CGSEA User's Guide

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Developers: Feng Zhang

License: GPL

URL: https://github.com/ChengSQXJTU/CGSEA

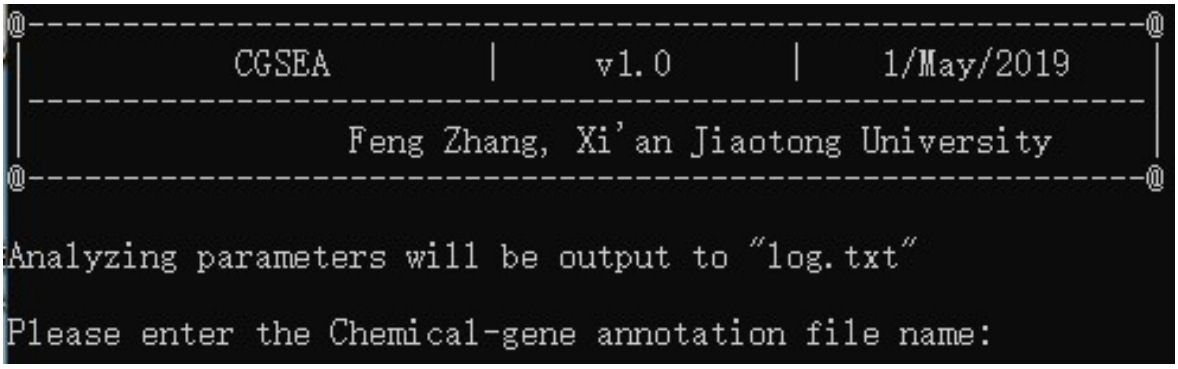
Email: fzhxjtu@xjtu.edu.cn

1. Installing and Running CGSEA

CGSEA is developed by C to interface with R for efficient data analysis. Please make sure that R (http://www.r-project.org/) has been installed on your system. CGSEA is a command line based program. Unzip the downloaded "CGSEA" package and run "CGSEA" program at your terminal window to start analysis.

Example:

./CGSEA



2. Parameter Setting

CGSEA will ask users to input a set of parameters before starting analysis:

[1] **Chemical-gene annotation file name**: Please input the storage path and name of Chemical-gene annotation file. We have provided a Chemical-gene annotation file in the CGSEA package. Users can also use the Chemical-gene annotation file prepared by their self**.** Please make your Chemical-gene annotation files using following format:

Example:

grandidone A MRPL20
methyl 5-aminolevulinate TCEB3
fluvalinate IQCC
….

Note: Each line of this file records a chemical (the first column) and corresponding gene (the second column).

[2] **Genome-wide gene expression association testing statistic file name**: Please

input the storage path and file name of genome-wide gene expression association testing statistics of target traits. The gene expression association testing statistics can be driven from transcriptome-wide association studies or gene expression profile studies. Please make your GWAS summary data files using following formats:

Example:

HES4 0.041
ISG15 3.276
SDF4 0.011
PER3 0.001
….

Note: Each line of this file record the gene (the first column) and corresponding expression association testing statistics (the second column).

[3] Permuation times: Permutations are used for *P* value calculation in CGSEA. More than 1,000 permutations are recommended for obtaining accurate *P* values. Note, too large permutation times will make CGSEA taking a long time to complete data analysis.

[4] Maximum sizes of chemical response geneset: Users need to define the maximum (fault value = 1000 genes) sizes of chemical response geneset analyzed by CGSEA.

[5] Minimum sizes of chemical response geneset: Users need to define the minimum (fault value = 5 genes) sizes of chemical response geneset analyzed by CGSEA.

3. Output files

CGSEA will output two result files:

[1] CGSEA_result.txt: Each line of this file records a chemical and corresponding enrichment analysis results.

Example:

Chemical name	**NES**	**P**
grandidone A	0.09	0.52
streptobiosamine	1.57	0.06

…

Note: NES denotes the normalized enrichment score statistics of CGSEA.

[2] **NESplot.pdf:** Plot of CGSEA analysis results of target trait. In generated figures, each point denotes a chemical. X-axis presents the total number of chemicals analyzed by CGSEA. Y-axis shows $-\log_{10}$ (*P* values) calculated by CGSEA.