Q2)

A researcher conducted a random dot motion discrimination task with 2 different motion coherence levels as different conditions. 30 participants performed 100 trials in each condition and the evidence accumulation was recorded. Column 1 of cell array = Condition 1 and each cell of Column 1 has one participant's data. Each cell has a 100 x 1000 matrix. Each row of the matrix = one trial for 1000 ms. The evidence accumulation starts from 300 and reaches the decision threshold at 600.The same convention applies to data from Column 2.

The data is attached herewith: Assignment2-NDM.mat'.

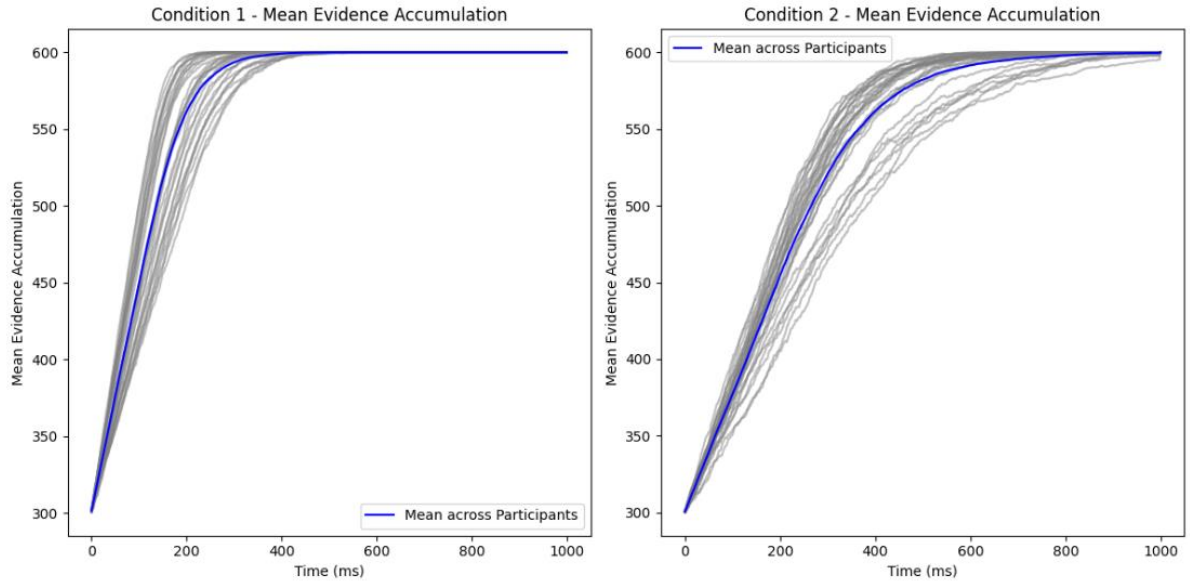
[links about importing MATLAB data arrays into Python and R

https://in.mathworks.com/help/matlab/matlab_external/matlab-arrays-as-python-variables.html

https://stackoverflow.com/questions/11671883/importing-an-array-from-matlab-into-r]

Now solve the following. Insert a figure (wherever required) and paste the MATLAB/Python/R code for the same. Any figure must provide all information necessary to interpret it including axes labels, captions/legends (simple figure titles as captions are not enough).

A i. Create two subplots for the two conditions separately. Plot the mean evidence accumulation (across 100 trials) of each participant in grey colour and the mean evidence accumulation (across 30 participants) in blue colour in each subplot.



