

Package ‘EWAScanner’

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Title Query and Analyse the 'EWAS Atlas' Database

Version 0.1.0

Description Provides a client for the 'EWAS Atlas' web services ([\(<https://ngdc.cncb.ac.cn/ewas/>](https://ngdc.cncb.ac.cn/ewas/); Li et al. (2019) [<doi:10.1093/nar/gky1027>](https://doi.org/10.1093/nar/gky1027)), allowing users to query epigenome-wide association study (EWAS) data by CpG (cytosine-phosphate-guanine) probe identifier, gene symbol, or genomic region, and to run trait, Gene Ontology, KEGG (Kyoto Encyclopedia of Genes and Genomes) pathway, and genomic location enrichment analyses on a set of CpG probes. Query functions support concurrent, rate-limited requests to the remote service. Results are returned as tidy data frames with dedicated summary and plotting methods, including word clouds of enriched 'EWAS Atlas' trait terms.

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URL <https://github.com/SAADAT-Abu/EWAScanner>

BugReports <https://github.com/SAADAT-Abu/EWAScanner/issues>

Depends R (>= 4.1.0)

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autoplot.ewas_enrichment
<i>Plot an EWAS Atlas enrichment result</i>

Description

Draws a dot plot of enrichment significance, mirroring the EWAS Atlas toolkit’s trait-enrichment chart: one row per term, position given by $-\log_{10}(p)$ and point size by the differentially-methylated CpG count.

Usage

```
## S3 method for class 'ewas_enrichment'
autoplot(object, type = "trait", top_n = 20L, ...)
```

Arguments

object	An ewas_enrichment object.
type	Which analysis result to plot (default "trait").
top_n	Number of top terms to display.
...	Unused.

Value

A ggplot object.

autoplot.ewas_result *Plot summary statistics for an EWAS Atlas query result*

Description

Plot summary statistics for an EWAS Atlas query result

Usage

```
## S3 method for class 'ewas_result'
autoplot(
  object,
  type = c("traits", "chromosome", "direction"),
  top_n = 15L,
  ...
)
```

Arguments

object	An ewas_result object.
type	One of "traits" (top trait frequency), "chromosome" (probes per chromosome), or "direction" (hyper-/hypomethylation balance).
top_n	Number of categories to show for type = "traits" or type = "chromosome".
...	Unused.

Value

A ggplot object.

ewas_enrichment *Run EWAS Atlas enrichment analysis on a set of CpG probes*

Description

Submits a probe set to the EWAS Atlas toolkit and retrieves one or more enrichment analyses run against it: EWAS trait-term enrichment, genomic location enrichment, Gene Ontology enrichment, KEGG pathway enrichment, tissue-specificity enrichment, and gene-expression correlation.

Usage

```
ewas_enrichment(
  probes,
  background = c("450K", "850K"),
  types = "trait",
  poll_interval = 5,
  timeout = 300,
  progress = interactive()
)
```

Arguments

probes	Character vector of CpG probe identifiers (20-5000).
background	One of "450K", "850K", or a character vector of probe identifiers to use as a custom background set.
types	Character vector of analyses to run: any of "trait" (EWAS Atlas trait-term enrichment), "genomic_location" (enrichment across gene/CpG-island-relative locations), "gene_ontology" (GO term enrichment), or "kegg" (KEGG pathway enrichment). Defaults to "trait".
poll_interval	Seconds between job-status polls.
timeout	Maximum seconds to wait for each analysis to finish.
progress	Logical; print progress messages while polling.

Details

The EWAS Atlas toolkit requires between 20 and 5000 probes per submission and computes results asynchronously; this function submits the job and polls for completion.

Value

An [ewas_enrichment](#) object.

Examples

```
probes <- c(
  "cg05575921", "cg00240195", "cg16419584", "cg11903855", "cg21566642",
  "cg23771366", "cg19859270", "cg00382138", "cg25648203", "cg01940273",
  "cg23576855", "cg00401753", "cg00300637", "cg12803068", "cg09935388",
  "cg01899089", "cg04180046", "cg00050873", "cg02228185", "cg18147296"
)
enr <- ewas_enrichment(probes, background = "850K", types = "trait")
top_traits(enr)
```

example_cpgs	<i>Example CpG probe list</i>
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Description

A small example dataset of Illumina CpG probe identifiers, useful for trying out [query_cpg\(\)](#) and [ewas_enrichment\(\)](#) without needing to supply your own probe list.

Usage

```
example_cpgs
```

Format

A data frame with 30 rows and 1 variable:

query_cpg Character. CpG probe identifier.

Source

Illustrative subset of probes with known EWAS Atlas trait associations.

