o conduct a repeated-measures ANOVA to compare the mean BMLD values across frequencies, you can follow these steps:

1. Organize your data into a table or spreadsheet with each row representing one subject and each column representing one frequency (125, 250, 500, 750, or 1000 Hz). Enter the BMLD value for each subject and frequency in the corresponding cell.
2. Open your preferred statistical software (e.g., SPSS, R, SAS) and import your data.
3. Choose the "ANOVA" option from the list of available analyses.
4. Specify the within-subjects factor as "Frequency" with five levels (125, 250, 500, 750, and 1000 Hz).
5. Specify the dependent variable as "BMLD."
6. Run the analysis and check the output for the F-test statistic and associated p-value. The F-test will indicate whether there are significant differences in BMLD between the different frequencies.
7. If the F-test is significant, you can perform a post-hoc analysis to determine which specific frequencies have significant differences. One option is to use a Bonferroni correction to adjust for multiple comparisons.
8. Interpret the results in light of your research question and specific aims.

It is important to note that this is a simplified overview of the steps involved in conducting a repeated-measures ANOVA. Depending on the specific software and statistical package you are using, the exact steps and options may vary. Additionally, it is important to carefully consider the assumptions underlying the ANOVA and check the validity of these assumptions before interpreting the results. If you are unsure about how to perform the analysis or interpret the results, consulting with a statistician or other expert may be helpful.

import pandas as pd

import statsmodels.api as sm

from statsmodels.formula.api import ols

# Load the BMLD data into a Pandas DataFrame

data = pd.read\_excel('bml\_data.xlsx')

# Specify the within-subjects factor as "Frequency" with five levels (125, 250, 500, 750, and 1000 Hz)

factor = 'Frequency'

levels = [125, 250, 500, 750, 1000]

# Specify the dependent variable as "BMLD"

dependent\_var = 'BMLD'

# Fit the repeated-measures ANOVA model

model = ols(f"{dependent\_var} ~ C({factor})", data=data).fit()

# Print the model summary

print(model.summary())

# Get the ANOVA table

aov\_table = sm.stats.anova\_lm(model, typ=2)

# Print the ANOVA table

print(aov\_table)

# Perform post-hoc tests with Bonferroni correction

from statsmodels.stats.multicomp import MultiComparison

mc = MultiComparison(data[dependent\_var], data[factor])

posthoc\_res = mc.allpairtest(stats.ttest\_rel, method='bonf')

# Print the post-hoc test results

print(posthoc\_res[0])

import pandas as pd

from scipy.stats import friedmanchisquare, rankdata

import numpy as np

# Load the data into a Pandas DataFrame

data = pd.read\_excel('bml\_data.xlsx')

# Run the Friedman test

f\_value, p\_value = friedmanchisquare(\*[data[data['Frequency'] == freq]['BMLD'].values for freq in data['Frequency'].unique()])

# Compute the ranks of the BMLD values for each frequency level

data['Rank'] = rankdata(-data['BMLD'].values).astype(int)

ranks = np.zeros((len(data['Frequency'].unique()), len(data)))

for i, freq in enumerate(data['Frequency'].unique()):

ranks[i, :] = data[data['Frequency'] == freq]['Rank'].values

# Compute the mean ranks and the rank differences between each frequency pair

mean\_ranks = np.mean(ranks, axis=1)

pairwise\_differences = np.abs(np.subtract.outer(mean\_ranks, mean\_ranks))

# Compute the critical value for the Nemenyi test

n\_groups = len(data['Frequency'].unique())

n\_samples = len(data)

q\_alpha = 2.343 \* np.sqrt(n\_groups \* (n\_groups + 1) / (6 \* n\_samples))

# Perform the post-hoc Nemenyi test for all frequency pairs

for i in range(n\_groups):

for j in range(i+1, n\_groups):

diff = mean\_ranks[i] - mean\_ranks[j]

q = diff / np.sqrt((n\_groups \* (n\_groups + 1)) / (6 \* n\_samples))

p = 1 - np.sum(pairwise\_differences > np.abs(diff)) / (n\_groups \* (n\_groups - 1) / 2)

print(f"Comparison between frequencies {data['Frequency'].unique()[i]} and {data['Frequency'].unique()[j]}:")

print(f" Difference in mean ranks: {diff:.2f}")

print(f" Z-value: {q:.2f}")

print(f" p-value: {p:.4f}")

if np.abs(q) > q\_alpha:

print(" Significant at alpha=0.05")

else:

print(" Not significant at alpha=0.05")

# Print the test result

print(f"\nFriedman test: F = {f\_value:.2f}, p = {p\_value:.4f}")

The Friedman test is a non-parametric statistical test used to determine whether there are differences among three or more related groups. It is an extension of the Wilcoxon signed-rank test for paired samples to three or more groups.

The Friedman test generates two output values: the F-value and the p-value. The F-value is a test statistic that measures the degree of difference among the groups. It is calculated as follows:

F = (12 / (n \* k \* (k + 1))) \* Σ(R^2) - 3 \* n \* (k + 1)

where n is the number of observations per group, k is the number of groups, and R is the rank of each observation. The F-value is compared to a critical value from the chi-squared distribution with k-1 degrees of freedom to determine statistical significance.

The p-value is the probability of obtaining a test statistic as extreme as or more extreme than the observed F-value, assuming the null hypothesis is true. A p-value less than the chosen significance level (usually 0.05) indicates that the observed differences among the groups are unlikely to be due to chance alone, and thus the null hypothesis can be rejected. Conversely, a p-value greater than the chosen significance level suggests that the observed differences are not statistically significant and that the null hypothesis cannot be rejected.