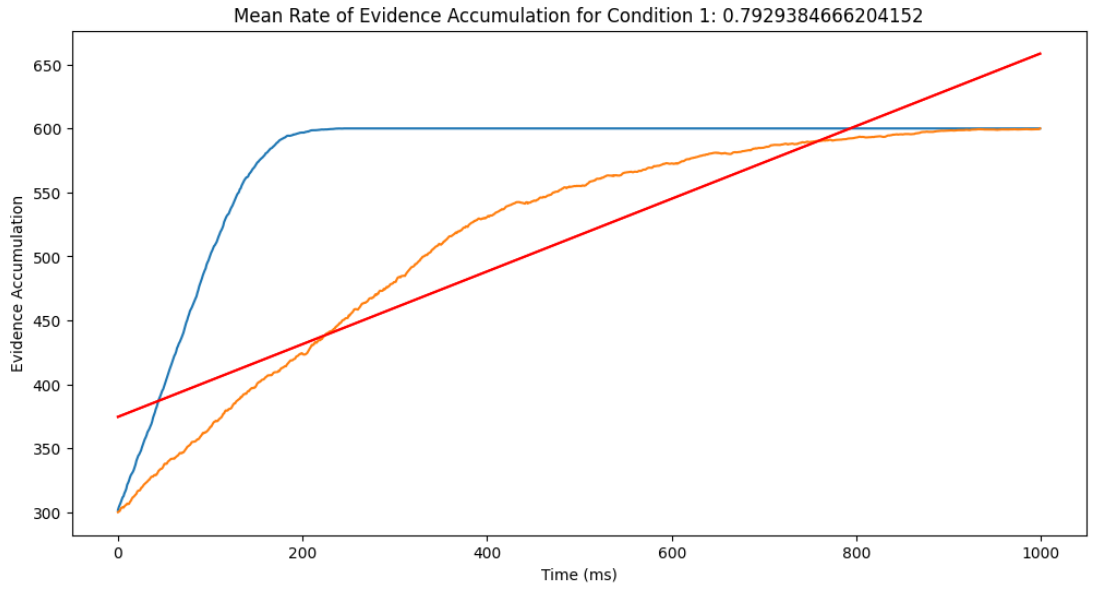
Code is:

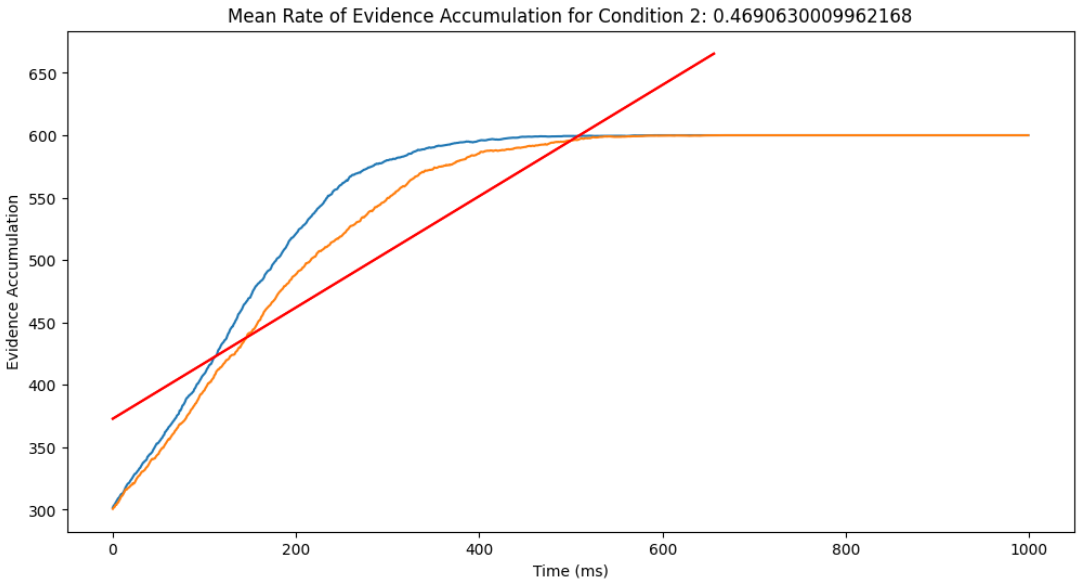
```
#!/usr/bin/env python
# coding: utf-8

# Create two subplots for the two conditions separately. Plot the mean
evidence
# accumulation (across 100 trials) of each participant in grey colour and the
mean
# evidence accumulation (across 30 participants) in blue colour in each
subplot.

# In[20]:


import os
import scipy.io as sio
import numpy as np
import matplotlib.pyplot as pl


# In[21]:


# Load data from the .mat file
dataset = sio.loadmat("NDM_Assignment2.mat")


# In[22]:


# Extract the data
dataset = dataset['NDM_Assignment2']

fig, axs = plt.subplots(1, 2, figsize=(12, 6))
labels = ["Condition 1", "Condition 2"]
idx = 0

while idx < 2:
    label = labels[idx]
    data = dataset[:, idx]


    mean_participants = np.empty((len(data), 1000))
    mean_trials = np.empty((len(data), 1000))

    # Calculate the mean evidence accumulation
    i = 0
    while i < len(data):
        participant_data = data[i]
        mean_trials[i] = np.mean(participant_data,axis =0 )
```

```
        i += 1

    # Calculate the mean evidence accumulation
    mean_participants = np.mean(mean_trials,axis =0)

    # Plot the mean evidence accumulation
    i = 0
    while i < len(mean_trials):
        axs[idx].plot(mean_trials[i], color='grey', alpha=0.5)
        i += 1

    # Plot the mean evidence accumulation
    axs[idx].plot(mean_participants, color='blue', label="Mean across
Participants")

    axs[idx].set_title(f"{label} - Mean Evidence Accumulation")
    axs[idx].set_xlabel("Time (ms)")
    axs[idx].set_ylabel("Mean Evidence Accumulation")
    axs[idx].legend()

    idx += 1

# Display the plots
plt.tight_layout()
plt.show()
```

