values, "extracted_text.csv")
```

```
In [ ]: import pandas as pd

# Read the CSV file into a dataframe
df = pd.read_csv("/content/extracted_text.csv", sep="\t", header=None)

# Filter rows based on the condition
filtered_df = df[df[0].str.startswith(("HbA1c-NGSP", "LDL", "HDL", "Seru..."))]

# Reset the index of the filtered dataframe
filtered_df.reset_index(drop=True, inplace=True)

# Store the filtered dataframe to CSV without headers
filtered_df.to_csv("filtered_data.csv", header=False, index=False)

# Print the filtered dataframe
print(filtered_df)
```

0	Serum,ferritin,levels,between,15-30,ug/L,may,r...
1	HDL,Chol.,1.0,1.3,1.2,1.3,mmol/L,(>1.2)
2	LDL,Chol.,H,3.7,H,3.8,2.9,H,3.8,mmol/L,(<3.0)
3	HDL,cholesterol,>1.0,mmol/L
4	LDL,cholesterol,<2.5,mmol/L,(<1.8,mmol/L,for,v...)
5	HDL,(1.0-2.0),mmol/L,1.0,1.2,1.3
6	LDL,(1.5-3.4),mmol/L,3.0,2.8,2.3
7	Serum,(3.4-5.4),mmol/L,6.8,4.5,5.0
8	Serum,Folate,36.1,nmol/L,(>,9.0)
9	Serum,Vitamin,B12,Assay:
10	Serum,Active,B12,Assay:

```
In [ ]: import pandas as pd
import re

# Read the CSV file into a dataframe
df = pd.read_csv("/content/extracted_text.csv", sep="\t", header=None)

# Filter rows based on the condition
filtered_df = df[df[0].str.match(r'(Serum|HbA1c-NGSP|LDL|HDL).*\d')]

# Reset the index of the filtered dataframe
filtered_df.reset_index(drop=True, inplace=True)

# Store the filtered dataframe to CSV without headers
filtered_df.to_csv("filtered_data.csv", header=False, index=False)

# Print the filtered dataframe
print(filtered_df)
```

```
0
0 Serum,ferritin,levels,between,15-30,ug/L,may,r...
1 HDL,Chol.,1.0,1.3,1.2,1.3,mmol/L,(>1.2)
2 LDL,Chol.,H,3.7,H,3.8,2.9,H,3.8,mmol/L,(<3.0
3 HDL,cholesterol,>1.0,mmol/L
4 LDL,cholesterol,<2.5,mmol/L,(<1.8,mmol/L,for,v...
5 HDL,(1.0-2.0),mmol/L,1.0,1.2,1.3
6 LDL,(1.5-3.4),mmol/L,3.0,2.8,2.3
7 Serum,(3.4-5.4),mmol/L,6.8,4.5,5.0
8 Serum,Folate,36.1,nmol/L,(>,9.0)
9 Serum,Vitamin,B12,Assay:
10 Serum,Active,B12,Assay:
```

Extracting data from Selected report pages(first_page, last_page)

```
In [ ]: import pytesseract
from pdf2image import convert_from_path

def convert_image_to_text(image):
    text = pytesseract.image_to_string(image)
    return text

def get_text_from_pdf_range(pdf_file, start_page, end_page):
    text = ""
    images = convert_from_path(pdf_file, first_page=start_page, last_page=end_page)
    for page_number, image in enumerate(images, start=start_page):
        page_text = convert_image_to_text(image)
        print("Page", page_number, ":", page_text)
        text += page_text
    return text
```

```
In [ ]: report1 = get_text_from_pdf_range(path_to_pdf, 1, 5)
```

Page 1 : KONKISA, SUJATHA

303/35 WALDRON RD, SEFTON. 2162

Phone: 99115858

Birthdate: 01/12/1955 Sex: F Medicare Number: 2734521624
Your Reference: 00120677 Lab Reference: 884122152-E-Thyroid
Function

Laboratory: Douglass Hanly Moir Pathology eOrder

Addressee: DR GEETA TADIMALLA Referred by: DR GEETA TADIMALLA
Name of Test: Thyroid Function

Requested: 09/10/2022 Collected: 10/10/2022 Reported: 10/10/2022
19:42

Clinical notes: HEALTH CHECK UP

```
In [ ]: values=extract_values(report1)  
save_to_csv(values, "report_1.csv")
```



```
In [ ]: import pandas as pd
import re
import warnings

# Ignore warnings
warnings.filterwarnings("ignore")

# Read the CSV file into a dataframe
df = pd.read_csv("/content/report_1.csv", sep="\t", header=None)

# Filter rows based on the condition
filtered_df = df[df[0].str.match(r'(Date|Time|Cholesterol|Triglycerides|'))

# Remove "F" values from the "Time" row
filtered_df.loc[filtered_df[0].str.startswith('Time'), 0] = filtered_df.
filtered_df.loc[filtered_df[0].str.startswith('Time'), 0] = filtered_df.

# Remove "H" values from the "LDL-" row
filtered_df.loc[filtered_df[0].str.startswith('LDL'), 0] = filtered_df.l

# Remove "H" values from the "Cholesterol" row
filtered_df.loc[filtered_df[0].str.startswith('Cholesterol'), 0] = filte

# Reset the index of the filtered dataframe
filtered_df.reset_index(drop=True, inplace=True)

# Delete rows with far greater length
max_length = filtered_df[0].str.len().max()
filtered_df = filtered_df[filtered_df[0].str.len() < max_length]

# Delete 2 rows above "Date" if it follows "Time" row
rows_to_delete = []
for i in range(1, len(filtered_df)):
    if filtered_df.iloc[i][0].startswith('Date') and filtered_df.iloc[i-1][0].startswith('Time'):
        rows_to_delete.extend([i-2, i-1])

filtered_df = filtered_df.drop(rows_to_delete)

# Drop duplicate rows
filtered_df = filtered_df.drop_duplicates()

# Combine "HDL" and "Chol." into one value
# filtered_df[0] = filtered_df[0].str.replace('Date,16/01/21,18/09/21,22', 'Date')
filtered_df[0] = filtered_df[0].str.replace('Time,F-Fast,0910,0903,1014,1015', 'Time')
filtered_df[0] = filtered_df[0].str.replace('HDL,Chol.,', 'HDL-Chol.')
filtered_df[0] = filtered_df[0].str.replace('LDL,Chol.,', 'LDL-Chol.')
filtered_df[0] = filtered_df[0].str.replace('HDL,cholesterol,', 'HDL-cholesterol')
filtered_df[0] = filtered_df[0].str.replace('LDL,cholesterol,', 'LDL-cholesterol')
filtered_df[0] = filtered_df[0].str.replace('Date,of,Service:', 'Date_of_Service')

# Drop rows starting with "HDL-cholesterol" and "LDL-cholesterol"
filtered_df = filtered_df[~filtered_df[0].str.startswith('HDL-cholesterol')]
filtered_df = filtered_df[~filtered_df[0].str.startswith('LDL-cholesterol')]
# filtered_df = filtered_df[~filtered_df[0].str.startswith('Non-HDL-cholesterol')]
filtered_df = filtered_df[~filtered_df[0].str.startswith('Date_of_Service')]

# Reset the index again
filtered_df.reset_index(inplace=True)
```

```
filtered_df.reset_index(drop=True, inplace=True)

# Split rows separated by commas into a dataframe
filtered_df = filtered_df[0].str.split(',', expand=True)

# df_2 = filtered_df[['Date', '16/01/21', '18/09/21', '22/01/22', '10/10/22']]
df_2 = filtered_df.iloc[:, 0:5].transpose()

df_2.columns = df_2.iloc[0]

# Remove the first row from the split dataframe
df_2 = df_2[1:]

df_2['Date'] = pd.to_datetime(df_2['Date'])

# Make the first row the header and replace "None" values in the first row
filtered_df.loc[0, filtered_df.loc[0].isna()] = ['Units', 'Reference']
filtered_df.columns = filtered_df.iloc[0]

# Remove the first row from the split dataframe
filtered_df = filtered_df[1:]

# Reset the index of df_2
# df_2.reset_index(drop=True, inplace=True)

print(df_2)

# Store the filtered dataframe to CSV without headers
filtered_df.to_csv("result_1.csv", header=True, index=False)

# Print the filtered dataframe
# print(filtered_df)
```

	Date	Time	Cholesterol	Triglycerides	HDL-Chol	LDL-Chol
0						
1	2021-01-16	09:10	5.3	1.2	1.0	3.7
2	2021-09-18	09:03	5.7	1.2	1.3	3.8
3	2022-01-22	10:14	4.6	1.0	1.2	2.9
4	2022-10-10	09:02	5.6	1.0	1.3	3.8


```
In [ ]: import pandas as pd
import re
import warnings

# Ignore warnings
warnings.filterwarnings("ignore")

# Read the CSV file into a dataframe
df = pd.read_csv("/content/report_1.csv", sep="\t", header=None)

# Filter rows based on the condition
filtered_df = df[df[0].str.match(r'(Date|Time|Sodium|Potassium|Chloride|'))

# Reset the index of the filtered dataframe
filtered_df.reset_index(drop=True, inplace=True)

# Delete rows with far greater length
max_length = filtered_df[0].str.len().max()
filtered_df = filtered_df[filtered_df[0].str.len() < max_length]

filtered_df[0] = filtered_df[0].str.replace('Date,16/01/21,18/09/21,22/0
filtered_df[0] = filtered_df[0].str.replace('Time,F-Fast,0910,F,0903,F,1
filtered_df[0] = filtered_df[0].str.replace('Total,cholesterol', 'Total_
filtered_df[0] = filtered_df[0].str.replace('Total,Protein', 'Total Prot
filtered_df[0] = filtered_df[0].str.replace('Corr,Calcium', 'Corr Calcium
filtered_df[0] = filtered_df[0].str.replace('eGFR,>90,88,76,mL/min/1.73m
filtered_df[0] = filtered_df[0].str.replace('Urate,0.30,0.30,0.29,mmol/L
filtered_df[0] = filtered_df[0].str.replace('Calcium,2.34,2.25,2.51,mmol
filtered_df[0] = filtered_df[0].str.replace('Corr Calcium,2.40,2.37,2.51
filtered_df[0] = filtered_df[0].str.replace('Phosphate.', 'Phosphate')
filtered_df[0] = filtered_df[0].str.replace('Date,of,Service:', 'Date_of

# Drop rows starting with "HDL-cholesterol" and "LDL-cholesterol"
filtered_df = filtered_df[~filtered_df[0].str.startswith('LDL')]
filtered_df = filtered_df[~filtered_df[0].str.startswith('Total_choleste
filtered_df = filtered_df[~filtered_df[0].str.startswith('Date_of_servic

# Drop duplicate rows
filtered_df = filtered_df.drop_duplicates()

# Delete 2 rows above "Date" if it follows "Time" row
rows_to_delete = []
for i in range(1, len(filtered_df)):
    if filtered_df.iloc[i][0].startswith('Date') and filtered_df.iloc[i-1][0].startswith('Time'):
        rows_to_delete.extend([i-2, i-1])

filtered_df = filtered_df.drop(rows_to_delete)

# Reset the index of the filtered dataframe
filtered_df.reset_index(drop=True, inplace=True)

# Split rows separated by commas into a dataframe
filtered_df = filtered_df[0].str.split(',', expand=True)

# Make the first row the header and replace "None" values in the first row
filtered_df.loc[0, filtered_df.loc[0].isna()] = ['Units', 'Reference']
```

```

filtered_df.columns = filtered_df.iloc[0]

# Remove the first row from the split dataframe
filtered_df = filtered_df[1:]

df_4 = filtered_df[['Date', '16/01/21', '18/09/21', '10/10/22']].transpo

# Set the first row as the column names
df_4.columns = df_4.iloc[0]

# Remove the first row and reset the index
df_4 = df_4[1:].reset_index(drop=True)

df_4['Date'] = pd.to_datetime(df_4['Date'], format='%d/%m/%y')

df_4['eGFR'] = df_4['eGFR'].str.replace(r'>|<', '')
df_4['ALT'] = df_4['ALT'].str.replace(r'>|<', '')

print(df_4)

```

	Date	Time	Sodium	Potassium	Chloride	Bicarbonate	Urea	Creatinine
0	2021-01-16	09:10	141	4.5	105		27	3.0
1	2021-09-18	09:03	136	4.4	104		24	4.4
2	2022-10-10	09:02	140	4.4	101		28	5.2

	eGFR	Urate	...	Phosphate	Bili.Total	ALP	GGT	LD	AST	ALT	Total Protein
0	90	0.30	...	0.95		3	64	11	130	14	8
1	88	0.30	...	1.07		8	77	11	133	15	8
2	76	0.29	...	1.03		7	76	12	151	17	6

	Albumin	Globulin
0	40	31
1	37	31
2	43	28

[3 rows x 22 columns]

In []: `print(filtered_df.columns)`

```
Index(['Date', '16/01/21', '18/09/21', '10/10/22', 'Units', 'Reference'], dtype='object', name=0)
```

```
In [ ]: df_4
```

Out[18]:

	Date	Time	Sodium	Potassium	Chloride	Bicarbonate	Urea	Creatinine	eGFR	Urate	...	Pt
0	2021-01-16	09:10	141	4.5	105	27	3.0	60	90	0.30	...	
1	2021-09-18	09:03	136	4.4	104	24	4.4	65	88	0.30	...	
2	2022-10-10	09:02	140	4.4	101	28	5.2	70	76	0.29	...	

3 rows × 22 columns

```
In [ ]: print(df_2)
```

	Date	Time	Cholesterol	Triglycerides	HDL-Chol	LDL-Chol	
1	2021-01-16	09:10		5.3	1.2	1.0	3.7
2	2021-09-18	09:03		5.7	1.2	1.3	3.8
3	2022-01-22	10:14		4.6	1.0	1.2	2.9
4	2022-10-10	09:02		5.6	1.0	1.3	3.8


```
In [ ]: import matplotlib.pyplot as plt
import pandas as pd

data = {
    'Date': ['16/01/21', '18/09/21', '22/01/22', '10/10/22'],
    'Time': ['09:10', '09:03', '10:14', '09:02'],
    'Cholesterol': [5.3, 5.7, 4.6, 5.6],
    'Triglycerides': [1.2, 1.2, 1.0, 1.0],
    'HDL-Chol': [1.0, 1.3, 1.2, 1.3],
    'LDL-Chol': [3.7, 3.8, 2.9, 3.8]
}

df_1 = pd.DataFrame(data)

# Convert date strings to datetime format
df_1['Date'] = pd.to_datetime(df_1['Date'], format='%d/%m/%y')

# Create a list of variables to plot
variables = ['Cholesterol', 'Triglycerides', 'HDL-Chol', 'LDL-Chol']
thresholds = {'Cholesterol': (3.9, 5.2),
              'Triglycerides': (0.5, 1.7),
              'HDL-Chol': (1.0, 2.0),
              'LDL-Chol': (1.5, 3.4)}

# Calculate the number of rows and columns for the subplots
num_plots = len(variables)
num_rows = int(num_plots * 0.5)
num_cols = int(num_plots / num_rows) if num_plots % num_rows == 0 else num_plots

