

Bayesian Restricted Likelihood Methods: Conditioning on Insufficient Statistics in Bayesian Regression

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Abstract

Bayesian methods have proven themselves to be successful across a wide range of scientific problems and have many well-documented advantages over competing methods. However, these methods run into difficulties for two major and prevalent classes of problems: handling data sets with outliers and dealing with model misspecification. We outline the drawbacks of previous solutions to both of these problems (e.g., use of heavy-tailed likelihoods) and propose a new method as an alternative. When working with the new method, we summarize the data through a set of insufficient statistics, targeting inferential quantities of interest, and update the prior distribution with the summary statistics rather than the complete data. By careful choice of conditioning statistics, we retain the main benefits of Bayesian methods while reducing the sensitivity of the

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analysis to features of the data not captured by the conditioning statistics. For reducing sensitivity to outliers, classical robust estimators (e.g., M-estimators) are natural choices for conditioning statistics. With these choices, the method can be thought of as a blend of classical robust estimation and Bayesian methods.

A major contribution of this work is the development of a data augmented Markov chain Monte Carlo (MCMC) algorithm for the linear model and a wide range of choices for summary statistics. We demonstrate the method on an insurance agency data set containing many outliers and subject to model misspecification. Success is manifested in better predictive performance for data points of interest as compared to competing methods.

KEYWORDS: Approximate Bayesian computation, Markov chain Monte Carlo, M-estimation, Robust regression.

1 Introduction

Bayesian methods have provided successful solutions to a wide range of scientific problems, with their value having been demonstrated both empirically and theoretically. In simple settings, the success of the methods is often attributed to formal optimality properties, sometimes derived through the laws of subjective probability and sometimes through admissibility and the complete class theorems of decision theory. In complex settings, the hierarchical model allows one to create and fit sophisticated models that may, for example, pool information across similar problems.

The development of Bayesian inference relies on a complete Bayesian model consisting of three elements: the prior distribution, the loss function, and the likelihood or sampling density. While formal optimality of Bayesian methods is unquestioned if one accepts the validity of all three of these elements, a healthy skepticism encourages

us to question each of them. Concern about the prior distribution has been addressed through the development of techniques for subjective elicitation (Garthwaite et al., 2005; O’Hagan et al., 2006) and objective Bayesian methods (Berger, 2006). Concern about the loss function is reflected in, for example, the extensive literature on Bayesian hypothesis tests (Kass and Raftery, 1995).

The focus of this work is the development of techniques to handle imperfections in the likelihood. These imperfections often show themselves through the presence of outliers—cases not reflecting the phenomenon under study. There are three main solutions to Bayesian outlier-handling. The first is to replace the basic sampling density with a mixture model which includes one component for the “good” data and a second component for the “bad” data. With this approach, the prior distribution is updated with the mixture model likelihood to obtain the complete-data posterior distribution and the good component of the sampling density is used for prediction of future good data. The second approach replaces the basic sampling density with a thick-tailed density in an attempt to discount outliers, yielding techniques that often provide solid estimates of the center of the distribution but do not easily translate to predictive densities for further good data. The third approach fits a flexible (typically nonparametric) model to the data, producing a Bayesian version of a density estimate for both good and bad data. In recent development, inference is made through the use of robust inference functions (Lee and MacEachern, 2014).

The traditional strategies for handling outliers all have their drawbacks. While we view the sampling density for the good data as stable, the outlier-generating processes may be transitory in nature, constantly shifting as the source of bad data changes. This prevents us from appealing to large-sample arguments to claim that, with enough data, we can nail down a model for both good and bad data combined. Instead of attempting to model both good and bad data, we propose a novel strategy for handling

outliers. In a nutshell, we begin with a complete model as if all of the data are good. Rather than driving the move from prior to posterior by the full likelihood, we use only the likelihood driven by a few summary statistics which typically target inferential quantities of interest. We call this likelihood a restricted because conditioning is done on a restricted set of data; the set which satisfies the observed summary statistics. This is a formal update of the prior distribution based on the sampling density of the summary statistics. The novelty of the work is twofold. We make use of classical robust estimators as summary statistics in a formal Bayesian framework, using the sampling density of the estimators as a replacement for the sampling density of the data. Second, we advance the argument that conditioning on an insufficient summary of the data is sound practice, rather than merely being done for computational and modelling convenience.

The remainder of the paper develops....

2 Restricted Likelihood

2.1 Examples

To describe the use of the restricted likelihood, we begin with a pair of simple examples for the one-sample problem. For both, the model takes the data $\mathbf{y} = (y_1, \dots, y_n)$ to be a random sample of size n from a continuous distribution indexed by a parameter vector $\boldsymbol{\theta}$, with pdf $f(y|\boldsymbol{\theta})$. The standard, or full, likelihood is $L(\boldsymbol{\theta}|\mathbf{y}) = \prod_{i=1}^n f(y_i|\boldsymbol{\theta})$.

The first example considers the case where a known subset of the data are known to be bad in the sense of not informing us about $\boldsymbol{\theta}$. This case mimics the setting where outliers are identified and discarded before doing a formal analysis. Without loss of generality, we label the good cases 1 through $n - k$ and the bad cases $n - k + 1$ through n . The relevant likelihood to be used to move from prior distribution to

posterior distribution is clearly $L(\boldsymbol{\theta}|y_1, \dots, y_{n-k}) = \prod_{i=1}^{n-k} f(y_i|\boldsymbol{\theta})$. For an equivalent analysis, we rewrite the full likelihood as the product of two pieces:

$$L(\boldsymbol{\theta}|\mathbf{y}) = \left(\prod_{i=1}^{n-k} f(y_i|\boldsymbol{\theta}) \right) \left(\prod_{i=n-k+1}^n f(y_i|\boldsymbol{\theta}) \right). \quad (1)$$

We wish to keep the first piece and drop the second for better inference on $\boldsymbol{\theta}$.

The second example involves deliberate censoring of small and large observations. This is sometimes done as a precursor to the analysis of reaction time experiments (e.g., Ratcliff, 1993) where very small and large reaction times are physiologically implausible; explained by either anticipation or lack of attention of the subject. With lower and upper censoring times at t_1 and t_2 , the post-censoring sampling distribution is of mixed form, with masses $F(t_1|\boldsymbol{\theta})$ at t_1 and $1 - F(t_2|\boldsymbol{\theta})$ at t_2 , and density $f(y|\boldsymbol{\theta})$ for $y \in (t_1, t_2)$. We adjust the original data y_i , producing $c(y_i)$ by defining $c(y_i) = t_1$ if $y_i \leq t_1$, $c(y_i) = t_2$ if $y_i \geq t_2$, and $c(y_i) = y_i$ otherwise. The adjusted update is performed with $L(\boldsymbol{\theta}|c(\mathbf{y}))$. Letting $g(t_1|\boldsymbol{\theta}) = F(t_1|\boldsymbol{\theta})$, $g(t_2|\boldsymbol{\theta}) = 1 - F(t_2|\boldsymbol{\theta})$, and $g(y|\boldsymbol{\theta}) = f(y|\boldsymbol{\theta})$ for $y \in (t_1, t_2)$, we may rewrite the full likelihood as the product of two pieces

$$L(\boldsymbol{\theta}|\mathbf{y}) = \left(\prod_{i=1}^n g(c(y_i)|\boldsymbol{\theta}) \right) \left(\prod_{i=1}^n f(y_i|\boldsymbol{\theta}, c(y_i)) \right), \quad (2)$$

Only the first part is retained the analysis. Several more examples are detailed in Lewis (2014).

2.2 Generalization

To generalize the approach in (1) and (2), we write the full likelihood in two pieces with a conditioning statistic $T(\mathbf{y})$, as indicated below:

$$L(\boldsymbol{\theta}|\mathbf{y}) = f(T(\mathbf{y})|\boldsymbol{\theta}) f(\mathbf{y}|\boldsymbol{\theta}, T(\mathbf{y})). \quad (3)$$

Here, $f(T(\mathbf{y})|\boldsymbol{\theta})$ is the conditional pdf of $T(\mathbf{y})$ given $\boldsymbol{\theta}$ and $f(\mathbf{y}|\boldsymbol{\theta}, T(\mathbf{y}))$ is the conditional pdf of \mathbf{y} given $\boldsymbol{\theta}$ and $T(\mathbf{y})$. In the dropped case example, the conditioning statistic is $T(\mathbf{y}) = (y_1, \dots, y_{n-k})$. In the censoring example, the conditioning statistic is $T(\mathbf{y}) = (c(y_1), \dots, c(y_n))$. We refer to $f(T(\mathbf{y})|\boldsymbol{\theta})$ as the restricted likelihood and $L(\boldsymbol{\theta}|\mathbf{y}) = f(\mathbf{y}|\boldsymbol{\theta})$ as the full likelihood.

Bayesian methods can make use of a restricted likelihood since $T(\mathbf{y})$ is a well-defined random variable with a probability distribution indexed by $\boldsymbol{\theta}$. This leads to the restricted likelihood posterior

$$\pi(\boldsymbol{\theta}|T(\mathbf{y})) = \frac{\pi(\boldsymbol{\theta})f(T(\mathbf{y})|\boldsymbol{\theta})}{m(T(\mathbf{y}))}, \quad (4)$$

where $m(T(\mathbf{y}))$ is the marginal distribution of $T(\mathbf{y})$ under the prior distribution. Predictive statements for further (good) data rely on the model. For another observation, say y_{n+1} , we would have the predictive density

$$f(y_{n+1}|T(\mathbf{y})) = \int f(y_{n+1}|\boldsymbol{\theta})\pi(\boldsymbol{\theta}|T(\mathbf{y})) d\boldsymbol{\theta}. \quad (5)$$

2.3 Literature review

Direct use of restricted likelihood appears in many areas of the literature. The motivation is often similar to ours: concern about outliers or, more generally, model

misspecification. For example, the use of rank likelihoods is discussed by Savage (1969), Pettitt (1983, 1982), and more recently by Hoff et al. (2013). Lewis et al. (2012) make use of order statistics and robust estimators for $T(\mathbf{y})$ in the location-scale setting. Asymptotic properties of restricted posteriors are studied by Doksum and Lo (1990), Clarke and Ghosh (1995), Yuan and Clarke (2004), and Hwang et al. (2005). The tenor of these asymptotic results is that, for a variety of conditioning statistics with non-trivial regularity conditions on prior, model, and likelihood, the posterior distribution resembles the asymptotic sampling distribution of the conditioning statistic.

Restricted likelihoods have also been used as practical approximations to a full likelihood. For example, Pratt (1965) appeals to heuristic arguments regarding approximate sufficiency to justify the use of the restricted likelihood of the sample mean and standard deviation. Approximate sufficiency is also appealed to in the use of Approximate Bayesian Computation (ABC), which is related to our method. ABC is a collection of posterior approximation methods which has recently experienced success in applications to epidemiology, genetics, and quality control (see, for example, Tavaré et al., 1997; Pritchard et al., 1999; Marjoram et al., 2003; Fearnhead and Prangle, 2012). Interest typically lies in the full data posterior and ABC is used for computational convenience as an approximation. Consequently, effort is made to choose an approximately sufficient $T(\mathbf{y})$ and update to the ABC posterior by using the likelihood $L(\boldsymbol{\theta}|\mathcal{B}(\mathbf{y}))$, where $\mathcal{B}(\mathbf{y}) = \{\mathbf{y}^* | \rho(T(\mathbf{y}), T(\mathbf{y}^*)) < \epsilon\}$, ρ is a metric, and ϵ is a tolerance level. This is the likelihood “conditioned” on the collection of data sets which result in a $T(\cdot)$ within ϵ of the observed $T(\mathbf{y})$. With an approximately sufficient $T(\cdot)$ and a small enough ϵ , heuristically $L(\boldsymbol{\theta}|\mathcal{B}(\mathbf{y})) \approx L(\boldsymbol{\theta}|T(\mathbf{y})) \approx L(\boldsymbol{\theta}|\mathbf{y})$. Consequently, the ABC posterior approximates the full data posterior and efforts have been made to formalize what is meant by approximate sufficiency (e.g., Joyce

and Marjoram, 2008). ABC is related to our method in that the “conditioning” is on something other than the data \mathbf{y} . However, we specifically seek to condition on an insufficient statistic to guard against misspecification in parts of the likelihood. Additionally, we develop methods where the conditioning is exact (i.e. $\epsilon = 0$).

This work extends the development of Bayesian restricted likelihood by arguing that deliberate choice of $T(\mathbf{y})$ is sound practice and also by expanding the class of conditioning statistics in which exact conditioning can be achieved. Our methods do not rely on asymptotic properties, nor do they rely on approximate conditioning.

3 Illustrative Examples

Before discussing computational details, the method is applied to two simple examples on well known data sets to demonstrate its effectiveness in situations where outliers are a major concern. The full model in each case fits into the Bayesian linear regression framework discussed in Section 4.

The first example is an analysis of Simon Necomb’s 66 measurements of the speed of light; two of which are significant outliers in the lower tail. The full model is a standard location-scale Bayesian model:

$$\beta \sim N(23.6, 2.04^2), \sigma^2 \sim IG(5, 10), y_i \stackrel{iid}{\sim} N(\beta, \sigma^2), i = 1, 2, \dots, n = 66, \quad (6)$$

where y_i denotes the i^{th} measurement of the passage time of light. β is interpreted as the passage time of light with σ^2 representing measurement error. Four versions of the restricted likelihood are fit with conditioning statistics: 1) Huber’s M-estimator for location with Huber’s ‘proposal 2’ for scale 2) Tukey’s M-estimator for location with Huber’s ‘proposal 2’ for scale 3) LMS (least median squares) for location with

associated estimator of scale and 4) LTS (least trimmed squares) for location with associated estimator of scale. Associated tuning parameters for the M-estimators are chosen to achieve 95% efficiency under normality Huber (1964) and for comparability, roughly 5% of the residuals are trimmed for LTS. Additionally, two other common approaches to outlier handling are fit: 1) replacing the normal distribution with a t-distribution and, 2) replacing the normal distribution with a mixture of two normals. The t-model assumes $y_i \stackrel{iid}{\sim} t_\nu(\beta, \sigma^2)$ with $\nu = 5$. The prior on σ^2 is $IG(5, \frac{\nu-2}{\nu}10)$ so the prior on the variance is the same as the other models. The mixture takes the form: $y_i \stackrel{iid}{\sim} pN(\beta, \sigma^2) + (1-p)N(\beta, 10\sigma^2)$ assuming the prior $p \sim \text{beta}(20, 1)$ on the probability of belonging to the ‘good’ component.

