A guide for interpreting ROI statistical comparisons in SAMBA

19 March 2019 (Tuesday)
Alternate title: "compare_group_stats_exec_v2: a guide to interpreting its output"
The code referenced herein: /cm/shared/workstation_code_dev/analysis/SAMBA/label_stats/compare_group_stats_exec_v2.m

This function performs basic statistical comparisons between two groups. The group names, number in each group, and run numbers of group members are included in the first two lines of the output file.

Each file contains the comparisons for a particular MRI biomarker/contrast: acd, fa, dwi, rd, etc.

The comparisons are made for each Region of Interest (ROI). The mean value of the particular contrast within each ROI for each individual has been previously measured and are the atomic units in the statistical calculations. Currently the structure names are not included, and ROIs are identified by their number as they appear in the label volumes.

A guide to the various column names*:

* "*XXX*" is used in place of the names of Group 2 and Group 1, which are arbitrarily specified (e.g. "treated" and "controls", "knock_out" and "wild_type", etc).
* Note that the t-tests are: Group 2 - Group 1. Keep this in mind when interpreting the polarity of the related statistics.

ROI: The identifying lookup number for the region of interest/label.
mean_XXX: The mean value of the individual means of the XXX group.
std_XXX: The standard deviation of the individual means of the XXX group.
sem_XXX: Standard Error of the Mean for the XXX group.
                     This is calculated by dividing the std by the square root of the number of individuals in the XXX Group.
ci1_XXX: The lower bound of the Confidence Interval of the XXX group statistics, calculated as *mean - 1.96*std.*
ci2_XXX: The upper bound of the Confidence Interval of the XXX group statistics, calculated as *mean + 1.96*std.*
hypothesis: Accept the null-hypothesis: 0; Reject null hypothesis: 1. This is returned from the *ttest2* function in MATLAB.
p_value: The p-value as calculated by the [parametric] *ttest2* function in MATLAB.
ppermute: The p-value of the permutation test (n=1000), as calculated by the *mattest* function in MATLAB.
P_FDR_0p05_BH: The adjusted *ttest2* p-value from the Benjamini & Hochberg False Discovery Rate correction, with $q = 0.05$.

Google "fdr_bh matlab" to find the relevant code in the MATLAB File Exchange website.

CI_1:   Lower bound of the Confidence Interval as returned from the *ttest2* function in MATLAB.
             This is the "100*(1-ALPHA)% confidence interval for the true difference of population means."

CI_2:   Upper bound of the Confidence Interval as returned from the *ttest2* function in MATLAB.

t_stats: The t-statistic (test statistic), as calculated by the *ttest2* function in MATLAB.

cohen_d: Cohen's *d*, "an effect size used to indicate the standardised difference between two means."
             Calculated here as the (mean_Group_2 - mean_Group_1) / pooled_std.
             NOTE THE POLARITY, i.e. + when G2 is larger than G1.

difference: The difference in means, divided by the mean of Group 1, multiplied by 100%.
             Calculated as 100*(mean_Group_2 - mean_Group_1) / mean_Group_1.
             NOTE THE POLARITY, i.e. + when G2 is larger than G1.