# Create subplots in a grid layout
fig, axes = plt.subplots(num_rows, num_cols, figsize=(12, 8))
fig.suptitle('Variable Levels Over Time', fontsize=16)

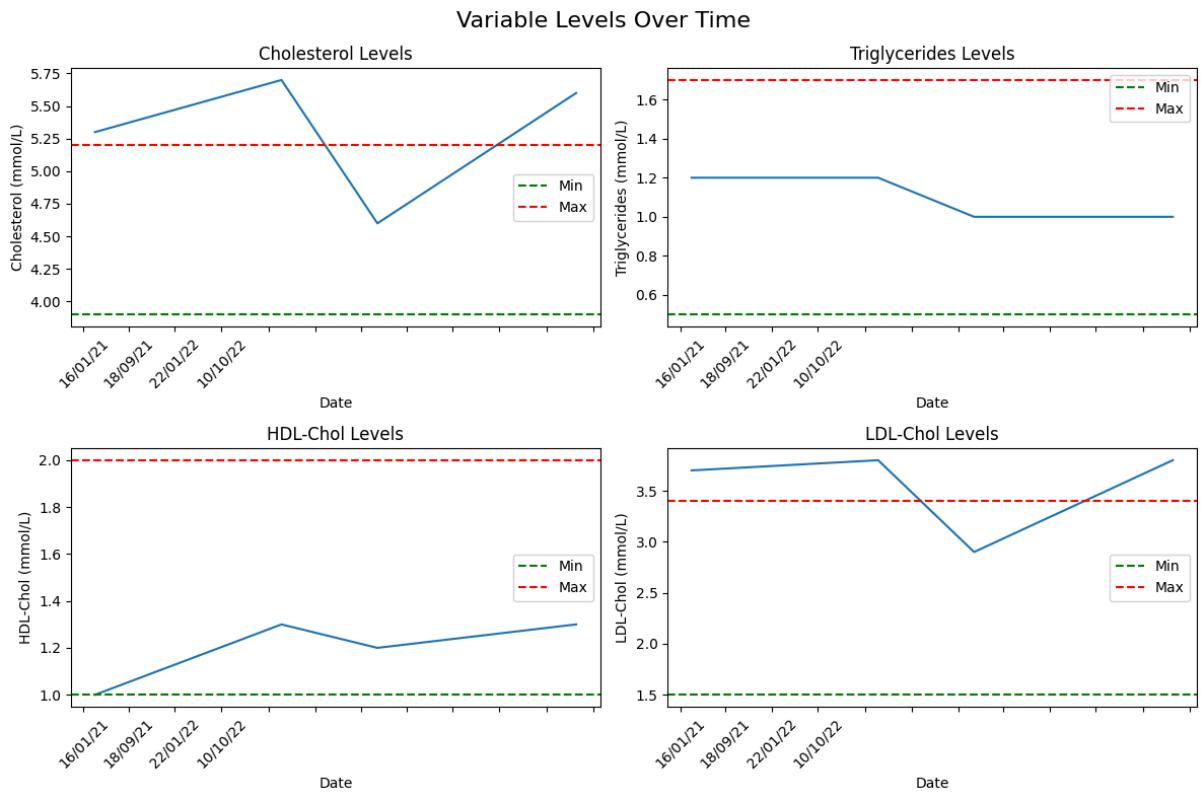
# Plot each variable in a separate subplot
for i, var in enumerate(variables):
    row = i // num_cols
    col = i % num_cols
    ax = axes[row, col] if num_rows > 1 else axes[col]

    # Plot line chart
    ax.plot(df_1['Date'], df_1[var])
    ax.set_xlabel('Date')
    ax.set_ylabel(var + ' (mmol/L)')
    ax.set_title(var + ' Levels')
    ax.set_xticklabels(df_1['Date'].dt.strftime('%d/%m/%y'), rotation=45)

    # Specify horizontal line types for thresholds
    if var in thresholds:
        min_val, max_val = thresholds[var]
        ax.axhline(y=min_val, color='g', linestyle='--', label='Min')
        ax.axhline(y=max_val, color='r', linestyle='--', label='Max')
        ax.legend()

# Remove any empty subplots
if num_plots < num_rows * num_cols:
    if num_rows > 1:
        axes[-1, -1].axis('off')
```

```
else:  
    axes[-1].axis('off')  
  
plt.tight_layout()  
plt.show()
```




```
In [ ]: import seaborn as sns
import matplotlib.pyplot as plt
import pandas as pd

# Convert date strings to datetime format
df_2['Date'] = pd.to_datetime(df_2['Date'], format='%d/%m/%y')

# Create a list of variables to plot
variables = ['Cholesterol', 'Triglycerides', 'HDL-Chol', 'LDL-Chol']
thresholds = {'Cholesterol': (3.9, 5.2),
              'Triglycerides': (0.5, 1.7),
              'HDL-Chol': (1.0, 2.0),
              'LDL-Chol': (1.5, 3.4)}

# Calculate the number of rows and columns for the subplots
num_plots = len(variables)
num_rows = int(num_plots ** 0.5)
num_cols = int(num_plots / num_rows) if num_plots % num_rows == 0 else num_plots

# Create subplots in a grid layout
fig, axes = plt.subplots(num_rows, num_cols, figsize=(12, 8))
fig.suptitle('Variable Levels Over Time', fontsize=16)

# Plot each variable in a separate subplot using Seaborn's lineplot
for i, var in enumerate(variables):
    row = i // num_cols
    col = i % num_cols
    ax = axes[row, col] if num_rows > 1 else axes[col]

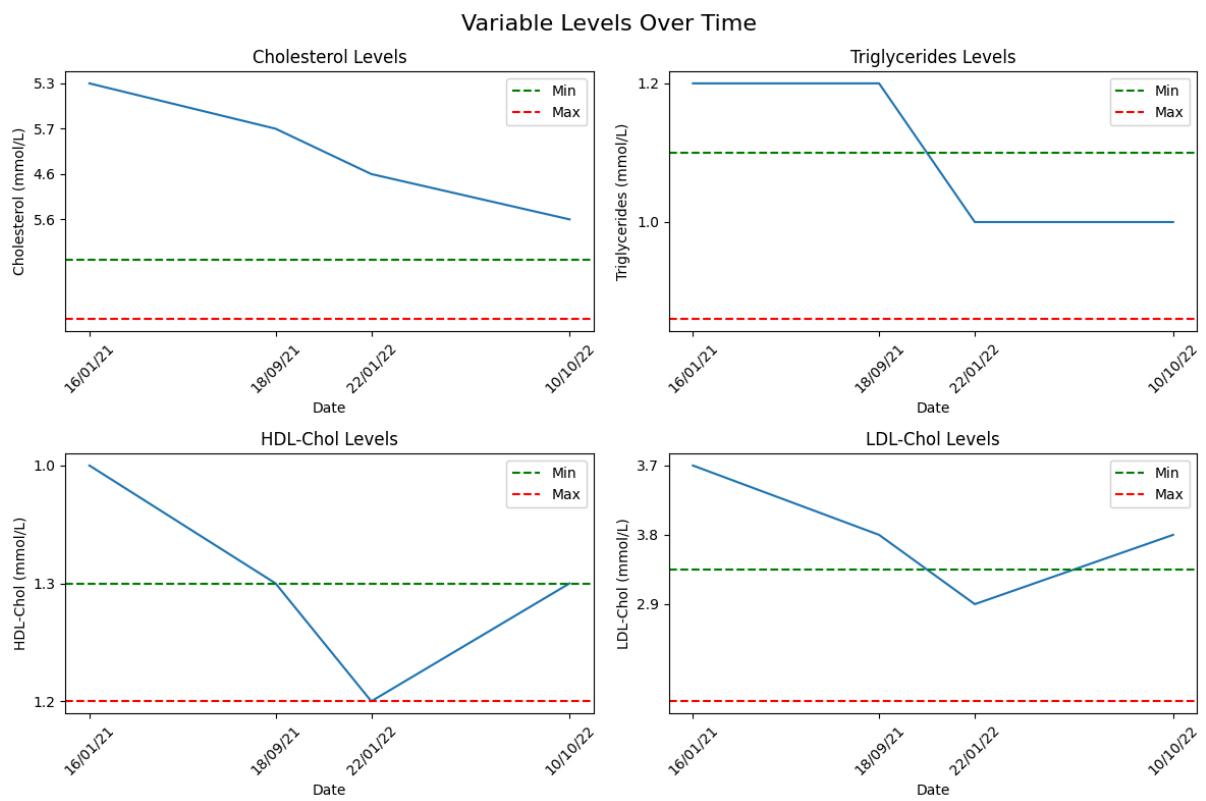
    # Plot line chart using Seaborn's lineplot
    sns.lineplot(data=df_2, x='Date', y=var, ax=ax)
    ax.set_xlabel('Date')
    ax.set_ylabel(var + ' (mmol/L)')
    ax.set_title(var + ' Levels')

    # Specify horizontal line types for thresholds
    if var in thresholds:
        min_val, max_val = thresholds[var]
        ax.axhline(y=min_val, color='g', linestyle='--', label='Min')
        ax.axhline(y=max_val, color='r', linestyle='--', label='Max')
        ax.legend()

    # Set the x-axis tick locations and labels
    ax.set_xticks(df_2['Date'])
    ax.set_xticklabels(df_2['Date'].dt.strftime('%d/%m/%y'), rotation=45)

# Remove any empty subplots
if num_plots < num_rows * num_cols:
    if num_rows > 1:
        axes[-1, -1].axis('off')
    else:
        axes[-1].axis('off')

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



```
In [ ]: report2 = get_text_from_pdf_range(path_to_pdf, 6, 6)
```

Page 6 : 93–Jan–2023 81:82 UTC To: 61296884568 61272544546 p.l

Lumus Imaging National Capital Private Hospital

Level 2, 5 Hospital Road

lumus rarer ies
imaging Tel; 0261958900
Fax: 0261958905

ABN: 65 080 595 937

9/01/2023 11:54 AM AEDT

Patient ID: 2856472
Dr Nikhil Jaiswal Order: 91.40313269
33 Colbee Court Exam Date: 9/01/2023 11:00 AM AEDT
PHILLIP ACT 2606

Re: SUJATHA KONKISA – DOB: 1/12/1955
76/44 JERRABOMBERRA AVENUE NARRABUNDAH ACT 2604

ULTRASOUND-GUIDED LEFT BREAST CHEST WALL CORE BIOPSY

Clinical notes:
Previous left breast cancer

Report:

Following informed verbal and written Consent, 4 passes using a 14-gauge core biopsy needle of the spiculated left chest wall lesion in the 12 o'clock position were performed under ultrasound guidance using aseptic technique.

Tissue was sent to pathology for examination
No immediate post-procedure complications were encountered.
Electronically Signed by: Dr Martin Dobes

Copies to: Dharmi Somasundaram, GEETA TADIMALLA
Sonographer: J. Butt

Page 1 of 1

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Our network of over 135 locations will now be part of the Lumus imaging® Network

We are transitioning to our new Lumus Imaging brand. Learn more at lumusimaging.com.au
We accept all referrals, including Healthcare imaging Services referrals

```
In [ ]: values=extract_values(report2)
         save_to_csv(values, "report_2.csv")
```



```
In [ ]: import pandas as pd
import re
import warnings

# Ignore warnings
warnings.filterwarnings("ignore")

# Read the CSV file into a dataframe
df = pd.read_csv("/content/report_2.csv", sep="\t", header=None)

# Filter rows based on the condition
filtered_df = df[df[0].str.match(r'(Date|Time|Cholesterol|Triglycerides|'))

# Remove "F" values from the "Time" row
filtered_df.loc[filtered_df[0].str.startswith('Time'), 0] = filtered_df.
filtered_df.loc[filtered_df[0].str.startswith('Time'), 0] = filtered_df.

# Remove "H" values from the "LDL-" row
filtered_df.loc[filtered_df[0].str.startswith('LDL'), 0] = filtered_df.l

# Remove "H" values from the "Cholesterol" row
filtered_df.loc[filtered_df[0].str.startswith('Cholesterol'), 0] = filte

# Reset the index of the filtered dataframe
filtered_df.reset_index(drop=True, inplace=True)

# Delete rows with far greater length
max_length = filtered_df[0].str.len().max()
filtered_df = filtered_df[filtered_df[0].str.len() < max_length]

# Delete 2 rows above "Date" if it follows "Time" row
rows_to_delete = []
for i in range(1, len(filtered_df)):
    if filtered_df.iloc[i][0].startswith('Date') and filtered_df.iloc[i-2][0].startswith('Time'):
        rows_to_delete.extend([i-2, i-1])

filtered_df = filtered_df.drop(rows_to_delete)

# Drop duplicate rows
filtered_df = filtered_df.drop_duplicates()

# Combine "HDL" and "Chol." into one value
filtered_df[0] = filtered_df[0].str.replace('Time,F-Fast', 'Time')
filtered_df[0] = filtered_df[0].str.replace('HDL,Chol.,', 'HDL-Chol,')
filtered_df[0] = filtered_df[0].str.replace('LDL,Chol.,', 'LDL-Chol,')
filtered_df[0] = filtered_df[0].str.replace('HDL,cholesterol,', 'HDL-cholesterol')
filtered_df[0] = filtered_df[0].str.replace('LDL,cholesterol,', 'LDL-cholesterol')
filtered_df[0] = filtered_df[0].str.replace('Date,of,Service:', 'Date_of_Service')

# Drop rows starting with "HDL-cholesterol" and "LDL-cholesterol"
filtered_df = filtered_df[~filtered_df[0].str.startswith('HDL-cholesterol')]
filtered_df = filtered_df[~filtered_df[0].str.startswith('LDL-cholesterol')]
# filtered_df = filtered_df[~filtered_df[0].str.startswith('Non-HDL-cholesterol')]
filtered_df = filtered_df[~filtered_df[0].str.startswith('Date_of_Service')]

# Reset the index again
filtered_df.reset_index(drop=True, inplace=True)
```

```
# Split rows separated by commas into a dataframe
filtered_df = filtered_df[0].str.split(',', expand=True)

# Make the first row the header and replace "None" values in the first row
# filtered_df.columns = filtered_df.iloc[0]
# filtered_df.loc[0, filtered_df.loc[0].isna()] = ['Units', 'Reference']

# Remove the first row from the split dataframe
filtered_df = filtered_df[1:]

# Store the filtered dataframe to CSV without headers
filtered_df.to_csv("result_2.csv", header=True, index=False)

# Print the filtered dataframe
print(filtered_df)
```

Empty DataFrame

Columns: []

Index: []

```
In [ ]: report3 = get_text_from_pdf_range(path_to_pdf, 7, 7)
```

Page 7 : KONKISA, SUJATHA

76/44 JERRABOMBERRA AVENUE, NARRABUNDAH. 2604

Birthdate: 01/12/1955 Sex: F Medicare Number: 27345216242
Your Reference: 91.40313269 Lab Reference: 91.40313269 2
Laboratory: Lumus Imaging National Capital Private Hospital
Addressee: Dr GEETA TADIMALLA Referred by: Dr Nikhil Jaiswal
Copy to:

GEETA TADIMALLA
Dharmi Somasundaram

Name of Test: US Core Biopsy Breast – Unilateral with consult
Requested: 09/01/2023 Collected: 09/01/2023 Reported: 30/01/2023
15:24

*kaKAKK ADDENDUM #1 ***4 x eR
Results have been returned from ACT Pathology:

Diagnostic Summary:

A. Left chest wall biopsy: Invasive breast carcinoma of no special type (ductal carcinoma), predicted grade 2.

Please see the full report from ACT Pathology.

