

# Package: naturdata (via r-universe)

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## Contents

get_condition . . . . .	3
ndb_aggregate_pinpoint . . . . .	3
ndb_append_coords . . . . .	4
ndb_calc_avg . . . . .	4
ndb_calc_cover_ratio . . . . .	5
ndb_calc_jord_cn . . . . .	6
ndb_calc_n_arter . . . . .	6

ndb_calc_n_store_stammer . . . . .	7
ndb_calc_weighted_assessment . . . . .	7
ndb_clean_artsliste . . . . .	8
ndb_clean_kemi . . . . .	9
ndb_clean_lysaaben_struktur . . . . .	9
ndb_clean_plantekemi . . . . .	10
ndb_clean_skov_doedtved . . . . .	11
ndb_clean_skov_struktur . . . . .	11
ndb_clean_stamdata . . . . .	12
ndb_connect . . . . .	12
ndb_create_tbl . . . . .	13
ndb_disconnect . . . . .	13
ndb_filter_artsliste . . . . .	14
ndb_filter_lysaaben_prog . . . . .	14
ndb_filter_skov_prog . . . . .	15
ndb_get . . . . .	15
ndb_get_artsgruppe . . . . .	16
ndb_get_artsliste_pf . . . . .	16
ndb_get_artsnavne . . . . .	17
ndb_get_artsscorer . . . . .	17
ndb_get_arttraits . . . . .	18
ndb_get_doedtved . . . . .	19
ndb_get_ellenberg . . . . .	19
ndb_get_laver . . . . .	20
ndb_get_lysaaben_struktur . . . . .	20
ndb_get_mosser . . . . .	21
ndb_get_novana_aktids . . . . .	21
ndb_get_plantekemi . . . . .	22
ndb_get_schema . . . . .	22
ndb_get_skov_struktur . . . . .	23
ndb_get_skov_trae_diam_naturtype . . . . .	23
ndb_get_skov_traeregistrering . . . . .	24
ndb_get_stamdata . . . . .	24
ndb_get_tbl . . . . .	25
ndb_label . . . . .	25
ndb_labels . . . . .	26
ndb_names . . . . .	26
ndb_rename . . . . .	27
ndb_to_percent . . . . .	27
ndb_update_import_job . . . . .	28
ndb_write_artsliste . . . . .	28
ndb_write_to_db . . . . .	29
nogo_naturtyper . . . . .	29
replace_na_if . . . . .	30

---

get_condition	<i>Generate a condition string</i>
---------------	------------------------------------

---

**Description**

Generate a condition string based on the input arguments. This function is only to be used in `replace_na_if()`.

**Usage**

```
get_condition(column, progIds, naturtypeIds = NULL, year = NULL, year_cond)
```

**Arguments**

column	name	The name of the column to replace values in
progIds	int	The progIds to modify values within
naturtypeIds	int	The naturtypeIds to modify values within
year	int	The year to use in the condition. See year_cond
year_cond	chr	The condition to apply on year

---

ndb_aggregate_pinpoint	<i>Calculate number of pins hit by an aggregated species group</i>
------------------------	--

---

**Description**

Calculate number of pins hit by an aggregated species group as the unique number of pins hit by the group.

**Usage**

```
ndb_aggregate_pinpoint(pp)
```

**Arguments**

pp	chr	The pinpoint hits as character string of the format "[1,2,4,16]"
----	-----	--

**Value**

int	The number of pins
-----	--------------------

**Examples**

```
tibble::tibble(
  aktId = 1,
  artId = 1:2,
  pinpoint = c("[3,7,9,11,13,14,16]", "[1,2,3]")
) |>
  dplyr::summarize(hyppighed = ndb_aggregate_pinpoint(pinpoint),
                  .by = aktId)
```

---

ndb_append_coords	<i>Extract x and y from WKT</i>
-------------------	---------------------------------

---

**Description**

Coordinates are stored as WKT on the database in the column geomText This function will extract the x and y from geomText and add them as columns to data.

