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Assessing Identification Risk in Survey Microdata using Log-linear Models

CHRIS SKINNER and NATALIE SHLOMO*

ABSTRACT. This article considers the assessment of the risk of identification of respondents in survey microdata, in the context of applications at the United Kingdom (UK) Office for National Statistics (ONS). The threat comes from the matching of categorical 'key' variables between microdata records and external data sources and from the use of log-linear models to facilitate matching. While the potential use of such statistical models is well-established in the literature, little consideration has been given to model specification nor to the sensitivity of risk assessment to this specification. In numerical work not reported here, we have found that standard techniques for selecting log-linear models, such as chi-squared goodness of fit tests, provide little guidance regarding the accuracy of risk estimation for the very sparse tables generated by typical applications at ONS, for example tables with millions of cells formed by cross-classifying six key variables, with sample sizes of 10 or 100 thousand. In this article we develop new criteria for assessing the specification of a log-linear model in relation to

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the accuracy of risk estimates. We find that, within a class of 'reasonable' models, risk estimates tend to decrease as the complexity of the model increases. We develop criteria which detect 'underfitting' (associated with overestimation of the risk). The criteria may also reveal 'overfitting' (associated with underestimation) although not so clearly, so we suggest employing a forward model selection approach. Our criteria turn out to be related to established methods of testing for overdispersion in Poisson log-linear models. We show how our approach may be used for both file-level and record-level measures of risk. We evaluate the proposed procedures using samples drawn from the 2001 UK Census where the true risks can be determined and show that a forward selection approach leads to good risk estimates. There are several 'good' models between which our approach provides little discrimination. The risk estimates are found to be stable across these models, implying a form of robustness. We also apply our approach to a large survey dataset. There is no indication that increasing the sample size necessarily leads to the selection of a more complex model. The risk estimates for this application display more variation but suggest a suitable upper bound.

KEY WORDS: Confidentiality; Disclosure; Key variable; Matching; Model specification.

1 INTRODUCTION

Statistical agencies often wish to provide researchers with access to survey microdata, but must balance this aim against the need to protect the confidentiality of the respondents. In particular, many agencies have policies which require them to control the risk of identification. For example, the key 'confidentiality guarantee' in the United Kingdom (UK) National Statistics Code of Practice (National Statistics, 2004, p.7) is that 'no statistics will be produced that are likely to identify an individual'.

The developing field of statistical disclosure limitation methodology provides agencies with many methods to protect confidentiality and, in particular, to assess identification risk (Willenborg and de Waal, 2001; Doyle, Lane, Theeuws and Zayatz, 2001). Traditional methods to assess identification risk include the use of rules and check lists based on institutional experience, simple data-based summary measures and re-identification experiments (Federal Committee on Statistical Methodology, 1994). Such methods can be somewhat ad hoc, however, and number of authors (e.g. Paass, 1988; Duncan and Lambert, 1989; Fuller, 1993; Trottni and Fienberg, 2002) have proposed statistical modelling frameworks which permit identification risk to be assessed following clear statistical principles. Identification may be treated as a form of statistical inference by a potential ‘intruder’, who is assumed to make efficient use of available information to facilitate identification through specified models. There have been some applications of such modelling approaches to assessing risk. Reiter (2005) applied the approach of Duncan and Lambert (1989) to the Current Population Survey. Paass (1988) applied discriminant analysis to two microdata files from the German Federal Statistical Office. Bethlehem, Keller and Pannekoek (1990) applied a Poisson-Gamma model to Dutch data. Nevertheless, more research on issues arising in applications is needed if modelling methods are to become part of the standard risk assessment ‘toolkit’ of statistical agencies. In particular, more understanding is needed of how to specify models and of how sensitive risk assessment approaches are to specification.

The purpose of this article is to investigate the use of log-linear modelling methods in some risk assessment problems which have arisen at the UK Office for National Statistics (ONS) when releasing microdata from social surveys. In addition to considering here one particular survey application, we draw samples from the 2001 UK Census to mimic social survey data in a setting where population values are available for validation. In line with the Code of Practice mentioned above, the aim is to

protect against identification which could arise from an intruder matching a micro-data record to a known population individual using the values of variables which are both available in the microdata and traceable or visible externally. These variables are called key variables (Bethlehem et al., 1990). For the kinds of social survey applications considered by ONS, these key variables are invariably categorical, e.g. sex, age, ethnicity, religion, place of residence or occupation. Previous work has shown that, when multivariate categorical key variables are available, an intruder might be able to use log-linear modelling to improve their chances of identifying records (Skinner and Holmes, 1998; Fienberg and Makov, 1998; Dobra, Fienberg and Trottni, 2003; Fienberg and Slavkovic, 2005; Elamir and Skinner, 2006). However, this work has given little attention to the important practical issue of how to specify these models or to the sensitivity of risk assessment to model specification.

The main aim of this paper is to develop and investigate approaches to specifying log-linear models, which are suitable for use in practice by a statistical agency for the very large and sparse cross-classified tables arising in the kinds of application considered here and which directly address the risk assessment objectives. We shall argue that these objectives can be represented as certain prediction problems and thus differ from the standard kinds of objectives of log-linear modelling (e.g. Bishop, Fienberg and Holland, 1975). Our approach will be to develop diagnostic criteria of model adequacy for such prediction purposes, which we shall refer to as minimum error tests. Thus, in practice, our proposed approach involves (i) specifying the key variables, (ii) selecting one or more log-linear models which fit well according to these criteria and (iii) using the well-fitting models to obtain risk estimates.

The kinds of risk measures considered here, based on log-linear modelling, may be used to assess the impact of recoding the key variables, which is the primary method of disclosure limitation used at present by ONS in the release of social survey microdata,

alongside the use of restrictions on access arrangements, such as via licenses or on-site laboratories.

The article is organised as follows. The framework for identification risk assessment is set out in Section 2, with the associated log-linear models discussed in Section 3. Section 4 describes possible criteria for assessing the model and Section 5 describes how these might be used to specify a model. Section 6 extends the methodology of Sections 2-5 to complex sampling schemes. Applications to census samples and to a social survey are presented in Sections 7 and 8 respectively. Finally, Section 9 contains a discussion and areas for future research.

2 IDENTIFICATION RISK ASSESSMENT

Following several authors (e.g. Paass, 1988; Duncan and Lambert; 1989; Bethlehem et al., 1990), we consider a microdata file consisting of records for a sample of individuals from a finite population. We imagine an intruder with access to the file as well as to auxiliary information on the values of the key variables for some known individuals in the population. The intruder matches the two data sources in order to identify one or more records in the microdata. We suppose the intruder assesses whether there is a microdata record and a known individual for which the probability that the former belongs to the latter is high (Paass, 1988; Duncan and Lambert, 1989). Our basic definition of identification risk is the value of this probability when the microdata record does indeed belong to the known individual.

We conceive of this probability as conditional on data, which might reasonably be assumed available to the intruder, and defined with respect to a model and assumptions, which are justifiable from analysis of the data and from knowledge of the processes (sample selection, measurement error etc.) generating the data. We treat the key

variables as given by a specified scenario, as in Paass (1988). In the kinds of census and social survey applications of concern here, we may assume that the key variables are categorical. A stronger assumption that we shall make is that the key variables are measured in the same way in the two sources, so there is no measurement error to create discrepancies. Ignoring such discrepancies may be expected to lead to overestimation of risk and the risk estimates reported in this article may therefore be considered to be conservative. The treatment of measurement error would be a key extension of our approach but is beyond the scope of this paper.

To introduce our basic measure of identification risk, let F_k be the population count in cell k of the multi-way contingency table formed by cross-classifying the key variables (with cells labelled $k = 1, \dots, K$). Under the above assumptions, together with weak exchangeability assumptions about the selection of records and known population individuals, and the assumption that F_k is known to the intruder, the definition of identification risk above, i.e. the probability that a microdata record may be identified, takes the form $1/F_k$, where k is the cell to which the record belongs (Duncan and Lambert, 1989). The risk is maximum when the record is population unique, i.e. $F_k = 1$. In practice, the agency should ensure that key variables are not released where intruders are able to determine small values of F_k using, for example, population lists (Skinner, Marsh, Openshaw and Wymer, 1994). A more realistic measure is therefore given by $E(1/F_k) = \sum_r P(F_k = r)/r$, where $P(F_k = r)$ denotes the probability that $F_k = r$ under the model ($r=1, 2, \dots$), given data available to the intruder (Skinner and Holmes, 1998). Given the particular concern about population uniqueness (e.g. Bethlehem et al., 1990), a related risk measure of interest is $P(F_k = 1)$, the probability of population uniqueness. This is the first term in the sum $\sum_r P(F_k = r)/r$ and so is a less conservative measure than $E(1/F_k)$. We shall treat the data available to the intruder as the sample counts f_k and we shall express the two risk measures of interest

as $E(1/F_k | f_k)$ and $P(F_k = 1 | f_k)$. Under a “working model” that the pairs (F_k, f_k) are independent, these measures will be the conditional expectation of $1/F_k$ and the conditional probability that $F_k = 1$, respectively, given the data f_1, \dots, f_K . For simplicity, we shall retain $E(1/F_k | f_k)$ and $P(F_k = 1 | f_k)$ as definitions of our measures of interest, even under possible departures from this assumption. The first risk measure will generally be highest when $f_k = 1$, i.e. in sample unique cells. Moreover, the probability of population uniqueness is only non-zero when $f_k = 1$. Consideration of worst cases thus leads to a focus on the measures $r_{1k} = P(F_k = 1 | f_k = 1)$ and $r_{2k} = E[1/F_k | f_k = 1]$.

