

# Package: corella (via r-universe)

May 15, 2026

**Title** Prepare, Manipulate and Check Data to Comply with Darwin Core Standard

**Version** 0.1.4

**Description** Helps users standardise data to the Darwin Core Standard, a global data standard to store, document, and share biodiversity data like species occurrence records. The package provides tools to manipulate data to conform with, and check validity against, the Darwin Core Standard. Using 'corella' allows users to verify that their data can be used to build 'Darwin Core Archives' using the 'galaxias' package.

**Depends** R (>= 4.3.0)

**Imports** cli, dplyr, glue, hms, lubridate, purrr, rlang, sf, stringr, tibble, tidyr, uuid

**Suggests** gt, knitr, nanoparquet, ozmaps, readr, rmarkdown, testthat (>= 3.0.0), withr

**License** GPL-3

**URL** <https://corella.ala.org.au/R/>

**BugReports** <https://github.com/AtlasOfLivingAustralia/corella/issues>

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**Encoding** UTF-8

**VignetteBuilder** knitr

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.2

**Config/testthat/edition** 3

**LazyData** true

**Config/pak/sysreqs** libabsl-dev cmake libgdal-dev gdal-bin libgeos-dev libicu-dev libssl-dev libproj-dev libsqli3-dev libudunits2-dev

**Repository** <https://atlasoflivingaustralia.r-universe.dev>

**Date/Publication** 2025-06-11 05:53:47 UTC

**RemoteUrl** <https://github.com/AtlasOfLivingAustralia/corella>

**RemoteRef** HEAD

**RemoteSha** 0069f379c78caf5aa9849c563c1f0a3115694ba6

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---

basisOfRecord\_values *Accepted value functions*

---

### Description

When creating a Darwin Core Archive, several fields have a vocabulary of acceptable values. These functions provide a vector of terms that can be used to fill or validate those fields.

### Usage

basisOfRecord\_values()

countryCode\_values()

### Value

A vector of accepted values for that use case.

**See Also**

[occurrence\\_terms\(\)](#) or [event\\_terms\(\)](#) for valid Darwin Core *terms* (i.e. column names).

**Examples**

```
# See all valid basis of record values
basisOfRecord_values()
```

---

check\_dataset

*Check a dataset for Darwin Core conformance*

---

**Description**

Run a test suite of checks to test whether a `data.frame` or `tibble` conforms to Darwin Core Standard.

While most users will only want to call `suggest_workflow()`, the underlying check functions are exported for detailed work, or for debugging. This function is useful for users experienced with Darwin Core Standard or for final dataset checks.

**Usage**

```
check_dataset(.df)
```

**Arguments**

`.df` A tibble against which checks should be run

**Details**

`check_dataset()` is modelled after `devtools::test()`. It runs a series of checks, then supplies a summary of passed/failed checks and error messages.

Checks run by `check_dataset()` are the same that would be run automatically by various `set_` functions in a piped workflow. This function allows users with only minor expected updates to check their entire dataset without the need for `set_` functions.

**Value**

Invisibly returns the input data frame, but primarily called for the side-effect of running check functions on that input.

**Examples**

```
df <- tibble::tibble(
  scientificName = c("Crinia Signifera", "Crinia Signifera", "Litoria peronii"),
  latitude = c(-35.27, -35.24, -35.83),
  longitude = c(149.33, 149.34, 149.34),
  eventDate = c("2010-10-14", "2010-10-14", "2010-10-14"),
  status = c("present", "present", "present")
)

# Run a test suite of checks for Darwin Core Standard conformance
# Checks are only run on columns with names that match Darwin Core terms
df |>
  check_dataset()
```

---

composite_id	<i>Create unique identifier columns</i>
--------------	---

---

**Description**

A unique identifier is a pattern of words, letters and/or numbers that is unique to a single record within a dataset. Unique identifiers are useful because they identify individual observations, and make it possible to change, amend or delete observations over time. They also prevent accidental deletion when more than one record contains the same information (and would otherwise be considered a duplicate).

The identifier functions in *corella* make it easier to generate columns with unique identifiers in a dataset. These functions can be used within `set_events()`, `set_occurrences()`, or (equivalently) `dplyr::mutate()`.

**Usage**

```
composite_id(..., sep = "-")

sequential_id(width)

random_id()
```

**Arguments**

...	Zero or more variable names from the tibble being mutated (unquoted), and/or zero or more <code>_id</code> functions, separated by commas.
sep	Character used to separate field values. Defaults to "-"
width	(Integer) how many characters should the resulting string be? Defaults to one plus the order of magnitude of the largest number.

**Details**

Generally speaking, it is better to use existing information from a dataset to generate identifiers. For this reason we recommend using `composite_id()` to aggregate existing fields, if no such composite is already present within the dataset. Composite IDs are more meaningful and stable; they are easier to check and harder to overwrite.

It is possible to call `sequential_id()` or `random_id()` within `composite_id()` to combine existing and new columns.

**Value**

An amended tibble containing a column with identifiers in the requested format.