Electronically Signed by: Dr Martin Dobes
e KKK ORIGINAL REPORT *****4

ULTRASOUND-GUIDED LEFT BREAST/CHEST WALL CORE BIOPSY

Clinical notes:

Previous left breast cancer.

Report:

Following informed verbal and written consent, 4 passes using a 14-gauge core biopsy needle of the spiculated left chest wall lesion in the 12 o'clock position were performed under ultrasound guidance using aseptic technique.

Tissue was sent to pathology for examination.
No immediate post-procedure complications were encountered.

Electronically Signed by: Dr Martin Dobes

Copies to: Dharmi Somasundaram, GEETA TADIMALLA

Sonographer: J. Butt

cc: SOMASUNDARAM, Dr Dharmi, Jenke Circuit KAMBAH ACT 2902

```
In [ ]: values=extract_values(report3)
         save_to_csv(values, "report_3.csv")
```



```
In [ ]: import pandas as pd
import re
import warnings

# Ignore warnings
warnings.filterwarnings("ignore")

# Read the CSV file into a dataframe
df = pd.read_csv("/content/report_3.csv", sep="\t", header=None)

# Filter rows based on the condition
filtered_df = df[df[0].str.match(r'(Date|Time|Cholesterol|Triglycerides|'))

# Remove "F" values from the "Time" row
filtered_df.loc[filtered_df[0].str.startswith('Time'), 0] = filtered_df.
filtered_df.loc[filtered_df[0].str.startswith('Time'), 0] = filtered_df.

# Remove "H" values from the "LDL-" row
filtered_df.loc[filtered_df[0].str.startswith('LDL'), 0] = filtered_df.l

# Remove "H" values from the "Cholesterol" row
filtered_df.loc[filtered_df[0].str.startswith('Cholesterol'), 0] = filte

# Reset the index of the filtered dataframe
filtered_df.reset_index(drop=True, inplace=True)

# Delete rows with far greater length
max_length = filtered_df[0].str.len().max()
filtered_df = filtered_df[filtered_df[0].str.len() < max_length]

# Delete 2 rows above "Date" if it follows "Time" row
rows_to_delete = []
for i in range(1, len(filtered_df)):
    if filtered_df.iloc[i][0].startswith('Date') and filtered_df.iloc[i-2][0].startswith('Time'):
        rows_to_delete.extend([i-2, i-1])

filtered_df = filtered_df.drop(rows_to_delete)

# Drop duplicate rows
filtered_df = filtered_df.drop_duplicates()

# Combine "HDL" and "Chol." into one value
filtered_df[0] = filtered_df[0].str.replace('Time,F-Fast', 'Time')
filtered_df[0] = filtered_df[0].str.replace('HDL,Chol.,', 'HDL-Chol,')
filtered_df[0] = filtered_df[0].str.replace('LDL,Chol.,', 'LDL-Chol,')
filtered_df[0] = filtered_df[0].str.replace('HDL,cholesterol,', 'HDL-cholesterol')
filtered_df[0] = filtered_df[0].str.replace('LDL,cholesterol,', 'LDL-cholesterol')
filtered_df[0] = filtered_df[0].str.replace('Date,of,Service:', 'Date_of_Service')

# Drop rows starting with "HDL-cholesterol" and "LDL-cholesterol"
filtered_df = filtered_df[~filtered_df[0].str.startswith('HDL-cholesterol')]
filtered_df = filtered_df[~filtered_df[0].str.startswith('LDL-cholesterol')]
# filtered_df = filtered_df[~filtered_df[0].str.startswith('Non-HDL-cholesterol')]
filtered_df = filtered_df[~filtered_df[0].str.startswith('Date_of_Service')]

# Reset the index again
filtered_df.reset_index(drop=True, inplace=True)
```

```
# Split rows separated by commas into a dataframe
filtered_df = filtered_df[0].str.split(',', expand=True)

# Make the first row the header and replace "None" values in the first row
# filtered_df.columns = filtered_df.iloc[0]
# filtered_df.loc[0, filtered_df.loc[0].isna()] = ['Units', 'Reference']

# Remove the first row from the split dataframe
filtered_df = filtered_df[1:]

# Store the filtered dataframe to CSV without headers
filtered_df.to_csv("result_3.csv", header=True, index=False)

# Print the filtered dataframe
print(filtered_df)
```

Empty DataFrame
Columns: []
Index: []

In []: report4 = get_text_from_pdf_range(path_to_pdf, 8, 10)

Page 8 : NATA Accreditation Numbers
TCH #2508 = Calvary #15024

Requesting Dr:
Martin Alexander
Dobes

Copies to: @LABRRCCRECI|PIENTS@

Recipient' Dr G. Tadimalia
Address: Lane Street Medical Centre
WENTWORTHVILLE NSW

Fax #: 02 9688 4500

25-Jan-2023 1:27 UIC To: 61296884580

ACT Pathology j

PO BOX 11 WENTWORTHVILLE NSW 2127

In []: values=extract_values(report4)
save_to_csv(values, "report_4.csv")


```
In [ ]: import pandas as pd
import re
import warnings

# Ignore warnings
warnings.filterwarnings("ignore")

# Read the CSV file into a dataframe
df = pd.read_csv("/content/report_4.csv", sep="\t", header=None)

# Filter rows based on the condition
filtered_df = df[df[0].str.match(r'(Date|Time|Cholesterol|Triglycerides|HDL|LDL|Chol.)')]

# Remove "F" values from the "Time" row
filtered_df.loc[filtered_df[0].str.startswith('Time'), 0] = filtered_df.
filtered_df.loc[filtered_df[0].str.startswith('Time'), 0] = filtered_df.

# Remove "H" values from the "LDL-" row
filtered_df.loc[filtered_df[0].str.startswith('LDL'), 0] = filtered_df.l

# Remove "H" values from the "Cholesterol" row
filtered_df.loc[filtered_df[0].str.startswith('Cholesterol'), 0] = filte

# Drop duplicate rows
filtered_df = filtered_df.drop_duplicates()

# Reset the index of the filtered dataframe
filtered_df.reset_index(drop=True, inplace=True)

# Delete rows with far greater length
max_length = filtered_df[0].str.len().max()
filtered_df = filtered_df[filtered_df[0].str.len() < max_length ]

# Delete 2 rows above "Date" if it follows "Time" row
rows_to_delete = []
for i in range(1, len(filtered_df)):
    if filtered_df.iloc[i][0].startswith('Date') and filtered_df.iloc[i-1][0].startswith('Time'):
        rows_to_delete.extend([i-2, i-1])

filtered_df = filtered_df.drop(rows_to_delete)

# Drop duplicate rows
filtered_df = filtered_df.drop_duplicates()

# Combine "HDL" and "Chol." into one value
filtered_df[0] = filtered_df[0].str.replace('Time,F-Fast', 'Time')
filtered_df[0] = filtered_df[0].str.replace('HDL,Chol.,', 'HDL-Chol,')
filtered_df[0] = filtered_df[0].str.replace('LDL,Chol.,', 'LDL-Chol,')
filtered_df[0] = filtered_df[0].str.replace('HDL,cholesterol,', 'HDL-cholesterol')
filtered_df[0] = filtered_df[0].str.replace('LDL,cholesterol,', 'LDL-cholesterol')
filtered_df[0] = filtered_df[0].str.replace('Date,of,Service:', 'Date_of_Service')

# Drop rows starting with "HDL-cholesterol" and "LDL-cholesterol"
filtered_df = filtered_df[~filtered_df[0].str.startswith('HDL-cholesterol')]
filtered_df = filtered_df[~filtered_df[0].str.startswith('LDL-cholesterol')]
# filtered_df = filtered_df[~filtered_df[0].str.startswith('Non-HDL-cholesterol')]
filtered_df = filtered_df[~filtered_df[0].str.startswith('Date_of_Service')]
```

```

# Reset the index again
filtered_df.reset_index(drop=True, inplace=True)

# Split rows separated by commas into a dataframe
filtered_df = filtered_df[0].str.split(',', expand=True)

# Make the first row the header and replace "None" values in the first row
# filtered_df.columns = filtered_df.iloc[0]
# filtered_df.loc[0, filtered_df.loc[0].isna()] = ['Units', 'Reference']

# Remove the first row from the split dataframe
filtered_df = filtered_df[1:]

# Store the filtered dataframe to CSV without headers
filtered_df.to_csv("result_4.csv", header=True, index=False)

# Print the filtered dataframe
print(filtered_df)

```

Empty DataFrame
Columns: []
Index: []

In []: report5 = get_text_from_pdf_range(path_to_pdf, 11, 17)

Page 11 : KONKISA, SUJATHA

20 DEMPSEY ST, DENHAM COURT. 2565

Phone: 61540023

Birthdate: 01/12/1955 Sex: F Medicare Number: 2734521624

Your Reference: 00126939 Lab Reference: 23-21907242-FBE-0
Laboratory: Laverty Pathology

Addressee: DR ESHWAR MADAS Referred by: DR ESHWAR MADAS

Name of Test: HAEMATOLOGY (FBE-0)

Requested: 13/02/2023 Collected: 16/02/2023 Reported: 16/02/2023
18:35

Clinical notes: 3monthly Checkup.

In []: values=extract_values(report5)
save_to_csv(values, "report_5.csv")


```
In [ ]: import pandas as pd
import re
import warnings

# Ignore warnings
warnings.filterwarnings("ignore")

# Read the CSV file into a dataframe
df = pd.read_csv("/content/report_5.csv", sep="\t", header=None)

# Filter rows based on the condition
filtered_df = df[df[0].str.match(r'(Date|Time|Chol|Trig|HbA1c-NGSP|HbA1c|HDL|Non-HDL|Cholesterol|Triglycerides)')]

# Reset the index of the filtered dataframe
filtered_df.reset_index(drop=True, inplace=True)

# Drop duplicate rows
filtered_df = filtered_df.drop_duplicates()

# Combine "HDL" and "Chol." into one value
filtered_df[0] = filtered_df[0].str.replace('Date,Collected,19,Nov,20,16')
filtered_df[0] = filtered_df[0].str.replace('Time,Collected', 'Time,,')
filtered_df[0] = filtered_df[0].str.replace('Non-HDL,\(\<,3.4\)', 'Non-HDL,\(<,3.4\)')
filtered_df[0] = filtered_df[0].str.replace('Chol,', 'Cholesterol,')
filtered_df[0] = filtered_df[0].str.replace('Trig,', 'Triglycerides,')

# Remove "&" values from the "HbA1c-NGSP" row
filtered_df.loc[filtered_df[0].str.startswith('HbA1c-NGSP'), 0] = filtered_df[0].str.replace('&', '')

# Combine "HDL" and "Chol." into one value
filtered_df[0] = filtered_df[0].str.replace('Chol/HDL\(<4.5\)', 'Chol/HDL\(<4.5\)&')

# Reset the index again
filtered_df.reset_index(drop=True, inplace=True)

# Regular expression pattern
pattern = r'Chol/HDL\(<,(\d+\.\d+)\)\&'

# Replace the pattern with the desired format
filtered_df[0] = filtered_df[0].str.replace(pattern, r'Chol/HDL,\(<\1\),\2')

# Drop duplicate rows
filtered_df = filtered_df.drop_duplicates()

# Split rows separated by commas into a dataframe
filtered_df = filtered_df[0].str.split(',', expand=True)

# print(filtered_df)

df_3 = filtered_df.iloc[:, [0, 3, 4, 5]].T
df_3.columns = df_3.iloc[0]

# Remove the first row from the split dataframe
df_3 = df_3[1:]

df_3.reset_index(drop=True, inplace=True)
```

```
df_3['Date'] = pd.to_datetime(df_3['Date'])

print(df_3)

# Make the first row the header
filtered_df.columns = filtered_df.iloc[0]

# Remove the first row from the split dataframe
filtered_df = filtered_df[1:]

# Store the filtered dataframe to CSV without headers
filtered_df.to_csv("result_5.csv", header=True, index=False)

# Print the filtered dataframe
# print(filtered_df)
```

	Date	Time	HbA1c-NGSP	HbA1c-IFCC	Cholesterol	Triglycerides	HD
L	LDL	\					
0	2020-11-19	08:15	6.8	51	4.7	1.5	1.
0	3.0						
1	2022-11-16	07:30	5.7	39	4.5	1.2	1.
2	2.8						
2	2023-02-16	08:57	5.7	39	4.1	1.0	1.
3	2.3						

	Non-HDL	Chol/HDL
0	3.7	4.7
1	3.3	3.8
2	2.8	3.2


```
df_5['eGFR'] = df_5['eGFR'].str.replace(r'<>', '')
df_5['ALT'] = df_5['ALT'].str.replace(r'<>', '')

print(df_5)

print(filtered_df)
```

	Date	Time	Sodium	Potassium	Bicarbonate	An	Gap	Urea	Creat	eGF
0	2020-11-19	08:15	141	4.3		26	13	4.6	60	8
1	2022-11-16	07:30	140	4.3		24	20	5.3	65	7
2	2023-02-16	08:57	142	4.1		24	22	6.0	70	None

	Urate	AST	ALT	GGT	Alk	Phos	Protein	Albumin	Glob	Calcium	Corr	Cal
0	0.32	...	11	7	11		72	66	39	27	2.43	2.59
1	0.30	...	16	9	8		64	70	42	28	2.57	None
2	None	...	14	7	10		67	68	42	26	None	None

	Phosphate
0	1.10
1	1.01
2	None

[3 rows x 21 columns]

	0	1	2	3	4	5
0	Date	Reference	Units	19/11/20	16/11/22	16/02/23
1	Time			08:15	07:30	08:57
2	Sodium	(135–145)	mmol/L	141	140	142
3	Potassium	(3.6–5.4)	mmol/L	4.3	4.3	4.1
4	Bicarbonate	(22–32)	mmol/L	26	24	24
5	An Gap	(10–20)	mmol/L	13	20	22
6	Urea	(2.5–9.0)	mmol/L	4.6	5.3	6.0
7	Creat	(45–90)	umol/L	60	65	70
8	eGFR	mL/min/1.73m ²	>90	84	78	None
9	Urate	(0.14–0.36)	mmol/L	0.32	0.30	None
10	Bili	(<15)	umol/L	5	4	6
11	AST	(<35)	U/L	11	16	14
12	ALT	(<30)	U/L	<7	9	7
13	GGT	(<35)	U/L	11	8	10
14	Alk Phos	(30–115)	U/L	72	64	67
15	Protein	(60–82)	g/L	66	70	68
16	Albumin	(36–48)	g/L	39	42	42
17	Glob	(20–39)	g/L	27	28	26
18	Calcium	(2.10–2.60)	mmol/L	2.43	2.57	None
19	Corr Calcium	(2.10–2.60)	2.51	2.59	None	None
20	Phosphate	(0.75–1.50)	mmol/L	1.10	1.01	None