These are referred to as record-level or per record measures (Willenborg and de Waal, 2001, p.52) since they vary between records. More generally, we write $r_k = E[g(F_k) | f_k = 1]$, where $g(F) = I(F = 1)$ or $1/F$ in the case of r_{1k} or r_{2k} , respectively. Estimation of such record-level measures may help the agency identify and target ‘high risk’ records for the application of ‘local’ disclosure limitation methods. Nevertheless, agencies often also need measures of risk at the file level in their decision making processes, such as in the assessment of recoding options, and this leads to consideration of aggregating such record-level measures (Lambert, 1993; Fienberg and Makov, 1998). Here, we consider simply summing the record-level measures across sample unique records, to give $\tau^* = \sum_{SU} r_k$ and, in particular:

$$\tau_1^* = \sum_{SU} r_{1k} = \sum_{SU} P(F_k = 1 | f_k = 1), \quad (1)$$

the expected number of sample uniques that are population unique, and

$$\tau_2^* = \sum_{SU} r_{2k} = \sum_{SU} E(1/F_k | f_k = 1), \quad (2)$$

the expected number of correct matches for sample uniques, where $SU = \{k : f_k = 1\}$ denotes sample unique cells. Our focus will be on situations where K is large (and the

(F_k, f_k) may be treated as independent) so that a law of large numbers implies that τ^* will closely approximate $\tau = \sum_k I(f_k = 1)g(F_k)$, which takes the particular forms $\tau_1 = \sum_k I(f_k = 1, F_k = 1)$ or $\tau_2 = \sum_k I(f_k = 1)/F_k$. Such measures may be more appealing to some statistical agencies since they have a model-free interpretation.

For any of the measures above, the problem of risk assessment becomes one of statistical inference if the f_k are observed but the F_k are not. In the case of τ , we may view this as a problem of finite population prediction.

3 LOG-LINEAR MODELS

Models are required not only for the explicit definition of most of the risk measures in the previous section, but also for inference about these measures. Following standard methods for contingency tables (e.g. Bishop et al., 1975) and previous work on disclosure control (e.g. Bethlehem et al., 1990), we consider models where the F_k are realisations of independent Poisson random variables with means λ_k ($k = 1, \dots, K$). We write $F_k \sim P(\lambda_k)$. In order to develop relatively simple procedures, we shall first assume that the sample is drawn by Bernoulli sampling where individuals in cell k have the same known inclusion probability π_k so that the sample counts f_k are also independent Poisson random variables $f_k \sim P(\pi_k \lambda_k)$. We extend our approach to complex sampling schemes in Section 6. Under the Bernoulli sampling assumption, we have $F_k | f_k \sim P[\lambda_k(1 - \pi_k)] + f_k$ so that the record level measures may be expressed as $r_{1k} = \exp[-(1 - \pi_k)\lambda_k] = h_1(\lambda_k)$, say, and, $r_{2k} = \{1 - \exp[-(1 - \pi_k)\lambda_k]\} / [(1 - \pi_k)\lambda_k] = h_2(\lambda_k)$ say, or, more generally, $r_k = E[g(F_k) | f_k = 1] = h(\lambda_k)$, say, where $h(\lambda)$ is a monotonic decreasing function of λ . We write the aggregated risk measures as:

$$\tau^* = \sum_k I(f_k = 1)h(\lambda_k). \quad (3)$$

The modelling assumptions so far are generally insufficient to make precise inference about these risk measures since the measures depend on unknown λ_k values for cells where the observed counts f_k are just one. Following principles of small domain estimation, we therefore “borrow strength” (Rao, 2003; p.2) between cells by supposing the λ_k are related via the log-linear model:

$$\log \lambda_k = \mathbf{x}'_k \boldsymbol{\beta}, \quad (4)$$

where \mathbf{x}_k is a $q \times 1$ design vector, depending on the values of the key variables in cell k , and $\boldsymbol{\beta}$ is a $q \times 1$ parameter vector. Typically, we shall specify \mathbf{x}_k to include main effects and low order interactions of the categorical key variables (Bishop et al., 1975). Since the f_k are the outcomes of independent $P(\pi_k \lambda_k)$ random variables, the maximum likelihood (ML) estimator $\hat{\boldsymbol{\beta}}$ may be obtained by solving the score equations:

$$\sum_k [f_k - \pi_k \exp(\mathbf{x}'_k \boldsymbol{\beta})] \mathbf{x}_k = 0, \quad (5)$$

using numerical techniques. The risk measures in Section 2 may then be estimated by replacing λ_k by $\hat{\lambda}_k = \exp(\mathbf{x}'_k \hat{\boldsymbol{\beta}})$ in the expressions above, for example $\hat{\tau} = \sum_k I(f_k = 1) h(\hat{\lambda}_k)$. Such an approach has been described in Skinner and Holmes (1998) and Elamir and Skinner (2006), who have shown how it may generate useful risk measures. See also Fienberg and Makov (1998), Dobra et al. (2003). The problem addressed in this paper is that inference may be sensitive to the specification of (4). We propose an approach in the next section to check the adequacy of this specification. We shall assume that, given a specified model of form (4), inference proceeds in the simple manner above, i.e. by plugging $\hat{\lambda}_k$ in for λ_k in the risk measure expressions. Other more sophisticated approaches are possible, for example averaging over alternative models (Fienberg and Makov, 1998), but will not be considered here.

4 CRITERIA FOR MODEL ASSESSMENT

4.1 Rationale

We seek criteria for assessing whether the vector \mathbf{x}_k in the log-linear model in (4) may be expected to lead to accurate estimated risk measures. One approach would be to use goodness-of-fit criteria such as Pearson or likelihood-ratio tests. These are not designed for finite population prediction problems, however. Moreover, the usual conditions on the average cell size n/K required for their validity (e.g. at least 1 or 5) do not hold for the large and sparse tables typical of the kinds of applications considered here. For example, the survey that is assessed in Section 7 has 127,200 records in 2,366,000 cells defined by six identifying key variables, and the average cell size is 0.05. Some work on sparse tables (Koehler, 1986) suggests that the Pearson test is preferable to the likelihood ratio test in such circumstances. Nevertheless, our empirical work has suggested that neither of these criteria, nor other standard approaches such as Akaike's Information Criterion, are very successful in deciding whether the disclosure risk measures will be well estimated and we shall not consider them further here.

Instead, we consider an approach motivated directly by our aim to estimate the risk measures accurately. Specifically, we seek a criterion for choosing a specification of model (4) which minimises the error (in a sense to be defined) of $\hat{\tau} = \sum_k I(f_k = 1)h(\hat{\lambda}_k)$ as an estimator of $\tau^* = \sum_k I(f_k = 1)h(\lambda_k)$ or as a predictor of $\tau = \sum_k I(f_k = 1)g(F_k)$. See Rao and Wu (2001) for a general discussion of the use of prediction criteria in model selection. Empirical work suggests that, within a neighbourhood of 'reasonable' models, $\hat{\tau}$ tends to decline as the model becomes more complex. To provide some heuristic theoretical reasoning for this phenomenon, let $\tilde{\boldsymbol{\beta}}$ be the solution of

$$\sum_k [\lambda_k - \exp(\mathbf{x}'_k \tilde{\boldsymbol{\beta}})] \mathbf{x}_k = 0, \quad (6)$$

interpreted as an ‘average’ value of $\hat{\beta}$ across its sampling distribution and let $\tilde{\lambda}_k = \exp(\mathbf{x}'_k \tilde{\beta})$ be a corresponding ‘average’ value of $\hat{\lambda}_k$. We can think of the estimation error $\hat{\lambda}_k - \lambda_k$ as composed of the sum of a ‘sampling error’ $\hat{\lambda}_k - \tilde{\lambda}_k$ and a ‘misspecification error’ $\tilde{\lambda}_k - \lambda_k$ and, via these components, consider two problems.

Overfitting: this is the case where the model is ‘too complex’ in the sense that the sampling error is positively associated with f_k (in the extreme case of a saturated model $\hat{\lambda}_k = f_k/\pi_k$) and where this sampling error is the dominant component of estimation error. We consider applications where the expected sample size per cell is less than one so that $I(f_k = 1)$ tends to be positively associated with f_k . Since h is a monotonic decreasing function, we may expect that, in the presence of overfitting, $I(f_k = 1)$ tends to be positively associated with $\hat{\lambda}_k - \lambda_k$ and negatively associated with $h(\hat{\lambda}_k) - h(\lambda_k)$ and thus for $\hat{\tau}$ to underestimate τ^* . Another reason to expect this outcome is that overfitting may produce too many fitted marginal zero counts where sample marginal counts are random zeros, leading to fitted cell counts being too high for the non-zero cells of the table and risk measures being underestimated.