**Examples**

```
df <- tibble::tibble(
  eventDate = paste0(rep(c(2020:2024), 3), "-01-01"),
  basisOfRecord = "humanObservation",
  site = rep(c("A01", "A02", "A03"), each = 5)
)

# Add composite ID using a random ID, site name and eventDate
df |>
  set_occurrences(
    occurrenceID = composite_id(random_id(),
                                site,
                                eventDate)
  )

# Add composite ID using a sequential number, site name and eventDate
df |>
  set_occurrences(
    occurrenceID = composite_id(sequential_id(),
                                site,
                                eventDate)
  )
```

---

country\_codes

*Dataset of supported Country Codes*


---

**Description**

A tibble of ISO 3166-1 alpha-2 codes for countries, which are the accepted standard for supplying countryCode in Darwin Core Standard.

**Usage**

```
country_codes
```

**Format**

A tibble containing valid country codes (249 rows x 3 columns). Column descriptions are as follows:

**name** ISO 3166-1 alpha-2 code, pointing to its ISO 3166-2 article.

**code** English short name officially used by the ISO 3166 Maintenance Agency (ISO 3166/MA).

**year** Year when alpha-2 code was first officially assigned.

**Source**

[Wikipedia](#).

**See Also**

[set\\_locality\(\)](#) for assigning countryCode within a tibble; [countryCode\\_values\(\)](#) to return valid codes as a vector.

---

darwin\_core\_terms      *Dataset of supported Darwin Core terms*

---

**Description**

The Darwin Core Standard is maintained by Biodiversity Information Standards, previously known as the Taxonomic Databases Working Group and known by the acronym 'TDWG'. This tibble is the full list of supported terms, current as of 2024-12-10.

Users can use [occurrence\\_terms\(\)](#) and [event\\_terms\(\)](#) as convenience functions to access these terms.

**Usage**

```
darwin_core_terms
```

**Format**

A tibble containing valid Darwin Core Standard terms (206 rows x 6 columns). Column descriptions are as follows:

**class** TDWG group that a term belongs to.

**term** Column header names that can be used in Darwin Core

**url** Stable url to information describing the term.

**definition** Human-readable definition of the term.

**comments** Further information from TDWG.

**examples** Examples of how the field should be populated.

**set\_functions** Function in corella that supports Darwin Core term.

**Source**

Slightly modified version of a [table supplied by TDWG](#).

**See Also**

[occurrence\\_terms\(\)](#) and [event\\_terms\(\)](#) to get terms for use in `dplyr::select()`

---

occurrence\_terms      *Select support functions*

---

**Description**

When creating a Darwin Core archive, it is often useful to select only those fields that conform to the standard. These functions provide a vector of terms that can be used in combination with `dplyr::select()` and `dplyr::any_of()` to quickly select Darwin Core terms for the relevant data type (events, occurrences, media).

**Usage**

```
occurrence_terms()
```

```
event_terms()
```

**Value**

A vector of accepted (but not mandatory) values for that use case.

**See Also**

[basisOfRecord\\_values\(\)](#) or [countryCode\\_values\(\)](#) for valid entries *within* a field.

**Examples**

```
# Return a vector of accepted terms in an Occurrence-based dataset
occurrence_terms() |> head(10L) # first 10 terms

# Use this vector to filter a data frame
df <- tibble::tibble(
  name = c("Crinia Signifera", "Crinia Signifera", "Litoria peronii"),
  latitude = c(-35.27, -35.24, -35.83),
  longitude = c(149.33, 149.34, 149.34),
  eventDate = c("2010-10-14", "2010-10-14", "2010-10-14"),
  measurement1 = c(24.3, 24.9, 20.1), # example measurement column
  measurement2 = c(0.92, 1.03, 1.09) # example measurement column
)

df |>
  dplyr::select(any_of(occurrence_terms()))
```

---

 set\_abundance

*Set, create or modify columns with abundance information*


---

## Description

In some field methods, it is common to observe more than one individual per observation; to observe abundance using non-integer measures such as mass or area; or to seek individuals but not find them (abundance of zero). As these approaches use different Darwin Core terms, this function assists in specifying abundances to a tibble using Darwin Core Standard.

In practice this is no different from using `mutate()`, but gives some informative errors, and serves as a useful lookup for how columns with abundance information are represented in the Darwin Core Standard.

## Usage

```
set_abundance(
  .df,
  individualCount = NULL,
  organismQuantity = NULL,
  organismQuantityType = NULL,
  .keep = "unused"
)
```

## Arguments

<code>.df</code>	A data.frame or tibble that the column should be appended to.
<code>individualCount</code>	The number of individuals present
<code>organismQuantity</code>	A number or enumeration value for the quantity of organisms. Used together with <code>organismQuantityType</code> to provide context.
<code>organismQuantityType</code>	The type of quantification system used for <code>organismQuantity</code> .
<code>.keep</code>	Control which columns from <code>.data</code> are retained in the output. Note that unlike <code>dplyr::mutate()</code> , which defaults to "all" this defaults to "unused"; i.e. only keeps Darwin Core columns, and not those columns used to generate them.

## Details

Examples of `organismQuantity` & `organismQuantityType` values:

- 27 (`organismQuantity`) individuals (`organismQuantityType`)
- 12.5 (`organismQuantity`) % biomass (`organismQuantityType`)
- r (`organismQuantity`) Braun-Blanquet Scale (`organismQuantityType`)
- many (`organismQuantity`) individuals (`organismQuantityType`)

**Value**

A tibble with the requested fields added/reformatted.

