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Accurate Parametric Inference for Small Samples

Alessandra R. Brazzale and Anthony C. Davison

Abstract. We outline how modern likelihood theory, which provides essentially exact inferences in a variety of parametric statistical problems, may routinely be applied in practice. Although the likelihood procedures are based on analytical asymptotic approximations, the focus of this paper is not on theory but on implementation and applications. Numerical illustrations are given for logistic regression, nonlinear models, and linear non-normal models, and we describe a sampling approach for the third of these classes. In the case of logistic regression, we argue that approximations are often more appropriate than ‘exact’ procedures, even when these exist.

Key words and phrases: Conditional inference, heteroscedasticity, logistic regression, Lugannani–Rice formula, Markov chain Monte Carlo, nonlinear model, R, regression-scale model, saddlepoint approximation, spline, statistical computing.

1. INTRODUCTION

Monte Carlo inference has developed remarkably over the last 30 years. Bootstrap procedures (Efron, 1979) are used for a wide range of problems (Efron and Tibshirani, 1993, Davison and Hinkley, 1997). Markov chain Monte Carlo simulation has transformed Bayesian modelling (Robert and Casella, 2004). The combination of iterative simulation with importance sampling and improved algorithms for full enumeration of discrete sample spaces has had a strong impact on the analysis of contingency tables (Forster, McDonald and Smith, 1996, Smith, Forster and McDonald, 1996, Diaconis and Sturmfels, 1998, Mehta, Patel and Senchaudhuri, 2000). More recently there has been a rise in Bayesian nonparametric modelling (Denison et al., 2002), which parallels the use of the bootstrap

for nonparametric frequentist inference. All these techniques use simulation to avoid tailoring analytical work to specific problems.

Parallel with these developments has been the development of analytical approximations for parametric inference in small samples, initiated by Fisher (1934) but largely overlooked until new developments were stimulated by Efron and Hinkley (1978) and Barndorff-Nielsen and Cox (1979). A flood of subsequent work is summarized in the books of Barndorff-Nielsen and Cox (1994), Pace and Salvani (1997), and Severini (2000). The efforts of many researchers, particularly O. E. Barndorff-Nielsen, (1983, 1986) and D. A. S. Fraser (e.g., Fraser, 1990; Fraser, Reid and Wu, 1999) and their co-workers, have led to an elegant theory of near-exact inference based on small samples from parametric models. Its theoretical basis is saddlepoint and related approximation (Daniels, 1954, 1987), and further developments have been well described by Reid (1988, 1995, 2003). These methods are highly accurate in many situations, but are nevertheless under-used compared to the simulation procedures mentioned above. One reason for this may be their arcane basis in the conditionality principle, ancillary statistics and marginalization, and another may be the forbidding technical details, but the main reason is undoubtedly the lack of suitable software. Unlike the bootstrap libraries available in general-purpose

Alessandra R. Brazzale is Associate Professor of Statistics, Department of Social, Cognitive and Quantitative Sciences (DSSCQ) University of Modena and Reggio Emilia, Viale Allegri 9, 42100 Reggio Emilia, Italy (e-mail: alessandra.brazzale@unimore.it) and Institute of Biomedical Engineering, Italian National Research Council. Anthony C. Davison is Professor of Statistics, Institute of Mathematics (IMA-FSB-EPFL), École Polytechnique Fédérale de Lausanne, Station 8, 1015 Lausanne, Switzerland (e-mail: anthony.davison@epfl.ch).

languages such as S-PLUS (S-PLUS, 2007) and R (R Development Core Team, 2007) or specialized software such as WinBUGS (Lunn et al., 2000) or *LogXact* (Cytel Inc., 2007), small-sample parametric asymptotics have been implemented piecemeal, usually by specialists in the area for their personal use.

This paper describes the implementation and use of libraries of software for higher order inference for several special classes of model: for linear exponential families such as logistic regression models, for nonnormal linear models and for nonlinear regression models with heteroscedastic normal errors. Its objective is to make higher order inference for such models available for use by those without a command of the technical details. We also describe how Markov chain Monte Carlo may be used not only to assess conditional coverage and related properties of some of our methods, but also for inference. A related, more extended, account may be found in Brazzale, Davison and Reid (2007), which gives many further examples. Butler (2007) gives ample evidence for the accuracy of the approximations that underlie some of the theory used herein.

Section 2 outlines developments in parametric asymptotics that undergird the numerical approximations whose implementation is described in Section 3. Application to logistic regression is described in Section 4, where we argue that the conservatism and fragility of exact inference in this context should lead us to prefer approximation. In Section 5 we discuss regression-scale models with nonnormal errors, outline how both analytical approximation and Markov chain Monte Carlo simulation may be used for approximate conditional inference, and compare them empirically. Section 6 describes how the approximate methods may be applied to nonlinear regression models, which are often fitted using small samples from bioassays or toxicological studies. The paper concludes with a brief discussion and appendices containing technical details.

2. BACKGROUND

2.1 First Order Inference

Initially we consider a parametric statistical model with density $f(y; \theta)$, where $\theta \in \Theta \subseteq \mathbb{R}^d$ is a d -dimensional parameter and $y = (y_1, \dots, y_n)$ a vector of continuous responses. Let $L(\theta) \propto f(y; \theta)$ denote the likelihood and $\ell(\theta) = \log L(\theta)$ the log likelihood functions. Under mild conditions the maximum likelihood estimate $\hat{\theta}$ may be found by solving the score

equation $\ell_\theta(\hat{\theta}) = 0$, and its asymptotic variance is approximated using the inverse of the observed information matrix $j(\hat{\theta})$. We distinguish between quantities of primary interest and others not of direct concern by writing $\theta = (\psi, \lambda)$, where ψ is a low-dimensional parameter of interest and λ is a nuisance parameter whose dimension may be appreciably larger than that of ψ . This partitioning entails corresponding splits of the score vector $\ell_\theta(\psi, \lambda)$ into $\ell_\psi(\psi, \lambda)$ and $\ell_\lambda(\psi, \lambda)$, and of the observed information function $j(\psi, \lambda)$ into the sub-matrices $j_{\psi\psi}(\psi, \lambda)$, $j_{\psi\lambda}(\psi, \lambda)$, $j_{\lambda\psi}(\psi, \lambda)$ and $j_{\lambda\lambda}(\psi, \lambda)$.

Exact inference for linear exponential families and location-scale models was discussed by Fisher (1934) in a paper largely ignored for many years. Even where available, in principle, the effort needed to implement exact methods in all but the simplest cases means they are seldom used in practice, but are typically replaced by asymptotic approximations derived by assuming that the sample size n , or, more generally, some information index, tends to infinity. We then eliminate the nuisance parameter λ by replacing it by the constrained maximum likelihood estimate $\hat{\lambda}_\psi$ obtained by maximizing $\ell(\psi, \lambda)$ with respect to λ for fixed ψ . Inference about ψ may then be performed using the profile log likelihood function $\ell_p(\psi) = \max_\lambda \ell(\psi, \lambda) = \ell(\psi, \hat{\lambda}_\psi)$. The corresponding observed information function, $j_p(\psi) = -\partial^2 \ell_p(\psi) / \partial \psi \partial \psi^T$, can be expressed in terms of the full observed information function through the identity

$$j_p(\psi) = j_{\psi\psi}(\hat{\theta}_\psi) - j_{\psi\lambda}(\hat{\theta}_\psi) \{j_{\lambda\lambda}(\hat{\theta}_\psi)\}^{-1} j_{\lambda\psi}(\hat{\theta}_\psi),$$

where $\hat{\theta}_\psi = (\psi, \hat{\lambda}_\psi)$. For scalar ψ , inference on the parameter of interest may be based on the Wald statistic, $j_p(\hat{\psi})^{1/2}(\hat{\psi} - \psi)$, score statistic, $\{j_p(\hat{\psi})\}^{-1/2} \ell_\psi(\psi, \hat{\lambda}_\psi)$, or on the likelihood root,

$$(1) \quad r(\psi) = \text{sign}(\hat{\psi} - \psi) [2\{\ell_p(\hat{\psi}) - \ell_p(\psi)\}]^{1/2},$$

which have standard normal distributions up to the order $O(n^{-1/2})$. When the sample size is small these first order approximations are often inaccurate, especially in complex models.

2.2 Higher Order Inference

The keys to refining the limiting behavior of the most important likelihood quantities are two higher order density approximations: Barndorff-Nielsen's (1983) p^* formula and the tangent exponential model p_{TEM} developed by Fraser, Reid and Wu (1999). Apart from

an $O(n^{-1})$ norming constant, the first gives the density of the maximum likelihood estimate at the observed data and at other points having the same value of an ancillary statistic, though these must be known. The second is an exponential model whose distribution function at the observed data differs from that of the conditional model by $O(n^{-3/2})$ under the observed conditioning (Fraser, Andrews and Wong, 2005). Both approximations are exact for transformation models and give excellent results generally. In full exponential families they agree with the saddlepoint approximation to the density of the minimal sufficient statistic given by Barndorff-Nielsen and Cox (1979).

