HW5

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Question 1

A) Install packages

```
# install.packages(c("rstan","rstanarm","shinystan"))
```

B)

Forum: Identifiability across levels in occupancy model

(https://discourse.mc-stan.org/t/identifiability-across-levels-in-occupancy-model/5340)

I will be using occupancy models at the species level with covariates. I can use this data to teach my model probabilty of detection and probability of site occupied to then extrapolate into the future and estimate the effects habitat disturbances have on reptile species.

Question 2

Choice 1: Dall et al. 2005: "Information and its use by animals in evolutionary ecology"

Are foraging animals Bayesians? Why or why not?

I believe foraging animals are Bayesians. They are using prior information to reduce the cost and increase success. There is a genetic and physiological disposition that animals have to guide them to certain foraging areas; however, over time they learn through personal experience (trail and error) and social experience (observing others). Reptiles are solitary yet social animals in that they do not implment child reering or rely on each other for survival, but they also do not live completely in solitary (hibernaculum and basking locations are shared among and cross species). The neonatal rattlesnakes do not depend on parents retrieving their first meal; however, they stick around and observe foraging locations. Reptiles are highly philopatric, making their way to the same summer foraging area every year and return to the same hibernacula eah year. Determining a least-cost paths to not waste energy on the first forgaging of the season is important for survival. Also, ensuring a last meal before returning to the hibernacula. They gain information socially and personally to increase probabiltiy of survival.

Question 3: Probability of land on Earth

```
# P(H|D) = P(D|H) * P(H) / P(D)
prob_earth <-  0.3  # P(pixel from Earth that is land) = 0.30
prob_mars <-  1 # P(pixel from Mars that is land) = 1.0
prob_earth_mars <-  0.5 # P(pixel is from Earth or Mars) = 0.5
postprob_earth_land <-  0.23 # given posterior probability that pixel is from Earth
```

```
prob_pixel <-  (prob_earth * prob_earth_mars) + (prob_mars * prob_earth_mars)
# P(pixel is from Earth or Mars given priors) =
  # P(land pixel is Earth) * P(land pixel is from Earth or Mars) +
  # P(land pixel is from Mars) * P(land pixel is from Earth or Mars)
prob_pixel
```

```
## [1] 0.65
```

```
prob_pixel_earth <-  prob_earth * prob_pixel
#P(pixel is from Earth given priors)
prob_pixel_earth
```

```
## [1] 0.195
```

```
prob_pixel_land <-  prob_earth * prob_pixel / postprob_earth_land
# P(pixel is from Earth given posterior probability = 0.23)
prob_pixel_land
```

```
## [1] 0.8478261
```

There is a 84.7% probability that a pixel selected randomly fro either plant will be "land".

Question 4: Panda Mama

What is the probability that her next birth will also be twins?

```
p_sppA_twins <- 0.1  # P(species A producing twins)
p_sppB_twins <- 0.2  # P(species B producing twins)
p_sppA_sppB <- 0.5  # P(being either species A or B)
# P(two twin births in a row) =
  #posterior probability of twins for species A + posterior probability of twins for species B

# probability of twins at a single point of time (without prior knowledge)
p_twins <- (p_sppA_twins * p_sppA_sppB + p_sppB_twins * p_sppA_sppB)

# posterior probability of twins for species A =
  # (P(species A producing twins) * prior) / P(twins at a single point of time)
postp_twins_A <- (p_sppA_twins * p_sppA_sppB)/(p_twins)

# posterior probability of twins for species B =
  # (P(species B producing twins) * prior) / P(twins at a single point of time)
postp_twins_B <- (p_sppB_twins * p_sppA_sppB)/(p_twins)
# P(two twin births in a row)
p_two_twins <- (postp_twins_A * p_sppA_twins) + (postp_twins_B * p_sppB_twins)
p_two_twins
```

```
## [1] 0.1666667
```

A) Compute the probability that the panda we have is from species A, assuming we have only observed the first birth and that it was twins.

```
postp_twins_A
```

```
## [1] 0.3333333
```

B) Suppose the same panda mother has a second birth and that it is not twins, but a singleton infant. Compute the posterior probability that this panda is species A.

```
p_sppA_singleton <- 1 - p_sppA_twins # P(species A produce singleton)
p_sppB_singleton <- 1 - p_sppB_twins # P(species B produce singleton)

# P(first giving birth to twins, then to a singleton) in general
p_singleton <- (p_sppA_twins * p_sppA_singleton * p_sppA_sppB) +
  (p_sppB_twins * p_sppB_singleton * p_sppA_sppB)
p_singleton
```

```
## [1] 0.125
```

```
p_TS_sppA <- p_sppA_twins * p_sppA_singleton # P(species A produce twins then a singleton)
p_TS_sppA
```

```
## [1] 0.09
```

```
post_p_sppA <- (p_TS_sppA * p_sppA_sppB) / p_singleton
post_p_sppA
```

```
## [1] 0.36
```

The posterior probability that the mother is species A beecause she gave birth to twins then a singleton is 36%

C) A genetic test claims to identify the species of our mother panda. Compute the posterior probability that your panda is species A.

```
p_ID_T_sppA <- 0.8 # P(identifying correctly sppA as sppA)
p_ID_T_sppB <- 0.65 # P(identifying correctly sppB as sppB)
p_ID_F_sppA <- 0.2 # P(misidentifying  sppB as sppA)
p_ID_F_sppB <- 0.35 # P(misidentifying  sppA as sppB)
p_test_sppA <- (p_ID_T_sppA * p_sppA_sppB) + (p_ID_F_sppB * p_sppA_sppB)
# P(identifying sppA correctly and misidentifying sppB)
post_p_test_sppA <- (p_ID_T_sppA * p_sppA_sppB) / p_test_sppA
post_p_test_sppA
```

```
## [1] 0.6956522
```

The posterior probability that the panda mother is species A is 69.6%, this based on the genetic testing correctly identifying sppA

C.2) Compute the posterior probability that your panda is species A based on the gentic testing and the birthing information.

```
p_ID_T_sppA # P(identifying correctly sppA as sppA)
```

```
## [1] 0.8
```

```
post_p_sppA
```

```
## [1] 0.36
```

```r
# posterior probability that the mother is sppA given the birthing information
p_sppA_test_births <- (p_ID_T_sppA * post_p_sppA) + (p_ID_F_sppB * (1 - post_p_sppA))
# P(identifying sppA as sppA based on genetic testing and birthing information)
post_p_sppA_TB <- (p_ID_T_sppA * post_p_sppA) / p_sppA_test_births
post_p_sppA_TB
```

```
## [1] 0.5625
```

The posterior probability that the panda mother is species is A is 56.3%, this is based on the genetic testing and the prior birthing information.