--- DATA ANALYSIS PLAN ---

Data preperation

1. Data validation and exclusion

1.1 Participant comment review

Participant comments after testing will be reviewed to validate a proper test result. Comments pertaining to technical difficulties and/or disturbances that may have affected the test result will be reviewed by at least two of the authors and lead to exclusion if so judged.

1.2 Non-native speaker exclusion

Furthermore, participants who are non-native Swedish speakers will be excluded in the analysis for CERAD learning, CERAD recall and FAS.

2. Index score for Stroop

Index scores will be calculated for the second part of Stroop test (color-word incongruence) by taking the number of correctanswers divided by the time in seconds.

3. Data standardization

Data will then be standardized from raw scores according to the normative regression models for each cognitive test using age, education, input method and sex as predictors resulting in Z-scores, indicating standard deviations above or below expected score. For a full overview of the multiple linear regression models used, and how they were calculated, see (Mindmore, 2022; van den Hurk et al., 2021).

4. Normality check

To test for normality, data will be visually inspected, and a subsequent Shapiro-Wilk test will be conducted.

Primary analysis

5. Primary hypothesis analysis

For the primary hypothesis, if data is acceptably normally distributed: parametric independent sample one-tailed t-tests will be used to test for differences between the patient group compared to norms. Otherwise a one-sided Wilcoxon signed rank test will be conducted.

Exploratory analysis

6. Generating virtual control group

a control group will be generated by using the predicted scores from normative regression models for the participants included in the study, leading to a virtual control group.

7. ANOVA for each test

After which an ANOVA with the three groups will be done.

8. Post-huc Tukey HSDs

Tukey post-hoc test will be done to test for pairwise comparisons

9. Simple linear regressions in memory domain

The tests in the memory domain (CERAD learning, CERAD delayed recall and Corsi) will be correlated to the sum-score of 6-QEMP using simple linear regression.

10. Simple linear regressions between subjective symptoms and cognitive test results

Each cognitive test will be correlated to the sum-scores of the SMBQ using simple linear regression.

Importing the necessary packages and loading data files

In [15]:
```
from mindmore_standardisation import mindmore_standardis
import pandas as pd
import numpy as np
from matplotlib import pyplot as plt
from scipy import stats
from statsmodels.stats.multicomp import pairwise_tukeyhs
import seaborn as sns
from test_occasion_calculator import what_test_occassion
from mindmore_standardisation import mindmore_standardis
```

```
from MindmoreVirtualControls import MindmoreVirtualContr
import datetime
import EDA
import pingouin as pg

DataFile = pd.read_csv('Data/merged_datafile.csv',encodi
DataFile.rename(columns={'ICBTvs.TAU Sub _sum_Förmätn':'
```

```
C:\Users\FRF8\Anaconda3\envs\ICBTvsTAU\lib\site-packages
\outdated\utils.py:14: OutdatedPackageWarning: The packa
ge outdated is out of date. Your version is 0.2.1, the l
atest is 0.2.2.
Set the environment variable OUTDATED_IGNORE=1 to disabl
e these warnings.
  return warn(
C:\Users\FRF8\Anaconda3\envs\ICBTvsTAU\lib\site-packages
\outdated\utils.py:14: OutdatedPackageWarning: The packa
ge pingouin is out of date. Your version is 0.5.2, the l
atest is 0.5.3.
Set the environment variable OUTDATED_IGNORE=1 to disabl
e these warnings.
  return warn(
```

1. Data validation and exclusion

1.1 Participant comment review

At this point in analysis, all patient comments have been reviewed and no results were excluded for this reason.

1.2 Non-native speaker exclusion

Marking participants for exclusion if non-native for CERAD and FAS

In [2]:

```
DataFile.loc[DataFile.MotherTongue == 0, 'Exclude'] = "E
DataFile.loc[DataFile.Exclude == 'Exclude FAS, CERAD', '

DataFile.loc[DataFile.Exclude == 'Exclude FAS, CERAD', '
DataFile.loc[DataFile.Exclude == 'Exclude FAS, CERAD', '
DataFile.loc[DataFile.Exclude == 'Exclude FAS, CERAD', '
```

```
# Let's see how many are now excluded from the analysis
print("The number of excluded participants for CERAD Lea
      DataFile['CERAD_LEARNING'].isna().sum()))

print("The number of excluded participants for CERAD_DEL
DataFile['CERAD_DELAYED'].isna().sum()))

print("The number of excluded participants for FAS_INDEX
DataFile['FAS_INDEX'].isna().sum()))
```

```
The number of excluded participants for CERAD Learning i
s: 21
The number of excluded participants for CERAD_DELAYED i
s: 21
The number of excluded participants for FAS_INDEX is: 22
```

2. Index scores for Stroop

Due to a product update, index scores had already been calculated by the product

3. Data standardization

Starting out with #3, standardisation. For a full review of the script. See mindmore_standardisation.py

In [3]:

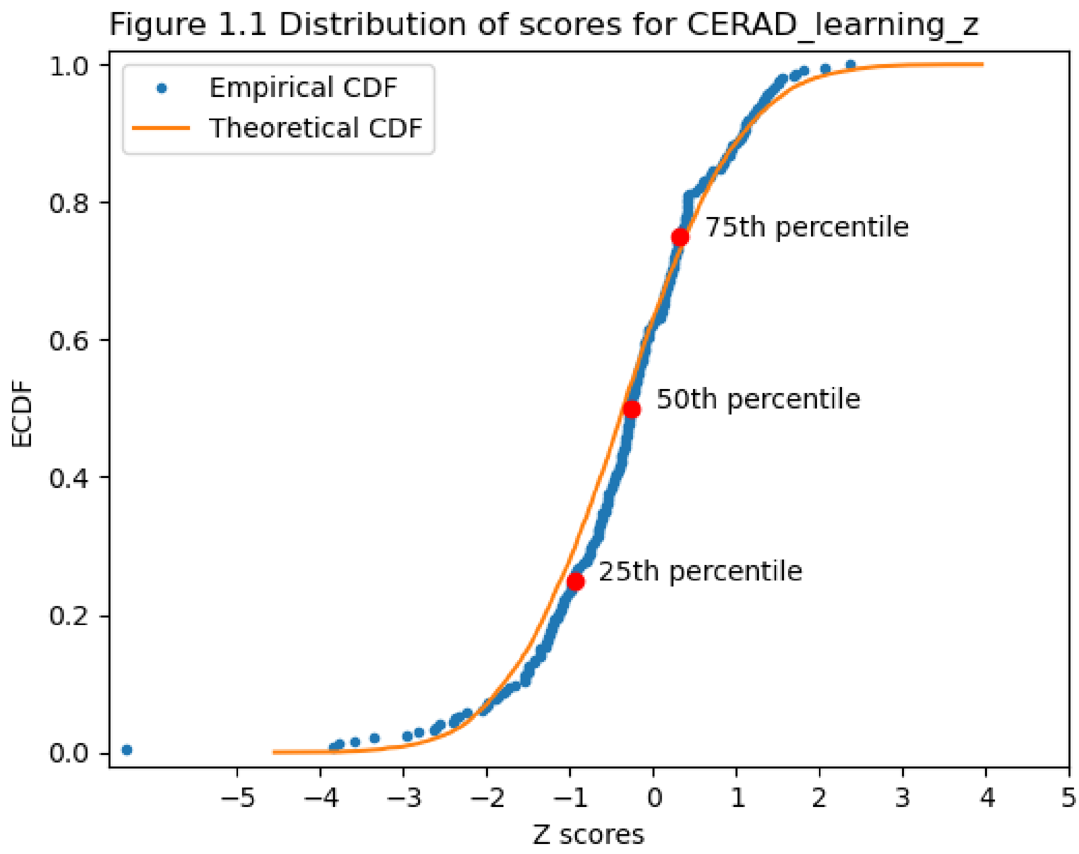
```
x = mindmore_standardiser(DataFile)
merged_datafile = x.CERAD_learning()
merged_datafile = x.CERAD_recall()
merged_datafile = x.CORSI_FWD()
merged_datafile = x.FAS()
merged_datafile = x.SDMT()
merged_datafile = x.Stroop_index_standardizer()
merged_datafile = x.Stroop_inhibition_standardiser()
```

4. Normality check

Let's move on to step #4, visually inspecting data and then conducting a ShapiroWilk test for Normality