**Examples**

```
df <- tibble::tibble(
  scientificName = c("Cacatua (Licmetis) tenuirostris",
                    "Cacatua (Licmetis) tenuirostris",
                    "Cacatua (Licmetis) tenuirostris"),
  n_obs = c(1, 3, 4)
)

df |>
  set_abundance(individualCount = n_obs)
```

---

set_collection	<i>Set, create or modify columns with museum- or collection-specific information</i>
----------------	--

---

**Description**

Format fields that specify the collection or catalog number of a specimen or occurrence record to a tibble using Darwin Core Standard.

In practice this is no different from using `mutate()`, but gives some informative errors, and serves as a useful lookup for fields in the Darwin Core Standard.

**Usage**

```
set_collection(
  .df,
  datasetID = NULL,
  datasetName = NULL,
  catalogNumber = NULL,
  .keep = "unused"
)
```

**Arguments**

.df	A data.frame or tibble that the column should be appended to.
datasetID	An identifier for the set of data. May be a global unique identifier or an identifier specific to a collection or institution.
datasetName	The name identifying the data set from which the record was derived.
catalogNumber	A unique identifier for the record within the data set or collection.
.keep	Control which columns from .data are retained in the output. Note that unlike <code>dplyr::mutate()</code> , which defaults to "all" this defaults to "unused"; i.e. only keeps Darwin Core columns, and not those columns used to generate them.

**Details**

Examples of datasetID values:

- b15d4952-7d20-46f1-8a3e-556a512b04c5

Examples of datasetName values:

- Grinnell Resurvey Mammals
- Lacey Ctenomys Recaptures

Examples of catalogNumber values:

- 145732
- 145732a
- 2008.1334
- R-4313

**Value**

A tibble with the requested fields added/reformatted.

**Examples**

```
df <- tibble::tibble(
  name = c("Crinia Signifera", "Crinia Signifera", "Litoria peronii"),
  eventDate = c("2010-10-14", "2010-10-14", "2010-10-14"),
  catalog_num = c("16789a", "16789c", "08742f"),
  dataset = c("Frog search", "Frog search", "Frog search")
)

# Reformat columns to Darwin Core terms
df |>
  set_collection(
    catalogNumber = catalog_num,
    datasetName = dataset
  )
```

---

set\_coordinates

*Set, create or modify columns with spatial information*

---

**Description**

This function helps format standard location fields like latitude and longitude point coordinates to a tibble using Darwin Core Standard.

**Usage**

```
set_coordinates(
  .df,
  decimalLatitude = NULL,
  decimalLongitude = NULL,
  geodeticDatum = NULL,
  coordinateUncertaintyInMeters = NULL,
  coordinatePrecision = NULL,
  .keep = "unused"
)
```

**Arguments**

<code>.df</code>	A data.frame or tibble that the column should be appended to.
<code>decimalLatitude</code>	The latitude in decimal degrees.
<code>decimalLongitude</code>	The longitude in decimal degrees.
<code>geodeticDatum</code>	The datum or spatial reference system that coordinates are recorded against (usually "WGS84" or "EPSG:4326"). This is often known as the Coordinate Reference System (CRS). If your coordinates are from a GPS system, your data are already using WGS84.
<code>coordinateUncertaintyInMeters</code>	(numeric) Radius of the smallest circle that contains the whole location, given any possible measurement error. <code>coordinateUncertaintyInMeters</code> will typically be around 30 (metres) if recorded with a GPS after 2000, or 100 before that year.
<code>coordinatePrecision</code>	(numeric) The precision that <code>decimalLatitude</code> and <code>decimalLongitude</code> are supplied to. <code>coordinatePrecision</code> should be no less than 0.00001 if data were collected using GPS.
<code>.keep</code>	Control which columns from <code>.df</code> are retained in the output. Note that unlike <code>dplyr::mutate()</code> , which defaults to "all" this defaults to "unused"; i.e. only keeps Darwin Core columns, and not those columns used to generate them.

**Details**

In practice this is no different from using `mutate()`, but gives some informative errors, and serves as a useful lookup for how spatial columns are represented in the Darwin Core Standard.

Example values are:

- `geodeticDatum` should be a valid EPSG code

**Value**

A tibble with the requested columns added/reformatted.

**See Also**

[set\\_locality\(\)](#) for provided text-based spatial information.

**Examples**

```
df <- tibble::tibble(
  scientificName = c("Crinia Signifera", "Crinia Signifera", "Litoria peronii"),
  latitude = c(-35.27, -35.24, -35.83),
  longitude = c(149.33, 149.34, 149.34),
  eventDate = c("2010-10-14", "2010-10-14", "2010-10-14")
)

# Reformat columns to Darwin Core Standard terms
df |>
  set_coordinates(
    decimalLongitude = longitude,
    decimalLatitude = latitude
  )
```

---

set\_coordinates\_sf      *Set, create or modify columns with sf spatial information*

---

**Description**

This function helps format standard location fields like longitude and latitude point coordinates to a tibble using Darwin Core Standard.

It differs from `set_coordinates()` by accepting `sf` geometry columns of class `POINT` as coordinates (rather than numeric lat/lon coordinates). The advantage of using an `sf` geometry is that the Coordinate Reference System (CRS) is automatically formatted into the required `geodeticDatum` column.

