# Bayesian Model

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## 1 Bayesian Generalized Linear Model

### 1.1 Not Hierarchical Statistical Model

We want to fit a model to our data, where the occurence of the species ($y_{i,j}$) for site $i$ in projected area $j$ is modeled as,

$$\begin{aligned} y_{i,j} \sim & \text{Bernoulli}(p_{i,j}) \\ \text{logit}(p_{i,j}) = & \beta_0 + \beta_1 \times \text{dist.human}_{i,j} \end{aligned}$$

#### 1.1.1 Priors

$$\begin{aligned} \beta_0 \sim & \text{Logistic}(0, 1) \\ \beta_1 \sim & \text{Logistic}(0, 1) \end{aligned}$$

#### 1.1.2 Alternative Priors

$$\begin{aligned} \beta_0 \sim & \text{Normal}(\mu = 0, \sigma = 1.5) \\ \beta_1 \sim & \text{Normal}(\mu = 0, \sigma = 1.5) \end{aligned}$$

### 1.2 JAGS syntax for this model

```
model {

# Priors
  b0 ~ dlogis(0,1)
  b1 ~ dlogis(0,1)

#Alternative priors on the logit scale
#Note that JAGS parameters for the Normal distribution
#are mu (mean) and the precision, which is
#the inverse of the variance,
#i.e., tau = 1/sigma^2
  b0 ~ dnorm(0,1/1.5^2)
  b1 ~ dnorm(0,1/1.5^2)

# Likelihood
  for (i in 1:N) {
     y[i] ~ dbern(p[i])
     logit(p[i]) <- b0 + b1*dist.human[i]
  } #End loop

} #End Model
```