The posteriors of β under each model appear in top of Figure 1. As expected, the posterior under the normal model is pulled downward by the two outliers while the heavy tailed model provides robustness against them. The restricted likelihood methods using the M-estimators and LTS statistics also achieve robustness against the outliers. Conditioning on LMS however, results in a posterior similar to the one under the normal model. The M-estimators provide the most precise posteriors in this case. This is reflected in more precise predictions than the heavy-tailed and mixture model as illustrated by the predictive distributions displayed in the bottom of Figure 1.

As a second example, a data set measuring the number of telephone calls in Belgium from 1950-1973 is analyzed. The outliers in this case are due to a change in units on which calls were recorded for part of the dataset. The full model is a standard normal Bayesian linear regression:

$$\boldsymbol{\beta} \sim N_2(\boldsymbol{\mu}_0, \boldsymbol{\Sigma}_0), \sigma^2 \sim IG(a, b), \mathbf{y} \sim N(X\boldsymbol{\beta}, \sigma^2 I), \quad (7)$$

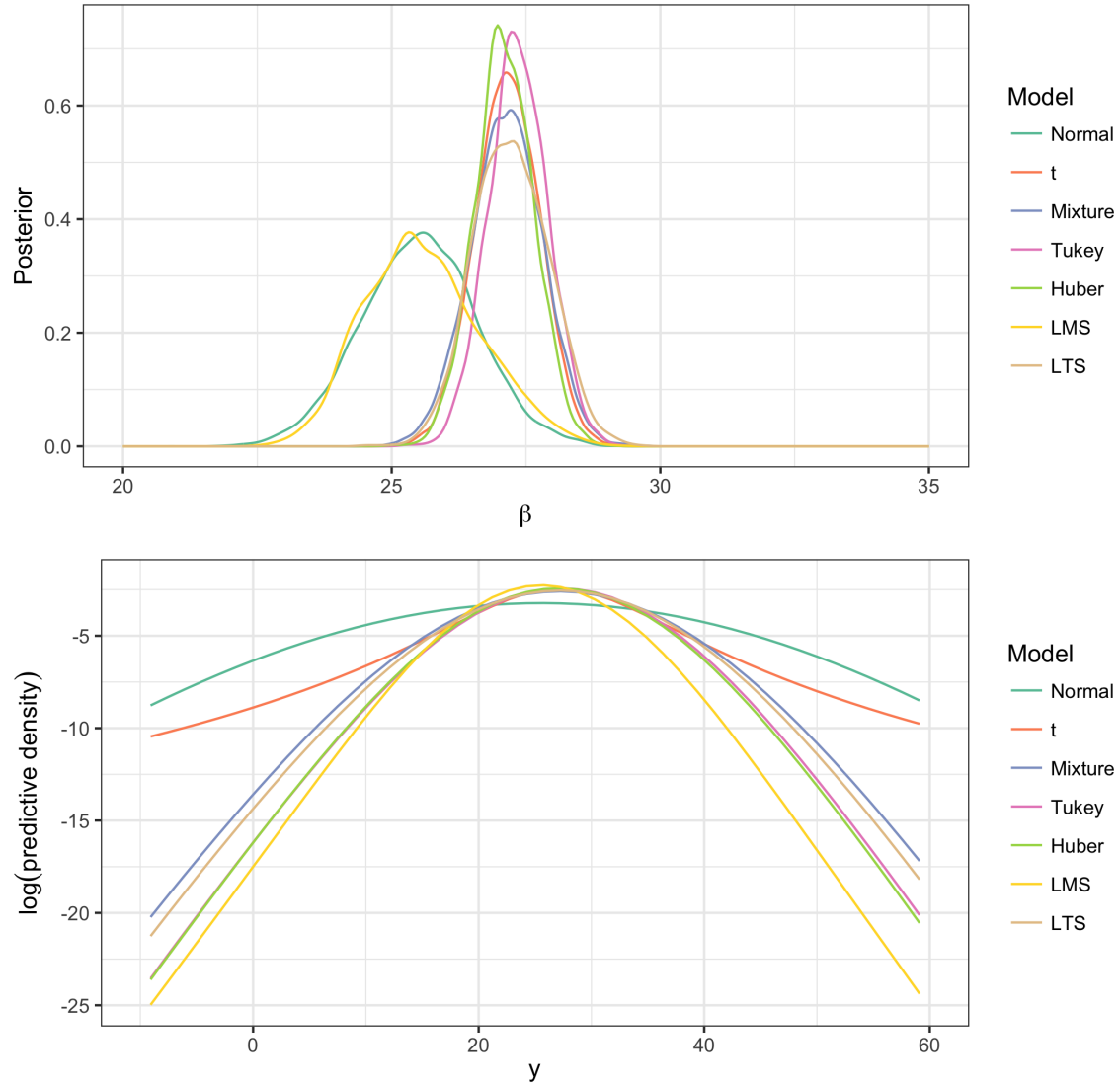


Figure 1: Top: Posteriors of the location parameter β under the normal theory model, the t-model, and four restricted likelihood models for Newcomb's speed of light measurements. Bottom: Posterior predictive distribution of the speed of light under the normal theory model, the t-model, and four restricted likelihood models.

where $\boldsymbol{\beta} = (\beta_0, \beta_1)^\top$, \mathbf{y} is the vector of the logarithm of the number of calls, and \mathbf{X} is the $n \times 2$ design matrix. Prior parameters are fixed via a fit to the first 3 data points. In particular, $\Sigma_0 = g\sigma_0^2(\mathbf{X}^\top \mathbf{X})^{-1}$, with $\sigma_0 = 0.03$ and $\mu_0 = (1.87, 0.03)^\top$; the MLEs fit to the first three data points. There are $n = 21$ remaining data points and the parameter g is set to 21 reflecting a unit information prior. Finally $a = 2$ and $b = 1$ for the normal theory and restricted likelihood models.

Four models are compared: 1) the normal theory base model 2) A two component normal mixture model, 3) a t-model, and 4) a restricted likelihood model conditioning on Tukey’s M-estimator for the slope and intercept with Huber’s ‘proposal 2’ for scale. The mixture model assumes different mean regression functions and variances for each component, but keeps the same, relatively non-informative priors. The probability of belonging to the first component is given a *beta*(5, 1) prior. The heavy-tailed model fixes the degrees of freedom to 5 with the same adjustment to the prior on σ^2 as above.

The data and 95% credible bands of the posterior predictive distribution under each model are displayed in Figure 2. The normal theory model is only fit to the obvious non-outlying points. Since the t-model assumes the data are heavy-tailed, the posterior predictive distribution is much wider. On the other hand, the predictive distribution under the restricted likelihood approach is much more precise and is close to that of the normal theory fit that discards the outliers. It is also close to the two component mixture results where the predictive distribution is formulated using only the good component. The mixture model involves explicitly modeling the outlier generating mechanism. In more more complex situations where the outlier generating mechanism is transient (i.e. ever changing and more complex than just a unit error in the recording), modeling the outliers becomes more difficult. Like classical robust estimation, the restricted likelihood approach avoids explicitly modeling the outliers.

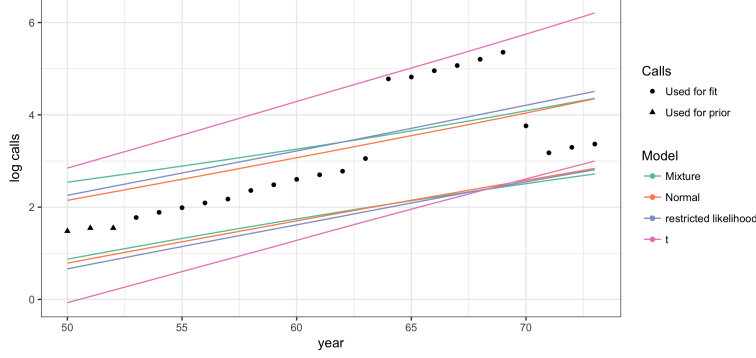


Figure 2: Predictive distribution of $\log(\text{calls})$ under the Normal theory model fit to the non-outliers, the restricted likelihood model with Tukey’s M-estimator for the slope and intercept with Huber’s ‘proposal 2’ for scale, and a heavy-tailed t-distribution model. The first three data points were used to specify the prior with the remaining points used in the posterior fits. See details in the Appendix.

4 Restricted Likelihood for the Linear Model

The simple examples in the previous section highlight that productive use of the restricted likelihood relies on a good choice of $T(\mathbf{y})$. This work focuses on robustness in linear models where natural choices include many used above: M-estimators in the tradition of Huber (1964), least median squares (LMS), and least trimmed squares (LTS). For these choices the restricted likelihood is not available in closed form, making computation of the restricted posterior a challenge. For low-dimensional statistics $T(\mathbf{y})$ and parameters $\boldsymbol{\theta}$, direct computational strategies described in Lewis (2014) can be used to estimate the restricted posterior conditioned on essentially any statistic. These strategies rely on density estimation $f(T(\mathbf{y})|\boldsymbol{\theta})$ using samples of $T(\mathbf{y})$ for many values of $\boldsymbol{\theta}$; a strategy which breaks down in higher dimensions. This section outlines a data-augmented MCMC algorithm that can be applied to the Bayesian linear model when $T(\mathbf{y})$ consists of estimates of the regression coefficients and scale parameter.

4.1 The Bayesian linear model

We focus on the use of restricted likelihood for the Bayesian linear model with a standard formulation:

$$\begin{aligned}\boldsymbol{\theta} &= (\boldsymbol{\beta}, \sigma^2) \sim \pi(\boldsymbol{\theta}) \\ y_i &= x_i^\top \boldsymbol{\beta} + \epsilon_i, \text{ for } i = 1, \dots, n\end{aligned}\tag{8}$$

where x_i and $\boldsymbol{\beta} \in \mathbb{R}^p$, $\sigma^2 \in \mathbb{R}^+$, and the ϵ_i are independent draws from a distribution with center 0 and scale σ . X denotes the design matrix whose rows are x_i^\top .

For the restricted likelihood model, conditioning statistics are assumed to be of the form $T(\mathbf{y}) = (\mathbf{b}(X, \mathbf{y}), s(X, \mathbf{y}))$ where $\mathbf{b}(X, \mathbf{y}) = (b_1(X, \mathbf{y}), \dots, b_p(X, \mathbf{y}))^\top \in \mathbb{R}^p$ is an estimator for the regression coefficients and $s(X, \mathbf{y}) \in \{0\} \cup \mathbb{R}^+$ is an estimator of the scale. Throughout, observed data and summary statistic is denoted by \mathbf{y}_{obs} and $T(\mathbf{y}_{obs}) = (\mathbf{b}(X, \mathbf{y}_{obs}), s(X, \mathbf{y}_{obs}))$, respectively. Several conditions are imposed on the model and statistic to ensure validity of the MCMC algorithm:

- C1.** The $n \times p$ design matrix, X , whose i^{th} row is x_i^\top , is of full column rank.
- C2.** The ϵ_i are a random sample from some distribution which has a density with respect to Lebesgue measure on the real line and for which the support is the real line.
- C3.** $\mathbf{b}(X, \mathbf{y})$ is almost surely continuous and differentiable with respect to \mathbf{y} .
- C4.** $s(X, \mathbf{y})$ is almost surely positive, continuous, and differentiable with respect to \mathbf{y} .
- C5.** $\mathbf{b}(X, \mathbf{y} + X\mathbf{v}) = \mathbf{b}(X, \mathbf{y}) + \mathbf{v}$ for all $\mathbf{v} \in \mathbb{R}^p$.
- C6.** $\mathbf{b}(X, a\mathbf{y}) = a\mathbf{b}(X, \mathbf{y})$ for all constants a .

C7. $s(X, \mathbf{y} + X\mathbf{v}) = s(X, \mathbf{y})$ for all $\mathbf{v} \in \mathbb{R}^p$.

C8. $s(X, a\mathbf{y}) = |a|s(X, \mathbf{y})$ for all constants a .

Properties C5 and C6 of \mathbf{b} are called *regression* and *scale equivariance*, respectively. Properties C7 and C8 of s are called *regression invariance* and *scale equivariance*. Many estimators satisfy the above properties, including simultaneous M-estimators (Huber and Ronchetti, 2009; Maronna et al., 2006) for which the R package `brlm` (github.com/jrlewi/brlm) is available to implement the MCMC described here. Further software development is required to extend the MCMC implementation beyond these M-estimators. The package also implements the direct computational methods described in Lewis (2014). These methods are effective in lower dimensional problems and were used in several of the examples in Section 3.

4.2 Computational strategy

The general style of algorithm we present is a data augmented MCMC targeting $f(\boldsymbol{\theta}, \mathbf{y} | T(\mathbf{y}) = T(\mathbf{y}_{obs}))$, the joint distribution of $\boldsymbol{\theta}$ and the full data given the summary statistic $T(\mathbf{y}_{obs})$. The Gibbs sampler (Gelfand and Smith, 1990) iteratively samples from the full conditionals

1. $\pi(\boldsymbol{\theta} | \mathbf{y}, T(\mathbf{y}) = T(\mathbf{y}_{obs}))$
2. $f(\mathbf{y} | \boldsymbol{\theta}, T(\mathbf{y}) = T(\mathbf{y}_{obs}))$.

When \mathbf{y} has the summary statistic $T(\mathbf{y}) = T(\mathbf{y}_{obs})$, the first full conditional is the same as the full data posterior $\pi(\boldsymbol{\theta} | \mathbf{y})$. In this case, the condition $T(\mathbf{y}) = T(\mathbf{y}_{obs})$ is redundant. This allows us to make use of conventional MCMC steps for this generation. For typical regression models, algorithms abound. Details of the recommended

algorithms depend on details of the prior distribution and sampling density and we assume this can be done (see e.g., Liu, 1994; Liang et al., 2008).