**Usage**

```
set_coordinates_sf(.df, geometry = NULL, .keep = "unused")
```

**Arguments**

<code>.df</code>	A data.frame or tibble that the column should be appended to.
<code>geometry</code>	The latitude/longitude coordinates as <code>sf POINT</code> class
<code>.keep</code>	Control which columns from <code>.data</code> are retained in the output. Note that unlike <code>dplyr::mutate()</code> , which defaults to "all" this defaults to "unused"; i.e. only keeps Darwin Core columns, and not those columns used to generate them.

**Value**

A tibble with the requested columns added/reformatted.

**See Also**

[set\\_coordinates\(\)](#) for providing numeric coordinates, [set\\_locality\(\)](#) for providing text-based spatial information.

**Examples**

```
df <- tibble::tibble(
  scientificName = c("Crinia Signifera", "Crinia Signifera", "Litoria peronii"),
  latitude = c(-35.27, -35.24, -35.83),
  longitude = c(149.33, 149.34, 149.34),
  eventDate = c("2010-10-14", "2010-10-14", "2010-10-14")
) |>
sf::st_as_sf(coords = c("longitude", "latitude")) |>
sf::st_set_crs(4326)

# Reformat columns to Darwin Core Standard terms.
# Coordinates and CRS are automatically detected and reformatted.
df |>
  set_coordinates_sf()
```

---

 set\_datetime

*Set, create or modify columns with date and time information*


---

**Description**

This function helps format standard date/time columns in a tibble using Darwin Core Standard. Users should make use of the [lubridate package](#) to format their dates so corella can read them correctly.

In practice this is no different from using `mutate()`, but gives some informative errors, and serves as a useful lookup for how spatial fields are represented in the Darwin Core Standard.

**Usage**

```
set_datetime(
  .df,
  eventDate = NULL,
  year = NULL,
  month = NULL,
  day = NULL,
  eventTime = NULL,
  .keep = "unused",
  .messages = TRUE
)
```

**Arguments**

<code>.df</code>	A <code>data.frame</code> or <code>tibble</code> that the column should be appended to.
<code>eventDate</code>	The date or date + time that the observation/event occurred.
<code>year</code>	The year of the observation/event.
<code>month</code>	The month of the observation/event.
<code>day</code>	The day of the observation/event.
<code>eventTime</code>	The time of the event. Use this term for Event data. Date + time information for observations is accepted in <code>eventDate</code> .
<code>.keep</code>	Control which columns from <code>.data</code> are retained in the output. Note that unlike <code>dplyr::mutate()</code> , which defaults to "all" this defaults to "unused"; i.e. only keeps Darwin Core fields, and not those fields used to generate them.
<code>.messages</code>	(logical) Should informative messages be shown? Defaults to TRUE.

**Details**

Example values are:

- `eventDate` should be class `Date` or `POSIXct`. We suggest using the `lubridate` package to define your date format using functions like `ymd()`, `mdy()`, `dmy()`, or if including date + time, `ymd_hms()`, `ymd_hm()`, or `ymd_h()`.

**Value**

A `tibble` with the requested columns added/reformatted.

**Examples**

```
df <- tibble::tibble(
  name = c("Crinia Signifera", "Crinia Signifera", "Litoria peronii"),
  latitude = c(-35.27, -35.24, -35.83),
  longitude = c(149.33, 149.34, 149.34),
  date = c("2010-10-14", "2010-10-14", "2010-10-14"),
  time = c("10:08:12", "13:01:45", "14:02:33")
)

# Use the lubridate package to format date + time information
# eventDate accepts date + time
df |>
  set_datetime(
    eventDate = lubridate::ymd_hms(paste(date, time))
  )
```

---

 set\_events

*Set, create or modify columns with Event information*


---

## Description

Identify or format columns that contain information about an **Event**. An "Event" in Darwin Core Standard refers to an action that occurs at a place and time. Examples include:

- A specimen collecting event
- A survey or sampling event
- A camera trap image capture
- A marine trawl
- A camera trap deployment event
- A camera trap burst image event (with many images for one observation)

In practice this function is used no differently from `mutate()`, but gives users some informative errors, and serves as a useful lookup for fields in the Darwin Core Standard.

## Usage

```
set_events(
  .df,
  eventID = NULL,
  eventType = NULL,
  parentEventID = NULL,
  .keep = "unused",
  .keep_composite = "all"
)
```

## Arguments

<code>.df</code>	A data.frame or tibble that the column should be appended to.
<code>eventID</code>	A unique identifier for an individual Event.
<code>eventType</code>	The type of Event
<code>parentEventID</code>	The parent event under which one or more Events sit within.
<code>.keep</code>	Control which columns from <code>.df</code> are retained in the output. Note that unlike <code>dplyr::mutate()</code> , which defaults to "all" this defaults to "unused"; i.e. only keeps Darwin Core columns, and not those columns used to generate them.
<code>.keep_composite</code>	Control which columns from <code>.df</code> are kept when <code>composite_id()</code> is used to assign values to <code>eventID</code> , defaulting to "all". This has a different default from <code>.keep</code> because composite identifiers often contain information that is valuable in other contexts, meaning that deleting these columns by default is typically unwise.