In []: df_5

Out[35]:

	Date	Time	Sodium	Potassium	Bicarbonate	An Gap	Urea	Creat	eGFR	Urate	...	AST	ALT
0	2020-11-19	08:15	141	4.3	26	13	4.6	60	84	0.32	...	11	7
1	2022-11-16	07:30	140	4.3	24	20	5.3	65	78	0.30	...	16	9
2	2023-02-16	08:57	142	4.1	24	22	6.0	70	None	None	...	14	7

3 rows × 21 columns

In []: import pandas as pd

```
# Read the two CSV files into dataframes
df1 = pd.read_csv("result_1.csv")
df2 = pd.read_csv("result_5.csv")

# Merge the dataframes based on the 'Date' column
merged_df = df1.merge(df2, on='Date', how='outer')

# Merge the "Units" and "Reference" columns
merged_df['Reference'] = merged_df['Reference_x'].fillna('') + merged_df['Reference_y'].fillna('')
merged_df['Units'] = merged_df['Units_x'].fillna('') + merged_df['Units_y'].fillna('')

# Drop the unnecessary columns
merged_df = merged_df.drop(['Units_x', 'Reference_x', 'Units_y', 'Reference_y'])

# Print the updated merged dataframe
merged_df
```

Out[36]:

	Date	16/01/21	18/09/21	22/01/22	10/10/22	19/11/20	16/11/22	16/02/23	Reference
0	Time	09:10	09:03	10:14	09:02	08:15	07:30	08:57	
1	Cholesterol	5.3	5.7	4.6	5.6	4.7	4.5	4.1	(<5.5(3.9-5.2)
2	Triglycerides	1.2	1.2	1.0	1.0	1.5	1.2	1.0	(<2.0)(0.5-1.7)
3	HDL-Chol	1.0	1.3	1.2	1.3	NaN	NaN	NaN	(>1.2)
4	LDL-Chol	3.7	3.8	2.9	3.8	NaN	NaN	NaN	(<3.0)
5	HbA1c-NGSP	NaN	NaN	NaN	NaN	6.8	5.7	5.7	(4.0-6.0)
6	HbA1c-IFCC	NaN	NaN	NaN	NaN	51	39	39	(20-42)
7	HDL	NaN	NaN	NaN	NaN	1.0	1.2	1.3	(1.0-2.0)
8	LDL	NaN	NaN	NaN	NaN	3.0	2.8	2.3	(1.5-3.4)
9	Non-HDL	NaN	NaN	NaN	NaN	3.7	3.3	2.8	(<3.4)
10	Chol/HDL	NaN	NaN	NaN	NaN	4.7	3.8	3.2	(<4.5)

In []: `import pandas as pd`

```
# Read the two CSV files into dataframes
# df1 = pd.read_csv("result_1.csv")
# df2 = pd.read_csv("result_5.csv")

# Merge the dataframes based on the 'Date' column
merged_df = df_2.merge(df_3, on='Date', how='outer')

merged_df['Time'] = merged_df['Time_x'].combine_first(merged_df['Time_y'])
merged_df['Cholesterol'] = merged_df['Cholesterol_x'].combine_first(merged_df['Cholesterol_y'])
merged_df['Triglycerides'] = merged_df['Triglycerides_x'].combine_first(merged_df['Triglycerides_y'])

# Merge "HDL-Chol" and "HDL" columns
merged_df['HDL'] = merged_df['HDL-Chol'].fillna(merged_df['HDL'])

# Merge "LDL-Chol" and "LDL" columns
merged_df['LDL'] = merged_df['LDL-Chol'].fillna(merged_df['LDL'])

merged_df = merged_df[['Date', 'Time', 'Cholesterol', 'Triglycerides', 'HDL', 'LDL', 'HbA1c-NGSP', 'HbA1c-IFCC', 'Non-HDL', 'Chol/HDL']]

# Convert the 'Date' column to date type
merged_df['Date'] = pd.to_datetime(merged_df['Date'])

# Print the updated merged dataframe
merged_df = merged_df.sort_values('Date')

merged_df.reset_index(drop=True, inplace=True)

# Save the merged dataframe to a CSV file
merged_df.to_csv("merged_data_1.csv", index=False)

merged_df
```

Out[37]:

	Date	Time	Cholesterol	Triglycerides	HDL	LDL	HbA1c-NGSP	HbA1c-IFCC	Non-HDL	Chol/HDL
0	2020-11-19	08:15	4.7	1.5	1.0	3.0	6.8	51	3.7	4.7
1	2021-01-16	09:10	5.3	1.2	1.0	3.7	NaN	NaN	NaN	NaN
2	2021-09-18	09:03	5.7	1.2	1.3	3.8	NaN	NaN	NaN	NaN
3	2022-01-22	10:14	4.6	1.0	1.2	2.9	NaN	NaN	NaN	NaN
4	2022-10-10	09:02	5.6	1.0	1.3	3.8	NaN	NaN	NaN	NaN
5	2022-11-16	07:30	4.5	1.2	1.2	2.8	5.7	39	3.3	3.8
6	2023-02-16	08:57	4.1	1.0	1.3	2.3	5.7	39	2.8	3.2

In []:

In []: merged_df

Out[38]:

	Date	Time	Cholesterol	Triglycerides	HDL	LDL	HbA1c-NGSP	HbA1c-IFCC	Non-HDL	Chol/HDL
0	2020-11-19	08:15	4.7	1.5	1.0	3.0	6.8	51	3.7	4.7
1	2021-01-16	09:10	5.3	1.2	1.0	3.7	NaN	NaN	NaN	NaN
2	2021-09-18	09:03	5.7	1.2	1.3	3.8	NaN	NaN	NaN	NaN
3	2022-01-22	10:14	4.6	1.0	1.2	2.9	NaN	NaN	NaN	NaN
4	2022-10-10	09:02	5.6	1.0	1.3	3.8	NaN	NaN	NaN	NaN
5	2022-11-16	07:30	4.5	1.2	1.2	2.8	5.7	39	3.3	3.8
6	2023-02-16	08:57	4.1	1.0	1.3	2.3	5.7	39	2.8	3.2


```
In [ ]: import seaborn as sns
import matplotlib.pyplot as plt
import pandas as pd
from matplotlib.dates import AutoDateLocator, AutoDateFormatter

sns.set(style="darkgrid")

# Convert date strings to datetime format
merged_df['Date'] = pd.to_datetime(merged_df['Date'], format='%d/%m/%y')

# Create a list of variables to plot
variables = ['Cholesterol', 'Triglycerides', 'HbA1c-NGSP', 'HbA1c-IFCC',
              'LDL', 'Non-HDL', 'Chol/HDL']
thresholds = {'Cholesterol': (3.9, 5.2),
              'Triglycerides': (0.5, 1.7),
              'HDL': (1.0, 2.0),
              'LDL': (1.5, 3.4),
              'HbA1c-NGSP': (4.0, 6.0),
              'HbA1c-IFCC': (20, 42),
              'Non-HDL': (3.4, 4.1),
              'Chol/HDL': (3.9, 5.2)}

# Calculate the number of rows and columns for the subplots
num_plots = len(variables)
num_rows = int(num_plots ** 0.5)
num_cols = int(num_plots / num_rows) if num_plots % num_rows == 0 else n

# Create subplots in a grid layout
fig, axes = plt.subplots(num_rows, num_cols, figsize=(15, 12))
fig.suptitle('Variable Levels Over Time', fontsize=16)

# Plot each variable in a separate subplot using Seaborn's lineplot
for i, var in enumerate(variables):
    row = i // num_cols
    col = i % num_cols
    ax = axes[row, col] if num_rows > 1 else axes[col]

    # Plot line chart using Seaborn's lineplot with markers and labels
    sns.lineplot(data=merged_df, x='Date', y=var, ax=ax, marker='o', mar

    # Convert the marker values column to numeric type
    merged_df[var] = pd.to_numeric(merged_df[var], errors='coerce')

    # Annotate marker values
    for x_val, y_val in zip(merged_df['Date'], merged_df[var]):
        if not pd.isnull(y_val):
            if merged_df[var].diff().iloc[1] > 0:
                xytext = (5, -5)
                ha = 'left'
            else:
                xytext = (-5, 5)
                ha = 'right'
            ax.annotate(f'{y_val:.1f}', (x_val, y_val), xytext=xytext, t

            ax.set_xlabel('Date')
            ax.set_ylabel(var + ' (mmol/L)')
            ax.set_title(var + ' Levels')
```

```

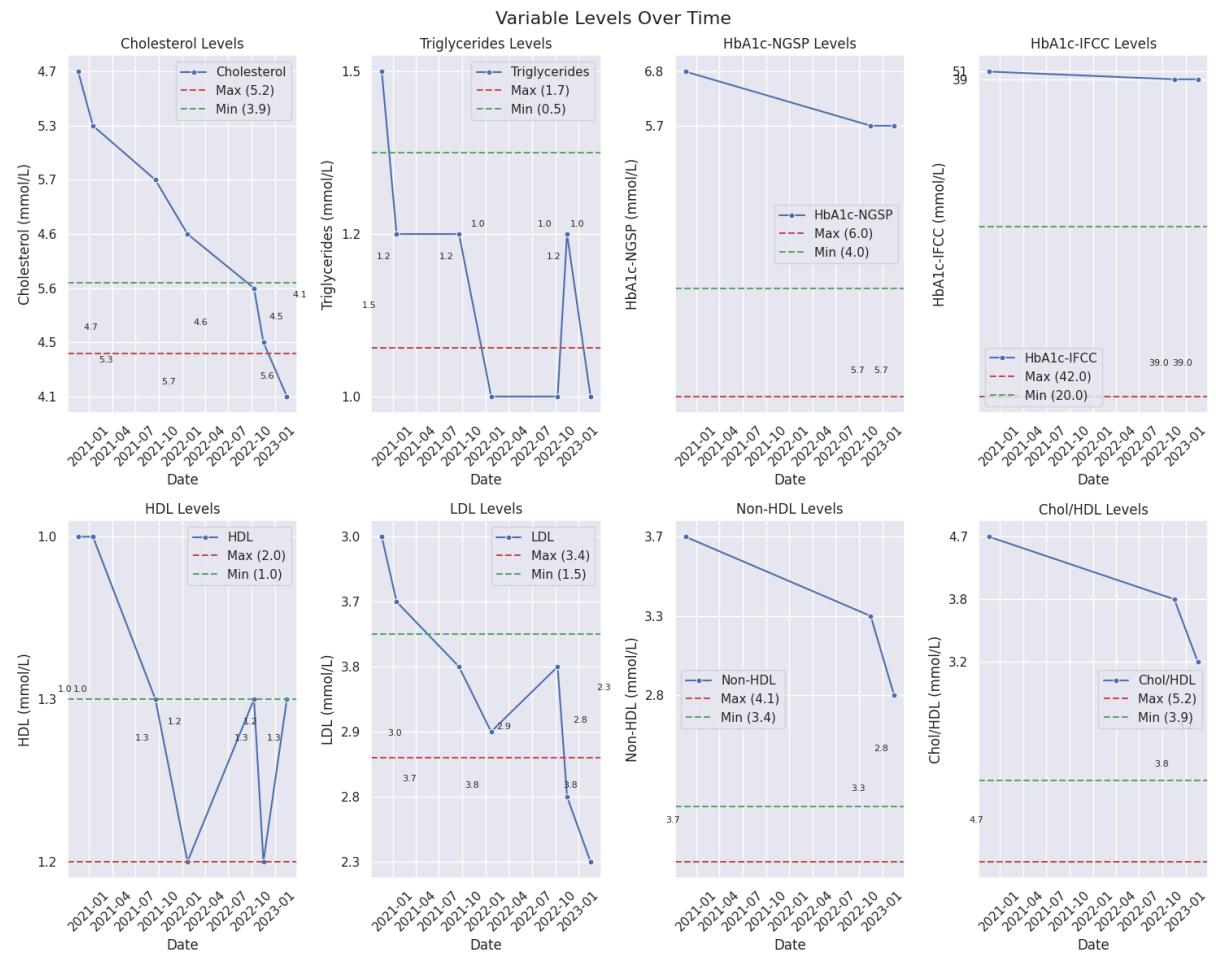
# Specify horizontal line types for thresholds
if var in thresholds:
    min_val, max_val = thresholds[var]
    ax.axhline(y=max_val, color='r', linestyle='--', label=f'Max ({max_val})')
    ax.axhline(y=min_val, color='g', linestyle='--', label=f'Min ({min_val})')
    ax.legend()

# Configure x-axis tick locations and labels
locator = AutoDateLocator()
formatter = AutoDateFormatter(locator)
ax.xaxis.set_major_locator(locator)
ax.xaxis.set_major_formatter(formatter)
plt.setp(ax.xaxis.get_majorticklabels(), rotation=45)

# Remove any empty subplots
if num_plots < num_rows * num_cols:
    if num_rows > 1:
        axes[-1, -1].axis('off')
    else:
        axes[-1].axis('off')

plt.tight_layout(rect=[0, 0, 1, 0.96])
plt.tight_layout()
plt.show()