These density approximations are mainly useful for deriving approximate distribution functions for appropriate pivots, from which we obtain P-values and confidence intervals for the parameters of interest. For scalar ψ , these approximate distribution functions have the forms

$$(2) \quad \Phi^*(r) = \Phi(r) + \phi(r) \left(\frac{1}{r} - \frac{1}{q} \right)$$

and

$$(3) \quad \Phi(r^*) = \Phi \left(r + \frac{1}{r} \log \frac{q}{r} \right),$$

for r given at (1) and q defined as

$$(4) \quad q = \frac{|\varphi(\hat{\theta}) - \varphi(\hat{\theta}_\psi) \varphi_\lambda(\hat{\theta}_\psi)|}{|\varphi_\theta(\hat{\theta})|} \left\{ \frac{|j(\hat{\theta})|}{|j_{\lambda\lambda}(\hat{\theta}_\psi)|} \right\}^{1/2},$$

where $\Phi(\cdot)$ and $\phi(\cdot)$ represent the standard normal distribution and density functions. Here, $\varphi(\theta)$ is a reparametrization based at the observed data and used to provide a third order distribution function approximation through the tangent exponential model, and $\varphi_\theta(\theta)$ and $\varphi_\lambda(\theta)$ represent the $d \times d$ matrix with (i, j) element $\partial\varphi_i/\partial\theta_j$ and the $d \times (d - 1)$ matrix with (i, j) element $\partial\varphi_i/\partial\lambda_j$. Special expressions for (4) can be found in Appendix A.1. Expression (2) is known as a Lugannani–Rice-type approximation, and the quantity r^* in the Barndorff-Nielsen-type approximation (3) is known as a modified likelihood root. Under ordinary repeated sampling, approximations (2) and (3) are exact up to the third order, that is,

$$\begin{aligned} \text{pr}(R \leq r; \theta) &= \Phi^*(r) + O(n^{-3/2}), \\ \text{pr}(R^* \leq r^*; \theta) &= \Phi(r^*) + O(n^{-3/2}). \end{aligned}$$

In comparison, the likelihood root r itself is standard normal only to the first order, $O(n^{-1/2})$. A rather subtle Taylor series expansion of $\Phi(r^*)$ around r , taking into account the dependence of $\varphi(\theta)$ on the observed data

point, shows that $\Phi(r^*) = \Phi^*(r) + O(n^{-3/2})$, rising to $O(n^{-1})$ if this dependence is not accommodated; in particular the more accurate results holds for linear exponential families (Jensen, 1992), in which $\varphi(\theta)$ does not depend on the observed data. In an exponential family of order one, $\Phi^*(r)$ equals the Lugannani and Rice (1980) tail area approximation. In the presence of nuisance parameters, it gives the approximation due to Skovgaard (1987).

2.3 Related Ideas

An alternative to the ideas outlined in Section 2.2 is first to adjust the profile likelihood $L_p(\psi) = \exp\{\ell_p(\psi)\}$ to account for the presence of nuisance parameters, and then to correct the first order statistics obtained therefrom in order to improve the standard normal approximation. Pierce and Peters (1992) call these sequential approximations, as contrasted with the more common double approximations (Barndorff-Nielsen and Cox, 1979).

The general form of the adjusted profile likelihood is

$$(5) \quad L_a(\psi) = L_p(\psi)M(\psi),$$

with suitably defined correction term $M(\psi)$; see Appendix A.2. When an exact conditional or marginal likelihood function for ψ exists, this is approximated to the order $O(n^{-1})$ by the adjusted profile likelihood function. In stratified models with the number of nuisance parameters proportional to the number of strata, Sartori et al. (1999) showed that $M(\psi)$ corrects for the presence of the nuisance parameters. The maximizing value $\hat{\psi}_a$ usually has a smaller finite-sample bias than does $\hat{\psi}$, and the likelihood root $r_a(\psi)$ based on L_a has a distribution that is closer to normal than does $r(\psi)$. Insight into why likelihood roots obtained from adjusted likelihoods tend to achieve most of the distributional improvement achieved by higher order methods, despite their null distribution being standard normal only to the first order, is provided by Sartori (2003) in a two-index asymptotics setting and by DiCiccio and Efron (1996), who relate their findings to the bootstrap.

If the parameter of interest is vector, formula (3) cannot be used. Skovgaard (2001) suggests adjusting the likelihood ratio statistic $w(\psi) = 2\{\ell_p(\hat{\psi}) - \ell_p(\psi)\}$, which has the χ^2 distribution with $d_0 = \text{dim}(\psi)$ degrees of freedom up to the order $O(n^{-1})$. His proposed adjusted likelihood ratio statistic

$$(6) \quad w^* = w\{1 - w^{-1} \log u\}^2,$$

with correction term u suitably defined, is also asymptotically distributed as $\chi_{d_0}^2$, but behaves much better

than w in small samples. If ψ is scalar, then $u = r/q$ with q given by (4), and (6) reduces to $(r^*)^2$.

The above discussion applies only to continuous response models. For discrete responses, analogous results are in general unavailable. However, for distributions such as the binomial and Poisson whose support has, or can easily be transformed to, a lattice structure, the use of a slightly modified form of (2) provides approximations to tail probabilities with error $O(n^{-1})$ (Severini, 2000, Section 6.3.3). Pierce and Peters (1992) discuss continuity correction for the asymptotic approximations. As discussed in Section 4, the uncorrected version can be interpreted as an approximation to the mid-P value (Agresti, 2002, page 20)

$$p_{\text{mid}}(x; \psi) = \text{pr}(X < x; \psi) + \frac{1}{2} \text{pr}(X = x; \psi)$$

for a suitable lattice random variable X . Further discussion is given by Pierce and Peters (1999), Davison and Wang (2002), and Davison, Fraser and Reid (2006), who indicate that use of r^* unmodified in standard discrete cases approximates the mid-P value with error of the order $O(n^{-1})$. From a practical point of view, the most reassuring point is perhaps not the precise asymptotic order of these approximations, but rather the fact that they are relative, and thus give accurate values even for small tail probabilities.

3. IMPLEMENTATION

3.1 General

Many journal pages and several books have been devoted to the ideas sketched in Section 2, but their widespread adoption in practice has been limited by the lack of suitable software. The R package bundle `hoa`, short for higher order asymptotics, is intended to make these methods readily accessible by providing easy-to-use and self-contained code for routine data analysis with logistic regression models, nonnormal linear models and nonlinear models with nonconstant variance (Brazzale, 2005). These models are widely used in applications: logistic regression is a common tool in epidemiology and medicine; nonnormal linear models comprise models used in survival and reliability analyses; and nonlinear heteroscedastic models are increasingly used in biostatistics, for instance, in herbicide bioassays and ecotoxicity tests. The code is organized as four packages, three of which—`cond`, `marg` and `nlreg`—refer to the model classes just mentioned. A fourth—`csampling`—contains conditional sampling routines for nonnormal linear models and was used to produce the results presented

in Section 5. The code is freely available from <http://statwww.epfl.ch/AA> or can be downloaded from CRAN (<http://cran.r-project.org>).

The remainder of this section sketches the core ideas that make it possible to implement higher order asymptotics in a numerical computing environment with limited facilities for algebraic manipulation. The issues inherent to the implementation for logistic and nonlinear models are described in Brazzale (1999) and Bellio and Brazzale (2003), respectively. The complete design strategy can be found in Brazzale (2000), Chapter 6.

3.2 Building-Blocks

The complexity of the algebraic expressions involved is the main obstacle to the implementation of higher order asymptotics in numerical computing environments, most of which have inefficient symbolic manipulation capabilities, if any at all. The key to our implementation of the methods presented in Section 2 is to identify building-blocks into which the higher order statistics can be decomposed and which are provided or can efficiently be handled by the computing device. This builds upon the observation of Davison (1988) that in linear exponential families the output of standard fitting routines suffices to calculate the $q(\psi)$ and $M(\psi)$ correction terms of Section 2. Brazzale (2000), Section 6.1, derives the corresponding building-blocks for nonnormal linear and nonlinear heteroscedastic regression models. The first of these classes is characterized by the design matrix X , the standardized residuals a , minus the logarithm of the density function of the error term, $g_0(\varepsilon) = -\log f(\varepsilon)$, and its first two derivatives (see Brazzale, Davison and Reid, 2007, Section 8.6.2). For nonlinear regression models the only requirements are the mean and variance functions $\mu(x; \beta)$ and $w(x; \beta, \rho)^2$ and their first two derivatives (see Brazzale, Davison and Reid, 2007, Section 8.6.3). Two design strategies were adopted to make these quantities available in `hoa`: either they are provided by special constructs, called *family objects*, or they are derived as needed by exploiting the algebraic manipulation function `deriv3` available in R; see Bellio and Brazzale (2003).

3.3 Pivot Profiling

Inferences provided by fitting routines available in statistical computing environments such as S-PLUS and R are generally based upon first order asymptotics. Most often the Wald statistic is used, because its linearity in the interest parameter ψ yields simple readily computed confidence intervals. The likelihood ratio

statistic is parametrization-invariant, and hence more reliable, but its nonlinearity in ψ means that construction of confidence intervals entails re-fitting the model for all the required values of ψ . We deal with this by using cubic splines to interpolate values of $r(\psi)$ and related quantities among values calculated exactly for a grid encompassing the required range of ψ . In R this may be achieved by using different *offsets*, for each of which the necessary output is retrieved and statistics calculated. Estimates and confidence bounds are read off from significance functions such as (2) and (3) using the fitted splines.

Numerical interpolation of higher order solutions works very well for analytic functions such as the profile and adjusted profile likelihoods, but quantities such as r^* have a singularity at $\psi = \hat{\psi}$, and the numerical values calculated may be unstable if ψ is close to $\hat{\psi}$. This problem is particularly acute for logistic regression. Nonnormal linear models are much less affected, and in our experience numerical instabilities are almost absent for nonlinear models. To avoid singularities in the first two model classes, we implemented a hybrid algorithm that uses two-step polynomial interpolation of the higher order statistics for values of ψ in a small interval around $\hat{\psi}$. The higher order solutions are expressed as polynomials of the likelihood root r , which itself is written as a polynomial in ψ , and the coefficients of these polynomials are estimated by least squares. For nonlinear models, it suffices to avoid exact computation of the higher order statistics for values of ψ very close to the maximum likelihood estimate.

The procedure just described represents the bulk of the approximate conditional inference routines in the `cond`, `marg` and `nlreg` packages, which enable inference for the three model classes of the `hoa` bundle. See Section 6.3.2 and Appendix B.2 of [Brazzale \(2000\)](#) for further details.

3.4 Markov Chain Monte Carlo

The generation of observations conditional on an ancillary statistic is useful for inferential purposes such as the calculation of confidence intervals and P-values whenever the exact conditional density is unknown or difficult to obtain without simulation. Such an approach is described in an unpublished technical report by [Casella, Wells and Tanner \(1994\)](#), who emphasize sampling-based calculations for pivotal inference using the Gibbs sampler.