**Usage**

```
ndb_append_coords(data)
```

**Arguments**

data	data.frame containing a WKT string in geomText
------	--

**Details**

Coordinates in geomText are in UTM32 (EPSG 25832)

**Value**

data with augmented with utm\_x and utm\_y

---

ndb_calc_avg	<i>Calculate the average across multiple columns</i>
--------------	--

---

**Description**

Calculate the average of e.g. vegetationheight which is recorded by four measurements each in it own column. The average is only calculated where there are at least min\_n\_values non-na values.

**Usage**

```
ndb_calc_avg(tbl, prefix, min_n_values = 3)
```

**Arguments**

tbl	The table with the columns to average over.
prefix	chr The string with which the columns are selected (using <code>dplyr::starts_with()</code> ).
min_n_values	int Number of required non-na values (Default 3).

**Value**

tibble Table with aktId and the calculated average as prefix\_avg

---

ndb\_calc\_cover\_ratio *Calculate the cover ratio*

---

**Description**

Calculate the cover ratio as the ratio between species A to the sum of species A and species B The cover ratio is defined as

$$\frac{\text{species A}}{\text{sum}(\text{species A, species B})}$$

**Usage**

```
ndb_calc_cover_ratio(species_A, species_B)
```

**Arguments**

species_A	int The number of pins hitting species A.
species_B	int The number of pins hitting species B.

**Value**

The ratio of species A to the sum of species A and species B.

**Examples**

```
ndb_calc_cover_ratio(10L, 5L)
```

---

ndb\_calc\_jord\_cn      *Calculate jord\_CN*

---

### Description

The function will calculate the ratio between jord\_C and jord\_N while performing checks for whether both are within the detection limit. Lastly the function will ensure that the calculated ratio is within 10 and 60.

### Usage

```
ndb_calc_jord_cn(tbl)
```

### Arguments

tbl                    A table containing the columns jord\_C, jord\_N, jord\_C\_under\_detektionsgraensen and jord\_N\_under\_detektionsgraensen.

### Value

tbl augmented with the jord\_CN column

---

ndb\_calc\_n\_arter      *Calculate the number of unique species observations*

---

### Description

Art, Hybrid, Sektion, Superart are counted as unique observations. Form and Variant are counted as their parent species.

### Usage

```
ndb_calc_n_arter(artsliste, artsnavne)
```

### Arguments

artsliste            data.frame with artId, aktId and taxonomi  
artsnavne            data.frame returned by [ndb\\_get\\_artsnavne\(\)](#)

### Value

tibble with artId & n\_arter

### See Also

[ndb\\_get\\_artsnavne\(\)](#)

---

 ndb\_calc\_n\_store\_stammer

*Calculate the number of large trunks*


---

### Description

Function to calculate the number of large trunks. What constitutes a large trunk is dependent on the naturetype. Since the naturetype can vary over time and is sometimes interpreted from previous registrations n\_store\_stammer needs to be re-calculated (in some situations).

### Usage

```
ndb_calc_n_store_stammer(nt, traeregistrering, traediameter)
```

### Arguments

nt	A table with (at least) aktId & naturtypeId
traeregistrering	The table data.skov_traeregistrering from naturdata_kalo. This is a list of the species measured in the plot.
traediameter	The list lists.trae_diameter_naturtype. This is a table with the criteria for when a certain tree species is considered large (growth is naturetype dependent).

### Details

The circle diameter has varied over time between 10 and 15m. To accomodate for that observations from the 10m circle are scaled up by the ratio of the areas of two circles with radii 15 and 10 is given by:  $\frac{\pi \cdot 15^2}{\pi \cdot 10^2} = \frac{225}{100} = \frac{9}{4} \approx 2.25$

### Value

Table with aktId and n\_store\_stammer\_15m

---

 ndb\_calc\_weighted\_assessment

*Calculate an area weighted assessment*


---

### Description

Calculate a weighted assessment where the area within and outside the NATURA 2000 sites is used as weights.