Firstly creating a visualizations for all standardized scores

In [4]:
```
EDA.EDA(merged_datafile)
```



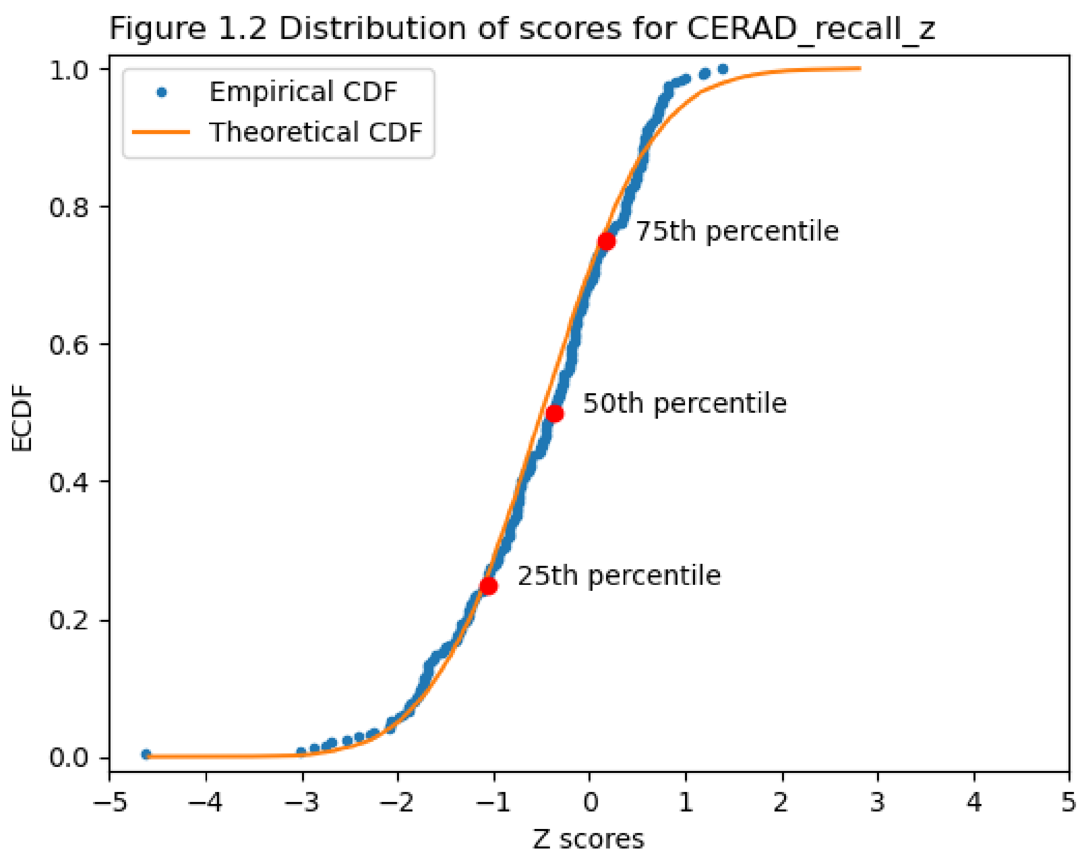


Figure 1.3 Distribution of scores for CORSI_FWD_z

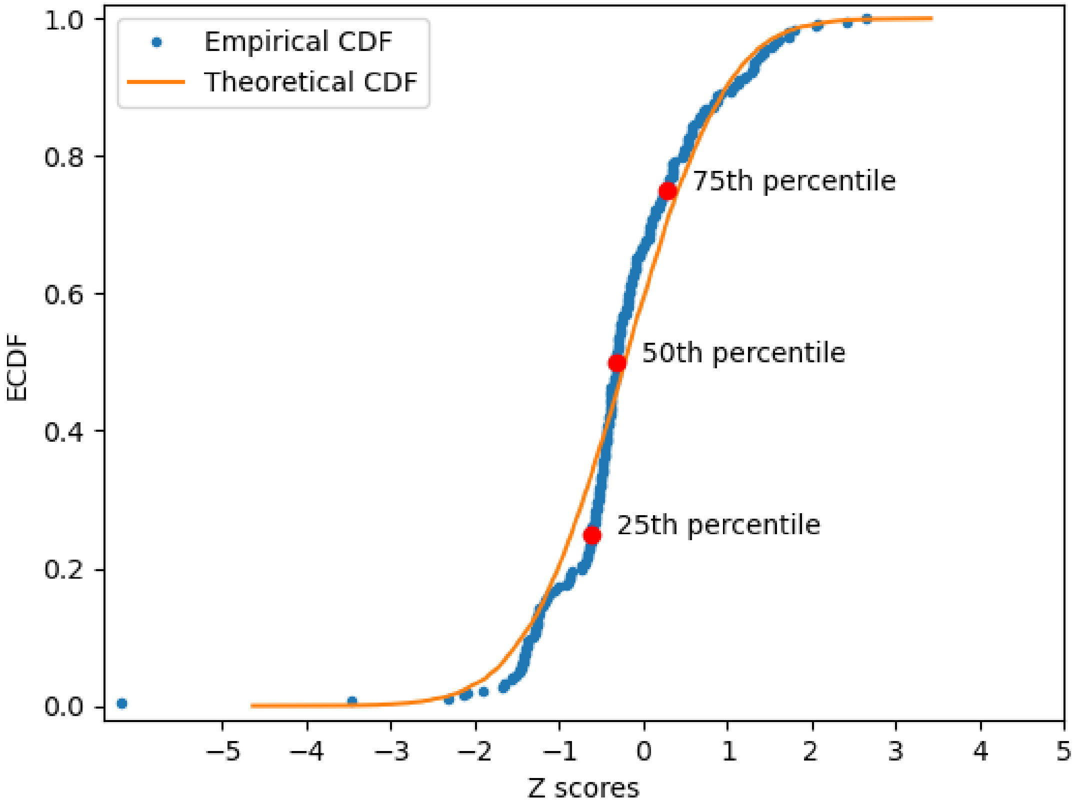


Figure 1.4 Distribution of scores for FAS_z

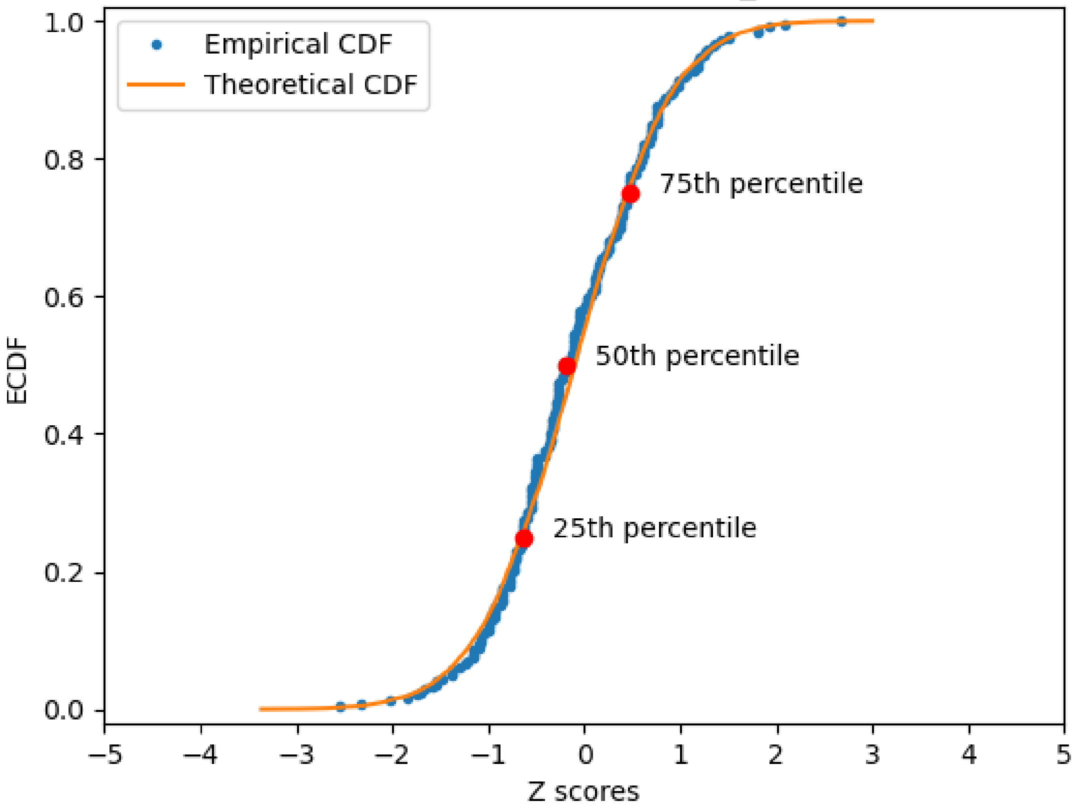


Figure 1.5 Distribution of scores for SDMT_z

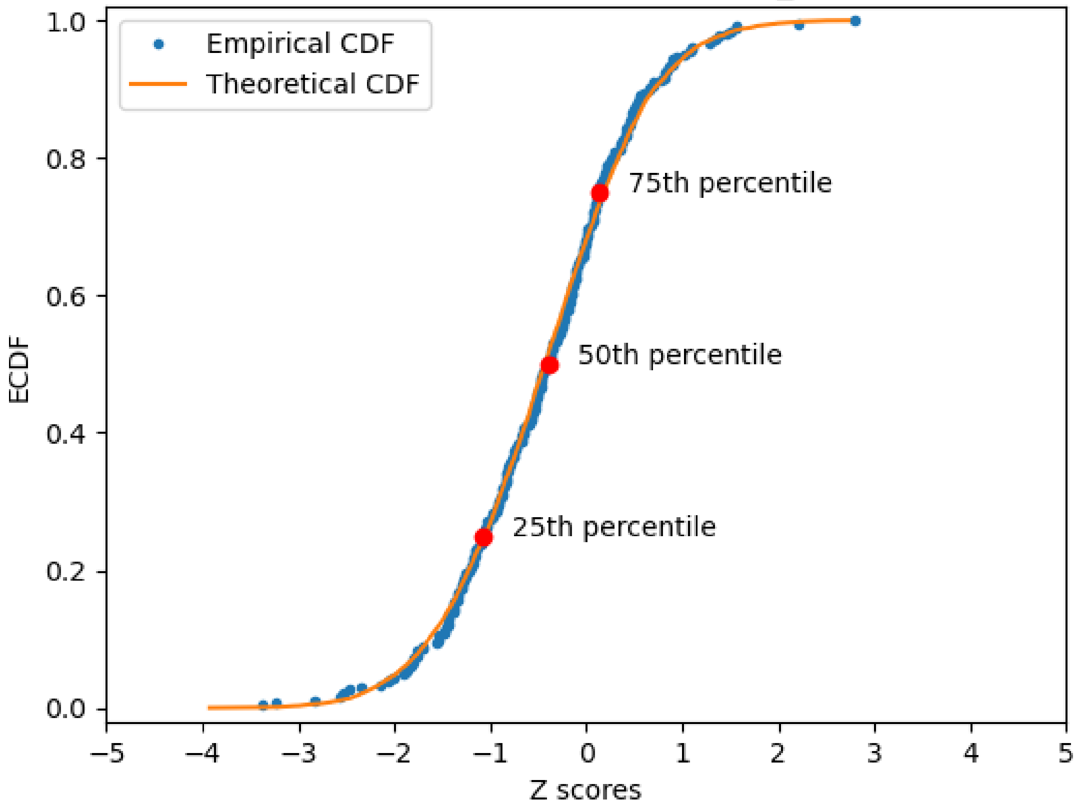
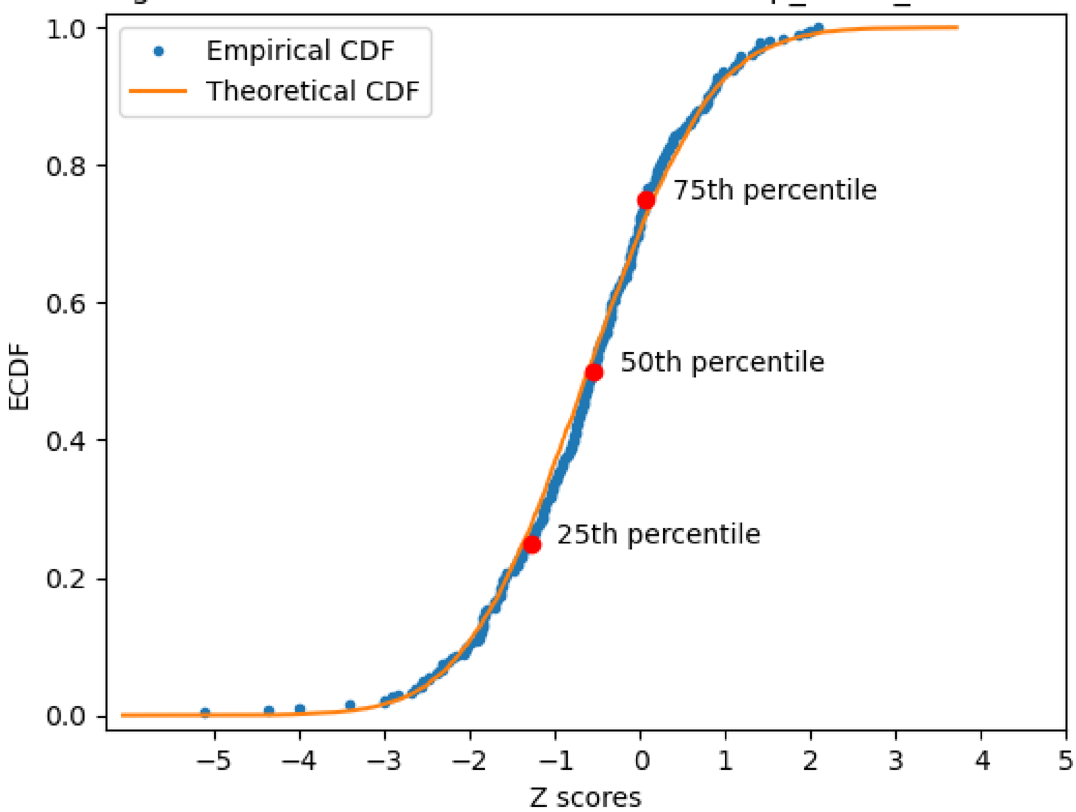
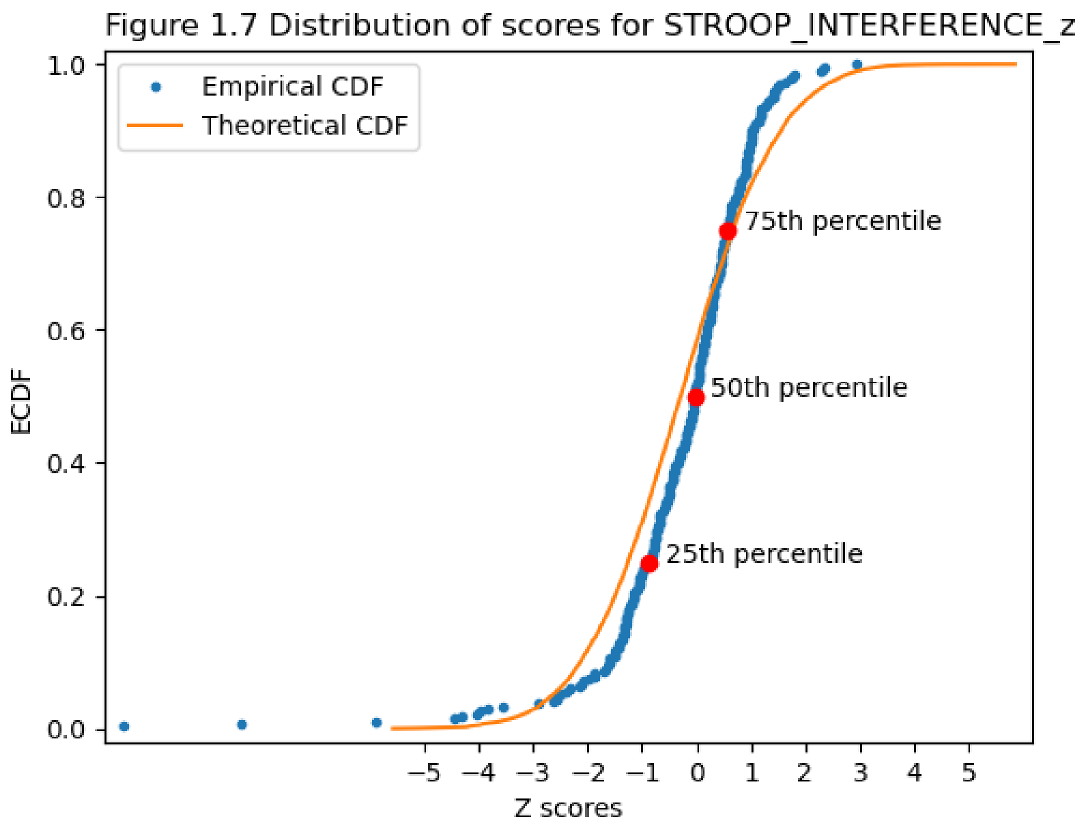


Figure 1.6 Distribution of scores for Stroop_index_z





Looking at the data, we can see that it is fairly normally distributed with some extreme outliers. Let's do the Shapiro-Wilk test for normality.

