

9.3 Multiple Coins From Multiple Mints

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2023-06-20

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9.3.1 Independent Mints

American coins can usually be identified with which mint they came from. For example, recent 1-cent coins minted in Denver have a “D” under the year on their obverse (“head”) side. Suppose we want to estimate the mint parameters μ_m of the different mints. We will assume that the two mints’ parameters are independent of each other, and estimate them separately from each other.

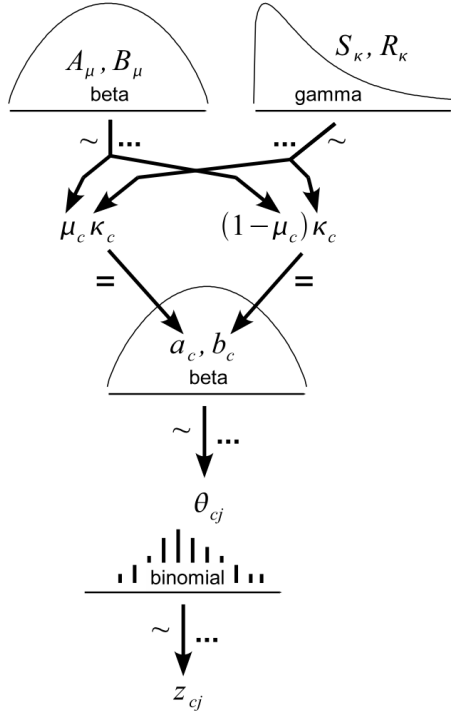


Figure 9.15: Hierarchical diagram for model of data from the filtration-condensation experiment, with program in Section 9.5.2 (FilconBrugs.R). This diagram is much like Figure 9.7, except for two changes. First, the distribution at the bottom of the hierarchy is binomial instead of Bernoulli, because the data are sums across trials instead of individual trials. Second, the estimated parameters all have a subscript c that denotes the condition from which the data were drawn. In other words, this structure is copied separately for each condition.

This situation arises in real research quite regularly. For example, give each participant a 20-item test, and mark the answers correct or wrong, so each subject has a score in the range 0–20. Randomly assign the subjects to one of two conditions for taking the test: noisy environment and quiet environment. We would like to know whether the noise/quiet affected test performance, so we compare the estimates of μ_{noise} and μ_{quiet} .

```
for ( condIdx in 1:nCond ) {
  a[condIdx] <- mu[condIdx] * kappa[condIdx]
```

```

    b[condIdx] <- (1-mu[condIdx]) * kappa[condIdx]
    # Hyperprior on mu and kappa:
    mu[condIdx] ~dbeta( Amu , Bmu )
    kappa[condIdx] ~dgamma( Skappa , Rkappa )
  }
# Constants for hyperprior:
Amu <- 1
Bmu <- 1
Skappa <- pow(meanGamma,2)/pow(sdGamma,2)
Rkappa <- meanGamma/pow(sdGamma,2)
meanGamma <- 10
sdGamma <- 10
}

```

The model specification uses nested indexing (as we’ve seen in a previous section) in line 16, which says that the underlying propensity θ for an individual subject is distributed as a beta distribution that has shape parameters `a[cond[subjIdx]]` and `b[cond[subjIdx]]` specific to the condition of the that subject.

The BUGS model uses a binomial likelihood distribution for total correct, instead of using the Bernoulli distribution for individual trials.

