QUICK START GUIDE
Step by step instructions to run the analysis

INITIAL SETTINGS

1. Download R and RStudio

Ensure that you have R version 4.4.1 or higher installed on your computer. The necessary software for this analysis can be found at:

- *R*: https://cran.r-project.org/
- *RStudio*: https://posit.co/downloads/
- *Rtools*: https://cran.r-project.org/bin/windows/Rtools/rtools44/rtools.html

1.1 Open R project

On your computer, navigate to your working directory that contains the R project and initial files. Then, click on the R project named *KoalaModellingAnalysis.Rproj*.

RStudio will open and automatically load a script called 01-initial-script.R.

1.2 01-initial-script.R

The initial function will download the latest code from GitHub https://github.com/seq-koala-monitoring/stats-model/tree/main) and configure the working directory to ensure that the analyses run properly. You also need to provide an API code that allows R to download a few soil variables from TERN. Please, follow the steps below:

1. Navigate to https://geonetwork.tern.org.au/geonetwork/srv/eng/new.account
2. Create an account

We designed this project to give users flexibility to adjust parameters while still achieving reliable results. If you need to modify any spatial parameter from the default, adjust the arguments in the fcn_set_parameters function.

The parameters are:

- <u>primary_grid_size</u>: A numeric value representing the spatial dimensions (in metres) of each cell in the analysis and mapping grid. Default: *500*
- <u>secondary_grid_size</u>: A numeric value that multiplies the primary grid size to create a coarser grid. Default: *10*
- <u>line_transect_buffer</u>: A numeric value (in metres) for the estimated effective width of line transects (i.e., one side of the line transect). Default: *28.7*
- <u>cov_impute_buffer</u>: A numeric value (in metres) for the buffer around areas for covariate imputation. Default: *0*
- <u>area_buffer</u>: A numeric value (in metres) defining the buffer around the study area. Default: *0*
- <u>monitoring_units</u>: The filename (with extension and within quotation marks) of the spatial layer containing boundaries of monitoring units, such as previous genetic populations. Default: *Population_boundaries_v2.shp*
- <u>gen_pop_column_id</u>: A string (within quotation marks) specifying the column name that identifies each monitoring unit in the spatial layer. Default: *"GENPOP_ID"*
- <u>update_database</u>: Should the koala survey database be updated with new data? Default: TRUE

For example:

<u>Example 1)</u>

Modify the primary grid size from 500m to 250m

fcn_set_parameters(primary_grid_size = 250)

<u>Example 2)</u>

Modify the primary grid size from 500m to 250m AND the shapefile containing the boundaries of monitoring units

fcn_set_parameters(primary_grid_size = 250, monitoring_units = "new_monit_units.shp")

Lastly, you will be redirected to a new tab with a file named *covariate_processing.R*. This file will gather all the covariates needed for the Bayesian state-space model that estimates densities of koalas across South East Queensland.

COVARIATES AND KOALA SURVEY DATA

2. Download covariates

The R script *covariate_processing.R* opened in the last step was designed to update the covariates required for the Bayesian state-space model used to estimate koala densities across Southeast Queensland.

The basic workflow involves checking if the input folder already has the latest covariate file. If it doesn't, the code will automatically download, process, and save the most recent file the correct location.

Before anything, start fresh by clicking Session > Restart R. After that, please, select all lines by pressing Ctrl + A on a Windows PC or Command + A on a Mac. Then, run these lines by pressing Ctrl + Enter on a Windows PC or Command + Return on a Mac. Alternatively, you can click on Source near the top right corner of the script panel. This code may take anywhere from a few minutes to days to run, depending on how many files need updating and your computer's specifications.

When you see "THIS CODE HAS FINISHED" in the Console panel (usually at the bottom left), you're ready to start processing these covariates. You will be automatically redirected to a new tab with a file named *data_processing.R*. This file prepare all the data for the Bayesian state-space model

NOTE:

1) Disregard any warnings on the task bar about packages that are not installed

3. Update survey database and process data for modelling

The R script *data_processing.R*, opened in the previous step, is designed to process all covariate data related to the survey data. It also formats the data appropriately for the Bayesian state-space model used to estimate koala densities in Southeast Queensland.

The basic workflow involves three main steps:

- Updating the koala survey database
- Extracting covariate values for the transects in the koala survey database

- Preparing the data for the modelling phase

Before anything, make sure that the table *group_observers_lookup.csv*, originally found in *input > group_observers*, is up to date. It is important to keep the date format as dd/mm/yyyy and always save it as a csv. Note that the *group_observers* column is only for tracking changes and is not used in the analysis.

In RStudio, start fresh by clicking Session > Restart R. After that, please, select all lines by pressing Ctrl + A on a Windows PC or Command + A on a Mac. Then, run these lines by pressing Ctrl + Enter on a Windows PC or Command + Return on a Mac. Alternatively, you can click on Source near the top right corner of the script panel.

When you see "THIS CODE HAS FINISHED" in the Console panel (usually at the bottom left), you're ready to the modelling stage. You will be automatically redirected to a new tab with a file named *model_runs.R*. This file will perform the Bayesian state-space models.

NOTE:

1) Disregard any warnings on the task bar about packages that are not installed

2) This code may take anywhere from a few minutes to days to run, depending on how many files need updating and your computer's specifications.