Conditional inference may also be used to assess the quality of small-sample solutions. Studies of the properties of the methods presented in Section 2 ([DiCiccio,](#)

[Field and Fraser, 1990](#), [DiCiccio and Field, 1991](#), [Ronchetti and Ventura, 2000](#)) focused on their numerical accuracy, stability and sensitivity to model failure. So far as we know, there has been no numerical investigation of these properties conditional on an ancillary statistic; [Severini \(1999\)](#) and [Ventura \(1997\)](#) grouped their simulation results by the levels of two nearly independent functions of the ancillary, but this does not amount to a fully conditional simulation. [Trotter and Tukey \(1956\)](#) were the first to simulate conditionally on an ancillary statistic in the special case of normal samples, but there have been few contributions since ([Durbin, 1961](#); [Bondesson, 1982](#); [Fraser, Lee and Reid, 1990](#); [Morgenthaler and Tukey, 1991](#)).

The `csampling` package of the `hoa` bundle includes a conditional sampler for general regression-scale models and extends [Bondesson's \(1982\)](#) method by replacing an acceptance-rejection algorithm by the Metropolis–Hastings algorithm ([Robert and Casella, 2004](#), Chapter 7). Section 5.2 describes a simulation study performed using this package.

4. LOGISTIC REGRESSION

4.1 Likelihood Approximation

After the linear model, logistic regression of binary responses y_1, \dots, y_n on covariates $(z_1, x_1), \dots, (z_n, x_n)$ is perhaps the most widely used parametric regression procedure. Let X , Z and y denote the $n \times p$, $n \times k$ and $n \times 1$ matrices whose i th rows are respectively x_i^\top , z_i^\top and y_i . The log likelihood

$$\begin{aligned} \ell(\psi, \lambda) &= y^\top Z \psi + y^\top X \lambda \\ &\quad - \sum_{i=1}^n \log\{1 + \exp(z_i^\top \psi + x_i^\top \lambda)\} \end{aligned}$$

corresponds to a linear exponential family with canonical parameter (ψ, λ) and sufficient statistic $(t, s) = (Z^\top y, X^\top y)$, so the higher order approximations described above are particularly simple and can be obtained by re-arranging the output of standard routines for fitting logistic models ([Davison, 1988](#)); see also [Daniels \(1958\)](#), [Barndorff-Nielsen and Cox \(1979\)](#), [Pierce and Peters \(1992\)](#) and [Strawderman, Casella and Wells \(1996\)](#). Such approximations are provided by our `cond` package.

EXAMPLE 1 (Urine data). For illustration, we take data on the presence or not of crystals in urine samples ([Andrews and Herzberg, 1985](#), page 249). Full data on the six quantitative covariates are available for 77 individuals, and we consider the coefficient ψ of the

variable urea representing urea concentration (millimoles/litre) in a logistic regression model also containing the five other covariates and an intercept. The R code for first order and higher order inferences is

```
> uri.glm <- glm( r ~ gravity + ph +
+               osmo + conduct +
+               urea + calc,
+               family = binomial,
+               data = urine )
> summary( uri.glm )
> uri.urea <- cond( uri.glm,
+                 offset = urea )
> summary( uri.urea )
> plot( uri.urea )
```

The first two instructions fit the model by maximum likelihood and then print the results, and the last four lines of code compute, summarize and plot the first and higher order approximations. The maximum likelihood estimate and its standard error are $\hat{\psi} = -0.0320$ (0.0161), yielding a Wald statistic of -1.99 with two-sided P-value $2\Phi(-1.99) = 0.047$. An approximation to the conditional maximum likelihood estimate and its standard error is obtained by maximizing the adjusted profile log likelihood and taking its curvature at the maximum; this gives $\hat{\psi}_a = -0.0276$ (0.0149), yielding an approximate conditional Wald statistic of -1.85 and P-value 0.064. The 95% confidence intervals for ψ based on these two Wald pivots are respectively $(-0.0636, -0.0004)$ and $(-0.0568, 0.0016)$, and those based on the likelihood root r , and the modified likelihood root r^* are

$(-0.0668, -0.0025)$ and $(-0.0587, 0.0005)$. Thus, the estimated coefficient changes by around 14%, more than might be anticipated with six nuisance parameters and 77 observations, and there are corresponding changes to the confidence intervals.

Figure 1 shows two of the graphs provided by the `plot` command: note the large difference between first and higher order inference summaries, which suggests that the latter should be used as a matter of course with binary data models. The adjusted profile likelihood corrects for the finite sample bias in the maximum likelihood estimator, in analogy to the conditional likelihood function, while the modified likelihood root also accounts for the nonnormality of the ordinary and adjusted likelihood functions.

A simple information computation sheds some light on the size of the higher order correction in the example above. Suppose that we have independent observations y'_1, \dots, y'_n from the logistic density $\exp(y'_i - \lambda - z_i \psi) / \{1 + \exp(y'_i - \lambda - z_i \psi)\}^2$, where the z_i are known scalar covariates. The asymptotic variance v_{cont} of the maximum likelihood estimator of ψ based on the continuous y'_i is a corner of the Fisher information matrix, which is easily seen to be $3(\tilde{X}^T \tilde{X})^{-1}$, where \tilde{X} denotes the entire design matrix, whose i th row here is $(1, z_i)$. If only the sign of the y'_i is known, so the continuous observations are replaced by binary variables, the asymptotic variance of the maximum likelihood estimator of ψ is a corner of the matrix $(\tilde{X}^T W \tilde{X})^{-1}$, where W denotes the $n \times n$ diagonal matrix $\text{diag}\{\pi_1(1 - \pi_1), \dots, \pi_n(1 - \pi_n)\}$, with

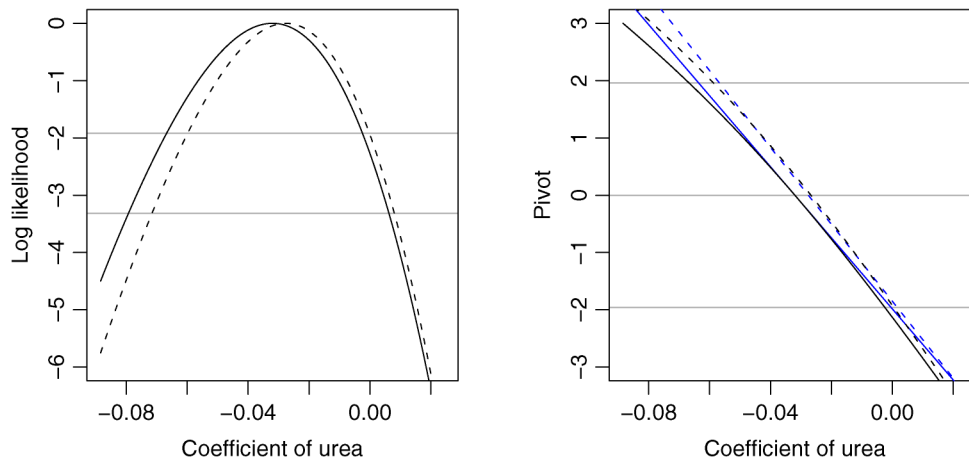


FIG. 1. Graphical output comparing first (solid) and higher order (dashes) inference summaries for the urine data. Left: profile log likelihood $\ell_p(\psi)$ (solid) and adjusted profile log likelihood $\ell_a(\psi)$ (dashes), with horizontal gray lines indicating 0.95 and 0.99 confidence sets for ψ . Right: likelihood root $r(\psi)$ (solid, curved) and modified likelihood root $r^*(\psi)$ (dashes, curved), and Wald pivots based on the profile likelihood (solid, straight) and the adjusted profile likelihood (dashes, straight). The horizontal gray lines are at the 0.025, 0.5 and 0.975 standard normal quantiles.

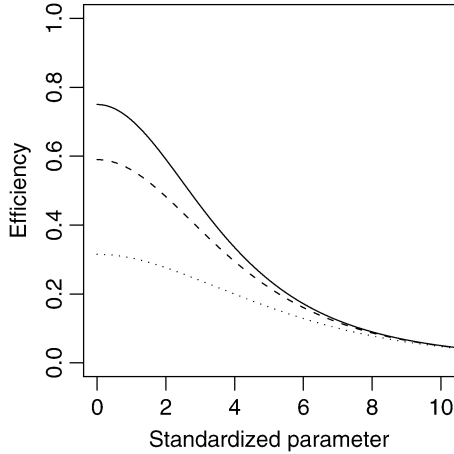


FIG. 2. Efficiency of logistic regression for estimation of ψ relative to estimation with corresponding continuous responses from the logistic distribution, as a function of the standardized parameter δ for the continuous model, for $\lambda = 0$ (solid), $\lambda = 1$ (dashes) and $\lambda = 2$ (dots).

$\pi_i = \exp(\lambda + z_i \psi) / \{1 + \exp(\lambda + z_i \psi)\}^2$. The ratio of these asymptotic variances gives some idea of the information content of the binary data compared to the continuous data. Figure 2 shows this ratio as a function of the standardized parameter $\delta_{\text{cont}} = \psi / (v_{\text{cont}})^{1/2}$ when the covariate z takes $n = 21$ equi-spaced values ranging from -3 to 3 . The maximum value 0.75 occurs when $\lambda = \psi = 0$, but the ratio drops fast as δ_{cont} increases. A value of $\delta_{\text{cont}} = 5$ that would be easily distinguished from 0 using the continuous data would correspond to a value of around 2 based on the binary data, and this would be much less easily distinguished from zero.

If the same computation is applied to the urine data, then the numbers of continuous observations equivalent to the 77 binary observations range from 7 to 19 , depending on the parameter considered, with a value of 16 or so for ψ . In this light the difference between first order and higher order results seems much more explicable: we are fitting a model with 6 nuisance parameters to the equivalent of fewer than 20 continuous observations, and so one would expect an appreciable “degrees of freedom” adjustment. Section 4.2 of Brazzale, Davison and Reid (2007) gives related discussion.