```




```
In [ ]: import seaborn as sns
import matplotlib.pyplot as plt
import pandas as pd
from matplotlib.dates import AutoDateLocator, AutoDateFormatter

sns.set(style="darkgrid")

# Convert date strings to datetime format
merged_df['Date'] = pd.to_datetime(merged_df['Date'], format='%d/%m/%y')

# Create a list of variables to plot
variables = ['Cholesterol', 'Triglycerides', 'HbA1c-NGSP', 'HbA1c-IFCC',
             'LDL', 'Non-HDL', 'Chol/HDL']
thresholds = {'Cholesterol': (3.9, 5.2),
              'Triglycerides': (0.5, 1.7),
              'HDL': (1.0, 2.0),
              'LDL': (1.5, 3.4),
              'HbA1c-NGSP': (4.0, 6.0),
              'HbA1c-IFCC': (20, 42),
              'Non-HDL': (3.4, 4.1),
              'Chol/HDL': (3.9, 5.2)}

# Calculate the number of rows and columns for the subplots
num_plots = len(variables)
num_rows = int(num_plots ** 0.5)
num_cols = int(num_plots / num_rows) if num_plots % num_rows == 0 else n

# Create subplots in a grid layout
fig, axes = plt.subplots(num_rows, num_cols, figsize=(15, 12))
fig.suptitle('Variable Levels Over Time', fontsize=16)

# Plot each variable in a separate subplot using Seaborn's lineplot
for i, var in enumerate(variables):
    row = i // num_cols
    col = i % num_cols
    ax = axes[row, col] if num_rows > 1 else axes[col]

    # Plot line chart using Seaborn's lineplot with markers and labels
    sns.lineplot(data=merged_df, x='Date', y=var, ax=ax, marker='o', mar

    # Convert the marker values column to numeric type
    merged_df[var] = pd.to_numeric(merged_df[var], errors='coerce')

    # Annotate marker values
    for x_val, y_val in zip(merged_df['Date'], merged_df[var]):
        if not pd.isnull(y_val):
            if merged_df[var].diff().iloc[1] > 0:
                xytext = (5, -5)
                ha = 'left'
            else:
                xytext = (-5, 5)
                ha = 'right'
            ax.annotate(f'{y_val:.1f}', (x_val, y_val), xytext=xytext, t

            ax.set_xlabel('Date')
            ax.set_ylabel(var + ' (mmol/L)')
            ax.set_title(var + ' Levels')
```

```
# Specify horizontal line types for thresholds
if var in thresholds:
    min_val, max_val = thresholds[var]
    ax.axhline(y=max_val, color='r', linestyle='--', label=f'Max ({max_val})')
    ax.axhline(y=min_val, color='g', linestyle='--', label=f'Min ({min_val})')
    ax.legend()

# Configure x-axis tick locations and labels
locator = AutoDateLocator()
formatter = AutoDateFormatter(locator)
ax.xaxis.set_major_locator(locator)
ax.xaxis.set_major_formatter(formatter)
plt.setp(ax.xaxis.get_majorticklabels(), rotation=45)

# Remove any empty subplots
if num_plots < num_rows * num_cols:
    if num_rows > 1:
        axes[-1, -1].axis('off')
    else:
        axes[-1].axis('off')

plt.tight_layout(rect=[0, 0, 1, 0.96])
import seaborn as sns
import matplotlib.pyplot as plt
import pandas as pd
from matplotlib.dates import AutoDateLocator, AutoDateFormatter

sns.set(style="darkgrid")

# Assuming you have already loaded 'merged_df' and defined 'variables' as
# a list of column names

# Convert date strings to datetime format
merged_df['Date'] = pd.to_datetime(merged_df['Date'], format='%d/%m/%y')

# Create a list of variables to plot
# (omitted for brevity)

# Calculate the number of rows and columns for the subplots
# (omitted for brevity)

# Create subplots in a grid layout with colorful background
fig, axes = plt.subplots(num_rows, num_cols, figsize=(15, 12), facecolor='white')
fig.suptitle('Variable Levels Over Time', fontsize=16)

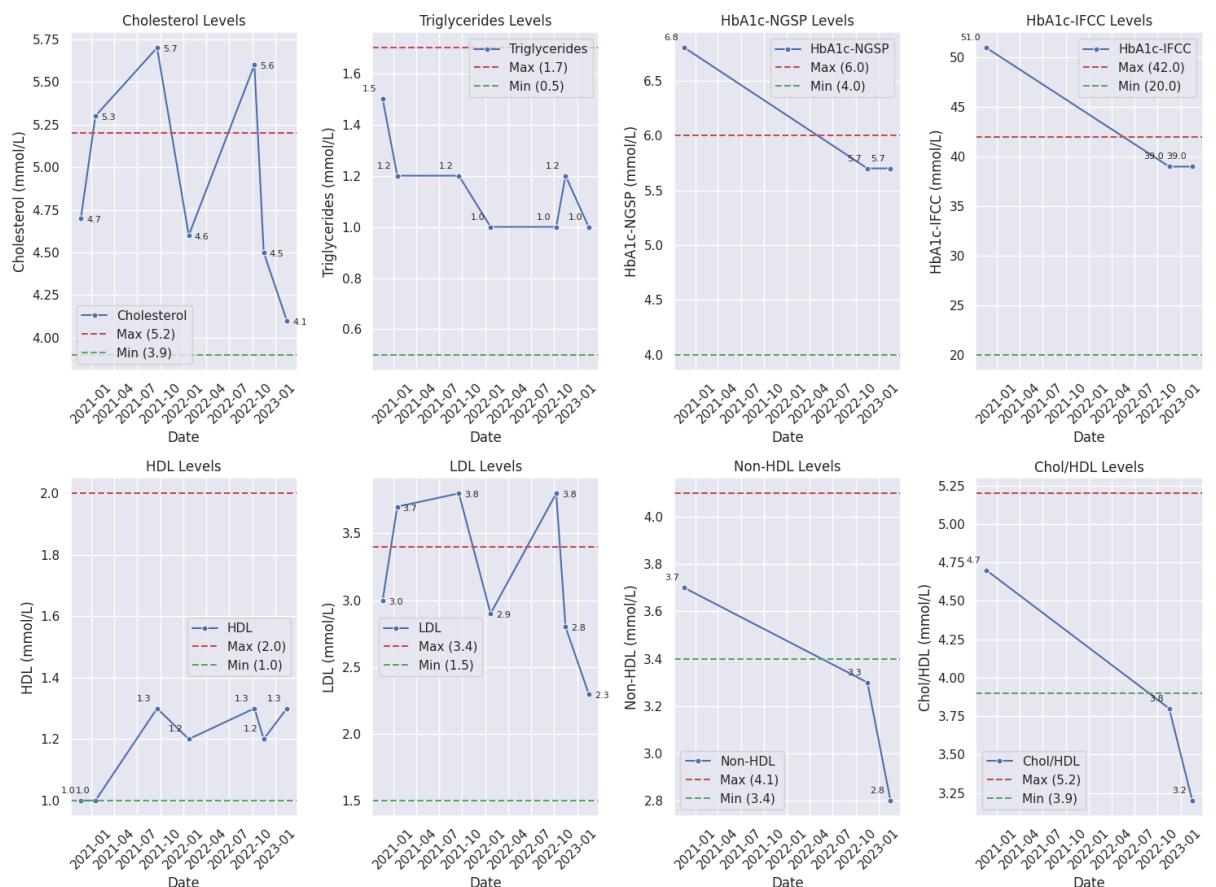
# Plot each variable in a separate subplot using Seaborn's lineplot
# (omitted for brevity)

# Remove any empty subplots
# (omitted for brevity)

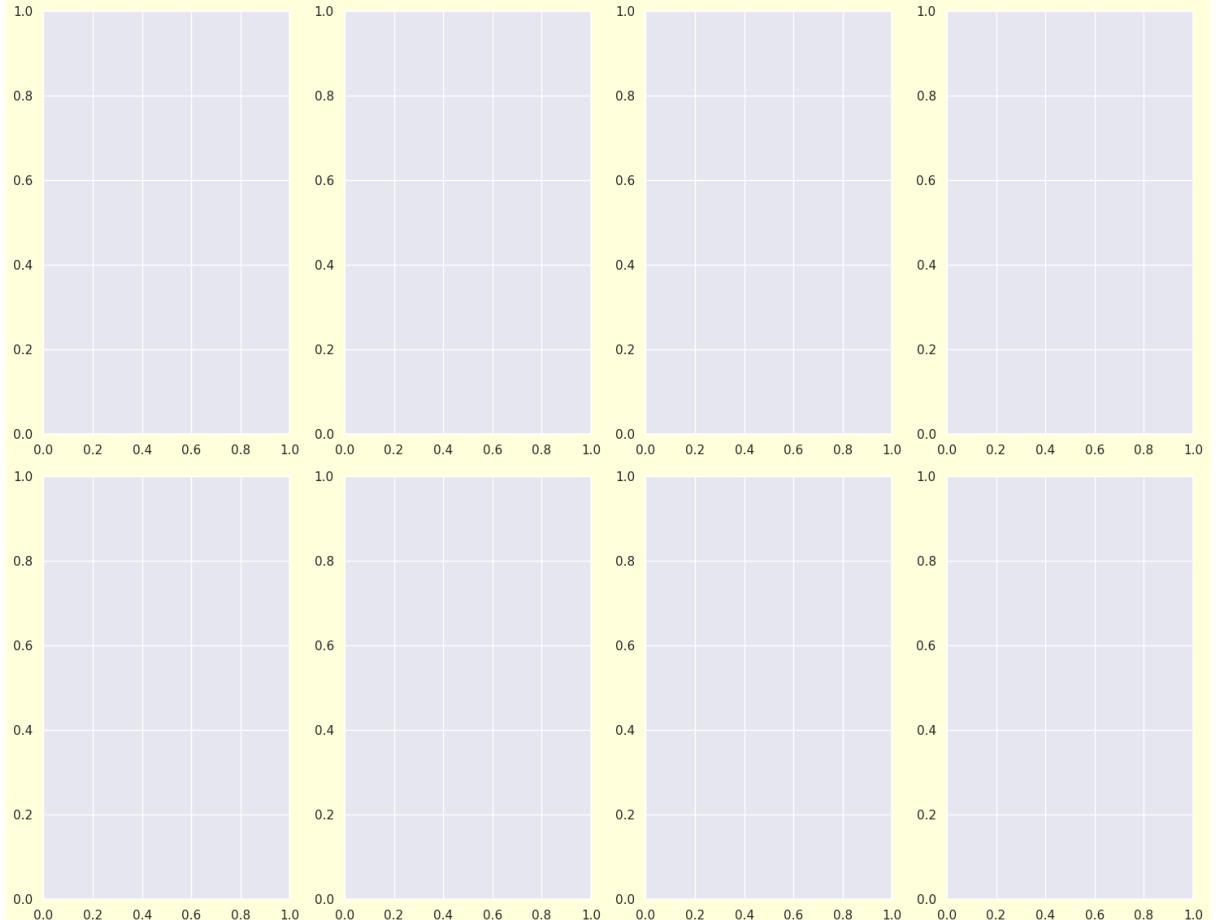
plt.tight_layout(rect=[0, 0, 1, 0.96])
plt.tight_layout()
plt.show()

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

Variable Levels Over Time



Variable Levels Over Time



<Figure size 640x480 with 0 Axes>


```
In [ ]: import seaborn as sns
import matplotlib.pyplot as plt
import pandas as pd
from matplotlib.dates import DateFormatter

sns.set(style="whitegrid")

# Read the merged DataFrame from the CSV file
merged_df = pd.read_csv("merged_data_1.csv")

# Convert the 'Date' column to datetime format
# merged_df['Date'] = pd.to_datetime(merged_df['Date'], infer_datetime_f

# Define the list of variables for the bar charts
variables = ['Cholesterol', 'Triglycerides', 'HbA1c-NGSP', 'HbA1c-IFCC',
              'LDL', 'Non-HDL', 'Chol/HDL']

# Calculate the number of rows and columns for the subplots
num_plots = len(variables)
num_rows = int(num_plots * 0.5)
num_cols = int(num_plots / num_rows) if num_plots % num_rows == 0 else n

# Create subplots in a grid layout
fig, axes = plt.subplots(num_rows, num_cols, figsize=(15, 12))
fig.suptitle('Variable Levels Over Time (Bar Charts)', fontsize=16)

# Plot bar charts for each variable using Seaborn's barplot
for i, var in enumerate(variables):
    row = i // num_cols
    col = i % num_cols
    ax = axes[row, col] if num_rows > 1 else axes[col]

    # Create the bar chart using Seaborn's barplot
    sns.barplot(data=merged_df, x='Date', y=var, ci=None, ax=ax)

    # Convert the y-axis labels to 1 decimal place
    ax.yaxis.set_major_formatter('{:.1f}'.format)

    ax.set_xlabel('Date')
    ax.set_ylabel(var + ' (mmol/L)')
    ax.set_title(var + ' Levels')

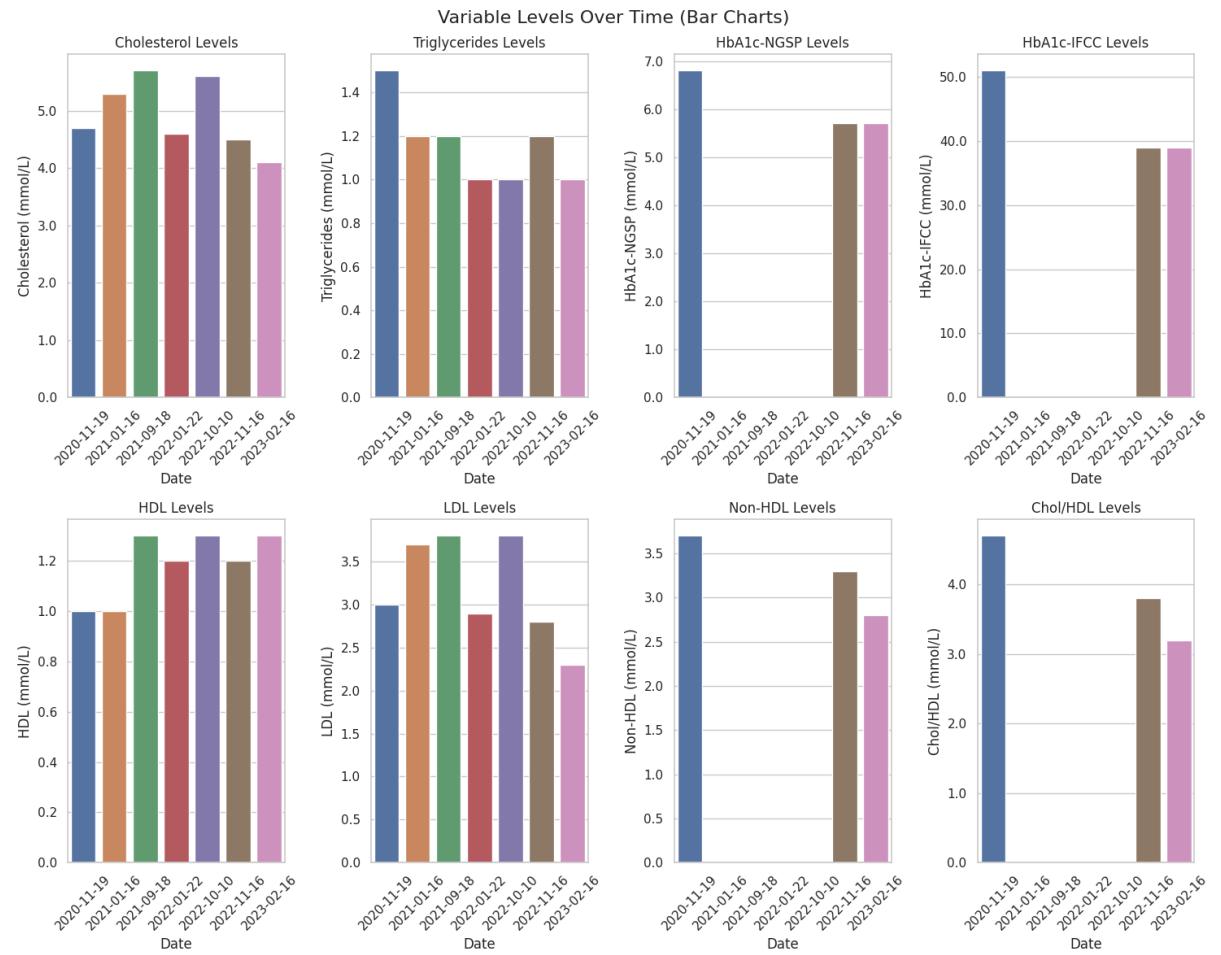
    # Format x-axis tick labels to display only date (without time)
    # date_format = DateFormatter("%Y-%m-%d")
    # ax.xaxis.set_major_formatter(date_format)

