

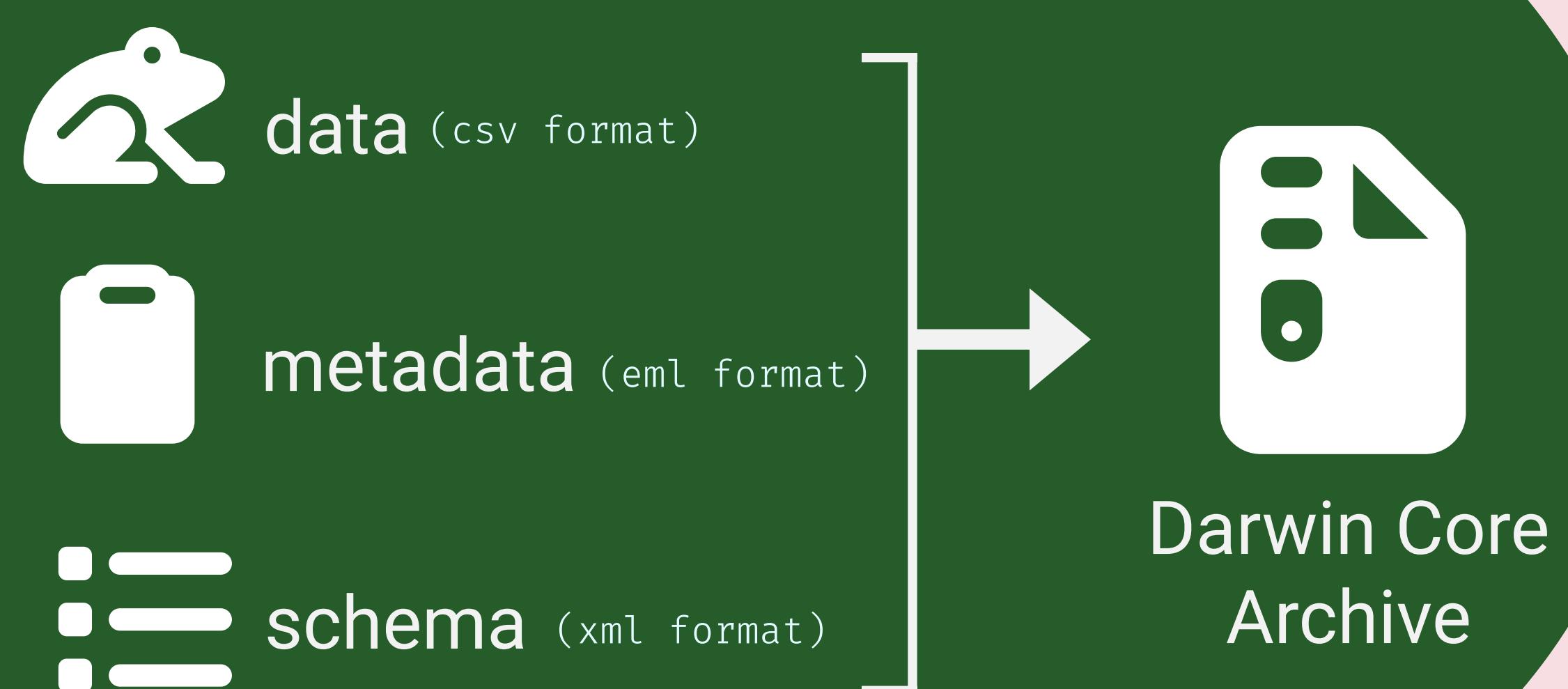


# galaxias

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



```
library(galaxias)
```

### Standardise data

```
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()
```

Scan QR code to go to webpage



galaxias  
website



ALA  
blog post



Intro  
video

