

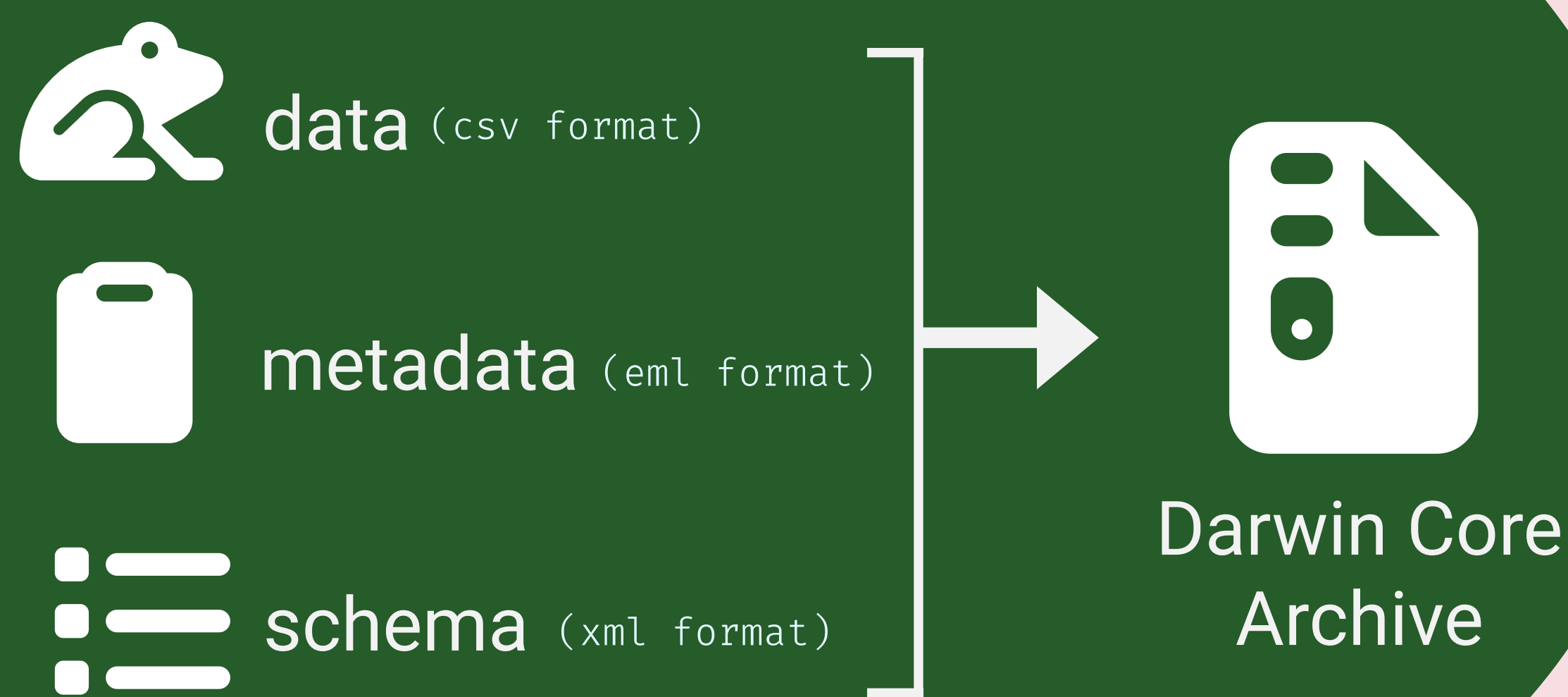


galaxias

An R and Python interface designed to simplify the process of converting biodiversity data into Darwin Core Archives, the accepted format to submit data to data infrastructures like the Atlas of Living Australia (ALA) or the Global Biodiversity Information Facility (GBIF).

Poster design by Dax Kellie

What's a Darwin Core Archive?



These formats are easy for machines to ingest, but difficult for a user to make

The Process

to bundle and share biodiversity data with galaxias



data



metadata



archive



validate



submit

Scan QR code to go to webpage



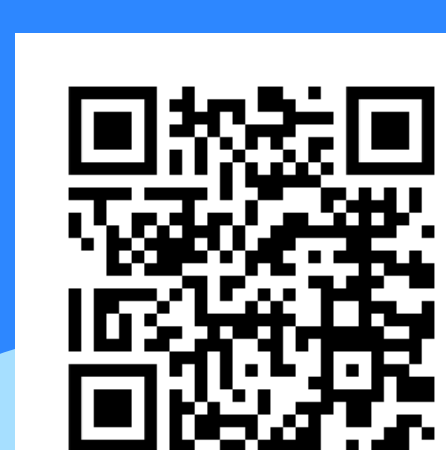
galaxias
website



ALA
blog post



Intro
video



Standardise data

```
library(galaxias)

my_data_dwc <- df >
  set_occurrences(occurrenceID = composite_id(location_id,
                                              sequential_id()),
                  basisOfRecord = "humanObservation") >
  set_coordinates(decimalLatitude = latitude,
                  decimalLongitude = longitude) >
  set_locality(country = "Australia",
               locality = "Canberra") >
  set_datetime(eventDate = lubridate::dmy(date)) >
  set_scientific_name(scientificName = species,
                     taxonRank = "species") >
  set_taxonomy(kingdom = "Animalia",
               family = "Cacatuidae")

use_data(my_data_dwc) # add data to directory
```



Write metadata

```
use_metadata_template("metadata.Rmd")
use_metadata("metadata.Rmd") # add metadata to directory
```



Package for sharing

```
# (auto-builds schema)
build_archive("my_dwca.zip") # convert to Darwin Core Archive
```



Quality check

```
check_directory() # local quality checks
check_archive("my_dwca.zip") # GBIF quality checks
```



Share

```
# open submission page
submit_archive()
```