For a typical model and conditioning statistic, the second full conditional $f(\mathbf{y}|\boldsymbol{\theta}, T(\mathbf{y}) = T(\mathbf{y}_{obs}))$ is not available in closed form. We turn to Metropolis-Hastings (Hastings, 1970), using the strategy of proposing full data $\mathbf{y} \in \mathcal{A} := \{\mathbf{y} \in \mathbb{R}^n | T(\mathbf{y}) = T(\mathbf{y}_{obs})\}$ from a well defined distribution with support \mathcal{A} and either accepting or rejecting the proposal. Let $\mathbf{y}_p, \mathbf{y}_c \in \mathcal{A}$ represent the proposed and current full data, respectively. Denote the proposal distribution for \mathbf{y}_p by $p(\mathbf{y}_p|\boldsymbol{\theta}, T(\mathbf{y}_p) = T(\mathbf{y}_{obs})) = p(\mathbf{y}_p|\boldsymbol{\theta}, \mathbf{y}_p \in \mathcal{A}) = p(\mathbf{y}_p|\boldsymbol{\theta})$. The last equality follows from the fact that our $p(\cdot|\boldsymbol{\theta})$ assigns probability one to the event $\{\mathbf{y}_p \in \mathcal{A}\}$. These equalities still hold if the dummy argument \mathbf{y}_p is replaced with \mathbf{y}_c . The conditional density is

$$\begin{aligned} f(\mathbf{y}|\boldsymbol{\theta}, \mathbf{y} \in \mathcal{A}) &= \frac{f(\mathbf{y}|\boldsymbol{\theta})I(\mathbf{y} \in \mathcal{A}|\mathbf{y}, \boldsymbol{\theta})}{\int_{\mathcal{A}} f(\mathbf{y}|\boldsymbol{\theta})d\mathbf{y}} \\ &= \frac{f(\mathbf{y}|\boldsymbol{\theta})}{\int_{\mathcal{A}} f(\mathbf{y}|\boldsymbol{\theta})d\mathbf{y}} \end{aligned}$$

for $\mathbf{y} \in \mathcal{A}$. This includes both \mathbf{y}_p and \mathbf{y}_c . The Metropolis-Hastings acceptance probability is the minimum of 1 and R where,

$$R = \frac{f(\mathbf{y}_p|\boldsymbol{\theta}, \mathbf{y}_p \in \mathcal{A}) p(\mathbf{y}_c|\boldsymbol{\theta}, \mathbf{y}_c \in \mathcal{A})}{f(\mathbf{y}_c|\boldsymbol{\theta}, \mathbf{y}_c \in \mathcal{A}) p(\mathbf{y}_p|\boldsymbol{\theta}, \mathbf{y}_p \in \mathcal{A})} \quad (9)$$

$$= \frac{f(\mathbf{y}_p|\boldsymbol{\theta})}{\int_{\mathcal{A}} f(\mathbf{y}|\boldsymbol{\theta})d\mathbf{y}} \frac{\int_{\mathcal{A}} f(\mathbf{y}|\boldsymbol{\theta})d\mathbf{y} p(\mathbf{y}_c|\boldsymbol{\theta})}{f(\mathbf{y}_c|\boldsymbol{\theta}) p(\mathbf{y}_p|\boldsymbol{\theta})} \quad (10)$$

$$= \frac{f(\mathbf{y}_p|\boldsymbol{\theta}) p(\mathbf{y}_c|\boldsymbol{\theta})}{f(\mathbf{y}_c|\boldsymbol{\theta}) p(\mathbf{y}_p|\boldsymbol{\theta})}. \quad (11)$$

For the models we consider, evaluation of $f(\mathbf{y}|\boldsymbol{\theta})$ is straightforward. Therefore, the difficulty in implementing this Metropolis-Hastings step manifests itself in the ability to both simulate from and evaluate $p(\mathbf{y}_p|\boldsymbol{\theta})$; the well defined distribution with support

\mathcal{A} . We now discuss such an implementation method for the linear model in (8).

4.2.1 Construction of the proposal

Our computational strategy relies on proposing \mathbf{y} such that $T(\mathbf{y}) = T(\mathbf{y}_{obs})$ where $T(\cdot) = (\mathbf{b}(X, \cdot), s(X, \cdot))$ satisfies the conditions C3-C8. It is not a simple matter to do this directly, but with the specified conditions, it is possible to scale and shift any \mathbf{z}^* which generates a positive scale estimate to such a \mathbf{y} via the following Theorem whose proof is in the appendix.

Theorem 4.1. *Assume that conditions C4-C8 hold. Then, any vector $\mathbf{z}^* \in \mathbb{R}^n$ with conditioning statistic $T(\mathbf{z}^*)$ for which $s(X, \mathbf{z}^*) > 0$ can be transformed into \mathbf{y} with conditioning statistic $T(\mathbf{y}) = T(\mathbf{y}_{obs})$ through the transformation*

$$\mathbf{y} = h(\mathbf{z}^*) := \frac{s(X, \mathbf{y}_{obs})}{s(X, \mathbf{z}^*)} \mathbf{z}^* + X \left(\mathbf{b}(X, \mathbf{y}_{obs}) - \mathbf{b}(X, \frac{s(X, \mathbf{y}_{obs})}{s(X, \mathbf{z}^*)} \mathbf{z}^*) \right).$$

Using the theorem, the general idea is to first start with a sample \mathbf{z}^* from a known distribution, say $p(\mathbf{z}^*)$, and transform via $h(\cdot)$ to $\mathbf{y} \in \mathcal{A}$. The proposal density $p(\mathbf{y}|\boldsymbol{\theta})$ is then a change-of-variables adjustment on $p(\mathbf{z}^*)$ derived from $h(\cdot)$. In general however, the mapping $h(\cdot)$ is many-to-one: for any $\mathbf{v} \in \mathbb{R}^n$ and any $c \in \mathbb{R}^+$, $c\mathbf{z}^* + X\mathbf{v}$ map to the same \mathbf{y} . This makes the change-of-variables adjustment difficult. We handle this point by first noticing that the set \mathcal{A} is an $n-p-1$ dimensional space: there are p constraints imposed by the regression coefficients and one further constraint imposed by the scale. Hence, we restrict the initial \mathbf{z}^* to an easily understood $n-p-1$ dimensional space. Specifically, this space is the unit sphere in the orthogonal complement of the column space of the design matrix. Denote the column space and its orthogonal complement with $\mathcal{C}(X)$ and $\mathcal{C}^\perp(X)$, respectively. With \mathbf{z}^* on this sphere, $c\mathbf{z}^* + X\mathbf{v}$ is clearly not (unless $c = 1$ and $\mathbf{v} = \mathbf{0}$) since every point on the

sphere is both in $\mathcal{C}^\perp(X)$ and has $\|\mathbf{z}^*\| = 1$. Thus the mapping has become one-to-one making the change of variables more feasible.

With the domain of $h(\cdot)$ restricted to the unit sphere in $\mathcal{C}^\perp(X)$, the range is still the entirety of \mathcal{A} . This is important so that the support of the proposal distribution (i.e. the $h(\cdot)$) contains the support of the target $f(\mathbf{y}|\theta, \mathbf{y} \in \mathcal{A})$; a necessary condition for convergence of the Metropolis-Hastings algorithm (in this case the supports are both \mathcal{A}). To see that the range of $h(\cdot)$ is \mathcal{A} , consider any $\mathbf{y} \in \mathcal{A}$ and its projection onto $\mathcal{C}^\perp(X)$: $Q\mathbf{y}$ where $Q = I - XX^\top$ ¹. It is easy to show that $\mathbf{z}^* = Q\mathbf{y}/\|Q\mathbf{y}\|$ is on the unit sphere and $h(\mathbf{z}^*) = \mathbf{y}$.

Given the one-to-one and onto mapping from the sphere to \mathcal{A} , the general proposal strategy is summarized as follows:

1. Sample \mathbf{z}^* from a distribution with known density on the unit sphere in $\mathcal{C}^\perp(X)$.
2. Set $\mathbf{y} = h(\mathbf{z}^*)$ and calculate the Jacobian of this transformation in two steps.
 - (a) Scale from unit sphere to the set $\Pi(\mathcal{A}) := \{\mathbf{z} \in \mathbb{R}^n \mid \exists \mathbf{y} \in \mathcal{A} \text{ s.t. } \mathbf{z} = Q\mathbf{y}\}$.

This is the projection of \mathcal{A} onto $\mathcal{C}^\perp(X)$ and, by condition C7, every element of this set has $s(X, \mathbf{z}) = s(X, \mathbf{y}_{obs})$. Specifically, set $\mathbf{z} = \frac{s(X, \mathbf{y}_{obs})}{s(X, \mathbf{z}^*)} \mathbf{z}^*$. There are two pieces of this Jacobian: one for the scaling and one for the mapping of the sphere onto $\Pi(\mathcal{A})$. The latter piece is given in equation (12).

- (b) Shift from $\Pi(\mathcal{A})$ to \mathcal{A} : $\mathbf{y} = \mathbf{z} + X(\mathbf{b}(X, \mathbf{y}_{obs}) - \mathbf{b}(X, \mathbf{z}))$. This shift is along the column space of X to the unique element in \mathcal{A} . The Jacobian of this transformation is given by equation (13).

The final proposal distribution including the complete Jacobian is given in equation (14) with details in the next section. Before giving these details we provide

¹We have used condition C1 to assume without loss of generality that the columns of X form an orthonormal basis for $\mathcal{C}(X)$ (i.e., $X^\top X = I$).

a visualization of each of the sets described above to aid in the understanding of the strategy we are taking. Figure 3 depicts an artificial low-dimensional location-scale example. In the figure, $n = 3$, $p = 1$, and the conditioning statistic is $T(\mathbf{y}) = (\min(\mathbf{y}), \sum(y_i - \min(\mathbf{y}))^2)$. The set \mathcal{A} is depicted for $T(\mathbf{y}_{obs}) = (0, 1)$ which we describe as a “warped triangle” in light blue, with each side corresponding to a particular coordinate of \mathbf{y} being the minimum value of zero. The other two coordinates are restricted by the scale statistic to lie on the quarter circle of radius one in the positive orthant. In this example, the column vector $X = \mathbf{1}$ (shown as a reference) spans $\mathcal{C}(X)$ and the unit sphere in $\mathcal{C}^\perp(X)$ is a unit circle on the orthogonal plane (shown in red). This is the sphere from which the initial sample \mathbf{z}^* is taken. $\Pi(\mathcal{A})$, the projection of \mathcal{A} onto the orthogonal plane is depicted as the bowed triangle in dark blue. We will come back to this artificial example in the next section in an attempt to visualize the Jacobian calculations

4.2.2 Evaluation of the proposal density

We now explain each step in computing the Jacobian described above.

Scale from unit sphere to $\Pi(\mathcal{A})$

The first step is constrained to $\mathcal{C}^\perp(X)$ where the unit sphere is transformed to $\Pi(\mathcal{A})$. We further break this step into two substeps: first, the distribution on the unit sphere is transformed to that along a sphere of radius $r = \|\mathbf{z}\| = s(X, \mathbf{y}_{obs})/s(X, \mathbf{z}^*)$. This contributes a factor of $r^{-(n-p-1)}$ to the Jacobian. Second, the new sphere is then deformed to $\Pi(\mathcal{A})$. This deformation contributes an attenuation to the Jacobian equal to the ratio of infinitesimal volumes in the tangent spaces of the sphere and $\Pi(\mathcal{A})$ at \mathbf{z} . Restricting ourselves to the $n - p$ dimensional space $\mathcal{C}^\perp(X)$, this ratio is the cosine of the angle between the normal vectors of the two sets at \mathbf{z} . The normal to the sphere is its radius vector \mathbf{z} . The normal to $\Pi(\mathcal{A})$ is given in the following

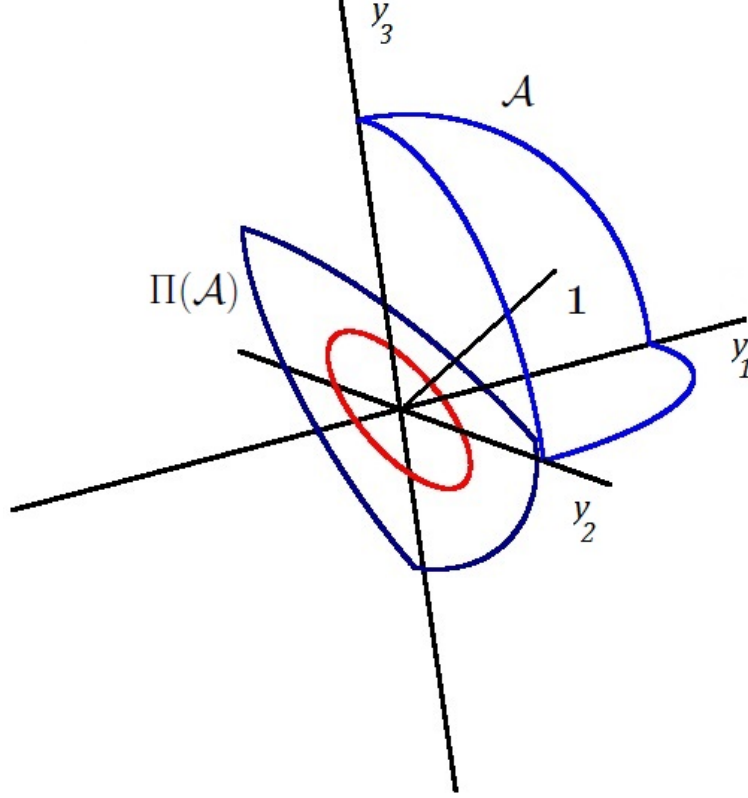


Figure 3: A depiction of \mathcal{A} , $\Pi(\mathcal{A})$, and the unit circle for the illustrative example where $b_1(\mathbf{1}, \mathbf{y}) = \min(\mathbf{y}) = 0$ and $s(\mathbf{1}, \mathbf{y}) = \sum (y_i - b_1(\mathbf{1}, \mathbf{y}))^2 = 1$. \mathcal{A} is the combination of three quarter circles, one on each plane defined by $y_i = 0$. The projection of this manifold onto the deviation space is depicted by the bowed triangular shape in the plane defined by $\sum y_i = 0$. The circle in this plane represents the sample space for the intermediate sample \mathbf{z}^* . Also depicted is the vector $\mathbf{1}$, the design matrix for the location and scale setting.

lemma.

Lemma 4.2. *Assume that conditions C1-C2, C4, and C7 hold. Let $\mathbf{y} \in \mathcal{A}$. Let $\nabla s(X, \mathbf{y})$ denote the gradient of the scale statistic with respect to the data vector evaluated at \mathbf{y} . Then $\nabla s(X, \mathbf{y}) \in \mathcal{C}^\perp(X)$ and is normal to $\Pi(\mathcal{A})$ at $\mathbf{z} = Q\mathbf{y}$ in $\mathcal{C}^\perp(X)$.*

As a result of the lemma, the contribution to the Jacobian of this attenuation is

$$\cos(\gamma) = \frac{\nabla s(X, \mathbf{y})^\top \mathbf{z}}{\|\nabla s(X, \mathbf{y})\| \|\mathbf{z}\|}, \quad (12)$$

where γ is the angle between the two normal vectors. This step is visualized in Figure 4 for the artificial location-scale example. The figure pictures only the $\mathcal{C}^\perp(X)$, which in this case is a plane. The original unit sphere (here, the solid circle) is first stretched to the dashed sphere contributing $r^{-(n-p-1)}$ to the Jacobian as seen in panel (a). In panel (b), the dashed circle is transformed onto $\Pi(\mathcal{A})$ contributing $\cos(\gamma)$ to the Jacobian. The normal vectors in panel (b) are orthogonal to the tangent vectors of $\Pi(\mathcal{A})$ and the circle. As stated above, the Jacobian is the ratio of infinitesimal lengths along these tangent vectors. This is the same as the ratio of the infinitesimal lengths of the normal vectors (i.e., $\cos(\gamma)$). This generalization extends to higher dimensions where the ‘lengths’ along the tangent vectors become volumes along the tangent spaces.