### Usage

```
ndb_calc_weighted_assessment(Ai, Au, ni, nu, vi, vu)
```

**Arguments**

A <sub>i</sub>	Area inside NATURA 2000 sites
A <sub>u</sub>	Area outside the NATURA 2000 sites
n <sub>i</sub>	Number of plots inside NATURA 2000
n <sub>u</sub>	Number of plots outside NATURA 2000
v <sub>i</sub>	Proportion of plots that meet the criteria inside the NATURA 2000 sites
v <sub>u</sub>	Proportion of plots that meet the criteria outside the NATURA 2000 sites

**Details**

The weighted assessment is defined as:  $v = \frac{A_i \sqrt{n_i} v_i + A_u \sqrt{n_u} v_u}{A_i \sqrt{n_i} + A_u \sqrt{n_u}}$

**Value**

The weighted assesment

---

ndb\_clean\_artsliste    *Function to clean the artsliste table*

---

**Description**

Cases with hyppighed > 16 are set to NA. Cases where hyppighed == 0 & isPinpoint == 1 are changed to isPinpoint == 0 and isProevfelt == 1

**Usage**

```
ndb_clean_artsliste(tbl)
```

**Arguments**

tbl	tibble The raw.artsliste table
-----	--------------------------------

**Value**

tbl cleaned

---

ndb_clean_kemi	<i>Function to clean the raw.kemi table</i>
----------------	---

---

**Description**

The function will insert a value of half the detection limit for values less than the detection limit (0.05 for jord\_C and 0.01 for jord\_N). For pH values outside 2.5 - 8.5 will be replaced with NA. In case vand\_ph is missing vand\_ph2 is used instead. The vand\_ph2 is not included in the returned table.

**Usage**

```
ndb_clean_kemi(tbl)
```

**Arguments**

tbl	tibble The raw.kemi table
-----	---------------------------

**Details**

The ratio between jord\_C and jord\_N is also calculated and added to the returned table.

**Value**

tbl cleaned

---

ndb_clean_lysaaben_struktur	<i>Function to clean the raw.lysaaben_struktur table</i>
-----------------------------	--

---

**Description**

This function will perform several clean-up steps.

- Replace vegetationshojde > 300 with NA
- Replace areas over 78.5 and <= 80 with 78.5
- Replace areas over 80 with NA
- Replace negative values with NA

**Usage**

```
ndb_clean_lysaaben_struktur(tbl)
```

**Arguments**

tbl	tibble The raw.lysaaben_struktur table
-----	--

## Details

In addition NA's are replaced with 0 under these conditions #TODO

hoeljer\_5m\_observeret is not written to data as this is the raw interval strings which are not used currently.

## Value

tbl cleaned

---

ndb\_clean\_plantekemi *Function to clean the plantekemi table*

---

## Description

The function will ensure that all species have artId and that all naturtypeId's are valid (i.e. not marine or aquatic). The function will also insert a value of half the detection limit for values less than the detection limit (0.03 for plante\_N and 0.01 for plante\_P) and add julian date as a column. Cases where samples have been taken from species that was not part of the protocol are removed (Dunet dueurt, Søbomme, Ager-padderok, Uomsat dødt organisk materiale). Lastly a few cases where multiple artId for the same artsNavn are set to the correct artID.

## Usage

```
ndb_clean_plantekemi(tbl, nogo_naturtyper)
```

## Arguments

tbl                    tibble The raw.plantekemi table  
nogo\_naturtyper       integer Vector of illegal naturtypeId's.

## Details

The julianDate column is calculated using `lubridate::yday()`.

---

`ndb_clean_skov_doedtved`*Function to clean the skov\_doedtved table*

---

**Description**

To have valid column names when pivoting to wider formats values with å in retning are replaced with aa. Cases where nedbrydning != 1:5 are set to NA. The comment column is dropped.

