# Notes on Bayesian Analysis of Difference in Prevalence 

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## Introduction

The aim of this work is to extend the theory developed in BayesianPrevalence.pdf to the situation where two prevalences are being compared by using the difference in prevalence. We consider two different experimental designs:

Case 1: A test procedure is applied with two distinct groups of units and the difference in prevalence between the two groups is estimated by using Bayesian posterior inference;

Case 2: Two different test procedures are applied with a single group of units and the difference is prevalence between the two tests is estimated by using Bayesian posterior inference.

## Case 1

Within each of the two distinct populations, the units are of two types: a unit either does or does not possess a definable effect. In population 1, a proportion, $\gamma_{1}$ possess the definable effect, while the proportion of this population which do not possess this effect is $1-\gamma_{1}$. Similarly, in population 2 a proportion, $\gamma_{2}$, possess a definable effect, while the proportion of this population which do not possess this effect is $1-\gamma_{2}$.

A random sample of $n_{i}$ units is selected from the $i$ th population $(i=1,2)$ and each unit undergoes a test procedure, in which the presence of the defined effect is investigated using a significance test. It is assumed that for each unit the significance level for the $i$ th test is $a_{i}$ (1specificity), or false positive rate, and the power, or sensitivity, of the $i$ th test is $b_{i}\left(0<a_{i}<b_{i} \leq 1\right)$. Thus, for the $i$ th test, the probability that a randomly selected unit from the population who does not possess the defined effect will produce a significant result is $a_{i}$, whereas the probability that a randomly selected unit from the population who does possess the defined effect will produce a significant result is $b_{i}$.

A binary variable - shows a significant effect or does not show a significant effect - is recorded for each unit in each of the samples and we suppose that the total number of units who show a significant effect, out of the $n_{i}$ tested, is $k_{i,}(i=1,2)$. Let $\theta_{i}$ be the probability that a randomly selected unit from the $i$ th population would show a significant effect. Then

$$
\begin{equation*}
\theta_{i}=\left(1-\gamma_{i}\right) a_{i}+\gamma_{i} b_{i}=a_{i}+\left(b_{i}-a_{i}\right) \gamma_{i}, \quad(i=1,2) \tag{1}
\end{equation*}
$$

We will develop the modelling in terms of the parameters $\theta_{1}, \theta_{2}$, and later use (1) to find appropriate results in terms of the prevalence difference, $\gamma_{1}-\gamma_{2}$.

In designed studies, the aim would be to set the levels of sensitivity and specificity to be equal for both tests, i.e. $a_{1}=a_{2} \equiv a$ and $b_{1}=b_{2} \equiv b$. Otherwise the comparison of the prevalences would be biased, a priori. The general situation where specificity and sensitivity, respectively, are not assumed to be equal for both tests will be described in the sequel.

## Modelling

For each of the tests, we assume that the test results on the performance of the units are independent and that the parameter $\theta_{i}$ is the same for all units who undertake the test. Let the random variable $X_{i}$ denote the number of units out of the $n_{i}$ tested which show a significant effect at significance level $a$. Then $X_{i}$ follows a binomial distribution and

$$
\begin{equation*}
\operatorname{Pr}\left(X_{i}=k_{i} \mid \theta_{i}\right)=\binom{n_{i}}{k_{i}} \theta_{i}^{k_{i}}\left(1-\theta_{i}\right)^{n_{i}-k_{i}}, \quad k_{i}=0,1, \ldots, n_{i}, \quad\left(0<\theta_{i}<1, i=1,2\right) . \tag{2}
\end{equation*}
$$

Also $X_{1}$ and $X_{2}$ are independent given $\theta_{1}, \theta_{2}$.
We now define prior distributions to characterise the prior uncertainty about the $\theta_{i}$. First, we note that under the uncontroversial assumption that $b_{i}>a_{i}$ for the $i$ th test, we find from (1) that $\theta_{i}>a_{i}$. Also, since $\gamma_{i}<1$, we find that $\theta_{i}<b_{i}$. The claim regarding the assumption that $b_{i}>a_{i}$ is perfectly reasonable since it would make no sense to employ a test procedure for which the power is less than the significance level. It follows that $a_{1}<\theta_{1}<b_{1}$ and $a_{2}<\theta_{2}<b_{2}$