Shift from $\Pi(\mathcal{A})$ to \mathcal{A}

The final piece of the Jacobian comes from the transformation from $\Pi(\mathcal{A})$ to \mathcal{A} . This step involves a shift of \mathbf{z} to \mathbf{y} along the column space of X . Since the shift depends on \mathbf{z} , the density on the set $\Pi(\mathcal{A})$ is deformed by the shift. The contribution of this deformation to the Jacobian is, again, the ratio of the infinitesimal volume along $\Pi(\mathcal{A})$ at \mathbf{z} to the corresponding volume along \mathcal{A} at \mathbf{y} . The ratio is calculated by considering the volume of the projection of a unit hypercube in the tangent space of \mathcal{A} at \mathbf{y} onto $\mathcal{C}^\perp(X)$. Computational details are given in the following lemmas and subsequent theorem. Throughout, let $\mathcal{T}_y(\mathcal{A})$ and $\mathcal{T}_y^\perp(\mathcal{A})$ denote the tangent space to \mathcal{A} at \mathbf{y} and its orthogonal complement respectively.

Lemma 4.3. *Assume that conditions C1-C5 and C7-C8 hold. Then the $p+1$ gradient*

vectors $\nabla s(X, \mathbf{y}), \nabla b_1(X, \mathbf{y}), \dots, \nabla b_p(X, \mathbf{y})$ form a basis for $\mathcal{T}_y^\perp(\mathcal{A})$ with probability one.

The lemma describes construction of a basis for $\mathcal{T}_y^\perp(\mathcal{A})$. This leads to a basis for $\mathcal{T}_y(\mathcal{A})$. Both of these bases can be orthonormalized. Let $A = [a_1, \dots, a_{n-p-1}]$ and $B = [b_1, \dots, b_{p+1}]$ denote the matrices whose columns contain the orthonormal bases for $\mathcal{T}_y(\mathcal{A})$ and $\mathcal{T}_y^\perp(\mathcal{A})$, respectively. The columns in A define a unit hypercube in $\mathcal{T}_y(\mathcal{A})$ and their projections onto $\mathcal{C}^\perp(X)$ define a parallelepiped. We defer construction of A until later.

Lemma 4.4. *Assume that conditions C1-C5 and C7-C8 hold. Then the $n \times (n-p-1)$ dimensional matrix $P = QA$ is of full column rank.*

As a consequence of this lemma, the parallelepiped spanned by the columns of P is not degenerate (it is $n-p-1$ dimensional), and its volume is given by

$$\text{Vol}(P) := \sqrt{\det(P^\top P)} = \prod_{i=1}^r \sigma_i \quad (13)$$

where $r = \text{rank}(P) = n-p-1$ and $\sigma_1 \geq \sigma_2 \geq \dots \geq \sigma_r > 0$ are the singular values of P (e.g., Miao and Ben-Israel (1992)). Combining Lemmas 4.3 and 4.4 above leaves us with the following result concerning the calculation of the desired Jacobian.

Theorem 4.5. *Assume that conditions C1-C5 and C7-C8 hold. Then the Jacobian of the transformation from the distribution along $\Pi(\mathcal{A})$ to that along \mathcal{A} is equal to the volume given in (13).*

The proposal density

Putting all the pieces of the Jacobian together we have the following result. Any dependence on other variables, including current states in the Markov chain, is made implicit.

Theorem 4.6. *Assume that conditions C1-C8 hold. Let \mathbf{z}^* be sampled on the unit sphere in $\mathcal{C}^\perp(X)$ with density $p(\mathbf{z}^*)$. Using the transformation of \mathbf{z}^* to $\mathbf{y} \in \mathcal{A}$ described in Theorem 4.1, the density of \mathbf{y} is*

$$p(\mathbf{y}) = p(\mathbf{z}^*)r^{-(n-p-1)}\cos(\gamma)\text{Vol}(P) \quad (14)$$

where $r = s(X, \mathbf{y}_{obs})/s(X, \mathbf{z}^*)$, and $\cos(\gamma)$ and $\text{Vol}(P)$ are as in equations (12) and (13), respectively.

In practice, computing A directly to find P and $\text{Vol}(P)$ is computationally intensive as it involves orthogonalization of n vectors in n -dimensional space. To find a matrix A , supplement B with a set of n linearly independent columns on the right, and apply Gram-Schmidt orthonormalization to the matrix. This algorithm is infeasibly slow when n is large because it is $\mathcal{O}(n^3)$ and must be repeated at each iterate of the MCMC when a complete data set is drawn. Fortunately, we can make use of results related to *principal angles* found in Miao and Ben-Israel (1992) to compute the volume in (13) using B and an orthonormal basis for $\mathcal{C}(X)$ (The definition of principal angles can be found in the cited text). Recall, B is constructed by orthogonalization of a basis for $\mathcal{T}_y^\perp(\mathcal{A})$. Since this space is of dimension $p + 1$, applying Gram-Schmidt to find the orthonormal basis is much faster, the algorithm is $\mathcal{O}(np^2)$, and there is a considerable reduction in computational burden when $n \gg p$. Further, the singular values of $P = QA$ are also the singular values of $W^\top A$ (recall, $Q = WW^\top$), which can be easily obtained through B . The following corollary formally states how computation of A can be circumvented.

Corollary 4.7. *Let U be a matrix whose columns form an orthonormal basis for $\mathcal{C}(X)$. Then the non-unit singular values of $U^\top B$ are the same as the non-unit singular values of $W^\top A$.*

Thus, we can compute $\text{Vol}(P)$ by finding the singular values of $U^\top B$, reducing the computational burden substantially.

5 Simulations

5.1 Simulation 1

5.2 Simulation 2

Data generating model:

$$\begin{aligned}\theta_i &\sim N(\mu, \tau^2), \quad i = 1, 2, \dots, 90 \\ y_{ij} &\sim (1 - p_i)N(\theta_i, \sigma^2) + p_iN(\theta_i, m_i\sigma^2), \quad j = 1, 2, \dots, n_i\end{aligned}\tag{15}$$

with $\mu = 0, \tau^2 = 1, \sigma^2 = 4$. The values of p_i, m_i , and n_i depend on the group and are formed using 5 replicates of the full factorial design over factors p_i, m_i, n_i with levels $p_i = .1, .2, .3$, $m_i = 9, 25$, and $n_i = 25, 50, 100$. The full model for fitting is a corresponding normal model without contamination:

$$\begin{aligned}\mu &\propto 1, \quad \tau^2 \propto \tau^{-2}, \\ \theta_i &\sim N(\mu, \tau^2), \quad \sigma_i^2 \sim IG(a_s, b_s), \quad i = 1, 2, \dots, 90, \\ y_{ij} &\sim N(\theta_i, \sigma_i^2), \quad j = 1, 2, \dots, n_i\end{aligned}\tag{16}$$

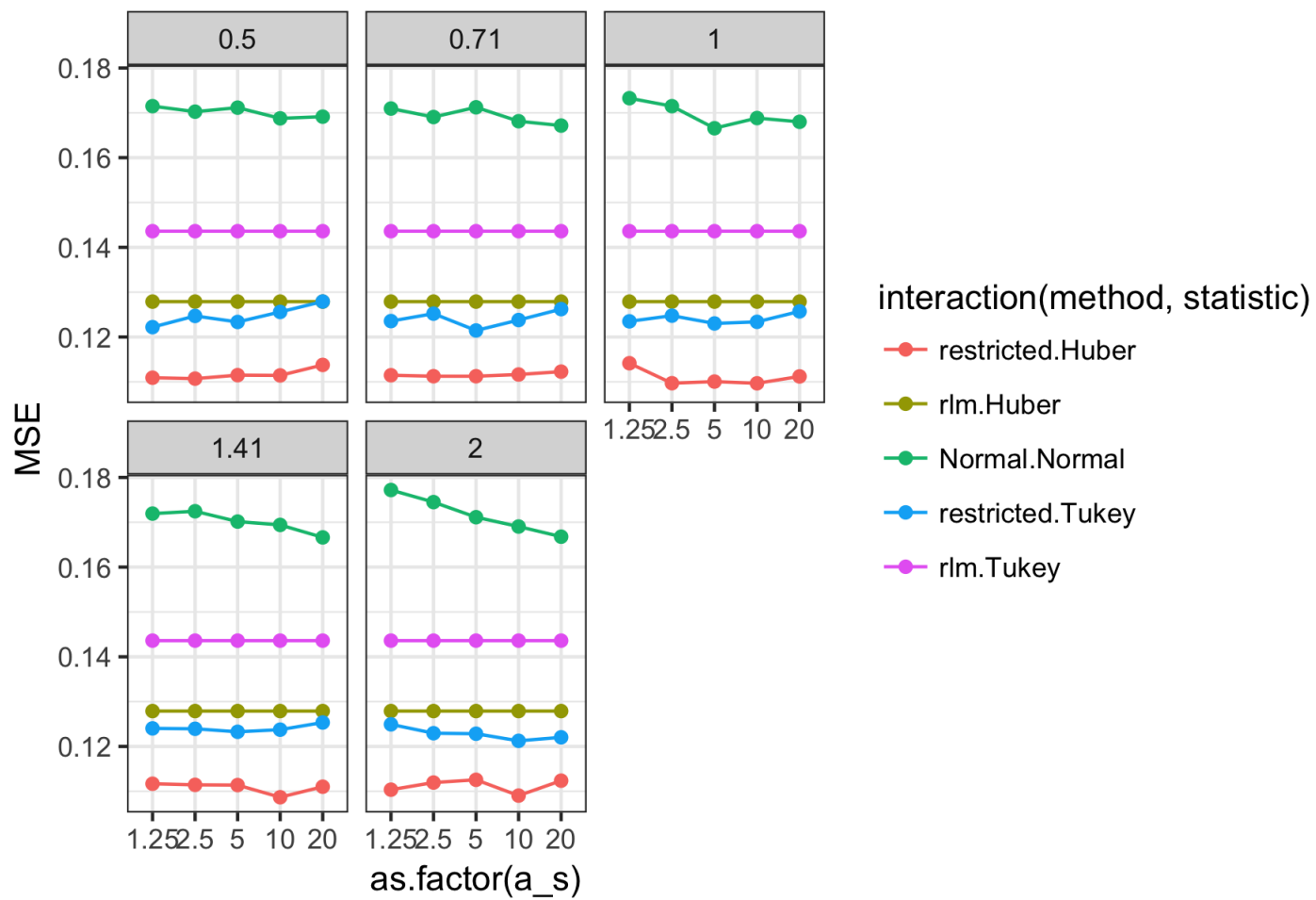
For the restricted likelihood versions we condition on robust M-estimators of location and scale in each group: $T_i(\mathbf{y}_i) = (\hat{\theta}_i, \hat{\sigma}_i^2), i = 1, 2, \dots, 90$. The two versions used are Huber's and Tukey's location estimator both coupled with Huber's scale estimator. The estimates from the Bayesian models are compared to these estimates. To complete the specification of model (16) we must specify a_s and b_s . For this we use

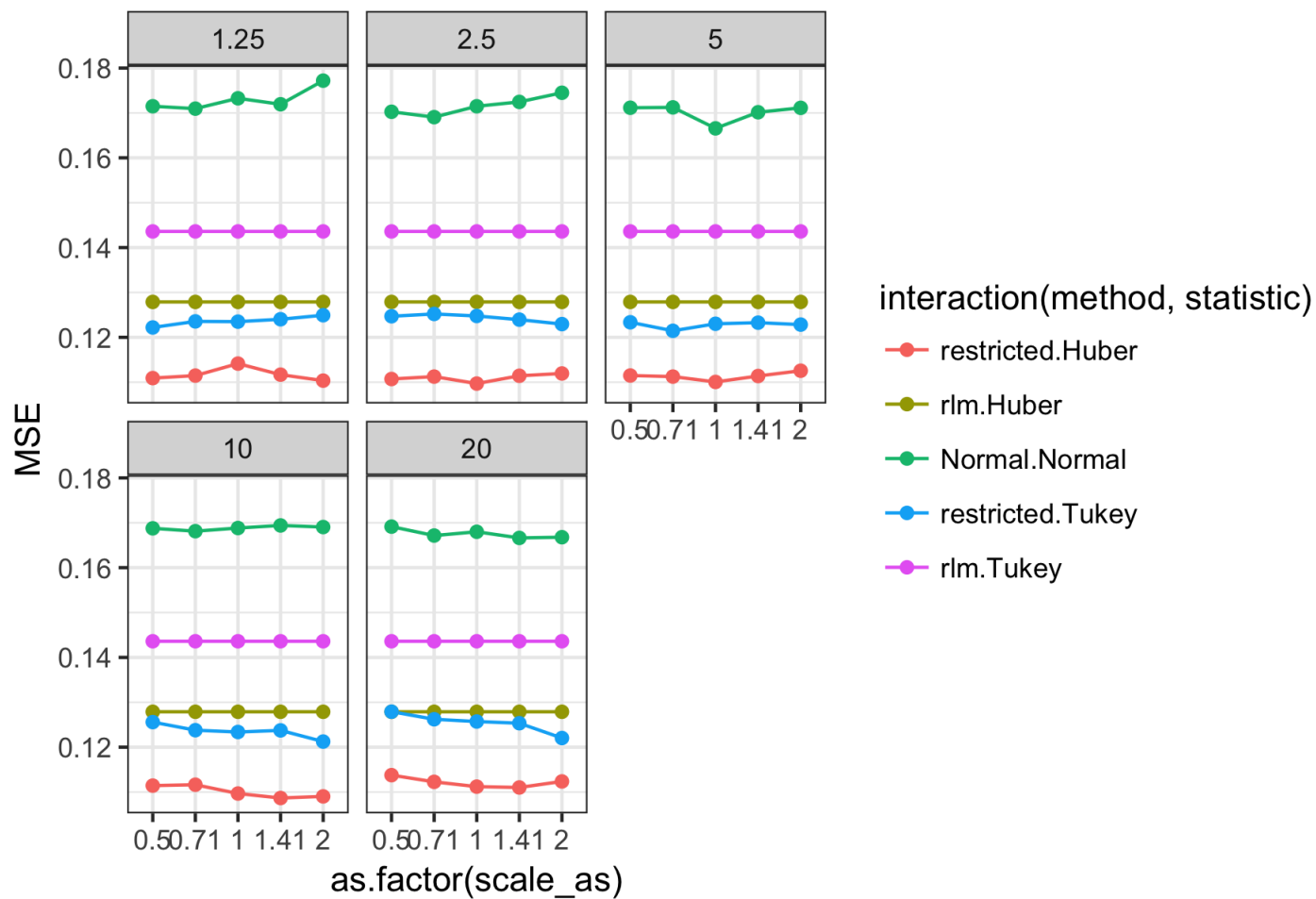
a variety of values representing different levels of prior knowledge. For each we set $b_s = 4a_sc_s$ resulting in a prior mean for each σ_i^2 of $\frac{4c_s a_s}{a_s - 1}$, $a_s > 1$. The larger a_s , the more informative the prior. With $c_s = 1$ the shrinkage (for large a_s) is to the true value of $\sigma^2 = 4$ of the variance of the good component of data in the data generating model. We consider $a_s = 1.25, 2.5, 5, 10, 20$ and $c_s = 1/2, 1/\sqrt{2}, 1, \sqrt{2}, 2$. Values of $c_s \neq 1$ will result in shrinkage towards the wrong value of σ^2 with strength growing with a_s .