4.2 Exact Inference

In a logistic regression model, exact inference for the interest parameter ψ is available from the conditional density function of T given the value of S ,

$$(7) \quad \text{pr}(T = t \mid S = s; \psi) = \frac{\exp(y^\top Z \psi)}{\sum_{u \in \mathcal{A}_s} \exp(u^\top Z \psi)},$$

where $\mathcal{A}_s = \{y : y^\top X = s, y \in \{0, 1\}^n\}$. The function (7) does not depend on λ , and this greatly simplifies inference (Cox, 1958). The main practical difficulty in using (7) is the enumeration of the elements of \mathcal{A}_s , but recent computational advances have brought this into reach, at least in simple cases. One possibility is to use the network algorithm (Mehta and Patel, 1995, Mehta, Patel and Senchaudhuri, 2000) provided by commercial software such as LogXact, but although helpful in simple problems, it can be impractically slow when there are several covariates. Forster, McDonald and Smith (2003) propose a Markov chain Monte Carlo algorithm for more complex models, but as their chain may be reducible, there is no guarantee that \mathcal{A}_s would be fully explored even if the chain were to be run forever. Their algorithm has been implemented in the `elrm` package of R by Zamar, McNeney and Graham (2007).

Apart from the enumeration of \mathcal{A}_s , there are two deeper problems, both linked to the exactness of (7): the conservatism of exact tests and confidence intervals, which leads to overly-wide intervals and overly-large P-values, and the fragility of exact conditional inference in certain discrete cases. We now discuss these, illustrated by data with $n = 16$ binary responses:

$$y^\top = (1 \ 0 \ 1 \ 0 \ 1 \ 1 \ 1 \ 0 \\ 0 \ 0 \ 0 \ 0 \ 1 \ 0 \ 0 \ 0),$$

covariate matrices

$$X^\top = \frac{1}{2} \begin{pmatrix} 2 & 2 & 2 & 2 & 2 & 2 & 2 & 2 \\ -3 & -3 & -3 & -3 & -1 & -1 & -1 & -1 \\ 2 & 2 & 2 & 2 & 2 & 2 & 2 & 2 \\ -1 & 1 & 1 & 1 & 1 & 3 & 3 & 3 \end{pmatrix},$$

$$Z^\top = \frac{1}{2} \begin{pmatrix} -3 & -1 & 1 & 3 & -3 & -1 & 1 & 3 \\ -3 & -1 & 1 & 3 & -3 & -1 & 1 & 3 \end{pmatrix},$$

and corresponding sufficient statistics $s = X^\top y = (6, -3)$ and $t = Z^\top y = -4$. In this case the full sample space has 2^{16} elements, reducing to 8008 and 13 elements respectively when conditioned on the first component of s and on both components of s . We use this example in the next two subsections.

4.3 Conservatism of Exact Inference

Exact inference in discrete response models typically leads to conservative tests and confidence intervals. A striking illustration of this in the context of simple binomial models is given by Agresti and Coull (1998), who show how exact intervals such as that due

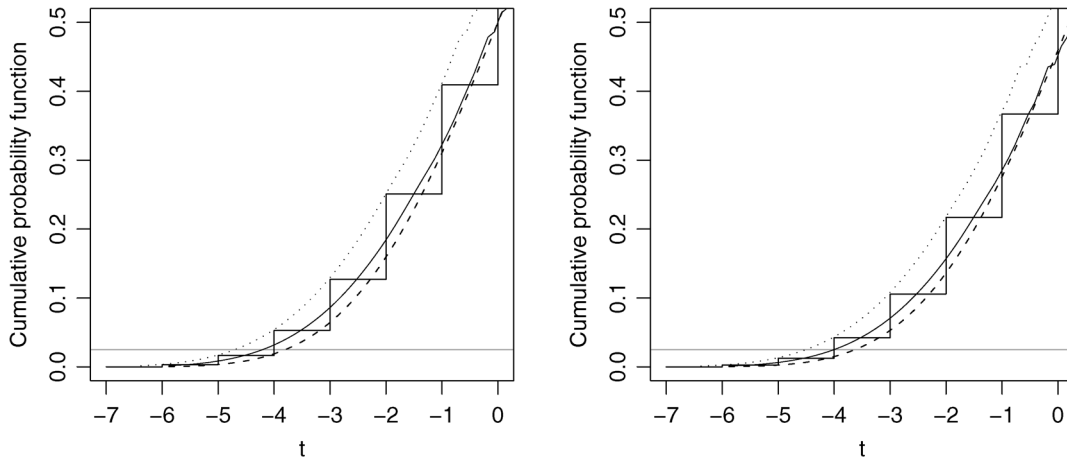


FIG. 3. Exact conditional distribution of T in logistic example (step function), with $\Phi\{r^*(t)\}$ (solid), $\Phi\{r(t)\}$ (dashes), and $\Phi\{r^*(t + 1/2)\}$ (dots), shown for $t = -6, \dots, 0$. Left: $\psi = 0$. Right: $\psi = 0.05$. The horizontal gray lines are at 0.025.

to Clopper and Pearson (1934) are conservative for all values of the underlying parameter, while approximate intervals based on likelihood quantities have overall coverage closer to the nominal level. For a variety of viewpoints on this and some solutions, see Agresti and Caffo (2000), Brown, Cai and DasGupta (2001) and Geyer and Meeden (2005).

In the case of our simple example, Figure 3 shows the lower tail of the exact conditional distribution function of T when $\psi = 0$, obtained by computing the generating function for the combinatorial terms; it has support on the set $\{-6, -5, \dots, 6\}$. Also shown are the approximate conditional distributions obtained by taking $\Phi\{r(t; 0)\}$, $\Phi\{r^*(t; 0)\}$, and $\Phi\{r^*(t + 1/2; 0)\}$, for a grid of values of t in the range $(-6, 6)$; the corresponding datasets were constructed to retain the original value of the conditioning statistic s . These approximations correspond respectively to first order and higher order procedures, and to use of the higher order procedure with a continuity correction. Use of the function $\Phi\{r^*(t; \psi)\}$ for $\psi = 0$ yields a continuous approximation to the exact conditional distribution function that closely matches the mid-points of the jumps in the step-function and thus the mid-P value.

Table 1 compares P-values and confidence limits for these data. The results for mid-P and the modified likelihood root are fairly close, and give tighter inferences than does the exact solution, which is close to the modified likelihood root, plus continuity correction. The kink at $t = 0$ in the approximations involving r^* is due to a numerical instability. Although a different expression given as a limit for $r \rightarrow 0$ is available, it is rarely used in practice because errors in P-values that are close to 0.5 are unimportant.

TABLE 1
One-sided P-values for testing $\psi = 0$ and limits of nominally equi-tailed 95% confidence intervals for ψ , for the artificial logistic regression example

	P-values	Limits of confidence interval
Exact	0.0528	(-2.992, 0.158)
mid-P	0.0346	(-2.690, 0.069)
Wald	0.0399	(-2.572, 0.144)
Wald, modified	0.0475	(-2.290, 0.183)
Likelihood root, r	0.0190	(-2.950, -0.060)
Modified likelihood root, r^*	0.0318	(-2.506, 0.050)
with continuity correction	0.0557	(-2.906, 0.172)

The equi-tailed exact confidence interval (ψ_-, ψ_+) with level $(1 - 2\alpha)$ has limits given by the solutions to the equations

$$(8) \quad \begin{aligned} \text{pr}(T \geq t \mid S = s; \psi_-) &= \alpha, \\ \text{pr}(T \leq t \mid S = s; \psi_+) &= \alpha, \end{aligned}$$

whereas the limits of the intervals based on r and r^* are the solutions in ψ of the equations

$$\Phi\{r(t; \psi)\} = \alpha, 1 - \alpha, \quad \Phi\{r^*(t; \psi)\} = \alpha, 1 - \alpha,$$

respectively. The right-hand panel of Figure 3 shows the conditional distribution for T for $\psi = 0.05$, which for $t < 0$ slightly depresses the probabilities relative to taking $\psi = 0$, and illustrates why the exact intervals are wider, and hence more conservative, than are these approximate ones: it is necessary to take $\psi_+ > 0.05$ to satisfy the right-hand equation in (8); in fact, the first line of Table 1 shows that $\psi_+ = 0.158$ is required.

4.4 Fragility of Exact Conditional Inference

The second issue is the sensitivity of the set \mathcal{A}_s , and hence of exact conditional inference, to the matrix X . It seems reasonable to require that small changes to X , for instance, due to rounding of the explanatory variables, should lead to small changes in confidence intervals and P-values. To test this, we jittered the second column x_2 of the matrix X in the simple example of Section 4.2. When the elements of x_2 were perturbed by adding normal noise with standard deviation 0.01, rounded to 3 decimal places, the value of s changed to (6, -3.013), and the support points of the conditional distribution reduced from $\{-6, -5, \dots, 6\}$ to $\{-4, -2, 0\}$. The exact tail probability for t , $\text{pr}(T \leq t \mid S = s; \psi = 0)$, changed from 0.0528 to 0.3333, and mid-P from 0.0347 to 0.167, but $\Phi\{r^*(t)\}$ changed only from 0.0318 to 0.0316.

An attempt to assess the fragility of the inference for the urine data failed: when the covariates are scaled to zero mean and unit variance, and rounded to the nearest integer, giving 5–6 rounded values for each covariate, one million iterations of the algorithm described by Forster, McDonald and Smith (2003), designed to enumerate the conditional sample space for the urea effect, found 13 support points. A Markov chain run with rounding to the first decimal place failed to move at all, suggesting that, with this degree of precision in the covariates, the conditional distribution for the urea effect is degenerate. Thus, exact conditional inference seems to be out of reach for these data.

To compare more systematically the effects of perturbing the covariate on exact and approximate conditional inferences, we repeated this experiment 1000 times, by adding noise with standard deviation 0.01 to x_2 , and rounding to different precisions. Table 2 gives the sizes of the resulting conditional sample spaces.

TABLE 2

Changes in number of support points of conditional sample space for a logistic regression model when a covariate is perturbed by adding small amounts of noise, rounded to different numbers of decimal places. As the number of decimal places increases, the conditioning becomes increasingly restrictive

Decimal places	Number of support points of conditional sample space												
	1	2	3	4	5	6	7	8	9	10	11	12	13
1													1000
2	9	8	16	13	33	50	65	103	150	206	181	138	28
3	129	212	191	167	141	101	38	15	4	1			
4	730	221	46	3									

Small changes to the covariates may sharply change the conditional sample space, and thus may severely affect exact conditional inferences and derived quantities such as mid-P values, but the approximate conditional inferences barely change: for each level of rounding, the average values of r and r^* were -2.076 and -1.855 across the 1000 simulated datasets, with standard errors of around 0.004 and 0.0035 for all levels of rounding; the values of r and r^* are of course constant when rounding to one decimal place. The mid-P values are computed with respect to the exact distribution, and hence are very sensitive to changes in the covariates; the ‘approximating mid-P value’ $\Phi(r^*)$ might in such cases be regarded as having been computed from an approximating continuous distribution (Davison and Wang, 2002).