Underfitting: this is the case where $\tilde{\lambda}_k$ is ‘oversmoothed’, so that there is negative association between $\tilde{\lambda}_k - \lambda_k$ and λ_k , and misspecification error is the dominant component of estimation error. It follows that $\hat{\lambda}_k - \lambda_k$ is also negatively associated with λ_k . Now, we expect f_k to be positively associated with λ_k and thus (when the expected sample size per cell is less than one) for $I(f_k = 1)$ to be negatively associated with $\hat{\lambda}_k - \lambda_k$ and positively associated with $h(\hat{\lambda}_k) - h(\lambda_k)$ and thus for $\hat{\tau}$ to overestimate τ^* . Another reason to expect this outcome is that structural zero counts in tables may fail to be fitted correctly in the presence of underfitting, leading to expected cell counts tending to be too low for the non-zero cells of the table and risk measures being overestimated.

Our empirical experience (as will be illustrated in Sections 6 and 7) is that it is harder to detect the impact of overfitting than underfitting. Our development of a data-based criterion for minimising estimation error is therefore led by consideration of the impact of the latter.

4.2 Development of Criterion

We represent the impact of underfitting by the component of the bias of $\hat{\tau}$ as an estimator of τ^* or predictor of τ arising from misspecification of the model, that is from the difference between $\tilde{\lambda}_k$ and λ_k , i.e:

$$B = \sum_k E[I(f_k = 1)][h(\tilde{\lambda}_k) - h(\lambda_k)] = \sum_k \pi_k \lambda_k \exp(-\pi_k \lambda_k) [h(\tilde{\lambda}_k) - h(\lambda_k)]. \quad (7)$$

We approximate the term $h(\tilde{\lambda}_k)$ in this expression by

$$h(\tilde{\lambda}_k) \doteq h(\lambda_k) + h'(\lambda_k)(\tilde{\lambda}_k - \lambda_k) + h''(\lambda_k)(\tilde{\lambda}_k - \lambda_k)^2/2, \quad (8)$$

using a quadratic expansion of $h(\tilde{\lambda}_k)$ around λ_k . For example, when $h(\lambda) = h_1(\lambda)$, we obtain $h'(\lambda_k) = -(1 - \pi_k)h_1(\lambda_k)$ and $h''(\lambda_k) = (1 - \pi_k)^2 h_1(\lambda_k)$. To illustrate the quality of the approximation, consider the value $\lambda_k = 1$ which might be taken to be the value of most concern, being the value when $F_k = 1$ is most likely. Figure 1 plots $h(\tilde{\lambda})$ and its approximation in (8) against $\tilde{\lambda}$ for $\pi_k=0.05$ and the two choices of h function considered above equation (3). The approximation works well for the range of $\tilde{\lambda}$ values plotted and potential problems with the approximation at the extremes are mitigated by the lower bound $\lambda_k > 0$ and the damping effect of $\exp(-\pi_k \lambda_k)$ in (7) for large values of λ_k .

Substituting approximation (8) into (7) gives:

$$B \doteq \sum_k \pi_k \lambda_k \exp(-\pi_k \lambda_k) [h'(\lambda_k)(\tilde{\lambda}_k - \lambda_k) + h''(\lambda_k)(\tilde{\lambda}_k - \lambda_k)^2/2]. \quad (9)$$

Since $E(f_k) = \mu_k = \pi_k \lambda_k$ and $E[(f_k - \pi_k \tilde{\lambda}_k)^2 - f_k] = \pi_k^2 (\lambda_k - \tilde{\lambda}_k)^2$, it follows that, for a large number of cells, expression (9) may be approximated by

$$\tilde{B} = \sum_k \lambda_k \exp(-\mu_k) \{-h'(\lambda_k)(f_k - \pi_k \tilde{\lambda}_k) + h''(\lambda_k)[(f_k - \pi_k \tilde{\lambda}_k)^2 - f_k]/(2\pi_k)\}. \quad (10)$$

In the case of underfitting, when $f_k - \pi_k \tilde{\lambda}_k$ may be reasonably approximated by $f_k - \pi_k \hat{\lambda}_k$, a natural estimator of \tilde{B} and hence of B is

$$\hat{B} = \sum_k \hat{\lambda}_k \exp(-\hat{\mu}_k) \{-h'(\hat{\lambda}_k)(f_k - \hat{\mu}_k) + h''(\hat{\lambda}_k)[(f_k - \hat{\mu}_k)^2 - f_k]/(2\pi_k)\}. \quad (11)$$

We write \hat{B} as \hat{B}_1 or \hat{B}_2 when $h(\lambda) = h_1(\lambda)$ or $h(\lambda) = h_2(\lambda)$ respectively, for example

$$\hat{B}_1 = \sum_k \hat{\lambda}_k \exp(-\hat{\lambda}_k)(1 - \pi_k) \{(f_k - \hat{\mu}_k) + (1 - \pi_k)[(f_k - \hat{\mu}_k)^2 - f_k]/(2\pi_k)\}. \quad (12)$$

We have argued that \hat{B} may be viewed as an estimator of the bias of $\hat{\tau}$ in the presence of underfitting, when this bias may be expected to be positive. The properties of \hat{B} in the case of overfitting are more difficult to assess. As will be discussed further below, we expect the first part of expression (11) involving $(f_k - \hat{\mu}_k)$ to contribute less than the second component involving $[(f_k - \hat{\mu}_k)^2 - f_k]$. In the second component, we expect that overfitting will lead to $(f_k - \hat{\mu}_k)^2$ tending to be less than $(f_k - \mu_k)^2$ and thus, since $E[(f_k - \mu_k)^2] = E(f_k)$, we may expect the second component to tend to be negative and hence for \hat{B} to be negative. We thus conclude that \hat{B} will tend to be negative in the presence of overfitting, although we do not suggest that it will estimate the bias of $\hat{\tau}$ in this case. We refer to \hat{B} as a *minimum error criterion*, since it is constructed with the aim of minimising the error of $\hat{\tau}$ as an estimator of τ^* or predictor of τ .

4.3 Test Statistics

We propose to use the closeness of \hat{B} to zero as evidence of an absence of underfitting. We emphasise that this criterion is designed to assess the quality of the risk estimates arising from the model, not whether the model is correct, i.e. the purpose is estimation not testing. Nevertheless, we need to quantify ‘closeness’ to zero since \hat{B} will differ from zero because of sampling error, even in the absence of underfitting, and thus we consider estimating the variance of \hat{B} . We assume that it is reasonable to approximate the distribution of \hat{B} by the distribution of \tilde{B} . This approximation may be justified by standard asymptotic theory for contingency tables where the cells (and K) are fixed and the population and sample sizes per cell increase. Alternatively, it may be justified in an asymptotic framework (Haberman, 1977) in which K increases alongside the population and sample sizes and where the contribution of the sampling error in $\hat{\beta}$ via the $\hat{\lambda}_k$ to the variance of \hat{B} becomes negligible relative to the contribution of the terms involving f_k in (11). This framework seems more realistic for our applications, where K is large and the cell sizes may be small, but the two-way and three-way marginal counts upon which $\hat{\beta}$ is based tend to increase with sample size.

If the model is correctly specified, so that $\tilde{\lambda}_k = \lambda_k$ and $f_k \sim P(\mu_k)$, then \tilde{B} has zero expectation and, using standard results for the first four moments of a Poisson random variable, $\text{var}(\tilde{B}) = \sum_k a_k^2 \mu_k + 2b_k^2 \mu_k^2$, where $a_k = -\lambda_k \exp(-\pi_k \lambda_k) h'(\lambda_k)$ and $b_k = \lambda_k \exp(-\pi_k \lambda_k) h''(\lambda_k) / (2\pi_k)$. For $h(\lambda) = h_1(\lambda)$, we have $a_k = (1 - \pi_k) \lambda_k \exp(-\lambda_k)$ and $b_k = (1 - \pi_k)^2 \lambda_k \exp(-\lambda_k) / (2\pi_k)$ and for $h(\lambda) = h_2(\lambda)$, we have $a_k = \exp(-\pi_k \lambda_k) r_{2k} - \exp(-\lambda_k)$ and $b_k = \{\exp(-\pi_k \lambda_k) r_{2k} - \exp(-\lambda_k) [1 + (1 - \pi_k) \lambda_k / 2]\} / [\pi_k \lambda_k]$, where r_{2k} is given above (3).

A natural estimator of $\text{var}(\tilde{B})$ is given by

$$\nu = \sum_k \hat{a}_k^2 \hat{\mu}_k + 2\hat{b}_k^2 \hat{\mu}_k^2, \quad (13)$$

where $\hat{\mu}_k = \pi_k \hat{\lambda}_k$, and

$$\hat{a}_k = -\hat{\lambda}_k \exp(-\hat{\mu}_k) h'(\hat{\lambda}_k), \quad (14)$$

and

$$\hat{b}_k = \hat{\lambda}_k \exp(-\hat{\mu}_k) h''(\hat{\lambda}_k) / (2\pi_k). \quad (15)$$

An alternative variance estimator is obtained by assuming just that $\tilde{\lambda}_k = \lambda_k$ and the f_k are independent with mean and variance equal to μ_k but without assuming that the third and fourth moments follow those of a Poisson distribution. In this case, we obtain $\text{var}(\tilde{B}) = \sum_k E\{a_k(f_k - \mu_k) + b_k[(f_k - \mu_k)^2 - f_k]\}^2$ and an alternative estimator of $\text{var}(\tilde{B})$ is given by

$$\nu_R = \sum_k \{\hat{a}_k(f_k - \hat{\mu}_k) + \hat{b}_k[(f_k - \hat{\mu}_k)^2 - f_k]\}^2, \quad (16)$$

where the subscript R denotes robust.