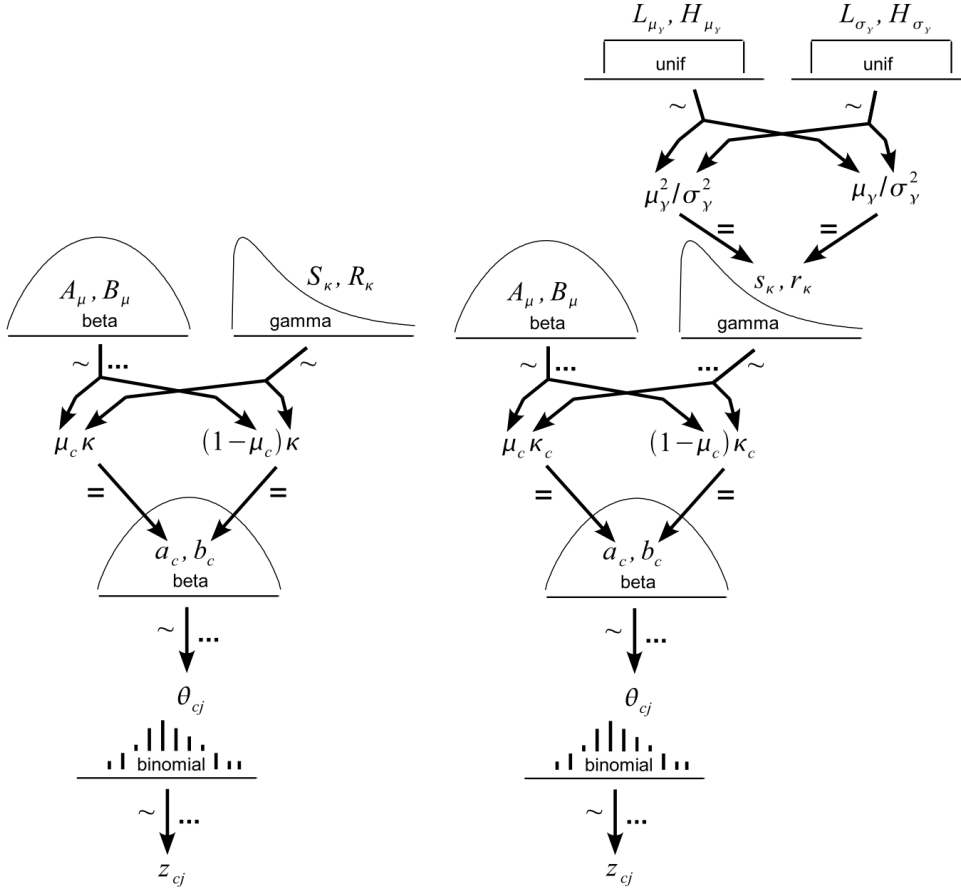
Although BUGS specifies the binomial density as `dbi`, R specifies it as `dbinom`.) This use of the binomial is just a convenience for shortening the program. If the data were specified as trial-by-trial outcomes instead of as total correct, then the model could include a trial-by-trial loop and use a Bernoulli likelihood function.

9.3.2 Dependent Mints

In some experimental designs, we might assume that the different treatment conditions are totally independent of each other.

In the context of minting coins, this is assuming that the parameter values of one mint are completely disconnected from the parameter values of another mint. This assumption of total disconnection was used to analyze the data from the filtration-condensation experiment in the previous section.

On the other hand, we could treat the mint parameters as being mutually informative, perhaps because the same governmental agency oversees the creation of all the mints.



We can consider again the filtration-condensation experiment. In the previous section’s analysis, we estimated each condition’s parameters completely separately from the other conditions. But this assumption of complete informational insulation between conditions might be losing some useful information. In particular, consider the κ_c parameters, which indicate how tightly the individual subjects’ accuracies cluster around the group average μ_c .

9.3.3 Individual Differences and Meta-Analysis

In experiments with human participants, one of the striking results is vast variation between people. Seat ten people at a simple response-time task, and you will get ten different mean response times.

These various results across people are referred to as **individual differences**. We could estimate parameters for each individual completely insulated from estimates of other individuals. Alternatively, we could believe that the individual results are all taken from a common overarching distribution, because all the individuals were of the same species. We could specify the dependence of individual performance parameters on the overarching distribution, and then our estimates of the individual parameters would be influenced by results from other individuals, via the co-dependence on the hyperparameter.

Hierarchical models can also be used for **meta-analysis**. The idea is that different replications of an experiment are independent representatives of an overarching distribution of effect magnitudes. Each experiment’s data informs a posterior distribution regarding its own first-level parameters, but the other experiments’ data also influence the estimates because of their dependency on the overarching parameter.