A single (maybe need to do more...each run through takes about 3 hours on my laptop and current code, maybe 10 different sets would suffice) set of data is generated from (15). The models compared are: the full model (16), the two restricted likelihood versions of this full model, classical robust linear models fit individually to each group.

We compare fits of each model using $MSE = \frac{1}{90} \sum_{i=1}^{90} (\hat{\theta}_i - \theta_i)^2$ with $\hat{\theta}_i$ the estimate of θ_i from the corresponding model.

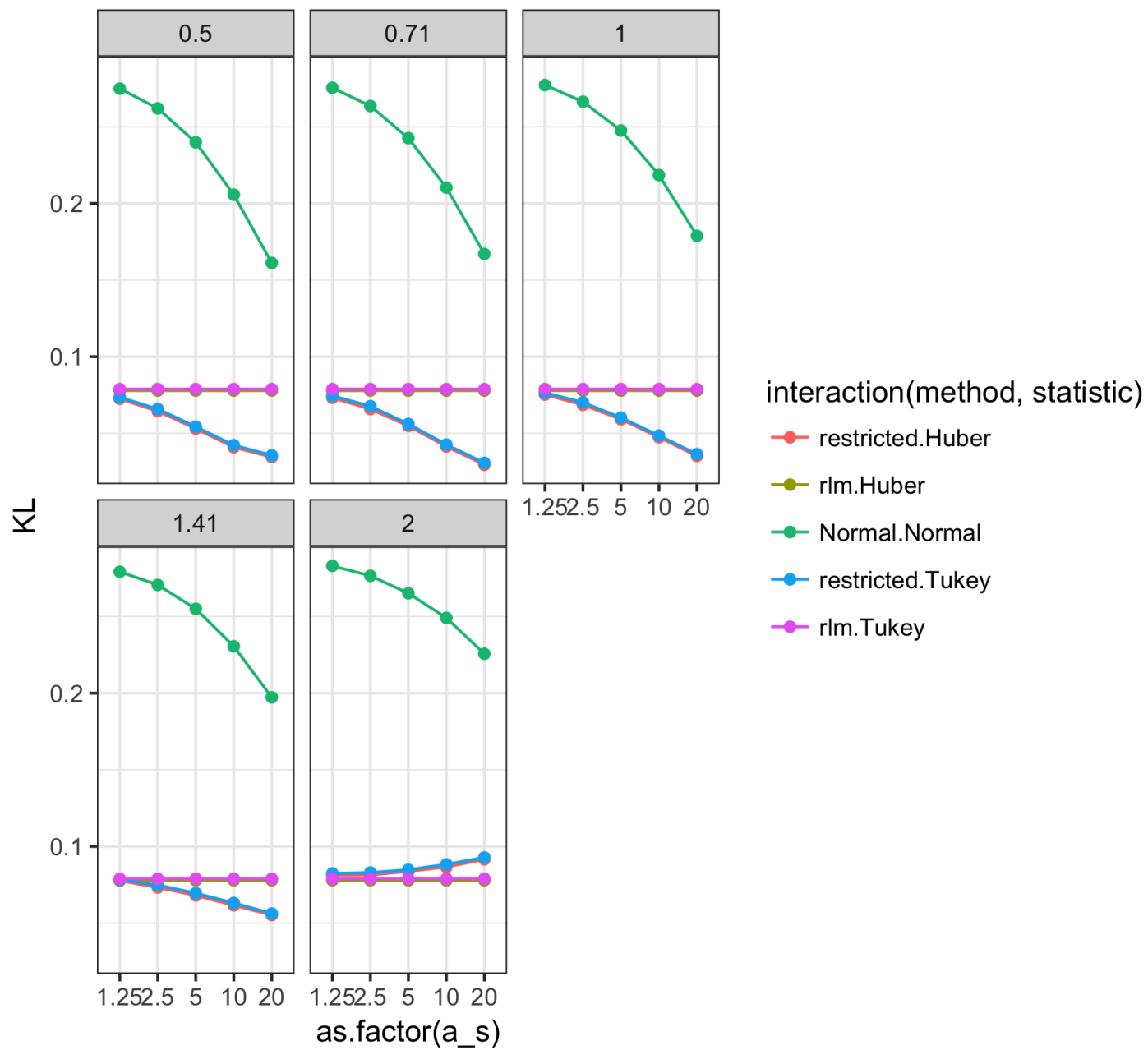
Results for MSE

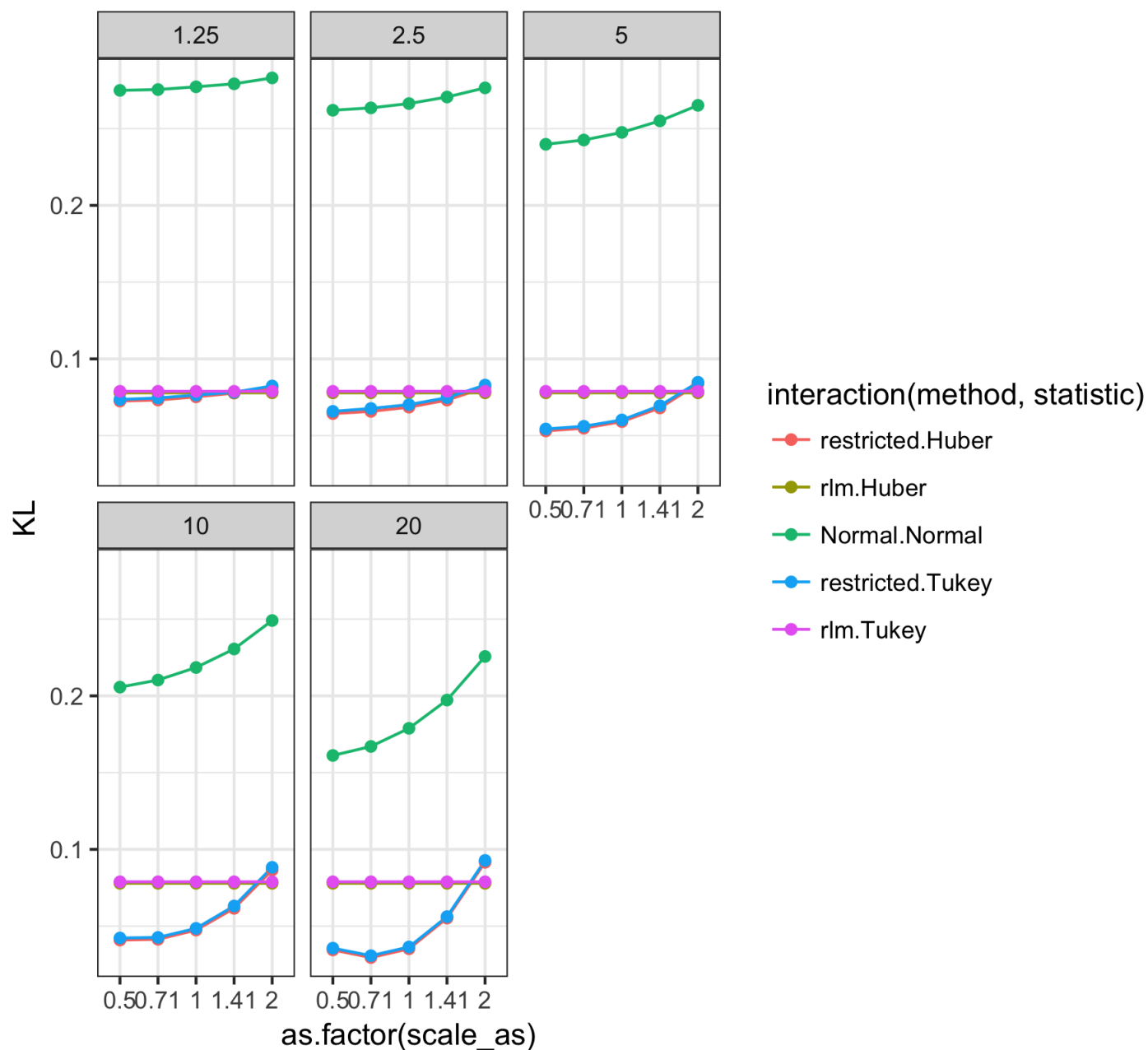




Big picture - restricted methods beating corresponding robust regressions (labeled rlm). MSE robustness to prior on σ_i^2

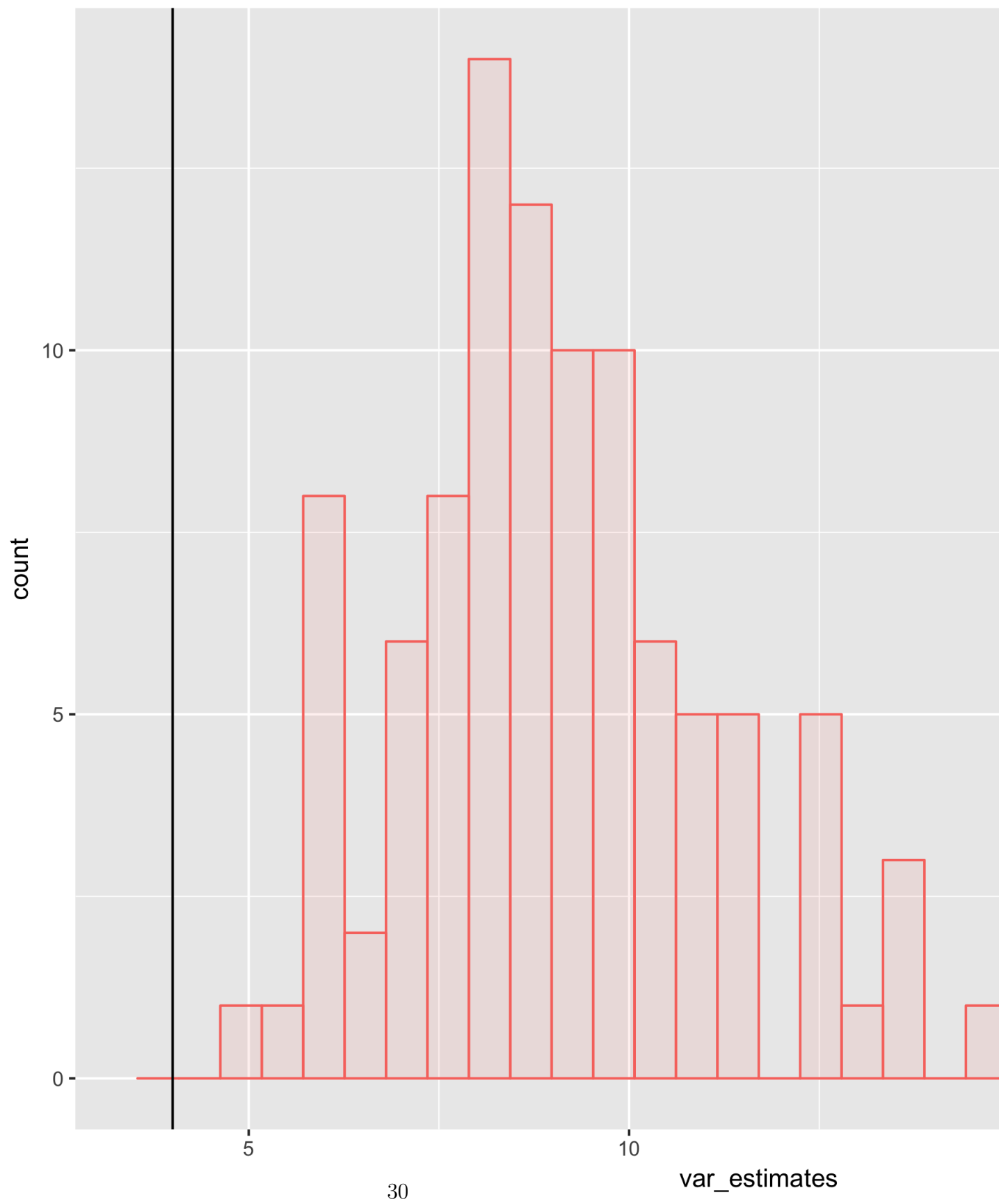
Results for KL (plots are average of the KLs computed for each group):





One explanation for the idea that 'shrinking towards smaller values' may do slightly better than shrinking toward the true value is the fact that we used default tuning parameters to define M-Estimators. For the amount of contamination in each group, the expected value of the variance estimate (Huber's proposal 2) is larger than $\sigma^2 = 4$. The histogram below demonstrates a sample of variance estimates for data

generated from one of the contamination groups....the estimates are consistently above 4. Thus it appears the prior mean must be smaller than the true value to get the 'correct' amount of shrinkage. There is a suggestion that if the prior is too strong (large a_s), at some point, shrinking to too small a value degrades performance....which would be expected.



6 Applications

We illustrate the methods developed in Sections 2 and 4 with a pair of regression models for data from Nationwide Insurance Company, which concern prediction of the performance of insurance agencies. The data contain outliers and are subject to model misspecification. In particular, a group of the data do not follow the same generative process as the data of interest. It would be extremely challenging to model some features of the data. In our analysis, we follow the standard practice when demonstrating the benefits of robust methods. We work with a naive model for the data which ignores certain features of the problem. We do this both to create a situation where all can agree that the model for the full data \mathbf{y} is imperfect and to preserve the confidentiality of selected aspects of modelling done by Nationwide. We wish to provide inference for the ‘good’ portion of the data. The two models we fit either treat the analysis as a single regression or as a collection of related regressions. Details of the models, prior distributions, and conditioning statistics are given in the next two subsections.