These results supplement the finding of Pace, Salvan and Ventura (2004) that rounding of the response has little effect on higher order likelihood procedures.

5. REGRESSION-SCALE MODELS

5.1 Exact Inference

Nonnormal linear models, also known as regression-scale models, belong to the wider class of transformation models. They may be written using matrix notation as

$$(9) \quad y = X\beta + \sigma\varepsilon,$$

where X is a fixed $n \times p$ design matrix with unknown regression coefficient $\beta \in \mathbb{R}^p$, $\sigma > 0$ is a scale parameter, and $\varepsilon = (\varepsilon_1, \dots, \varepsilon_n)$ represents an n -dimensional vector of errors which are independently and identically distributed according to a known though not necessarily normal density $f(\cdot)$ on \mathbb{R} . If the maximum likelihood estimates $(\hat{\beta}, \hat{\sigma})$ exist and are finite, there exists a one-to-one change of variables from $y = (y_1, \dots, y_n)$ to $(\hat{\beta}, \hat{\sigma}, a)$, where $a_i = (y_i - x_i^\top \hat{\beta})/\hat{\sigma}$, $i = 1, \dots, n$, are the standardized residuals of the model and x_i^\top is the i th row of X . The pair $(\hat{\beta}, \hat{\sigma})$ forms a transformation variable, whereas the vector of standardized residuals $a = (a_1, \dots, a_n)$ is ancillary with respect to β and σ . As shown by Fraser (1979), Section 6.1.5, the functionally unique separation of β and σ is obtained from the pivots $Z_1 = (\hat{\beta} - \beta)/\hat{\sigma}$ and $Z_2 = \hat{\sigma}/\sigma$, whose joint distribution given a is known up to a normalizing constant. Fisher (1934), Fraser (1979) and others suggest that inference on the parameters (β, σ) should be made conditionally on a . Conditional confidence intervals for single parameters are based on the marginal densities of the corresponding

pivots, obtained by integrating out the remaining components in

$$(10) \quad \begin{aligned} f_{Z_1, Z_2|a}(z_1, z_2 | a) \\ = c(a) z_2^{n-1} \prod_{i=1}^n f\{(x_i^\top z_1 + a_i) z_2\} |X^\top X|^{1/2}. \end{aligned}$$

Lawless (1972, 1973, 1978) gives applications to Cauchy, logistic, Weibull, and extreme value distributions and, Kappenmann (1975) to the Laplace distribution under a location-scale model.

Exact calculation of the marginal distribution for the pivots of interest usually involves multidimensional numerical integration, and can be difficult. For instance, the normalizing constant is given by

$$\begin{aligned} c(a)^{-1} = \int_0^{+\infty} \int_{-\infty}^{+\infty} \dots \int_{-\infty}^{+\infty} z_2^{n-1} \\ \cdot \prod_{i=1}^n f\{(x_i^\top z_1 + a_i) z_2\} \\ \cdot |X^\top X|^{1/2} dz_{11} \\ \dots dz_{1p} dz_2, \end{aligned}$$

where $z_{1l} = (\hat{\beta}_l - \beta_l)/\hat{\sigma}$. The required computational effort rapidly becomes infeasible, especially if the number of parameters is large and the dimension of the interest parameter is low. There are two ways to overcome this problem. The first is to use the higher order theory presented in Section 2, which applies rather naturally to regression-scale models. The tail area approximations (2) and (3) agree with those proposed by DiCiccio, Field and Fraser (1990) and by Fraser, Lee and Reid (1990) for the marginal distribution functions of the pivots Z_1 and Z_2 . All these methods are available through the package `margin` of the `hoar` bundle, which is equivalent in its design, syntax and use to the `cond` package. Examples of application are given in Section 5.2 of Brazzale, Davison and Reid (2007) and in Section 5.3.2 of Brazzale (2000).

The second way to avoid numerical calculation of the normalizing constant in (10) is to use Markov chain Monte Carlo (MCMC) techniques to simulate from the conditional distribution.

5.2 Monte Carlo Simulation

Classical simulation techniques generate observations that are independent and identically distributed by sampling directly from the target density. In our case this is not possible, as the normalizing constant $c(a)$ in (10) is generally unknown. Among possibilities for

dealing with this are the conditional sampler available through the `rsm.sample` routine of the `csampling` package, which implements the Metropolis–Hastings algorithm. This routine samples not from the conditional density (10) of the pivots, but from that of the maximum likelihood estimates $(\hat{\beta}, \hat{\sigma})$, namely,

$$(11) \quad \begin{aligned} f_{\hat{\beta}, \hat{\sigma}|a}(\hat{\beta}, \hat{\sigma} | a; \beta, \sigma) \\ = c(a) \frac{\hat{\sigma}^{n-p-1}}{\sigma^n} \prod_{i=1}^n f[\{x_i^\top (\hat{\beta} - \beta) + \hat{\sigma} a_i\}/\sigma] \\ \cdot |X^\top X|^{1/2}. \end{aligned}$$

Because of the one-to-one relationship between the maximum likelihood estimates and the pivots (Z_1, Z_2) given a , both approaches yield the same results, but sampling from (11) makes it easier to investigate the distributions of higher order statistics. The pseudo-code for the conditional sampler may be written as:

- Choose a candidate generation density $f_c(\cdot)$.
- Choose an initial value $(\hat{\beta}_0, \hat{\sigma}_0)$.
- For $t = 1, \dots, T$

1. Generate $(\hat{\beta}_c, \hat{\sigma}_c)$ from $f_c(\cdot)$. Take

$$(\hat{\beta}_t, \hat{\sigma}_t) = \begin{cases} (\hat{\beta}_c, \hat{\sigma}_c) & \text{with probability } \pi, \\ (\hat{\beta}_{t-1}, \hat{\sigma}_{t-1}) & \text{with probability } 1 - \pi, \end{cases}$$

where

$$\pi = \min \left\{ \frac{f(\hat{\beta}_c, \hat{\sigma}_c | a; \beta_0, \sigma_0) f_c(\hat{\beta}_{t-1}, \hat{\sigma}_{t-1})}{f(\hat{\beta}_{t-1}, \hat{\sigma}_{t-1} | a; \beta_0, \sigma_0) f_c(\hat{\beta}_c, \hat{\sigma}_c)}, 1 \right\},$$

a is the ancillary and (β_0, σ_0) the simulation parameters.

- 2. Reconstitute the sample $y_t = (y_{1t}, \dots, y_{nt})$, where $y_{it} = x_i^\top \hat{\beta}_t + \hat{\sigma}_t a_i$.

The main implementation issue is the choice of $f_c(\cdot)$. We found it best to make the transformation $\log \hat{\sigma}$, giving the target density support \mathbb{R}^{p+1} , and to sample from a multivariate Student t distribution with low degrees of freedom and with shape close to that of the target density. Details can be found in Brazzale (2000), Chapter 7.

The following two subsections summarize the results of a study inspired by Example 3 of DiCiccio, Field and Fraser (1990). The `rsm.sample` routine was used to retrieve the empirical distribution of the pivots $Z_1 = (\hat{\beta} - \beta)/\hat{\sigma}$ and $Z_2 = \hat{\sigma}/\sigma$ for a fixed value of the ancillary statistic, and to investigate the empirical accuracy of the tail area approximations (2) and (3).

5.3 Conditional Distribution of Pivotal Quantities

We considered a sample of size $n = 10$ from a linear regression model with the 10×6 design matrix

$$X^T = \begin{bmatrix} 0.686 & 0.640 & 0.908 & 0.886 & 0.508 \\ 0.566 & 0.632 & 0.130 & 0.480 & 0.669 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 1 & 1 & 1 & 1 & 1 \\ 0.255 & 0.197 & 0.056 & 0.646 & 0.317 \\ 0.930 & 0.869 & 0.204 & 0.961 & 0.321 \\ 1 & 1 & 1 & 1 & 1 \\ 0.255 & 0.197 & 0.056 & 0.646 & 0.317 \\ 0.930 & 0.869 & 0.204 & 0.961 & 0.321 \\ 1 & 1 & 1 & 1 & 1 \end{bmatrix}$$

and errors that follow the standard log-Weibull distribution. This is a rather extreme scenario, with only 4 residual degrees of freedom and with highly correlated estimators of the regression coefficients. The sample configuration a on which to condition was chosen by random sampling from the standard log-Weibull distribution using the same parameter values as in DiCiccio, Field and Fraser (1990). We repeated the study for various choices of a , all of which yielded similar results. The candidate generation density—a multivariate t_5 distribution—was rescaled and centered so as to optimize the acceptance rate, of about 25% and 30%, as was assessed in a pilot study. According to Corollary 4 of Tierney (1994), the resulting Markov chain is uniformly ergodic. The sampler was run for $T = 100,000$ iterations, reached stationarity very quickly, and mixed well. The corresponding R code is given in the demonstration file for the `csampling` package.

Figure 4 shows the conditional distributions of the pivots $Z_{13} = (\hat{\beta}_3 - \beta_3)/\hat{\sigma}$ and $\log Z_2 = \log(\hat{\sigma}/\sigma)$ for

a particular choice of the sample configuration a . Both distributions are notably nonnormal; the finite sample distribution of $\log Z_2$ is, furthermore, heavily biased. Non-normal distributions were also observed for the remaining five regression coefficients. Table 3 compares the exact distribution functions of the two pivots with the approximations obtained from the likelihood root r and the modified likelihood root r^* . The first order approximation performs rather poorly, especially for the scale parameter, while the third order solution competes well in this rather extreme scenario.