Calculate the rate of mean evidence accumulation (across participants) for each of the two conditions separately and report on the title of each subplot.

Graphs:






```
# Calculate the rate of mean evidence accumulation (across participants) for
each of the
# two conditions separately and report on the title of each subplot.
# [Hint: Fit a straight line to the data between the starting point of mean
evidence
# accumulation and the earliest point of reaching the threshold of maximum
evidence to
# calculate the average rate.]

# In[7]:


import scipy.io
```

```
import numpy as np
import matplotlib.pyplot as plt
from scipy.stats import linregress


# In[9]:


# Load the MATLAB file
data = scipy.io.loadmat("NDM_Assignment2.mat")
data['NDM_Assignment2']


# In[22]:


# Assuming that the data is stored in two variables 'Condition1' and
'Condition2'
condition1 = data['NDM_Assignment2'][0]
condition2 = data['NDM_Assignment2'][1]

def CalculateRate(condition, ConditionName):
    # Initialize a list where we store the rates of each participant
    Rates = []

    # Now looping over each participant's data using a while loop
    participant_index = 0
    while participant_index < len(condition):
        ParticipantData = condition[participant_index]

        # Calculate the mean evidence accumulation across each trial
        MeanEvidence = np.mean(ParticipantData, axis=0)

        Start_index = np.where(MeanEvidence >= 300)[0][0]
        End_index = np.where(MeanEvidence >= 600)[0][0]

        # Fit a straight line to the data between start and end indices
        slope, intercept, _, _, _ = linregress(range(Start_index,
End_index+1), MeanEvidence[Start_index:End_index+1])

        # Append the slope (rate of evidence accumulation) to the list
        Rates.append(slope)

        # Increment the participant index
        participant_index += 1

    # Calculate the mean rate across participants
    mean_rate = np.mean(Rates)
```

```
    # Plot mean evidence accumulation for each participant with fitted line
    plt.figure(figsize=(12, 6))
    plt.title(f'Mean Rate of Evidence Accumulation for {ConditionName}:
{mean_rate}')
    plt.xlabel('Time (ms)')
    plt.ylabel('Evidence Accumulation')

    # Reset the participant index and loop again to create the plots
    participant_index = 0
    while participant_index < len(condition):
        ParticipantData = condition[participant_index]

        mean_evidence = np.mean(ParticipantData, axis=0)
        plt.plot(mean_evidence)
        plt.plot(range(Start_index, End_index+1), intercept +
slope*range(Start_index, End_index+1), 'r', label='fitted line')

        # Increment the participant index
        participant_index += 1

    plt.show()

# Calculate and plot rate for each condition
CalculateRate(condition1, 'Condition 1')
CalculateRate(condition2, 'Condition 2')


# In[ ]:




# In[ ]:
```