The conjugate prior for $\theta_{i}$ is the beta distribution so, bearing in mind the constraint on $\theta_{i}$, we assume that the prior distribution for $\theta_{i}$ is the following truncated beta distribution with probability density function

$$
\begin{equation*}
p\left(\theta_{i} \mid r_{i}, s_{i}\right)=\frac{1}{B\left(r_{i}, s_{i}\right)} \frac{\theta_{i}^{r_{i}-1}\left(1-\theta_{i}\right)^{s_{i}-1}}{\left[F\left(b ; r_{i}, s_{i}\right)-F\left(a ; r_{i}, s_{i}\right)\right]}, \quad a_{i}<\theta_{i}<b_{i}, \quad\left(r_{i}>0, s_{i}>0, i=1,2\right), \tag{3}
\end{equation*}
$$

where $F\left(x ; r_{i}, s_{i}\right)$ is the cumulative distribution function (cdf) of $\theta_{i}$.
The selection of values for the parameters $r_{i}, s_{i}$ depends on prior information about $\theta_{i}$. In the absence of any prior information about $\theta_{i}$ we will use the choice $r_{i}=1, s_{i}=1$ in practical applications, while keeping the notation general in the formulation. This corresponds to the a priori assumption that the prior uncertainty regarding $\theta_{i}$ can be represented by a uniform distribution on the interval $\left(a_{i}, b_{i}\right),(i=1,2)$. We also assume a priori that $\theta_{1}$ and $\theta_{2}$ are independent. Given the conditional independence of $X_{1}$ and $X_{2}$, given $\theta_{1}, \theta_{2}$, this means that $\theta_{1}$ and $\theta_{2}$ are independent a posteriori given the binomial data from the test results. This means that the posterior distribution of $\left(\theta_{1}, \theta_{2}\right)$ given the binomial data factorises into a product of two truncated beta distributions.

Defining $m_{i 1} \equiv k_{i}+r_{i}, m_{i 2} \equiv n_{i}-k_{i}+s_{i}(i=1,2)$, the posterior distribution for $\left(\theta_{1}, \theta_{2}\right)$ given the binomial data is
$p\left(\theta_{1}, \theta_{2} \mid k_{1}, k_{2}, r_{1}, r_{2}, s_{1}, s_{2}\right)=C \theta_{1}^{m_{11}-1}\left(1-\theta_{1}\right)^{m_{12}-1} \theta_{2}^{m_{21}-1}\left(1-\theta_{2}\right)^{m_{22}-1}, \quad a_{1}<\theta_{1}<b_{1}, a_{2}<\theta_{2}<b_{2}$,
where

$$
\begin{equation*}
C=\frac{1}{\operatorname{Beta}\left(m_{11}, m_{12}\right)\left[F\left(b ; m_{11}, m_{12}\right)-F\left(a ; m_{11}, m_{12}\right)\right] \operatorname{Beta}\left(m_{21}, m_{22}\right)\left[F\left(b ; m_{21}, m_{22}\right)-F\left(a ; m_{21}, m_{22}\right)\right]} \tag{4}
\end{equation*}
$$

and $F(x ; \lambda, \mu)$ is the $c d f$ of a Beta distribution having parameters $\lambda, \mu$.

## Posterior density of prevalence difference by simulation

We wish to compute a HPD interval for the difference between the probabilities of a significant result in the two tests, $\theta_{1}-\theta_{2}$ and then convert it into a corresponding HPD interval for the prevalence difference,

$$
\begin{equation*}
\gamma_{1}-\gamma_{2}=\frac{\theta_{1}-a_{1}}{b_{1}-a_{1}}-\frac{\theta_{2}-a_{2}}{b_{2}-a_{2}}, \tag{5}
\end{equation*}
$$

making use of (1). Since the posterior distributions of $\theta_{1}$ and $\theta_{2}$ are independent, we can draw values from truncated beta distributions independently for $\theta_{1}$ and for $\theta_{2}$.