Given our assumptions above, $\hat{B}/\sqrt{\nu}$ or $\hat{B}/\sqrt{\nu_R}$ have an approximate standard normal distribution under the hypothesis that the expected value of \hat{B} is zero. We shall refer to the associated tests as *minimum error tests*. They are diagnostic tests, designed to assess whether a model displays evidence of underfitting or overfitting for estimation purposes and not to test whether a given model is correct.

4.4 Relation to Existing Tests of Overdispersion

The expression for \hat{B} in (11) or (12) may be considered as the sums of two components $\hat{B} = \hat{B}_a + \hat{B}_b$. The first component, $\hat{B}_a = \sum_k \hat{a}_k(f_k - \hat{\mu}_k)$, is of the same form as the

estimating function appearing in (5) so that if $\boldsymbol{\beta}$ is estimated using ML and the vector of weights \hat{a}_k is in the linear space spanned by \mathbf{x}_k then this component will be zero. In general, this argument suggests that the first component may be less important than the second component, $\hat{B}_b = \sum_k b_k [(f_k - \hat{\mu}_k)^2 - f_k]$. We shall consider this empirically in Section 6. The component \hat{B}_b may be interpreted as an estimator of the degree of overdispersion or underdispersion, since f_k and $(f_k - \hat{\mu}_k)^2$ are unbiased estimators of the conditional mean and variance of f_k respectively, again ignoring differences between $\hat{\boldsymbol{\beta}}$ and $\boldsymbol{\beta}$ and assuming $\mu_k = \exp(\mathbf{x}'_k \boldsymbol{\beta})$. Hence, an average of $[(f_k - \hat{\mu}_k)^2 - f_k]$ is a measure of overdispersion or underdispersion. This reveals a close connection between the proposed test procedure above and existing tests of overdispersion. In particular, Cameron and Trivedi (1998, p.78) construct $z_k = [(f_k - \hat{\mu}_k)^2 - f_k] / \hat{\mu}_k$ and test whether it has zero expectation by referring the test statistic $\hat{\kappa} / \sqrt{\nu_{\kappa}}$ in the usual way to a standard normal distribution, where $\hat{\kappa} = K^{-1} \sum_{k=1}^K z_k$, and $\nu_{\kappa} = \sum_{k=1}^K (z_k - \hat{\kappa})^2 / [K(K-1)]$. This is a score test of $H_0 : \kappa = 0$ for a model with a conditional variance of the form $(1 + \kappa)\mu_k$. It can also test for underdispersion.

5 USE OF MODEL ASSESSMENT CRITERIA

We propose to use the criteria developed in the previous section to select a specification of the log-linear model in (4) via a search algorithm. The criteria might also be used as a diagnostic approach to assess whether a given specified model may be expected to provide adequate risk measures.

Since the criterion \hat{B} in (11) and the associated minimum error tests were derived primarily as a means to detect underfitting (and numerical work we have undertaken suggests that indeed they are more effective for this purpose than for detecting overfit-

ting) we suggest a forward search algorithm, starting from simpler models and adding terms until the specification is judged to be adequate.

In many empirical experiments that we have undertaken, we have found that the independence log-linear model tends to underfit and leads to overestimation of the disclosure risk measures. At the other extreme, the all 3-way interactions model tends to overfit and leads to underestimation of the risk measures. Thus we expect a reasonable solution to lie between these extremes and indeed the all 2-way interactions log-linear model often leads to good estimates of the risk measures for the types of datasets and size of keys that are used in practice. As a practical approach, we suggest first computing the criteria of Section 4 for the independence model and the all 2-way interactions model. If the latter model shows no sign of underfitting then we propose starting with the independence model and adding the 2-way interaction terms for different pairs of key variables, chosen sequentially in order to reduce \hat{B} , until a model is identified which is judged to show no evidence of underfitting. On the other hand, if the all 2-way interactions model is found to exhibit underfitting, then we propose to start a similar forward model search algorithm from this model as the initial model, adding 3-way interaction terms for different triples of key variables. As in any model search algorithm for a hierarchical log-linear model, the inclusion of a higher order term containing an interaction implies that all subsidiary lower order effects should also be included.

Given the alternative choices of test procedures, as well as the alternative measures of overdispersion mentioned in Section 4.4, there are alternative possible stopping rules for the search algorithm. We shall discuss these in the context of the real applications in the next sections. There will, of course, be no single ‘correct’ model and there are likely to be a number of models between which the criteria will not discriminate. We suggest that in the disclosure risk assessment context, it is sensible to produce risk

estimates for each of a number of such ‘reasonable models’ and to use the differences between the estimates as a diagnostic to check the sensitivity of the measures to the specification of the model.

6 COMPLEX SAMPLING SCHEMES

Social surveys almost always employ complex sampling schemes, especially stratification and multi-stage sampling, and use survey weights. In this section we consider how the methods developed in Sections 2-5 require adapting in such circumstances.

The same broad rationale and interpretations provided in Section 2 for the risk measures τ_1 and τ_2 still apply under complex sampling. For example, τ_2 may still be interpreted as the expected number of correct matches for sample uniques, if the intruder is equally likely to match a sampled individual in cell k to any one of the F_k population individuals. The assumptions in Section 3 that $F_k \sim P(\lambda_k)$ and that the λ_k obey the log-linear model in (4) are also unaffected by the complex sampling. What may be affected are the risk expressions $r_{1k} = \exp[-(1 - \pi_k)\lambda_k]$ and $r_{2k} = \{1 - \exp[-(1 - \pi_k)\lambda_k]\}/[(1 - \pi_k)\lambda_k]$. These expressions still hold if $P(f_k = 1 | F_k) = F_k\pi_k(1 - \pi_k)^{F_k-1}$, as for example when the conditional distribution of f_k given F_k is $\text{Bin}(F_k, \pi_k)$. We shall argue in this section that, in fact, $P(f_k = 1 | F_k) \approx F_k\pi_k(1 - \pi_k)^{F_k-1}$ will tend in general to be a good approximation in practice in social surveys, subject if necessary to some judicious choice of key variables. Moreover, we shall present empirical evidence in Section 7 that, the extent to which this approximation holds in practice in social surveys is sufficient to avoid complex sampling inducing serious bias into estimates of the risk measures τ_1 and τ_2 . To assess the approximation $P(f_k = 1 | F_k) \approx F_k\pi_k(1 - \pi_k)^{F_k-1}$ further, we note that it holds if each of two conditions hold:

C1: the inclusion probabilities of individuals within cell k are all approximately equal to π_k ;

C2: individuals within cell k are selected approximately independently.

Consider C1 first. In social surveys, the greatest variations in individual inclusion probabilities tend to arise from differences between major strata, especially geographical strata. It is common to include such major stratification variables as key variables since they will typically be very visible, e.g. state of residence. In this case, there will be no between-stratum component to the variation in inclusion probabilities within cells, providing support for C1. Even if there are design variables, which are not natural key variables, but do lead to major variations in inclusion probabilities, they could be included as key variables to ensure that C1 provides a good approximation.

The main practical threat to condition C2 in social surveys comes from multi-stage sampling and the possibility that the sampling of individuals within cells is clustered. For example, in the extreme case when a cell falls within a single cluster (and no subsampling is employed), either the cluster is sampled so that $f_k = F_k$ or the cluster is not sampled so that $f_k = 0$. It follows that, in this case, $P(F_k = 1 \mid f_k = 1) = 1$ and $E(1/F_k \mid f_k = 1) = 1$ so that the earlier expressions for r_{1k} and r_{2k} would be misleading. In practical applications, this extreme possibility seems very unlikely. The number of sample individuals in a primary sampling unit in social surveys is usually limited in order to avoid loss of precision, and the cross-classification of key variables, such as sex, age group, ethnicity, religion, place of residence or occupation, will typically cut across the primary sampling units and divide them by many more cells than the sample sizes within the primary sampling units. We do not suggest that there will never be individuals from the same cell within a common cluster, e.g. few key variables in practice would split twin children of the same sex living in the same family, but we shall suggest from our empirical work that the degree of clustering in cells tends not to

lead to a degree of over-dispersion of the Binomial distribution which would seriously bias the risk estimates.

Cluster sampling might also lead to correlation between values of f_k in different cells and thus to departures from the “working assumption” that the (F_k, f_k) are independent. This will not, however, lead to bias in the estimation of τ_1 or τ_2 since these are linear in k . Thus, if \hat{r}_{1k} and \hat{r}_{2k} unbiasedly estimate $P(F_k = 1 | f_k = 1)$ and $E(1/F_k | f_k = 1)$ respectively, then $\sum_{SU} \hat{r}_{1k}$ and $\sum_{SU} \hat{r}_{2k}$ will unbiasedly estimate τ_1 and τ_2 respectively, irrespective of any correlation between the f_k .

We next turn to estimation. The λ_k can be estimated consistently under complex sampling using pseudo maximum likelihood estimation (Rao and Thomas, 2003), where the estimating equation in (5) is modified by replacing f_k by \hat{F}_k , obtained by summing the survey weights across sample individuals in cell k , and by removing π_k . The resulting estimates $\hat{\lambda}_k$ are plugged into the expressions for r_{1k} and r_{2k} . The value of π_k in these expressions is replaced by the estimate $\hat{\pi}_k = f_k/\hat{F}_k$. Note that the risk measures only depend upon π_k for sample unique cells and $\hat{\pi}_k$ in this case is simply the reciprocal of the weight for the sample unique case, and this will simply be the inclusion probability of that case if inverse inclusion probability weighting is employed. If the only variation in inclusion probabilities is between major strata, the λ_k could be consistently estimated alternatively by simply ensuring that the strata are represented by a key variable and that the main effects of this key variable are included in the model, with π_k in (5) replaced by $\hat{\pi}_k$.

