Package: ghettoblaster (via r-universe)

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Title NCBI BLAST web client

Version 0.0.1

Description NCBI BLAST web client.

License `use_mit_license()`

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Imports httr2, dplyr, stringr, glue, brio, xml2, purrr, worrms, future, furrr, tidyr

Repository https://pieterprovoost.r-universe.dev

RemoteUrl https://github.com/pieterprovoost/ghettoblaster

RemoteRef HEAD

RemoteSha 3b6735e40885512e5e1d43c85e80eee3f3270c48

Contents

`blast`   *Run a BLAST search*

Description

Run a BLAST search

Usage

```
blast(sequence, max_num_seq = 100, verbose = FALSE, add_worms = FALSE)
```

Arguments

sequence	A DNA sequence
max_num_seq	The maximum number of sequences to return
verbose	Whether to print status messages
add_worms	Whether to add WoRMS taxonomy information

Value

A data frame with the BLAST results

`get_results`   *Get the results of a BLAST request*

Description

Get the results of a BLAST request

Usage

```
get_results(rid)
```

Arguments

rid	A request ID

Value

A data frame with the results

| get_taxonomy | *Get WoRMS taxonomy for a list of species names* |

Description

Get WoRMS taxonomy for a list of species names

Usage

```
get_taxonomy(species_names)
```

Arguments

species_names   A character vector of species names

Value

A data frame with the taxonomy, input names in column input

| ghettoblaster | *NCBI BLAST web client* |

Description

This package provides a simple interface to the NCBI BLAST web service.

| submit_sequence | *Submit a sequence to NCBI BLAST* |

Description

Submit a sequence to NCBI BLAST

Usage

```
submit_sequence(sequence, program = "blastn", max_num_seq = 100)
```

Arguments

sequence	A DNA sequence
program	The BLAST program to use
max_num_seq	The maximum number of sequences to return

Value

A request ID

wait_until_ready	*Wait until a BLAST request is ready*

Description

Wait until a BLAST request is ready

Usage

```
wait_until_ready(rid, verbose = FALSE)
```

Arguments

rid	A request ID
verbose	Whether to print status messages

Value

TRUE if the request is ready, FALSE in case of an unexpected status

worms_for_names	*Get WoRMS taxonomy for a list of species names*

Description

Get WoRMS taxonomy for a list of species names

Usage

```
worms_for_names(...)
```

Arguments

species_names	A character vector of species names

Value

A data frame with the taxonomy, input names in column input

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