How can we make a random draw from a truncated distribution? The following procedure achieves this:

- First, draw a random number from the uniform distribution on the interval

$$
\left[F\left(a_{1} ; m_{11}, m_{12}\right), F\left(b_{1} ; m_{11}, m_{12}\right)\right]
$$

- Second, apply the inverse cdf method to find the corresponding random number which follows the Beta $\left(m_{11}, m_{12}\right)$ distribution, truncated by $a_{1}<\theta_{1}<b_{1}$. This gives the first simulated value for $\theta_{1}$. Repeat these steps for the required number of times.

Similarly, simulated values of $\theta_{2}$ are obtained as follows:

- First, draw a random number from the uniform distribution on the interval

$$
\left[F\left(a_{2} ; m_{21}, m_{22}\right), F\left(b_{2} ; m_{21}, m_{22}\right)\right]
$$

- Second, apply the inverse cdf method to find the corresponding random number which follows the Beta $\left(m_{21}, m_{22}\right)$ distribution, truncated by $a_{2}<\theta_{2}<b_{2}$. This gives the first simulated value for $\theta_{2}$. Repeat these steps for the required number of times.

The simulated values of the prevalence difference, $\gamma_{1}-\gamma_{2}$ are then available from (5) for each simulated pair $\left(\theta_{1}, \theta_{2}\right)$.

## Case II

In this case, two different test procedures are applied to a sample of $n$ units. Within the population of units there is a prevalence $\gamma_{1}$ in relation to Test 1 and a prevalence $\gamma_{2}$ in relation to Test 2. Let $\theta_{i}$ be the probability that a randomly selected unit from the population will show a significant result on the $i$ th test $(i=1,2)$ Then

$$
\begin{equation*}
\theta_{i}=\left(1-\gamma_{i}\right) a_{i}+\gamma_{i} b_{i}=a_{i}+\left(b_{i}-a_{i}\right) \gamma_{i}, \quad(i=1,2) . \tag{6}
\end{equation*}
$$

## Modelling

Each unit provides one of four mutually exclusive results, and we denote the observed data by a vector $\mathbf{k}=\left\{k_{11}, k_{120}, k_{01}, k_{00}\right\}$, the elements of which are defined as follows:

- $k_{11}$ is the number of subjects which have a significant result on both tests;
- $k_{10}$ is the number of subjects which have a significant result on Test 1 and a non-significant result on Test 2;
- $k_{01}$ is the number of subjects which have a non-significant result on Test 1 and a significant result on Test 2;
- $k_{00}$ is the number of subjects which have a non-significant result on both tests;
and these observed frequencies sum to $n$, i.e. $\sum_{i, j} k_{i j}=n$.
There is a vector $\boldsymbol{\theta}$ of population parameters defined as follows:
- $\theta_{11}$ is the population proportion of subjects which have a significant result on both tests;
- $\theta_{10}$ is the population proportion of subjects which have a significant result on Test 1 and a non-significant result on Test 2;
- $\theta_{01}$ is the population proportion of subjects which have a non-significant result on Test 1 and a significant result on Test 2;
- $\theta_{00}$ is the population proportion of subjects which have a non-significant result on both tests;
with $\theta_{i j}>0$ and $\sum_{i, j} \theta_{i j}=1$, so that $\boldsymbol{\theta}$. Let the random vector $\mathbf{X}$ describe the observed counts, $k_{i j}$. Then $\mathbf{X}$ follows a multinomial model with pmf

$$
\operatorname{Pr}(\mathbf{X}=\mathbf{k} \mid \boldsymbol{\theta}) \propto \theta_{11}^{k_{11}} \theta_{10}^{k_{10}} \theta_{01}^{k_{01}}\left(1-\theta_{11}-\theta_{10}-\theta_{01}\right)^{k_{00}} .
$$

We take the prior on $\boldsymbol{\theta}$ to be a Dirichlet distribution which is defined on the 3-simplex:

$$
p(\boldsymbol{\theta}) \propto \theta_{11}^{r_{11}} \theta_{10}^{r_{10}} \theta_{01}^{r_{01}}\left(1-\theta_{11}-\theta_{10}-\theta_{01}\right)^{r_{00}} .
$$

Then the posterior distribution of $\boldsymbol{\theta}$, given the observed data $\mathbf{k}$ is

$$
\begin{equation*}
p(\boldsymbol{\theta} \mid \mathbf{k}) \propto \theta_{11}^{m_{11}} \theta_{10}^{m_{10}} \theta_{01}^{m_{01}}\left(1-\theta_{11}-\theta_{10}-\theta_{01}\right)^{m_{00}}, \tag{7}
\end{equation*}
$$

where $m_{i j}=k_{i j}+r_{i j},(i=0,1)$.
In the absence of specific prior information, we assume in the simulations that $r_{i j}=1$ for $i=0,1$, so that the prior distribution is uniform on the 3-simplex; clearly other values could be used, depending on the available prior information. Indeed, other forms of prior distribution could be used in general.

The marginal probabilities $\theta_{1}, \theta_{2}$ may be expressed in terms of the components of $\boldsymbol{\theta}$ as

$$
\begin{equation*}
\theta_{1}=\theta_{11}+\theta_{10}, \quad \theta_{2}=\theta_{11}+\theta_{01}, \tag{8}
\end{equation*}
$$

so that from (6), (8)

$$
\begin{equation*}
\gamma_{1}-\gamma_{2}=\frac{\theta_{11}+\theta_{10}-a_{1}}{b_{1}-a_{1}}-\frac{\theta_{11}+\theta_{01}-a_{2}}{b_{2}-a_{2}} . \tag{9}
\end{equation*}
$$

The marginal probabilities $\theta_{1}, \theta_{2}$ are subject to the constraints

$$
\begin{equation*}
a_{1}<\theta_{1}<b_{1}, \quad a_{2}<\theta_{2}<b_{2} \tag{10}
\end{equation*}
$$

which are in terms of the elements of $\boldsymbol{\theta}$ :

$$
\begin{equation*}
a_{1}<\theta_{11}+\theta_{10}<b_{1}, \quad a_{2}<\theta_{11}+\theta_{01}<b_{2} . \tag{11}
\end{equation*}
$$

So the posterior distribution of $\boldsymbol{\theta}$ given $\mathbf{k}$ is the truncated Dirichlet distribution defined by the pdf in (7) subject to the constraints in (11). As in Case I, we determine the pdf of the prevalence difference by making use of Monte Carlo simulation. We first describe the 'stick-breaking' method (Wikipedia, article on Dirichlet processes) for simulation from a standard Dirichlet distribution, and then we extend this method to deal with simulation from a truncated Dirichlet distribution.

## Simulating random Dirichlet data

When the parameters in $\theta$ are constrained only by the usual 'simplex' constraints, a simple approach if given by the 'stick-breaking' method. This is based on the following standard distributional results.

The marginal distribution of $\theta_{11}$ given the data is

$$
\theta_{11} \sim \operatorname{Beta}\left(m_{11}, m_{10}+m_{01}+m_{00}\right) .
$$

Consideration of the conditional distribution of $\theta_{10}$ given $\theta_{11}$ and the data leads to

$$
\frac{\theta_{10}}{1-\theta_{11}} \sim \operatorname{Beta}\left(m_{10}, m_{01}+m_{00}\right)
$$

Consideration of the conditional distribution of $\theta_{01}$ given $\theta_{11}, \theta_{10}$ and the data leads to

$$
\frac{\theta_{10}}{1-\theta_{11}-\theta_{10}} \sim \operatorname{Beta}\left(m_{01}, m_{00}\right)
$$

Finally, $\theta_{00}$ is computed by using

$$
\theta_{00}=1-\theta_{11}-\theta_{10}-\theta_{01} .
$$

The resulting simulation scheme follows.

1. Draw $u_{11}$ randomly from the $\operatorname{Beta}\left(m_{11}, m_{10}+m_{01}+m_{00}\right)$ distribution. Set $\theta_{11}=u_{11}$.
2. Draw $u_{10}$ randomly from the $\operatorname{Beta}\left(m_{10}, m_{01}+m_{00}\right)$ distribution. Set $\theta_{10}=\left(1-u_{11}\right) u_{10}$.
3. Draw $u_{01}$ randomly from the $\operatorname{Beta}\left(m_{01}, m_{00}\right)$ distribution. Set $\theta_{01}=\left(1-u_{11}-u_{10}\right) u_{01}$.
4. Set $\theta_{00}=1-\theta_{11}-\theta_{10}-\theta_{01}$.

## Simulating random truncated Dirichlet data

Given the nature of the constraints on the parameters in $\boldsymbol{\theta}$, a new approach is required to define an appropriate method of simulation. We adapt the 'stick-breaking' method to our requirements and
develop a 'stick-breaking' method for Dirichlet data under truncation given by the constraints in (11), as follows.

1. Set limits for $\theta_{11}: l o=0, \mathrm{hi}=\min \left(b_{1}, b_{2}\right)$.
2. Make a random draw, $z_{11}$, from the uniform distribution on the interval

$$
\left[F\left(\mathrm{lo} ; m_{11}, m_{10}+m_{01}+m_{00}\right), F\left(\mathrm{hi} ; m_{11}, m_{10}+m_{01}+m_{00}\right)\right] .
$$

3. Find the corresponding $u_{11}$, by the inverse cdf method, which follows the required truncated beta distribution. Set $\theta_{11}=u_{11}$.
4. Set limits for $\theta_{10}: l o=\max \left(\left(a_{1}-\theta_{11}\right) /\left(1-\theta_{11}\right), 0\right), \mathrm{hi}=\left(b_{1}-\theta_{11}\right) /\left(1-\theta_{11}\right)$.
5. Make a random draw, $z_{10}$, from the uniform distribution on the interval

$$
\left[F\left(\mathrm{lo} ; m_{10}, m_{01}+m_{00}\right), F\left(\mathrm{hi} ; m_{10}, m_{01}+m_{00}\right)\right] .
$$

6. Find the corresponding $u_{10}$, by the inverse cdf method, which follows the required truncated beta distribution. Set $\theta_{10}=\left(1-u_{11}\right) u_{10}$.
7. Set limits for $\theta_{01}: l o=\max \left(\left(a_{2}-\theta_{11}\right) /\left(1-\theta_{11}-\theta_{10}\right), 0\right), \mathrm{hi}=\min \left(\left(b_{2}-\theta_{11}\right) /\left(1-\theta_{11}-\right.\right.$ $\left.\left.\theta_{10}\right), 1\right)$.
8. Make a random draw, $z_{01}$, from the uniform distribution on the interval

$$
\left[F\left(\mathrm{lo} ; m_{01}, m_{00}\right), F\left(\mathrm{hi} ; m_{01}, m_{00}\right)\right] .
$$

9. Find the corresponding $u_{01}$, by the inverse cdf method, which follows the required truncated beta distribution. Set $\theta_{01}=\left(1-u_{11}-u_{10}\right) u_{01}$.
10. Set $\theta_{00}=1-\theta_{11}-\theta_{10}-\theta_{01}$.
11. Then $\left(\theta_{11}, \theta_{10}, \theta_{01}, \theta_{00}\right)$ is a random draw from the Dirichlet distribution in (7) subject to the constraints in (11).
12. Compute an estimate of the difference in prevalence:

$$
\gamma_{1}-\gamma_{2}=\frac{\theta_{11}+\theta_{10}-a_{1}}{b_{1}-a_{1}}-\frac{\theta_{11}+\theta_{01}-a_{2}}{b_{2}-a_{2}}
$$

For given data, this simulate procedure will provide an estimate of the posterior distribution for $\gamma_{1}-\gamma_{2}$, from which other posterior quantities can be estimated.

We finally consider how, given information about the true prevalences, a multinomial data set can be randomly generated.

## Simulating random multinomial data, given prevalence information

In this case, two different test procedures are applied to a sample of $n$ units. Within the population of units there are four different prevalences:
$\gamma_{11}$ the proportion of units in the population that possesses the 'definable effect' on both tests
$\gamma_{10}$ the proportion of units in the population that possesses the 'definable effect' on test 1 but not test 2
$\gamma_{01}$ the proportion of units in the population that possesses the 'definable effect' on test 2 but not test 1
$\gamma_{00}$ the proportion of units in the population that possesses the 'definable effect' on neither test
It is of particular interest to estimate the difference between the marginal prevalences:

$$
\gamma_{1}=\gamma_{11}+\gamma_{10}, \quad \gamma_{2}=\gamma_{11}+\gamma_{01}
$$

for Test 1 and for Test 2, respectively.
In order to simulate a random vector from the multinomial distribution, We require to express the $\theta_{i j}$ 's in terms of the $\gamma_{i j}$ 's.

## Probabilities of the Tests' outcomes

We denote the test outcomes by $O$. Then $O$ can be,,,+++--+-- , which denote significant result on both tests, significant result on Test 1 but not Test 2 etc. For each of these outcomes there are four possible ground truth situations. Let $G$ denote the ground truth. Then $G$ has values ,,,+++--+-- , which denote the possibilities 'has the definable effect on both tests', 'has the definable effect only on Test 2', 'has the definable effect only on Test 2', 'has teh definable effect on neither test.

We assume that the test statistics for the two tests are conditionally independent given each value of $G$. Then the conditional probability that the result is ++ given that the ground truth is +- is given by $b_{1} b_{2}$. In fact there are sixteen possible combinations of outcomes and ground truths. We illustrate how to obtain $\theta_{11}$, which is the (unconditional) probability of obtaining a significant result on both tests, i.e. the outcome ++ . Then

$$
\begin{array}{ll}
\operatorname{Pr}(O=++\mid G=++)=b_{1} b_{2}, & \operatorname{Pr}(O=++\mid G=+-)=b_{1} a_{2}, \\
\operatorname{Pr}(O=++\mid G=-+)=a_{1} b_{2}, & \operatorname{Pr}(O=++\mid G=--)=a_{1} a_{2} .
\end{array}
$$

The ground truth probabilities are

$$
\operatorname{Pr}(G=++)=\gamma_{11}, \quad \operatorname{Pr}(G=+-)=\gamma_{10}, \quad \operatorname{Pr}(G=-+)=\gamma_{01}, \quad \operatorname{Pr}(G=--)=\gamma_{00} .
$$

It follows from the law of total probability that

$$
\theta_{11}=b_{1} b_{2} \gamma_{11}+b_{1} a_{2} \gamma_{10}+a_{1} b_{2} \gamma_{01}+a_{1} a_{2} \gamma_{00} .
$$

By using similar arguments, we obtain

$$
\theta_{10}=b_{1}\left(1-b_{2}\right) \gamma_{11}+b_{1}\left(1-a_{2}\right) \gamma_{10}+a_{1}\left(1-b_{2}\right) \gamma_{01}+a_{1}\left(1-a_{2}\right) \gamma_{00},
$$

which may be expressed as

$$
\theta_{10}=a_{1}+\left(b_{1}-a_{1}\right) \gamma_{1 .}-\theta_{11} .
$$

Also

$$
\theta_{01}=\left(1-b_{1}\right) b_{2} \gamma_{11}+\left(1-b_{1}\right) a_{2} \gamma_{10}+\left(1-a_{1}\right) b_{2} \gamma_{01}+\left(1-a_{1}\right) a_{2} \gamma_{00},
$$

which may be written as

$$
\theta_{01}=a_{2}+\left(b_{2}-a_{2}\right) \gamma_{.1}-\theta_{11} .
$$

$\theta_{00}$ is found by subtraction as $1-\theta_{11}-\theta_{10}-\theta_{01}$.
It is worth noting that we recover equations of the marginal proportions of significant results for the two tests, as

$$
\theta_{1}=\theta_{11}+\theta_{10}=a_{1}+\left(b_{1}-a_{1}\right) \gamma_{1 .,}
$$

and

$$
\theta_{2}=\theta_{11}+\theta_{01}=a_{2}+\left(b_{2}-a_{2}\right) \gamma_{.1} .
$$

## Independent prevalences

If the prevalences are assumed to be independent in the sense that

$$
\gamma_{11}=\gamma_{1} \gamma_{2}, \quad \gamma_{10}=\gamma_{1}\left(1-\gamma_{2}\right), \quad \gamma_{01}=\left(1-\gamma_{1}\right) \gamma_{2}, \quad \gamma_{00}=\left(1-\gamma_{1}\right)\left(1-\gamma_{.2}\right)
$$

then, after some algebra, we find that

$$
\theta_{11}=\theta_{1} \theta_{2}, \quad \theta_{10}=\theta_{1}\left(1-\theta_{2}\right), \quad \theta_{01}=\left(1-\theta_{1}\right) \theta_{2}, \quad \theta_{00}=\left(1-\theta_{1}\right)\left(1-\theta_{2}\right) .
$$

It is worth considering the posterior distribution for $\boldsymbol{\theta}$ in this case, which is proportional to

$$
\theta_{1}^{m_{11}+m_{10}}\left(1-\theta_{1}\right)^{m_{01}+m_{00}} \times \theta_{2}^{m_{11}+m_{01}}\left(1-\theta_{2}\right)^{m_{10}+m_{00}} .
$$

In other words it factorises into the product of two beta pdfs - a form that is the same as in Case 1. This indicates that making the assumption of independence in Case 2 doesn't make sense, since this just reduces to the case of two different groups and one test.

## Defining general prevalences for data simulation

There is a simple way to express the general dependence among the the prevalences.
Re-consider the ground truth information. We define two binary variables to represent this. Let $G_{1}$ equal 1 when the defined effect associated with Test 1 is present in the population, and zero otherwise. Let $G_{2}$ equal 1 when the defined effect associated with Test 2 is present in the population, and zero otherwise. Then, the joint distribution of $G_{1}$ and $G_{2}$ is

$$
\begin{array}{ll}
\operatorname{Pr}\left(G_{1}=1, G_{2}=1\right)=\gamma_{11}, & \operatorname{Pr}\left(G_{1}=1, G_{2}=0\right)=\gamma_{10} \\
\operatorname{Pr}\left(G_{1}=0, G_{2}=0\right)=\gamma_{01}, & \operatorname{Pr}\left(G_{1}=0, G_{2}=0\right)=\gamma_{00}
\end{array}
$$

and the marginal distribution are

$$
\begin{array}{ll}
\operatorname{Pr}\left(G_{1}=1\right)=\gamma_{1}, & \operatorname{Pr}\left(G_{1}=0\right)=1-\gamma_{1}, \\
\operatorname{Pr}\left(G_{2}=1\right)=\gamma_{2}, & \operatorname{Pr}\left(G_{2}=0\right)=1-\gamma_{2} .
\end{array}
$$

It seems natural to consider the correlation between $G_{1}$ and $G_{2}$. Denote this by $\rho_{12}$. This is the correlation between the presences of the defined effects associated with Test 1 and Test 2 in the population. We now derive an expression for this correlation.