We finally turn to the use of the minimum error test criteria for the choice of the model. We propose to use the same expression for \hat{B} as in (11) with π_k replaced by $\hat{\pi}_k$, with $\hat{\mu}_k = \hat{\pi}_k \hat{\lambda}_k$ and with $\hat{\lambda}_k$ estimated as above. The motivation for this expression follows as in Section 4.2. The leading term, $\hat{\lambda}_k \exp(-\hat{\lambda}_k)$ in \hat{B} only acts to weight the remaining factor in parentheses which is designed to approximate zero for the

preferred model, and thus the impact of complex sampling on this leading term should be of low relative importance for model choice. The term $f_k - \hat{\mu}_k$ may alternatively be expressed as $\hat{\pi}_k(\hat{F}_k - \hat{\lambda}_k)$, i.e. a multiple of the term featuring in the pseudo score equation and a similar argument to that in Section 4.2 suggests that this term should be of lesser importance than the final term: $(f_k - \hat{\mu}_k)^2 - f_k$. This latter term is the one which seems of most concern in the case of complex sampling. It is based on the Poisson assumption that f_k unbiasedly estimates its own variance. For general complex designs this may not be the case, but under conditions C1 and C2 above we may expect it to hold approximately. The concern is that multistage sampling might lead to slight overdispersion of f_k , with a tendency for f_k to underestimate its own variance, possibly making \hat{B} too large when in fact the model is appropriate. This might lead us to select a more complex model than is appropriate. We find no evidence of such a tendency, however, in the application in Section 7.

7 APPLICATION TO CENSUS SAMPLES

We now apply the proposed methods to samples drawn from the 2001 UK population census. Treating one region of $N=944,793$ individuals as the population, we compute the true aggregated risk measures and compare them to the estimated risk measures for both simple random samples and complex samples from this population and thus examine the performance of the model choice criteria.

We consider two keys defined by six traceable and visible key variables. The first key is defined by (number of categories in parentheses): area (2), sex (2), age (101), marital status (6), ethnicity (17) and economic activity (10), giving $K=412,080$ cells. The second has 73,440 cells and is defined as the first key except that age is grouped

into 18 bands. Our choice of key variables follows considerations at ONS and in Dale and Elliot (2001). To fit the log-linear models, we used iterative proportional fitting (IPF) (Bishop et al., 1975) which is simple to program and directly generates the fitted values $\hat{\mu}_k$ for the risk estimates. Log-linear model fitting procedures in standard statistical software will often not cope with the large numbers of variables and cells in our setting. Therefore we have written a special application in SAS to implement IPF. We experienced no problems of convergence despite the presence of many cells with $f_k = 0$. Our estimation method dealt ‘automatically’ with zero marginal counts corresponding to a given model, because of, for example, impossible combinations of key variable values (structural zeros). When there is a zero on a margin that is used to fit the model, no parameter is estimated and the fitted internal cell values are also zero.

Table 1 presents true and estimated values of τ_1 and τ_2 for three simple random samples with 0.5%, 1% and 2% sampling fractions and for three log-linear models: the independence model, the all 2-way interactions model and the all 3-way interactions model. We see a consistent pattern of estimates decreasing with increasing model complexity, with the independence model always leading to overestimation and the all 3-way interactions model always leading to underestimation. The all 2-way interactions model performs better, mostly generating underestimates but twice generating overestimates. The errors of estimation of $\hat{\tau}_1$ and $\hat{\tau}_2$ always share the same sign and suggest that a fitting criterion which ‘works’ for one measure should also work for the other measure. The five test statistics also tend to have the same signs. The serious overestimation (and underfitting) of the independence model is consistently predicted by the large positive values of all five test statistics. The signs of the five test statistics are also always the same for the all 2-way interactions model and all consistently predict whether $\hat{\tau}_1$ and $\hat{\tau}_2$ will overestimate or underestimate τ_1 and τ_2 respectively. The

underestimation (and overfitting) of the all 3-way interactions model is consistently predicted by the negative signs of the test statistics $\hat{\kappa}/\sqrt{\nu_\kappa}$, $\hat{B}_2/\sqrt{\nu}$ and $\hat{B}_2/\sqrt{\nu_R}$. There are inconsistencies, however, in the behaviour of $\hat{B}_1/\sqrt{\nu}$ and $\hat{B}_1/\sqrt{\nu_R}$, especially for the smaller sample sizes, and this suggests that these tests should be used primarily to detect underfitting.

Although the test statistics have similar signs, their magnitudes vary. The two test statistics, using a variance estimator based upon the Poisson assumption, seem most sensitive (i.e. have the largest values) to underfitting, but least sensitive to overfitting. In contrast, the test statistics based upon the variance estimator ν_R (or the Cameron-Trivedi test) are more sensitive to overfitting and less sensitive to underfitting.

Table 2 presents some values of the underlying statistics \hat{B}_1 and \hat{B}_2 for the large key. For the all 2-way interactions model, there is some similarity between these values and those of the estimation errors $\hat{\tau}_1 - \tau_1$ and $\hat{\tau}_2 - \tau_2$, respectively, as might be expected as the former are intended to estimate the expectation of the latter. For example, for the 1% sample and the large key, we have $\hat{B}_1 = -59.3$, $\hat{\tau}_1 - \tau_1 = -54.1$ and $\hat{B}_2 = -72.9$, $\hat{\tau}_2 - \tau_2 = -75.8$. Nevertheless, the statistics \hat{B}_1 and \hat{B}_2 were derived using approximations around the true model and when the assumed model provides a poor fit, as for the independence and all 3-way interactions models, we observe that \hat{B}_1 and \hat{B}_2 bear little relation to the estimation errors. Moreover, there will be no reliable interpretation of the values of \hat{B}_1 or \hat{B}_2 when they are of a similar magnitude to their standard errors, the case that will be of most interest in our approach to model selection. Henceforth, we shall therefore only consider the values of the test statistics associated with \hat{B}_1 and \hat{B}_2 , not the unstandardized values. Table 2 also includes breakdowns of the \hat{B}_1 and \hat{B}_2 statistics according to the $\hat{B} = \hat{B}_a + \hat{B}_b$ decomposition in Section 4.4. As discussed there, we observe that the second component \hat{B}_b dominates for the independence and all 2-way interactions models, i.e. except for the case of serious overfitting. Thus, as

discussed in Section 4.4., the tests based on \hat{B} are similar to tests of overdispersion when the model underfits.

We now undertake a forward model search, as discussed in Section 5, for the data defined by the large key and the 1% sample ($n=9,448$). Table 1 suggests that the independence model underfits and the all 2-way interactions model overfits. We therefore start from the independence model and consider adding 2-way interaction terms until we find a model for which there is no evidence of lack of fit. Table 3 presents results of the best fitted models obtained for each round of a forward search, starting with the independence model, labelled as Model I. Note that the 1-way (main effects) terms become obsolete when adding in 2-way interaction terms that contain them. The first four rounds are clear-cut in the sense that, at each round, there is a clear choice of the set of 2-way interactions which best reduces all of the test criteria. The set of interaction terms between age and economic activity, denoted $\{a^*ec\}$, is included in round 1 (leading to the model denoted 1). Three further rounds leads to the addition of the sets $\{a^*et\}$, $\{a^*m\}$ and $\{s^*ec\}$ to give Model 4. This model provides a good fit in the sense that the values of all the test statistics based upon \hat{B}_1 or \hat{B}_2 are less than 2 (although the Cameron-Trivedi test still suggests some underfitting). It is less clear how to proceed beyond Model 4. A simple approach in practice might be a forward search using only one criterion (we suggest $\hat{B}_2/\sqrt{\nu}$ in Section 8) stopping at the round prior to which the criterion becomes negative for every added term. Here, we adopt a more informal approach, selecting more than one model at a round if they are nearly indistinguishable with respect to the multiple criteria and permitting very slight negative values of one or two criteria. Thus, at round 5, we select two models, 5a and 5b, which each provide improvements over model 4 but neither appears to be uniformly better than the other in terms of all the criteria. We fail to find any terms to add to Model 5a without one of the criteria becoming strongly negative and thus treat Model

5a as one candidate ‘terminal’ model. There are, however, three models, 6b, 6c, and 6d, which may be obtained from Model 5b and which appear reasonable. Model 6b is again a candidate terminal model since we cannot add any terms without one of the criteria becoming strongly negative. Finally we obtain an additional two candidate terminal models, 7c and 7d from Models 6c and 6d. We thus have four potential ‘terminal’ models, 5a, 6b, 7c and 7d. In fact each of these models gives very similar estimates $\hat{\tau}_1$ and $\hat{\tau}_2$ of around 148 and 336 respectively, implying a robustness of the search procedure to the choice of criterion. Moreover, similar estimates are obtained from models 4, 5b, 6c and 6d, implying a robustness to the precise form of the stopping rule.