---

set\_individual\_traits *Set, create or modify columns with information of individual organisms*

---

### Description

Format fields that contain measurements or attributes of individual organisms to a tibble using Darwin Core Standard. Fields include those that specify sex, life stage or condition. Individuals can be identified by an individualID if data contains resampling.

In practice this is no different from using `mutate()`, but gives some informative errors, and serves as a useful lookup for fields in the Darwin Core Standard.

### Usage

```
set_individual_traits(
  .df,
  individualID = NULL,
  lifeStage = NULL,
  sex = NULL,
  vitality = NULL,
  reproductiveCondition = NULL,
  .keep = "unused"
)
```

### Arguments

<code>.df</code>	A data.frame or tibble that the column should be appended to.
<code>individualID</code>	An identifier for an individual or named group of individual organisms represented in the Occurrence. Meant to accommodate resampling of the same individual or group for monitoring purposes. May be a global unique identifier or an identifier specific to a data set.
<code>lifeStage</code>	The age class or life stage of an organism at the time of occurrence.
<code>sex</code>	The sex of the biological individual.
<code>vitality</code>	An indication of whether an organism was alive or dead at the time of collection or observation.
<code>reproductiveCondition</code>	The reproductive condition of the biological individual.
<code>.keep</code>	Control which columns from .data are retained in the output. Note that unlike <code>dplyr::mutate()</code> , which defaults to "all" this defaults to "unused"; i.e. only keeps Darwin Core columns, and not those columns used to generate them.

### Details

Examples of lifeStage values:

- zygote

- larva
- adult
- seedling
- flowering

Examples of vitality values:

- alive
- dead
- uncertain

Examples of reproductiveCondition values:

- non-reproductive
- pregnant
- in bloom
- fruit bearing

## Value

A tibble with the requested fields added/reformatted.

## See Also

[set\\_scientific\\_name\(\)](#) for adding scientificName and authorship information.

## Examples

```
df <- tibble::tibble(
  name = c("Crinia Signifera", "Crinia Signifera", "Litoria peronii"),
  latitude = c(-35.27, -35.24, -35.83),
  longitude = c(149.33, 149.34, 149.34),
  eventDate = c("2010-10-14", "2010-10-14", "2010-10-14"),
  id = c(4421, 4422, 3311),
  life_stage = c("juvenile", "adult", "adult")
)

# Reformat columns to Darwin Core Standard
df |>
  set_individual_traits(
    individualID = id,
    lifeStage = life_stage
  )
```

---

set_license	<i>Set, create or modify columns with license and rights information</i>
-------------	--

---

### Description

Format fields that contain information on permissions for use, sharing or access to a record to a tibble using Darwin Core Standard.

In practice this function is no different from using `mutate()`, but gives some informative errors, and serves as a useful lookup for fields in the Darwin Core Standard.

### Usage

```
set_license(
  .df,
  license = NULL,
  rightsHolder = NULL,
  accessRights = NULL,
  .keep = "unused"
)
```

### Arguments

<code>.df</code>	A data.frame or tibble that the column should be appended to.
<code>license</code>	A legal document giving official permission to do something with the resource. Must be provided as a url to a valid license.
<code>rightsHolder</code>	Person or organisation owning or managing rights to resource.
<code>accessRights</code>	Access or restrictions based on privacy or security.
<code>.keep</code>	Control which columns from .data are retained in the output. Note that unlike <code>dplyr::mutate()</code> , which defaults to "all" this defaults to "unused"; i.e. only keeps Darwin Core columns, and not those columns used to generate them.

### Details

Examples of license values:

- <http://creativecommons.org/publicdomain/zero/1.0/legalcode>
- <http://creativecommons.org/licenses/by/4.0/legalcode>
- CC0
- CC-BY-NC 4.0 (Int)

Examples of rightsHolder values:

- The Regents of the University of California

Examples of accessRights values:

- not-for-profit use only (string example)
- <https://www.fieldmuseum.org/field-museum-natural-history-conditions-and-suggested-norms-use-col> (URI example)

**Value**

A tibble with the requested fields added/reformatted.

**See Also**

[set\\_observer\(\)](#) for adding observer information.

**Examples**

```
df <- tibble::tibble(
  name = c("Crinia Signifera", "Crinia Signifera", "Litoria peronii"),
  latitude = c(-35.27, -35.24, -35.83),
  longitude = c(149.33, 149.34, 149.34),
  eventDate = c("2010-10-14", "2010-10-14", "2010-10-14"),
  attributed_license = c("CC-BY-NC 4.0 (Int)", "CC-BY-NC 4.0 (Int)", "CC-BY-NC 4.0 (Int)")
)

# Reformat columns to Darwin Core Standard
df |>
  set_license(
    license = attributed_license
  )
```

---

set\_locality

*Set, create or modify columns with locality information*

---

**Description**

Locality information refers to a description of a place, rather than a spatial coordinate. This function helps to format columns with locality information to a tibble using Darwin Core Standard.

In practice this is used no differently from `mutate()`, but gives some informative errors, and serves as a useful lookup for fields in the Darwin Core Standard.