Using the probability distributions of $G_{1}$ and $G_{2}$, it follows that

$$
\begin{array}{ll}
\mathbb{E}\left(G_{1}\right)=\gamma_{1}, & \mathbb{E}\left(G_{1}^{2}\right)=\gamma_{1}, \\
\mathbb{E}\left(G_{2}\right)=\gamma_{2}, & \mathbb{E}\left(G_{2}^{2}\right)=\gamma_{2} .
\end{array}
$$

Hence, we may write the variances of $G_{1}$ and $G_{2}$, as well as the covariance of $G_{1}$ and $G_{2}$ as follows.

$$
\begin{aligned}
\operatorname{var}\left(G_{1}\right) & =\mathbb{E}\left(G_{1}^{2}\right)-\mathbf{E}\left(G_{1}\right)^{2}=\gamma_{1}\left(1-\gamma_{1}\right), \\
\operatorname{var}\left(G_{2}\right) & =\mathbb{E}\left(G_{2}^{2}\right)-\mathbf{E}\left(G_{2}\right)^{2}=\gamma_{2}\left(1-\gamma_{2}\right), \\
\operatorname{cov}\left(G_{1}, G_{2}\right) & =\mathbb{E}\left(G_{1} G_{2}\right)-\mathbf{E}\left(G_{1}\right) \mathbb{E}\left(G_{2}\right)=\gamma_{11}-\gamma_{1} \gamma_{2} .
\end{aligned}
$$

Therefore, when $0<\gamma_{1}<1$ and $0<\gamma_{2}<1$ we can expression the correlation between $G_{1}$ and $G_{2}$ as

$$
\rho_{12}=\operatorname{cor}\left(G_{1}, G_{2}\right)=\frac{\operatorname{cov}\left(G_{1}, G_{2}\right)}{\sqrt{\operatorname{var}\left(G_{1}\right) \operatorname{var}\left(G_{2}\right)}}=\frac{\gamma_{11}-\gamma_{1} \gamma_{2}}{\sqrt{\gamma_{1}\left(1-\gamma_{1}\right) \gamma_{2}\left(1-\gamma_{2}\right)}} .
$$

We see that the correlation is equal to zero when $\gamma_{11}=\gamma_{1} \gamma_{2}$, i.e. the prevalences are 'independent'. The correlation is equal to 1 when $\gamma_{10}=\gamma_{01}=0$, and then the marginal prevalences are equal. The correlation is equal to -1 when $\gamma_{11}=\gamma_{00}=0$, and the marginal prevalences are typically unequal, but can be equal.

Note, however, that in the 'edge cases' in which one or both of the marginal prevalences, $\gamma_{1}, \gamma_{2}$, is equal to zero there can be no correlation between $G_{1}$ and $G_{2}$, since their covariance is equal to zero, and so $\rho_{12}=0$.

In order to set up a simulation of the multinomial data we require to specify the marginal prevalences, $\gamma_{1}, \gamma_{2}$, as well the correlation between the presences of the defined effects, $\rho_{12}$. Then we set

$$
\gamma_{11}=\gamma_{1} \gamma_{2}+\rho_{12} \sqrt{\gamma_{1}\left(1-\gamma_{1}\right) \gamma_{2}\left(1-\gamma_{2}\right)}
$$

and also

$$
\begin{aligned}
& \gamma_{10}=\gamma_{1}-\gamma_{11} \\
& \gamma_{01}=\gamma_{2}-\gamma_{11} \\
& \gamma_{00}=1-\gamma_{11}-\gamma_{10}-\gamma_{01}
\end{aligned}
$$

This formula is also valid when either or both of the marginal prevalences is equal to zero. We compute the $\theta_{i j}$ as follows

$$
\begin{aligned}
& \theta_{11}=b_{1} b_{2} \gamma_{11}+b_{1} a_{2} \gamma_{10}+a_{1} b_{2} \gamma_{01}+a_{1} a_{2} \gamma_{00}, \\
& \theta_{10}=a_{1}+\left(b_{1}-a_{1}\right) \gamma_{1 .}-\theta_{11}, \\
& \theta_{01}=a_{2}+\left(b_{2}-a_{2}\right) \gamma_{.1}-\theta_{11}, \\
& \theta_{00}=1-\theta_{11}-\theta_{10}-\theta_{01} .
\end{aligned}
$$

These values of $\theta_{i j}$ can then be used to generate random multinomial counts for the required number of participants.

