STAT 447 Assignment 6

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Question 1: Efficacy of Vaccines

In this exercise we will model the effectiveness of COVID vaccines using clinical trials data. Each trial consists of two arms: vaccinated (i.e., treated) and control (i.e., not treated). For a typical trial we know

- The total number of patients in each arm: t_v (vaccinated), t_c (control).
- The number of patients that got infected with the SARS-CoV-2 virus in each arm: n_v and n_c.

We model n_v and n_c as Binomial random variables. The unknown parameter for these distributions will depend on two numbers in $[0, 1]$

The first is Incidence (denoted p): the probability that a patient in the trial will become infected without being treated with the vaccine.

The second is Effectiveness (denoted e) the decrease in incidence that the vaccine provides.

We will take betaMP(μ, λ) distributions rather than beta(α, β). In this instance $\mu \in [0, 1]$ is the *mean* and $\lambda > 0$ is a *precision* parameter.

The following bijection holds regarding these parameters:

$$\mu = \frac{\alpha}{\alpha + \beta}, \text{ and } \lambda = \alpha + \beta \iff \alpha = \mu\lambda, \text{ and } \beta = (1 - \mu)\lambda$$

There are a few priors in this experiment.

Firstly, we have the Mean and Precision Priors of Effectiveness, given by a Uniform and Exponential distribution, respectively:

$$\mu_e \sim \text{unif}(0, 1), \text{ and } \lambda_e \sim \exp(0.001)$$

This gives us the Effectiveness, as a Likelihood given these Beta Parameters.

$$\big(e \mid \{\mu_e, \lambda_e\}\big) \sim \text{betaMP}(\mu_e, \lambda_e)$$

We then arrive at the number of infected inoculated individuals n_v, which arises as a function of the total number of individuals (the known value t_v), the incidence p (whose formulation will be discussed next) and e (discussed above).

$$\big(n_\text{v} \mid \{e, p\}\big) \sim \text{binom}(t_\text{v}, p(1 - e))$$

Now, we discuss the Bayesian framework for *all* individuals overall (i.e. "Incidence.")

We have mean incidence and precision assigned priors as follows:

$$\mu_\text{p} \sim \text{betaMP}(0.1, 10), \text{ and } \lambda_\text{p} \sim \exp(0.001)$$

Similarly, we have the likelihood for incidence given these parameters:

$$\big(p \mid \{\mu_{\mathrm{p}}, \lambda_{\mathrm{p}}\}\big) \sim \mathrm{betaMP}(\mu_{\mathrm{p}}, \lambda_{\mathrm{p}})$$

Then, the number of infections in the control group:

$$\big(n_{\mathrm{c}} \mid p\big) \sim \mathrm{binom}(t_{\mathrm{c}}, p)$$

Part 1

Expand the model in Equation 1 into a hierarchical model that covers both vaccines. The parameters $\{\mu_{\mathrm{e}}, \lambda_{\mathrm{e}}, \mu_{\mathrm{p}}, \lambda_{\mathrm{p}}\}$ must be shared across vaccines.

In contrast, each vaccine must have its own (e, p) pair.

First, we note the hyper-parameter choice for each of these variables. For uniform μ_{e}, we declared parameters $\{a_{\mathrm{e}}, b_{\mathrm{e}}\}$ as $\{0, 1\}$. Similarly, we declared λ_{e} and λ_{p} as exponential random variables with parameters $\ell_{\mathrm{e}} = \ell_{\mathrm{p}} = 0.001$. Finally we declared μ_{p} as a Beta MP random variable with parameters $\{\vartheta_{\mathrm{p}}, s_{\mathrm{p}}\}$ as $\{0.1, 10\}$. We include these hyper-parameters as constants in our Graphical model, to reflect the fact that these choices were made by us, the designers, and could be changed.

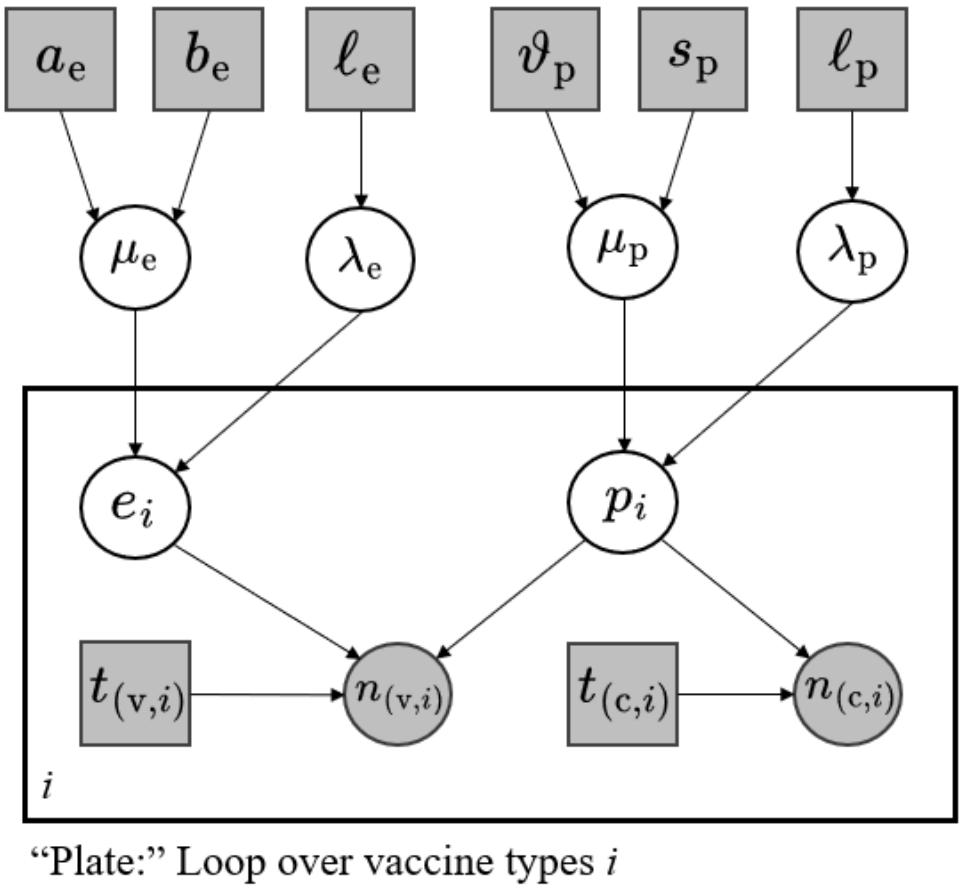

Figure 1: Graph Model of Vaccine Hierarchy

Part 2

Now, with this framework presented, we will inspect the data before implementing Hierarchical Model to describe the setting.

```
df = present = read.csv("vaccines.csv")
colnames(present) = c("Trials", "Arms", "Group Sizes", "Number of Cases")
kable(present)
```

Trials	Arms	Group Sizes	Number of Cases
Pfizer-BioNTech	vaccinated	18198	8
Pfizer-BioNTech	control	18325	162
Moderna-NIH	vaccinated	14134	11
Moderna-NIH	control	14073	185

We need to do a `simPPLe` implementation for this, too. The PPL function should return the indicator that Moderna is more effective than Pfizer. We include a hidden code cell that defines the `BetaMP` Distribution.