**Usage**`ndb_clean_skov_doedtved(tbl)`**Arguments**

<code>tbl</code>	tibble The raw.skov_doedtved table
------------------	------------------------------------

**Value**`tbl cleaned`

---

`ndb_clean_skov_struktur`*Function to clean the skov\_struktur table*

---

**Description**

Columns with coverage in the 5 m circle have areas adjusted to 78.5 m<sup>2</sup> when values are between 78.5 - 80, coverage over 80 are set to NA. In all cases negative values are replaced with NA. For progId 133, 134 with naturtypeId 9999 NA are replaced with 0. Count and area columns are converted to integer. For for all coverage variables NAs are replaced with 0. For n\_hulheder\_15m and n\_raad\_15m NAs are only replaced from 2011 and onwards.

**Usage**`ndb_clean_skov_struktur(tbl)`**Arguments**

<code>tbl</code>	tibble The raw.skov_struktur table
------------------	------------------------------------

**Details**

The sum of hulheder\_15m and raad\_15m is also calculated by this function as n\_hulheder\_raad\_samlet\_15m

---

ndb_clean_stamdata	<i>Function to clean the raw.stamdata table</i>
--------------------	---

---

**Description**

Currently just sets naturtypeId to NA when status is not "Godkendt data" (statusId = 100).

**Usage**

```
ndb_clean_stamdata(tbl)
```

**Arguments**

tbl	tibble The raw.stamdata table
-----	-------------------------------

**Value**

tbl cleaned

---

ndb_connect	<i>Connect to naturdata_kalo</i>
-------------	----------------------------------

---

**Description**

The function assumes that server, database, uid & pwd are stored in the .Renvron file using the variable names NATURDATA\_KALO\_SERVER, NATURDATA\_KALO\_DB, NATURDATA\_KALO\_UID & NATURDATA\_KALO\_PWD

**Usage**

```
ndb_connect()
```

**Details**

Note that the ODBC Driver 17 for SQL Server is required.

**Value**

OdbcConnection

---

ndb_create_tbl	<i>Create and write table</i>
----------------	-------------------------------

---

**Description**

This wraps `DBI::dbWriteTable()` to create a new table

**Usage**

```
ndb_create_tbl(con, obj, schema = "data", table)
```

**Arguments**

con	An OdbcConnection
obj	Table to write
schema	chr Name of the schema
table	chr Name of the table to create

**Details**

create\_tbl will overwrite any existing table.

**Value**

TRUE, invisibly

---

ndb_disconnect	<i>Disconnect from database</i>
----------------	---------------------------------

---

**Description**

Simple wrapper around `DBI::dbDisconnect()`

**Usage**

```
ndb_disconnect(con)
```

**Arguments**

con	OdbcConnection
-----	----------------

ndb\_filter\_artsliste *Filter the artsliste table*

---

**Description**

Filter artslisten to only have observations where isPinpoint, isProvefelt or is5m has the value of 1.

**Usage**

```
ndb_filter_artsliste(artsliste)
```

**Arguments**

artsliste      The artsliste table

**See Also**

[ndb\\_get\\_artsliste\\_pf\(\)](#)

---

ndb\_filter\_lysaaben\_prog

*Filter to only program IDs for lysåben*

---

**Description**

Filter on progId to only 117,119,131:132,142,144

**Usage**

```
ndb_filter_lysaaben_prog(tbl)
```

**Arguments**

tbl            A table that contains the column progId

**Value**

tbl filtered

---

ndb\_filter\_skov\_prog     *Filter to only skov programs*

---

**Description**

Filter on progId to only 133, 134 or 140

**Usage**

ndb\_filter\_skov\_prog(tbl)

**Arguments**

tbl                    A table that contains the column progId

**Value**

tbl filtered

---

ndb\_get                    *Get a specified table from the database*

---

**Description**

Get a specified table from the database

**Usage**

ndb\_get(con, schema, tbl)