In [6]:
```
standardised = merged_datafile.filter(regex='z$')
ShapiroWilk = []
for columns in standardised:
    ShapiroWilk.append(stats.shapiro(standardised[column

col = standardised.columns.tolist()
ShapiroWilk = pd.DataFrame(ShapiroWilk, index=col).sort_

print(ShapiroWilk.round(2))
```

	statistic	pvalue
FAS_z	0.99	0.55
SDMT_z	0.99	0.44
Stroop_index_z	0.99	0.02
CERAD_recall_z	0.97	0.00
CERAD_learning_z	0.95	0.00
CORSI_FWD_z	0.93	0.00
STROOP_INTERFERENCE_z	0.83	0.00

Based of these tests as well as a visual inspection of the data, FAS and SDMT follow rules of normality which means that we will do a one-sample t-test for these two tests, and a Wilcoxon signed-rank test for the others. Beginning with the t-tests.

Primary analysis

5. Primary hypothesis analysis

In [7]:

```
t_test = []
normal = standardised[['FAS_z', 'SDMT_z']]
for columns in normal:
        a = normal[columns].dropna()
        t_test.append(stats.ttest_1samp(a, 0, alternativ

col = normal.columns.tolist()
t_test = pd.DataFrame(t_test, index = col)

t_test.round(4)

t_test = t_test.rename(columns = {'statistic': 't_test_s
```

And to calculate effect size (Cohen's d)

In [8]:

```
t_test['CohensD'] = 0
t_test = t_test.reset_index()
def CohensDOS(row):
    return normal[row['index']].mean()/normal[row['index

t_test['CohensD'] = t_test.apply(lambda row: CohensDOS(r
t_test = t_test.set_index('index')
```

And for the non-normal inferential statistics.

In [9]:

```
Wilcoxon = []

nonnormal = standardised[['CERAD_learning_z', 'CERAD_rec
                          'CORSI_FWD_z', 'Stroop_index_z
                          ]]

for columns in nonnormal:
```

```
        a = nonnormal[columns].dropna()
        Wilcoxon.append(stats.wilcoxon(a, alternative='l

col = nonnormal.columns.tolist()
Wilcoxon = pd.DataFrame(Wilcoxon, index = col)

Wilcoxon.round(4)

Wilcoxon = Wilcoxon.rename(columns = {'statistic': 'Wilc
```

Calculating effect size for Wilcoxon using Rank-Biserial correlation (Kirby, 2014)

In [10]:

```
Wilcoxon['RankBiserial'] = 0

Wilcoxon = Wilcoxon.reset_index()

def RankBiserial(row):

    d = nonnormal[nonnormal[row['index']] != 0]
    d = nonnormal[row['index']].dropna()

    r = stats.rankdata(abs(d))
    rsum = r.sum()
    r_plus = np.sum((d > 0) * r)
    r_minus = np.sum((d < 0) * r)
    rbc = r_plus / rsum - r_minus / rsum
    return rbc


Wilcoxon['RankBiserial'] = Wilcoxon.apply(lambda row: Ra
Wilcoxon = Wilcoxon.set_index('index')
```

Summarizing it into a descriptive table

In [11]:

```
DescriptiveTable = standardised.describe()
DescriptiveTable = DescriptiveTable.transpose()

DescriptiveTable = DescriptiveTable.merge(t_test, left_i
                       how='outer').merge(Wilcoxon, left
                                              right_index=Tr
DescriptiveTable.drop(labels=['25%', '50%', '75%'], axis

print(DescriptiveTable.round(8))
```

```
                       count      mean       std
min       max  \
CERAD_learning_z       245.0 -0.334515  1.128791  -6.327
918  2.371209
CERAD_recall_z         245.0 -0.501192  0.921808  -4.617
542  1.392112
CORSI_FWD_z            266.0 -0.218479  0.950105  -6.211
740  2.642359
FAS_z                  244.0 -0.106253  0.818160  -2.547
825  2.681607
SDMT_z                 266.0 -0.440868  0.924864  -3.375
359  2.792290
STROOP_INTERFERENCE_z  266.0 -0.278261  1.445925 -10.524
169  2.939983
Stroop_index_z         266.0 -0.617332  1.126034  -5.106
889  2.094363

                       t_test_statistic  pvalue_x   Cohe
nsD  \
CERAD_learning_z                    NaN       NaN
NaN
CERAD_recall_z                      NaN       NaN
NaN
CORSI_FWD_z                         NaN       NaN
NaN
FAS_z                         -2.028605  0.021795 -0.129
868
SDMT_z                        -7.774494  0.000000 -0.476
685
STROOP_INTERFERENCE_z               NaN       NaN
NaN
Stroop_index_z                      NaN       NaN
NaN

                       Wilcoxon_statistic  pvalue_y  Ran
kBiserial
CERAD_learning_z                  10390.0  0.000013
-0.310436
CERAD_recall_z                     6983.0  0.000000
-0.536552
CORSI_FWD_z                       12174.0  0.000004
-0.314353
FAS_z                                 NaN       NaN
NaN
SDMT_z                                NaN       NaN
NaN
STROOP_INTERFERENCE_z             15224.0  0.021916
```

```
-0.142576
Stroop_index_z                       7699.0   0.000000
-0.566388
```

From the t-tests and the Wilcoxon tests we can observe a difference between patients with stress related mental disorders and the normative sample on every measure. Let's see if we can visualize it with the means for each cognitive test with 95% confidence interval (assuming normality)

In [12]:

```
def W_array(array, conf=0.95): # function that returns W
    t = stats.t(df = len(array) - 1).ppf((1 + conf) /2)
    W = t * np.std(array, ddof=1) / np.sqrt(len(array))
    return W # the error

CI = list()
mean_list = list()
for columns in standardised:
    CI.append((W_array(standardised[columns]))) # makes
    mean_list.append(np.mean(standardised[columns])) # s

#Getting the order correct
mean_list.reverse()
column_list = standardised.columns.tolist()
column_list.reverse()

plt.errorbar(x=mean_list, y=range(len(standardised.colum
plt.axvline(0, ls='--') # this is only to demonstrate th
                          # of the 95% CI contain the ac
plt.yticks(range(len(standardised.columns.tolist())),col
plt.xlabel("Figure X. Mean Z-score. A Z-score of 0 would

plt.show();
```

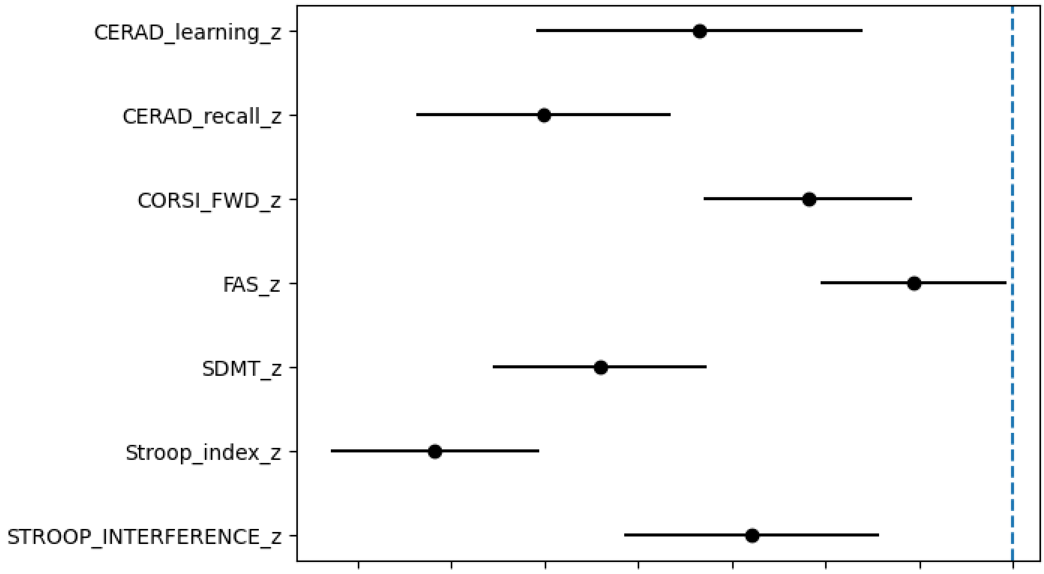


Figure X. Mean Z-score. A Z-score of 0 would indicate no difference from norms

Exploratory analysis

6. Generating virtual control group

In [13]:

```
ControlGroup = merged_datafile.copy()

ControlGroup['diagnosis'] = "Virtual control"

x = MindmoreVirtualControl(ControlGroup)
ControlGroup = x.CERAD_learning()
ControlGroup = x.CERAD_recall()
ControlGroup = x.CORSI_FWD()
ControlGroup = x.FAS()
ControlGroup = x.SDMT()
ControlGroup = x.Stroop_index_VC()
ControlGroup = x.Stroop_inhibition_VC()

ControlGroup = ControlGroup.drop(columns=['CERAD_learnin
'CORSI_FWD_z', 'FAS_z', 'SDMT_z', 'Stroop_index_z',
'STROOP_INTERFERENCE_z', 'SubjectiveMemory', 'CERAD_LEAR
'CERAD_DELAYED_PREDICTED', 'FAS_predicted'])

# And now standardizing this file for a more appropriate
x = mindmore_standardiser(ControlGroup)
ControlGroup = x.CERAD_learning()
ControlGroup = x.CERAD_recall()
```

```
ControlGroup = x.CORSI_FWD()
ControlGroup = x.FAS()
ControlGroup = x.SDMT()
ControlGroup = x.Stroop_index_standardizer()
ControlGroup = x.Stroop_inhibition_standardiser()


# And excluding the participants as was previously gener
ControlGroup.loc[ControlGroup.MotherTongue == 0, 'Exclud
ControlGroup.loc[ControlGroup.Exclude == 'Exclude FAS, C

ControlGroup.loc[ControlGroup.Exclude == 'Exclude FAS, C
ControlGroup.loc[ControlGroup.Exclude == 'Exclude FAS, C
ControlGroup.loc[ControlGroup.Exclude == 'Exclude FAS, C
```

7. ANOVA for each test

Now that a virtual control group is generated, we can move on to do an ANOVA with our three groups. Please note that we are no longer looking at standardised scores but instead an comparison of the predicted score of a generated control group vs the actual scores for each diagnostic group

In [17]:
```
#Now that a virtual control group is generated, we can m
# with our three groups. Please note that we are looking

AnovaGroup = pd.concat([merged_datafile, ControlGroup])

# AnovaGroup.to_csv('Exports/DataWControlGroup20221125.c

ADGroup = AnovaGroup[AnovaGroup['diagnosis'] == 'Adjustm
EDGroup = AnovaGroup[AnovaGroup['diagnosis'] == 'Exhaust
VirtualGroup = AnovaGroup[AnovaGroup['diagnosis'] == 'Vi

AnovaCol = ['CERAD_learning_z', 'CERAD_recall_z',
'CORSI_FWD_z', 'FAS_z', 'SDMT_z', 'Stroop_index_z',
'STROOP_INTERFERENCE_z']
ANOVA = []
for x in AnovaCol:
    AD = ADGroup[x].dropna()
    ED = EDGroup[x].dropna()
    VG = VirtualGroup[x].dropna()
```

```
    # ANOVA.append(stats.f_oneway(AD, ED, VG))
    ANOVA.append(pg.anova(data = AnovaGroup, dv=x, betwe


ANOVA = pd.concat(ANOVA)
ANOVA = ANOVA.set_index(pd.Series(AnovaCol))

ANOVA = ANOVA.round({'F':2, "np2":2, "p-unc":3})

ANOVA[['ddof1', 'ddof2', 'F', 'p-unc', 'np2']] = ANOVA[[
                'ddof2', 'F', 'p-unc', 'np2']].apply(lam

print(ANOVA)
```

```
                          Source  ddof1  ddof2      F  p-un
c   np2
CERAD_learning_z       diagnosis      2    508   6.79   .00
1   .03
CERAD_recall_z         diagnosis      2    508  14.27     .
0   .05
CORSI_FWD_z            diagnosis      2    529    3.8   .02
3   .01
FAS_z                  diagnosis      2    507    .85   .42
7    .0
SDMT_z                 diagnosis      2    529  11.26     .
0   .04
Stroop_index_z         diagnosis      2    529  26.91     .
0   .09
STROOP_INTERFERENCE_z  diagnosis      2    529   3.97    .0
2   .01
```

8. Post-huc Tukey HSDs

It seems we have a significant result in difference between the groups for all of our cognitive tests. Let's do the post-hoc analysis using pairwise comparisons with Tukey HSD. We'll also include a visualization.