6.1 Nationwide Data

The Nationwide Insurance Company sells many of its insurance policies through agencies which provide direct service to policy holders. The contractual agreements between Nationwide and these agencies vary. Of major interest to Nationwide is the prediction of future performance of agencies where, for our purposes, performance is measured by the total number of households an agency services (‘household count’). A serviced household is one in which at least one person living at that residence has at least one policy written through the agency. We used data from previous years to build a model to forecast future household count. In particular, we use agency char-

acteristics, as measured during a single month in 2010, to predict household counts in the corresponding month in 2012. The characteristics used are household count and two measurements of agency size/experience. The two measurements of agency size/experience are, roughly, the number of employed persons at the agency and the length of time the agency has been affiliated with Nationwide. The household counts (response and predictor) have been square rooted to stabilize variance. The data are proprietary, and to mask them all variables have been individually centered and scaled and identifiers (agency/agent names and state labels) have been removed. All subsequent analysis is done on this scale. As an exploratory view, a plot of the square root of count in 2012, against that in 2010 is shown in Figure 5. The different colors represent the varying contractual agreements as they stood in 2010. ‘Type 1’ agencies are of special interest. Among the open agencies, a strong linear correlation exists. The specific linear relationship depends on agency type. The data are characterized by a large number of agencies which were open in 2010 but closed sometime before 2012, as represented by the horizontal band at 0. We use these data as a test bed for our techniques, fitting models that do not account for agency closures or contract type. Our expectation is that ~~the incomplete restricting the~~ likelihood will facilitate prediction for the good part of the data.

6.2 Regression model

The first analysis that we consider is based on a single regression. We use the following standard normal theory regression model

$$\boldsymbol{\beta} \sim N_p(\boldsymbol{\mu}_0, \Sigma_0); \quad \sigma^2 \sim IG(a_0, b_0); \quad y_i = \mathbf{x}_i^\top \boldsymbol{\beta} + \epsilon_i, \quad \epsilon_i \stackrel{iid}{\sim} N(0, \sigma^2), \quad i = 1, \dots, n, \quad (17)$$

where $\boldsymbol{\beta}$ is a four dimensional vector ($p = 4$) of regression coefficients for the intercept, square root of count in 2010, and the two size/experience measures, and y_i is the square rooted household count in 2012 for the i^{th} agency with covariate vector \boldsymbol{x}_i . Although the mean of covariates and response have been removed, we include the intercept as fitting is done on a holdout set to evaluate predictive performance. The hyper-parameters $a_0, b_0, \boldsymbol{\mu}_0$ and Σ_0 are all fixed and set from a robust regression fit to the data from the time period two years before. Letting $\hat{\boldsymbol{\beta}}$ represent the estimate of the coefficients from this fit we set $\boldsymbol{\mu}_0 = \hat{\boldsymbol{\beta}}$ and $\Sigma_0 = n \cdot \text{var}(\hat{\boldsymbol{\beta}})$ where here n is the sample size of the prior data set. The hyperparameters for σ^2 are set so that the prior mean is s^2 , the estimated variance from the robust regression, and the spread of the prior covers the range of plausible values with high probability. All values are then transformed appropriately to match the current scale of the data. In the end we take $\boldsymbol{\mu}_0 = (0.18, 0.81, 0.01, -0.02)^\top$ and set the mean of σ^2 to 0.014 and standard deviation to 0.033.

We compare four Bayesian models: the standard Bayesian normal theory model, two restricted likelihood models, both with simultaneous M-estimators, and a heavy-tailed model. For the restricted likelihood methods we use the same simultaneous M-estimators as in Section ?? adapted to linear regression. The heavy-tailed model replaces the normal sampling density in (17) with a t -distribution with $\nu = 3$ degrees of freedom. We also fit the corresponding classical robust regressions and a least squares regression.

6.2.1 Method of model comparison

We wish to examine the performance of the models in a fashion that preserves the essential features of the problem. Since we are concerned with outliers and model misspecification, we understand that our models are imperfect and so prefer to use

an out-of-sample measure of fit. This leads us to cross-validation. We repeatedly split the data into training and validation sets. We fit the model to the training data and assess its performance on the validation data.

The presence of numerous outliers in the data implies that both training and validation data will contain outliers. For this reason, the evaluation must be robust to a certain fraction of bad data. The two main strategies are to robustify the evaluation function (e.g., Ronchetti et al., 1997) or to retain the desired evaluation function and trim cases (Jung et al., 2014). Here, we pursue the trimming approach with log predictive density for the Bayesian models and log plug-in maximum likelihood for the classical fits used as the evaluation function.

The trimmed evaluation proceeds as follows in our context. The evaluation function for case i in the hold-out data is the log predictive density, say $\log(f(y_i))$, with the conditioning on the summary statistic suppressed. The trimming fraction is set at $0 \leq \alpha < 1$. To score a method, we first identify a base method. Denote the predictive density under this method by $f_b(y)$. Under the base method, $\log(f_b(y_i))$ is computed for each case in the validation sample, say $i = 1, \dots, M$. Order the validation sample according to the ordering of $\log(f_b(y_i))$ and denote this ordering by $y_{(1)}^b, y_{(2)}^b, \dots, y_{(M)}^b$. That is, for $i < j$ $\log(f_b(y_{(i)}^b)) < \log(f_b(y_{(j)}^b))$. All of the methods are then scored on the validation sample with the mean trimmed log marginal pseudo likelihood,

$$TLM_b(A) = (M - [\alpha M])^{-1} \sum_{i=[\alpha M]+1}^M \log(f_A(y_{(i)}^b)),$$

where f_A corresponds to the predictive distribution under the method “A” being scored. In other words, the $[\alpha M]$ observations with the smallest values of $\log(f_b(y))$ are removed from the validation sample and all of the methods are scored using only the remaining $M - [\alpha M]$ observations. This process is advantageous to the base

method. A method that performs poorly when it is the base method is discredited. For a complete evaluation, we allow each method to appear as the base method. For brevity, we present only a selection of results in our subsequent analyses.

6.2.2 Comparison of predictive performance

Model performance is assessed using the mean and standard deviation of the TLM across 100 different splits into training and validation samples. First, we include all observations in each validation sample to calculate TLM for each split. We then repeat the evaluation using only certain subsets of the validation sample that are of special interest. Subsets include open agencies, open ‘Type 1’ agencies, and ‘Type 1’ agencies. For brevity, we include results for the ‘Type 1’ agencies only. As noted, assessing model predictions on this set of agencies is of special interest to the company. A range of training sample sizes was used and we include results from $n = 25, 100, 1000$, and 2000 out of a total of 3180 agencies. The trimming fraction, α , ranges from 0 to 0.3. A classical robust regression to the prior data assigns zero weight to around 16% of observations; in essence removing these from the analysis. This informed the range of trimming fractions chosen. In practice, we would set α slightly larger than 0.16.

Model evaluation for ‘Type 1’ agencies is shown in Figure 6 for training sample sizes $n = 25, 100$, and 1000. The t -model is used as the base method to compute TLM. The models pictured are: classical robust regression with Tukey’s ψ function (rlm-T), restricted likelihood with Tukey ψ (restr.-T), classical robust regression with Huber’s ψ function (rlm-H), restricted likelihood with Huber’s ψ (restr.-H), and the thick tailed t -model (t). The normal theory models perform poorly due to the numerous outliers and are left out of the figures. Appearing in the figures are the mean TLM across validations set for each model and each trimming fraction, α (along the x -axis).

The error bars depicted are one standard deviation of the TLM above and below the mean. The range of the vertical axis is chosen to enhance important features and as a result, some evaluation measures extend below this range. In particular, the restricted likelihood methods perform poorly if no trimming is done; reflecting that these methods are not intended to fit well to outliers. Recall that we expect about 15-16% outliers in the validation sets, thus trimming fractions slightly larger than this amount are needed in order to assess fits to the ‘good’ data. For $n = 25$, the thick tailed model prevails across trimming fractions, although less so for $\alpha \geq 0.15$. For sample sizes as low as $n = 100$, the restricted likelihood methods outperform the heavy-tailed model with the Tukey version performing the best. The stronger performance of restricted likelihood based on Tukey’s method and the t model is to be expected, as many of the residuals are so extreme that trimming is better than winsorizing (as Huber’s method effectively does). As expected, with enough data, the Bayesian methods and their classical counterparts perform similarly, although there is a persistent slight edge in favor of the Bayesian restricted likelihood methods. We attribute this advantage to the weakly informative prior distribution which pulls the estimates slightly toward better values. The similarity occurs as early as $n = 100$.

6.3 Hierarchical regression model

Nationwide agencies span many states and insurance regulations and the competitive environment varies between states. A natural extension to the previous analysis is a hierarchical regression model, grouping agencies within each state to reflect similar business environments. Using the same study design with the same training and validation splits, we re-analyze the data using the following hierarchical regression

model:

$$\begin{aligned} \boldsymbol{\beta} &\sim N_p(\boldsymbol{\mu}_0, a\Sigma_0); \quad \boldsymbol{\beta}_j \stackrel{iid}{\sim} N_p(\boldsymbol{\beta}, b\Sigma_0); \quad \sigma_j^2 \sim IG(a_0, b_0); \\ \mathbf{y}_{ij} &= \mathbf{x}_{ij}^\top \boldsymbol{\beta}_j + \epsilon_{ij}, \quad \epsilon_{ij} \stackrel{iid}{\sim} N(0, \sigma_j^2), \quad i = 1, \dots, n_j, \quad j = 1, \dots, J \end{aligned} \tag{18}$$

where y_{ij} represents the i^{th} observation in the j^{th} state, n_j is the total number of agencies in each state, and J is the number of states. \mathbf{x}_{ij} is a four dimensional vector comprised of the same covariates as above. $\boldsymbol{\beta}_j$ represents the individual regression coefficient vector for state j . We match this model to the non-hierarchical model in several ways. First, $\boldsymbol{\mu}_0$, Σ_0 , a_0 , and b_0 are fixed as before. We constrain $a+b=1$ in an attempt to partition the total variance between the individual $\boldsymbol{\beta}_j$'s and the overall $\boldsymbol{\beta}$. We take $b \sim \text{beta}(v_1, v_2)$. Using the previous data set, we assess the variation between individual estimates of the $\boldsymbol{\beta}_j$ to set v_1 and v_2 to allow for a reasonable amount of shrinkage. To allow for dependence across the σ_j^2 we first take $(z_1, \dots, z_J) \sim N_J(\mathbf{0}, \Sigma_\rho)$ with $\Sigma_\rho = (1 - \rho)I + \rho\mathbf{1}\mathbf{1}^\top$. Then we set $\sigma_j^2 = H^{-1}(\Phi(z_j))$ where H is the cdf of an $IG(a_0, b_0)$ and Φ is the cdf of a standard normal. This results in the specified marginal distribution, while introducing correlation via ρ . We assume $\rho \sim \text{beta}(a_\rho, b_\rho)$ with mean $\mu_\rho = a_\rho/(a_\rho + b_\rho)$ and precision $\psi_\rho = a_\rho + b_\rho$. The parameters μ_ρ and ψ_ρ are given beta and gamma distributions, respectively. We fix the parameters of these distributions by again considering fits to individual states from the previous data set. More precise details on setting v_1, v_2 and the the priors on μ_ρ and ψ_ρ are given in the appendix. We note that we tried a range of other fixed hyper-parameters resulting in negligible differences in the results.

Using the same techniques as in the previous section, we fit the normal theory hierarchical model above, a thick tailed t version with $\nu = 3$ d.f., and two restricted likelihood versions (Huber's and Tukey's) of the model. For the incomplete restricted

methods, we condition on robust regression estimates fit separately within each state. We also fit classical robust regression counterparts and a least squares regression separately within each state.

We digress briefly to note that for the restricted likelihood methods no additional computational strategies outside of those discussed in Section 4.2 are needed to fit the hierarchical models described here. Since we condition on statistics which are computed within each state, the model’s conditional independence between the states allows the data augmentation described earlier to be performed independently within each state. Updates of hyperparameters follow conventional MCMC procedures. We note that different types of statistics could be chosen for each state, if desired, allowing for a large amount of flexibility.

Selected results for the hierarchical fits appear in Figure 7. Hierarchical models naturally require more data and so we consider only training sizes of $n = 1000$ and 2000 . Again, the t -model is used as the base method for computing TLM. Trimming fractions between 0.15 and 0.3 are displayed, as patterns for smaller trimming fractions are similar to those from the non-hierarchical fits. That is, without sufficient trimming, the Bayesian restricted likelihood fits’ evaluation measure is poor. Again, the normal theory fits, both Bayesian and classical, perform poorly and are left out of the figures. We see that the restricted likelihood with Tukey’s estimator performs best in each case (assuming sufficient trimming). Huber’s version also tops the thick tailed model for $n = 2000$. The Bayesian restricted likelihood fits considerably outperform their respective individual classical robust fits for training size of $n = 1000$. This observation remains, though marginally so, for $n = 2000$. The advantage of the hierarchical models seen here is due to the pooling of information across states, resulting in better predictive performance as compared to both the thick tailed competitor as well the respective classical fits.

6.4 Comparison of hierarchical and non-hierarchical fits

The performance of the methods for the hierarchical and non-hierarchical models can be contrasted through our cross validations studies. We focus on Tukey’s and Huber’s conditioning statistic and concentrate our evaluation on the ‘Type 1’ agencies. Table 1 displays the mean TLM for each model and range of trimming fractions. Our summary below focuses exclusively on realistic trimming fractions, $\alpha \geq 0.15$, and Tukey’s conditioning statistic.

We first note that for the non-hierarchical model, there is little difference between mean TLM for $n = 1000$ and $n = 2000$, with the numbers differing only in the third decimal place (see rows 1 and 3 of the table). This is due to the posterior predictive distributions having stabilized. The mean TLMs for the hierarchical model show a greater change with increases of about 0.05 to 0.08 as the training sample size changes from 1000 to 2000 (see rows 2 and 4 of the table). For calibration, the mean TLM for a normal with mean 0.5 and variance 1 is approximately this size when trimming is done under a standard normal base model. Thus, the increase in mean TLM is substantial. We attribute the change for the hierarchical model to the improvement in fits, particularly for states with fewer agencies.