**Arguments**

con                    Connection to the database  
schema                chr Name of the schema where tbl lives  
tbl                    chr Name of table

---

ndb\_get\_artsgruppe     *Get the artsgruppe\_planter table*

---

**Description**

Get the artsgruppe\_planter table

**Usage**

```
ndb_get_artsgruppe(con)
```

**Arguments**

con                    Connection to the database

**Value**

A lazy table

**Source**

lists.artsgruppe\_planter

---

ndb\_get\_artsliste\_pf     *Get the artsliste table*

---

**Description**

Get the artsliste table and filter it to only have observations where isPinpoint, isProvefelt or is5m has the value of 1.

**Usage**

```
ndb_get_artsliste_pf(con)
```

**Arguments**

con                    Connection to the database

**Source**

data.artsliste

**See Also**

[ndb\\_filter\\_artsliste\(\)](#)

---

ndb\_get\_artsnavne      *Get the list of species names*

---

### Description

Get the list of species names and filter to only include either plants (when `taxon = 'plants'`) or only bryophytes when `taxon = 'bryophytes'`. 'Plants' is defined as species from the phyla *Tracheophyta*, *Magnoliophyta*, *Pinophyta* and *Pteridophyta*. 'Bryophytes' is defined as the classes *Bryopsida* and *Polytrichopsida*.

### Usage

```
ndb_get_artsnavne(con, taxon)
```

### Arguments

con	Connection to the database
taxon	chr Either "bryophytes" or "plants".

### Details

In addition to filtering, the function will also ensure that Form and Variant are treated as their parent species by `ndb_calc_n_arter()` whereas Art, Underart, Hybrid, Sektion and Superart are treated as unique observations.

Source: `lists.artsNavne`

### Value

A tibble with species names.

### See Also

[ndb\\_calc\\_n\\_arter\(\)](#)

---

ndb\_get\_artsscorer      *Get the list of artsscorer per species*

---

### Description

Get the list of artsscorer per species

### Usage

```
ndb_get_artsscorer(con)
```

**Arguments**

con                    Connection to the database

**Value**

A lazy table

**Source**

lists.artsScore

---

ndb\_get\_arttraits        *Get the list of traits*

---

**Description**

Get the list of traits

**Usage**

```
ndb_get_arttraits(con)
```

**Arguments**

con                    Connection to the database

**Value**

A lazy table

**Source**

lists.arttraits

---

ndb_get_doedtved	<i>Get the skov doedtved table</i>
------------------	------------------------------------

---

**Description**

Get the skov doedtved table

**Usage**

```
ndb_get_doedtved(con)
```

**Arguments**

con	Connection to the database
-----	----------------------------

**Value**

A lazy table

**Source**

```
data.skov_doedtved
```

---

ndb_get_ellenberg	<i>Get the Ellenberg values</i>
-------------------	---------------------------------

---

**Description**

Get the list of Ellenberg values (the English version) plus T\_EllTysk. It is somewhat misleading that T\_EllTysk is in lists.ellenberg\_engelsk, but it is not a mistake.

**Usage**

```
ndb_get_ellenberg(con)
```

**Arguments**

con	Connection to the database
-----	----------------------------

**Value**

A lazy table

**Source**

```
lists.ellenberg_engelsk
```

---

ndb_get_laver	<i>Get the list of lichen species names</i>
---------------	---

---

**Description**

Get the list of lichen species names (i.e. species in class *Lecanoromycetes*). The returned species list will have a column `isLav` with all 1L's.

**Usage**

```
ndb_get_laver(con)
```

**Arguments**

con	Connection to the database
-----	----------------------------

**Value**

A tibble with lichen species names.