Whole code:

```
#!/usr/bin/env python
# coding: utf-8

# Create two subplots for the two conditions separately. Plot the mean
evidence
# accumulation (across 100 trials) of each participant in grey colour and the
mean
```

```
# evidence accumulation (across 30 participants) in blue colour in each
subplot.

# In[20]:


import os
import scipy.io as sio
import numpy as np
import matplotlib.pyplot as pl


# In[21]:


# Load data from the .mat file
dataset = sio.loadmat("NDM_Assignment2.mat")


# In[22]:


# Extract the data
dataset = dataset['NDM_Assignment2']

fig, axs = plt.subplots(1, 2, figsize=(12, 6))
labels = ["Condition 1", "Condition 2"]
idx = 0

while idx < 2:
    label = labels[idx]
    data = dataset[:, idx]


    mean_participants = np.empty((len(data), 1000))
    mean_trials = np.empty((len(data), 1000))

    # Calculate the mean evidence accumulation
    i = 0
    while i < len(data):
        participant_data = data[i]
        mean_trials[i] = np.mean(participant_data,axis =0 )
        i += 1

    # Calculate the mean evidence accumulation
    mean_participants = np.mean(mean_trials,axis =0)

    # Plot the mean evidence accumulation
    i = 0
```

```
    while i < len(mean_trials):
        axs[idx].plot(mean_trials[i], color='grey', alpha=0.5)
        i += 1

    # Plot the mean evidence accumulation
    axs[idx].plot(mean_participants, color='blue', label="Mean across
Participants")

    axs[idx].set_title(f"{label} - Mean Evidence Accumulation")
    axs[idx].set_xlabel("Time (ms)")
    axs[idx].set_ylabel("Mean Evidence Accumulation")
    axs[idx].legend()

    idx += 1

# Display the plots
plt.tight_layout()
plt.show()


# Calculate the rate of mean evidence accumulation (across participants) for
each of the
# two conditions separately and report on the title of each subplot.
# [Hint: Fit a straight line to the data between the starting point of mean
evidence
# accumulation and the earliest point of reaching the threshold of maximum
evidence to
# calculate the average rate.]

# In[7]:


import scipy.io
import numpy as np
import matplotlib.pyplot as plt
from scipy.stats import linregress


# In[9]:


# Load the MATLAB file
data = scipy.io.loadmat("NDM_Assignment2.mat")
data['NDM_Assignment2']


# In[22]:
```

```
# Assuming that the data is stored in two variables 'Condition1' and
'Condition2'
condition1 = data['NDM_Assignment2'][0]
condition2 = data['NDM_Assignment2'][1]

def CalculateRate(condition, ConditionName):
    # Initialize a list where we store the rates of each participant
    Rates = []

    # Now looping over each participant's data using a while loop
    participant_index = 0
    while participant_index < len(condition):
        ParticipantData = condition[participant_index]

        # Calculate the mean evidence accumulation across each trial
        MeanEvidence = np.mean(ParticipantData, axis=0)

        Start_index = np.where(MeanEvidence >= 300)[0][0]
        End_index = np.where(MeanEvidence >= 600)[0][0]

        # Fit a straight line to the data between start and end indices
        slope, intercept, _, _, _ = linregress(range(Start_index,
End_index+1), MeanEvidence[Start_index:End_index+1])

        # Append the slope (rate of evidence accumulation) to the list
        Rates.append(slope)

        # Increment the participant index
        participant_index += 1

    # Calculate the mean rate across participants
    mean_rate = np.mean(Rates)

    # Plot mean evidence accumulation for each participant with fitted line
    plt.figure(figsize=(12, 6))
    plt.title(f'Mean Rate of Evidence Accumulation for {ConditionName}:
{mean_rate}')
    plt.xlabel('Time (ms)')
    plt.ylabel('Evidence Accumulation')

    # Reset the participant index and loop again to create the plots
    participant_index = 0
    while participant_index < len(condition):
        ParticipantData = condition[participant_index]

        mean_evidence = np.mean(ParticipantData, axis=0)
        plt.plot(mean_evidence)
```

```
        plt.plot(range(Start_index, End_index+1), intercept +
slope*range(Start_index, End_index+1), 'r', label='fitted line')

        # Increment the participant index
        participant_index += 1

    plt.show()

# Calculate and plot rate for each condition
CalculateRate(condition1, 'Condition 1')
CalculateRate(condition2, 'Condition 2')


# In[ ]:




# In[ ]:
```

ii) To compare the mean rate of evidence accumulation (across participants) between the two conditions, conduct an appropriate statistical test and report the results with test statistics and p values. What can be concluded about the motion coherence in the two conditions from the results? [2+1 points]

(Hint: If the data in each of the two groups follow a normal distribution, use a parametric statistical test for testing the difference of two independent group means. Otherwise, use a suitable non-parametric counterpart of the parametric test. https://in.mathworks.com/help/stats/hypothesis-tests-1.html). Normality assumption can be checked using Lilliefors test.)