**Usage**

```
set_locality(
  .df,
  continent = NULL,
  country = NULL,
  countryCode = NULL,
  stateProvince = NULL,
  locality = NULL,
  .keep = "unused"
)
```

**Arguments**

.df	A data.frame or tibble that the column should be appended to.
continent	(string) Valid continent. See details.
country	Valid country name. See country_codes.
countryCode	Valid country code. See country_codes.
stateProvince	A sub-national region.
locality	A specific description of a location or place.
.keep	Control which columns from .data are retained in the output. Note that unlike <code>dplyr::mutate()</code> , which defaults to "all" this defaults to "unused"; i.e. only keeps Darwin Core columns, and not those columns used to generate them.

**Details**

Values of continent should be one of "Africa", "Antarctica", "Asia", "Europe", "North America", "Oceania" or "South America".

countryCode should be supplied according to the [ISO 3166-1 ALPHA-2](#) standard, as per [TDWG advice](#). Examples of countryCode:

- AUS
- NZ
- BRA

Examples of locality:

- Bariloche, 25 km NNE via Ruta Nacional 40 (=Ruta 237)
- Queets Rainforest, Olympic National Park

**Value**

A tibble with the requested columns added/reformatted.

**See Also**

[set\\_coordinates\(\)](#) for numeric spatial data.

**Examples**

```
df <- tibble::tibble(
  scientificName = c("Crinia Signifera", "Crinia Signifera", "Litoria peronii"),
  latitude = c(-35.27, -35.24, -35.83),
  longitude = c(149.33, 149.34, 149.34),
  eventDate = c("2010-10-14", "2010-10-14", "2010-10-14"),
  countryCode = c("AU", "AU", "AU"),
  state = c("New South Wales", "New South Wales", "New South Wales"),
  locality = c("Melville Caves", "Melville Caves", "Bryans Swamp about 3km away")
)

# Reformat columns to Darwin Core Standard terms
```

```
df |>
  set_locality(
    countryCode = countryCode,
    stateProvince = state,
    locality = locality
  )

# Columns with valid Darwin Core terms as names are automatically detected
# and checked. This will do the same as above.
df |>
  set_locality(
    stateProvince = state
  )
```

---

set_measurements	<i>Convert columns with measurement data for an individual or event to Darwin Core standard</i>
------------------	---

---

## Description

**[Experimental]** This function is a work in progress, and should be used with caution.

In raw collected data, many types of information can be captured in one column. For example, the column name LMA\_g.m2 contains the measured trait (Leaf Mass per Area, LMA) and the unit of measurement (grams per meter squared, g/m2), and recorded in that column are the values themselves. In Darwin Core, these different types of information must be separated into multiple columns so that they can be ingested correctly and aggregated with sources of data accurately.

This function converts information preserved in a single measurement column into multiple columns (measurementID, measurementUnit, and measurementType) as per Darwin Core standard.

## Usage

```
set_measurements(.df, cols = NULL, unit = NULL, type = NULL, .keep = "unused")
```

## Arguments

.df	a data.frame or tibble that the column should be appended to.
cols	vector of column names to be included as 'measurements'. Unquoted.
unit	vector of strings giving units for each variable
type	vector of strings giving a description for each variable
.keep	Control which columns from .data are retained in the output. Note that unlike <code>dplyr::mutate()</code> , which defaults to "all" this defaults to "unused"; i.e. only keeps Darwin Core fields, and not those fields used to generate them.

## Details

Columns are nested in a single column `measurementOrFact` that contains Darwin Core Standard measurement fields. By nesting three measurement columns within the `measurementOrFact` column, nested measurement columns can be converted to long format (one row per measurement, per occurrence) while the original data frame remains organised by one row per occurrence. Data can be unnested into long format using `tidyr::unnest()`.

## Value

A tibble with the requested fields added.

## Examples

```
library(tidyr)

# Example data of plant species observations and measurements
df <- tibble::tibble(
  Site = c("Adelaide River", "Adelaide River", "AgnesBanks"),
  Species = c("Corymbia latifolia", "Banksia aemula", "Acacia aneura"),
  Latitude = c(-13.04, -13.04, -33.60),
  Longitude = c(131.07, 131.07, 150.72),
  LMA_g.m2 = c(NA, 180.07, 159.01),
  LeafN_area_g.m2 = c(1.100, 0.913, 2.960)
)

# Reformat columns to Darwin Core Standard
# Measurement columns are reformatted and nested in column `measurementOrFact`
df_dwc <- df |>
  set_measurements(
    cols = c(LMA_g.m2,
             LeafN_area_g.m2),
    unit = c("g/m2",
             "g/m2"),
    type = c("leaf mass per area",
             "leaf nitrogen per area")
  )

df_dwc

# Unnest to view full long format data frame
df_dwc |>
  tidyr::unnest(measurementOrFact)
```

---

set\_observer

*Set, create or modify columns with information of who made an observation*

---

**Description**

Format fields that contain information about who made a specific observation of an organism to a tibble using Darwin Core Standard.

In practice this is no different from using `mutate()`, but gives some informative errors, and serves as a useful lookup for fields in the Darwin Core Standard.