In [20]:
```
TukeyList = []

for x in AnovaCol:
    TukeyList.append(x)
    TukeyList.append(x)
    TukeyList.append(x)
```

```
TukeyHSD = []
counter = 1

for x in AnovaCol:
    AD = ADGroup[x].dropna()
    ED = EDGroup[x].dropna()
    VG = VirtualGroup[x].dropna()

    ANOVAGroupsNA = AnovaGroup.filter(items=[x, 'diagnos
    print(x+" results are "+str(stats.tukey_hsd(AD, ED,

    tukey = pairwise_tukeyhsd(endog=ANOVAGroupsNA[x],
                              groups=ANOVAGroupsNA['diagnosi
                              alpha=0.05)

    #Doing some plotting to visualize group differences
    tukey.plot_simultaneous(xlabel = "Figure "+str(count
    plt.show()

    sns.violinplot(data=ANOVAGroupsNA, x='diagnosis', y=
    plt.show()


    counter += 1


    tukeyTable = pd.DataFrame(data=tukey._results_table.
    print("Results for cognitive test "+x+" "+str(tukeyT
    TukeyHSD.append(tukeyTable)


TukeyHSD = pd.concat(TukeyHSD)

TukeyHSD = TukeyHSD.set_index(pd.Series(TukeyList))

TukeyHSD = TukeyHSD.round({'meandiff':2, 'p-adj':3,'lowe


TukeyHSD[['meandiff', 'p-adj', 'lower', 'upper']] = Tuke
               'meandiff', 'p-adj', 'lower', 'upper']].a

TukeyHSD['95% CI'] = "["+TukeyHSD['lower']+", "+TukeyHSD
TukeyHSD.drop(columns=['lower', 'upper', 'reject'], inpl
print(TukeyHSD)
```

CERAD_learning_z results are Tukey's HSD Pairwise Group Comparisons (95.0% Confidence Interval)

Comparison	Statistic	p-value	Lower CI	Upper CI
(0 - 1)	0.143	0.547	-0.177	0.463
(0 - 2)	-0.259	0.074	-0.537	0.019
(1 - 0)	-0.143	0.547	-0.463	0.177
(1 - 2)	-0.402	0.001	-0.671	-0.132
(2 - 0)	0.259	0.074	-0.019	0.537
(2 - 1)	0.402	0.001	0.132	0.671

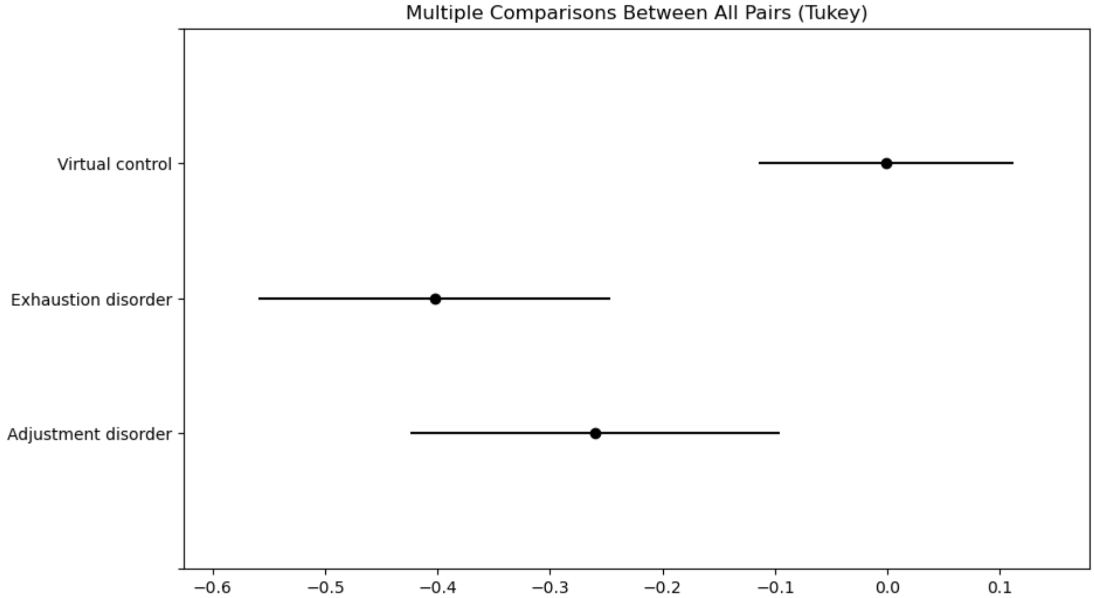
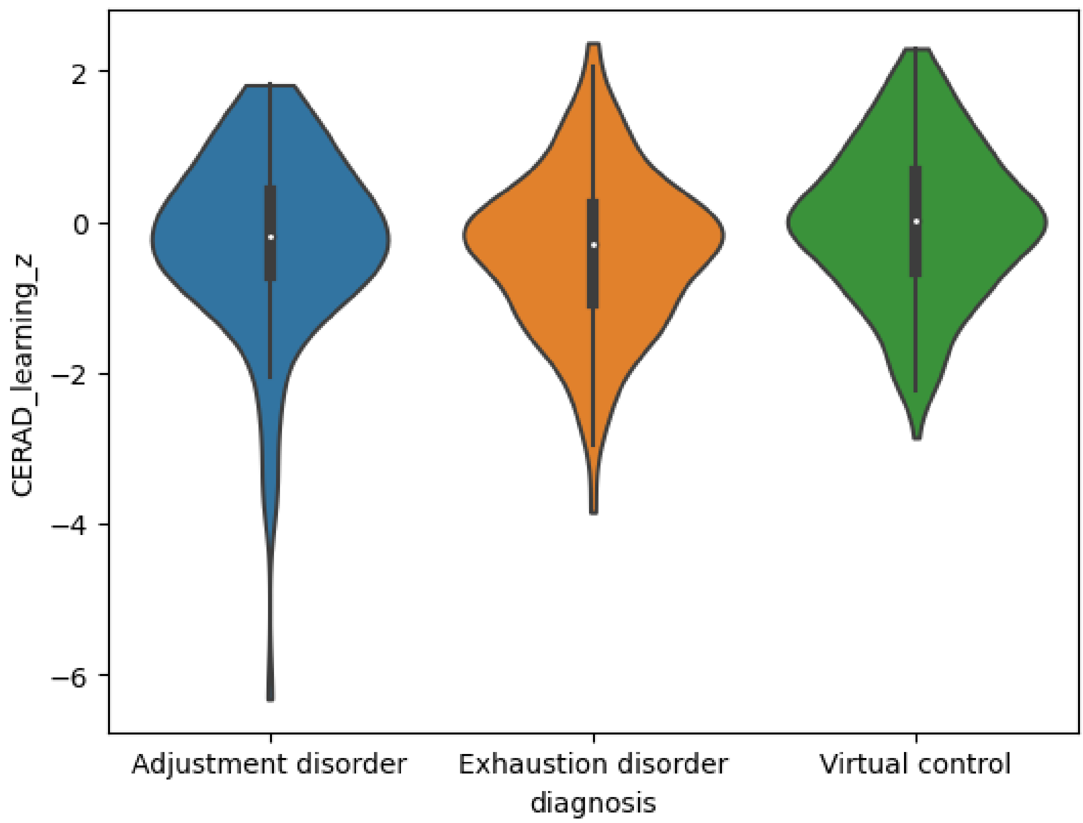


Figure 1. Tukey HSD for CERAD_learning_z



```
Results for cognitive test CERAD_learning_z
group1               group2  meandiff   p-adj   lower
upper  \
0  Adjustment disorder  Exhaustion disorder   -0.1428
0.5469 -0.4631  0.1775
1  Adjustment disorder      Virtual control    0.2587
0.0740 -0.0191  0.5365
2  Exhaustion disorder      Virtual control    0.4015
0.0014  0.1322  0.6709

   reject
0   False
1   False
2    True
CERAD_recall_z results are Tukey's HSD Pairwise Group Co
mparisons (95.0% Confidence Interval)
Comparison  Statistic  p-value  Lower CI  Upper CI
 (0 - 1)      0.092     0.688    -0.170     0.355
 (0 - 2)     -0.360     0.001    -0.588    -0.132
 (1 - 0)     -0.092     0.688    -0.355     0.170
 (1 - 2)     -0.452     0.000    -0.673    -0.231
 (2 - 0)      0.360     0.001     0.132     0.588
 (2 - 1)      0.452     0.000     0.231     0.673
```