T-test:
t-statistic: 12.87221400582511
P-value (t-test): 1.2035690396569046e-18
Difference in mean rate of evidence accumulation is significant of (t-test).

Now Using Mann-Whitney U test:
U-statistic: 900.0
P-value (Mann-Whitney U test): 3.019859359162157e-11

Difference in mean rate of evidence accumulation is significant of (Mann-Whitney U test).

[ ]:

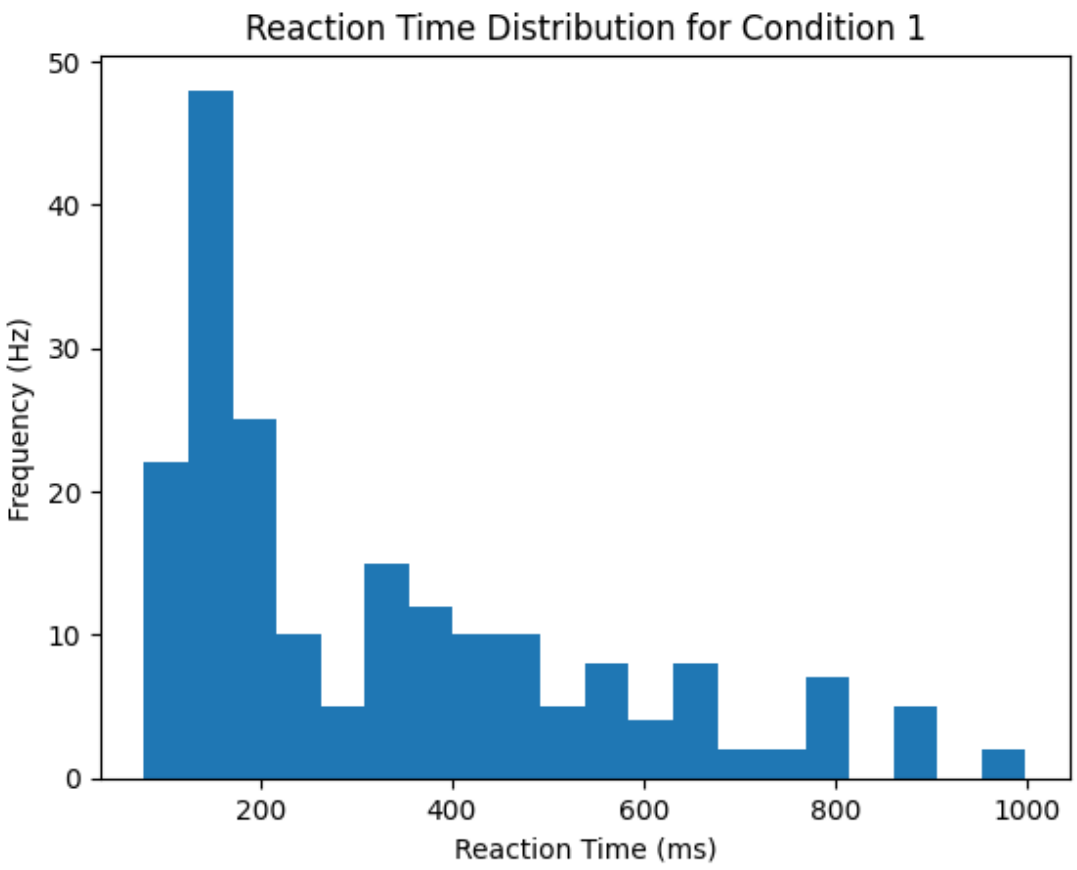
Code is:

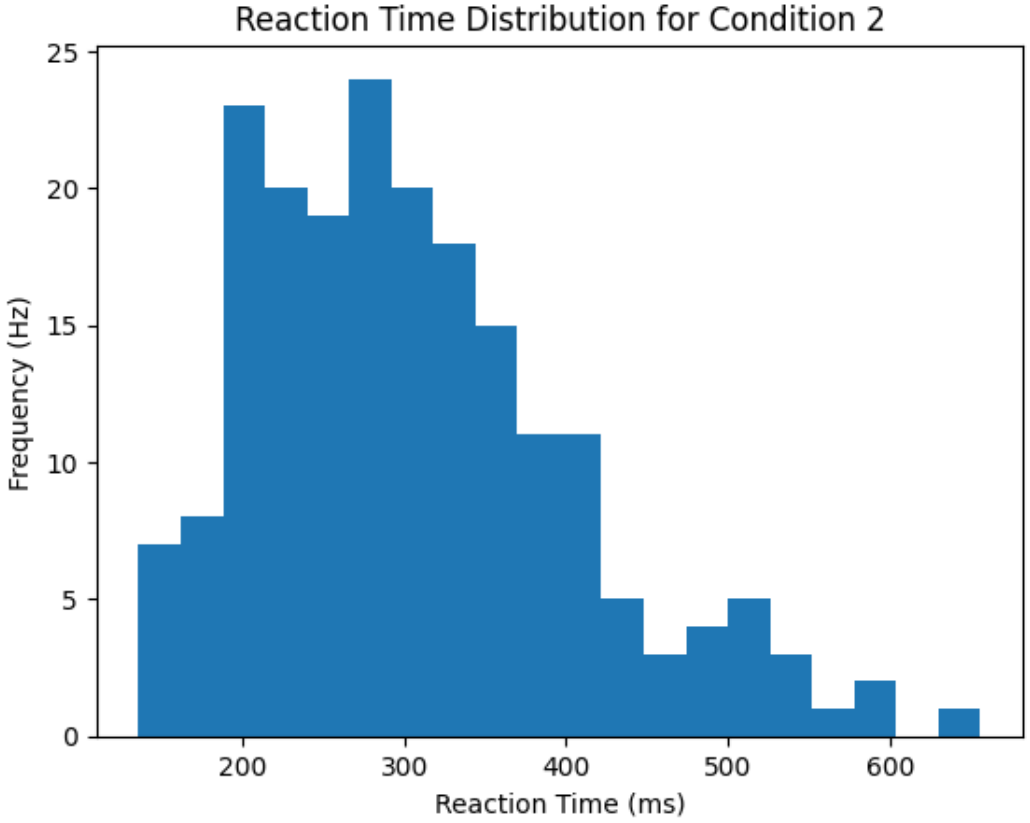
```
#!/usr/bin/env python
# coding: utf-8

# In[5]:


from scipy.stats import ttest_ind, mannwhitneyu
import numpy as np
import scipy.stats as stats
import os
import scipy.io as sio
import numpy as np
import matplotlib.pyplot as pl


# In[7]:


data = sio.loadmat("NDM_Assignment2.mat")
data['NDM_Assignment2']


# In[13]:


# Extract data for both conditions
Cond1Data = data['NDM_Assignment2'][:, 0]
Cond2Data = data['NDM_Assignment2'][:, 1]

# Convert the data to float
MeanCond1 = np.array([np.mean(participant) for participant in Cond1Data],
dtype=float)
MeanCond2 = np.array([np.mean(participant) for participant in Cond2Data],
dtype=float)


# Perform a two-sample independent t-test
TValue, PValue = ttest_ind(MeanCond1, MeanCond2)

# Perform a Mann-Whitney U test
Stat, PValueU = mannwhitneyu(MeanCond1, MeanCond2)

# Report the results
print("T-test:")
```

```
print(f"t-statistic: {TValue}")
print(f"P-value (t-test): {PValue}")
if PValue < 0.05:
    print("Difference in mean rate of evidence accumulation is significant  of
(t-test).")
else:
    print("No   significant difference in mean rate of evidence accumulation
of (t-test).")

print("\n Now Using Mann-Whitney U test:")
print(f"U-statistic: {Stat}")
print(f"P-value (Mann-Whitney U test): {PValueU}")
if PValueU < 0.05:
    print("Difference in mean rate of evidence accumulation is significant  of
(Mann-Whitney U test).")
else:
    print("No   significant difference in mean rate of evidence accumulation o
(Mann-Whitney U test).")


# In[ ]:
```

B i. i) From the data, calculate reaction time (RT) for all 100 trials of each participant. Divide the time axis in 20 bins and plot the mean RT for all 30 participants for both conditions separately. Plot one histogram of the reaction time distribution for each condition. Interpret the findings with respect to motion coherence.