**Usage**

```
set_observer(.df, recordedBy = NULL, recordedByID = NULL, .keep = "unused")
```

**Arguments**

<code>.df</code>	A data.frame or tibble that the column should be appended to.
<code>recordedBy</code>	Names of people, groups, or organizations responsible for recording the original occurrence. The primary collector or observer should be listed first.
<code>recordedByID</code>	The globally unique identifier for the person, people, groups, or organizations responsible for recording the original occurrence.
<code>.keep</code>	Control which columns from .data are retained in the output. Note that unlike <code>dplyr::mutate()</code> , which defaults to "all" this defaults to "unused"; i.e. only keeps Darwin Core columns, and not those columns used to generate them.

**Details**

Examples of `recordedBy` values:

- José E. Crespo

Examples of `recordedByID` values:

- `c("https://orcid.org/0000-0002-1825-0097", "https://orcid.org/0000-0002-1825-0098")`

**Value**

A tibble with the requested fields added/reformatted.

**Examples**

```
df <- tibble::tibble(
  name = c("Crinia Signifera", "Crinia Signifera", "Litoria peronii"),
  latitude = c(-35.27, -35.24, -35.83),
  longitude = c(149.33, 149.34, 149.34),
  eventDate = c("2010-10-14", "2010-10-14", "2010-10-14"),
  observer = c("David Attenborough", "David Attenborough", "David Attenborough")
)

# Reformat columns to Darwin Core terms
df |>
  set_observer(
    recordedBy = observer
  )
```

---

set_occurrences	<i>Set, create or modify columns with occurrence-specific information</i>
-----------------	---

---

### Description

Format fields uniquely identify each occurrence record and specify the type of record. `occurrenceID` and `basisOfRecord` are necessary fields of information for occurrence records, and should be appended to a data set to conform to Darwin Core Standard prior to submission.

In practice this is no different from using `mutate()`, but gives some informative errors, and serves as a useful lookup for fields in the Darwin Core Standard.

### Usage

```
set_occurrences(
  .df,
  occurrenceID = NULL,
  basisOfRecord = NULL,
  occurrenceStatus = NULL,
  .keep = "unused",
  .keep_composite = "all",
  .messages = TRUE
)
```

### Arguments

<code>.df</code>	a <code>data.frame</code> or <code>tibble</code> that the column should be appended to.
<code>occurrenceID</code>	A character string. Every occurrence should have an <code>occurrenceID</code> entry. Ideally IDs should be persistent to avoid being lost in future updates. They should also be unique, both within the dataset, and (ideally) across all other datasets.
<code>basisOfRecord</code>	Record type. Only accepts <code>camelCase</code> , for consistency with field names. Accepted <code>basisOfRecord</code> values are one of: <ul style="list-style-type: none"> <li>"humanObservation", "machineObservation", "livingSpecimen", "preservedSpecimen", "fossilSpecimen", "materialCitation"</li> </ul>
<code>occurrenceStatus</code>	Either "present" or "absent".
<code>.keep</code>	Control which columns from <code>.df</code> are retained in the output. Note that unlike <code>dplyr::mutate()</code> , which defaults to "all" this defaults to "unused"; i.e. only keeps Darwin Core columns, and not those columns used to generate them.
<code>.keep_composite</code>	Control which columns from <code>.df</code> are kept when <code>composite_id()</code> is used to assign values to <code>occurrenceID</code> , defaulting to "all". This has a different default from <code>.keep</code> because composite identifiers often contain information that is valuable in other contexts, meaning that deleting these columns by default is typically unwise.
<code>.messages</code>	Logical: Should progress message be shown? Defaults to TRUE.

**Details**

Examples of occurrenceID values:

- 000866d2-c177-4648-a200-ead4007051b9
- <http://arctos.database.museum/guid/MSB:Mamm:233627>

Accepted basisOfRecord values are one of:

- "humanObservation", "machineObservation", "livingSpecimen", "preservedSpecimen", "fossilSpecimen", "materialCitation"

**Value**

A tibble with the requested columns added/reformatted.

**See Also**

[basisOfRecord\\_values\(\)](#) for accepted values for the basisOfRecord field; [random\\_id\(\)](#), [composite\\_id\(\)](#) or [sequential\\_id\(\)](#) for formatting ID columns; [set\\_abundance\(\)](#) for occurrence-level counts.

**Examples**

```
df <- tibble::tibble(
  scientificName = c("Crinia Signifera", "Crinia Signifera", "Litoria peronii"),
  latitude = c(-35.27, -35.24, -35.83),
  longitude = c(149.33, 149.34, 149.34),
  eventDate = c("2010-10-14", "2010-10-14", "2010-10-14")
)

# Add occurrence information
df |>
  set_occurrences(
    occurrenceID = composite_id(random_id(), eventDate), # add composite ID
    basisOfRecord = "humanObservation"
  )
```

---

set_scientific_name	<i>Set, create or modify columns with scientific name &amp; authorship information</i>
---------------------	--

---

**Description**

Format the field scientificName, the lowest identified taxonomic name of an occurrence, along with the rank and authorship of the provided name to a tibble using Darwin Core Standard.

**Usage**

```
set_scientific_name(
  .df,
  scientificName = NULL,
  scientificNameAuthorship = NULL,
  taxonRank = NULL,
  .keep = "unused"
)
```

**Arguments**

`.df` A data.frame or tibble that the column should be appended to.

`scientificName` The full scientific name in the lower level taxonomic rank that can be determined.

`scientificNameAuthorship` The authorship information for `scientificName`.