**Source**

lists.artsNavne

---

ndb_get_lysaaben_struktur	<i>Get the lysaaben struktur table</i>
---------------------------	--

---

**Description**

Get the lysaaben struktur table

**Usage**

```
ndb_get_lysaaben_struktur(con)
```

**Arguments**

con	Connection to the database
-----	----------------------------

**Value**

A lazy table

**Source**

data.lysaaben\_struktur

---

ndb_get_mosser	<i>Get the artsnavne table only of bryophytes</i>
----------------	---

---

**Description**

Get the list of bryophyte species names (i.e. species in phylum *Bryophyta*).

**Usage**

```
ndb_get_mosser(con)
```

**Arguments**

con	Connection to the database
-----	----------------------------

**Value**

A tibble with bryophyte species names.

**Source**

lists.artsNavne

---

ndb_get_novana_aktids	<i>Get the list of aktId's from NOVANA</i>
-----------------------	--

---

**Description**

Get a list of aktId's where formaal == "NOVANA" and ansvarligMyndighed == "Milj\u00f8styrelsen"

**Usage**

```
ndb_get_novana_aktids(con)
```

**Arguments**

con	Connection to the database
-----	----------------------------

**Value**

A lazy table with progId, aktId & dato

**Source**

data.stamdata

---

ndb\_get\_plantekemi      *Get the plantekemi table*

---

**Description**

Return the plantekemi table

**Usage**

```
ndb_get_plantekemi(con)
```

**Arguments**

con                      Connection to the database

**Value**

A lazy table

**Source**

data.plantekemi

---

ndb\_get\_schema              *Get the database schema*

---

**Description**

Query the database for schemas, tables and their columns. Useful when only given a column name and need to find out where it lives on the database.

**Usage**

```
ndb_get_schema(con)
```

**Arguments**

con                      OdbcConnection

**Details**

The reporting scheme is rarely relevant and is not returned. The same goes for two tables trend\_p4 and tilstand\_p4#'

**Value**

A dataframe with

**schema** chr, Schema name

**table** chr, Table name

**column** chr, Column name

---

ndb\_get\_skov\_struktur *Get the skov struktur table*

---

**Description**

Get the skov struktur table

**Usage**

```
ndb_get_skov_struktur(con)
```

**Arguments**

con                      Connection to the database

**Value**

A lazy table

**Source**

data.skov\_struktur

---

ndb\_get\_skov\_trae\_diam\_naturtype  
*Get the trae diameter per naturtype table*

---

**Description**

This table holds information about the diameter a trunk should have for it to be considered "big".

**Usage**

```
ndb_get_skov_trae_diam_naturtype(con)
```

**Arguments**

con                      Connection to the database

**Value**

A lazy table

**Source**

list.trae\_diameter\_naturtype

---

ndb\_get\_skov\_traeregistrering

*Get the skov traeregistrering table*

---

**Description**

Get the skov traeregistrering table

**Usage**

ndb\_get\_skov\_traeregistrering(con)

**Arguments**

con                      Connection to the database

**Value**

A lazy table

**Source**

data.skov\_traeregistrering

---

ndb\_get\_stamdata

*Get the stamdata table*

---

**Description**

Get the stamdata table

**Usage**

ndb\_get\_stamdata(con)

**Arguments**

con                      Connection to the database

---

ndb_get_tbl	<i>Get table from the database and filter</i>
-------------	---

---

**Description**

Get table from the database and filter to only rows with `formaal == "NOVANA"` and `ansvarligMyn-dighed == "Miljøstyrelsen"`. Joins (both the `semi_join` on `novana` and the `left_join` on `kv`) are done on columns `progId` and `aktId`.

**Usage**

```
ndb_get_tbl(con, tbl, novana, kv = NULL)
```

**Arguments**

<code>con</code>	Connection to the database
<code>tbl</code>	chr Name of table
<code>novana</code>	lazy table Table with the <code>progId</code> & <code>aktId</code> that are from the NOVANA monitoring program.
<code>kv</code>	lazy table An optional table with status ("Godkendt data", "Indtastning påbegyndt") for the data.

**Details**

The filtering is done via the `dplyr::semi_join()` on `novana` which is a table of `progId` and `aktId` where only the entries relevant for NOVANA are included.