Direct comparison of the hierarchical and non-hierarchical models shows that, for $n = 1000$, the non-hierarchical model has uniformly (for α of interest) better mean TLM (rows 1 and 2). The differences are substantial, and the summaries primarily reflect greater stability of fits on a state-by-state basis under the non-hierarchical model. To a lesser extent, they reflect variation in the evaluation criterion which stems from modest validation sample size, particularly with larger trimming fractions. The trimmed cases are not proportionally distributed across states. The pattern changes for $n = 2000$ (rows 3 and 4), with the hierarchical model showing larger mean TLMs for trimming fractions 0.15 and 0.20. The improvement reflects the

	Trimming fraction (α)			
	0.15	0.2	0.25	0.3
Tukey ($n = 1000$)				
Non-Hier.	1.072 (0.014)	1.179 (0.022)	1.226 (0.029)	1.255 (0.033)
Hier.	1.021 (0.063)	1.110 (0.070)	1.157 (0.067)	1.187 (0.065)
Tukey ($n = 2000$)				
Non-Hier.	1.068 (0.029)	1.178 (0.007)	1.225 (0.011)	1.254 (0.014)
Hier.	1.094 (0.041)	1.189 (0.036)	1.221 (0.033)	1.242 (0.028)
Huber ($n = 1000$)				
Non-Hier.	1.020 (0.020)	1.114 (0.035)	1.157 (0.041)	1.184 (0.045)
Hier.	0.861 (0.073)	0.937 (0.079)	1.001 (0.074)	1.063 (0.064)
Huber ($n = 2000$)				
Non-Hier.	1.015 (0.021)	1.112 (0.014)	1.154 (0.019)	1.181 (0.023)
Hier.	0.930 (0.041)	1.014 (0.043)	1.080 (0.035)	1.148 (0.027)

Table 1: Mean (standard deviation) of TLM for ‘Type 1’ agencies for the Bayesian restricted likelihood non-hierarchical and hierarchical models for $n = 1000$ and 2000 .

ability of the hierarchical model to capture differences in regressions across the states which is realized when the training sample size is large enough. We attribute the better performance of the non-hierarchical model for the largest trimming fractions to variation in the evaluation.

7 Discussion

Many routine choices in an analysis react to the gap between reality and the statistical model, where a bit of set-up work improves inferential performance. Often, these choices can be recast in the framework of restricted likelihood presented here, lending them more formality and facilitating development of theoretical results. But a much greater benefit of our framework is that it leads us to blend classical estimation with Bayesian methods. Here, we use the likelihood from robust regression estimators to move from prior distribution to posterior distribution. Conditioning on the estimator, the update follows Bayes’ Theorem exactly. Computation is driven by MCMC meth-

ods, requiring only a modest supplement to existing algorithms. In another context, we might condition on the results of a set of estimating equations, designed to enforce lexical preferences for those features of the analysis considered most important, yet still producing inferences for secondary aspects of the problem. For example, the computational strategies we devised here allow us to apply the method to inference on quantiles of a regression model. In other settings, we envision conditioning on a mix of estimators and some of the observed data.

The framework we propose allows us to retain many benefits of Bayesian methods: it requires a full and complete model for the data; it lets us combine various sources of information both through the use of a prior distribution and through creation of a hierarchical model; it guarantees admissibility of our decision rules among the class based on the summary statistic $T(\mathbf{y})$; and it naturally leads us to focus on predictive inference.

This same framework retains many of the benefits of classical estimation. Great ingenuity has been used to create a wide variety of estimators in this tradition, many of which are designed to handle specific flaws in the model. The estimators are typically accompanied by asymptotic results on consistency and distribution. Many of these results carry over to our blend of classical and Bayesian methods, although regularity conditions differ. We expect our procedures to have strong large sample performance, especially in settings where pooling of information is of value.

This framework opens a number of questions, including a need to revisit such issues as model selection, model averaging for predictive performance, and the role of diagnostics. Perhaps the biggest question is which summary statistic to choose. For this, we recommend a choice based on the analyst’s understanding of the problem, model, reality, deficiencies in the model, inferences to be made, and the relative importance of various inferences. **In our words, to provide desirable inference, we recommend**

use of robust and relevant summary statistics in conjunction with Bayesian models.

8 Appendix

8.1 Proofs

Proof of Theorem 4.1.

Proof.

$$s(X, \mathbf{y}) = s\left(X, \frac{s(X, \mathbf{y}_{obs})}{s(X, \mathbf{z}^*)} \mathbf{z}^* + X \left(\mathbf{b}(X, \mathbf{y}_{obs}) - \mathbf{b}(X, \frac{s(X, \mathbf{y}_{obs})}{s(X, \mathbf{z}^*)} \mathbf{z}^*) \right)\right) \quad (19)$$

$$= \frac{s(X, \mathbf{y}_{obs})}{s(X, \mathbf{z}^*)} s(X, \mathbf{z}^*) = s(X, \mathbf{y}_{obs}), \quad \text{and} \quad (20)$$

$$\mathbf{b}(X, \mathbf{y}) = \mathbf{b}\left(X, \frac{s(X, \mathbf{y}_{obs})}{s(X, \mathbf{z}^*)} \mathbf{z}^* + X \left(\mathbf{b}(X, \mathbf{y}_{obs}) - \mathbf{b}(X, \frac{s(X, \mathbf{y}_{obs})}{s(X, \mathbf{z}^*)} \mathbf{z}^*) \right)\right) \quad (21)$$

$$= \mathbf{b}(X, \frac{s(X, \mathbf{y}_{obs})}{s(X, \mathbf{z}^*)} \mathbf{z}^*) + \mathbf{b}(X, \mathbf{y}_{obs}) - \mathbf{b}(X, \frac{s(X, \mathbf{y}_{obs})}{s(X, \mathbf{z}^*)} \mathbf{z}^*) \quad (22)$$

$$= \mathbf{b}(X, \mathbf{y}_{obs}) \quad (23)$$

□

Proof of Lemma 4.2.

Proof. We first show that $\nabla s(X, \mathbf{y}) \in \mathcal{C}^\perp(X)$. Recall that $H = I - Q$. By the regression invariance property C7 of s , we have

$$s(X, \mathbf{y}) = s(X, Q\mathbf{y} + H\mathbf{y}) = s(X, Q\mathbf{y}). \quad (24)$$

Thus, by the chain rule $\nabla s(X, \mathbf{y}) = Q\nabla s(X, Q\mathbf{y}) = Q\nabla s(X, \mathbf{z})$. Hence $X^\top \nabla s(X, \mathbf{y}) = 0$ as desired. From equation (24), all vectors $\mathbf{z}' \in \Pi(\mathcal{A})$ satisfy $s(X, \mathbf{z}') = s(X, \mathbf{y}) = s(X, \mathbf{y}_{obs})$, and so all directional derivatives of s along each tangent \mathbf{v} to $\Pi(\mathcal{A})$ in

$\mathcal{C}^\perp(X)$ at \mathbf{z} are equal to 0 (i.e., $\nabla s(X, \mathbf{z}) \cdot \mathbf{v} = 0$). Thus $\nabla s(X, \mathbf{z})$ is orthogonal to $\Pi(\mathcal{A})$ at \mathbf{z} . Since $\Pi(\mathcal{A})$ has dimension $n - p - 1$, $\nabla s(X, \mathbf{z})$ gives the unique (up to scaling and reversing direction) normal in the $n - p$ dimensional $\mathcal{C}^\perp(X)$. \square

Proof of Lemma 4.3

Proof. Without loss of generality, assume the columns of X form an orthonormal basis for $\mathcal{C}(X)$ and likewise the columns of W form an orthonormal basis for $\mathcal{C}^\perp(X)$. With earlier notation, $H = XX^\top$ and $Q = WW^\top$. The set \mathcal{A} is defined by the $p + 1$ equations $s(X, \mathbf{y}) = s(X, \mathbf{y}_{obs})$, $b_1(X, \mathbf{y}) = b_1(X, \mathbf{y}_{obs}), \dots, b_p(X, \mathbf{y}) = b_p(X, \mathbf{y}_{obs})$. Consequently, the gradients are orthogonal to \mathcal{A} . Let $\nabla \mathbf{b}(X, \mathbf{y})$ denote the $n \times p$ matrix with columns $\nabla b_1(X, \mathbf{y}), \dots, \nabla b_p(X, \mathbf{y})$. We seek to show the $n \times (p + 1)$ matrix $[\nabla \mathbf{b}(X, \mathbf{y}), \nabla s(X, \mathbf{y})]$ has rank $p + 1$. Using property C5, we have that

$$\mathbf{b}(X, \mathbf{y}) = \mathbf{b}(X, Q\mathbf{y} + H\mathbf{y}) = \mathbf{b}(X, Q\mathbf{y}) + X^\top \mathbf{y}$$

Then $\nabla \mathbf{b}(X, \mathbf{y}) = Q\nabla \mathbf{b}(X, Q\mathbf{y}) + X$ and

$$[XX^\top, WW^\top]^\top [\nabla \mathbf{b}(X, \mathbf{y}), \nabla s(X, \mathbf{y})] = \begin{pmatrix} X & \mathbf{0} \\ WW^\top \nabla \mathbf{b}(X, \mathbf{y}) & \nabla s(X, \mathbf{y}) \end{pmatrix} \quad (25)$$

The last column comes from Lemma 4.2. The matrix $[XX^\top, WW^\top]^\top$ is of full column rank (rank n), and so the rank of $[\nabla \mathbf{b}(X, \mathbf{y}), \nabla s(X, \mathbf{y})]$ is the same as the rank of the matrix on the right hand side of (25). This last matrix has rank $p + 1$ since $\nabla s(X, \mathbf{y}) \neq \mathbf{0}$ by C8, and so does $[\nabla \mathbf{b}(X, \mathbf{y}), \nabla s(X, \mathbf{y})]$. \square

Proof of Lemma 4.4

Proof. P is the projection of the columns of A onto $\mathcal{C}^\perp(X)$. For this to result in a loss of rank, a subspace of $\mathcal{T}_y(\mathcal{A})$ must belong to $\mathcal{C}(X)$. Following property C5, for

an arbitrary vector $X\mathbf{v} \in \mathcal{C}(X)$, $\mathbf{b}(X, \mathbf{y} + X\mathbf{v}) = \mathbf{b}(X, \mathbf{y}) + \mathbf{v}$. From the property, we can show that the directional derivative of \mathbf{b} along $X\mathbf{v}$ with $\mathbf{v} \neq \mathbf{0}$ is \mathbf{v} , which is a nonzero vector. Hence $X\mathbf{v} \notin \mathcal{T}_{\mathbf{y}}(\mathcal{A})$. \square

Proof of Corollary 4.7

Proof. The corollary relies on a lemma and theorem from Miao and Ben-Israel (1992) which we restate slightly for brevity of presentation. The principal angles between subspaces pluck off a set of angles between subspaces, from smallest to largest. The number of such angles is the minimum of the dimensions of the two subspaces. Miao and Ben-Israel's first result (their Lemma 1) connects these principal angles to a set of singular values, and hence to volumes.

Lemma 8.1. (*Miao, Ben-Israel*) *Let the columns of $Q_L \in \mathbb{R}^{n \times l}$ and $Q_M \in \mathbb{R}^{n \times m}$ form orthonormal bases for linear subspaces L and M respectively, with $l \leq m$. Let $\sigma_1 \geq \dots \geq \sigma_l \geq 0$ be the singular values of $Q_M^\top Q_L$. Then $\cos \theta_i = \sigma_i, i = 1, \dots, l$ where $0 \leq \theta_1 \leq \theta_2 \leq \dots \leq \theta_l \leq \frac{\pi}{2}$ are the principal angles between L and M .*

Miao and Ben-Israel's second result (their Theorem 3) makes a match between the principal angles between a pair of subspaces and the principal angles between their orthogonal complements.

Theorem 8.2. (*Miao, Ben-Israel*) *The nonzero principal angles between subspace L and M are equal to the nonzero principal angles between L^\perp and M^\perp .*

To establish the corollary, we appeal to Lemma 8.1 and Theorem 8.2. Translating Miao and Ben Israel's notation, we have $M = \mathcal{C}^\perp(X)$, $Q_M = W$, $L = \mathcal{T}_{\mathbf{y}}(\mathcal{A})$, and $Q_L = A$. By Theorem 8.2, the nonzero principal angles between $\mathcal{T}_{\mathbf{y}}(\mathcal{A})$ and $\mathcal{C}^\perp(X)$ are the same as the nonzero principal angles between $\mathcal{T}_{\mathbf{y}}^\perp(\mathcal{A})$ and $\mathcal{C}(X)$. By 8.1,

the non-unit singular values of $W^\top A$ are the same as the non-unit singular values of $U^\top B$. \square

8.2 Setting the hierarchical prior values

In setting the priors we use the same previous data set used to set the priors for the non-hierarchical model (Section 6.2) and several heuristic arguments. While the analyses in Section 6.3 set the hyper-parameters using what is described here, the results were not sensitive to these choices. This section describes the heuristics used in setting these prior parameters and is given for completeness. Using the previous data set we fit separate (robust) regressions to each state and a regression to the ~~entire~~ entirety of the data at once. Let the estimates for the fits to each state be $\hat{\beta}_1, \dots, \hat{\beta}_J, \hat{\sigma}_1, \dots, \hat{\sigma}_J$ and the estimates from the single regression be $\hat{\beta}$ and $\hat{\sigma}$. These are classical robust estimates using Tukey's regression and Huber's scale. Let n_j denote the number of observations in the j^{th} state and set $n = \sum n_j$.

First, consider v_1 and v_2 in the prior $b \sim \text{beta}(v_1, v_2)$. In the hierarchical model (18), $b = 0$ implies all the β'_j s are equal (no variation between states) and $b = 1$ implies the β'_j s vary about μ_0 according to $\Sigma_0 = n \cdot \text{var}(\hat{\beta})$ (see Section 6.2). We seek a prior measure for what we think b should be. In other words, how much prior uncertainty should we allow in β as opposed to the uncertainty amongst the β'_j s? Using the prior fit, a measure for uncertainty for β is $\Sigma_{\hat{\beta}} = \text{var}(\hat{\beta})$, the estimate of the covariance from the single regression. For the β'_j s, take $\delta_j = \hat{\beta}_j - \hat{\beta}$ and set the prior uncertainty to $\Sigma_{\delta} = n^{-1} \sum n_j \delta_j \delta_j^\top$. Consider the value $g = \left(|\Sigma_{\delta}| / |\Sigma_{\hat{\beta}}| \right)^{1/p}$. Heuristically, g is measure of the amount of uncertainty between the β'_j s to the amount of uncertainty in β . Now in the prior, we heuristically set the uncertainty in the β'_j s ($b\Sigma_0$) to be approximately equal to $g \cdot \text{var}(\hat{\beta})$. That is, $b\Sigma_0 \approx g \cdot \text{var}(\hat{\beta}) = \frac{g}{n} \Sigma_0$, suggesting $b \approx \frac{g}{n}$. Hence we set $E[b] = \frac{g}{n}$. The precision, $v_1 + v_2$, is set to be relatively high at 20,

completing the specification for the prior on b .

