

Wilcoxon秩和检验BioX

```
import pandas as pd
from scipy.stats import wilcoxon

# Load the Excel file to see its content
file_path = "C:/Users/xfc05/Documents/水产养殖数据假设检验.xlsx"
excel_data = pd.ExcelFile(file_path)

# Display the sheet names to understand the structure of the file
sheet_names = excel_data.sheet_names
print(sheet_names)

# Load the data from the '群体感应' sheet
data = pd.read_excel(file_path, sheet_name='群体感应')

# Display the first few rows of the dataframe to understand its structure
print(data.head())

# Organize data for analysis by creating a dictionary for each experimental
group
data_dict = {
    'WB600': data.iloc[5:7, 2].dropna().astype(float).tolist(),
    'pHT43': data.iloc[5:7, 3].dropna().astype(float).tolist(),
    'BsAiiA': data.iloc[5:7, 4].dropna().astype(float).tolist(),
    'BsYtnP': data.iloc[5:7, 5].dropna().astype(float).tolist(),
    'MtAiiM': data.iloc[5:7, 6].dropna().astype(float).tolist(),
    'AtAttM': data.iloc[5:7, 7].dropna().astype(float).tolist(),
    'AsAhLD': data.iloc[5:7, 8].dropna().astype(float).tolist(),
    'SsAhLS': data.iloc[5:7, 9].dropna().astype(float).tolist(),
    'BsAiiA+BsYtnP': data.iloc[5:7, 10].dropna().astype(float).tolist(),
    'BsAiiA+MtAiiM': data.iloc[5:7, 11].dropna().astype(float).tolist(),
    'BsYtnP+MtAiiM': data.iloc[5:7, 12].dropna().astype(float).tolist(),
    '商业菌': data.iloc[5:7, 13].dropna().astype(float).tolist()
}

# Display the organized data dictionary
print(data_dict)

# Perform Wilcoxon signed-rank test between each modified bacteria group and
the control group (WB600)
results = {}
control_group = data_dict['WB600']
```

```

for group, values in data_dict.items():
    if group != 'WB600': # Skip the control group for comparisons
        stat, p_value = wilcoxon(values, control_group)
        # Format the statistics to show more decimal places
        results[group] = {'statistic': f"{stat:.6f}", 'p_value': f"
{p_value:.6f}"}

# Display the Wilcoxon test results
print(results)

```

UserWarning: Sample size too small for normal approximation.

temp = _wilcoxon_iv(x, y, zero_method, correction, alternative, method, axis)

```

{'pHT43': {'statistic': '0.000000', 'p_value': '0.317311'}, 'BsAiiA': {'statistic': '0.000000', 'p_value':
'0.500000'}, 'BsYtnP': {'statistic': '0.000000', 'p_value': '0.500000'}, 'MtAiiM': {'statistic':
'0.000000', 'p_value': '0.500000'}, 'AtAttM': {'statistic': '0.000000', 'p_value': '0.317311'},
'AsAhID': {'statistic': '0.000000', 'p_value': '0.500000'}, 'SsAhIS': {'statistic': '0.000000', 'p_value':
'0.500000'}, 'BsAiiA+BsYtnP': {'statistic': '0.000000', 'p_value': '0.500000'}, 'BsAiiA+MtAiiM':
{'statistic': '0.000000', 'p_value': '0.500000'}, 'BsYtnP+MtAiiM': {'statistic': '0.000000', 'p_value':
'0.500000'}, '商业菌': {'statistic': '0.000000', 'p_value': '0.500000'}}

```