    # Rotate x-axis tick labels for better visibility
    plt.setp(ax.xaxis.get_majorticklabels(), rotation=45)

    # Remove any empty subplots
    if num_plots < num_rows * num_cols:
        if num_rows > 1:
            axes[-1, -1].axis('off')
        else:
            axes[-1].axis('off')

plt.tight_layout(rect=[0, 0, 1, 0.96])
```

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



In []: `merged_df['Date']`

Out[42]:

0	2020-11-19
1	2021-01-16
2	2021-09-18
3	2022-01-22
4	2022-10-10
5	2022-11-16
6	2023-02-16

Name: Date, dtype: object

```
In [ ]: merged_df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 7 entries, 0 to 6
Data columns (total 10 columns):
 #   Column           Non-Null Count  Dtype  
--- 
 0   Date             7 non-null      object 
 1   Time             7 non-null      object 
 2   Cholesterol      7 non-null      float64
 3   Triglycerides   7 non-null      float64
 4   HDL              7 non-null      float64
 5   LDL              7 non-null      float64
 6   HbA1c-NGSP      3 non-null      float64
 7   HbA1c-IFCC      3 non-null      float64
 8   Non-HDL          3 non-null      float64
 9   Chol/HDL         3 non-null      float64
dtypes: float64(8), object(2)
memory usage: 688.0+ bytes
```

```
In [ ]: import pandas as pd
```

```
# Merge the dataframes based on the 'Date' column
merged_df = df_4.merge(df_5, on='Date', how='outer')

merged_df['Time'] = merged_df['Time_x'].combine_first(merged_df['Time_y'])
merged_df['Sodium'] = merged_df['Sodium_x'].combine_first(merged_df['Sod'])
merged_df['Potassium'] = merged_df['Potassium_x'].combine_first(merged_d)
merged_df['Bicarbonate'] = merged_df['Bicarbonate_x'].combine_first(merg)
merged_df['Corr Calcium'] = merged_df['Corr Calcium_x'].combine_first(me
merged_df['Calcium'] = merged_df['Calcium_x'].combine_first(merged_df['C
merged_df['Phosphate'] = merged_df['Phosphate_x'].combine_first(merged_d
merged_df['Urea'] = merged_df['Urea_x'].combine_first(merged_df['Urea_y']
merged_df['eGFR'] = merged_df['eGFR_x'].combine_first(merged_df['eGFR_y'
merged_df['Urate'] = merged_df['Urate_x'].combine_first(merged_df['Urat
merged_df['Albumin'] = merged_df['Albumin_x'].combine_first(merged_df['A
merged_df['AST'] = merged_df['AST_x'].combine_first(merged_df['AST_y'])
merged_df['ALT'] = merged_df['ALT_x'].combine_first(merged_df['ALT_y'])
merged_df['GGT'] = merged_df['GGT_x'].combine_first(merged_df['GGT_y'])

# Drop the columns ending with "_x" and "_y"
merged_df.drop(columns=['Time_x', 'Time_y', 'Urea_x', 'Urea_y', 'eGFR_x'
                      'Urate_x', 'Urate_y', 'Albumin_x', 'Albumin_y',
                      'AST_y', 'ALT_x', 'ALT_y', 'GGT_x', 'GGT_y', 'So
                      'Potassium_x', 'Potassium_y', 'Bicarbonate_x', ' '
                      'Corr Calcium_x', 'Corr Calcium_y', 'Calcium_x',
                      'Corr Calcium_y', 'Calcium_y'])

merged_df = merged_df[['Date', 'Time', 'Urea', 'eGFR', 'Urate', 'Albumin
                      'Calcium', 'Corr Calcium', 'Phosphate', 'Bili.Total', 'ALP', 'LD
                      'Total Protein', 'Globulin', 'An Gap', 'Creat',
                      'Bili', 'Alk Phos', 'Protein', 'Glob']]]

# Convert all columns except the first two to float
merged_df[merged_df.columns[2:]] = merged_df[merged_df.columns[2:]].asty

# Save the merged dataframe to a CSV file
merged_df.to_csv("merged_data_2.csv", index=False)

merged_df
```

Out[44]:

	Date	Time	Urea	eGFR	Urate	Albumin	AST	ALT	GGT	Sodium	...	ALP	LD	Total Protein
0	2021-01-16	09:10	3.0	90.0	0.30	40.0	14.0	8.0	11.0	141.0	...	64.0	130.0	71.0
1	2021-09-18	09:03	4.4	88.0	0.30	37.0	15.0	8.0	11.0	136.0	...	77.0	133.0	68.0
2	2022-10-10	09:02	5.2	76.0	0.29	43.0	17.0	6.0	12.0	140.0	...	76.0	151.0	71.0
3	2020-11-19	08:15	4.6	84.0	0.32	39.0	11.0	7.0	11.0	141.0	...	NaN	NaN	NaN
4	2022-11-16	07:30	5.3	78.0	0.30	42.0	16.0	9.0	8.0	140.0	...	NaN	NaN	NaN
5	2023-02-16	08:57	6.0	NaN	NaN	42.0	14.0	7.0	10.0	142.0	...	NaN	NaN	NaN

6 rows × 28 columns


```
In [ ]: import seaborn as sns
import matplotlib.pyplot as plt
import pandas as pd
from matplotlib.dates import DateFormatter

sns.set(style="whitegrid")

# Read the merged DataFrame from the CSV file
merged_df = pd.read_csv("merged_data_2.csv")

# Convert the 'Date' column to datetime format
# merged_df['Date'] = pd.to_datetime(merged_df['Date'], infer_datetime_f

# Define the list of variables for the bar charts
variables = ['Urea', 'eGFR', 'Urate', 'Albumin', 'AST', 'ALT', 'GGT', 'S
    'Calcium', 'Corr Calcium', 'Phosphate', 'Bili.Total', 'ALP', 'LD'
    'Total Protein', 'Globulin', 'An Gap', 'Creat',
    'Bili', 'Alk Phos', 'Protein', 'Glob']

# Calculate the number of rows and columns for the subplots
num_plots = len(variables)
num_rows = int(num_plots * 0.5)
# num_cols = 3
num_cols = int(num_plots / num_rows) if num_plots % num_rows == 0 else n

# Create subplots in a grid layout
fig, axes = plt.subplots(num_rows, num_cols, figsize=(18, 20))
fig.suptitle('Variable Levels Over Time (Bar Charts)', fontsize=16)

# Plot bar charts for each variable using Seaborn's barplot
for i, var in enumerate(variables):
    row = i // num_cols
    col = i % num_cols
    ax = axes[row, col] if num_rows > 1 else axes[col]

    # Create the bar chart using Seaborn's barplot
    sns.barplot(data=merged_df, x='Date', y=var, ci=None, ax=ax)

    # Convert the y-axis labels to 1 decimal place
    ax.yaxis.set_major_formatter('{:.1f}'.format)

    ax.set_xlabel('Date')
    ax.set_ylabel(var + ' (mmol/L)')
    ax.set_title(var + ' Levels')

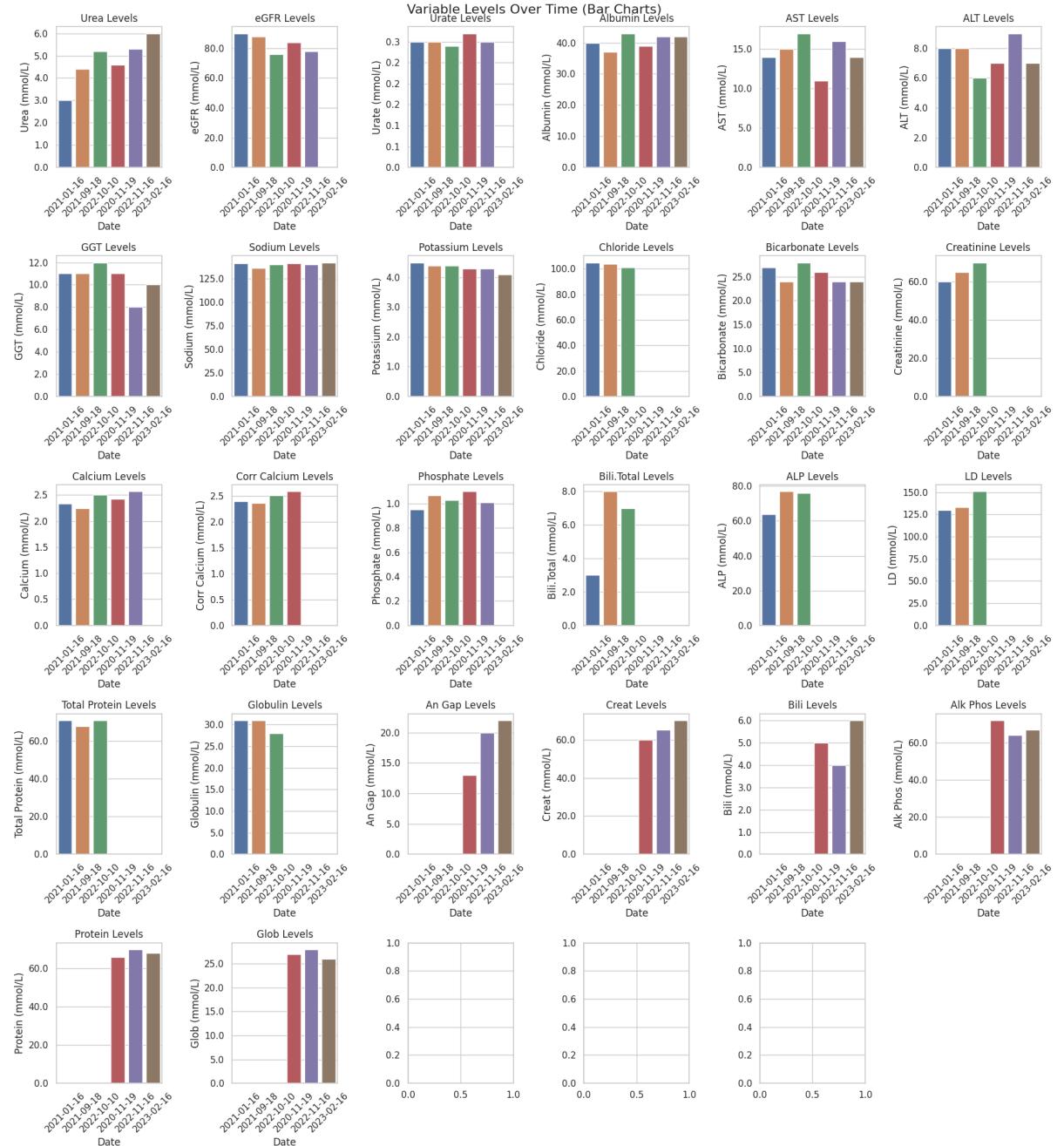
    # Format x-axis tick labels to display only date (without time)
    # date_format = DateFormatter("%Y-%m-%d")
    # ax.xaxis.set_major_formatter(date_format)

    # Rotate x-axis tick labels for better visibility
    plt.setp(ax.xaxis.get_majorticklabels(), rotation=45)

    # Remove any empty subplots
    if num_plots < num_rows * num_cols:
        if num_rows > 1:
            axes[-1, -1].axis('off')
        else:
```

```
axes[-1].axis('off')
```

```
plt.tight_layout(rect=[0, 0, 1, 0.96])
plt.tight_layout()
plt.show()
```




```
In [ ]: import seaborn as sns
import matplotlib.pyplot as plt
import pandas as pd
from matplotlib.dates import AutoDateLocator, AutoDateFormatter

sns.set(style="darkgrid")

merged_df = pd.read_csv("merged_data_2.csv")

# Create a list of variables to plot
variables = ['Urea', 'eGFR', 'Urate', 'Albumin', 'AST', 'ALT', 'GGT', 'S
    'Calcium', 'Corr Calcium', 'Phosphate', 'Bili.Total', 'ALP', 'LD'
    'Total Protein', 'Globulin', 'An Gap', 'Creat',
    'Bili', 'Alk Phos', 'Protein', 'Glob']

# Calculate the number of rows and columns for the subplot grid
num_plots = len(variables)
num_rows = int(num_plots ** 0.5)
num_cols = int(num_plots / num_rows) if num_plots % num_rows == 0 else n

# Create subplots in a grid layout
fig, axes = plt.subplots(num_rows, num_cols, figsize=(18, 20))
fig.suptitle('Variable Levels Over Time', fontsize=16)

# Plot each variable in a separate subplot using Seaborn's lineplot
for i, var in enumerate(variables):
    row = i // num_cols
    col = i % num_cols
    ax = axes[row, col] if num_rows > 1 else axes[col]

    # Plot line chart using Seaborn's lineplot with markers and labels
    sns.lineplot(data=merged_df, x='Date', y=var, ax=ax, marker='o', mar

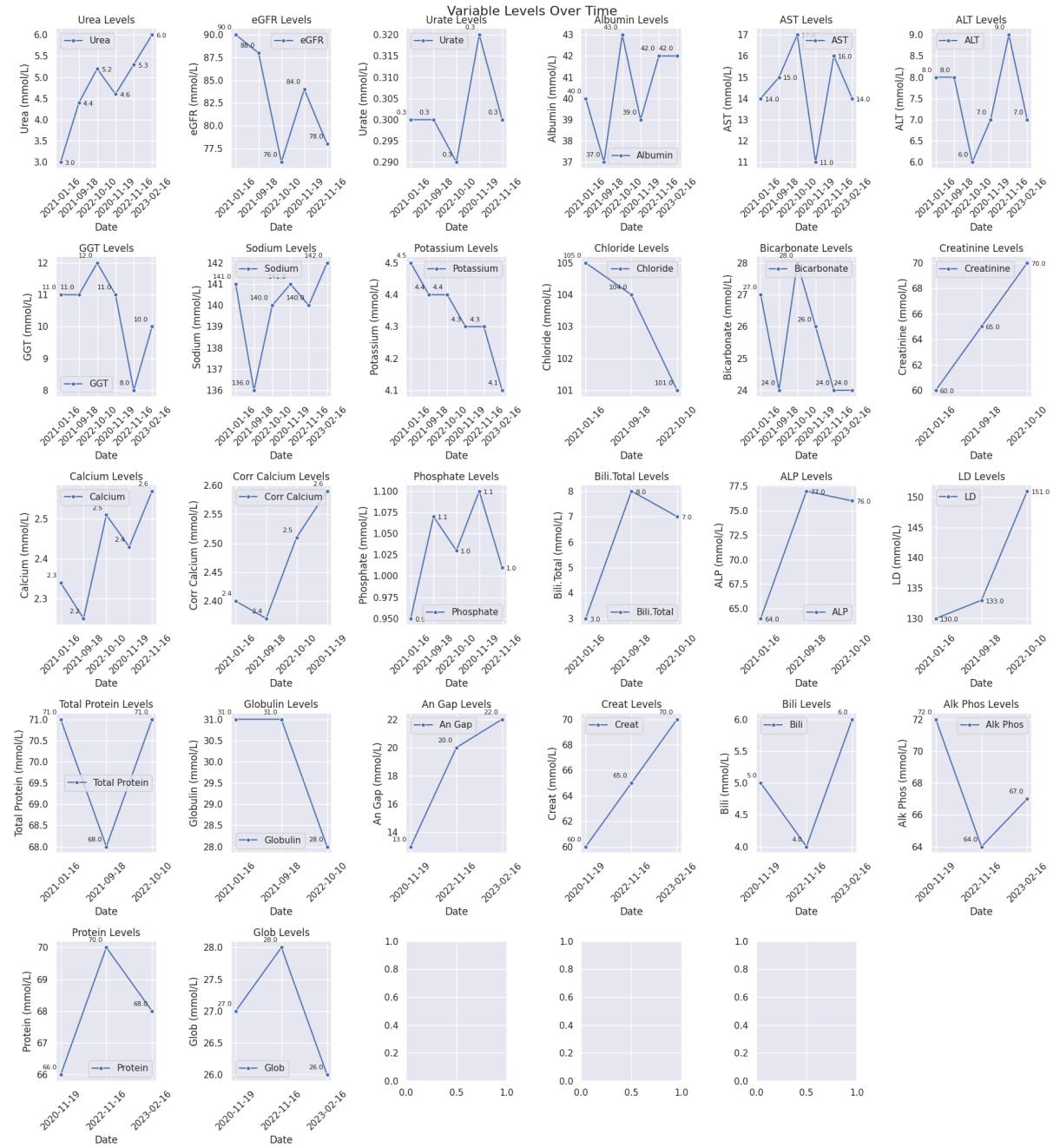
    # Annotate marker values
    for x_val, y_val in zip(merged_df['Date'], merged_df[var]):
        if not pd.isnull(y_val):
            if merged_df[var].diff().iloc[1] > 0:
                xytext = (5, -5)
                ha = 'left'
            else:
                xytext = (-5, 5)
                ha = 'right'
            ax.annotate(f'{y_val:.1f}', (x_val, y_val), xytext=xytext, t

    ax.set_xlabel('Date')
    ax.set_ylabel(var + ' (mmol/L)')
    ax.set_title(var + ' Levels')