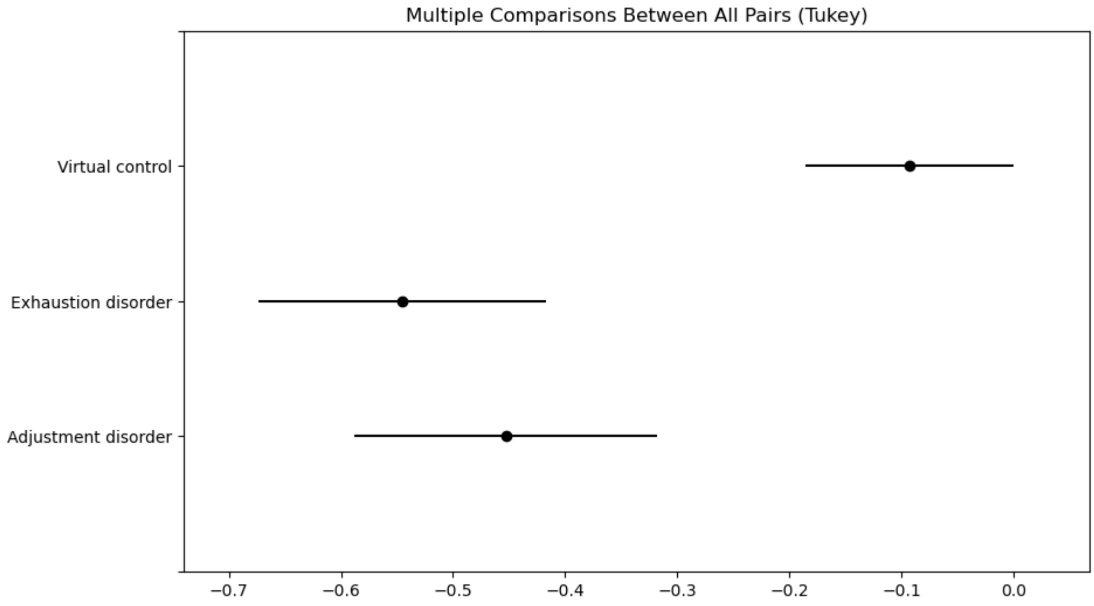
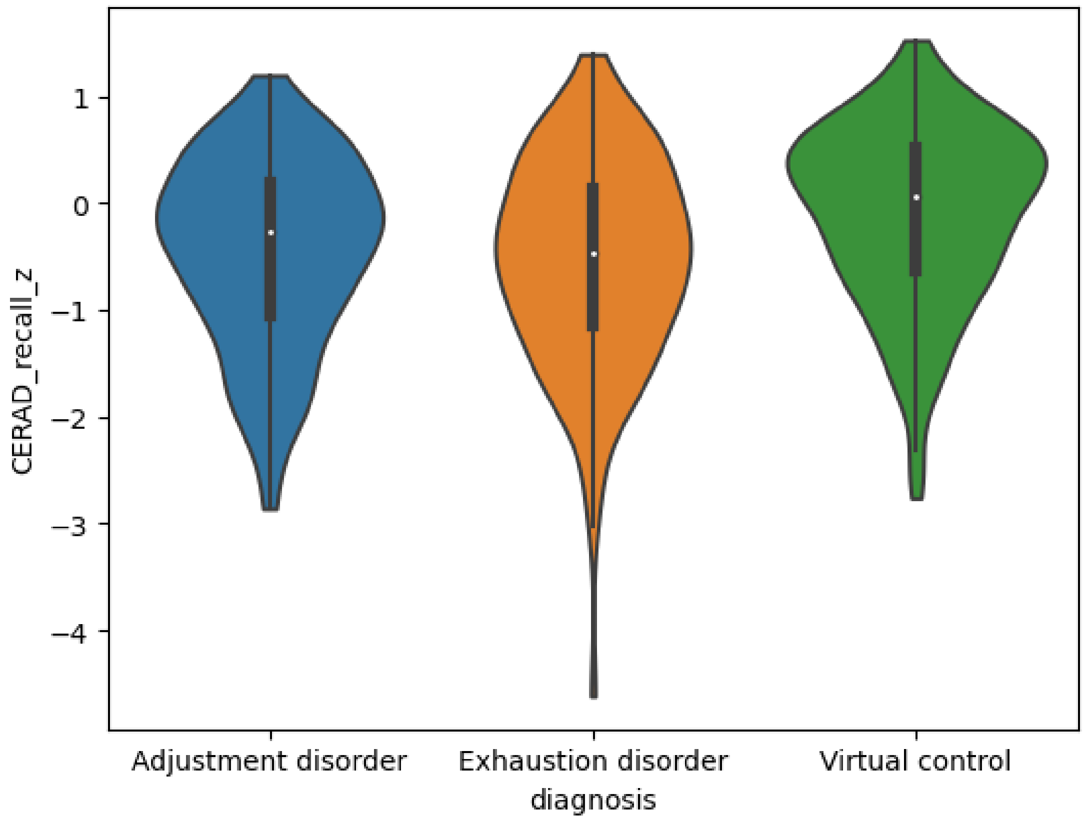


Figure 2. Tukey HSD for CERAD_recall_z




```
Results for cognitive test CERAD_recall_z
group1                  group2  meandiff   p-adj   lower
upper  \
0  Adjustment disorder  Exhaustion disorder   -0.0921
0.6877 -0.3547  0.1704
1  Adjustment disorder      Virtual control    0.3600
0.0007  0.1323  0.5877
2  Exhaustion disorder      Virtual control    0.4521
0.0000  0.2313  0.6729

   reject
0   False
1    True
2    True
CORSI_FWD_z results are Tukey's HSD Pairwise Group Compa
risons (95.0% Confidence Interval)
Comparison  Statistic  p-value  Lower CI  Upper CI
 (0 - 1)      0.008     0.998    -0.283     0.299
 (0 - 2)     -0.238     0.072    -0.491     0.016
 (1 - 0)     -0.008     0.998    -0.299     0.283
 (1 - 2)     -0.246     0.057    -0.497     0.005
 (2 - 0)      0.238     0.072    -0.016     0.491
 (2 - 1)      0.246     0.057    -0.005     0.497
```

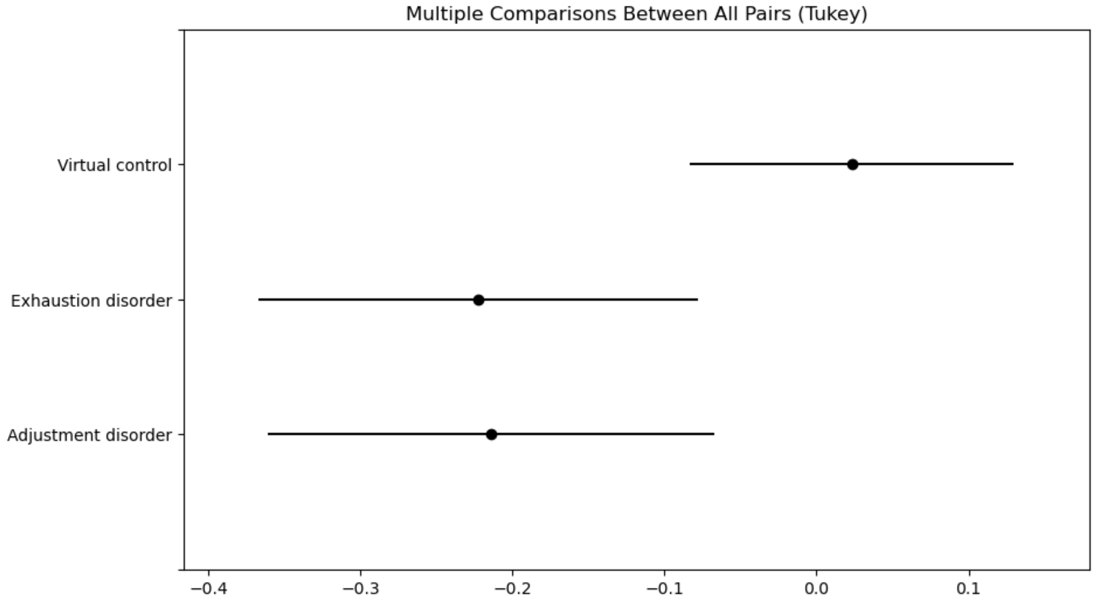
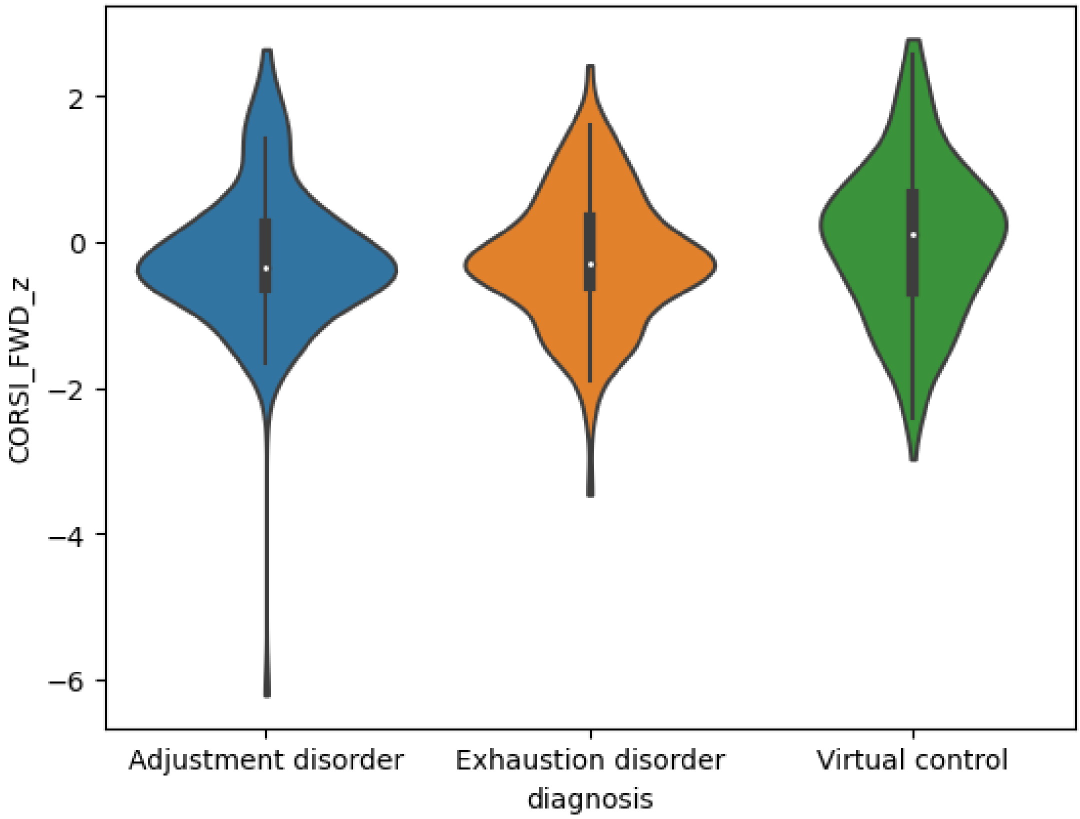


Figure 3. Tukey HSD for CORSI_FWD_z



```
Results for cognitive test CORSI_FWD_z                   g
roup1               group2  meandiff   p-adj   lower   u
pper  \
0  Adjustment disorder  Exhaustion disorder   -0.0080
0.9977 -0.2993  0.2833
1  Adjustment disorder      Virtual control    0.2376
0.0716 -0.0159  0.4911
2  Exhaustion disorder      Virtual control    0.2456
0.0567 -0.0054  0.4966

   reject
0   False
1   False
2   False
FAS_z results are Tukey's HSD Pairwise Group Comparisons
(95.0% Confidence Interval)
Comparison  Statistic  p-value  Lower CI  Upper CI
 (0 - 1)      0.147     0.409    -0.124     0.419
 (0 - 2)      0.055     0.847    -0.180     0.290
 (1 - 0)     -0.147     0.409    -0.419     0.124
 (1 - 2)     -0.093     0.608    -0.321     0.136
 (2 - 0)     -0.055     0.847    -0.290     0.180
 (2 - 1)      0.093     0.608    -0.136     0.321
```