Examples

```
data(example_cpgs)
head(example_cpgs)
```

plot_wordcloud	<i>Word cloud of EWAS Atlas trait terms</i>
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Description

Draws a word cloud sized by association frequency (for [ewas_result](#) objects) or by enrichment significance (for [ewas_enrichment](#) objects).

Usage

```
plot_wordcloud(x, max_words = 75L, colors = NULL, ...)

## S3 method for class 'ewas_result'
plot_wordcloud(x, max_words = 75L, colors = NULL, ...)

## S3 method for class 'ewas_enrichment'
plot_wordcloud(
  x,
  max_words = 75L,
```

```

    colors = NULL,
    type = "trait",
    weight = c("neglog10p", "count"),
    ...
  )

```

Arguments

x	An ewas_result or ewas_enrichment object.
max_words	Maximum number of trait terms to display.
colors	A vector of colors to cycle through.
...	Passed to methods.
type	Which enrichment analysis to plot the word cloud for (default "trait").
weight	Weighting statistic: "neglog10p" (default, significance) or "count" (differentially methylated CpG/gene count for the term).

Value

A ggplot object.

query_cpg	<i>Query the EWAS Atlas by CpG probe identifier</i>
-----------	---

Description

Retrieves trait associations and annotation for one or more Illumina CpG probe identifiers (e.g. "cg05575921") from the EWAS Atlas.

Usage

```
query_cpg(cpgs, workers = 2L, delay = 1, progress = interactive())
```

Arguments

cpgs	Character vector of CpG probe identifiers. Duplicates and missing values are dropped before querying.
workers	Integer; maximum number of concurrent requests. Defaults to 2, a conservative value intended to avoid overloading the remote service.
delay	Numeric; seconds to pause between batches of workers requests.
progress	Logical; print a simple progress message as batches complete.

Value

An [ewas_result](#) object.

Examples

```
res <- query_cpg(c("cg05575921", "cg11903855"), workers = 1, delay = 1)
summary(res)
```

query_gene	<i>Query the EWAS Atlas by gene symbol</i>
------------	--

Description

Retrieves probes and trait associations linked to one or more gene symbols (e.g. "AHRR") from the EWAS Atlas.

Usage

```
query_gene(genes, workers = 2L, delay = 1, progress = interactive())
```

Arguments

genes	Character vector of gene symbols.
workers	Integer; maximum number of concurrent requests. Defaults to 2, a conservative value intended to avoid overloading the remote service.
delay	Numeric; seconds to pause between batches of workers requests.
progress	Logical; print a simple progress message as batches complete.

Value

An [ewas_result](#) object.

Examples

```
res <- query_gene("AHRR", workers = 1, delay = 1)
summary(res)
```

`query_region`*Query the EWAS Atlas by genomic region*

Description

Retrieves probes and trait associations located within one or more genomic intervals (hg19 coordinates) from the EWAS Atlas.

Usage

```
query_region(  
  chr,  
  start = NULL,  
  end = NULL,  
  workers = 2L,  
  delay = 1,  
  progress = interactive()  
)
```

Arguments

<code>chr</code>	Chromosome (e.g. "1", "X"), or a data frame with columns <code>chr</code> , <code>start</code> , <code>end</code> giving one or more regions, in which case <code>start</code> and <code>end</code> are ignored.
<code>start</code>	Start position (hg19, 1-based).
<code>end</code>	End position (hg19, 1-based).
<code>workers</code>	Integer; maximum number of concurrent requests. Defaults to 2, a conservative value intended to avoid overloading the remote service.
<code>delay</code>	Numeric; seconds to pause between batches of workers requests.
<code>progress</code>	Logical; print a simple progress message as batches complete.

Value

An [ewas_result](#) object.

Examples

```
res <- query_region(chr = "5", start = 373000, end = 374000, workers = 1)  
summary(res)
```

summary.ewas_result	<i>Summarise an EWAS Atlas query result</i>
---------------------	---

Description

Summarise an EWAS Atlas query result

Usage

```
## S3 method for class 'ewas_result'
summary(object, top_n = 10L, ...)
```

Arguments

object	An ewas_result object.
top_n	Number of top traits to report.
...	Unused.

Value

Invisibly, a list with summary statistics; also printed.

top_traits.ewas_enrichment	<i>Rank traits by association frequency</i>
----------------------------	---

Description

Rank traits by association frequency

Usage

```
## S3 method for class 'ewas_enrichment'
top_traits(x, n = 10L, ...)

top_traits(x, n = 10L, ...)

## S3 method for class 'ewas_result'
top_traits(x, n = 10L, ...)
```

Arguments

x	An ewas_result or ewas_enrichment object.
n	Number of top traits to return.
...	Passed to methods.

Value

A data frame with columns `trait` and `n` (or `p/OR` for enrichment results), ordered from most to least significant/frequent.

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