5.4 Accuracy of Higher Order Approximations

Table 4 of DiCiccio, Field and Fraser (1990) reports the overall rates of noncoverage of the one-sided confidence intervals obtained from r and Φ^* for the parameters β_1, β_3 and $\log \sigma$ with a simulation of size 1000. However, as the authors themselves remark, these assessments are in terms of unconditional rather than conditional coverage.

Our Table 4 extends Table 4 of DiCiccio, Field and Fraser (1990): it gives the conditional rates of noncoverage of upper and lower confidence limits for the parameters β_1, β_3 and $\log \sigma$ obtained from the signed likelihood root pivot r , and the third order tail area approximations (2) and (3), for a particular choice of a . For the regression coefficients, the likelihood root yields confidence intervals which are too short, while the two higher order pivots work well. First order confidence intervals for $\log \sigma$ are heavily biased. Furthermore, we observed the feature mentioned by DiCiccio, Field and Fraser (1990): the tail area approximation $\Phi^*(r)$ breaks down. In about two-thirds of the samples the tail area exceeds 1. This is a drawback of Lugannani–Rice-type approximations, which need not give values within the interval $(0, 1)$. The modified likelihood root r^* does not suffer from this drawback and provides

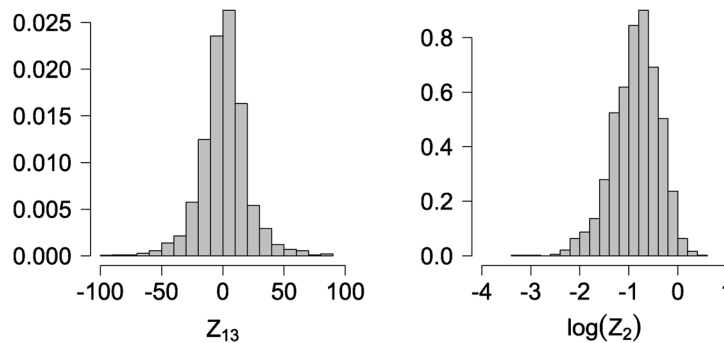


FIG. 4. Histograms of the pivots Z_{13} and Z_2 generated by the Metropolis–Hastings sampling (100,000 iterations). Only every 50th value is taken, after having discarded an initial sequence of length 5000.

TABLE 3

Exact and approximate tail probabilities for the pivots Z_{13} and $\log Z_2$ in the log-Weibull regression model with $n = 10$ and $p = 6$ considered by DiCiccio, Field and Fraser (1990), Example 3, for a particular choice of a . The approximations considered are $\Phi(r)$ and $\Phi(r^*)$, where r and r^* are the likelihood root and its third order modification. The exact distribution was generated by the Metropolis–Hastings sampling (100,000 iterations, burn-in 5000)

Pr($Z_{13} \leq z$)								
z	-52.3	-38.6	-29.0	-20.1	21.8	30.6	40.6	55.3
exact	0.01	0.025	0.05	0.1	0.9	0.95	0.975	0.99
$\Phi(r)$	< 0.001	< 0.001	0.001	0.008	0.996	0.999	1.000	1.000
$\Phi(r^*)$	0.006	0.016	0.035	0.082	0.913	0.962	0.984	0.995
Pr($\log Z_2 \leq z$)								
z	-2.13	-1.89	-1.69	-1.46	-0.30	-0.16	-0.05	0.07
exact	0.01	0.025	0.05	0.1	0.9	0.95	0.975	0.99
$\Phi(r)$	< 0.001	< 0.001	< 0.001	< 0.001	0.170	0.295	0.433	0.586
$\Phi(r^*)$	0.003	0.009	0.021	0.052	0.837	0.912	0.954	0.979

satisfactory values. Some insight into why this happens is provided by Figure 5, which shows the normal Q–Q plots of r and r^* for β_4 and σ . The finite-sample distribution of $r(\sigma)$ is heavily biased with respect to the

standard normal, whereas the tails of the distribution of $r(\beta_4)$ are too heavy. As noted in the previous paragraph, the conditional distributions of the maximum likelihood estimators are far from normal, so first or-

TABLE 4

Conditional rates of noncoverage of confidence intervals for β_1 , β_3 and $\log \sigma$ in the log-Weibull regression model with $n = 10$ and $p = 6$ considered by DiCiccio, Field and Fraser (1990), Example 3, for a particular choice of a . The tail area approximations used are based on the likelihood root, $\Phi(r)$, on its higher order modification, $\Phi(r^*)$, and the third order quantity, $\Phi^*(r)$. The coverages were calculated using a Metropolis–Hastings chain of length 100,000 after having discarded the first 5000 values. The coverages of confidence intervals for $\log \sigma$ using $\Phi^*(r)$ are not given, as this statistic breaks down

	Nominal	Upper confidence limit			Lower confidence limit		
		$\Phi(r)$	$\Phi(r^*)$	$\Phi^*(r)$	$\Phi(r)$	$\Phi(r^*)$	$\Phi^*(r)$
β_1	0.5	7.96	0.91	0.41	11.16	0.89	0.33
	1	10.53	1.71	0.85	14.05	1.58	0.52
	2.5	15.28	3.65	2.24	18.79	3.36	1.29
	5	19.61	6.37	4.45	23.07	6.19	2.81
	10	25.19	11.88	9.77	28.87	11.76	6.60
	25	36.19	25.98	25.22	39.05	26.71	23.63
β_3	0.5	8.29	0.86	0.35	10.89	1.03	0.40
	1	10.64	1.73	0.79	14.29	1.72	0.67
	2.5	15.15	3.89	2.22	19.23	3.69	1.69
	5	19.43	6.66	4.69	23.58	6.11	3.32
	10	25.24	11.82	9.63	29.61	11.30	6.76
	25	35.68	26.24	25.66	40.05	25.50	21.83
$\log \sigma$	0.5	44.38	1.53	–	0.00	0.34	–
	1	53.46	2.69	–	0.00	0.51	–
	2.5	65.68	5.66	–	0.00	1.17	–
	5	75.14	9.53	–	0.01	2.64	–
	10	83.66	17.10	–	0.06	5.97	–
	25	93.46	35.88	–	0.40	16.85	–

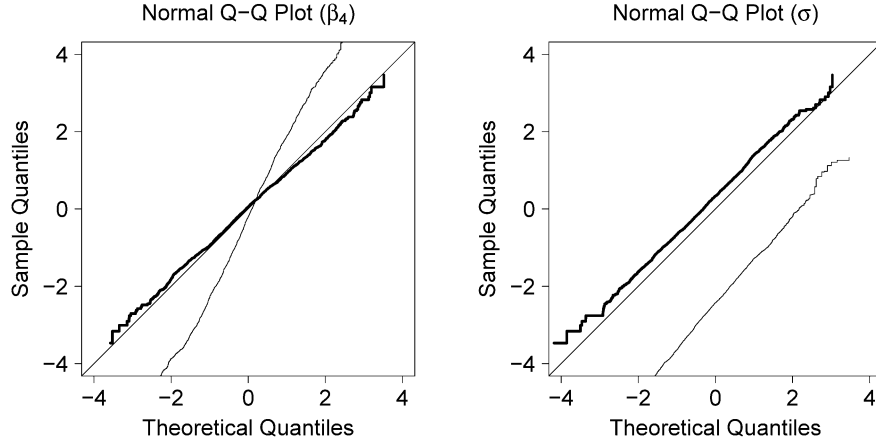


FIG. 5. Normal Q–Q plots of r (solid line) and r^* (bold line) for β_4 (left panel) and σ (right panel) obtained from the Metropolis–Hastings sampling (100,000 iterations), with diagonal line indicating perfect fit. The Q–Q plots only use every 50th simulated value, after having discarded an initial sequence of length 5000.

der asymptotics are not useful. Surprisingly, r^* works well for all seven parameters, especially since there are just $n = 10$ observations.

6. NONLINEAR MODELS

Nonlinear models are widely used in applied statistics, especially for modeling dose-response curves. We consider the general form

$$(12) \quad \begin{aligned} y_{ij} &= \mu(x_i; \beta) + w(x_i; \beta, \rho)\varepsilon_{ij}, \\ i &= 1, \dots, m, \quad j = 1, \dots, n_i, \end{aligned}$$

where m is the number of design points, n_i the number of replicates at design point x_i , y_{ij} represents the response of the j th experimental unit in the i th group, and the errors ε_{ij} are independent $N(0, 1)$ variates. The mean response is given by the nonlinear function $\mu(x_i; \beta)$, which depends on a vector of unknown regression coefficients β , while the function $w(x_i; \beta, \rho)$ may also depend on a vector ρ of variance parameters. If $w(\cdot)^2$ is constant, (12) becomes the classical nonlinear regression model. Inference on β and ρ is commonly based on first order approximations and linearization techniques (Seber and Wild, 1989, Chapter 5), plus graphical summaries such as profile and contour plots (Bates and Watts, 1988, Section 6.1), which allow one to assess the quality of distributional approximations for the likelihood ratio and Wald statistics. Bellio and Brazzale (1999) show that nonlinearity of the mean function and variance heterogeneity can lead to substantial inaccuracies in first order inferences, especially for the variance parameters, unless the sample size is large. This may be overcome

using the higher order solutions presented in Section 2, which are relatively easily derived in this case (Bellio, Jensen and Seiden, 2000). To do so, we re-write (12) as a curved exponential family of order $(2m, d)$, where d is the dimension of the parameter $\theta = (\beta, \rho)$. Expressions for the quantities needed to calculate the correction terms $q(\psi)$, $M(\psi)$ and $u(\psi)$ are listed in Brazzale, Davison and Reid (2007), Sections 8.6.2 and 8.6.3. We now present results of a data analysis performed with the `nlreg` package of the `hoa` bundle. Further examples may be found in Brazzale, Davison and Reid (2007), Chapters 5 and 6.

