

Package: oglnac (via r-universe)

October 6, 2026

Title Processing and Analysis of 'O-GlcNAcAtlas' Data

Version 0.1.6

Author Yaoxiang Li [aut, cre]

Maintainer Yaoxiang Li <liyaoxiang@outlook.com>

Description Provides tools for processing and analyzing data from the 'O-GlcNAcAtlas' database <<https://oglnac.org/>>, as described in Ma (2021) <[doi:10.1093/glycob/cwab003](https://doi.org/10.1093/glycob/cwab003)>. It integrates 'UniProt' <<https://www.uniprot.org/>> API calls to retrieve additional information. It is specifically designed for research workflows involving 'O-GlcNAcAtlas' data, providing a flexible and user-friendly interface for customizing and downloading processed results. Interactive elements allow users to easily adjust parameters and handle various biological datasets.

License GPL-3

URL <https://yaoxiangli.github.io/oglnac/>,
<https://github.com/YaoxiangLi/oglnac>

BugReports <https://github.com/YaoxiangLi/oglnac/issues>

Encoding UTF-8

RoxygenNote 7.3.2

Imports cli, jsonlite, glue

Suggests shiny, DT, bslib, readxl, pkgdown, testthat (>= 3.0.0),
tibble, curl

Config/testthat/edition 3

Repository <https://yaoxiangli.r-universe.dev>

Date/Publication 2026-05-27 03:34:34 UTC

RemoteUrl <https://github.com/yaoxiangli/oglnac>

RemoteRef HEAD

RemoteSha 2082a9b1d70cf279699e3ecfbb7ec639a030cfb0

Contents

compare_atlas_tables	2
compare_tibbles_uniprot	3
export_atlas_csv	4
launch_app	4
parse_uniprot_data	5
prepare_atlas_data	5
process_tibble_uniprot	6
process_tibble_uniprot_cached	7
retrieve_uniprot_data	8
validate_atlas_data	9
Index	10

compare_atlas_tables	<i>Compare Two Atlas Tables</i>
----------------------	---------------------------------

Description

Summarizes added, removed, and shared Atlas row IDs.

Usage

```
compare_atlas_tables(old_data, new_data, id_col = "id")
```

Arguments

- old_data Previous Atlas data frame.
- new_data Updated Atlas data frame.
- id_col Row identifier column. Defaults to "id".

Value

A one-row data frame with row and ID counts.

`compare_tibbles_uniprot`*Compare Input and Updated Tibbles*

Description

This function compares the original input tibble and the updated tibble, identifying and reporting any changes in the specified columns ('entry_name', 'protein_name', 'gene_name').

Usage

```
compare_tibbles_uniprot(  
  original_tibble,  
  updated_tibble,  
  entry_name_col = "entry_name",  
  protein_name_col = "protein_name",  
  gene_name_col = "gene_name"  
)
```

Arguments

`original_tibble` The original tibble before processing.

`updated_tibble` The tibble returned after processing.

`entry_name_col` The column name for entry names (default: "entry_name").

`protein_name_col` The column name for protein names (default: "protein_name").

`gene_name_col` The column name for gene names (default: "gene_name").

Value

None. Prints the differences between the tibbles.

Examples

```
# Example usage:  
  
# Original input tibble  
input_data <- tibble::tibble(  
  id = c(1, 2),  
  species = c("mouse", "rat"),  
  sample_type = c("brain", "liver"),  
  accession = c("O88737", "Q9R064"),  
  accession_source = c("UniProt", "UniProt")  
)  
  
# Process the tibble (this will add the entry_name, protein_name, and gene_name)
```

```
processed_data <- process_tibble_uniprot(input_data)

# Compare the original and processed tibbles
compare_tibbles_uniprot(input_data, processed_data)
```

export_atlas_csv	<i>Export O-GlcNAcAtlas Data as CSV</i>
------------------	---

Description

Writes a validated Atlas table to CSV with blank cells for missing values.

Usage

```
export_atlas_csv(data, file, dataset = NULL)
```

Arguments

data	A data frame containing Atlas records.
file	Output CSV path.
dataset	Optional dataset label: "unambiguous" or "ambiguous".

Value

The output file path, invisibly.

launch_app	<i>Launch oglnac Shiny App</i>
------------	--------------------------------

Description

This function launches a Shiny App for uploading, processing, and downloading UniProt data in CSV, TSV, or Excel format. Users can upload data, preview it, and select specific columns for processing. The processed data can be viewed and downloaded.

Usage

```
launch_app()
```

Value

None

Examples

```
if (interactive()) {
  oglnac::launch_app()
}
```

parse_uniprot_data	<i>Parse UniProt Data</i>
--------------------	---------------------------

Description

This function parses the data retrieved from the UniProt API to extract the entry name, protein name, and gene name.

Usage

```
parse_uniprot_data(uniprot_data)
```

Arguments

uniprot_data A list returned by the UniProt API query.