    # Rotate x-axis tick labels for better visibility
    plt.setp(ax.xaxis.get_majorticklabels(), rotation=45)

    # Remove any empty subplots
    if num_plots < num_rows * num_cols:
        if num_rows > 1:
            axes[-1, -1].axis('off')
        else:
            axes[-1].axis('off')
```

```
plt.tight_layout(rect=[0, 0, 1, 0.96])
plt.tight_layout()
plt.show()
```



In []: merged_df['Date']

Out[47]:

0	2021-01-16
1	2021-09-18
2	2022-10-10
3	2020-11-19
4	2022-11-16
5	2023-02-16

Name: Date, dtype: object

```
In [ ]: len(merged_df.columns.to_list())
```

```
Out[48]: 28
```

```
In [ ]: merged_df['Protein'].head(5)
```

```
Out[49]: 0      NaN  
1      NaN  
2      NaN  
3    66.0  
4    70.0  
Name: Protein, dtype: float64
```



```
In [ ]: import seaborn as sns
import matplotlib.pyplot as plt
import pandas as pd
from matplotlib.dates import AutoDateLocator, AutoDateFormatter

sns.set(style="darkgrid")

# Convert date strings to datetime format
merged_df['Date'] = pd.to_datetime(merged_df['Date'], format='%d/%m/%y')

# Create a list of variables to plot
#variables = ['Cholesterol', 'Triglycerides', 'HbA1c-NGSP', 'HbA1c-IFCC'
#             # 'LDL', 'Non-HDL', 'Chol/HDL']
#thresholds = {'Cholesterol': (3.9, 5.2),
#              # 'Triglycerides': (0.5, 1.7),
#              #'HDL': (1.0, 2.0),
#              #'LDL': (1.5, 3.4),
#              #'HbA1c-NGSP': (4.0, 6.0),
#              #'HbA1c-IFCC': (20, 42),
#              #'Non-HDL': (3.4, 4.1),
#              #'Chol/HDL': (3.9, 5.2)}

# Calculate the number of rows and columns for the subplots
num_plots = len(variables)
num_rows = int(num_plots ** 0.5)
num_cols = int(num_plots / num_rows) if num_plots % num_rows == 0 else n

# Create subplots in a grid layout
fig, axes = plt.subplots(num_rows, num_cols, figsize=(15, 12))
fig.suptitle('Variable Levels Over Time', fontsize=16)

# Plot each variable in a separate subplot using Seaborn's lineplot
for i, var in enumerate(variables):
    row = i // num_cols
    col = i % num_cols
    ax = axes[row, col] if num_rows > 1 else axes[col]

    # Plot line chart using Seaborn's lineplot with markers and labels
    sns.lineplot(data=merged_df, x='Date', y=var, ax=ax, marker='o', mar

    # Convert the marker values column to numeric type
    merged_df[var] = pd.to_numeric(merged_df[var], errors='coerce')

    # Annotate marker values
    for x_val, y_val in zip(merged_df['Date'], merged_df[var]):
        if not pd.isnull(y_val):
            if merged_df[var].diff().iloc[1] > 0:
                xytext = (5, -5)
                ha = 'left'
            else:
                xytext = (-5, 5)
                ha = 'right'
            ax.annotate(f'{y_val:.1f}', (x_val, y_val), xytext=xytext, t

            ax.set_xlabel('Date')
            ax.set_ylabel(var + ' (mmol/L)')
            ax.set_title(var + ' Levels')
```

```
# Specify horizontal line types for thresholds
if var in thresholds:
    min_val, max_val = thresholds[var]
    ax.axhline(y=max_val, color='r', linestyle='--', label=f'Max ({max})
    ax.axhline(y=min_val, color='g', linestyle='--', label=f'Min ({min}
    ax.legend()

# Configure x-axis tick locations and labels
locator = AutoDateLocator()
formatter = AutoDateFormatter(locator)
ax.xaxis.set_major_locator(locator)
ax.xaxis.set_major_formatter(formatter)
plt.setp(ax.xaxis.get_majorticklabels(), rotation=45)

# Remove any empty subplots
if num_plots < num_rows * num_cols:
    if num_rows > 1:
        axes[-1, -1].axis('off')
    else:
        axes[-1].axis('off')

plt.tight_layout(rect=[0, 0, 1, 0.96])
plt.tight_layout()
plt.show()
```

```
-----
ValueError                                Traceback (most recent call l
ast)
<ipython-input-50-8403595ceff2> in <cell line: 9>()
    7
    8 # Convert date strings to datetime format
--> 9 merged_df['Date'] = pd.to_datetime(merged_df['Date'], format='%d/%m/%y')
   10
   11 # Create a list of variables to plot

/usr/local/lib/python3.10/dist-packages/pandas/core/tools/datetimes.py
in to_datetime(arg, errors, dayfirst, yearfirst, utc, format, exact, unit, infer_datetime_format, origin, cache)
    1066         result = arg.map(cache_array)
    1067     else:
--> 1068         values = convert_listlike(arg._values, format)
    1069         result = arg._constructor(values, index=arg.index,
name=arg.name)
   1070     elif isinstance(arg, (ABCDataFrame, abc.MutableMapping)):

/usr/local/lib/python3.10/dist-packages/pandas/core/tools/datetimes.py
in _convert_listlike_datetimes(arg, format, name, tz, unit, errors, infer_datetime_format, dayfirst, yearfirst, exact)
    428
    429     if format is not None:
--> 430         res = _to_datetime_with_format(
    431             arg, orig_arg, name, tz, format, exact, errors, infer_datetime_format
   432         )

/usr/local/lib/python3.10/dist-packages/pandas/core/tools/datetimes.py
in _to_datetime_with_format(arg, orig_arg, name, tz, fmt, exact, errors, infer_datetime_format)
    536
    537     # fallback
--> 538     res = _array_strptime_with_fallback(
    539         arg, name, tz, fmt, exact, errors, infer_datetime_format
   540     )

/usr/local/lib/python3.10/dist-packages/pandas/core/tools/datetimes.py
in _array_strptime_with_fallback(arg, name, tz, fmt, exact, errors, infer_datetime_format)
    471
    472     try:
--> 473         result, timezones = array_strptime(arg, fmt, exact=exact,
errors=errors)
    474     except OutOfBoundsDatetime:
    475         if errors == "raise":


/usr/local/lib/python3.10/dist-packages/pandas/_libs/tslibs/strptime.pyx
in pandas._libs.tslibs.strptime.array_strptime()

ValueError: time data '2021-01-16' does not match format '%d/%m/%y' (ma
```

```
tch)
```

```
In [ ]:
```

```
In [ ]: len(merged_df.columns.unique().to_list())
```

```
In [ ]: merged_df.columns.to_list()
```

Extracting data from selected page

```
In [ ]: import pytesseract
        from pdf2image import convert_from_path

        def convert_image_to_text(image):
            text = pytesseract.image_to_string(image)
            return text

        def get_text_from_pdf_page(pdf_file, page_number):
            images = convert_from_path(pdf_file, first_page=page_number, last_page=page_number)
            if images:
                page_image = images[0]
                page_text = convert_image_to_text(page_image)
                print(page_text)
                return page_text
            else:
                return ""
```

HbA1c Values to CSV

```
In [ ]: data = get_text_from_pdf_page(path_to_pdf, 5)
```

```
In [ ]: import csv

def extract_hbalc_values(text):
    hbalc_values = []
    lines = text.split("\n")
    for line in lines:
        if "HbA1c-NGSP" in line:
            values = line.split()
            return values

def save_to_csv(values, filename):
    with open(filename, 'w', newline='') as csvfile:
        writer = csv.writer(csvfile)
        writer.writerow(["HbA1c Value"])
        writer.writerow(values)

hbalc_values = extract_hbalc_values(data)
save_to_csv(hbalc_values, "hbalc_values.csv")
```

HDL, LDL Values to CSV

```
In [ ]: data = get_text_from_pdf_page(path_to_pdf, 2)

In [ ]: import csv

def extract_ldl_hdl_values(text):
    ldl_values = []
    hdl_values = []
    lines = text.split("\n")
    for line in lines:
        if "LDL (1.5-3.4) mmol/L" in line:
            ldl_values.append(line)
        elif "HDL (1.0-2.0) mmol /i" in line:
            hdl_values.append(line)
    return ldl_values, hdl_values

def save_to_csv(ldl_values, hdl_values, filename):
    with open(filename, 'w', newline='') as csvfile:
        writer = csv.writer(csvfile)
        writer.writerow(hdl_values[0].split())
        writer.writerow(ldl_values[0].split())

ldl_values, hdl_values = extract_ldl_hdl_values(data)
save_to_csv(ldl_values, hdl_values, "ldl_hdl_values.csv")
```

##Using Apache Tika

```
In [ ]: !apt-get install openjdk-11-jdk-headless -qq > /dev/null
!pip install tika
!wget https://repo1.maven.org/maven2/org/apache/tika/tika-app/1.27/tika-
```

```
In [ ]: from tika import parser

# Parse the PDF file and extract the text
parsed = parser.from_file(path_to_pdf)
text = parsed['content']
print(text)
```

```
In [ ]:
```

```
In [ ]:
```

```
In [ ]: import re
from tika import parser

# Parse the PDF or text file using Apache Tika
#parsed = parser.from_file(path_to_pdf)

# Extract the content
content = parsed['content']

# Find the start and end positions of the desired values
start_index = content.find("Date Collected")
end_index = content.find("Reference intervals are")

# Extract the relevant substring containing the values
values_text = content[start_index:end_index]

# Define the pattern to extract key-value pairs
pattern = r"(\w+)\s+\((.*?)\)\s+(.*?)\s+(\S+)\s+(\S+)" 

# Extract the key-value pairs using regular expressions
values = {}
matches = re.findall(pattern, values_text)
for match in matches:
    key = match[0].strip()
    value = match[1].strip()
    values[key] = value

# Print the extracted values
for key, value in values.items():
    print(key + ':', value)
```

##Manual Cleaning

```
In [ ]: import pandas as pd
import re

# Clean the data and extract report values
clean_data = re.sub(r"\n\s*\n", "\n", data) # Remove empty lines
clean_data = re.sub(r"\s{2,}", " ", clean_data) # Replace multiple spaces

report_pattern = r"Request Number (\d+)\s+Date Collected ([\w\s\d]+)\s+T
reports = re.findall(report_pattern, clean_data, re.DOTALL)

report_data = []
for report in reports:
    report_number = report[0]
    date_collected = report[1]
    time_collected = report[2]
    specimen_type = report[3]
    report_text = report[4].strip()

    values = re.findall(r"([A-Za-z ]+) \(([\d.-]+\)) (\w+)", report_text)
    report_values = [(value[0], float(value[1]), value[2]) for value in values]

    report_data.append({
        "Report Number": report_number,
        "Date Collected": date_collected,
        "Time Collected": time_collected,
        "Specimen Type": specimen_type,
        "Report Values": report_values
    })

# Create a DataFrame from the extracted report data
df = pd.DataFrame(report_data)

# Print the DataFrame
print(df)
```

```
In [ ]: import re
import pandas as pd

# Define the regular expression pattern
pattern = r"(\w+)\s+\((.*?)\)\s+(\S+)\s+(\S+)""

# Find the match in the text
match = re.search(pattern, data)

# Create a DataFrame from the match
df = pd.DataFrame([match.groups()], columns=['Test', 'Reference Range', 'Unit'])

# Display the DataFrame
print(df)
```

```
In [ ]: data
```

```
In [ ]: import pandas as pd
import re

# Remove spaces between the last digit and the "mmol/L" unit
clean_data = re.sub(r'(\d)\s+(mmol/L)', r'\1\2', data)

# Replace the em dash "--" with a space
clean_data = re.sub(r'--', ' ', clean_data)

# Clean the data and extract report values
clean_data = re.sub(r"\n\s*\n", "\n", clean_data) # Remove empty lines
clean_data = re.sub(r"\s{2,}", " ", clean_data) # Replace multiple spaces

# Define the regular expression pattern to extract the data
pattern = r"(\w+)\s+\((.*?)\)\s+(\S+)\s+(\S+)\s+(\S+)""

# Find all matches in the data
matches = re.findall(pattern, clean_data)

# Format the "Reference Range" column
matches = [(test, f"{range} {unit}", date1, date2) for test, range, unit, date1, date2 in matches]

# Create a DataFrame from the matches
df = pd.DataFrame(matches, columns=['Test', 'Reference Range', '19 Nov 2023', 'Date 1', 'Date 2'])

# Display the DataFrame
print(df)
```

```
In [ ]: matches
```

```
In [ ]: import pandas as pd

# Assuming you have a DataFrame called "df"
df.to_csv('/content/output.csv', index=False)
```

In []: `import re`

```
# Extracting blood glucose levels
glucose_levels = re.findall(r"Blood glucose level.*?(\d+\.\d+-\d+\.\d+ mmol/L)", data)
print("Blood glucose levels:", glucose_levels)

# Extracting HbA1c value
hb_1c = re.findall(r"HbA1c < (\d+) mmol/mol", data)
print("HbA1c:", hb_1c)

# Extracting LDL-C value
ldl = re.findall(r"LDL-C < (\d+\.\d+) mmol/L", data)
print("LDL-C:", ldl)

# Extracting total cholesterol value
total_cholesterol = re.findall(r"Total cholesterol < (\d+\.\d+) mmol L", data)
print("Total cholesterol:", total_cholesterol)

