# Workshop 12: Occupancy models

This workshop will introduce basic single-season occupancy models (single and multi-species). If you have not already installed `JAGS`, you can download it here. You'll also need to install and load the `rjags` and `R2jags` libaries.

Download the data and all scripts here.

## Single-species, single-season

Let's start off by analyzing the data presented in lecture, but for a different species, the White-ruffed Manakin, *Corapipo altera*.

1. Open the file `single-species.R`. This file loads the data and, once filled in, will run a single-species, single-season occupancy model. Once you have loaded the data, you will have a multidimensional array, `X`, in your work-space. This array contains occurrence data for 308 species of birds across 44 sites, 3 visits to each. Subset `X` to view the occurrence data for just the White-ruffed Manakin, *Corapipo altera* (species code `wrma`).

2. Package up the data for the White-ruffed Manakin, so that it is appropriate for the model, as currently formulated. Run the model and plot the posterior distribution for both `psi` and `p` (the code to plot these is also there).

3. Modify the model to instead use normal priors for both `psi` and `p`. You will need to add a logit link function in order to ensure that these values remain between 0 and 1. Do the posteriors for `psi` and `p` look different when you do this?

4. In the workspace, you should have a vector `forest`. This specifies the type of site (`1` =forest, `0` =agriculture). Modify the model so that `forest` is now a predictor on the occurrence component of the model. Is there any evidence that White-ruffed Manakin occurrence is higher/lower in forests?

5. Repeat the above analysis for the species we examined in class, the Boat-billed Flycatcher, *Megarynchus pitangua* (species code `bbfl`).

# Multi-species, single-season

Next, we will analyze all of the species in one multi-species model.

1. Open the file `multi-species.R`. Run the analysis and generate the posteriors for both the White-ruffed Manakin and the Boat-billed Flycatcher. Are the trends generally consistent with what you saw in the single-species runs?

2. You should have a `sp.uniq` vector in your work-space. This codes for each species' evolutionary uniqueness. Modify this model so that the equation for occurrence now includes a species' evolutionary uniqueness as a predictor. Does a species' evolutionary uniqueness affect its overall rate occurrence?

3. As before, you should have a `forest` vector in your work-space. Include `forest` as a predictor on occurrence and interpret the model output.

4. Finally, add an interaction between `sp.uniq` and `forest` to your model. Interpret the model output. What is the biological meaning of this interaction?

Note: We could also include any of these predictors in the detectability component of our model. We haven't done that here, but for your own analyses, it important to think about the variables that might affect your rates of detection.