Graphs:


Reaction Time Distribution for Condition 1
Frequency (Hz)
Reaction Time (ms)
0
10
20
30
40
50
200
400
600
800
1000


Reaction Time Distribution for Condition 2
Frequency (Hz)
Reaction Time (ms)
0
5
10
15
20
25
200
300
400
500
600

Code:

```
#!/usr/bin/env python
# coding: utf-8

# In[1]:


import scipy.io
import numpy as np
import matplotlib.pyplot as plt


# In[3]:


mat_data = scipy.io.loadmat('NDM_Assignment2.mat')


# In[12]:


# Extract data for Condition 1 and Condition 2
cond1_data = mat_data['NDM_Assignment2'][0]
cond2_data = mat_data['NDM_Assignment2'][1]

# Function to calculate reaction time
def compute_ReactionTime(data):
    ReactionTime = []  # Change rt=[] to ReactionTime=[]
    index = 0  # Change participant_index to index
    while index < len(data):
        participant = data[index]
        TrailIndex = 0  # Change trial_index to TrailIndex
        while TrailIndex < len(participant):
            trial = participant[TrailIndex]
            ReactionTime.append(np.where(trial >= 600)[0][0])
            TrailIndex += 1
        index += 1
    return np.array(ReactionTime)

# Calculate reaction time for both conditions
rt_cond1 = compute_ReactionTime(cond1_data)
rt_cond2 = compute_ReactionTime(cond2_data)

# Plot reaction time for both conditions

condition=1
plt.hist(rt_cond1, bins=20)
plt.xlabel('Reaction Time (ms)')
plt.ylabel('Frequency (Hz)')
```

```
plt.title(f'Reaction Time Distribution for Condition {condition}')
plt.show()

condition=2
plt.hist(rt_cond2, bins=20)
plt.xlabel('Reaction Time (ms)')
plt.ylabel('Frequency (Hz)')
plt.title(f'Reaction Time Distribution for Condition {condition}')
plt.show()


# In[ ]:
```

ii) From the data, calculate the median bias of evidence accumulation (across participants) separately for condition 1 and condition 2. Conduct the appropriate statistical test to compare both with a reasoning. Report relevant test statistics and p values. [Use the hint in the previous question to conduct the test]

Ans:
Median Bias for Experiment 1: [600.0, 589.2167847205883]
Median Bias for Experiment 2: [600.0, 600.0]
Mann-Whitney U statistic: 1.0
P-value: 0.6170750774519738
T-value: -1.0
No, there is no significant difference between Experiment 1 and Experiment 2.
Since the p-value is greater than 0.05, there is no significant difference between Experiment 1 and Experiment 2.

Code:

```
# ii) From the data, calculate the median bias of evidence accumulation
(across
# participants) separately for condition 1 and condition 2. Conduct the
appropriate
# statistical test to compare both with a reasoning. Report relevant test
statistics and p
# values. [Use the hint in the previous question to conduct the test]

# In[21]:


import scipy.io
import numpy as np
from scipy.stats import mannwhitneyu, ttest_ind
```

```
# In[22]:


mat = scipy.io.loadmat('NDM_Assignment2.mat')
mat


# In[25]:


# Extracting data for Experiment 1 and Experiment 2
experiment1_data = mat['NDM_Assignment2'][0]
experiment2_data = mat['NDM_Assignment2'][1]

# Initialize lists to store median bias for each participant
median_bias_experiment1 = []
median_bias_experiment2 = []

# Iterate over participants to calculate the median bias for each
i = 0
while i < len(experiment1_data):
    median_bias_experiment1.append(np.median(experiment1_data[i]))
    i += 1

i = 0
while i < len(experiment2_data):
    median_bias_experiment2.append(np.median(experiment2_data[i]))
    i += 1

# Perform Mann-Whitney U test to compare medians
u_statistic, p_val = mannwhitneyu(median_bias_experiment1,
median_bias_experiment2)

# Perform t-test to calculate t-value
t_val, _ = ttest_ind(median_bias_experiment1, median_bias_experiment2)

# Report the results
print("Median Bias for Experiment 1:", median_bias_experiment1)
print("Median Bias for Experiment 2:", median_bias_experiment2)
print("Mann-Whitney U statistic:", u_statistic)
print("P-value:", p_val)
print("T-value:", t_val)

# Interpret the results
if p_val < 0.05:
    print("Yes there is a significant difference between Experiment 1 and
Experiment 2.")
```

```
else:
    print("No there is no significant difference between Experiment 1 and
Experiment 2.")


# In[ ]:
```