EXAMPLE 2 (*Herbicide bioassay*). Data set C3 of the `nlreg` package concerns an in vitro bioassay on the action of the herbicide chlorsulfuron on the callus area of colonies of *Brassica napus L.*, also known as oilseed rape. The experiment is described in Seiden, Kappel and Streibig (1998) and consists of $n = 51$ measurements of the callus area (in mm^2) for $m = 10$ different dose levels (in nmol/l). The design is unbalanced, as the number of replicates per dose varies from 5 to 8. Bellio, Jensen and Seiden (2000) discuss a model where the response variable is the logarithm of the callus area and the mean function is the logarithm of the four-parameter logistic function

$$(13) \quad \mu(x; \beta) = \beta_1 + \frac{\beta_2 - \beta_1}{1 + (x/\beta_4)^{\beta_3}}, \quad x \geq 0.$$

This yields a sigmoidal curve which decreases from an initial value β_2 to a limiting value β_1 when the concentration x tends to infinity. The parameter β_3 determines the shape of the curve, and β_4 corresponds to the EC_{50} .

A preliminary data analysis further suggests that the response variance might slightly decrease with its mean. The same authors suggest using the error-in-variable variance function

$$(14) \quad w(x; \beta, \kappa, \gamma, \sigma^2)^2 = \sigma^2 \left[1 + \kappa x^\gamma \left\{ \frac{\partial \mu(x; \beta) / \partial x}{\mu(x; \beta)} \right\}^2 \right],$$

$\kappa, \gamma, \sigma^2 > 0,$

where κ, γ and σ^2 are variance parameters.

The R code for first and higher order inference for the nonlinear model defined by (13) and (14) is

```
> C3.nl <-
+ nlreg(formula = log(area)~
+       log(b1+(b2-b1)/
+       (1+(dose/b4)^b3))
+       weights = ~(1+((k*dose^g*
+       (b2-b1)^2)/
+       (1+(dose/b4)^b3)^4*
+       b3^2*dose^(2*b3-2))/
+       b4^(2*b3)/(b1+(b2-b1)/
+       (1+(dose/b4)^b3))^2),
+       start = c(b1=2.2, b2=1700,
+       b3=2.8, b4=0.28,
+       g=2.7, k=1),
+       control = list(x.tol=1e-12,
+       rel.tol=1e-12,
+       step.min=1e-12),
+       data = C3, hoa = TRUE )
> summary( C3.nl )
> C3.prof <- profile( C3.nl,
+                   offset = "all" )
> contour( C3.prof, offset1 = b2,
+         offset2 = k, alpha = 0.95 )
> summary( ria.prof, twoside = TRUE )
```

The formula and weights arguments in the `nlreg` fitting routine determine respectively the mean and variance functions $\mu(\cdot)$ and $w(\cdot)^2$. The maximum likelihood estimate of σ^2 is available in closed form, but starting values for the other parameters must be provided through the `start` argument. All computations for σ^2 use the logarithmic scale. Because of the highly nonlinear model structure, we must refine the convergence criteria through the `control` argument. We obtain $\hat{\beta}_1 = 2.206$ (0.415), $\hat{\beta}_2 = 1662$ (117), $\hat{\beta}_3 = 2.841$ (0.360), $\hat{\beta}_4 = 0.2752$ (0.0452), $\hat{\gamma} = 2.605$ (0.793), $\hat{\kappa} = 1.009$ (0.580) and $\log \hat{\sigma}^2 = -1.888$ (0.234). The values in brackets are the standard errors, as returned by a call to `summary`. The option `hoa=TRUE` indicates that higher order solutions will be used in the subsequent calculations.

The `profile` and `contour` methods extend the original algorithm of Bates and Watts (1988), Chapter 6, to the higher order solutions presented in Section 2. The core routine is based upon pivot profiling as described in Section 3.3. By default, it computes the higher order statistics developed by Skovgaard (1996, 2001), although Fraser, Reid and Wu's (1999) version is available by setting `stats="fr"`. The option `offset="all"` means that all model parameters are to be profiled. Figure 6 shows the 95% approximate bivariate contour plots of the Wald, likelihood ratio and w^* pivots for the parameters β_2 and κ . The contours are plotted on the original scale (right panel) and on the r scale (left panel), respectively. On the latter scale the units are those of the likelihood root statistics. The more elliptical the contours are, the more quadratic is the likelihood; the closer the curves for w and w^* , the better the behavior of first order inferences.

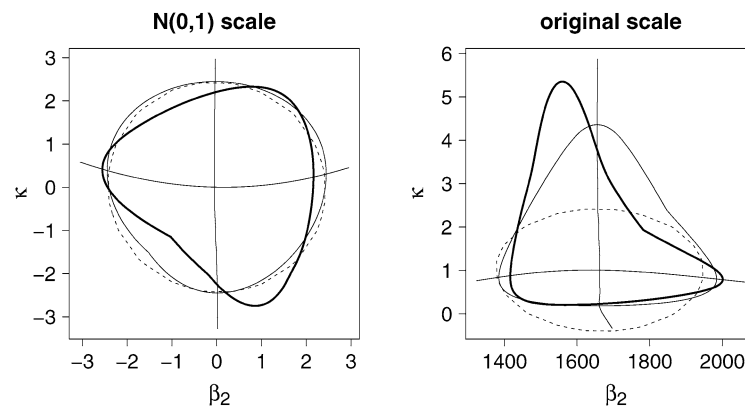


FIG. 6. Herbicide bioassay: data set C3. Approximate bivariate contour plots and profile traces for the parameters β_2 and κ obtained with the contour method of the `nlreg` package ($\alpha = 0.05$). The pivots used are as follows: likelihood root (—), modified likelihood root w^* (---) and Wald (- - -). Right panel: original scale; left panel: r scale.

The profile traces also shown represent the constrained maximum likelihood estimates of one parameter as a function of the other and show how the estimates affect each other. If the asymptotic correlation is zero, the angle between the traces is close to $\pi/2$, while an angle close to zero indicates strong correlation.

Two-sided confidence intervals can be obtained using the `summary` function. The 95% confidence intervals for the parameter κ are $(-0.1270, 2, 145)$, $(0.2697, 3.096)$, $(0.3264, 3.546)$ and $(0.3321, 3.803)$ for respectively the Wald, r and r^* pivots, these last computed using Skovgaard's (1996) and Fraser, Reid and Wu (1999) formulation. Both versions of r^* and the likelihood root, but not the Wald statistic, let us reject the null hypothesis of a constant variance function at the 5% level.

A common problem in nonlinear heteroscedastic regression is the estimation of the variance parameters, whose maximum likelihood estimators are usually heavily biased. More accurate estimates can be obtained from the adjusted profile likelihood using the fitting routine `mpl`:

```
> C3.mpl <- mpl( C3.nl )
> summary( C3.mpl )
```

We obtain $\hat{\gamma}_a = 2.654$ (0.834), $\hat{\kappa}_a = 1.081$ (0.711) and $\log \hat{\sigma}_a = -1.825$ (0.248), when the correction term $M(\psi)$ is based upon the p^* density approximation. The p_{TEM} approximation yields $\hat{\gamma}_a = 2.650$ (0.833), $\hat{\kappa}_a = 1.092$ (0.721) and $\log \hat{\sigma}_a = -1.827$ (0.248). The standard errors are obtained from the profile information matrix $j_p(\hat{\psi})$; this is possible because $|j_a(\hat{\psi})| = |j_p(\hat{\psi})| \{1 + O_p(n^{-1})\}$ and $\hat{\psi}_a - \hat{\psi} = O_p(n^{-1})$. The distance between the values obtained from the profile likelihood and the adjusted profile likelihood functions gives an idea of the bias of the ordinary maximum likelihood estimators. It is reassuring that both versions of the adjusted profile likelihood yield similar estimates.

7. DISCUSSION

The purpose of this paper is to show that highly accurate likelihood methods may be routinely used in data analysis, both to check whether standard approximations are adequate and to supplement them when they are inadequate. Libraries are available that implement these procedures for a variety of common models. Although available for the numerical computing environment R, it would be relatively straightforward to modify them for other packages. The classes of models discussed in this paper form a small subset of those

used in practice, but the same ideas can be extended to other classes for which some unifying structure can be identified, so that a common statistical computation setup is possible; see, for example, Guolo, Brazzale and Salvan (2006). In other cases a general approach requiring a small amount of programming is described by Brazzale, Davison and Reid (2007), Section 9.5.

In our work we have focused on so-called double saddlepoint approximations, although sequential saddlepoint approximations leading to inference based on expressions such as (5) should also be mentioned (Pierce and Peters, 1992; DiCiccio and Martin, 1993). The maximum likelihood estimator $\hat{\psi}_a$ provides good point estimates, for example, when estimating the variance parameters in a linear or nonlinear regression model; the bias correction is essentially what is provided by the use of REML through maximization of the restricted likelihood function. If an adjusted profile log likelihood derived from (5) is available, comparison of it with the corresponding profile log likelihood $\ell_p(\psi)$ gives valuable information about the bias of the maximum likelihood estimator, and if the adjusted profile log likelihood, $\log L_a(\psi)$, is close to quadratic, then it should be safe to base inference for ψ on the corresponding likelihood root statistic $r_a(\psi)$. However, if the profile log likelihoods are asymmetric, then inference based on $r^*(\psi)$ or, if available, $r_a^*(\psi)$, will be preferable. For instance, the asymmetry of both curves in the left-hand panel of Figure 1 is a warning to avoid using Wald statistics.

Different expressions are available for the correction terms $q(\psi)$ and $M(\psi)$ in (4) and (5). Though almost equivalent from the analytical and the numerical points of view, preference for one version or the other is not merely a matter of taste. Expression (15) in Appendix A.1 requires the availability of an exact ancillary statistic, and this is rarely the case. Skovgaard's (1996) sample space approximations circumvent this problem, but require the calculation of the covariances that are involved. Expression (16) of the Appendix is more versatile both in its derivation and implementation, but it seems unclear if it applies to dependent data. Bellio and Sartori (2006) illustrate the versatility of the higher order methods discussed in this paper.

A parallel literature on analytical approximations for Bayesian inference based on marginal posterior densities leads to remarkably similar expressions. Both the conceptual and mathematical developments are simpler, the first because arguments involving ancillarity are not required in the Bayesian paradigm, and the second because Laplace approximation for integrals is

used (Tierney and Kadane, 1986, Tierney, Kass and Kadane, 1989, DiCiccio, Field and Fraser, 1990). Elementary expositions are given by Davison (2003), Section 11.3.1 and Brazzale, Davison and Reid (2007), Section 8.7. The relation with matching and noninformative priors (Tibshirani, 1989, Reid, Mukerjee and Fraser, 2002) yields a close but imperfect rapprochement between objective Bayesian and Fisherian approaches. If so, the Holy Grail of objective statistical inference sought by Jeffreys and Fisher will have been reached—at least approximately! A recent example of this rapprochement is given by Davison and Sartori (2008).

