README

Code file documentation

- **Folder code_RWSPM:** contains all core functions for imposing "RegionWise Statistical Parametric Mapping".

  - Function *RWSPM* in "EWSPM.R" performs regional partitioning, distribution aggregation within each sub-region, and region-wise independence test.

  - Function *RW.MTCCT* in "EWSPM.R" identifies spatially contiguous regions where multiple adjacent subregions exhibit moderate but collectively meaningful associations.

  - Function *golden_section_search* in "slide_width.R" is used to select a sliding-region width by minimizing loss function defined in section 2.1 of manuscript.

- **Folder compared_method:**

  - The folder contains five subdirectories (code_GBJ, code_AdaMant, code_Rdcov, code_sKPCR, code_fvGWAS), each corresponding to one of the compared methods.

  - Code "Y_slide.R" is used for image partitioning and serves for the five compared methods in simulation.

- **Folder Simu_setting:** stores the simulation setting codes: "sim_s1.py" generates the data under the null hypothesis; "sim_s2.py", "sim_s3.py", and "sim_s4.py" generate data for Model 1 of

manuscript under different parameter settings. "sim_s5_x2.py",

"sim_s6_x2.py", and "sim_s7_x2.py" generate data for Model 2 of

manuscript under different parameter settings.

- **Folder code_simu_result:**

  - Code "DOR.R" generates box plots for six compared methods

    under settings 2-7, all results are summarized in Figure4 of

    manuscript.

  - Code "load_sim_result.R" loads and stores the results of the six

    compared methods under Settings 1-7.

  - Code "sum_sim_result.R" summarizes Type I error rate and

    power results under settings 1-7, all results are summarized in

    Table2 of manuscript.

- **Folder code_realdata:**

  - Due to data privacy and storage limitations, we did not put the

    original genotype data from ADNI online. Instead, a general

    illustrative set of scripts is included in the code_realdata folder,

    providing the code necessary to reproduce the real-data analysis

    presented in Section 5 of manuscript.

  - Before the performing the data application, the following input

    files are required:

1. The genetic data file (in our case, named as ADNI_1_3.RData),

2. The phenotype data files (in our case, named as left_hipp_ori.Rdata

and right_hipp_ori.Rdata),

3. The covarites information file (in our case, named as covarites_inf.Rdata),

4. The genetic data information file including chr, SNP, position, Alleles (in our case, named as snp_inf1_3.Rdata).

Step 1.

- Run "processing_realdata.R" to perform preprocessing of the phenotype data including regional partitioning, adjustment for covariate effects, and other related preparatory procedures.

Step 2.

- Run "rwspm rwspm_realdata.R" to impose our proposed method RWSPM on processed genetic-phenotype data.

- Run "realdata_sub_region.R" to segment phenotype data and serves for five compared methods.

- Run "realdata_gbj.R", "realdata_adaMant.R", "realdata_Rdcov.R", "realdata_ sKPCR.py", "realdata_fvGWAS.m" to impose five compared methods on processed genetic-phenotype data.

Step 3.

- Run "summarize_result.R" to summarize all reasults in real data analysis.

● The RWSPM is organized into an R package (*/.../RWSPM_0.1.0.tar.gz)*.