

# Package ‘uwinutils’

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**Type** Package

**Title** A suite of useful functions to query / report from the UWIN database

**Version** 0.1.0

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**Description** This is really only helpful to the handful of folks who have access to the backend of the UWIN database. However, it will hopefully make automated reporting much easier.

**License** GPL-2

**Encoding** UTF-8

**LazyData** true

**Depends** R (>= 3.5.3),  
magrittr,  
RMariaDB,  
doSNOW,  
progress,  
foreach

**Imports** dplyr,  
rstudioapi

**RoxygenNote** 6.1.1

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connect2db	<i>Connect to UWIN database</i>
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### Description

connect2db connects to the UWIN camera trapping database. It takes no arguments but will request for the password to the UWIN database when a connection is attempted.

### Usage

```
connect2db()
```

### Value

If the password is correctly input connect2db will return a MariaDBConnection called uwidb. to the global environment.

### Examples

```
## Not run:
connect2db()

## End(Not run)
```

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gsutil_copy	<i>Copy images from google cloud</i>
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### Description

gsutil\_copy takes in the object from images\_of and copies them to a specified folder.

### Usage

```
gsutil_copy(images_to_copy = NULL, output_folder = NULL, ncore = 2)
```

### Arguments

images_to_copy	The output data.frame from images_of.
ncore	a numeric scalar. The number of cores to use to copy images from google cloud. It defaults to 2.
output_to_folder	A character vector that denotes the full path of a folder to copy the images to. If the folder does not exist it will be created. A final slash cannot be placed at the end of the character. For example, "C:/users/data" works but "C:/users/data/" does not.

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hello	<i>Hello, World!</i>
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**Description**

Prints 'Hello, world!'.

**Usage**

```
hello()
```

**Examples**

```
hello()
```

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images_of	<i>Images of a species at a given study area</i>
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**Description**

images\_of queries the UWIN database for a selected species and study area.

**Usage**

```
images_of(species = NULL, studyArea = NULL, db = uwidb)
```

**Arguments**

species	A character vector of the species to be queried. If left as NULL then you can select the species you want in a pop up list. Multiple species can be selected by holding CTRL when clicking on them.
studyArea	The four letter capitalized study area abbreviation for a city. If left as NULL you can select the study area from a pop up list. Only one study area may be selected at a time.
db	The MariaDB connection to the UWIN database. Defaults to 'uwidb'

**Value**

a data.frame with the following columns: - filepath: the location of the image on google cloud - locationName: the site name the image was taken - photoName: the name of the image - common-Name: the species tagged in the images - numIndividuals: The number of individuals of the tagged species

**Examples**

```
## Not run:
my_images <- images_of()

## End(Not run)
```

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MODIFY	<i>Modify the records in the UWIN database.</i>
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### Description

MODIFY can be used, for example, to update or delete records in the UWIN database.

### Usage

```
MODIFY(sql = NULL, report = FALSE, db = uwidb)
```

### Arguments

sql	A SQL statement input as a character vector to be sent to the UWIN database.
report	Logical. Whether or not to report the number of rows affected. Defaults to FALSE.
db	The MariaDB connection to the UWIN database. Defaults to 'uwidb'

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SELECT	<i>Apply a select query to the UWIN database.</i>
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### Description

SELECT will send select SQL queries to the UWIN database and return the output.

### Usage

```
SELECT(sql = NULL, db = uwidb)
```

### Arguments

sql	A SQL statement input as a character vector to be sent to the UWIN database.
db	The MariaDB connection to the UWIN database. Defaults to 'uwidb'

### Value

A data.frame with the output from the SQL statement.

### Examples

```
## Not run:
my_sql <- 'SELECT * FROM Visits;'
SELECT(my_sql)

## End(Not run)
```

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