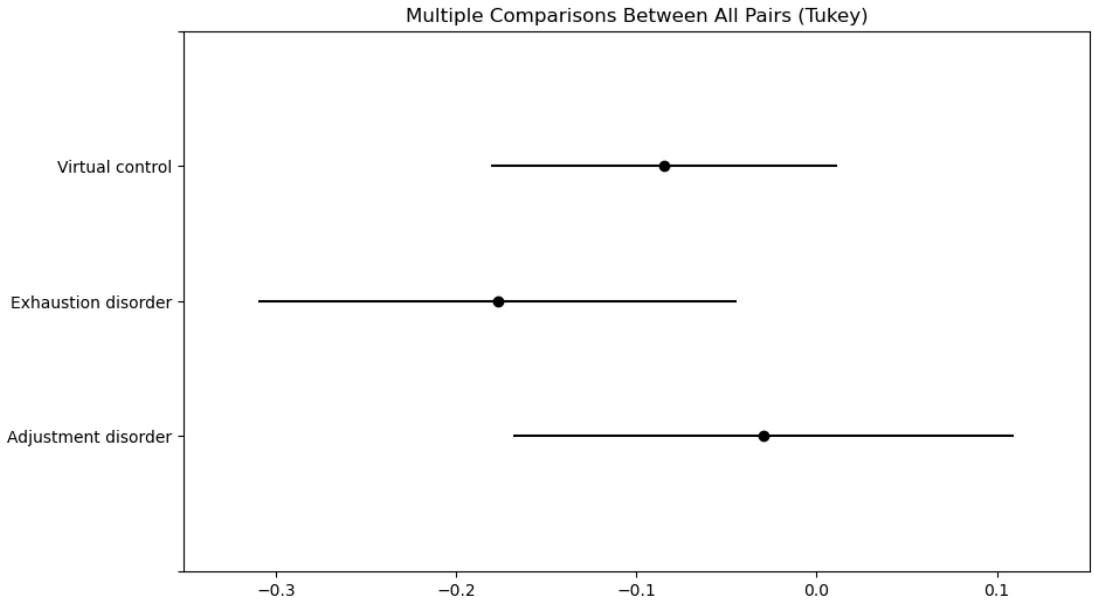
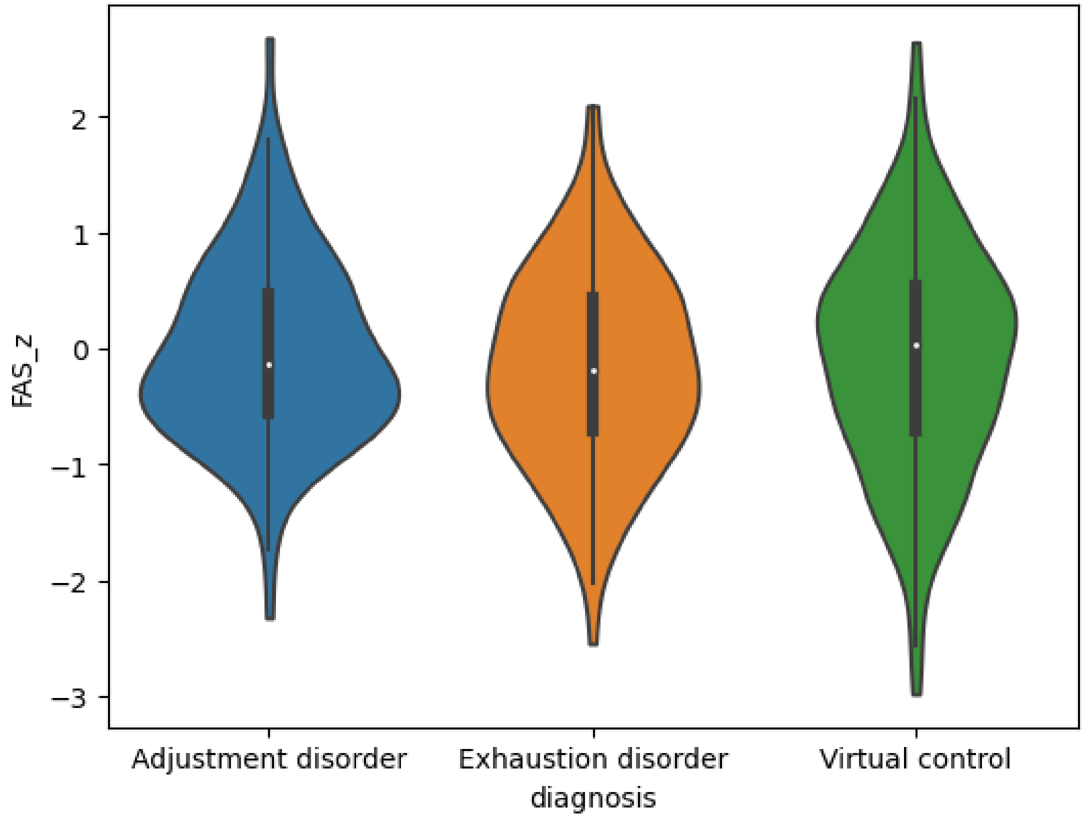


Figure 4. Tukey HSD for FAS_z




```
Results for cognitive test FAS_z                       group1
group2  meandiff   p-adj  lower   upper  \
0  Adjustment disorder  Exhaustion disorder   -0.1475
0.4089 -0.419  0.1240
1  Adjustment disorder      Virtual control   -0.0550
0.8466 -0.290  0.1801
2  Exhaustion disorder      Virtual control    0.0925
0.6079 -0.136  0.3210

   reject
0   False
1   False
2   False
SDMT_z results are Tukey's HSD Pairwise Group Comparison
s (95.0% Confidence Interval)
Comparison  Statistic  p-value  Lower CI  Upper CI
 (0 - 1)      0.205     0.197    -0.074     0.484
 (0 - 2)     -0.268     0.027    -0.511    -0.024
 (1 - 0)     -0.205     0.197    -0.484     0.074
 (1 - 2)     -0.473     0.000    -0.713    -0.232
 (2 - 0)      0.268     0.027     0.024     0.511
 (2 - 1)      0.473     0.000     0.232     0.713
```

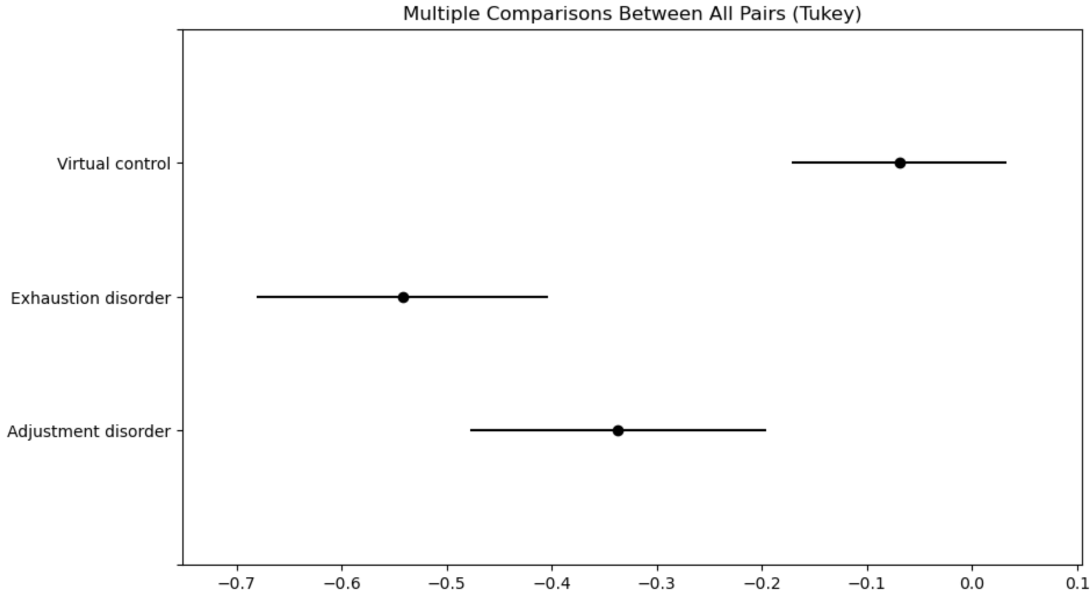
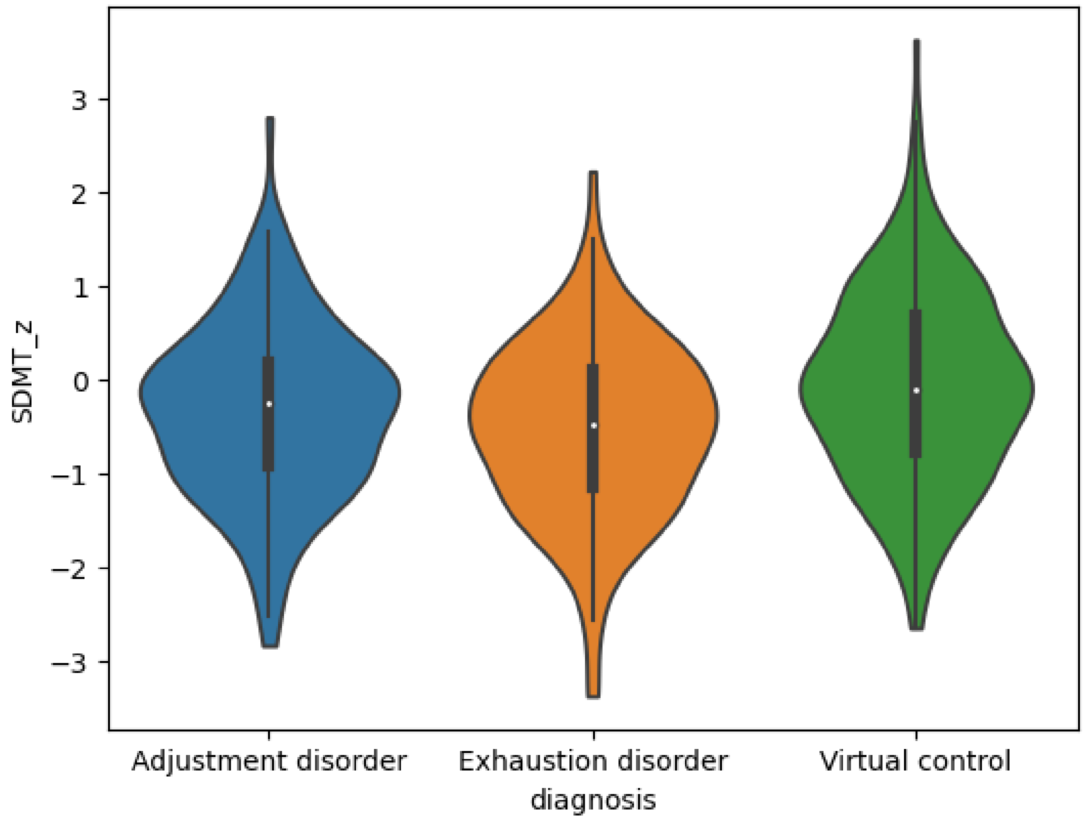


Figure 5. Tukey HSD for SDMT_z



```
Results for cognitive test SDMT_z                  group1
group2  meandiff   p-adj   lower   upper  \
0  Adjustment disorder  Exhaustion disorder   -0.2050
0.1970 -0.4844  0.0744
1  Adjustment disorder      Virtual control    0.2676
0.0269  0.0244  0.5107
2  Exhaustion disorder      Virtual control    0.4726
0.0000  0.2318  0.7133

   reject
0   False
1    True
2    True
Stroop_index_z results are Tukey's HSD Pairwise Group Co
mparisons (95.0% Confidence Interval)
Comparison  Statistic  p-value  Lower CI  Upper CI
 (0 - 1)      0.270     0.093    -0.034     0.573
 (0 - 2)     -0.505     0.000    -0.769    -0.241
 (1 - 0)     -0.270     0.093    -0.573     0.034
 (1 - 2)     -0.774     0.000    -1.036    -0.513
 (2 - 0)      0.505     0.000     0.241     0.769
 (2 - 1)      0.774     0.000     0.513     1.036
```