Value

A list containing 'entry_name', 'protein_name', and 'gene_name'.

Examples

```
# Example usage:

# Retrieve UniProt data
test_result <- retrieve_uniprot_data("088737")

# Parse the UniProt data
parsed_result <- parse_uniprot_data(test_result)

# Print the parsed result
print(parsed_result)
```

prepare_atlas_data	<i>Prepare O-GlcNAcAtlas Data for Export</i>
--------------------	--

Description

Adds or normalizes the ambiguous field used by the public static website.

Usage

```
prepare_atlas_data(data, dataset = NULL)
```

Arguments

`data` A data frame containing Atlas records.

`dataset` Optional dataset label: "unambiguous" or "ambiguous".

Value

A data frame ready to export.

```
process_tibble_uniprot
```

Process a Tibble of UniProt Data

Description

This function processes a tibble containing `accession` and `accession_source` columns. It retrieves data from the UniProt API for rows with `accession_source == "UniProt"` and overwrites or creates the `entry_name`, `protein_name`, and `gene_name` columns only if the parsed values are not NULL or NA.

Usage

```
process_tibble_uniprot(
  data,
  accession_col = "accession",
  accession_source_col = "accession_source",
  entry_name_col = "entry_name",
  protein_name_col = "protein_name",
  gene_name_col = "gene_name"
)
```

Arguments

`data` A tibble containing at least `accession` and `accession_source` columns.

`accession_col` The column name for accession numbers (default: "accession").

`accession_source_col` The column name for accession sources (default: "accession_source").

`entry_name_col` The column name for entry names (default: "entry_name").

`protein_name_col` The column name for protein names (default: "protein_name").

`gene_name_col` The column name for gene names (default: "gene_name").

Value

A tibble with UniProt data processed.

Examples

```
# Example usage:

# Load necessary library
library(tibble)

# Reduced example data as an R tibble
test_data <- tibble::tibble(
  id = c(1, 78, 83, 87),
  species = c("mouse", "mouse", "rat", "mouse"),
  sample_type = c("brain", "brain", "brain", "brain"),
  accession = c("O88737", "O35927", "Q9R064", "P51611"),
  accession_source = c("OtherDB", "UniProt", "UniProt", "UniProt"),
  entry_name = c("BSN_MOUSE", NA, "GORS2_RAT", NA),
  protein_name = c("Protein bassoon", NA, "Golgi reassembly-stacking protein2", NA),
  gene_name = c("Bsn", NA, "Gorasp2", NA)
)

# Process the tibble
result_data <- process_tibble_uniprot(test_data)

# Compare the original and processed tibbles
compare_tibbles_uniprot(test_data, result_data)
```

```
process_tibble_uniprot_cached
```

Process UniProt Data with a Local Cache

Description

Enriches a data frame like `process_tibble_uniprot()` while avoiding repeated UniProt requests for accessions already present in a local RDS cache.

Usage

```
process_tibble_uniprot_cached(
  data,
  cache_path = NULL,
  accession_col = "accession",
  accession_source_col = "accession_source",
  entry_name_col = "entry_name",
  protein_name_col = "protein_name",
  gene_name_col = "gene_name"
)
```

Arguments

data A data frame containing accession and accession source columns.
cache_path Optional RDS file path for cached parsed UniProt records.
accession_col The accession column name.
accession_source_col The accession source column name.
entry_name_col The entry name column name.
protein_name_col The protein name column name.
gene_name_col The gene name column name.

Value

A data frame with UniProt fields filled where available.

retrieve_uniprot_data *Retrieve Data from UniProt API*

Description

This function sends a GET request to the UniProt REST API and retrieves data based on the provided UniProt accession number.

Usage

```
retrieve_uniprot_data(accession)
```

Arguments

accession A character string representing the UniProt accession number.

Value

A list containing the retrieved data in JSON format, or NULL if the request fails.

Examples

```

# Example usage

result <- retrieve_uniprot_data("088737")
print(result)

```

validate_atlas_data	<i>Validate O-GlcNAcAtlas Data</i>
---------------------	------------------------------------

Description

Checks that an Atlas table has the columns needed by the public website and that dataset labels are not mixed accidentally.

Usage

```
validate_atlas_data(data, dataset = NULL)
```

Arguments

- data A data frame containing Atlas records.
- dataset Optional dataset label: "unambiguous" for dataset-I or "ambiguous" for dataset-II.

Value

A list with valid, errors, warnings, and summary.

Index

`compare_atlas_tables`, [2](#)
`compare_tibbles_uniprot`, [3](#)

`export_atlas_csv`, [4](#)

`launch_app`, [4](#)

`parse_uniprot_data`, [5](#)
`prepare_atlas_data`, [5](#)
`process_tibble_uniprot`, [6](#)
`process_tibble_uniprot_cached`, [7](#)

`retrieve_uniprot_data`, [8](#)

`validate_atlas_data`, [9](#)