Almost all the literature on higher order likelihood inference concerns regular models, yet nonregular situations are of growing interest. Testing for zero variance components plays a role in both spline smoothing applications and in generalized linear mixed models, for example, and the boundary hypotheses this entails lead to modifications of the usual limiting distributions. It would be valuable to have accurate and practicable analytical approximations for the more common nonregular situations. A first step in this direction is made by Castillo and López-Ratera (2006).

We have mainly discussed analytical approximations, but DiCiccio, Martin and Stern (2001), Lee and Young (2005), and DiCiccio and Young (2008) have used the parametric bootstrap to achieve high accuracy. As yet, the properties of this approach are understood only in certain, albeit important, cases, and rather large simulations seem to be needed for it to give solid gains over analytical approximation, which we believe to be sufficiently accurate for most applications. Differences in the first two decimal places of a P-value may influence decisions taken in practice, while variation in further places is crucial only in exceptional cases.

In this paper our concern is with implementation of accurate likelihood inference, which typically entails the elimination of parameters from likelihoods, by appropriate, often approximate, conditioning or marginalization. The different roles of conditioning in inference have been aired at length in the literature, and the interested reader may refer to Cox (1988) or Reid (1995), for instance, for more general discussion on this topic. The discussion of Section 4 might be misinterpreted as an attack on conditional inference, but it is rather intended to point out that the properties of statistical procedures labelled ‘exact’ merit critical examination. So-called exact inference may come at too high a price.

Why seek highly accurate inferences for a model that may be incorrect? Although we entirely agree that the robustness of conclusions plays a key role in applied work, we believe that this question is slightly beside the point. Provided the assumed model is found empirically acceptable, checking and, if necessary, improving the usual basis for inference seems worthwhile, even if the model might be falsified based on a larger sample. A Jesuitical reply might be: faced with an apparently Gaussian sample of size ten, should one base inference for its mean on a normal approximation or on the Student t distribution? A reader who would opt for the latter should also be willing on occasion to use the approaches described above. It would be worrying if the higher order methods were very sensitive to model failure, but published and unpublished work on this (Fraser, Wong and Wu, 1999, Bellio, 2000), as well as our own limited simulations, suggest that there is no dramatic breakdown of them under small model perturbations. It would be reassuring to have more evidence of this, however.

We hope that this paper will encourage others to use higher order methods in their applied work: a recipe may be appetizing in theory, but the proof of a pudding is in the eating.

APPENDIX: HIGHER ORDER APPROXIMATIONS

A.1 Modified Likelihood Root

The key element in using the modified likelihood root is the form of (4), whether computed using $\varphi(\theta)$ or using equivalent expressions.

Barndorff-Nielsen (1983) gives

$$q_1 = \frac{|\ell_{;\hat{\theta}}(\hat{\theta}) - \ell_{;\hat{\theta}}(\hat{\theta}_\psi) \ell_{\lambda;\hat{\theta}}(\hat{\theta}_\psi)|}{|\ell_{\theta;\hat{\theta}}(\hat{\theta})|} \cdot \left\{ \frac{|j(\hat{\theta})|}{|j_{\lambda\lambda}(\hat{\theta}_\psi)|} \right\}^{1/2}, \quad (15)$$

where the data vector y in $\ell(\theta; y)$ is expressed as a one-to-one function of the maximum likelihood estimator $\hat{\theta}$ and of an ancillary statistic a , whose distribution does not depend on θ . Expression (15) is obtained by formally setting $\varphi(\theta)^\top = \ell_{;\hat{\theta}}(\theta; \hat{\theta}, a)$. The numerator on the right-hand side of (15) is the determinant of a $d \times d$ matrix whose first column is the difference of sample-space derivatives $\ell_{;\hat{\theta}}(\hat{\theta}) - \ell_{;\hat{\theta}}(\hat{\theta}_\psi)$, defined as $\ell_{;\hat{\theta}}(\theta) = \ell_{;\hat{\theta}}(\theta; \hat{\theta}, a) = \partial \ell(\theta; \hat{\theta}, a) / \partial \hat{\theta}$, and whose remaining columns comprise the $d \times (d - 1)$ matrix of mixed derivatives $\ell_{\lambda;\hat{\theta}}(\theta) = \partial^2 \ell(\psi, \lambda; \hat{\theta}, a) / \partial \hat{\theta} \partial \lambda^\top$

evaluated at the constrained estimate $\hat{\theta}_\psi$. The denominator contains the $d \times d$ matrix of mixed derivatives $\ell_{\theta;\hat{\theta}}(\theta) = \partial^2 \ell(\theta; \hat{\theta}, a) / \partial \hat{\theta} \partial \theta^\top$ evaluated at $\hat{\theta}$.

A difficulty in using (15) is the need to differentiate $\ell(\theta; y)$ partially with respect to the maximum likelihood estimator $\hat{\theta}$, while holding fixed the value of a full-dimensional ancillary statistic a . Fraser, Reid and Wu (1999) bypass this difficulty in several ways. First, they note that only a second order, approximate, ancillary is needed, so the results apply to a broader range of models. Second, the ancillary is needed only at the observed data point, and this is given by tangents (V_1, \dots, V_d) defined in the directions corresponding to fixed values of the ancillary. Third, any differentiation in these directions is allowed, but differentiation with respect to $\hat{\theta}$ is irrelevant. Thus, the nominal reparameterization can be given as $\varphi(\theta)^\top = \ell_{;V}(\theta; y)$ using directional derivatives and yielding an expression which compares directly with (15),

$$(16) \quad q_2 = \frac{|\ell_{;V}(\hat{\theta}) - \ell_{;V}(\hat{\theta}_\psi) \ell_{\lambda;V}(\hat{\theta}_\psi)|}{|\ell_{\theta;V}(\hat{\theta})|} \cdot \left\{ \frac{|j(\hat{\theta})|}{|j_{\lambda\lambda}(\hat{\theta}_\psi)|} \right\}^{1/2}.$$

Here, $\varphi(\theta)$ is the canonical parameter of an exponential family with sufficient statistic $s = s(y) = \partial \ell(\hat{\theta}^0; y) / \partial \theta$, the score function evaluated at the maximum likelihood estimate $\hat{\theta}^0$ for a fixed point y^0 , which approximates the true model locally at y^0 with a relative error of the order $O(n^{-3/2})$ and whose log likelihood function and first derivative with respect to θ at the fixed point y^0 equal those of the original model. The canonical parameter φ is defined using a set of n vectors of length d through an $n \times d$ matrix V , with rows V_1, \dots, V_n , where $\ell_{;V}(\theta; y)$ indicates that the log likelihood is differentiated on the surface spanned by the columns of V . If the observations y_1, \dots, y_n are independent, then $\ell_{;V}(\theta; y) = \sum_{i=1}^n V_i \partial \ell(\theta; y) / \partial y_i$. In the continuous case, the V_i can be constructed as

$$V = - \left(\frac{\partial z}{\partial y^\top} \right)^{-1} \left(\frac{\partial z}{\partial \theta^\top} \right) \Big|_{\theta = \hat{\theta}},$$

using a vector of pivotal quantities $z = \{z_1(y_1, \theta), \dots, z_n(y_n, \theta)\}$, where each component $z_i(y_i, \theta)$ has a fixed distribution under the model. In the continuous case such a vector always exists in the form of the probability integral transformation $F(y_i; \theta)$.

Skovgaard (1996) develops an approximation to q_1 , which avoids specification of a by approximating the

sample space derivatives in (15) as

$$\begin{aligned} \ell_{;\hat{\theta}}(\hat{\theta}) - \ell_{;\hat{\theta}}(\hat{\theta}_\psi) &\doteq \{i(\hat{\theta})\}^{-1} j(\hat{\theta}) Q(\hat{\theta}, \hat{\theta}_\psi), \\ \ell_{\theta;\hat{\theta}}(\hat{\theta}_\psi) &\doteq \{i(\hat{\theta})\}^{-1} j(\hat{\theta}) S(\hat{\theta}, \hat{\theta}_\psi), \end{aligned}$$

using moments of quantities such as the expected Fisher information $i(\theta)$ and the covariances

$$\begin{aligned} S(\theta_1, \theta_2) &= \text{cov}_{\theta_1} \{ \ell_\theta(\theta_1), \ell_\theta(\theta_2) \}, \\ Q(\theta_1, \theta_2) &= \text{cov}_{\theta_1} \{ \ell_\theta(\theta_1), \ell(\theta_1) - \ell(\theta_2) \}. \end{aligned}$$

The covariances S and Q are often readily computed, either analytically or by simulation, though the resulting tail area approximation has error $O(n^{-1})$ rather than $O(n^{-3/2})$. In an as-yet unpublished work, Fraser and Reid (2009) point out that this version may be obtained by replacing $\varphi(\theta)$ by $\partial E\{\ell(\theta; y); \theta_0\} / \partial \theta_0$, evaluated at $\theta_0 = \hat{\theta}$.

A.2 Adjusted Profile Likelihood

The correction term $M(\psi)$ can be derived using the p^* approximation,

$$M_1(\psi) = |j_{\lambda\lambda}(\hat{\theta}_\psi)|^{1/2} / |\ell_{\lambda;\hat{\lambda}}(\hat{\theta}_\psi)|,$$

which gives rise to Barndorff-Nielsen (1983) modified profile likelihood, or using the tangent exponential model,

$$M_2(\psi) = |j_{\lambda\lambda}(\hat{\theta}_\psi)|^{1/2} / |\varphi_\lambda(\hat{\theta}_\psi)^\top \hat{V}_\lambda|,$$

where \hat{V}_λ is the $n \times (d - d_0)$ matrix obtained from $\hat{V} = V(\hat{\theta})$ by omitting the columns which relate to the parameter of interest (Fraser, 2003).

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