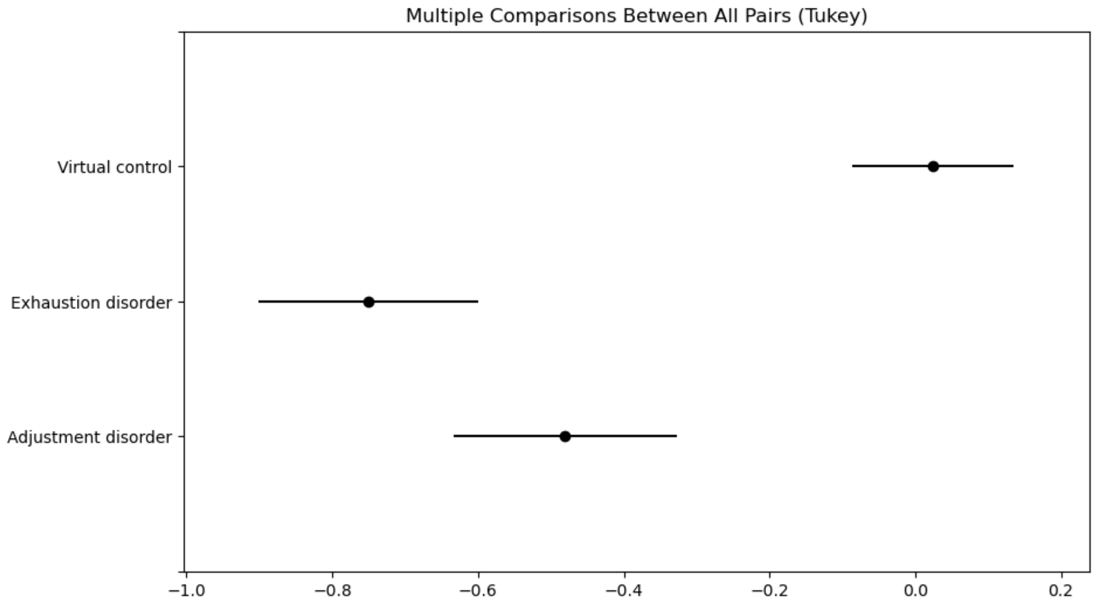
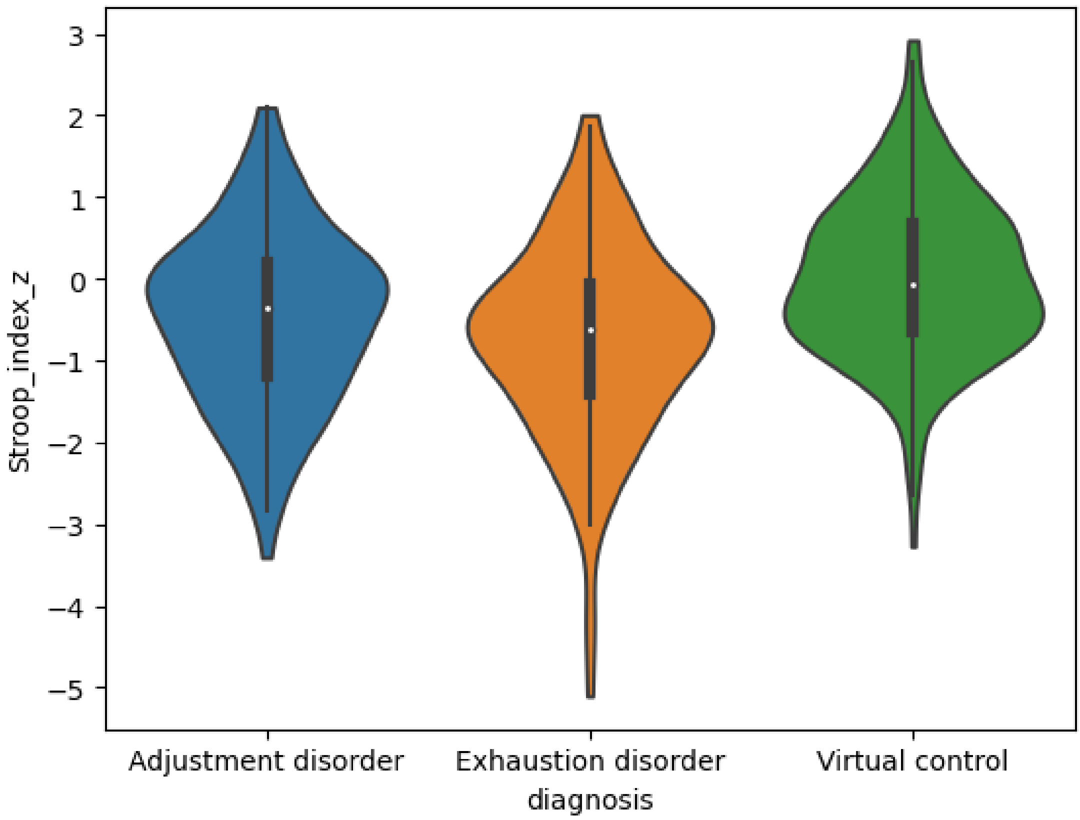


Figure 6. Tukey HSD for Stroop_index_z




```
Results for cognitive test Stroop_index_z
group1                   group2  meandiff   p-adj   lower
upper  \
0  Adjustment disorder  Exhaustion disorder   -0.2697
0.0928 -0.5729  0.0336
1  Adjustment disorder      Virtual control    0.5047
0.0000  0.2407  0.7686
2  Exhaustion disorder      Virtual control    0.7744
0.0000  0.5131  1.0356

   reject
0   False
1    True
2    True
STROOP_INTERFERENCE_z results are Tukey's HSD Pairwise G
roup Comparisons (95.0% Confidence Interval)
Comparison  Statistic  p-value  Lower CI  Upper CI
 (0 - 1)      0.300     0.132    -0.066     0.666
 (0 - 2)     -0.074     0.848    -0.392     0.244
 (1 - 0)     -0.300     0.132    -0.666     0.066
 (1 - 2)     -0.374     0.015    -0.689    -0.059
 (2 - 0)      0.074     0.848    -0.244     0.392
 (2 - 1)      0.374     0.015     0.059     0.689
```

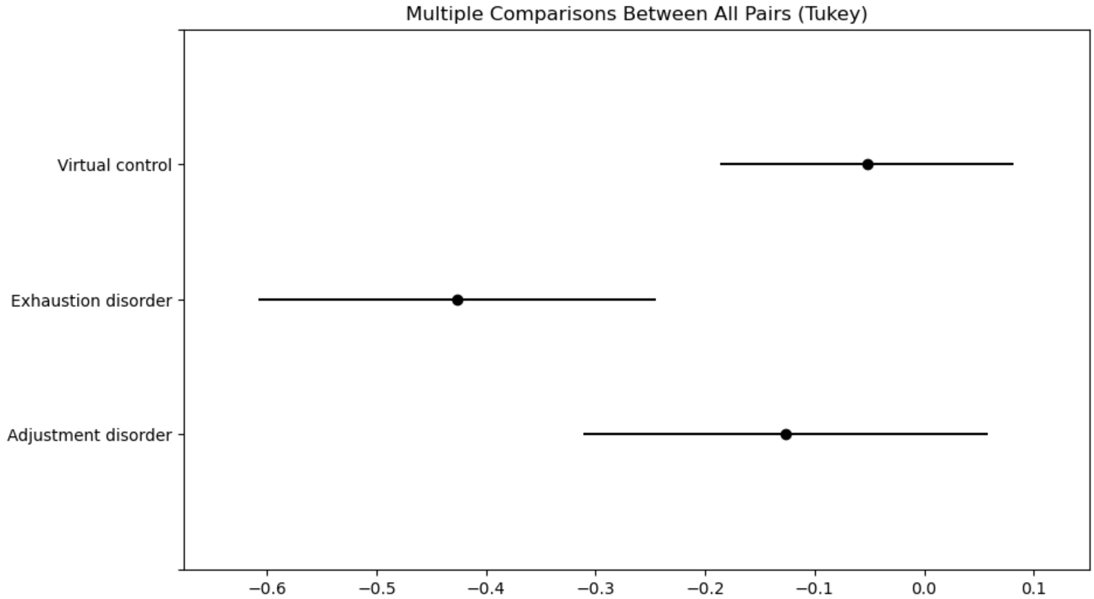
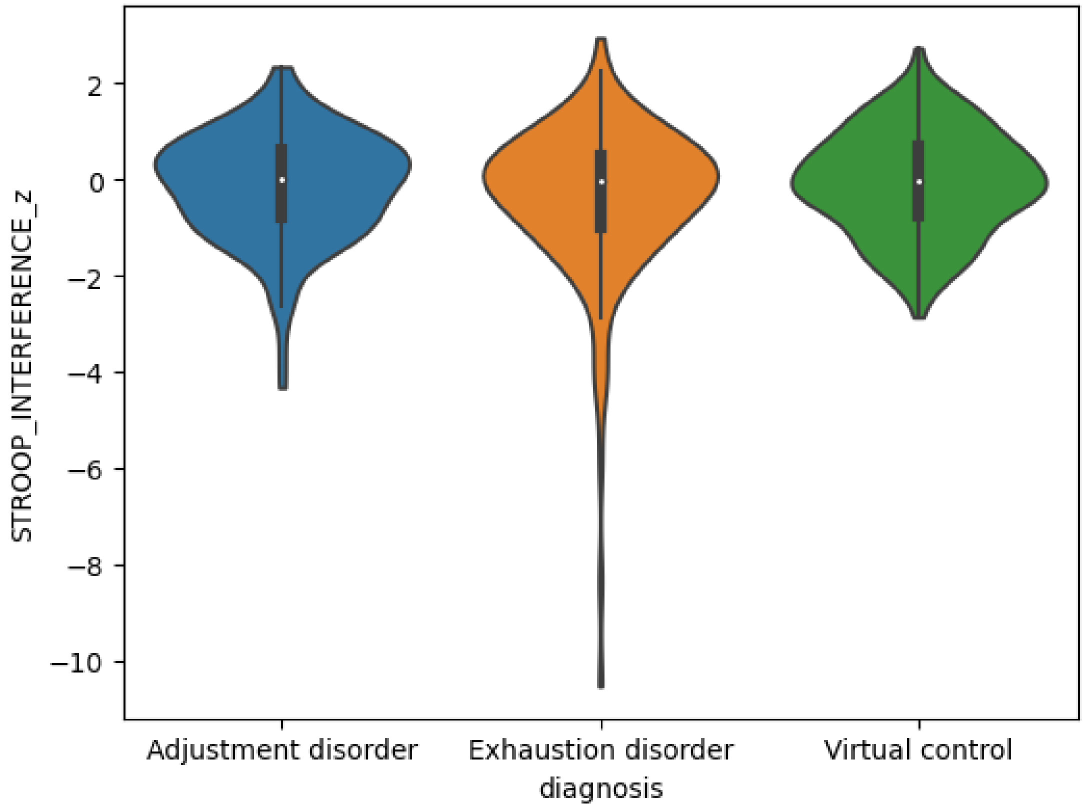


Figure 7. Tukey HSD for STROOP_INTERFERENCE_z



```
Results for cognitive test STROOP_INTERFERENCE_z
group1               group2  meandiff   p-adj   lower
upper  \
0  Adjustment disorder  Exhaustion disorder   -0.2998
0.1324 -0.6658  0.0661
1  Adjustment disorder      Virtual control    0.0740
0.8485 -0.2445  0.3925
2  Exhaustion disorder      Virtual control    0.3738
0.0152  0.0586  0.6891

   reject
0   False
1   False
2    True
                                           group1
group2 meandiff  \
CERAD_learning_z       Adjustment disorder  Exhaustion d
isorder    -0.14
CERAD_learning_z       Adjustment disorder      Virtual
control      .26
CERAD_learning_z       Exhaustion disorder      Virtual
control       .4
CERAD_recall_z         Adjustment disorder  Exhaustion d
isorder    -0.09
CERAD_recall_z         Adjustment disorder      Virtual
control      .36
CERAD_recall_z         Exhaustion disorder      Virtual
control      .45
CORSI_FWD_z            Adjustment disorder  Exhaustion d
isorder    -0.01
CORSI_FWD_z            Adjustment disorder      Virtual
control      .24
CORSI_FWD_z            Exhaustion disorder      Virtual
control      .25
FAS_z                  Adjustment disorder  Exhaustion d
isorder    -0.15
FAS_z                  Adjustment disorder      Virtual
control    -0.06
FAS_z                  Exhaustion disorder      Virtual
control      .09
SDMT_z                 Adjustment disorder  Exhaustion d
isorder     -0.2
SDMT_z                 Adjustment disorder      Virtual
control      .27
SDMT_z                 Exhaustion disorder      Virtual
control      .47
Stroop_index_z         Adjustment disorder  Exhaustion d
```

```
isorder    -0.27
Stroop_index_z         Adjustment disorder      Virtual
control       .5
Stroop_index_z         Exhaustion disorder      Virtual
control      .77
STROOP_INTERFERENCE_z  Adjustment disorder  Exhaustion d
isorder     -0.3
STROOP_INTERFERENCE_z  Adjustment disorder      Virtual
control      .07
STROOP_INTERFERENCE_z  Exhaustion disorder      Virtual
control      .37

                      p-adj        95% CI
CERAD_learning_z       .547  [-0.46, .18]
CERAD_learning_z       .074  [-0.02, .54]
CERAD_learning_z       .001    [.13, .67]
CERAD_recall_z         .688  [-0.35, .17]
CERAD_recall_z         .001    [.13, .59]
CERAD_recall_z           .0    [.23, .67]
CORSI_FWD_z            .998   [-0.3, .28]
CORSI_FWD_z            .072  [-0.02, .49]
CORSI_FWD_z            .057   [-0.01, .5]
FAS_z                  .409  [-0.42, .12]
FAS_z                  .847  [-0.29, .18]
FAS_z                  .608  [-0.14, .32]
SDMT_z                 .197  [-0.48, .07]
SDMT_z                 .027    [.02, .51]
SDMT_z                   .0    [.23, .71]
Stroop_index_z         .093  [-0.57, .03]
Stroop_index_z           .0    [.24, .77]
Stroop_index_z           .0   [.51, 1.04]
STROOP_INTERFERENCE_z  .132  [-0.67, .07]
STROOP_INTERFERENCE_z  .848  [-0.24, .39]
STROOP_INTERFERENCE_z  .015    [.06, .69]
```