In setting the parameters for the beta prior on μ_ρ and gamma prior on ψ_ρ we first take $\hat{z}_j = \Phi^{-1}(H(\hat{\sigma}_j^2))$. As in the prior we assume $(\hat{z}_1, \dots, \hat{z}_J) \sim N_J(\mathbf{0}, \Sigma_\rho)$ with $\Sigma_\rho = (1-\rho)I + \rho\mathbf{1}\mathbf{1}^\top$ and find the MLE, $\hat{\rho}_{mle}$, and observed inverse Fisher information, $I^{-1}(\rho_{mle})$. The mean of the beta prior on μ_ρ is set to $\hat{\rho}_{mle}$. Its variance is inflated somewhat and set to $2I^{-1}(\hat{\rho}_{mle})$. Since $\text{var}(\rho|\mu_\rho, \psi_\rho) = \mu_\rho(1-\mu_\rho)/(\psi_\rho+1)$ we replace μ_ρ with $\hat{\rho}_{mle}$, $\text{var}(\rho|\mu_\rho, \psi_\rho)$ with $2I^{-1}(\hat{\rho}_{mle})$, and set the mean of the gamma prior on ψ_ρ equal to $\hat{\rho}_{mle}(1-\hat{\rho}_{mle})/(2I^{-1}(\hat{\rho}_{mle})) - 1$. Finally, we arbitrarily set the variance of the gamma prior to be approximately the same as the mean.

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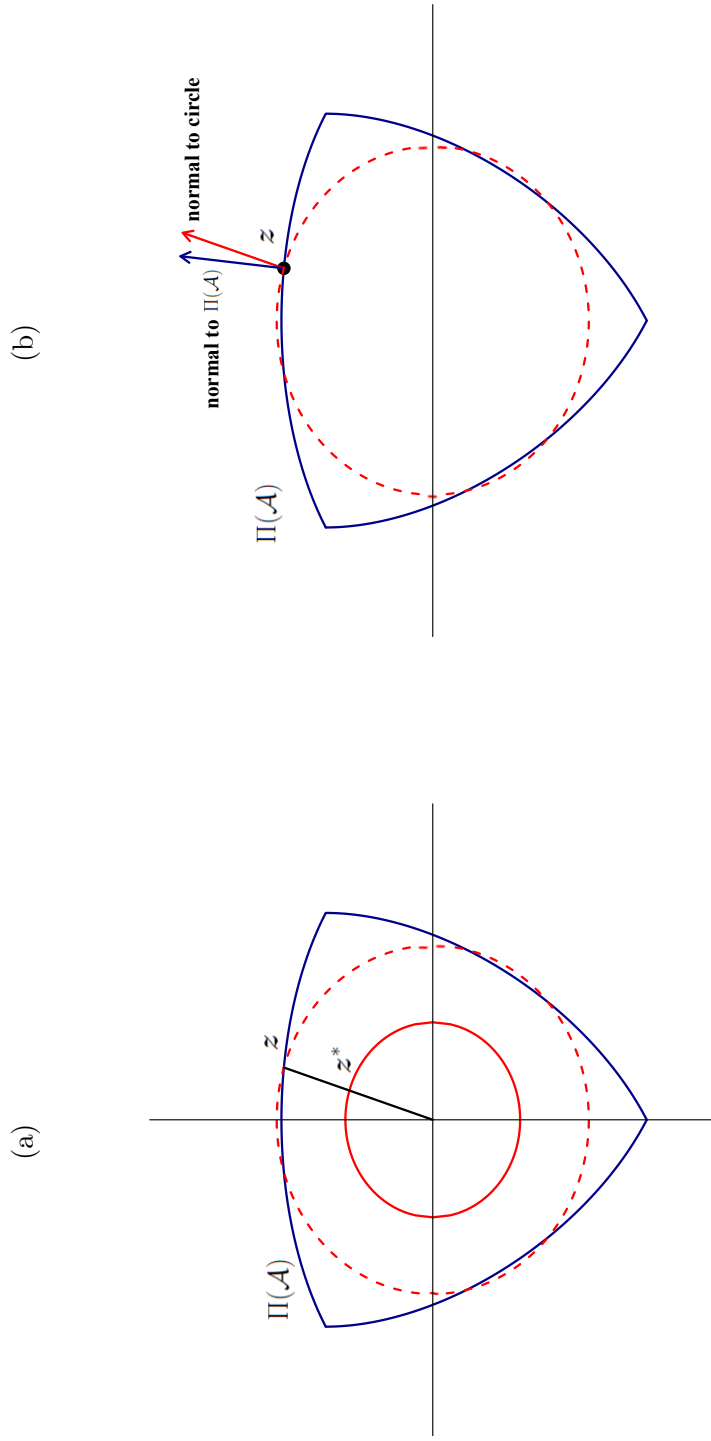


Figure 4: Panel (a) contains a depiction of the stretch from z^* to z . The adjustment for the stretch transforms the density along the unit circle to the density along the circle of radius $\|z\|$ (dashed circle). Panel (b) contains a depiction of the deformation from the distribution along the circle to the distribution along $\Pi(\mathcal{A})$. The adjustment can be seen to be the cosine of the angle between the normals to each manifold.

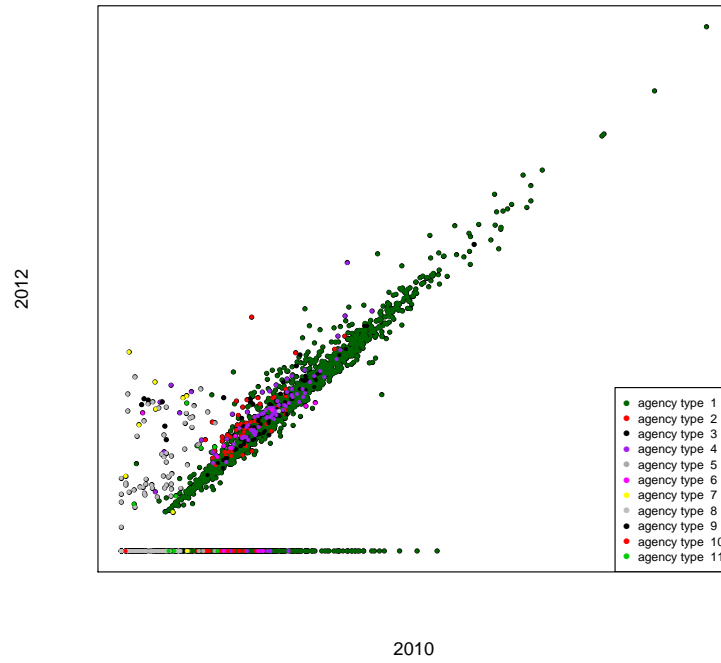
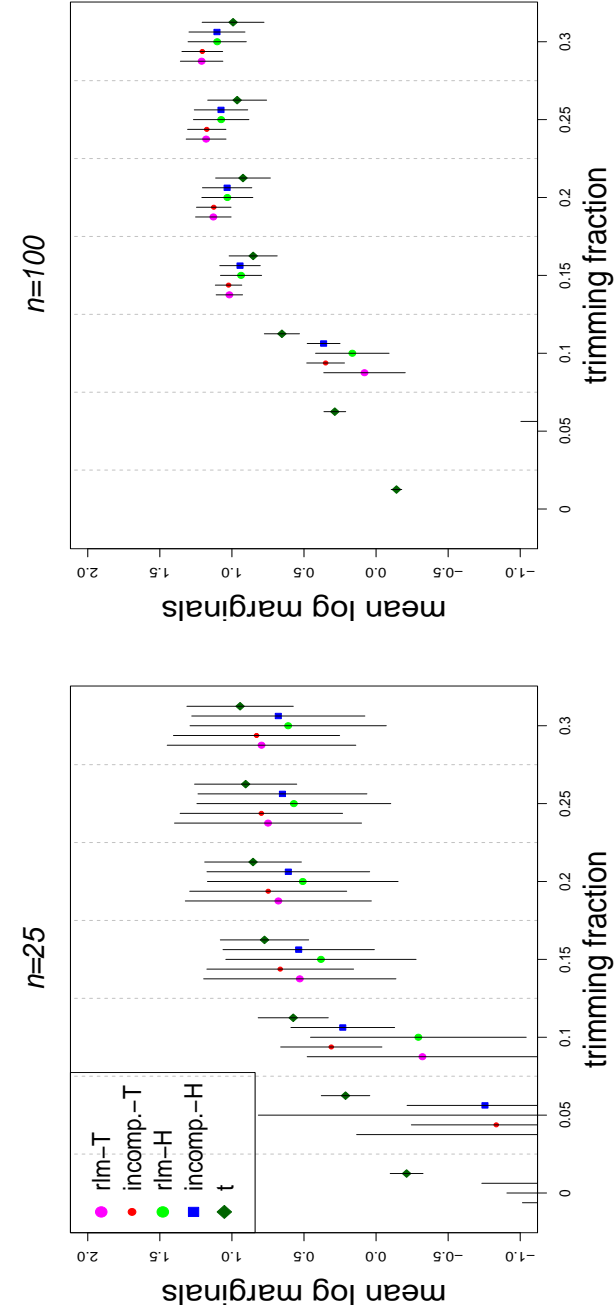


Figure 5: The square root of count in 2012 versus that in 2010 (after centering and scaling). The colors represent the varying contractual agreements as they stood in 2010. Agencies that closed during the 2010-2012 period are represented by the zero counts for 2012. Scalings on the axes are purposely left off for proprietary reasons.



(c)

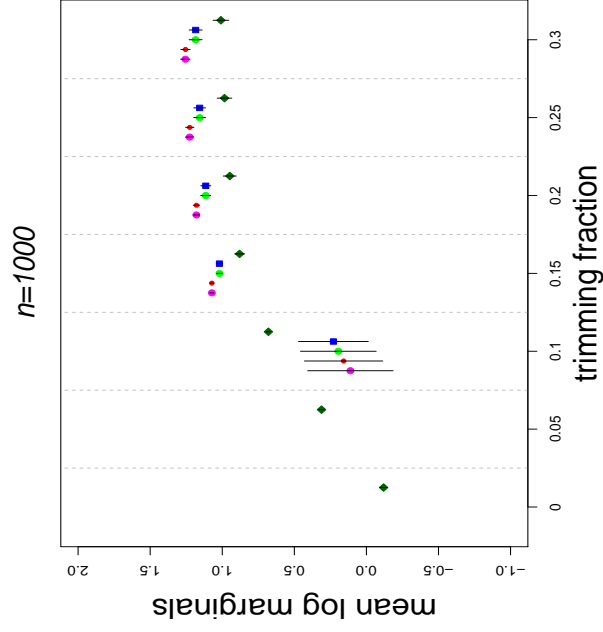


Figure 6: Model evaluation for ‘Type 1’ agencies for training sample sizes of $n = 25, 100$, and 1000 . The t -model is used as the base method to compute TLM. Plotted are the mean TLM for each model against the trimming fraction across the 100 cross-validation samples. Error bars correspond to one standard deviation of TLM above and below the mean. Models are labeled with the following abbreviations: ‘rlm’ corresponds to a classical robust fit, ‘restr.’ corresponds to our restricted likelihood method, and ‘t’ corresponds to the heavy-tailed t -distribution model. The letters ‘T’ and ‘H’ appearing after ‘rlm’ and ‘restr.’ correspond to the use of Tukey’s and Huber’s ψ respectively.

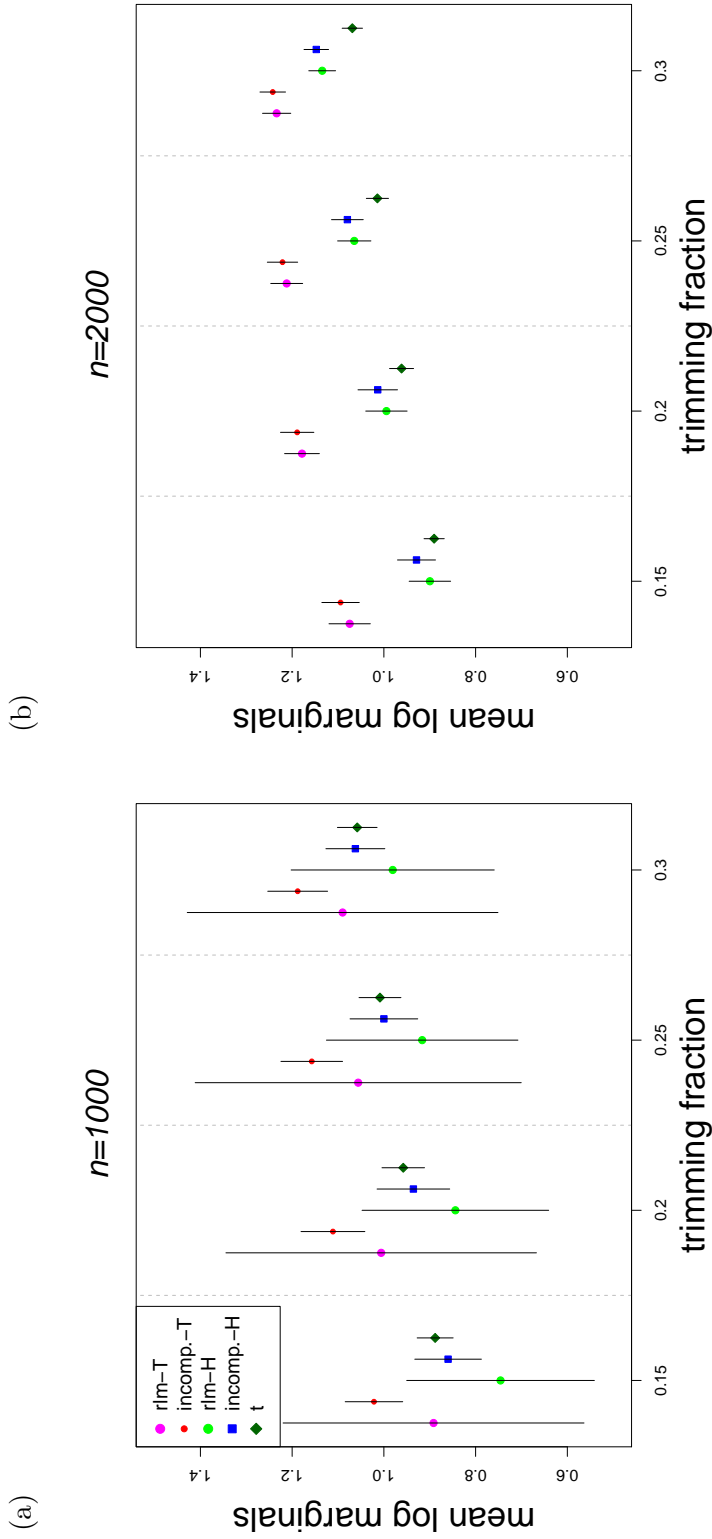


Figure 7: Model evaluation for ‘Type 1’ agencies under the hierarchical model for $n = 1000$ and 2000 . The t -model is used as the base method to compute TLM. Plotted are the mean TLM for each model against the trimming fraction across the 100 cross-validation samples. Error bars correspond to one standard deviation of TLM above and below the mean. Models are labeled using the same notation as the previous figure. Only the relevant trimming fractions ($\alpha \geq .15$) are pictured.