**Value**

lazy table

---

ndb_label	<i>Given the variable name, return the label</i>
-----------	--

---

**Description**

The names of the variables (aka. `indikator`s) used on `Naturdata_kalo` are not well suited for use on a webpage or figure. This function will return a more meaningful, but verbose string.

**Usage**

```
ndb_label(data, ...)
```

**Arguments**

data	Vector of variable names
...	Not used

**Value**

data as label

**Examples**

```
ndb_label("val_vegetationshoejde_avg_5m")
```

---

ndb_labels	<i>Naturdata_kalo labels</i>
------------	------------------------------

---

**Description**

A named vector of variable (aka. indicator) labels. Not particularly useful on its own, but is the basis for the rename function [ndb\\_label\(\)](#)

**Usage**

```
ndb_labels
```

**Format**

A named vector of length 130

---

ndb_names	<i>Naturdata_kalo names</i>
-----------	-----------------------------

---

**Description**

A named vector of variable (aka. indicator) names. Not particularly useful on its own, but is the basis for the rename function [ndb\\_rename\(\)](#)

**Usage**

```
ndb_names
```

**Format**

A named vector of length 130

---

ndb_rename	<i>Rename either a data.frame or vector</i>
------------	---

---

### Description

The names of naturdata\_kalo where updated in 2024. This function makes it easy to convert old variable names to the new ones.

### Usage

```
ndb_rename(data, ...)
```

### Arguments

data	Vector of names or a data.frame with old names
...	Not used

### Details

Names in the deprecated Frekvens and Cover tables where not unique. To ensure that the function returns the correct names prefix the old names with "frekvens\_" or "cover\_". The ambiguous names where klokkeling, hedelyng, blåtop, stjerne-bredribbe and revling.

### Value

data renamed

### Examples

```
ndb_rename("antal_unik")

tibble::tibble(
  "enebaer_5m" = 1:3,
  "unknown" = "A") |>
  ndb_rename()
```

---

ndb_to_percent	<i>Convert from <math>m^2</math> cover to percent</i>
----------------	---

---

### Description

For communication of results it is often desirable to use percent rather than  $m^2$ . This function converts measurements in  $m^2$  to percent using the convention that a 5m circle has an area of 78.5  $m^2$  and a 15m circle an area of 706.9  $m^2$

**Usage**

```
ndb_to_percent(value, radius = NA)
```

**Arguments**

value	A measurement in $m^2$
radius	Radius of the circle (either 5 or 15)

---

```
ndb_update_import_job Update the import.jobs table
```

---

**Description**

Utility function to update the status, rundate and version in the import.jobs table

**Usage**

```
ndb_update_import_job(con, job, status, version)
```

**Arguments**

con	OdbcConnection
job	chr JobId e.g. "data.lysaaben_struktur"
status	chr The status which can be either running or complete
version	chr The current version of the project. This is passed to the script as a an input argument. See <a href="#">naturdata-raw-to-data</a>

**Value**

TRUE, invisibly

---

```
ndb_write_artsliste Write artsliste to database
```

---

**Description**

This a modified version of [ndb\\_write\\_to\\_db\(\)](#) where the rows in name are written species by species to avoid writing too large chunks.

**Usage**

```
ndb_write_artsliste(con, tbl, schema = "data", name)
```

**Arguments**

con	OdbcConnection to naturdata_kalo
tbl	tibble The table to be written
schema	chr Name of the schema to write to
name	chr Name of table to be written to schema

---

ndb_write_to_db	<i>Write table to database</i>
-----------------	--------------------------------

---

**Description**

The function will first call DELETE FROM before appending the contents of tbl.

**Usage**

```
ndb_write_to_db(con, tbl, schema = "data", name)
```

**Arguments**

con	OdbcConnection to naturdata_kalo
tbl	tibble The table to be written
schema	chr Name of the schema to write to
name	chr Name of table to be written to schema

**Value**

TRUE, invisibly

---

nogo_naturtyper	<i>No-go naturtyper</i>
-----------------	-------------------------

---

**Description**

A simple vector of marine and aquatic naturtypeId's. These are used for filtering tables to contain only the terrestrial types.