# Extracting HDL-C value
hdl = re.findall(r"_hdl > (\d+\.\d+) mmol/L", data)
print("HDL-C:", hdl)

# Extracting triglycerides value
triglycerides = re.findall(r"Triglycerides < (\d+\.\d+) mmol/L", data)
print("Triglycerides:", triglycerides)

# Extracting blood pressure value
blood_pressure = re.findall(r"Blood pressure S (\d+/\d+) mm Hg", data)
print("Blood pressure:", blood_pressure)

# Extracting BMI value
bmi = re.findall(r"BMI < (\d+) kg/m\?", data)
print("BMI:", bmi)

# Extracting urinary albumin excretion value
urinary_albumin = re.findall(r"Urinary albumin excretion < (\d+) kg/min", data)
print("Urinary albumin excretion:", urinary_albumin)

# Extracting alcohol intake value
alcohol_intake = re.findall(r"Alcohol intake S(\d+) standard drinks", data)
print("Alcohol intake:", alcohol_intake)

# Extracting physical activity duration
physical_activity = re.findall(r"At least (\d+) minutes walking", data)
print("Physical activity:", physical_activity)
```

In []: `pip install tika`

```
In [ ]: from tika import parser
import re

def extract_specific_values_from_pdf(pdf_path):
    parsed_pdf = parser.from_file(pdf_path)
    extracted_text = parsed_pdf['content']

    # Extracting blood glucose levels
    glucose_levels = re.findall(r"Blood glucose level Pre-prandial: (\d+.\d+)", extracted_text)
    if glucose_levels:
        print("Blood glucose levels:", glucose_levels)

    # Extracting HbA1c value
    hb_1c = re.findall(r"HbA1c < (\d+) mmol/mol", extracted_text)
    if hb_1c:
        print("HbA1c:", hb_1c)

    # Extract other desired values using similar pattern matching

# Provide the path to your PDF file
pdf_path = "/content/Pathology Report-Sujatha Konkisa[911].pdf"

extract_specific_values_from_pdf(pdf_path)

print(extract_specific_values_from_pdf(pdf_path))
```

```
In [ ]: import re
```

```
def extract_sections_from_text(data):
    # Extracting "serum/plasma glucose" section
    glucose_section = re.search(r"(serum/plasma glucose.*?)\n\n", extracted_text)
    if glucose_section:
        print("Serum/Plasma Glucose Section:")
        print(glucose_section.group(1))

    # Extracting "lipid studies" section
    lipid_section = re.search(r"(lipid studies.*?)\n\n", extracted_text, re.DOTALL)
    if lipid_section:
        print("Lipid Studies Section:")
        print(lipid_section.group(1))

    # Extracting "Glycated haemoglobin (HbA1c)" section
    hba1c_section = re.search(r"(Glycated haemoglobin \|(HbA1c\|).*)\n\n", extracted_text, re.DOTALL)
    if hba1c_section:
        print("Glycated Haemoglobin (HbA1c) Section:")
        print(hba1c_section.group(1))

    # Extracting "Urime microalbumin" section
    microalbumin_section = re.search(r"(Urime microalbumin.*?)\n\n", extracted_text, re.DOTALL)
    if microalbumin_section:
        print("Urime Microalbumin Section:")
        print(microalbumin_section.group(1))

# Assuming you have already extracted the text from the PDF and stored it
extracted_text = data

print(extract_sections_from_text(data))
```

```
In [ ]: glucose_section = re.search(r"(?i)(serum/plasma glucose.*?)\n\n", data, re.DOTALL)
print(glucose_section)
```

```
In [ ]: glucose_section_match = re.search(r"(?i)(serum/plasma\s*glucose.*?)\n\n", data, re.DOTALL)
if glucose_section_match:
    glucose_section = glucose_section_match.group(0)
    print("Serum/Plasma Glucose Section:")
    print(glucose_section)
```

```
In [ ]: import cv2
from pdf2image import convert_from_path
import numpy as np

# Convert PDF pages to PIL images
images = convert_from_path(path_to_pdf)

# Select the first page image
img = images[0]

# Convert PIL image to NumPy array
img_array = np.array(img)

# Resize the image
resized_img = cv2.resize(img_array, None, fx=0.5, fy=0.5)

# Convert image to grayscale
gray = cv2.cvtColor(resized_img, cv2.COLOR_BGR2GRAY)

# Convert image to black and white
adaptive_threshold = cv2.adaptiveThreshold(gray, 255, cv2.ADAPTIVE_THRESH
```

```
In [ ]: import cv2
import pytesseract
import numpy as np
from pdf2image import convert_from_path

# Open the PDF file and convert the first page to an image
images = convert_from_path(path_to_pdf, first_page=1, last_page=1)
img = np.array(images[0])

# Resize the image
resized_img = cv2.resize(img, None, fx=0.5, fy=0.5)

# Convert image to grayscale
gray = cv2.cvtColor(resized_img, cv2.COLOR_BGR2GRAY)

# Convert image to black and white using adaptive thresholding
_, binary_image = cv2.threshold(gray, 0, 255, cv2.THRESH_BINARY | cv2.TH

# Extract text from the binary image using Tesseract OCR
text = pytesseract.image_to_string(binary_image, config="--psm 3")

# Print the extracted text
print(text)
```

```
In [ ]: import PyPDF2
from pdf2image import convert_from_path
from google.colab.patches import cv2_imshow
import cv2
import numpy as np

# Open the PDF file
with open(path_to_pdf, "rb") as file:
    reader = PyPDF2.PdfReader(file)
    page = reader.pages[0] # Assuming you want to process the first page

# Convert the PDF page to an image
images = convert_from_path(path_to_pdf, first_page=1, last_page=1)
image = images[0]

# Convert PIL image to OpenCV format
image = cv2.cvtColor(np.array(image), cv2.COLOR_RGB2BGR)

# Resize the image
resized_image = cv2.resize(image, None, fx=0.5, fy=0.5)

# Convert image to grayscale
gray = cv2.cvtColor(resized_image, cv2.COLOR_BGR2GRAY)

# Convert image to black and white
_, binary_image = cv2.threshold(gray, 0, 255, cv2.THRESH_BINARY | cv2.THRESH_OTSU)

# Perform further processing on the binary image
# ...

# Display the resulting image
cv2_imshow(binary_image)

# Extract text from the binary image using Tesseract OCR
extracted_text = pytesseract.image_to_string(binary_image)

# Display the resulting text
print(extracted_text)
```

```
In [ ]: print(get_text_from_any_pdf(path_to_pdf))
```

```
In [ ]: from PyPDF2 import PdfReader

def get_text_from_any_pdf(path_to_pdf):
    text = ""

    with open(path_to_pdf, 'rb') as file:
        reader = PdfReader(file)
        num_pages = len(reader.pages)

        for page_number in range(num_pages):
            page = reader.pages[page_number]
            text += page.extract_text()

    return text

# Usage example
pdf_text = get_text_from_any_pdf('/content/Pathology Report-Sujatha Konk
print(pdf_text)
```

```
In [ ]: import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
```

```
In [ ]: extracted_text = (get_text_from_any_pdf(path_to_pdf)) # Your extracted
print(extracted_text)
```

```
In [ ]: def convert_pdf_to_images(pdf_path):
    images = convert_from_path(pdf_path)
    return images
```

```
In [ ]: from pdf2image import convert_from_path
from PIL import Image, ImageEnhance
import pytesseract

def convert_pdf_to_images(pdf_path):
    images = convert_from_path(pdf_path, dpi=300)
    return images

def extract_text_from_image(image):
    text = pytesseract.image_to_string(image)
    return text

images = convert_pdf_to_images(path_to_pdf)

extracted_text = []
for image in images:
    # Convert the image to grayscale
    grayscale_image = image.convert("L")

    # Enhance the image for better OCR accuracy (adjust the enhancement)
    enhanced_image = ImageEnhance.Contrast(grayscale_image).enhance(2.0)

    enhanced_image.show() # Display the enhanced image

    # Append the enhanced image to the list of images
    extracted_text.append(extract_text_from_image(enhanced_image))

# Print the extracted text
for text in extracted_text:
    print(text)
```

```
In [ ]: import numpy as np
import cv2
import pytesseract
from PIL import Image, ImageEnhance
from google.colab.patches import cv2_imshow

def preprocess_image(image):
    # Convert PIL image to NumPy array
    np_image = np.array(image)

    # Convert image to grayscale
    if np_image.ndim == 3:
        np_image = cv2.cvtColor(np_image, cv2.COLOR_RGB2GRAY)

    # Resize image for better OCR results
    resized_image = cv2.resize(np_image, (np_image.shape[1] * 3, np_image.shape[0] * 3))

    # Enhance contrast
    enhancer = ImageEnhance.Contrast(Image.fromarray(resized_image))
    contrast_image = enhancer.enhance(2) # Increase contrast (adjust the value)

    # Convert PIL image to NumPy array
    np_image = np.array(contrast_image)

    # Apply adaptive thresholding
    _, threshold_image = cv2.threshold(np_image, 0, 255, cv2.THRESH_BINARY)

    cv2_imshow(threshold_image)
    cv2.waitKey(0)
    cv2.destroyAllWindows()

    return threshold_image

def extract_text_from_image(image):
    processed_image = preprocess_image(image)
    text = pytesseract.image_to_string(processed_image)
    return text

def extract_data_from_pdf(pdf_path):
    images = convert_pdf_to_images(pdf_path)
    data = []
    for image in images:
        text = extract_text_from_image(image)
        data.append(text)
    return data
```

```
In [ ]: extract_data_from_pdf(path_to_pdf)
```

```
In [ ]: import numpy as np
import cv2
import pytesseract
from PIL import Image, ImageEnhance
from google.colab.patches import cv2_imshow

def preprocess_image(image):
    # Convert PIL image to NumPy array
    np_image = np.array(image)

    # Convert image to grayscale
    if np_image.ndim == 3:
        np_image = cv2.cvtColor(np_image, cv2.COLOR_RGB2GRAY)

    # Resize image for better OCR results
    resized_image = cv2.resize(np_image, (np_image.shape[1] * 3, np_image.shape[0] * 3))

    # Enhance contrast
    enhancer = ImageEnhance.Contrast(Image.fromarray(resized_image))
    contrast_image = enhancer.enhance(2) # Increase contrast (adjust the value)

    # Convert PIL image to NumPy array
    np_image = np.array(contrast_image)

    # Apply adaptive thresholding
    _, threshold_image = cv2.threshold(np_image, 0, 255, cv2.THRESH_BINARY)

    cv2_imshow(threshold_image)
    cv2.waitKey(0)
    cv2.destroyAllWindows()

    return threshold_image

def extract_text_from_image(image):
    processed_image = preprocess_image(image)
    text = pytesseract.image_to_string(processed_image)
    return text

def extract_data_from_pdf(pdf_path):
    images = convert_pdf_to_images(pdf_path)
    data = []
    for image in images:
        text = extract_text_from_image(image)
        lines = text.split("\n") # Split text by newline characters
        data.extend(lines) # Add each line to the data list
    return data
```

```
In [ ]: extract_data_from_pdf(path_to_pdf)
```

```
In [ ]: def extract_data_from_pdf(pdf_path):
    images = convert_pdf_to_images(pdf_path)
    data = []
    for image in images:
        text = extract_text_from_image(image)
        lines = text.split("\n") # Split text by newline characters
        cleaned_lines = [clean_text(line) for line in lines] # Clean each line
        data.extend(cleaned_lines) # Add each cleaned line to the data
    return data
```

```
In [ ]: import re
import string

def clean_text(text):
    # Remove leading/trailing whitespaces
    text = text.strip()

    # Convert to lowercase
    text = text.lower()

    # Remove punctuation
    text = text.translate(str.maketrans("", "", string.punctuation))

    # Remove unwanted characters
    text = re.sub(r"[^a-zA-Z0-9\s]", "", text)

    # Remove multiple spaces
    text = re.sub(r"\s+", " ", text)

    return text
```

```
In [ ]: clean_text(text)
```

```
In [ ]: def extract_data_from_pdf(pdf_path):
    images = convert_pdf_to_images(pdf_path)
    data = []
    for image in images:
        text = extract_text_from_image(image)
        lines = text.split("\n") # Split text by newline characters
        cleaned_lines = [clean_text(line) for line in lines] # Clean each line
        data.extend(cleaned_lines) # Add each cleaned line to the data
    return data
```

```
In [ ]: import re
import pandas as pd
from PyPDF2 import PdfReader

# Open the PDF file
with open('/content/Pathology Report-Sujatha Konkisa[911].pdf', 'rb') as file:
    # Initialize a PDF reader object
    pdf_reader = PdfReader(file)

    # Read the text from page 1
    page_text = pdf_reader.pages[0].extract_text()

    # Apply data cleaning and extraction on the page_text variable
    clean_data = re.sub(r'(\d)\s+(mmol/L)', r'\1\2', page_text)
    clean_data = re.sub(r'-', ' ', clean_data)
    clean_data = re.sub(r"\n\s*\n", "\n", clean_data)
    clean_data = re.sub(r"\s{2,}", " ", clean_data)

    # Define the regular expression pattern to extract the data
    pattern = r'(\w+)\s+\((.*?)\)\s+(-?[\d.]+(?:-[|\d.]+)?)\s+(-?[\d.]+(?:-[|\d.]+)?)'

    # Find all matches in the data
    matches = re.findall(pattern, clean_data)

    # Format the "Reference Range" column
    matches = [(test, f"{range} {unit}", date1, date2) for test, range, unit, date1, date2 in matches]

    # Create a DataFrame from the matches
    df = pd.DataFrame(matches, columns=['Test', 'Reference Range', '19 Nov 2023', 'Date'])

    # Display the DataFrame
    print(df)
```

```
In [ ]: import re
import pandas as pd
from pdf2image import convert_from_path
from PIL import Image
import pytesseract

def convert_pdf_to_img(pdf_file):
    return convert_from_path(pdf_file)

def convert_image_to_text(file):
    text = pytesseract.image_to_string(file)
    return text

def get_text_from_pdf_page(pdf_file, page_number):
    images = convert_pdf_to_img(pdf_file)
    if page_number >= 0 and page_number < len(images):
        image = images[page_number]
        text = convert_image_to_text(image)
        return text
    else:
        return ""

def extract_data_from_text(text):
    # Define the regular expression pattern to extract the data
    pattern = r'(\w+)\s+\((.*?)\)\s+(\$+)\s+(-?\d+\.\d+|\$+)\s+(-?\d+\.\$+)'

    # Find all matches in the text
    matches = re.findall(pattern, text)

    # Create a DataFrame from the matches
    df = pd.DataFrame(matches, columns=['Test', 'Reference Range', '19 N'])

    return df

# Specify the PDF file path
pdf_file = "/content/Pathology Report-Sujatha Konkisa[911].pdf"

# Specify the page number you want to extract (page numbers start from 0)
page_number = 0

# Get the text from the specified page of the PDF
text = get_text_from_pdf_page(pdf_file, page_number)

# Extract the data from the text
df = extract_data_from_text(text)

# Display the DataFrame
print(df)
```

In []:

In []:

In []: