

Probabilistic preference learning with the Mallows rank model

Valeria Vitelli

*Oslo Centre for Biostatistics and Epidemiology,
Department of Biostatistics, University of Oslo,
P.O.Box 1122 Blindern, NO-0317, Oslo, Norway*

VALERIA.VITELLI@MEDISIN.UIO.NO

Øystein Sørensen

*Oslo Centre for Biostatistics and Epidemiology,
Department of Biostatistics, University of Oslo,
P.O.Box 1122 Blindern, NO-0317, Oslo, Norway*

OYSTEIN.SORENSEN.1985@GMAIL.COM

Arnoldo Frigessi

*Oslo Centre for Biostatistics and Epidemiology,
University of Oslo and Oslo University Hospital,
P.O.Box 1122 Blindern, NO-0317, Oslo, Norway*

ARNOLDO.FRIGESSI@MEDISIN.UIO.NO

Elja Arjas

*Oslo Centre for Biostatistics and Epidemiology,
Department of Biostatistics, University of Oslo,
P.O.Box 1122 Blindern, NO-0317, Oslo, Norway*

ELJA.ARJAS@HELSINKI.FI

Editor:

Abstract

Ranking and comparing items is crucial for collecting information about preferences in many areas, including marketing and politics. The Mallows rank model is among the most successful approaches to analyse rank data, but its computational complexity has limited its use to a particular form based on Kendall distance. We develop computationally tractable methods for Bayesian inference in Mallows models with any right-invariant metric. Our method performs inference on the consensus ranking of the items, also when based just on partial rankings, such as top- k items or pairwise comparisons. We prove that items which none of the assessors has ranked, do not influence the maximum a posteriori consensus ranking, and can therefore be ignored. When assessors are many or heterogeneous, we propose a mixture model for clustering them in homogeneous subgroups, with cluster-specific consensus rankings, without any preprocessing. We develop approximate stochastic algorithms that allow a fully probabilistic analysis, leading to coherent quantifications of uncertainties. We make probabilistic predictions on the class membership of assessors based on their ranking of just some items, and predict missing individual preferences, as needed in recommendation systems. We test our approach using several experimental and benchmark datasets.

Keywords: Incomplete Rankings, Pairwise Comparisons, Preference Learning with uncertainty, Recommendation Systems, Markov Chain Monte Carlo.

1. Introduction

Various types of data have ranks as their natural scale. Companies recruit panels to rank novel products, and market studies are often based on interviews where competing services or items are compared or ranked. Analyzing preference data collected over the internet (e.g., movies, books, restaurants, political candidates, ...) receives much attention. A ranking represents a statement given by an assessor about the relative quality or relevance of the items being ranked. In addition to data that appear naturally as rankings, converting continuous data to ranks can lead to more

robust inference when assessors use different absolute scales that are not easily comparable. In the case of genomic data, for example, Afsari et al. (2014) classify phenotypes based on ranked RNA expressions, and the ARACNE algorithm (Margolin et al., 2006) uses ranked mutual information between pairs of genes to reconstruct gene regulatory networks. For the general background on statistical methods for rank data, we refer to the excellent monograph by Marden (1995) and the recent book by Alvo and Yu (2014).

There are three typical tasks for rank or preference data: (i) aggregate, merge, summarize multiple rankings to estimate the consensus ranking and discover shared patterns and structure; (ii) as assessors often rank only part of the items, predict the ranks of the remaining items at individual level; (iii) partition the assessors into classes, each sharing a consensus ranking of the items, and classify new assessors to a class. In this paper we interpret all three tasks (and their combinations) in a unified Bayesian inferential setting, which allows us to also quantify posterior uncertainty of the solutions. Uncertainty evaluations of the estimated preferences and class memberships is a fundamental aspect of information in marketing and decision making in general. For example, when predictions are too unreliable, actions based on these might better be postponed until more data are available and safer predictions can be made, so as not to unnecessarily annoy users or clients.

