Obtaining data from EWAS atlas

Standard operating procedure 7

Dec 31, 2023

Download epigenomic associations from EWAS atlas https://ngdc.cncb.ac.cn/ewas/browse available from China National Center for Bioinformatics.

EWAS Atlas is described in the study shown on the image below:

EWAS Atlas: a curated knowledgebase of epigenome-wide association studies

Mengwei Li [1] [2] [3], Dong Zou [1] [2], Zhaohua Li [1] [2] [4], Ran Gao [3] [5], Jian Sang [1] [2] [3], Yuansheng Zhang [1] [2] [3], Rujiao Li [1] [2], Lin Xia [1] [2] [3], Tao Zhang [1] [2] [3], Guangyi Niu [1] [2] [3], Yiming Bao [1] [2] [3] [4], Zhang Zhang [1] [2] [3] [5]

Affiliations + expand

Go to EWAS Atlas home page https://ngdc.cncb.ac.cn/ewas/browse and click **Downloads**

EWAS Atlas
@EWAS Open Platform

☰ Browse   💼 EWAS Toolkit   ⬇ Downloads   📊 Statistics   🖥 API   📁 Help   📊 EWAS Data Hub

Download By Trait

[▼]   ⬇Download

Batch Download

Description	Download	File size
Associations	EWAS_Atlas_associations.tsv	31.9MB
Studies	EWAS_Atlas_studies.tsv	81KB
Cohorts	EWAS_Atlas_cohorts.tsv	208KB
Probe annotations	EWAS_Atlas_probe_annotations.tsv	170.9MB
Trait to trait relationships	EWAS_trait_trait_logP.txt	0.9MB

Download EWAS atlas associations

Download By Trait

▼   ⬇Download

Batch Download

Description	Download	File size
Associations	EWAS_Atlas_associations.tsv	31.9MB
Studies	EWAS_Atlas_studies.tsv	81KB
Cohorts	EWAS_Atlas_cohorts.tsv	208KB
Probe annotations	EWAS_Atlas_probe_annotations.tsv	170.9MB
Trait to trait relationships	EWAS_trait_trait_logP.txt	0.9MB

Use R to search ***EWAS_atlas_associations.tsv*** file and save the associations with cardiovascular conditions of interest.

Before searching in R, verify which traits are present in the dataset by entering corresponding keywords in EWAS atlas search tab as shown below:

For example, typing in **cholesterol** will reveal cholesterol-related traits present in the dataset

After verifying that relevant traits are present in the dataset, we can use R grep to search for corresponding keywords and download selected associations as CSV files

```
# Read in associations
assoc <- read.table("EWAS_Atlas_associations.tsv", header = T,
                    quote = "\"", fill = T, sep = "\t")
head(assoc)

write.csv(assoc[grep("atherosclerosis", assoc$trait, ignore.case = T),],
          file = "atherosclerosis.csv")
```

After all relevant associations were downloaded, we can join all separate CSV files into a single master table