9. Simple linear regressions in memory domain

Now let's move on to the regressions. Firstly we'll start by looking at the relationship between subjective memory impairment and our memory tests

In [21]:

```
MemoryRegressions = []
MemTests = ['CERAD_learning_z', 'CERAD_recall_z', 'CORSI
```

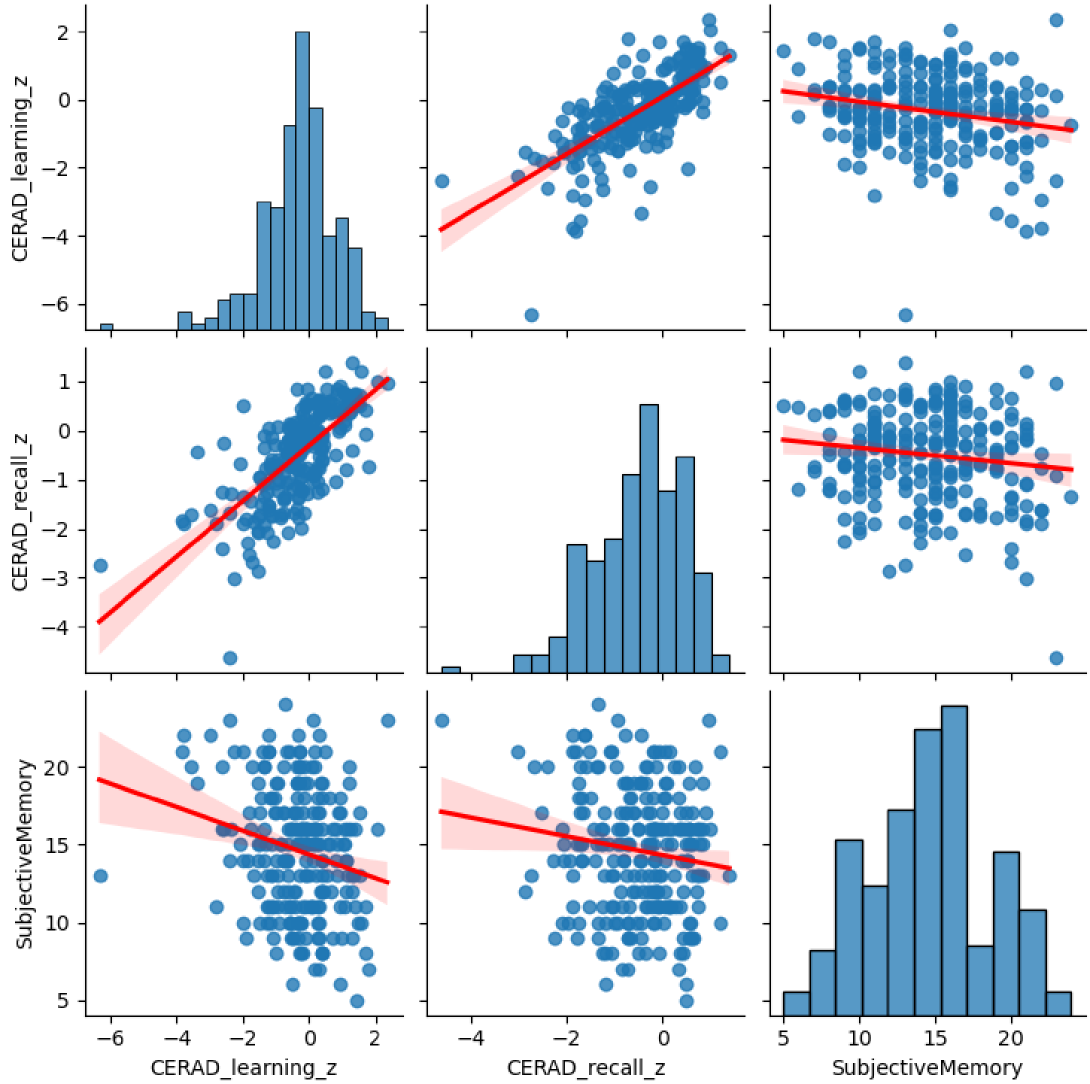
```
for tests in MemTests:
    a = merged_datafile[merged_datafile[tests].notnull()
    MemoryRegressions.append(stats.linregress(a[tests],
                                              y=a['Subje
                                              alternativ

MemoryRegressions = pd.DataFrame(MemoryRegressions, inde

print(MemoryRegressions)
```

```
                      slope  intercept    rvalue    pvalu
e    stderr
CERAD_learning_z -0.759242  14.370512 -0.214767  0.00071
4  0.221490
CERAD_recall_z   -0.601144  14.323201 -0.138865  0.02978
0  0.275013
CORSI_FWD_z      -0.142458  14.615492 -0.034191  0.57877
5  0.256283
```

Now there's seems to be a small association between subjective memory impairment and the CERAD tests. Let's plot it using a scatter plots

In [22]:
```
sns.pairplot(merged_datafile[['CERAD_learning_z', 'CERAD
                              , 'SubjectiveMemory']], ki
             plot_kws={'line_kws':{'color':'red'}})
```

Out[22]:
```
<seaborn.axisgrid.PairGrid at 0x1cb2a8675b0>
```



10. Simple linear regressions between subjective symptoms and cognitive test results

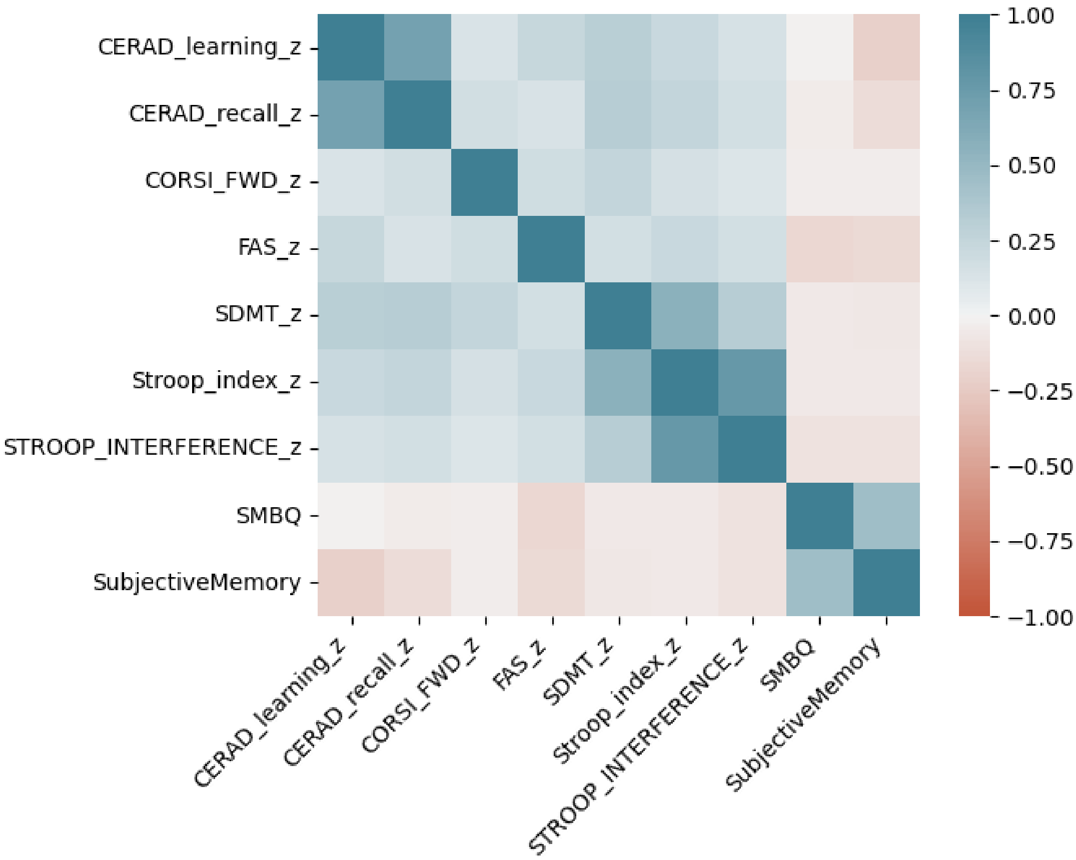
And now for the regressions for the subjective symtom measure SMBQ and the cognitive test results

In [23]:
```
LinearRegressions = []
for columns in AnovaCol:
        a = merged_datafile[merged_datafile[columns].not
        LinearRegressions.append(stats.linregress(a[colu
                                                  y=a['S
                                                  altern

LinearRegressions = pd.DataFrame(LinearRegressions, inde

print(LinearRegressions)
```

```
                          slope  intercept    rvalue
pvalue    stderr
CERAD_learning_z      -0.007443   5.205673 -0.009179  0.
886335  0.052015
CERAD_recall_z        -0.041136   5.187546 -0.041429  0.
518654  0.063642
CORSI_FWD_z           -0.035741   5.200838 -0.037893  0.
538344  0.058010
FAS_z                 -0.180406   5.183928 -0.161537  0.
011506  0.070848
SDMT_z                -0.057750   5.183186 -0.059600  0.
332882  0.059530
Stroop_index_z        -0.039627   5.184183 -0.049792  0.
418653  0.048921
STROOP_INTERFERENCE_z -0.060253   5.191880 -0.097217  0.
113687  0.037965
```

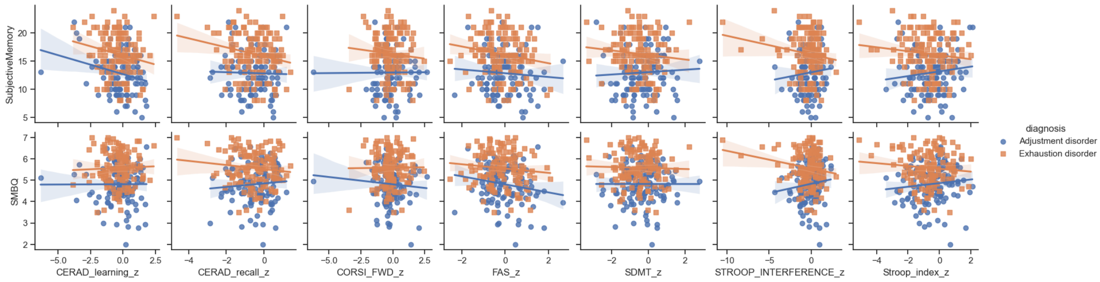
For FAS but not the other tests are we finding a relationship to SMBQ. Let's visualize the correlation matrix using a heatmap

In [53]:
```
Heatmap = merged_datafile[standardised.columns.tolist()+
corr = Heatmap.corr()
ax = sns.heatmap(
    corr,
    vmin=-1, vmax=1, center=0,
    cmap=sns.diverging_palette(20, 220, n=200),
    square=True
)
ax.set_xticklabels(
    ax.get_xticklabels(),
    rotation=45,
    horizontalalignment='right'
);
```



And we can also visualize the relationship between the subjective symptom ratings split by diagnosis

In [26]:
```
sns.set_theme(style="ticks")

sns.pairplot(merged_datafile[['CERAD_learning_z',
 'CERAD_recall_z',
 'CORSI_FWD_z',
 'FAS_z',
 'SDMT_z',
 'STROOP_INTERFERENCE_z',
 'Stroop_index_z',
                              'SubjectiveMemory', 'SMBQ'
                              'diagnosis']], hue='diagno
             kind='reg', y_vars=['SubjectiveMemory', 'SM
             x_vars=['CERAD_learning_z',
              'CERAD_recall_z',
              'CORSI_FWD_z',
              'FAS_z',
              'SDMT_z',
              'STROOP_INTERFERENCE_z',
              'Stroop_index_z'],
             markers=["o", "s"])

plt.show()
```


SubjectiveMemory
SMBQ
CERAD_learning_z
CERAD_recall_z
CORSI_FWD_z
FAS_z
SDMT_z
STROOP_INTERFERENCE_z
Stroop_index_z
diagnosis
Adjustment disorder
Exhaustion disorder

In [ ]: