Moving towards practical user-friendly synthesis: Scalable synthetic data methods for large confidential administrative databases using saturated count models

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Abstract

Over the past three decades, synthetic data methods for statistical disclosure control have continually developed; methods have adapted to account for different data types, but mainly within the domain of survey data sets. Certain characteristics of administrative databases - sometimes just the sheer volume of records of which they are comprised - present challenges from a synthesis perspective and thus require special attention. This paper, through the fitting of saturated models, presents a way in which administrative databases can not only be synthesized quickly, but also allows risk and utility to be formalised in a manner inherently unfeasible in other techniques. The paper explores how the flexibility afforded by two-parameter count models (the negative binomial and Poisson-inverse Gaussian) can be utilised to protect respondents’ - especially uniques’ - privacy in synthetic data. Finally an empirical example is carried out through the synthesis of a database which can be viewed as a good representative to the English School Census.
1 Introduction

There is an increasing demand for data to be made available to researchers. But this is coupled with greater demands, both legal and ethical, on the protection of personal data. Consequently, new data sources - and innovative ways of protecting data, are required.

Administrative databases originate because organisations need to hold individuals’ information for their day-to-day running. They have been largely under-explored as a potential data source, but - especially databases that belong to government departments - contain vast amounts of information, sometimes for an entire population. For this reason, administrative data are being used to enhance the 2021 UK census; and the UK’s National Statistician, Professor Sir Ian Diamond, has gone further and recommended that administrative data can help to replace future censuses (HM Government, 2018); censuses are, after all, notoriously expensive.

Often administrative databases are hidden away, with access limited to, for example, staff at government departments. When data are made available to researchers, it is usually via controlled environments, such as the Secure Research Service (SRS), a facility within the Office for National Statistics (ONS). To access data within the SRS, researchers have to first undertake formal training, then submit project applications and then, depending on the data’s confidentiality, process the data in safe rooms. While this procedure is necessary, it can be a time-consuming process that may deter researchers. In rare cases, it is possible to release open data, which is when data are released into the public domain for anyone to access.

Protecting data confidentiality is the main priority when disseminating administrative data. In the UK, the General Data Protection Regulation (GDPR) means that businesses and organisations are legally obliged to adhere to certain standards with regards to anonymisation when processing personal data (Information Commissioner’s Office, 2020). Traditionally, anonymisation is achieved through applying statistical disclosure control (SDC) methods (see Willenborg and De Waal (1996) for a review of such methods). Particularly stringent anonymisation techniques are required for administrative data - even if the data are released in a secure environment - since individuals do not supply their own information as they would in a survey and, as such, even minor disclosures could be very serious. Disclosures of sensitive information would also adversely affect the reputations of those involved in processing the data. Strict guarantees of privacy are essential.
The use of synthetic data (Rubin, 1993; Little, 1993) to protect data confidentiality continues to attract attention. Synthetic data sets occupy a unique position within the vast array of SDC methods. Whereas traditional methods typically perturb or suppress the original data until a satisfactory level of protection is attained, synthetic data methods involve constructing new data sets by simulating from models fitted to the original data.

In 1993 the *Journal of Official Statistics* published a special issue on data confidentiality. Two contributions therein planted the seed for the growth of synthetic data sets. Rubin (1993) proposed to multiply impute values for those individuals in the population who were not sampled in the original data and release simple random samples; these are now widely known as fully synthetic data sets (Raghunathan et al., 2003). Little (1993) proposed a similar idea whereby only the data’s sensitive values are replaced; these are now widely known as partially synthetic data sets (Reiter, 2003).

The idea is that the synthetic data preserve the statistical properties of the original data. In an ideal scenario, synthetic data provide analysts with identical inferences to those that would have been obtained had the analysis been performed on the real data, but as values are not real, disclosure risks are minimal. Re-identification becomes meaningless in fully synthetic data because individuals in the synthetic data do not directly pertain to individuals in the original data. This is especially beneficial for administrative data, when a database may hold information for an entire population, and so where there is no natural protection through sampling uncertainty, that is, uncertainty as to whether an individual was actually included in the original data.

The risk-utility trade-off is inherent in all data dissemination: high utility typically comes at the expense of high risk of disclosure. The ONS devised a spectrum (Bates et al., 2019) as a way of classifying the position of synthetic data with respect to this trade-off. At one end of the spectrum are “structural” synthetic data sets where only the data’s general structure are preserved, such as variable names and variable types; these could be employed as test data, that is, data on which researchers can first run their analyses - to identify, for example, any issues with code - before repeating their analyses on the original data. At the other end of the spectrum are “replica” synthetic data sets, which are designed to be analysed in place of the original data. As synthetic data sets are capable of substantially reducing disclosure risk, data
previously locked away could be made available to researchers in either secure environments or, potentially, as open data. The former could lie at the replica end of the spectrum with the later at the structural end.

Synthetic data arose from multiple imputation for missing data. Traditionally an appealing feature of multiple imputation was that the burden of imputing missing values fell on the imputer - a trained statistical modeller - rather than the analyst, who may be less well-versed in Statistics. This philosophy carried over into the development of synthesis methods. However, synthesis methods increasingly utilise complex computational techniques, necessitating specific non-trivial modelling decisions that require specialist training to implement effectively. This is coupled with data-holders (many of whom would not be trained in these advanced statistical methods) taking greater interest in producing their own synthetic data and thus retaining greater control over the synthesis process. There is thus growing appeal in developing synthesis methods that also ease the burden on the synthesizer while still generating appropriate synthetic data that satisfy data-holders’ requirements. This is a key motivating principle that underpins our proposed methodology.

This paper introduces synthesis methods whereby, through tweaking a parameter, the synthesizer can immediately generate synthetic data with different levels of disclosure risk to suit the data’s purpose and environment; that is, the parameter determines whether - using the terminology of Bates et al. (2019) - structural or replica synthetic data sets are generated (or somewhere in-between). The purpose of this paper is to show that synthetic data can address the significant challenges faced when gaining access to administrative databases, and result in a viable option for releasing data. We thus hope this will stimulate interest, and facilitate further development, into synthetic administrative databases.

This paper is structured as follows. Section 2 reviews existing synthesis methods, specifically in relation to categorical variables. Section 3 considers particular challenges faced when synthesizing large administrative databases - and thus motivates the development of new synthesis frameworks. Section 4 introduces this paper’s contribution to the field: the use of saturated models, that allow count distributions’ properties to be exploited. Section 5 looks at the problem posed by zero counts in the original data. And finally, Section 6 presents an empirical illustration: the synthesis of a database which is representative of the English Schools Census.
2 Existing methods of synthetic data generation

Suppose a synthesizer wishes to synthesize a microdata set \( Y = (Y_1, Y_2, \ldots, Y_p) \) comprising \( n \) units (\( n \) rows) completely observed over \( p \) variables (\( p \) columns), forming a \( n \times p \) matrix where the \((i,j)\)th element is the observed value \( Y_{ij} \): unit \( i \)'s observation on variable \( j \).

When all variables are categorical, there are a finite number of possible observations that any individual \( i \) can take, which is determined by the number of category combinations across variables. This means that, without loss of information, the data can be expressed as a frequency table, where the frequencies give the number of times the combinations of categories are observed. In general, if there are \( p \) categorical variables with \( m_1, \ldots, m_p \) categories, respectively, then the data can be cross-tabulated and expressed as a table with \( m_1 \times \ldots \times m_p \) cell counts, where each count gives the number of individuals who belong to a particular cell.

The first step in synthetic data generation involves modelling the joint multivariate distribution of the original data; for categorical data, this can be carried out at either the microdata level or at the aggregated (tabular) level. The second step involves generating synthetic values through simulating from these models fitted to the original data. Drechsler (2011) describes two broad methods for generating synthetic data: conditional and joint approaches.

2.1 Conditional approaches

The conditional approaches tend to model the original data at the microdata level by decomposing the original data’s joint multivariate distribution \( Y = (Y_1, Y_2, \ldots, Y_p) \) into a product of conditional univariate distributions, that is

\[
p(Y_1, Y_2, \ldots, Y_p) = p(Y_1) \prod_{j=2}^{p} p(Y_j \mid Y_{j-1}, \ldots, Y_2, Y_1).
\]  

(1)

Separate models can then be specified and fitted to each of these conditional distributions. This approach is flexible in the sense that it can account for different variable types, such as continuous, binary and categorical variables; for categorical variables, multinomial logistic regression models could be fitted to each variable, for example.
2.1.1 Multinomial logistic regression

Multinomial logistic regression models are an obvious choice for synthesizing categorical variables. Although not strictly a generalized linear model (GLM) owing to the multivariate response, the multinomial logistic regression model can be viewed as an extension to the (binary) logistic regression model to the case where the response has three or more levels.

When there are many regression coefficients, fitting these models is beyond the capabilities of the algorithms used in standard statistical software. However, when all of the model’s covariates are categorical, the time taken to obtain the regression coefficients’ maximum likelihood estimates (MLEs) can be substantially reduced by utilising the Poisson-multinomial equivalence: every multinomial model has a corresponding Poisson log-linear model; see Lang (1996). A specific advantage for large categorical data sets is that this allows the iterative proportional fitting (IPF) algorithm (Deming and Stephan, 1940) to be used, which provides a quick-and-easy route to obtain the model’s fitted values (the expected counts). However a downside of IPF is that, whilst expected counts are obtained, regression coefficients’ MLEs are not. This has implications for generating fully synthetic data as described by Rubin (1993), where parameters’ estimates and standard errors are intrinsic to deriving parameters’ posterior distributions.

2.1.2 Classification and regression trees (CART)

Developed by Breiman et al. (1984), CART can be viewed as a non-parametric analogue to the GLM. It was considered as a method to generate partially synthetic data by Reiter (2005). CART generates synthetic data sequentially, by growing a separate tree for each variable, conditional on all other other variables in the data. Its appeal has increased with the synthpop R package (Nowok et al., 2016), for which CART is the default synthesis method. A logical extension is the use of random forests for synthesis (Caiola and Reiter, 2010). Also developed by Breiman (2001), random forests grow multiple trees per variable. Drechsler and Reiter (2011) demonstrated the effectiveness of these non-parametric tree-based methods for synthesis, relative to model-based approaches.

Similarly, machine learning techniques are becoming an increasingly popular area of research in relation to synthetic data, such as the use of generative adversarial networks (GANs)
However, a disadvantage with many of these methods is that, while they can synthesize large categorical data sets, the time taken to execute the synthesis can render them infeasible.

2.1.3 The DPMPM synthesizer

Fully synthetic categorical data can be generated via Dirichlet process mixture of products of multinomial (DPMPM) distributions (Si and Reiter, 2013; Hu et al., 2014), which is the Bayesian analogue to the latent class model. Each individual is assumed to belong, independently, to one of \( F \geq 1 \) latent classes and then class-specific multinomial distributions are fitted, resulting in a mixture of multinomial distributions. The mixtures are estimated non-parametrically using Dirichlet process mixtures, and the use of mixtures takes away the need to specify models for every variable.

As the model has a fully Bayesian specification, Markov-Chain Monte Carlo (MCMC) methods are required to obtain inferences. It can be carried out via the \( \text{NPBayesImputeCat} \) R package (Hu et al., 2020); the package is capable of accounting for structural zeros. As with the non-parametric tree-based methods, it becomes infeasible to fit this method to large categorical data sets.

2.2 Joint modelling approaches

Alternatively, as categorical data can be equally expressed in a tabular format, that is, as a vector of counts, the data can be synthesized at the aggregated level, rather than the individual level by fitting a model to the entire cross-classified table.

2.2.1 The Poisson log-linear model

The entire data set can be modelled by a Poisson log-linear model, which assumes that the counts are independent and Poisson distributed. The model has a representation as a generalized linear model, in which it is parameterized by an intercept term, main effects and interaction effects. The interactions pertain to associations between variables; whenever an interaction is set to zero, independence is assumed between those variables. Model selection involves setting interactions to zero, that is, assuming the non-existence of certain relationships. The null
model assumes equiprobability: the expected cell counts are all equal. At the other extreme, the saturated model yields expected counts that are identical to the observed counts.

The model’s minimal sufficient statistics are the observed marginal tables for the highest order terms included in the model. For example, in the all two-way interaction model, all the observed two-way marginal tables. Practically, this means that the synthesizer does not require access to the full original table when synthesizing the data in this way. As with the multinomial model, expected counts from the fitted model can be obtained quickly via the IPF algorithm.

### 2.2.2 Hierarchical Bayesian Poisson log-linear model

Graham and Penny (2007) propose a hierarchical Bayesian Poisson log-linear model to synthesize categorical data. They model \( f_i \), the \( i \)th cell count of the multi-way table, as follows:

\[
\begin{align*}
  f_i | X_i, \lambda_i & \sim \text{Poisson}(\lambda_i) \\
  \lambda_i | X_i, \beta, \xi & \sim \text{Gamma}(\xi, \xi/\mu_i), \text{ with } \log(\mu_i) = X_i \beta.
\end{align*}
\]

A synthetic count \( f_i^{\text{syn}} \) is obtained by taking a draw from this model. The parameter \( \lambda_i \), the expected value of the \( i \)th cell count, is assumed to be Gamma distributed (the Poisson’s conjugate prior). The hyperparameter \( \xi \) controls the variance of \( \lambda_i \). The mean of \( \lambda_i \) is equal to \( \mu_i \), which, in turn, is the expected value for the \( i \)th cell, obtained from the Poisson log-linear model fitted to the original data; \( \beta \) is the vector of log-linear model parameters; and \( X_i \) is the vector of variable values which describe the \( i \)th cell. If prior distributions are also specified for the hyper-parameters \( \beta \) and \( \xi \), then the model has a fully Bayesian specification.

The Gamma prior means that the marginal distribution of \( f_i \) is the negative binomial distribution. This provides additional uncertainty - and therefore confidentiality protection - to the synthesis, as it means that both \( \lambda_i \) and \( f_i \) are stochastic. In addition, there is also model uncertainty as assumptions are made as to which interactions exist (the original counts are smoothed). Besides, since Graham and Penny propose a fully synthetic approach, the log-linear parameters \( \beta \) are also assumed to be stochastic; values are drawn from \( \beta \)'s posterior predictive distribution.
3 Challenges faced when synthesizing administrative data

Besides the usual challenges faced when synthesizing data - such as finding the optimal balance between risk and utility - there are additional challenges when synthesizing administrative databases. Henceforth it is assumed that all variables in our administrative database are categorical. This assumption is not as strong as it might first appear. Continuous variables are often subject to rounding, for example, ages given as integers. Continuous variables can also be categorized by the synthesizer: ages can be converted to integers. Besides, in an observed data set \( (n \) respondents), the continuous variables take a finite number of values (maximum of \( n \) values). This assumption allows the data to be expressed as a frequency table, with a vector of counts denoting the number of times each category combination is observed.

3.1 Large data sets

A major challenge when synthesizing administrative databases is their size: they are typically much larger than traditional survey data sets, both in terms of the number of records (rows) and the number of variables (columns). Variables with many categories increases the number of parameters to estimate and causes the computational times of many existing methods to increase dramatically.

The issue with computational time also extends to post-synthesis evaluations that examine the synthetic data’s risk and utility. For example, the Bayesian estimation of disclosure risk given in [Reiter et al. (2014)] is computationally intensive even for relatively small survey data sets, as it involves continually re-fitting the synthesis model for every individual in the data; ways, such as importance sampling, have already been incorporated to save time.

3.2 Random and structural zeros

The presence of large categorical variables means that multi-way tables are very sparse, that is, they have a high proportion of cells with zero counts. The zero cells can be said to comprise two sorts. The first sort - “random zeros” - are zero cells that arise through random chance: an individual with a given set of characteristics could have occurred but did not in the observed data. The second sort - “structural zeros” - are zeros that arise because a given set of characteristics is not possible, for example, a child aged three attending a secondary school.
It is desirable that post-synthesis, all structural zeros remain zero, and some random zeros are transformed into non-zero counts. Whenever random zeros are not synthesized to non-zeros, but some non-zeros are synthesized to zeros, it results in an inflated number of zeros in the synthetic data. This issue is discussed in greater detail in Section 5.

3.3 An unclearly defined sampling frame

Typically, administrative data are more akin to a census than a survey, and hence more akin to population data than sample data. Moreover, administrative data may not constitute a simple random sample; for example, the English School Census includes pupils who attend state-funded schools; pupils who attend privately-funded schools are excluded. This requires careful consideration from an inferential perspective.

Similarly, considerations are required from a risk perspective. The well established notions of sample uniqueness and population uniqueness - that is, belonging to a cell with a count of one in the sample and population, respectively - are less well-defined. Risk evaluations in SDC often revolve around estimating whether an individual, unique in the sample, is also unique in the population (Skinner et al., 1994). These concepts become hazy when dealing with administrative data.

3.3.1 Obtaining inferences from synthetic administrative data

In some cases it may be possible to assume that the data represent a sample drawn from a super-population. This facilitates the use of existing combining rules to obtain valid point estimates and variance estimates for a (super-) population parameter \( Q \) from synthetic data. There are two sources of uncertainty that need to be accounted for: the sampling uncertainty inherent in the original data; and the uncertainty owing to synthesis. (The original data are subject to the first source of uncertainty, but not the second.) The combining rules depend on - amongst other things - the type of synthetic data generated; for example, Reiter (2003) derives a valid variance estimator for population inferences from multiply imputed partially synthetic data.

For brevity, this paper focuses on generating just \( m = 1 \) synthetic data set. Under particular conditions - which include that the original data constitute a simple random sample - the
estimator given in Raab et al. (2016) provides valid variance estimates from just $m = 1$ synthetic data set,

$$\sqrt{\text{var}(\hat{Q})} = \bar{v}_m(n_{\text{syn}}/n + 1/m),$$

where $\bar{v}_m$ is the mean variance estimate across the $m$ synthetic data sets; $n_{\text{syn}}$ and $n$ are the “sample” sizes of the synthetic and original data, respectively; and $m$ is the number of synthetic data sets. However, we note that the proposed synthesis methods in this paper could easily be used to generate multiple synthetic data sets.

4 Scalable synthesis methods for large categorical data sets using saturated count models

Modelling for the purpose of generating synthetic data holds a unique position within statistical modelling: the objective is neither inferential nor predictive. Instead, the objective is solely to obtain synthetic data that resemble the original, but where disclosure risks are sufficiently low, that is, the model is not of interest per se. Our methodology exploits this, along with the notion that high-quality synthetic data are obtained by sufficiently moving away from the original data.

Saturated models have little value when, for example, estimating parameters from the data, but saturated models do perfectly preserve all associations in categorical data, which avoids distorting joint distributions at the modelling stage. Synthetic data are entirely dependent on the synthesis model, for example, omitting an interaction in a synthesis model would result in no association in the subsequent synthetic data. When the imputation model is less complex than the analyst’s model that is later fitted to the synthetic data, the analyst’s model is said to be “uncongenial” to the imputation model (Meng, 1994). Therefore, to preserve relationships, over-fitting is preferable to under-fitting; and fitting saturated models is over-fitting in its most extreme.

Saturated synthesis models eliminate bias and model uncertainty, so the synthetic data perfectly reproduce the properties of the original. Consequently, the synthetic counts have an unbiasedness property: as the synthetic sample size increases, the synthetic cell proportions
tend towards the proportions in the original data through the Central Limit Theorem.

There are two main advantages of the synthetic counts’ unbiasedness. First, having fewer sources of uncertainty in the synthesis - there is still, of course, the uncertainty that arises through simulation - means that the synthesizer has greater control of the variability in the system. As a result, certain properties of the synthetic data can be found analytically, rather than needing to be found empirically. For example, the probability that an original count of one is synthesized to one depends on the model’s probability mass function, only. As synthetic data generation is an iterative process - data sets are generated, evaluated, improved upon and then regenerated - knowing some properties beforehand may quicken this process: the synthesizer is not entirely in the dark.

Second, it may also mean that fewer synthetic data sets are required to obtain reliable inferences. The initial synthetic data literature was rooted in the multiple imputation due to non-response literature, see Rubin (1987), which seeks to capture the missing values’ underlying distribution. Bias and uncertainty are inevitable and so multiple synthetic data sets allow point estimates’ uncertainty to be properly accounted for. However, using saturated synthesis models gives greater credibility to inferences made using just one synthetic data set, as is the case in this paper. This in itself has two further advantages. It can reduce the disclosure risk: fewer records imply fewer potential re-identifications (Reiter and Mitra, 2009). Furthermore, it can simplify things for the analyst, as combining rules, which are required when there are multiple data sets, can be cumbersome, especially for non-statisticians. Instead, owing to the unbiasedness property of the synthetic data, generating just one synthetic data set is a viable option and, whilst variances may need to be adjusted to obtain valid population inferences (in situations where this is relevant), this is relatively more straightforward than computing and combining estimates from various different data sets.

4.1 The Poisson model

Suppose each count in the multi-way table is assumed to be independent and Poisson distributed, with mean equal to the observed count. Equivalently, suppose a saturated Poisson log-linear model is fitted to the entire table, so that expected cell counts in the fitted model are identical to the original counts. Synthetic counts can be generated by simulating from these
Poisson random variables, which adds stochastic error to the original counts and masks their true values.

The Poisson distribution’s probability mass function provides the probability that an arbitrary synthetic count \( f_{\text{syn}} \) equals \( N_2 \), given that the original count \( f \) equals \( N_1 \):

\[
p(f_{\text{syn}} = N_2 \mid f = N_1) = \frac{\exp(-N_1)N_1^{N_2}}{k_2!},
\]

where \( N_1 \) and \( N_2 \) are non-negative integers. The mean and variance of \( f_{\text{syn}} \) are both equal to \( N_1 \). While the Poisson distribution is degenerate when the mean is zero, practically, this does not cause problems for the method: whenever the original count is zero, the synthetic count is also zero. Note that this feature also naturally accounts for structural zeros present in the original data, which would remain zero.

So the synthesis involves simulation from a fully saturated log-linear model. As all original values are replaced, the data are completely synthesized by the terminology of [Raab et al. (2016)]. However, somewhat confusingly, the resulting data sets are partially synthetic in the sense of [Reiter (2003)], rather than fully synthetic in the sense of [Raghunathan et al. (2003)], as values are synthesized for the same individuals as in the original data. Finally, the synthesis is via the “plug-in approach” (Reiter and Kinney, 2012), that is, the Bayesian posterior predictive distribution is not used and synthetic values are drawn using the parameter estimates from the model. However, the fully Bayesian approach could also be implemented here as well.

It follows, naturally, that the expected “sample” size of the synthetic data \( n_{\text{syn}} \) is equal to \( n \), the sample size of the original data. The value \( n_{\text{syn}} \) is the sum of the cell counts in the multi-way table - the table’s grand total; and as these counts are independent Poisson random variables whose means sum to \( n \), \( n_{\text{syn}} \) is also a Poisson random variable with mean \( n \). Yet it need not be the case that \( \mathbb{E}[n_{\text{syn}}] = n \). As [Raab et al. (2016)] demonstrate, when synthesis involves replacing all original values, the synthetic sample size \( n_{\text{syn}} \) can be higher or lower than the original, \( n \).

4.2 The metrics \( \tau_1, \tau_2, \tau_3 \) and \( \tau_4 \)

The following four metrics are intrinsic to understanding the disclosure risk properties of this method. They measure the relationship between cell sizes in original and synthetic categorical
data. When parametric count models are used, these metrics can be represented analytically.

1. \( \tau_1(k) := \) The proportion of cells of size \( k \) in the synthetic data.

2. \( \tau_2(k) := \) The proportion of cells of size \( k \) in the observed data.

3. \( \tau_3(k) := \) The proportion of cells of size \( k \) in the original data, which remain of size \( k \) in the synthetic data.

4. \( \tau_4(k) := \) The proportion of cells of size \( k \) in the synthetic data, which were also of size \( k \) in the original data.

The metrics are linked in the following way:

\[
p(f = k | f^{\text{syn}} = k) \cdot p(f^{\text{syn}} = k) = p(f^{\text{syn}} = k | f = k) \cdot p(f = k)
\]

\[
\tau_4(k) \cdot \tau_1(k) = \tau_3(k) \cdot \tau_2(k)
\]  

(4)

Metrics \( \tau_1 \), \( \tau_2 \) and \( \tau_4 \) are conditional on the distribution of cell sizes in the original data, whereas \( \tau_3 \) is not. To illustrate, suppose an original data set is comprised entirely of cell counts of one and that the Poisson distribution is used to generate synthetic counts, then \( \tau_3(1) = \exp(-1) \) and \( \tau_4(1) = 1 \). Now suppose an original data set comprises a range of non-zero counts. Then \( \tau_3(1) = \exp(-1) \) remains unchanged, but \( \tau_4(1) \leq 1 \) because a synthetic cell count of one could have originated from any non-zero original cell. Hence \( \tau_4 \) depends on the original data, whereas \( \tau_3 \) does not. The next section illustrates how analytical expressions can be obtained for the four \( \tau \) metrics.

4.2.1 The metrics \( \tau_1 \) and \( \tau_2 \)

The metric \( \tau_1(k) \) is the proportion of cells of size \( k \) in the synthetic data, that is,

\[
\tau_1(k) = p(f^{\text{syn}} = k) \quad k = 0, 1, 2, \ldots
\]

(5)

which, by the law of total probability,

\[
= \sum_{j=0}^{\infty} p(f^{\text{syn}} = k | f = j) \cdot p(f = j) = \sum_{j=0}^{\infty} \frac{\exp(-j)j^k}{k!} \cdot \tau_2(j),
\]
where $\tau_2(k)$ is simply the proportion of cells with a count of $k$ in the original data that we denote by,

$$\tau_2(k) = p(f = k) \quad k = 0, 1, 2, \ldots .$$

(6)

### 4.2.2 The metric $\tau_3$

The metric $\tau_3(k)$ gives the proportion of cells of size $k$ in the original data, which remain of size $k$ in the synthetic data.

$$\tau_3(k) = p(f^\text{syn} = k | f = k) = \frac{\exp(-k)k^k}{k!} \quad k = 0, 1, 2, \ldots .$$

(7)

### 4.2.3 The metric $\tau_4$

Recall from (4) that $\tau_4(k)$ - the proportion of cells of size $k$ in the synthetic data, which were also of size $k$ in the original data - can be expressed in terms of the other $\tau$ metrics, that is, $\tau_4(k) = \tau_3(k)\tau_2(k)/\tau_1(k)$. The expression for $\tau_4(k)$ is therefore given as:

$$\tau_4(k) = p(f = k | f^\text{syn} = k) \quad k = 0, 1, 2, \ldots .$$

$$= \frac{\exp(-k)k^k}{k!} \cdot \tau_2(k) \left/ \left( \sum_{j=0}^{\infty} \frac{\exp(-j)j^k}{j!} \cdot \tau_2(j) \right) \right..$$

(8)

### 4.2.4 The $\tau$ metrics’ link to disclosure risk

The notion of disclosure risk is different for synthetic data in tabular format, than for microdata. When the original data are aggregated and synthesized, the direct links between individuals in the original and synthetic data are lost. To illustrate, suppose an original count of, say, 10 is synthesized to 8. Then it cannot be determined to whom those 8 individuals relate: do they relate to 8 of the original 10, and, if so, which 8? Or, more likely, the 8 would comprise at least one individual who originally belonged to a different cell, and so it is impossible to determine the synthesized values for a specific individual in the original data. Instead, disclosure risk here revolves around prediction disclosure (Skinner, 1992) (also known as attribute disclosure): the revealing of information about individuals’ sensitive values.
Uniques are individuals who belong to a cell with a count of one, and are considered to be most at risk of disclosure. An important value with respect to risk is $\tau_4(1)$: the proportion of uniques in the synthetic data which are also unique in the original data. This is arguably more important than $\tau_3(1)$: the proportion of uniques in the original data which are also unique in the synthetic data. This is because the former assumes knowledge of the synthetic data, which an attacker has access to. The latter assumes knowledge of the original, which an attacker cannot access.

### 4.3 Two-parameter count distributions

The Poisson variability (variance equal to the mean), may not provide sufficient protection to at-risk records in the original data. For example, with the Poisson, the metric $\tau_3(1)$ is always equal to $\exp(-1)$, and this cannot be altered by the synthesizer. The variability can be increased - without introducing bias - using overdispersed count models in place of the Poisson. These models are suitable when the sampling variance exceeds that which is expected from the Poisson. This may arise through, for example, clustered observations. These distributions - such as the negative binomial - tend to have multiple parameters, where one parameter controls the variability. With this additional flexibility, the synthesizer can determine ‘a priori’ the variability required to achieve a pre-specified desired level of confidentiality protection; that is, the synthesizer can decide where to position the synthetic data in relation to the risk-utility trade-off. Henceforth, all parameterisations are as presented in R package `gamlss.dist` (Stasinopoulos et al., 2007; Rigby et al., 2019), which provides a user-friendly way to access a plethora of distributions.

#### 4.3.1 Negative binomial (NBI)

The negative binomial distribution (NBI) is a two-parameter count model with a range of parameterisations. One parameterisation originates from a Poisson-Gamma mixture. Each synthetic count $f_{\text{syn}}$ is assumed to be Poisson distributed, but where the Poisson mean - in our case the original count $f$ - is itself stochastic, specifically, Gamma distributed. The marginal distribution of $f_{\text{syn}}$ is then NBI. As with the Poisson, the NBI’s probability mass function provides the probability that a synthetic count $f_{\text{syn}}$ equals $N_2$, given the original count $f$.
equals $N_1$,

\[
f^{\text{syn}} \mid f = N_1, \gamma \sim \text{Poisson}(N_1 \gamma) \quad \text{with} \quad \gamma \sim \text{Gamma}(1/\sigma, \sigma),
\]

\[
\Rightarrow f^{\text{syn}} \mid f = N_1, \sigma \sim \text{NBI}(N_1, \sigma)
\]

\[
p(f^{\text{syn}} = N_2 \mid f = N_1, \sigma) = \frac{\Gamma(N_2 + 1/\sigma)}{\Gamma(N_2 + 1) \cdot \Gamma(1/\sigma)} \cdot \left(\frac{\sigma N_1}{1 + \sigma N_1}\right)^{N_2} \cdot \left(\frac{1}{1 + \sigma N_1}\right)^{1/\sigma}. \quad (9)
\]

The parameter $\sigma$ controls the variance of the model. The Poisson($N_1$) distribution is recovered as $\sigma \to 0$. The mean and variance of $f^{\text{syn}}$ are given as:

\[
E[f^{\text{syn}} \mid f = N_1, \sigma] = N_1, \quad \text{and} \quad \text{Var}[f^{\text{syn}} \mid f = N_1, \sigma] = N_1 + \sigma N_1^2.
\]

As with the Poisson, explicit expressions can be derived for the various $\tau$ metrics.

### 4.3.2 Poisson-inverse Gaussian (PIG)

The Poisson-inverse Gaussian (PIG) is another explicit two-parameter count distribution, suitable for modelling data that are too overdispersed for the Poisson distribution. It is derived from an inverse Gaussian distribution mixed with the Poisson. The PIG distribution has similar properties to the NBI distribution: both have identical mean and variance functions. A subtle difference is that the PIG has a heavier right tail.

When the PIG is used for synthesis, the probability that an arbitrary synthetic count $f^{\text{syn}}$ equals $N_2$, given that the original count $f$ equals $N_1$ is,

\[
p(f^{\text{syn}} = N_2 \mid f = N_1, \sigma) = \left(\frac{2c}{\pi}\right)^{1/2} \cdot \frac{N_1^{N_2} \exp(1/\sigma) K_{N_2-1/2}(c)}{(c\sigma)^{N_2} N_2!}, \quad (10)
\]

where $c^2 = \frac{1}{\sigma^2} + \frac{2N_1}{\sigma}$ and $K_\lambda(t) = \frac{1}{2} \int_0^\infty x^{\lambda-1} \exp\left\{ -\frac{1}{2} t(x + x^{-1}) \right\} \, dx$. 

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is the modified Bessel function of the third kind. The Poisson($N_1$) is the limiting distribution as $\sigma \to 0$. As with the NBI model, the mean and variance are given as:

$$\mathbb{E}[f_{\text{syn}} = N_2 \mid f = N_1, \sigma] = N_1, \quad \text{and} \quad \text{Var}[f_{\text{syn}} = N_2 \mid f = N_1, \sigma] = N_1 + \sigma N_1^2.$$  

As with the Poisson and NBI, explicit expressions can be derived for the various $\tau$ metrics.

4.3.3 The synthesizer’s interpretation of two-parameter count distributions

In the Poisson model, the synthesizer does not have to set any model parameters. In two-parameter models, the synthesizer can raise $\sigma$ (in the parameterisations above) to generate synthetic data with a desired value for $\tau_3(1)$ or $\tau_4(1)$. This would reduce the synthetic data’s utility but, importantly, also reduce risk, as uniques in the original data are less likely to be unique in the synthetic data.

5 Dealing with zero counts through additive smoothing

There is a downside with using saturated models that needs addressing: cells with a count of zero (zero cells) in the original data always yield zero cells in the synthetic data, which results in too many zero cells being synthesized. The zero cells in the synthetic data comprise all zero cells in the original data, plus some non-zero cells that become zero through simulation. Depending on the number of excess zero cells, this could affect the utility of the synthetic data.

This issue also has implications for disclosure risk. The issue is not so much with the zero cells themselves, which are relatively low risk, but cells with counts of one (uniques). When zero cells remain zero, it follows that uniques in the synthetic data cannot have originated from zero cells; this increases the probability that uniques in the synthetic data originated from uniques in the original data, this then increases the value of $\tau_4(1)$. This is especially relevant for sparse data. In its most extreme, sparse categorical data are comprised entirely of zero cells and uniques. So again, if zero cells remain zero, then $\tau_4(1) = 1$ because a synthetic cell count of one must have originated from an original cell count of one.
The addition of a pseudocount $\alpha > 0$ to all non-structural zero cells in the original data (structural zeros should remain zero) opens up the possibility of zero counts being synthesized to non-zeros. For example, when $\alpha > 0$ is added to every non-structural zero cell in the original data, the probability that the corresponding synthetic cell count $f^{\text{syn}}$ is equal to $N_2$ is:

$$p(f^{\text{syn}} = N_2 \mid f = 0, \alpha) = \frac{\exp(-\alpha) \cdot \alpha^{N_2}}{N_2!},$$

when the Poisson model is used. The $\alpha > 0$ affects $\tau_1(k)$ and $\tau_4(k)$ for all $k$, two metrics that depend on the original data, as increasing $\alpha$ decreases the proportion of zero cells and increases the proportion of non-zero cells in the synthetic data; the values of $\tau_2(k)$ and $\tau_3(k)$ remain unaffected.

When $\alpha = 0$, the inequality $\tau_1(0) \geq \tau_2(0)$ holds, since zero cells in the synthetic data comprise all zero cells in the original data $\tau_2(0)$, plus those that randomly become zero through synthesis. However, as $\alpha$ increases, the difference between $\tau_1(0)$ and $\tau_2(0)$ narrows.

An attractive property might be for the synthetic data to have the same proportion of zero cells as the original data, that is, for $\tau_1(0) = \tau_2(0)$. Under the Poisson model this is achieved by setting

$$\alpha^* = -\log \left\{ 1 - \frac{1}{\tau_2(0)} \sum_{j=1}^{\infty} \exp(-j) \cdot \tau_2(j) \right\}.$$ 

The required value of $\alpha^*$ would also depend on $\sigma$ in the two-parameter distributions.

Although achieving $\tau_1(0) = \tau_2(0)$ is an attractive property, overall it has an adverse effect, as $\alpha$ effectively perturbs the original data - and therefore introduces bias into the synthesis - a small $\alpha$ is preferable with respect to data utility. However, $\alpha$ can also play a role in controlling disclosure risk. Zero cells with small $\alpha > 0$ added to their count are much more likely to be synthesized to have a count of one than any other non-zero value. For example, when $\alpha = 0.1$, a zero count is exactly twenty times more likely to be synthesized to have a count of one than two under the Poisson model. So $\alpha > 0$ increases the number of uniques in the synthetic data, and thereby decreases $\tau_4(1)$: the probability that a unique in the synthetic data originated from a unique in the observed data.

An alternative is to choose $\alpha$ such that $\tau_4(1) = p$, where the synthesizer decides what
\( p \in [0, 1] \) is acceptable (a pre-specified level of disclosure risk). Here the value of \( \alpha^* \) must be obtained numerically; under the Poisson model it satisfies,

\[
p = \exp(-1) \cdot \tau_2(1) \bigg/ \left( \alpha^* \exp(-\alpha^*) \cdot \tau_2(0) + \sum_{j=1}^{\infty} j \cdot \exp(-j) \cdot \tau_2(j) \right).
\]

Similar expressions can be derived for the two parameter synthesis models.

6 Empirical study

6.1 The data

The English School Census (ESC) is an administrative database that holds information about pupils in state-funded schools. Every school term the Department for Education (DfE) requests that all nursery, primary and secondary schools, which are fully or partly funded by the state, submit details about the school and its pupils. This is just one example of an administrative database held by a government department, other examples include, but are not limited to, the Patient Register (held by the Department of Health) and the Customer Information Survey (held by the Department for Work and Pensions).

For obvious reasons access to the ESC data, as well as any other administrative data, is highly restricted. However, in previous work conducted by the ONS, a carefully constructed data set using publicly available sources was created to be used as a substitute to the ESC, in order to develop synthesis methods for administrative data. The data have been generated using public 2011 census output tables involving various combinations of Local Authority, sex, age and ethnicity. Language attributes from the census have also been included and artificially expanded to match with categories in the ESC. School phase attributes were also incorporated, some adjustments for migration were applied, and non-response and invalid categories were added to various variables, again taking publicly available information from the census.

We do not consider the two variables measured at the school level for this illustration, and focus instead on the remaining five variables measured at the pupil level. Henceforth, we will

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1Specifically, information from the following public sources were used to create the data:
http://www.nomisweb.co.uk/census/2011; http://www.ons.gov.uk/ons/guide-method/census/2011/census-data/2011-census-user-guide/quality-and-methods/quality/quality-measures/response-and-imputation-rates/index.html; https://www.gov.uk/government/statistics/schools-pupils-and-their-characteristics-january-2014
Table 1: The ESCrep’s variables and their numbers of categories.

| Variable                  | Type     | # Categories |
|---------------------------|----------|--------------|
| Area Code/ Geography (V)  | Categorical | 326          |
| Ethnicity (W)             | Categorical | 20           |
| Sex (X)                   | Categorical | 4            |
| Age (Y)                   | Categorical | 19           |
| Language (Z)              | Categorical | 7            |

Table 2: Distribution of cell sizes in the ESCrep data.

| Cell count | Frequency | % of cells |
|------------|-----------|------------|
| 0          | 3,134,980 | 90.38      |
| 1          | 119,917   | 3.46       |
| 2          | 51,412    | 1.48       |
| 3          | 25,952    | 0.75       |
| 4          | 19,450    | 0.56       |
| 5          | 13,076    | 0.38       |
| 6          | 10,345    | 0.30       |
| 7          | 7,947     | 0.23       |
| 8          | 7,077     | 0.20       |
| 9          | 5,809     | 0.17       |
| 10         | 5,163     | 0.15       |
| 11 ≤       | 67,512    | 1.95       |
| Total      | 3,468,640 | 100        |

refer to this data set as the ESCrep where rep denotes representative. Table 1 summarises the variables present in the ESCrep illustration. The data comprise $n = 8,190,870$ pupils over five categorical variables, giving rise to a multi-way contingency table with $326 \times 20 \times 4 \times 19 \times 7 = 3.5 \times 10^6$ cells. The breakdown of the cell counts are given in Table 2; only 333,660 (9.6%) are non-zero so the data are sparse. There are no structural zeros. While the data are in a sense “simulated” this has been done using real data sources and care has been taken to ensure that the resulting data should reflect, at the very least, the typical structure present in the ESC. As such this is a good example to use to illustrate our synthesis methodology and we would expect similar performance when these methods are applied to the ESC as well as other similar large categorical administrative databases. Importantly, the data have not been generated from a statistical model and thus do not favour ‘a priori’ any given synthesis method.
6.2 The synthesis

The synthesis was carried out in R (version 3.6.3) using the methods described in this paper. The Poisson, NBI and PIG models were compared; just \( m = 1 \) data set was generated for each. The recorded central processing unit (CPU) times to carry this out were 0.2, 0.3 and 162 seconds, respectively; so notably longer for the PIG, albeit this is still much quicker than other methods.

Let \( V, W, X, Y \) and \( Z \) denote the five variables in the data, and let \( f_{vwxyz} \) denote the cell count of a particular cell in the cross-classified table corresponding to category \( v \in V, w \in W, x \in X, y \in Y \) and \( z \in Z \). A synthetic count was then drawn for this cell by,

\[
f_{vwxyz}^{\text{syn}} \sim \text{Poisson}(f_{vwxyz}),
\]

when the Poisson synthesis model was used; or, when either of the two-parameter distributions were used,

\[
f_{vwxyz}^{\text{syn}} \sim \text{NBI}(f_{vwxyz}, \sigma) \quad \text{or} \quad f_{vwxyz}^{\text{syn}} \sim \text{PIG}(f_{vwxyz}, \sigma).
\]

When the Poisson model was employed, the only parameter to be set was \( \alpha \), the pseudocount added to zero cells in the original data. When the two-parameter count models were employed, NBI and PIG, there was the additional “variance parameter” \( \sigma \) to consider.

As mentioned previously, one of the appealing features of using these saturated synthesis models is that it allows the synthesizer to determine properties of the synthesis model ‘a priori’ i.e. prior to synthetic data generation, thus reducing the amount of empirical evaluation necessary during the synthesis. For illustration, Figure 1 (left) compares the effect of \( \sigma \) on the risk metric \( \tau_4(1) \) for the NBI and PIG models: we see for large \( \sigma \) that the risk levels off for the NBI but continues to fall away for the PIG. Figure 1 (right) also looks at \( \tau_4(1) \), but looks at the combined effect of \( \sigma \) and \( \alpha \) when utilising the NBI synthesis model: for all \( \sigma \), \( \tau_4(1) \) declines steadily as \( \alpha \) increases. We see the NBI has a consistently lower \( \tau_4(1) \) value than the Poisson model, as expected.
Figure 1: Left plot shows the risk metric $\tau_d(1)$ as a function of $\sigma$ for when (solid line) the NBI model is used; and (dashed line) when the PIG model is used. Right plot shows, under the NBI synthesis model, how $\alpha$ and $\sigma$ affect $\tau_d(1)$, the proportion of uniques in the synthetic data that were also unique in the original data. The Poisson synthesis model is also present as a comparison here.

### 6.3 Descriptive summaries of risk and utility

Table 3 presents the proportion of cells - at the lowest level of aggregation (five-way margins) - that are with $p\%$ of their original size for different $\sigma$ and $\alpha$. The first block of results considers all cells, while the second block only considers non-zero cells (in the observed data). Smaller values of $p$ can be viewed as summaries of risk while larger values of $p$ measures of utility. We see that the Poisson model has the greatest utility but also the greatest risk. There is little to choose between the NBI and PIG models based on these summaries. As expected, greater $\sigma$ or $\alpha$ lead to greater divergences in original and synthetic cell sizes. These differences are also highlighted in Figures 2 and 3 which plot, for the NBI and PIG respectively, synthetic versus original counts, as well as percentage differences (between synthetic and original counts) versus original count. While the Poisson model ($\sigma = 0$ case) yields points that sit close to the 45° line - that is, strong correlation between synthetic and original counts - this correlation reduces as $\sigma$ increases for both NBI and PIG. The right panels all display a funnel shape, which indicate variability decreases as the observed cell count increases. This is an ideal profile for balancing risk and utility as the riskiest individuals are the ones corresponding to small cell counts, and so the ones we would want the most movement in during synthesis. It is interesting to note that even a relatively small value of $\sigma = 0.01$ introduces a substantive amount of variability into the synthetic cell counts.

Table 4 presents empirical values for the $\tau$ metrics, again for varying $\sigma$ and $\alpha$. The true
values are known prior to synthesis, but a small difference is expected owing to simulation noise. But for cell sizes that are prevalent in the original data - such as zeros and ones - this error is negligible. For example, the empirical value obtained for $\tau_3(1)$ when the Poisson model is used ($\sigma = 0, \alpha = 0$) is 0.3674, which is almost identical to the true value, $\exp(-1)=0.3679$. Table 4 illustrates the suitability of $\alpha$ in reducing risk. The values for $\tau_4(1)$ are substantially lower when $\alpha = 0.02$ than when $\alpha = 0$, for example, when the Poisson model is used, $\tau_4(1)$ equals 0.352 compared to 0.689. For a given $\alpha$ the NBI and PIG models almost always have a lower risk than the Poisson models when considering $\tau_3(1)$ and $\tau_4(1)$ metrics. It is particularly interesting to note varying profiles between synthesis methods and the metrics. For example, if one model has a lower $\tau_3(1)$ value than another this is not necessarily the case when comparing the corresponding $\tau_4(1)$ values. To illustrate, when $\alpha = 0, \sigma = 10$, for $\tau_3(1)$ under NBI, this value is 0.0711 < 0.1532 the value under PIG, but for $\tau_4(1)$, with these same parameter values, the value under NBI is 0.3910 > 0.3387 the value under PIG. The specific choice of synthesis model to use would depend on the synthesizer’s range of permitted values for $\tau_1, \tau_3,$ and $\tau_4$ and choosing the model that best satisfies these requirements.

6.4 Testing analytical validity through log-linear model analysis

In the synthetic data literature, specific utility (Snoke et al., 2018) is often assessed by comparing inferences, such as regression coefficients, obtained from the original and synthetic data. Metrics such as the confidence interval overlap (Karr et al., 2006), can then measure similarities between the estimates.

The synthesizer does not know of course what analyses users of the synthetic data would perform. The synthetic data may support certain analyses, while being “uncongenial” to others (Meng, 1994). Amongst the variables included in the data, which are best described as demographic, there is no obvious response variable. Instead, analysts may be interested in associations between variables, and so a log-linear analysis (Bishop et al., 1975) seems reasonable in this context. It is difficult to obtain parameter estimates and parameters’ variance estimates for the full five-variable data since large amounts of memory and storage are required. To
Table 3: Empirical results showing the proportion of synthetic cell counts that lie within \( p \% \) of the original count. The table includes values for different \( \sigma \) and \( \alpha \), looks at the NBI and PIG synthesis models and considers first all original cell counts and second only non-zero original cells.

| \( p \) | 0.5 | 1 | 5 | 10 | 50 | \( p \) | 0.5 | 1 | 5 | 10 | 50 |
|---|---|---|---|---|---|---|---|---|---|---|---|
| \( \sigma \) | \( \alpha = 0 \) | | | | | | | | | | |
| 0 (Pois.) | 0.927 | 0.927 | 0.931 | 0.935 | 0.967 | 0.927 | 0.927 | 0.931 | 0.935 | 0.967 | | | | | | | | |
| 0.1 | 0.924 | 0.924 | 0.926 | 0.928 | 0.961 | 0.925 | 0.925 | 0.926 | 0.928 | 0.961 | | | | | | | | |
| 0.5 | 0.920 | 0.920 | 0.922 | 0.946 | 0.921 | 0.921 | 0.921 | 0.923 | 0.949 | | | | | | | | |
| 1 | 0.917 | 0.917 | 0.917 | 0.918 | 0.937 | 0.918 | 0.918 | 0.919 | 0.920 | 0.942 | | | | | | | |
| 2 | 0.914 | 0.914 | 0.914 | 0.914 | 0.928 | 0.916 | 0.916 | 0.916 | 0.917 | 0.935 | | | | | | | |
| 5 | 0.910 | 0.910 | 0.910 | 0.910 | 0.918 | 0.913 | 0.913 | 0.913 | 0.914 | 0.927 | | | | | | | |
| 10 | 0.907 | 0.907 | 0.907 | 0.908 | 0.912 | 0.911 | 0.911 | 0.911 | 0.912 | 0.921 | | | | | | | |
| \( \alpha = 0.02 \) | | | | | | | | | | | | | | | | | | | |
| 0 (Pois.) | 0.909 | 0.910 | 0.913 | 0.917 | 0.949 | 0.909 | 0.910 | 0.913 | 0.917 | 0.949 | | | | | | | |
| 0.1 | 0.907 | 0.907 | 0.908 | 0.910 | 0.943 | 0.907 | 0.907 | 0.908 | 0.910 | 0.943 | | | | | | | |
| 0.5 | 0.902 | 0.902 | 0.903 | 0.904 | 0.928 | 0.903 | 0.903 | 0.903 | 0.905 | 0.931 | | | | | | | |
| 1 | 0.899 | 0.899 | 0.900 | 0.901 | 0.920 | 0.901 | 0.901 | 0.901 | 0.902 | 0.924 | | | | | | | |
| 2 | 0.896 | 0.896 | 0.896 | 0.897 | 0.911 | 0.899 | 0.899 | 0.899 | 0.900 | 0.918 | | | | | | | |
| 5 | 0.893 | 0.893 | 0.893 | 0.893 | 0.901 | 0.896 | 0.896 | 0.896 | 0.897 | 0.909 | | | | | | | |
| 10 | 0.891 | 0.891 | 0.891 | 0.891 | 0.896 | 0.895 | 0.895 | 0.895 | 0.895 | 0.905 | | | | | | | |
| \( \sigma \) | \( \alpha = 0 \) | | | | | | | | | | | | | | | | | | | |
| 0 (Pois.) | 0.242 | 0.245 | 0.280 | 0.327 | 0.658 | 0.242 | 0.245 | 0.280 | 0.327 | 0.658 | | | | | | | | |
| 0.1 | 0.214 | 0.215 | 0.226 | 0.252 | 0.592 | 0.217 | 0.218 | 0.229 | 0.256 | 0.598 | | | | | | | |
| 0.5 | 0.167 | 0.167 | 0.173 | 0.187 | 0.437 | 0.177 | 0.177 | 0.182 | 0.197 | 0.468 | | | | | | | |
| 1 | 0.136 | 0.136 | 0.140 | 0.150 | 0.347 | 0.153 | 0.153 | 0.157 | 0.167 | 0.395 | | | | | | | |
| 2 | 0.102 | 0.102 | 0.105 | 0.111 | 0.253 | 0.128 | 0.128 | 0.131 | 0.138 | 0.324 | | | | | | | |
| 5 | 0.059 | 0.059 | 0.061 | 0.064 | 0.145 | 0.097 | 0.097 | 0.099 | 0.104 | 0.238 | | | | | | | |
| 10 | 0.037 | 0.037 | 0.038 | 0.040 | 0.089 | 0.076 | 0.076 | 0.077 | 0.081 | 0.183 | | | | | | | |
| \( \alpha = 0.02 \) | | | | | | | | | | | | | | | | | | | |
| 0 (Pois.) | 0.242 | 0.245 | 0.279 | 0.326 | 0.657 | 0.242 | 0.245 | 0.279 | 0.326 | 0.657 | | | | | | | |
| 0.1 | 0.215 | 0.215 | 0.226 | 0.253 | 0.593 | 0.215 | 0.216 | 0.227 | 0.254 | 0.598 | | | | | | | |
| 0.5 | 0.167 | 0.167 | 0.172 | 0.186 | 0.437 | 0.175 | 0.176 | 0.181 | 0.196 | 0.468 | | | | | | | |
| 1 | 0.137 | 0.137 | 0.141 | 0.151 | 0.348 | 0.153 | 0.153 | 0.157 | 0.167 | 0.396 | | | | | | | |
| 2 | 0.102 | 0.102 | 0.105 | 0.111 | 0.253 | 0.128 | 0.128 | 0.130 | 0.138 | 0.324 | | | | | | | |
| 5 | 0.061 | 0.061 | 0.062 | 0.065 | 0.147 | 0.096 | 0.096 | 0.098 | 0.103 | 0.237 | | | | | | | |
| 10 | 0.037 | 0.037 | 0.037 | 0.039 | 0.088 | 0.076 | 0.076 | 0.077 | 0.081 | 0.182 | | | | | | | |
Figure 2: The plots on the left hand side plot the synthetic counts versus the original counts for different $\sigma$ when the NBI model is used for synthesis and the full five-variable data are synthesized. The plots on the right hand side plot original and synthetic counts’ percentage differences versus the original counts.
Figure 3: The plots on the left hand side plot the synthetic counts versus the original counts for different $\sigma$ when the PIG model is used for synthesis and the full five-variable data are synthesized. The plots on the right hand side plot original and synthetic counts’ percentage differences versus the original counts.
Table 4: Empirical values for the $\tau$ metrics for different $\sigma$ and $\alpha$ and for the NBI and PIG.

| $\sigma$ | $\tau_1(k)$ | $\tau_2(k)$ | $\tau_3(k)$ | $\tau_4(k)$ |
|----------|--------------|--------------|--------------|--------------|
| $\alpha = 0$ | 0 (Pois.) | α = 0 | $\alpha = 0.02$ | 0 (Pois.) |
| $0$ | 0.9190 | 0.9013 | 0.9804 | 0.9835 |
| $0.01$ | 0.9191 | 0.9012 | 0.9802 | 0.9834 |
| $0.1$ | 0.9204 | 0.9024 | 0.9803 | 0.9820 |
| $0.5$ | 0.9256 | 0.9078 | 0.9803 | 0.9764 |
| $1$ | 0.9317 | 0.9139 | 0.9804 | 0.9701 |
| $5$ | 0.9587 | 0.9415 | 0.9812 | 0.9427 |
| $10$ | 0.9713 | 0.9550 | 0.9819 | 0.9305 |

| $\alpha = 0.5$ | 0 (Pois.) | $\alpha = 0.02$ |
| $0$ | 0.9038 | 0.9804 |
| $0.01$ | 0.9034 | 0.9802 |
| $0.1$ | 0.9020 | 0.9803 |
| $0.5$ | 0.9078 | 0.9803 |
| $1$ | 0.9139 | 0.9804 |
| $5$ | 0.9415 | 0.9812 |

| $\alpha = 0$ | $\alpha = 0.02$ |
| 0 (Pois.) | 0.9190 | 0.9835 |
| 0.01 | 0.9191 | 0.9834 |
| 0.1 | 0.9204 | 0.9820 |
| 0.5 | 0.9256 | 0.9764 |
| 1 | 0.9317 | 0.9701 |
| 5 | 0.9587 | 0.9427 |
| 10 | 0.9713 | 0.9305 |

| $\alpha = 0.5$ | $\alpha = 0.02$ |
| 0 (Pois.) | 0.9190 | 0.9835 |
| 0.01 | 0.9191 | 0.9834 |
| 0.1 | 0.9204 | 0.9820 |
| 0.5 | 0.9256 | 0.9764 |
| 1 | 0.9317 | 0.9701 |
| 5 | 0.9587 | 0.9427 |
| 10 | 0.9713 | 0.9305 |
Table 5: This table shows how $\sigma$ and $\alpha$ affect the trimmed mean (top and bottom 10% excluded) percentage difference between log-linear parameter estimates obtained from the observed and synthetic data. The trimmed mean was used to subdue the effect of huge percentage differences arising through zero counts. For clarity, for an arbitrary original log-linear parameter estimate $q$ and its corresponding synthetic estimate $q^{\text{syn}}$, the percentage difference was calculated by $100 \times (q^{\text{syn}} - q)/q$.

|      | $\sigma = 0$ | $\sigma = 0.1$ | $\sigma = 0.5$ | $\sigma = 1$ | $\sigma = 2$ | $\sigma = 5$ | $\sigma = 10$ |
|------|--------------|----------------|----------------|--------------|--------------|--------------|--------------|
| **The NBI model** |              |                |                |              |              |              |              |
| $\alpha = 0$      | -1.7         | 3.9            | -12.0          | -0.1         | -18.7        | 10.6         | -108.4       |
| $\alpha = 0.005$  | -23.5        | -30.9          | -31.7          | -34.8        | -34.0        | 14.8         | -32.9        |
| $\alpha = 0.01$   | -32.5        | -33.2          | -33.7          | -38.9        | -47.8        | 41.0         | -64.7        |
| $\alpha = 0.015$  | -38.8        | -39.8          | -47.7          | -52.3        | -47.6        | -20.3        | -3.5         |
| $\alpha = 0.02$   | -37.1        | -34.0          | -44.4          | -40.9        | -27.7        | -42.0        | -33.5        |

|      | $\alpha = 0$ | -1.7          | -2.2           | 16.2         | 11.2         | -33.0        | -6.6         | 187.4        |
|      | $\alpha = 0.005$ | -23.5       | -21.7          | -28.4        | -21.7        | -33.0        | -73.6        | -990.4       |
|      | $\alpha = 0.01$ | -32.5       | -29.6          | -31.7        | -48.6        | -42.3        | 25.9         | -399.3       |
|      | $\alpha = 0.015$ | -38.8       | -26.4          | -36.6        | -37.6        | -20.6        | -64.4        | -504.0       |
|      | $\alpha = 0.02$ | -37.1       | -47.8          | -40.2        | -20.6        | -40.5        | -76.2        | 425.2        |

To relieve some of this pressure, the all two-way interaction model was fitted to three of the data’s five variables, ethnicity, age and language, resulting in 608 parameters.

The data were assumed to be a simple random sample drawn from a super-population and, as such, the estimator given in Raab et al. (2016) (equation 3), provides valid population inferences from the synthetic data. As $m = 1$ and $n^{\text{syn}} = n$, the variance estimate simplifies neatly to $\text{Var}(\hat{Q}) = 2v$ where $v$ is the variance estimate (square of the standard error) of the model parameter.

Potentially, estimability issues could have arisen through the presence of zero counts in either the original or synthetic data’s two-way marginal tables, which are the model’s sufficient statistics. This could have led to issues surrounding non-existence and non-identifiability of estimates (Fienberg et al., 2012), as there are some parameters included in the model with a true value of $-\infty$. For such parameters, R returned a large negative value, typically in the vicinity of -20, and no serious model fitting issues arose.
6.4.1 Results

Figures 4 and 5 present boxplots of confidence interval overlap values for the parameters from the log-linear model across different synthesis models. They demonstrate how increasing $\sigma$ and $\alpha$ causes utility to fall away. For example, irrespective of $\alpha$, whenever $\sigma = 10$, the median confidence interval overlap is zero. A high proportion of the overlap values are equal to $1/2$. This is owing to the nature - and perhaps a criticism - of the confidence interval overlap metric. Whenever an estimate’s standard error (and hence confidence interval) is infinite - which arises whenever an estimate pertains to a zero marginal count - the confidence interval overlap value is always $1/2$ because the infinite confidence interval entirely covers its finite counterpart and, conversely, the finite interval hardly covers the infinite one - the overlap metric averages these two “coverages”.

Table 5 presents (trimmed) mean percentage differences between synthetic and observed parameter estimates for different synthesis models. We see that setting $\alpha$ relatively small can have an adverse effect on utility. For example, when $\sigma = 0$ (the Poisson model) increasing $\alpha$ from 0 to 0.005 causes the (trimmed) mean percentage difference to rise from $-1.7\%$ to $-23.5\%$, demonstrating the bias arising from setting $\alpha > 0$. We note the general trend that increasing $\alpha$ and $\sigma$ tends to result in larger percentage differences.

6.5 Balancing risk and utility

A key question a synthesizer would have is which synthesis method offers the best balance between utility and risk. To address this question we can plot the risk-utility tradeoff from each generated synthetic data set. An example is displayed in Figure 6. Confidentiality protection has been measured on the y-axis via $1 - \tau_4(1)$ (1 - risk), and utility on the x-axis by mean confidence interval overlap. The original data sit at the point (1,0), that is, maximum utility and minimum confidentiality protection. All points must lie with the unit square $[0,1] \times [0,1]$ and the further from the origin the better the synthetic data.

This visualisation offers a convenient way to compare the performance of different synthesis methods. For example, it may be possible to strictly dominate one synthetic data set over another: the PIG model with $\sigma = 10$ provides greater utility and lower risk than the NBI model with $\sigma = 100$. In terms of picking an optimal synthetic data set, the choice depends on
Figure 4: These boxplots show how $\sigma$ and $\alpha$ affect log-linear parameters’ confidence interval overlap when the NBI distribution is used for synthesis. The left frame is the case where $\alpha = 0$; the middle frame where $\alpha = 0.1$; and the right frame where $\alpha = 0.02$.

Figure 5: These boxplots show how $\sigma$ and $\alpha$ affects confidence interval overlap when the PIG distribution is used for synthesis. The left frame is the case where $\alpha = 0$; the middle frame where $\alpha = 0.1$; and the right frame where $\alpha = 0.02$.

the priorities of the data holder and users. For example, it may be that synthetic data can only be released if the confidentiality protection is at least 0.5, in which case the synthetic data with the highest utility that satisfies this requirement could be released, here this would be the PIG model with $\sigma = 10$. Alternatively it may be that only data with a utility value of at least 0.5 would be deemed useful enough for release, in which case the synthetic data generated under a NBI model with $\sigma = 0.1$ would be chosen as the one with the highest confidentiality protection with utility at least 0.5.

In practice, a range of different metrics for utility and confidentiality protection could be created and feed into determining which synthesis method is optimal. The decision is also likely to be application specific.
7 Discussion and future work

There is no panacea for synthetic data generation. A compromise always needs to be struck between risk, utility and, in the case of large data sets, generative time. There are of course much more complex methods available to the synthesizer that may be more capable of capturing the data’s underlying distribution. However, besides taking longer computationally, these methods also lose interpretability for the synthesizer. Until undertaking post-synthesis evaluations they are often in the dark as to the effect of the synthesis. This method’s simplicity gives the synthesizer a handle on the synthetic data’s properties which, as well as being more convenient, may in turn invite greater transparency. We thus hope that this paper gives confidence to organisations that hold large administrative databases that generating synthetic data is not necessarily a computationally intensive and time consuming endeavour. Further, the organisations can easily tune the synthesis models in a very transparent way to achieve pre-specified levels of risk and/or utility.

The current “gold-standard” with regards to risk-guarantees is differential privacy (Dwork et al., 2006). Rinott et al. (2018) developed a differentially-private mechanism for perturbing categorical data expressed as a frequency table. The method involves adding random noise, dependent on a specific loss function, for example in one scenario discretised Laplacian noise is applied. Although not explicit, methods suggested by Rinott et al. are effectively generating
synthetic data through transforming the original data’s counts, as done in this paper. A comparison of the risk and utility of the data from that method, and the method described in this paper, may reveal interesting findings, for example, what value of $\sigma$ in the two-parameter synthesis models yields a similar level of risk? This may help to derive a lower bound for risk.

In this paper the case of generating $m = 1$ synthetic data set was considered. As [Raab et al. (2016)] point out, synthesis is not imputation: the true underlying values are known, hence a single data set is sufficient to obtain valid inferences. But $m > 1$ data sets can be generated and similar analytical expressions can be derived for the $\tau$ metrics. This effectively introduces another parameter for the synthesizer to set, thus providing further flexibility. Investigations unreported in this paper have shown promising signs for $m > 1$; for example, particularly for large $\sigma$, the gains in utility appear to outweigh the relatively small increase in risk.

Moreover, an optimal value for $n_{syn}$ (the sample size of the synthetic data) has not been sought. There is scope to set $n_{syn}$ lower than $n$ (the sample size of the original data). Given that the synthetic counts are unbiased, a smaller $n_{syn}$ may lead to proportionally larger gains in data confidentiality relative to the loss in utility. Disclosure risk would also decline due to the extra layer of sampling uncertainty: an attacker would not know whether an individual is represented in the synthetic data.

While the two-parameter count distributions allow the synthesizer to set the variance in the synthesis, they cannot control where the variability falls. They do not necessarily want the additional variability to manifest itself in say, a heavier right tail: this might have an adverse effect on the data’s subsequent utility. This relates to the distribution’s skewness; the skewness, like the variance, has implications for disclosure risk. Three-parameter count distributions - such as the Delaporte and Sichel distributions - would provide the synthesizer with control over the skewness in addition to the variance.

As mentioned earlier, this method exploits the notion that the quality of the synthetic data is more important than the underlying model used to generate it. This notion can be utilised further by specifying different models - different $\sigma$ values in the two-parameter count models - to different cell sizes in the original data. Smaller cell sizes could be synthesized using a relatively larger $\sigma$ than larger cells, which would inject more variability where it is needed.
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