`taxonRank` The taxonomic rank of `scientificName`.

`.keep` Control which columns from `.data` are retained in the output. Note that unlike `dplyr::mutate()`, which defaults to "all" this defaults to "unused"; i.e. only keeps Darwin Core columns, and not those columns used to generate them.

**Details**

In practice this function is used no differently from `mutate()`, but gives users some informative errors, and serves as a useful lookup for accepted column names in the Darwin Core Standard.

Examples of `scientificName` values (we specify the rank in parentheses, but users should not include this information):

- Coleoptera (order)
- Vespertilionidae (family)
- Manis (genus)
- *Ctenomys sociabilis* (genus + specificEpithet)
- *Ambystoma tigrinum diaboli* (genus + specificEpithet + infraspecificEpithet)

Examples of `scientificNameAuthorship`:

- (Györfi, 1952)
- R. A. Graham
- (Martinovský) Tzvelev

Examples of `taxonRank`:

- order
- genus
- subspecies
- infraspecies

**Value**

A tibble with the requested columns added/reformatted.

**See Also**

[set\\_taxonomy\(\)](#) for taxonomic name information.

**Examples**

```
df <- tibble::tibble(  
  name = c("Crinia Signifera", "Crinia Signifera", "Litoria peronii"),  
  latitude = c(-35.27, -35.24, -35.83),  
  longitude = c(149.33, 149.34, 149.34),  
  eventDate = c("2010-10-14", "2010-10-14", "2010-10-14")  
)  
  
# Reformat columns to Darwin Core Standard terms  
df |>  
  set_scientific_name(  
    scientificName = name  
  )
```

---

set\_taxonomy

*Set, create or modify columns with taxonomic information*

---

**Description**

Format fields that contain taxonomic name information from kingdom to species, as well as the common/vernacular name, to a tibble using Darwin Core Standard.

In practice this is no different from using `mutate()`, but gives some informative errors, and serves as a useful lookup for accepted column names in the Darwin Core Standard.

**Usage**

```
set_taxonomy(  
  .df,  
  kingdom = NULL,  
  phylum = NULL,  
  class = NULL,  
  order = NULL,  
  family = NULL,  
  genus = NULL,  
  specificEpithet = NULL,  
  vernacularName = NULL,  
  .keep = "unused"  
)
```

**Arguments**

.df	A data.frame or tibble that the column should be appended to.
kingdom	The kingdom name of identified taxon.
phylum	The phylum name of identified taxon.
class	The class name of identified taxon.
order	The order name of identified taxon.
family	The family name of identified taxon.
genus	The genus name of the identified taxon.
specificEpithet	The name of the first species or species epithet of the scientificName. <a href="#">See documentation</a>
vernacularName	The common or vernacular name of the identified taxon.
.keep	Control which columns from .data are retained in the output. Note that unlike <code>dplyr::mutate()</code> , which defaults to "all" this defaults to "unused"; i.e. only keeps Darwin Core columns, and not those columns used to generate them.

**Details**

Examples of specificEpithet:

- If scientificName is *Abies concolor*, the specificEpithet is *concolor*.
- If scientificName is *Semisulcospira gottschei*, the specificEpithet is *gottschei*.

**Value**

A tibble with the requested columns added/reformatted.

**See Also**

[set\\_scientific\\_name\(\)](#) for adding scientificName and authorship information.

**Examples**

```
df <- tibble::tibble(
  scientificName = c("Crinia Signifera", "Crinia Signifera", "Litoria peronii"),
  fam = c("Myobatrachidae", "Myobatrachidae", "Hylidae"),
  ord = c("Anura", "Anura", "Anura"),
  latitude = c(-35.27, -35.24, -35.83),
  longitude = c(149.33, 149.34, 149.34),
  eventDate = c("2010-10-14", "2010-10-14", "2010-10-14")
)

# Reformat columns to Darwin Core terms
df |>
  set_scientific_name(
    scientificName = scientificName
  ) |>
```

```
set_taxonomy(  
  family = fam,  
  order = ord  
)
```

---

`suggest_workflow`*Suggest a workflow to make data comply with Darwin Core Standard*

---

## Description

Checks whether a `data.frame` or `tibble` conforms to Darwin Core Standard and suggests how to standardise a data frame that is not standardised to minimum Darwin Core requirements. This is intended as users' go-to function for figuring out how to get started standardising their data.

Output provides a summary to users about which column names match valid Darwin Core terms, the minimum required column names/terms (and which ones are missing), and a suggested workflow to add any missing terms.

## Usage

```
suggest_workflow(.df)
```

## Arguments

`.df` A `data.frame`/tibble against which checks should be run

## Value

Invisibly returns the input `data.frame`/tibble, but primarily called for the side-effect of running check functions on that input.

## Examples

```
df <- tibble::tibble(  
  scientificName = c("Callocephalon fimbriatum", "Eolophus roseicapilla"),  
  latitude = c(-35.310, "-35.273"), # deliberate error for demonstration purposes  
  longitude = c(149.125, 149.133),  
  eventDate = c("14-01-2023", "15-01-2023"),  
  status = c("present", "present")  
)  
  
# Summarise whether your data conforms to Darwin Core Standard.  
# See a suggested workflow to amend or add missing information.  
df |>  
  suggest_workflow()
```

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