Instructions for replicating the Bayesian GLMM for the 2022 analysis of covariates associated with the illegal killing of elephants (PIKE)

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Users will need to have R statistical software, as well as RStudio installed and will need to install all the R packages that are loaded by the main R script – that is all the packages called by "library(packagename)" This can be done with the install.packages("packagename") command in R

1. First, create a new folder on your PC in which you will store the data file, the R script to run the analysis, and the model results file.
2. Open RStudio and go to Project, New Project, Existing directory…
3. Then navigate to and select the folder you created in step 1.
4. Open this new RStudio project (if not open already).
5. Open the script entitled "PIKE GLMM all.R" (via RStudio) which has the code for running the actual analysis. Note the user will first have to install the Bayesian analysis software JAGS on their computer, and then install the package R2Jags to allow R and JAGS to work together (see instructions below).
6. Run each line of this script "PIKE GLMM all.R" until the line that saves the model results. Note the model can take 20 minutes to a few hours to run depending on your computer's power.
7. The model results will be saved in the working directory.

Summarise model output and check model convergence and fit

8. In the same "PIKE GLMM all.R" script, there are lines of script (see # titles) to run the following using the model results produced earlier in the script:
    a. Create the Figure showing the 90% credibility interval for each of the covariates.
    b. Create a table of model results including the Gelman-Rubin convergence diagnostic.
    c. Produce MCMC trace plots to help confirm chain mixing and convergence.
    d. Calculate model fit (Bayesian p-value)

Instruction to install JAGS to work with R

1. If necessary, Download and install R and potentially a user interface to R like R Studio (see here for tips on getting started with R).
2. Download and install JAGS as per operating system requirements.
3. Install additional R packages: e.g., in R type: install.packages("R2jags")
9. (This last step is already in the s "PIKE GLMM all.R" script above).

Running supplementary models

The "PIKE GLMM all.R" script includes #NOTES that indicate how to exclude and include certain variables in the analysis by removing or adding "#" before variable names.