The model search is represented graphically in Figure 2. The points $(\hat{\tau}_2, \hat{B}_2/\sqrt{\nu})$ in the scatterplot correspond to all the models in Table 3 as well as all the models which were considered in the forward search but not selected. The points are scattered around a line with a positive slope which, as desired, is around zero when $\hat{\tau}_2$ is equal to the true value of τ_2 , although the search jumps across the true value $\hat{\tau}_2 = \tau_2$ when the term {a*m} is included (the change from Model 2 to 3). The plot tends to display some curvature (convexity) implying that the interval of values of τ_2 for well-fitting models is shorter above its true value than below, i.e. underfitting is easier to detect than overfitting.

We next examine the record-level risk measure \hat{r}_{2k} for the different models. Figure 3 presents a scatterplot of $1/F_k$ against \hat{r}_{2k} for 2,304 sample uniques under Model 5a in Table 3 of the 1% Census sample with the large key. Table 4 provides a corresponding cross-classification of these values within bands. We observe a strong positive relationship with a Spearman rank correlation of 0.80, i.e. the model is effective in using the key variable information to predict $1/F_k$. Nevertheless, it is good news from the

point of view of disclosure protection that the prediction is far from perfect with, for example, many population unique cells not being picked up by high \hat{r}_{2k} values. The values of $1/F_k$ range above and below the diagonal line in Figure 3, as anticipated if \hat{r}_{2k} is to be interpreted as an expected value of $1/F_k$. There is no strong evidence of the \hat{r}_{2k} being smoothed to have smaller dispersion than the $1/F_k$ with similar marginal distributions observed in Table 4.

Table 1 enabled comparison of two different keys. To extend this comparison to an even more demanding key, we now add a 9 category religion variable to the large key to produce $K=3,798,720$ cells. Taking a 1% sample, we now find that over 70% of the non-zero cells are sample unique. The number of population uniques in the sample has risen to $\tau_1=311$ (compared to $\tau_1=159$ without religion), representing over 3% of the 9448 sample cases. Results are presented in Table 5. As for the two keys in Table 1 with a 1% sample, the all 2-way interactions model (II) provides a reasonable fit although, as before, there is some evidence of overfitting. Forward selection from the independence model (I) works well, as in Table 3. The minimum error test criteria suggest the addition of five 2-way interaction terms and the resulting estimates of τ_1 and τ_2 are close to their true values.

We next consider the impact of complex sampling by adopting a sampling and weighting system, typical of household survey designs implemented at government statistical agencies. From the same population, we drew a stratified sample using two strata defined by the area key variable. Sampling fractions were 1:65 in the first area and 1:125 in the second area. In each stratum a systematic sample of households was selected after sorting by finer geographical detail and all persons in the sampled households were included, so the sample of individuals is clustered by household. Differential non-response was generated at the household level based on household size: 20% non-

response for small households, 10% for intermediate size households and 5% for large households. The resulting number of responding individuals represented 1% of the population, enabling comparisons with the 1% sample in Table 3. We constructed sample weights based on generalized regression estimators for 96 weighting classes defined by area, sex and 24 age groups. The weights were calculated to ensure that all individuals in a household receive the same weight and also that the sum of the individual weights in the sample in each weighting class equals the known population total.

The large key with six key variables was used again. The values of the true risk measures are $\tau_1 = 136$ and $\tau_2 = 331.8$, not very different from the values $\tau_1 = 159$ and $\tau_2 = 355.9$ for the 1% simple random sample. The estimates obtained using the methods described in Section 6 are given in Table 6. The results are broadly similar to those found for the simple random sample in Table 3. A good fit is obtained in Model 4 by the inclusion of four 2-way interactions as well as the main effects. This is similar to Model 4 in Table 3, with three of the 2-way interactions the same. The estimates $\hat{\tau}_1 = 132$ and $\hat{\tau}_2 = 334.1$ are even closer to the true values than for the simple random sample. Four other well-fitting models, 5a-5d, are also included in Table 6 and indicate as earlier that the risk estimates are fairly stable across these models. The observed robustness of the results to the complex design seems likely to arise here from the impact of household clustering being mitigated by the fact that the age and sex key variables cut across clusters and by the inclusion of the stratifying variable as a key variable. We also carried out a similar experiment based on the same design without the clustering. This was to assess whether cluster sampling tended to inflate \hat{B} resulting in a different choice of model. We obtained no evidence of this effect.

8 APPLICATION TO SOCIAL SURVEY DATA

We now describe an application to a social survey with a sample size of $n = 127,200$ individuals drawn with equal probability sampling from the adult population of the UK. Although the true values of τ_1 and τ_2 are no longer available for validation, we can still compare the behaviour of the alternative criteria and the stability of risk estimates. The microdata first underwent disclosure control based on initial recoding or suppression of key variables. The visible and traceable key variables that were used for the evaluations were: area (20), sex (2), age in years (top-coded at 90) (91), marital status (5), ethnicity (13) and economic activity (10) resulting in a key of $K = 2,336,000$ cells. There were 13,954 sample uniques. Some results are presented in Table 7. There is clear underfitting of the independence model and clear overfitting of the all 3-way interactions model. The all 2-way interactions model, however, appears to provide a reasonable fit. It is interesting that this model ‘fits’ despite the sample size being much larger than in the census samples. The all 2-way interactions model cannot be exactly true. Experience with the increasing power of conventional goodness-of-fit tests with sample size might lead us to expect that this model would be rejected for a sample as large as this. This is not what we see. Table 1 provides further evidence that increasing the sample size does not necessarily result in the selection of a more complex model. We see no tendency in this table for the test statistics for the all 2-way interactions model to deviate more significantly from zero the larger the sample size. Such evidence lends further support for the practical feasibility of using our criteria across a range of survey settings.

Returning to Table 7, since the values of some of the test statistics for the all 2-way interactions model approach 2, we consider adding in 3-way interactions. Among the twenty possible combinations of 3 from 6 key variables, we present results for the

eight models (1a-1h) which reduced the values of all the minimum error test criteria (without making any negative). Selecting the two of these models (1c and 1d) with the smallest values of $\hat{B}_2/\sqrt{\nu}$ we also present results for nine further models which lead to a reduction of all the minimum error test criteria by adding in 3-way interaction terms.

We observe that the value of the Cameron-Trivedi test now differs clearly from the minimum error tests. We have found such discrepancies with other survey examples, both in positive and negative directions. Table 3 provides examples of relatively minor discrepancies in the opposite direction for Models 4 and 5a for the census data, where the Cameron-Trivedi test indicates significant underfitting, unlike the other test criteria. Exploration of these discrepancies indicates a number of sources, mainly related to the fact that the Cameron-Trivedi statistic is not designed with a focus on sample uniques. In particular, cells with higher expected frequencies $\hat{\mu}_k$ may make a more important contribution to the Cameron-Trivedi statistic than the minimum error criteria, because the contributions of these cells are downweighted less severely by $1/\hat{\mu}_k$ than by $\exp(-\hat{\mu}_k)$. Moreover, we have found a number of survey examples where the \hat{B}_b term no longer dominated $\hat{B} = \hat{B}_a + \hat{B}_b$ (see Section 4.4.). Our broad conclusion is that it is inappropriate to use the Cameron-Trivedi statistic as a general diagnostic criterion for the risk measures considered here, since it is not designed for this purpose.

The values of $\hat{\tau}_1$ and $\hat{\tau}_2$ are spread across the intervals (157.6, 266.9) and (681.5, 845.3) respectively for the well-fitting models in Table 7, exhibiting rather greater variation than in Table 3. We observe that the impact of adding in extra terms is either to reduce the risk measures (e.g. adding terms to Model II) or to have little effect (e.g. adding terms to Model 1d). The values 264.9 and 844.5 of $\hat{\tau}_1$ and $\hat{\tau}_2$ for the all 2-way interactions model act as reasonable upper bounds. A clear lower bound is less easy to obtain and this appears to reflect the greater difficulty in detecting overfitting than underfitting. Fortunately, for risk assessment purposes, an upper bound is usually

considered to be of greater importance. The variation of values of $\hat{\tau}_1$ and $\hat{\tau}_2$ provides some guidance to the sensitivity of the risk estimate provided by this upper bound.

9 DISCUSSION

We have examined the use of Poisson log-linear models to estimate disclosure risk measures for microdata, with applications to census and survey samples. As in Skinner and Holmes (1998) and Elamir and Skinner (2006), we have found that an all 2-way interactions model often leads to reasonable estimates. We have sought to improve on the use of this model as a default, by developing diagnostic criteria for model choice, suitable for risk assessment with the kinds of large and sparse contingency tables spanned by key variables that are typical in practical applications in official statistics. We have shown that our criteria do help to select models that show appreciable improvements in risk estimation relative to the all 2-way interactions model, especially by enabling us to detect overestimation arising from underfitting models. Since our criteria are more effective at detecting underfitting than overfitting, we have proposed a forward selection approach to model selection. There will invariably be several models which are effectively indistinguishable in terms of our criteria. We have found empirically that the risk estimates tend to be rather stable across the simplest models which show no evidence of underfitting. We have found that there may be additional more complex models, obtained by adding terms to the simplest models without leading to significant overfitting (or underfitting), and they may display somewhat more variable risk estimates, but these estimates always tend to be lower than those for the simpler models. Thus the risk estimates for the simplest well-fitting models tend to provide a good upper bound and a conservative approach to risk assessment.

