Downloading significant associations from genome-wide epigenetic associations studies

Standard operating procedure 8

Yaroslav Ilnytskyy
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Study eligibility

Accept the following studies:

- Epigenome-wide studies focused on detecting associations between the methylation levels of single CpGs and relevant traits. If the study is based on differentially methylated region, please highlight it in the excel sheet.
- The studies are based on microarrays or next generation sequencing
- The study has significant CpGs with p-values less than 0.001 or q-values below 0.05
- The study must have a Pubmed ID

Association eligibility

Record the following associations:

- The p-value of the association is below 0.001 or the q-value less than 0.05
- Probe/CpG id is provided for microarray study
- Genome coordinates and genome version is provided for the sequencing studies

Column description

See the excel file with example of EWAS data table attached to this email

Columns:

probeID: probe/CpG id, for example cg15556765, this column is filled out for microarray studies only

chr: chromosome id (this column is filled out for sequencing studies only)

pos: chromosomal position (filled out for sequencing studies only)

genome_version: version of human genome assembly, for example GRCh37

beta_coefficient: beta coefficient that reflects the strength of association between CpG methylation and quantitative expression of the trait. This data type is applicable to studies that aim to find associations between CpG methylation level and continuous traits

methylation_change: hyper- or hypo-methylated in condition of interest. This column applies to case/control studies

Column description (continued)

p-value: p-value of the association

method: microarray or sequencing

platform: microarray platform, for example HumanMethylation450K or sequencing type, like Illumina sequencing

condition: condition or trait of interest

comparison: description of cases and controls or the association with continuous variable

ethnicity: ethnicity of the patient cohort

cohort_size: size of the patient cohort, cases plus controls

PMID: pubmed ID