Week 3 in-class exercise

Suppose there are two species of panda bear. Both are equally common in the wild and live in the same places. They look exactly alike and eat the same food, and there is yet no genetic assay capable of telling them apart. They differ however in their family sizes. Species A gives birth to twins 10% of the time, otherwise birthing a single infant. Species B births twins 20% of the time, otherwise birthing singleton infants. Assume these numbers are known with certainty, from many years of field research. Now suppose you are managing a captive panda breeding program. You have a new female panda of unknown species, and she has just given birth to twins.

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

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

3) 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.

A common boast of Bayesian statisticians is that Bayesian inference makes it easy to use all of the data, even if the data are of different types. So suppose now that a veterinarian comes along who has a new genetic test that she claims can identify the species of our mother panda. But the test, like all tests, is imperfect. This is the information you have about the test:

The probability it correctly identifies a species A panda is 0.8.
The probability it correctly identifies a species B panda is 0.65.

The vet administers the test to your panda and tells you that the test is positive for species A.
4) First ignore your previous information from the births and compute the posterior probability that your panda is species A.

5) Then redo your calculation, now using the birth data as well.

Homework

Prepare a document with your answers and the R code you used to solve all 4 problems.