We considered four different criteria, depending on the choice of risk measure (\hat{B}_1 vs. \hat{B}_2) and the choice of variance estimator (ν vs. ν_R). We found that models which ‘work’ for one risk measure (τ_1 or τ_2) tend to work also for the other risk measure. However, our results suggest a slight preference for \hat{B}_2 compared to \hat{B}_1 since the former did not generate misleading results for the all 3-way interactions model in Table 1. There may also be a slight preference for ν rather than ν_R if a forward selection approach is to be used since it appears to lead to a test statistic $\hat{B}_2/\sqrt{\nu}$ with more power for rejecting underfitting models.

We have suggested that differences between risk estimates for alternative well-fitting models may be used to represent uncertainty in a form of sensitivity analysis. Further research would be needed to assess the impact of sampling error in the parameter estimates and the construction of confidence intervals, although we suspect such sampling error effects are somewhat less important than the impact of model choice. One critical assumption in this paper is that there are no discrepancies in the values of the key variables between the microdata and the intruder’s other data source; we plan to extend our approach to handle such discrepancies. Another assumption is that the population frequencies are generated by a Poisson model. Our model assessment criteria aimed at balancing underfitting and overfitting have, in fact, allowed for possible under- or over-dispersion in this Poisson model and our numerical work using census samples has validated the performance of our procedures (based upon the Poisson assumption) in a set-up making no use of the Poisson model. We have therefore identified no need to consider more complex assumptions in this part of the model. We do consider that it may be useful to investigate ways of achieving more simplicity, in particular since our approach can generate significant computational demands when there are many cells. In particular, it would be useful to research ways of splitting the risk assessment by subpopulations (defined by key variables) in order to simplify computation.

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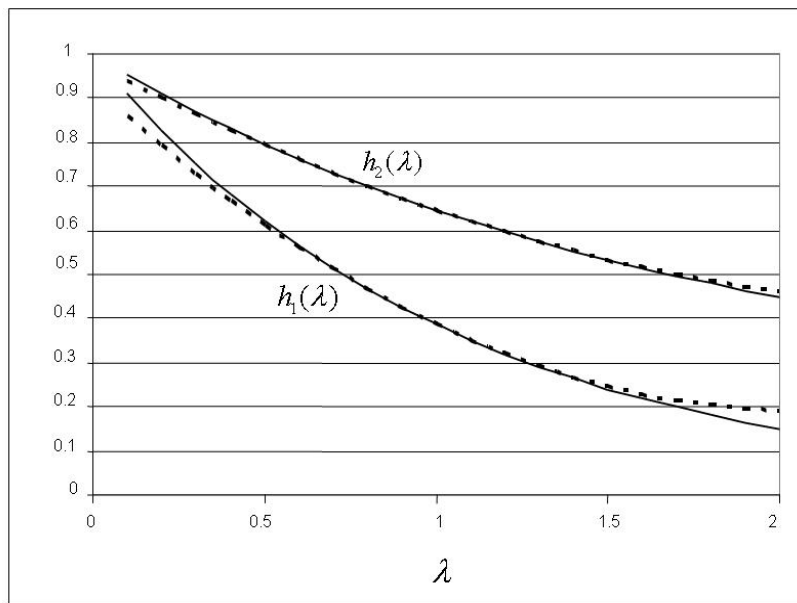


Figure 1: Quadratic approximations of $h(\lambda)$ functions for $\pi = 0.05$. Solid lower line is $h_1(\lambda)$. Solid upper line is $h_2(\lambda)$. Dotted lines are approximations from equation (8).

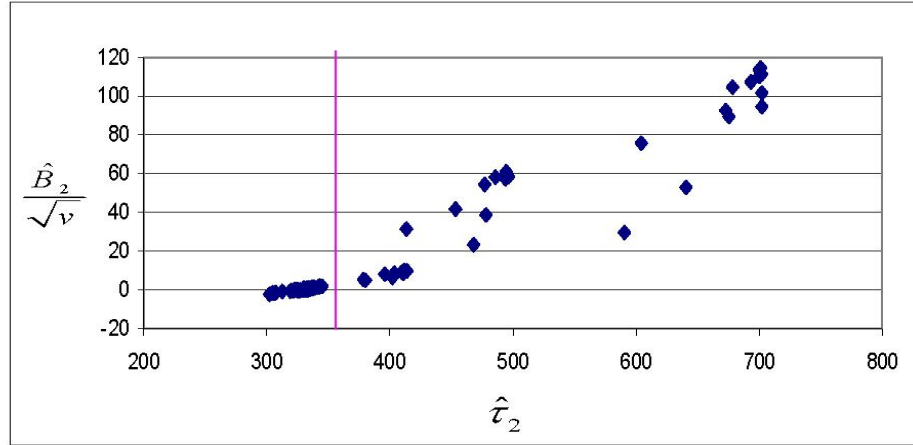


Figure 2: Scatterplot of $\frac{\hat{B}_2}{\sqrt{v}}$ against $\hat{\tau}_2$ for all models considered in forward search, summarised in Table 2.

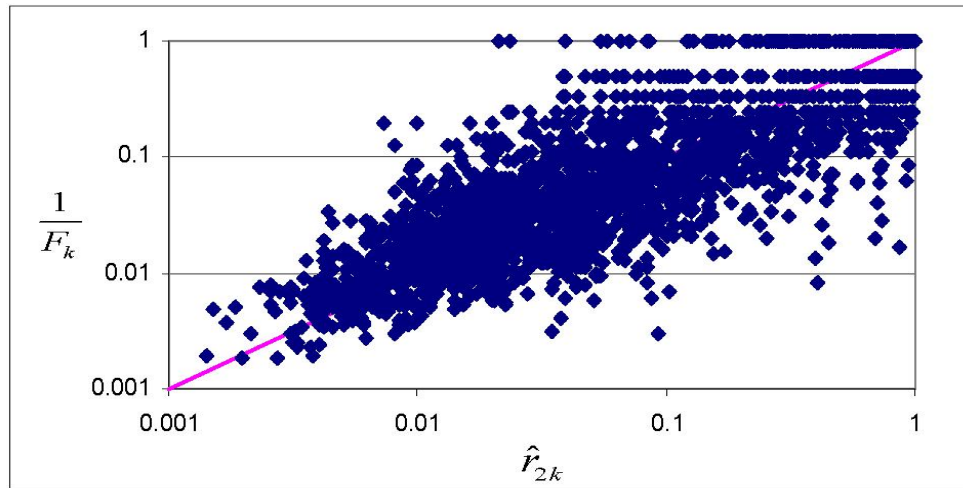


Figure 3: Scatterplot (on logarithmic scales) of $1/F_k$ against \hat{r}_{2k} for 2,304 sample uniques for model 5a in Table 2 with 1% census sample and large key.

Table 1: *Aggregated Risk Measures and Test Statistics for Samples Drawn from the 2001 UK Census.*

n	Model	τ_1	τ_2	$\hat{\tau}_1$	$\hat{\tau}_2$	Test Statistics				
						$\hat{\kappa}/\sqrt{\nu_\kappa}$	$\hat{B}_1/\sqrt{\nu}$	$\hat{B}_1/\sqrt{\nu_R}$	$\hat{B}_2/\sqrt{\nu}$	$\hat{B}_2/\sqrt{\nu_R}$
<i>Small Key K = 73440</i>										
4724	I	23	68.2	54.2	126.9	8.6	12.5	3.3	30.4	7.2
	II			16.0	52.2	-3.6	-0.5	-6.4	-0.8	-2.9
	III			0.0	7.1	-26.4	0.0	2.2	-1.0	-13.1
9448	I	39	127.1	99.3	230.2	8.6	32.1	4.2	60.6	6.8
	II			37.8	117.9	-3.9	-1.3	-9.0	-1.6	-4.2
	III			0.5	24.7	-28.8	-0.2	-2.8	-2.3	-14.3
18896	I	75	215.3	174.3	355.7	9.6	70.7	6.1	125.5	9.1
	II			85.5	222.0	2.0	0.7	0.5	0.7	0.6
	III			11.0	82.1	-28.6	-1.2	-7.4	-4.1	-20.8
<i>Large Key K = 412080</i>										
4724	I	80	183.9	197.4	385.1	10.6	16.8	4.8	53.1	7.4
	II			35.9	112.3	-8.0	-0.5	-1.6	-1.0	-1.4
	III			0.0	11.0	-40.7	0.0	1.1	-1.3	-19.3
9448	I	159	355.9	386.6	701.2	14.4	48.5	8.0	114.2	8.8
	II			104.9	280.1	-10.3	-1.6	-11.1	-2.7	-4.9
	III			1.1	42.2	-45.1	-0.3	-3.0	-3.1	-22.1
18896	I	263	628.9	672.0	1170.5	16.8	105.2	10.3	226.1	10.4
	II			252.0	591.3	-5.7	-1.1	-1.5	-1.5	-1.8
	III			11.3	150.2	-51.9	-1.3	-8.5	-7.0	-37.0

Model I = independence model, Model II = all 2-way interactions model, Model III = all 3-way interactions model.