**Usage**

```
nogo_naturtyper
```

**Format**

A vector of 21 integer values

---

replace_na_if	<i>Replace NA values based on a set of conditions</i>
---------------	---

---

**Description**

Replace NA in a column with 0 when conditions based on progId and optionally naturtypeId are true.

**Usage**

```
replace_na_if(  
  tbl,  
  column,  
  progIds,  
  naturtypeIds = NULL,  
  year = NULL,  
  year_cond  
)
```

**Arguments**

tbl	Input table
column	name The name of the column to replace values in
progIds	int The progIds to modify values within
naturtypeIds	int The naturtypeIds to modify values within
year	int The year to use in the condition. See year_cond
year_cond	chr The condition to apply on year

**Value**

tbl with column modified.

# Index

## \* datasets

- ndb\_labels, 26
- ndb\_names, 26
- nogo\_naturtyper, 29

DBI::dbDisconnect(), 13  
DBI::dbWriteTable(), 13  
dplyr::semi\_join(), 25  
dplyr::starts\_with(), 5

get\_condition, 3

lubridate::yday(), 10

ndb\_aggregate\_pinpoint, 3  
ndb\_append\_coords, 4  
ndb\_calc\_avg, 4  
ndb\_calc\_cover\_ratio, 5  
ndb\_calc\_jord\_cn, 6  
ndb\_calc\_n\_arter, 6  
ndb\_calc\_n\_arter(), 17  
ndb\_calc\_n\_store\_stammer, 7  
ndb\_calc\_weighted\_assessment, 7  
ndb\_clean\_artsliste, 8  
ndb\_clean\_kemi, 9  
ndb\_clean\_lysaaben\_struktur, 9  
ndb\_clean\_plantekemi, 10  
ndb\_clean\_skov\_doedtved, 11  
ndb\_clean\_skov\_struktur, 11  
ndb\_clean\_stamdata, 12  
ndb\_connect, 12  
ndb\_create\_tbl, 13  
ndb\_disconnect, 13  
ndb\_filter\_artsliste, 14  
ndb\_filter\_artsliste(), 16  
ndb\_filter\_lysaaben\_prog, 14  
ndb\_filter\_skov\_prog, 15  
ndb\_get, 15  
ndb\_get\_artsgruppe, 16  
ndb\_get\_artsliste\_pf, 16  
ndb\_get\_artsliste\_pf(), 14  
ndb\_get\_artsnavne, 17  
ndb\_get\_artsnavne(), 6  
ndb\_get\_artsscorer, 17  
ndb\_get\_arttraits, 18  
ndb\_get\_doedtved, 19  
ndb\_get\_ellenberg, 19  
ndb\_get\_laver, 20  
ndb\_get\_lysaaben\_struktur, 20  
ndb\_get\_mosser, 21  
ndb\_get\_novana\_aktids, 21  
ndb\_get\_plantekemi, 22  
ndb\_get\_schema, 22  
ndb\_get\_skov\_struktur, 23  
ndb\_get\_skov\_trae\_diam\_naturtype, 23  
ndb\_get\_skov\_traeregistrering, 24  
ndb\_get\_stamdata, 24  
ndb\_get\_tbl, 25  
ndb\_label, 25  
ndb\_label(), 26  
ndb\_labels, 26  
ndb\_names, 26  
ndb\_rename, 27  
ndb\_rename(), 26  
ndb\_to\_percent, 27  
ndb\_update\_import\_job, 28  
ndb\_write\_artsliste, 28  
ndb\_write\_to\_db, 29  
ndb\_write\_to\_db(), 28  
nogo\_naturtyper, 29

replace\_na\_if, 30  
replace\_na\_if(), 3