Modeling sums of exchangeable binary variables

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ABSTRACT

We introduce a new model for sums of exchangeable binary random variables. The proposed distribution is an approximation to the exact distributional form, and relies on the theory of completely monotone functions and the Laplace transform of a gamma distribution function. Using Monte Carlo methods, we show that this new model compares favorably to the beta-binomial model with respect to estimating the success probability of the Bernoulli trials and the correlation between any two variables in the exchangeable set. We apply the new methodology to two classic data sets and the results are summarized.

1. Introduction

Correlated binary outcomes, either by design or through natural conditions, is a common occurrence in many fields. Examples include measuring a Bernoulli outcome in a repeated measures study, teratological risk assessment, studies of familial diseases and genetic traits, and group randomization studies, among many others. Of immediate concern around the world, COVID-19 positivity tests within a family or geographical unit introduce potentially correlated binary outcomes.

Kuk (2004) provides a nice introduction to developmental toxicity studies and the statistical issues therein. We will summarize the details from their paper as its development is closely related to what is presented here. In a standard developmental toxicity study, pregnant laboratory animals are often randomly assigned to receive varying dose levels of a toxic substance during a major period of organogenesis. Their lives are usually terminated before giving birth, their uterus is subsequently removed and examined for possible birth defects. For each litter in such a study, there is a sequence of Bernoulli random variables $X_1, X_2, ..., X_m$ where $X_i = 0, 1$, denoting the absence or presence of the birth defect.

It is commonly assumed that members of the same litter will behave more similarly than nonlittermates and, therefore, one may assume a degree of correlation between littermates. Kuk (2004) notes that litter effect can be accounted for by assuming the intralitter correlation is induced by a random effect that is shared by all fetuses in the same litter. This random effect accounts for all of the environmental and genetic factors that littermates share in common. Pang and Kuk (2005) point out that, “failure to account for litter effect and the overdispersion it induces will lead to estimates with overstated precision.”
In earlier work, Williams (1975) states that it is necessary to model variation between fetuses in the same litter and variation between litters receiving the same treatment. It is this insight that leads to the development of the beta binomial model for application to toxicological experiments involving reproduction and teratogenicity. Williams (1975) essentially assumes that the probability of response varies as a beta distribution between dose groups to model the overdispersion due to litter effect. It should be noted that Skellam (1948) was first to propose the idea of using the beta distribution to describe variation in the probability parameter of the binomial distribution. For a large portion of the past 40+ years, the beta binomial distribution has been the gold standard when it comes to modeling clustered binary data. Additional models include a correlated binomial model proposed by Kupper and Haseman (1978), a correlated beta binomial model discussed by Paul (1979) and Pack (1986), an extended beta binomial model introduced by Prentice (1986), and “additive” and “multiplicative” generalizations of the binomial given in Altham (1978).

George and Bowman (1995) developed an exact distribution for sums of exchangeable binary variables. In addition, they propose an approximating model for \( \lambda_k = P(X_1 = X_2 = \cdots = X_k = 1), k = 1, 2, \ldots, m \) using \( \lambda_k = f(k; \beta) \) where \( f \) is the completely monotone folded-logistic function. A drawback to this model is that with only a single parameter \( \beta \), this model lacks the flexibility of many two-parameter models, such as the beta binomial model, when estimating success probability and intra-cluster correlation.

Kuk (2004) notes that the shape of the beta binomial probability function is often U-shaped, J-shaped, or reverse J-shaped instead of unimodal with the mode near the expected value of \( mp \). Hence, all of the probability mass could be concentrated at 0 and \( m \), and a value near the “expected” value could be very unlikely. Essentially what happens is that the beta binomial, and other existing distributions, tend to underestimate the risk of at least one littermate having a birth defect. Kuk (2004) introduced the \( q \)-power model that is based on the exchangeable theory developed in George and Bowman (1995). The shared response model, introduced in Pang and Kuk (2005), can model the data without overestimating the probability of no affected fetuses.

In this manuscript, we propose a new (approximate) distribution for handling exchangeable binary data. Our model is based on the theory of George and Bowman (1995), and is similar to Kuk (2004), Yu and Zelterman (2008), and Bowman (2016) in its development. Background information related to several previous models, and our new model are introduced in Section 2. In Section 3, we present the results of a large-scale Monte Carlo study designed to assess several statistical properties of the proposed model relative to those of existing methods. Two classic examples are analyzed in Section 4 and our concluding remarks are reported in Section 5.

2. Model development

2.1. Prior research

Modeling finite sums of exchangeable binary random variables is explored in detail in the papers of George and Bowman (1995), Bowman and George (1995), and George and Kodell (1996), among other papers outlined in Section 1. An exact distribution for the sum of exchangeable binary random variables is derived in George and Bowman (1995). We summarize their results in order to develop our proposed model.
Let $Y = (Y_1, Y_2, ..., Y_m)^T$ denote a vector of exchangeable binary random variables. By exchangeable, we mean that

$$(Y_1, Y_2, ..., Y_k)^T \sim D(Y_{\pi(1)}, Y_{\pi(2)}, ..., Y_{\pi(k)})^T$$

for any permutation $\pi$ of the integers $\{1, 2, ..., k\}$. We are interested in making inferences on the quantity $S_m = \sum_{j=1}^{m} Y_j$ for $k \leq m$. From a straightforward application of the Inclusion-Exclusion principle in probability, the exact distribution of these sums can be shown to be

$$P[S_m = s] = \left(\begin{array}{c} m \\ s \end{array}\right) \sum_{k=0}^{m-s} (-1)^k \left(\begin{array}{c} m-s \\ k \end{array}\right) p_{s+k}, \text{ for } s = 0, 1, ..., m. \quad (1)$$

where,

$$p_j = P[Y_1 = 1, Y_2 = 1, ..., Y_j = 1], j = 1, 2, ..., m, \text{ and } 1 = p_0 \geq p_1 \geq p_2 \geq \cdots \geq p_m \quad (2)$$

Parameter estimates of $p_1, ..., p_m$, and hence any $k^{th}$-order correlation can be found in the following way. An observation $S_m = s$ is simply an indicator random variable following a multinomial distribution having cell probabilities given by $P[S_m = j]$ for $j = 0, 1, ..., m$. Using the inversion formula

$$p_j = \sum_{k=0}^{m-j} \left(\begin{array}{c} m-j \\ k \end{array}\right) \left(\begin{array}{c} m \\ k \end{array}\right) P[S_m = m - k]$$

we can find the desired estimates. Variance estimates are computed based on the distributional properties of multinomial probabilities. Rather than estimating each individual $p_j$ using a saturated approach, it is possible to model these parameters using a function which preserves the constraints given above, namely that

$$1 = p_0 \geq p_1 \geq p_2 \geq \cdots \geq p_m, \text{ and } \sum_{k=0}^{m-s} (-1)^k \left(\begin{array}{c} m-s \\ k \end{array}\right) p_{s+k} \geq 0. \quad (3)$$

George and Bowman (1995) suggest using the folded-logistic function to model the sequences of probabilities in order to approximate the model defined in Equation (1). The folded-logistic function is defined by

$$p_x(\beta) = \frac{2}{1 + (x + 1)^\beta}$$

for $x \geq 0$ and $\beta > 0$. Under this parameterization, Equation (1) becomes

$$P[S_m = s; \beta] = \left(\begin{array}{c} m \\ s \end{array}\right) \sum_{k=0}^{m-s} (-1)^k \left(\begin{array}{c} m-s \\ k \end{array}\right) \frac{2}{1 + (s + k + 1)^\beta}, \quad (4)$$

for $s = 0, 1, ..., m$. The estimation problem is now reduced to estimating a single parameter, $\beta$, rather than estimating the $m$ individual $p$'s.
Kuk (2004) introduces two additional distributions based on the theory of completely monotone functions. Note that a function \( \varphi \) is completely monotone if it possesses derivatives \( \varphi^{(n)} \) of all orders and \( (-1)^n \varphi^{(n)}(\lambda) \geq 0 \), for \( \lambda > 0 \). In the first, Kuk models the sequence of probabilities \( 1 = p_0 \geq \cdots \geq p_m \) by
\[
\lambda_k = P(X_1 = X_2 = \cdots = X_k = 1) = p_1^k
\]
where \( k = 0, 1, \ldots, m \) and \( 0 \leq p_1 \leq 1 \). The parameter \( p \) is the marginal response probability and the parameter \( \gamma \) controls the degree of association between littermates. A value of \( \gamma = 1 \) corresponds to independence between littermates while a value of \( \gamma = 0 \) corresponds to complete dependence between littermates. Under this parameterization, Equation (1) can be written as
\[
P(S_m = s; p, \gamma) = \left( \frac{m}{s} \right) \sum_{k=0}^{m-s} (-1)^k \binom{m-s}{k} p^{(s+k)\gamma}.
\]
Kuk refers to this model as the \( p \)-power distribution.

Kuk mentions that one may also use the same type of power-family model for \( X' = 1 - X \). In this case, \( q = 1 - p = P(X' = 1) = P(X = 0) \) and, therefore,
\[
\lambda_k = P(X'_1 = X'_2 = \cdots = X'_k = 1) = P(X_1 = X_2 = \cdots = X_k = 0) = q^k
\]
This results in the \( q \)-power probability distribution given by
\[
P(S_m = s; q, \gamma) = P(S'_m = m - s|q, \gamma) = \left( \frac{m}{s} \right) \sum_{k=0}^{s} (-1)^k \binom{s}{k} (q^{m-s+k})^\gamma
\]
where \( 0 \leq q, \gamma \leq 1 \). Kuk advocates for the use of the \( q \)-power distribution over the \( p \)-power distribution when modeling overdispersed binary data.

### 2.2. Laplace Transform of the gamma (LapGam) distribution

Our development relies on the theory presented in Section 2.1, along with the following theory on the difference operator \( \Delta \), as given in Feller (1971). The difference operator \( \Delta \) is defined on a sequence \( \{c_n\} \) to be \( \Delta c_n = c_{n+1} - c_n \). If we apply the difference operator to the new sequence \( \Delta c_n \), we get another sequence \( \Delta^2 c_n = \Delta(\Delta c_n) \). Similarly, the higher-order differences are defined recursively by \( \Delta^r c_n = \Delta(\Delta^{r-1} c_n) \), where \( \Delta^1 = \Delta \). It can be shown that the \( r^{th} \)-order difference can be written as
\[
\Delta^r c_n = \sum_{k=0}^{r} \binom{r}{k} (-1)^{r+k} c_{n+k}.
\]
This leads to the following definition.

**Definition 2.1** (Feller V2). A sequence \( \{c_n\} \) such that \( (-1)^r \Delta^r c_n \geq 0 \) for all combinations \( r, \nu \) is called a completely monotone sequence.

Applying these results to the sequence \( \{p_n\} \) given above, we see that if \( \{p_n\} \) is completely monotone, then the constraints defined in Equation (3) are satisfied. We will model such a sequence using a completely monotone function. Our main result, summarized next, is a direct application of the following theorem using the gamma distribution function.
Theorem 2.2 (Feller V2). A function \( \varphi \) on \((0, \infty)\) is the Laplace transform of a probability distribution \( F \), iff it is completely monotone, and \( \varphi(0) = 1 \).

Result 2.1. The function \( p_x \) defined by
\[
p_x(a, b) = \frac{1}{1 + bx^a}
\]
for \( x \geq 0 \) and \( \beta, x > 0 \) is a completely monotone function.

To see this, let \( F \) be the distribution function of a gamma random variable with mean \( \alpha \beta \) and variance \( \alpha \beta^2 \), for parameters \( \alpha, \beta > 0 \). The Laplace transform of \( F \) is given by
\[
\varphi_x(a, b) = \int_0^\infty e^{-\lambda x} dF(x) = \frac{1}{(1 + \beta \lambda)^a}.
\]
Therefore, \( p_x(a, b) \) is a completely monotone function by Feller’s result given above.

Similarly to the ideas presented in George and Bowman (1995) and Kuk (2004), we will use this function as a model for the sequence \( 1 = p_0 \geq p_1 \geq \cdots \geq p_m \). Therefore, an approximate distribution of \( S_m \) under this parameterization is
\[
P(S_m = s; \alpha, \beta) = \binom{m}{s} \sum_{k=0}^{m-s} (-1)^k \binom{m-s}{k} \frac{1}{[1 + \beta(s + k)]^a}
\]
for \( s = 0, 1, \ldots, m \). We will refer to this distribution as the Laplace transform of the gamma distribution, or the LapGam for short.

We wish to emphasize that the distribution defined in Equation (10) is constructed from the gamma distribution function and the theory of completely monotone functions. There are no doubt additional distributions similar to the LapGam that can be defined using distribution functions characterized by multiple parameters. Hopefully the theory presented here will spur additional work in the area.

2.3. Estimation

Let \( S_{m1}, S_{m2}, \ldots, S_{mn} \) be a random sample of sums of exchangeable binary random variables defined by \( S_{mi} = \sum_{j=1}^{m} Y_{ij} \) where \( P[Y_{ij} = 1] = p_i \). We will assume that \( S_{mi} \) follows the distribution given by Equation (1) with
\[
p_{s+k} = p_{s+k}(x, \beta) = \frac{1}{[1 + \beta(s + k)]^a}.
\]
Thus, the log-likelihood function for this sample can be written as
\[
\begin{align*}
  l_n(x, \beta; s) &= \log \left( \prod_{i=1}^{n} P[S_m = s_i; \alpha, \beta] \right) \\
  &= \sum_{i=1}^{n} \log \left( \binom{m}{s_i} \right) + \sum_{i=1}^{n} \log \left( \sum_{k=0}^{m-s_i} (-1)^k \binom{m-s_i}{k} p_{s+k}(x, \beta) \right) \\
  &= \sum_{i=1}^{n} \log \left( \binom{m}{s_i} \right) + \sum_{i=1}^{n} \log \left( \sum_{k=0}^{m-s_i} \frac{(-1)^k \binom{m-s_i}{k}}{[1 + \beta(s + k)]^a} \right).
\end{align*}
\]
Our interest is in finding maximum likelihood estimators (MLEs) $\hat{\alpha}$ and $\hat{\beta}$. It is straightforward to write a Newton-Raphson algorithm to maximize the likelihood given in Equation (12), or simply use an optimization method in R or python to find the MLEs. We have found that either approach is numerically stable in optimizing several different variants of this likelihood, for example, as when using the semiparametric approach described in Section 4.2. The delta method (Lehmann 1999) can then be

**Figure 1.** The estimated sampling distributions of $\hat{p}$ using the beta binomial, folded-logistic, LapGam, and $q$-power models. Each row and column correspond to particular values of $p$ and $p$, respectively, which were used to generate the data in each simulation. The horizontal dashed lines serve as references for the targeted values of $p$ to be estimated.
utilized to find estimators of the probability parameters and correlations (of potentially all orders).

3. Monte Carlo simulation

In order to assess the performance of the LapGam model in a controlled environment, we conducted a large-scale Monte Carlo study. Three additional models were chosen as a basis of comparison in this simulation study: the George and Bowman (1995) model given in Equation (4), the beta binomial model (16) using the parameterization defined in Prentice (1986), and the \( q \)-power model (6) defined in Kuk (2004). The models were evaluated in terms of estimating the binary response probability \( p \) and first-order correlation \( \rho \) for sums of correlated binary variables. We considered 40 different scenarios corresponding to \( p = 0.1, 0.2, 0.3, 0.4, \) and \( 0.5 \) and \( \rho = 0.05, 0.10, 0.15, \) and \( 0.20 \). We varied the number of Bernoulli trials using \( m = 10 \) and \( m = 15 \). For every scenario, \( B = 1000 \) samples of size 100 were simulated. The data for this simulation study were generated using the bindata() package (Leisch, Weingessel, and Hornik 1998) available in the R software (R Core Team 2020). For the sake of brevity, we only discuss the results of the simulations when \( m = 10 \) in this manuscript. The \( m = 15 \) scenario is similar to what is shown here. A comprehensive summary of the full set of simulation results is available from the author upon request.

We first discuss the results of estimating \( p \), the success probability. The simulated sampling distributions of \( \hat{p} \) can be see in Figure 1. Specifically, each row \( (p) \) and column \( (\rho) \) combination corresponds to the parameter values that were used to generate the data. Each box shows the estimated sampling distributions of \( \hat{p} \) under the four models in question. As can be seen in this figure, the beta binomial and the LapGam models perform almost identically across the ten different scenarios presented here. On the other hand, the estimates of \( p \) based on the folded-logistic and \( q \)-power models show evidence of bias in certain situations. For example, there is noticeable bias in both when the intra-cluster correlation is high \((0.2)\) and the success probability is low \((0.1)\).

Figure 2 shows the results when estimating \( \rho \). Each row \( (\rho) \) and column \( (p) \) combination indicates the parameter values that were used to generate the data and shows the estimated sampling distributions of \( \hat{\rho} \) under the four models in question. Similar to the story told above, the beta binomial and LapGam models tend to perform well at estimating \( \rho \) in each scenario, whereas the other two show some bias. The folded-logistic model, in particular, does a bad job at estimating \( \rho \) when the success probability is 0.5 and the individual trials are weakly correlated \( \rho = 0.05 \).

4. Examples

4.1. Brassica data

The following example consists of data presented in Skellam (1948) and Altham (1978) on the secondary association of chromosomes in *Brassica*, a group of plants belonging to the Mustard family (botany.com). If the probability of association is constant within and across nuclei and the individual bivalents are independent, then the counts can be assumed to follow a binomial distribution. However, Skellam (1948) and Altham (1978)
discuss the fact that these data are overdispersed relative to a binomial model and that the beta binomial (and other models) provide an adequate fit. Table 1 provides a summary of the data and the expected counts under five models: binomial, beta binomial, folded-logistic, LGa, and the $q$-power model.

The $p$-values for the chi-square goodness of fit statistics for the beta binomial, LGa, and the $q$-power models are 0.8594, 0.8621, and 0.9993, respectively. On the other hand, the usual binomial and the folded logistic fits are rejected according to the chi-

**Figure 2.** The estimated sampling distributions of $\hat{p}$ using the beta binomial, folded-logistic, LapGam, and $q$-power models. Each row and column correspond to particular values of $\rho$ and $p$, respectively, which were used to generate the data in each simulation. The horizontal dashed lines serve as references for the targeted values of $\rho$ to be estimated.
A square test with p-values equal to 0.0439 and 0.0048, respectively. The probability of association for a given bivalent and the correlation among pairs of bivalents are given in Table 2. As can be seen in this classic example, it is difficult to distinguish which model provides the best summary of these data between the beta binomial, LGa, and the \( q \)-power models. It is fairly easy to discount the estimates based on the folded-logistic function, however.

### 4.2. Brazil data

Our second example consists of data related to a survey of deaths in children from a particularly poor region in northeast Brazil. The raw data were reported in Sastry (1997) and reproduced in Yu and Zelterman (2008). The data consist of 1051 unique families with a total of 2946 children. The number of children in the families ranged from one to eight, with two being the most frequent. The outcome of interest is a binary variable indicating childhood mortality. The data are assumed to be exchangeable as they are overdispersed within families relative to a binomial model.

As discussed in Yu and Zelterman (2008), it appears that the mortality rate and within-family correlation differ as a function of family size. They account for this difference using a quadratic function of \( m \), family size, in the logit of \( \mu \), mortality rate, and the log of \( \gamma \) in the beta binomial model specification defined in Equation (16). Rather than requiring strict functional forms, we take a semi-parametric approach to fitting the beta binomial and LapGam models to the Brazil data. That is, we model the logit of \( \mu \) and the log of \( \gamma \) using cubic splines in \( m \), i.e.,

\[
\text{logit}[\mu(m)] = s(m)\eta_1
\]

and

\[
\log[\gamma(m)] = s(m)\eta_2
\]

where \( s(m) \) is the cubic-spline basis representation of \( m \) and \( \eta_1 \) and \( \eta_2 \) are vectors of parameters to be estimated from the data. Similarly, we handle within-family differences in \( \alpha \) and \( \beta \) from Equation (10) using the log, or

\[
\log[\alpha(m)] = s(m)\eta_3
\]

and

\[
\log[\beta(m)] = s(m)\eta_4
\]

Again, \( \eta_3 \) and \( \eta_4 \) are estimable parameter values and \( s(m) \) is the cubic-spline basis representation of \( m \).

### Table 1. The observed and expected counts for the *Brassica* data using the binomial, folded-logistic, beta binomial, LapGam, and \( q \)-power models.

|  | Observed | Binomial | FL | BB | LapGam | \( q \)-power |
|---|---|---|---|---|---|---|
| 0 | 32 | 24.86 | 50.59 | 33.97 | 33.97 | 32.43 |
| 1 | 103 | 103.24 | 90.57 | 97.16 | 97.20 | 102.02 |
| 2 | 122 | 142.93 | 104.45 | 127.67 | 127.61 | 122.69 |
| 3 | 80 | 65.96 | 91.39 | 78.20 | 78.23 | 79.86 |
The estimated deviances for the semi-parametric fits of the beta binomial and LapGam models are 18.79 and 19.09, respectively. The estimated mortality rates and within-family correlations are presented in Figure 3. The estimates associated with the beta binomial model are given as circles along the solid line and the LapGam estimates are shown using triangles on dashed lines. The estimated probabilities are virtually identical across the two models whereas there are noticeable differences in within-family correlation. As a comparison to Yu and Zelterman (2008) and for completeness, the estimated deviance using a quadratic function of $m$ in $a$ and $b$ is 19.16, suggesting a slightly better fit when using the semi-parametric model.

### 5 Discussion

In this paper, we introduced a new model, LapGam, for approximating the distribution of sums of exchangeable binary variables. The model is developed using a novel application of completely monotone functions and the difference operator to the exact distribution as developed in George and Bowman (1995). In addition, we demonstrate the efficacy of maximum likelihood estimation of the LapGam using a large-scale simulation study. Lastly, we demonstrate the use of this model by applying the results to two classic applications.

The simulation study shows that this new LapGam model performs as well as the well-known beta binomial distribution under a wide variety of simulated conditions. These results provide confidence in our conclusions associated with the two classic examples that we analyzed in Section 4.

As other authors have noted (Yu and Zelterman 2008) and references therein), the exact distribution, as well as its many approximations, rarely out perform the beta binomial

### Table 2. The parameter estimates of $p$ and $q$ using the folded-logistic, beta binomial, LapGam, and $q$-power models.

|                | FL     | BB     | LapGam | $q$-power |
|----------------|--------|--------|--------|-----------|
| $p$            | 0.567  | 0.581  | 0.581  | 0.581     |
| $q$            | 0.214  | 0.087  | 0.087  | 0.087     |

Figure 3. The left panel shows the estimated mortality rates as functions of $m$ for the beta binomial model (circles, solid line) and the LapGam model (triangles, dashed). The right panel shows the estimated within-family correlation for each family size ranging from two to eight for the beta binomial model (circles, solid line) and the LapGam model (triangles, dashed).
model when applied to estimating parameters in sums of exchangeable binary variables. This is the case here as well. However, we did show that our new proposal, the LapGam model, performs as well as the beta binomial model in all of our simulated scenarios.

In closing, we wish to emphasize that the theory and numerical results that are presented in this manuscript should serve a building block for future research on sums of exchangeable Bernoulli variables. That is, we provide a recipe for the exploration of additional models using the theory of completely monotone functions and distribution functions, as presented in Feller (1971). There are likely similar results to those presented in Section 2.1 that could lead to interesting theoretical and methodological developments. Hopefully these future studies will come to fruition.

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Appendix

Background information

Most of the substantial work on sequences of exchangeable binary variables revolves around the famous theorem of Bruno de Finetti as stated in Diaconis (1977).

**Theorem A.1** (de Finetti). Let \( \{Y_i\}_{i=1}^{\infty} \) be an infinite sequence of random variables with \( \{Y_i\}_{i=1}^{m} \) exchangeable for each \( m \); then there is a unique probability measure \( \mu \) on \([0, 1]\) such that for each fixed sequence of zeros and ones \( \{e_i\}_{i=1}^{m} \), we have

\[
P[Y_1 = e_1, \ldots, Y_m = e_m] = \int_0^1 p^r(1-p)^{m-r} \, d\mu(p)
\]

where \( s = \sum e_i \).

Several comments are in order regarding this theorem. Perhaps most important is the fact that the unique measure \( \mu \) exists only if we have an infinite sequence of exchangeable binary random variables \( \{Y_i\}_{i=1}^{\infty} \). This result is known to fail for finite sets, say \( \{Y_i\}_{i=1}^{r} \), of exchangeable binary variables. Fortunately, two finite forms of de Finetti’s theorem are developed in Diaconis (1977) and are restated here for completeness.

**Theorem A.2** (Diaconis 1977). Let \( \{Y_i\}_{i=1}^{r} \) be an exchangeable sequence which can be extended to an exchangeable sequence of length \( k > r \). Then there is a measure \( \mu_k \) on \([0, 1]\) such that if \( e_1, e_2, \ldots, e_r \) is any sequence of zeros and ones and \( s = \sum_{i=1}^{r} e_i \), then

\[
\left| P[Y_1 = e_1, \ldots, Y_r = e_r] - \int_0^1 p^r(1-p)^{r-s} \, d\mu_k(p) \right| < \frac{c}{k},
\]

where \( c \) is a constant that does not depend on the sequence \( e_r \).
Corollary A.3. Let \( \{Y_i\}_{i=1}^{\infty} \) be an infinite sequence of random variables with \( \{Y_i\}_{i=1}^{m} \) exchangeable for each \( m \); then there is a unique probability measure \( \mu \) on \([0, 1]\) such that for each fixed sequence of zeros and ones \( \{e_i\}_{i=1}^{m} \), we have

\[
P[S_m = s] = \binom{m}{s} \int_0^1 p^s (1-p)^{m-s} \, d\mu(p)
\]

where \( s = \sum e_i = 0, 1, \ldots, m \).

Results such as the previous three are potentially one motivation, but certainly not the only one, for using the beta binomial distribution to model sums of correlated binary variables, see e.g. Skellam (1948), Griffiths (1973), Williams (1975), and Prentice (1986). The beta binomial model is defined on \( S_m \) for sums of correlated binary random variables having latent response probability \( p \) as

\[
P[S_m = s|p] = \binom{m}{s} p^s (1-p)^{m-s} \text{ for } s = 0, 1, \ldots, m, (14)
\]

where \( p \sim \text{Beta}(\alpha, \beta) \). This implies that, unconditionally,

\[
P[S_m = s] = \int \binom{m}{s} p^s (1-p)^{m-s} \, dG(p)
\]

\[
= \binom{m}{s} \Gamma(\alpha, \beta) \int_0^1 p^{s+\beta-1} (1-p)^{m+\beta-s-1} \, dp
\]

\[
= \binom{m}{s} B(\alpha+s, m+\beta-s) \frac{B(\alpha+s, m+\beta-s)}{B(\alpha, \beta)}, \text{ for } s = 0, 1, \ldots, m
\]

(15)

with \( B(a, b) = \frac{\Gamma(a)\Gamma(b)}{\Gamma(a+b)} \). The critical, yet non-verifiable assumptions in using such a model as the distribution of finite sums of exchangeable binary variables are that: (i) the set of exchangeable variables can be embedded into an infinite sequence of exchangeable binary random variables, and (ii) the unique measure given in Theorem A.1, \( \mu \), is a beta distribution function.

Prentice (1986) introduces an alternative form of the beta binomial distribution by defining \( \mu = \alpha(\alpha + \beta)^{-1} \) and \( \gamma = \rho(1-\rho)^{-1} \). The mass function under this parameterization is defined by

\[
P[S_m = s; \mu, \gamma] = \binom{m}{s} \prod_{a=0}^{s-1} \left( \frac{\mu + \gamma a}{1 - \mu + \gamma a} \right) \prod_{a=0}^{m-s-1} \left( \frac{\mu - \gamma a}{1 - \mu - \gamma a} \right)
\]

(16)

\( s = 0, 1, \ldots, m \), for \( 0 < \mu < 1 \) and \( \gamma > 0 \). Using this form, \( \rho = \gamma(1+\gamma)^{-1} \) and small negative correlations are permissible. In fact, one can show that

\[
\rho \geq \max\{-\mu(m - \mu - 1)^{-1}, -\mu(m - \mu - 1)^{-1}\},
\]

or equivalently,

\[
\gamma \geq \max\{-\mu(m - 1)^{-1}, \bar{\mu}(m - 1)^{-1}\},
\]

where \( \bar{\mu} = 1 - \mu \). Note that usual binomial variation corresponds to \( \gamma = 0 \), whereas, binomial variation corresponds to infinite parameter values under the original parameterization.