Table 2: *Aggregated Risks Measures and Components of Model Choice Criteria for Samples Drawn from the 2001 UK Census with a Large Key.*

n	Model	τ_1	τ_2	$\hat{\tau}_1$	$\hat{\tau}_2$	Components of Test Criteria					
						\hat{B}_1	\hat{B}_{1a}	\hat{B}_{1b}	\hat{B}_2	\hat{B}_{2a}	\hat{B}_{2b}
4724	I	80	183.9	197.4	385.1	1178.9	-11.8	1190.7	2555.4	11.2	2544.2
	II			35.9	112.3	-16.8	4.2	-21.0	-23.7	1.7	-25.4
	III			0.0	11.0	0.1	-0.6	0.7	-6.1	-3.0	-3.1
9448	I	159	355.9	386.6	701.2	3400.8	-12.1	3412.8	5463.2	25.2	5437.9
	II			104.9	280.1	-59.3	6.6	-65.9	-72.9	2.4	-75.2
	III			1.1	42.2	-2.1	-1.6	-0.6	-24.1	-5.9	-18.3
18896	I	263	628.9	672.0	1170.5	7269.9	-32.1	7302.0	10618.0	55.7	10562.0
	II			252.0	591.3	-43.6	3.9	-47.5	-43.0	2.5	-45.5
	III			11.3	150.2	-17.0	-5.1	-11.9	-84.7	-9.3	-75.4

Table 3: *Models Selected by a Forward Search for 1% Census Sample with Large Key and Simple Random Sampling Design.*

Model	$\hat{\tau}_1$	$\hat{\tau}_2$	Test Statistics				
			$\hat{\kappa}/\sqrt{\nu_\kappa}$	$\hat{B}_1/\sqrt{\nu}$	$\hat{B}_1/\sqrt{\nu_R}$	$\hat{B}_2/\sqrt{\nu}$	$\hat{B}_2/\sqrt{\nu_R}$
I	386.6	701.2	14.4	48.5	8.0	114.2	8.8
II	104.9	280.1	-10.3	-1.6	-11.1	-2.7	-4.9
1: I + {a*ec}	243.4	494.3	6.5	54.8	3.3	59.2	3.5
2: 1 + {a*et}	180.1	411.6	13.3	3.1	1.4	9.8	4.5
3: 2 + {a*m}	152.3	343.3	5.2	0.9	0.6	1.7	1.1
4: 3 + {s*ec}	149.2	337.5	2.7	0.3	0.2	0.9	0.6
5a: 4 + {ar*a}	148.5	337.1	2.3	0.0	0.0	0.8	0.6
5b: 4 + {s*m}	147.7	335.3	2.2	0.0	0.0	0.7	0.4
6b: 5b + {ar*a}	147.0	335.0	1.8	-0.2	-0.2	0.6	0.4
6c: 5b + {ar*m}	148.9	337.1	2.1	0.0	0.0	0.7	0.5
6d: 5b + {m*ec}	146.3	331.4	1.1	-0.2	-0.2	0.0	0.0
7c: 6c + {m*ec}	147.5	333.2	1.0	-0.3	-0.3	0.1	0.0
7d: 6d + {ar*a}	145.6	331.0	0.7	-0.4	-0.4	0.0	0.0

Area-ar, Sex-s, Age-a, Marital Status-m, Ethnicity-et, and Economic Activity-ec; true values are $\tau_1 = 159$, $\tau_2 = 355.9$

Table 4: *Cross-classification of $1/F_k$ against \hat{r}_{2k} for Sample Uniques within Bands for Model 5a of 1% Census Sample with Large Key.*

$1/F_k$	\hat{r}_{2k}			
	0 - 0.1	0.1 - 0.5	0.5 - 1	Total
0 - 0.1	1391	150	11	1552
0.1 - 0.5	162	253	76	491
0.5 - 1	26	91	144	261
Total	1579	494	231	2304

Table 5: *Models Selected by a Forward Search for 1% Census Sample with Very Large Key ($K=3,708,720$)*

Model	$\hat{\tau}_1$	$\hat{\tau}_2$	Test Statistics				
			$\hat{\kappa}/\sqrt{\nu_\kappa}$	$\hat{B}_1/\sqrt{\nu}$	$\hat{B}_1/\sqrt{\nu_R}$	$\hat{B}_2/\sqrt{\nu}$	$\hat{B}_2/\sqrt{\nu_R}$
I	962.7	1386.3	6.3	108.1	5.5	129.6	8.4
II	251.8	560.9	-0.4	-0.9	-1.0	-2.3	-3.2
1: I + {a*ec}{ar*a}	716.0	1094.0	4.1	58.5	4.7	40.6	5.9
2: 1 + {s*a}{ar*ec}	715.2	1092.7	4.0	58.3	4.6	39.0	5.5
3: 2 + {et*r}{a*m}	419.0	777.3	3.6	16.7	3.2	30.2	3.3
4: 3 + {a*et}{s*ec}	356.3	687.4	1.4	1.1	0.9	1.6	1.4
5: 4 + {m*r}{ec*r}	320.9	662.4	1.0	0.5	0.5	0.4	0.4

Area-ar, Sex-s, Age-a, Marital Status-m, Ethnicity-et, Economic Activity-ec, Religion -r; true values are $\tau_1 = 311$, $\tau_2 = 663.1$

Table 6: *Models Selected by a Forward Search for 1% Census Sample with Large Key and Complex Survey Design.*

Model	$\hat{\tau}_1$	$\hat{\tau}_2$	Test Statistics				
			$\hat{\kappa}/\sqrt{\nu_\kappa}$	$\hat{B}_1/\sqrt{\nu}$	$\hat{B}_1/\sqrt{\nu_R}$	$\hat{B}_2/\sqrt{\nu}$	$\hat{B}_2/\sqrt{\nu_R}$
I	378.5	701.8	14.0	8.2	50.7	8.5	114.5
II	103.5	283.5	-2.0	-1.5	-1.0	-3.6	-2.2
1: I + {a*m}	297.8	590.4	14.7	6.3	20.6	9.0	38.1
2: 1 + {a*et}	231.3	514.0	19.1	5.2	13.4	8.3	21.1
3: 2 + {a*ec}	153.8	357.0	7.1	2.5	3.8	3.1	4.6
4: 3 + {et*ec}	132.0	334.1	6.4	0.2	0.2	0.8	0.8
5a: 4 + {ar*a}	132.8	335.8	5.6	0.2	0.1	0.7	0.7
5b: 4 + {s*m}	129.0	331.3	6.0	0.0	0.0	0.8	0.7
5c: 4 + {ar*ec}	131.3	333.6	6.1	-0.1	-0.1	0.5	0.5
5d: 4 + {m*ec}	128.3	327.4	5.6	-0.1	-0.1	0.3	0.4

Area-ar, Sex-s, Age-a, Marital Status-m, Ethnicity-et, and Economic Activity-ec; true values are $\tau_1 = 136$, $\tau_2 = 331.8$

Table 7: *Models Selected by a Forward Search for a Social Survey.*

Model	$\hat{\tau}_1$	$\hat{\tau}_2$	Test Statistics				
			$\hat{\kappa}/\sqrt{\nu_\kappa}$	$\hat{B}_1/\sqrt{\nu}$	$\hat{B}_1/\sqrt{\nu_R}$	$\hat{B}_2/\sqrt{\nu}$	$\hat{B}_2/\sqrt{\nu_R}$
I	879.5	2301.6	15.51	561.4	9.77	1206.7	9.19
II	264.9	844.5	0.68	1.80	0.99	1.93	1.41
III	10.5	211.4	-82.74	-0.48	-9.12	-3.54	-43.15
1a: II+{ar*s*et}	263.5	840.9	-0.02	0.96	0.66	1.59	1.23
1b: II+{ar*s*ec}	263.4	843.0	0.51	1.35	0.98	1.83	1.35
1c: II+{ar*a*m}	232.1	787.6	-3.01	1.61	0.88	0.94	0.70
1d: II+{ar*a*ec}	217.9	748.3	-3.65	1.46	0.76	0.36	0.30
1e: II+{ar*et*ec}	191.2	739.2	-0.94	0.98	0.69	1.27	0.99
1f: II+{s*m*et}	266.9	845.3	0.58	1.73	0.95	1.83	1.35
1g: II+{a*m*et}	188.5	727.8	-0.96	1.50	0.88	1.24	0.90
1h: II+{m*et*ec}	244.3	813.0	0.16	1.59	0.89	1.35	1.03
2c1: 1c+{ar*s*et}	230.5	784.1	-5.38	0.53	0.43	0.49	0.41
2c2: 1c+{ar*s*ec}	231.2	786.4	-3.22	1.52	0.83	0.84	0.63
2c3: 1c+{ar*et*ec}	157.6	681.5	-6.99	0.32	0.28	0.04	0.03
2c4: 1c+{s*a*m}	232.5	785.0	-3.54	1.61	0.88	0.88	0.65
2c5: 1c+{s*a*et}	226.7	772.7	-4.41	1.39	0.81	0.78	0.59
2c6: 1c+{s*m*et}	234.2	788.7	-3.21	1.55	0.85	0.90	0.67
2d1: 1d+{ar*s*et}	216.0	745.2	-6.77	0.91	0.56	0.16	0.13
2d2: 1d+{ar*s*ec}	217.8	747.8	-3.76	1.45	0.76	0.28	0.23
2d3: 1d+{s*m*ec}	216.6	743.8	-3.86	1.43	0.75	0.32	0.26

Area-ar, Sex-s, Age-a, Marital Status-m, Ethnicity-et, and Economic Activity-ec