Two of the most commonly used models for preference learning are the Plackett-Luce (Luce, 1959; Plackett, 1975) and Mallows models (Mallows, 1957). The Plackett-Luce model is a stage-wise probabilistic model on permutations, while the Mallows model is based on a distance between rankings. Inferring the parameters of the Plackett-Luce distribution is typically done by maximum likelihood estimation, using a minorize/maximize (MM) algorithm (Hunter, 2004). A Bayesian approach was first proposed by Guiver and Snelson (2009). Caron and Teh (2012) perform Bayesian inference in a Plackett-Luce model with time-dependent preference probabilities, and further develop the framework in Caron et al. (2014), where a Dirichlet process mixture is used to cluster assessors based on their preferences. The Plackett-Luce model is limited by the specific data generation mechanism, but inference is quite efficient. The Mallows models, on the other hand, are richer because of the flexible choice of distance. However for most distances exact inference is very demanding, because the normalizing constant is very expensive to compute. Therefore most work on Mallows models has been limited to one particular form of the model which uses the Kendall distance, for which the normalizing constant can be computed analytically. Maximum Likelihood inference about the consensus ranking in the Mallows model is generally NP-hard, and heuristic algorithms for this have been developed: Lu and Boutilier (2014) is the most interesting proposal in this setting, making use of their Repeated Insertion Model (RIM) based on the EM algorithm, while also allowing for clustering data in the form of pairwise preferences. However, the approach focuses on the Kendall distance only, and it provides no uncertainty quantification. Another interesting EM-based approach is Khan et al. (2014), which is driven by expectation propagation approximate inference and scales to very large datasets without requiring strong factorization assumptions. Among probabilistic approaches, Meilă and Chen (2010) use Dirichlet process mixtures to perform Bayesian clustering in the Mallows model, but they again focus on the Kendall distance only. Jacques and Biernacki (2014) also propose clustering of possibly partial rankings, but in the context of the Insertion Sorting Rank (ISR) model, and they develop an R package called *Rankcluster* for running their method (Jacques et al., 2014). Hence, the approach is probabilistic but it is far from the Mallows. See Section 4 for a more detailed presentation of related work.

The contributions of this paper can be summarized as follows. We develop a Bayesian framework for inference in Mallows models with any right-invariant metric. In this way the full power of the Mallows models is exploited, as there is no reason to believe that the footrule or Spearman distance would be less useful than Kendall's. We propose a new Metropolis-Hastings iterative

algorithm, which converges to the Bayesian posterior distribution, except for an approximation of the normalizing constant, which is efficiently computed off-line, using an importance sampling scheme. Using data augmentation techniques, our methods also allow for incomplete rankings, as in the important cases of top- k rankings, pairwise comparisons, and ranks missing at random. For the common situation when the pool of assessors is inhomogeneous and cannot be assumed to share a common consensus, we develop a new Bayesian clustering scheme which embeds the Mallows model. Our approach unifies clustering, classification and preference prediction in a single inferential procedure, thus leading to coherent posterior credibility levels of learned rankings and predictions. The probabilistic Bayesian setting allows us to naturally compute complex probabilities of interest, like the probability that an item has consensus ranking higher than a given level, or the probability that the consensus ranking of an item is higher than that of another item of interest. For incomplete rankings this can be done also at the individual assessor level.

In Section 2, we introduce the Bayesian Mallows model for rank data, and discuss the choice of distance measure (Section 2.1) and prior distribution (Section 2.2). In Section 2.3, we show how efficient Bayesian computation can be performed for this model, using a novel leap-and-shift proposal distribution. We develop and test an importance sampling scheme for computing the normalizing constant, based on a pseudo-likelihood approximation of the Mallows model. Section 3 is dedicated to partial rankings and clustering of assessors. In Section 3.1 we extend the Bayesian Mallows approach to partial rankings, and we prove some results on the effects of unranked items on the consensus ranking (Section 3.1.1). Section 3.2 considers data in the form of ordered subsets or pairwise comparisons of items. In Section 3.3 we describe a mixture model to deal with the possible heterogeneity of assessors, finding cluster-specific consensus rankings. In Section 3.4 we merge the two latter generalizations, hence allowing for clustering assessors from pairwise comparisons data. Section 3.5 is dedicated to prediction, when both the cluster assignment and personalized preference learning are carried out for new assessors.

In Section 4 we review related methods which have been proposed in the literature. In Section 5, we then move to illustrations and applications. Section 5.1 starts with our potato experiment, where the true ranking is known, to illustrate the use of the Mallows model for data in the form of full rankings, and to investigate convergence of our algorithms (see also Appendix A). We then continue with case studies, which illustrate the different incomplete data situations considered. This includes the Sushi and MovieLens benchmark data. Section 6 presents some conclusions and extensions. In Appendix B we show some further results on one of the experiments. In Appendix C we perform some simulation experiments in order to gain further insight into how the model works when increasing the level of uncertainty or the number of assessors.

2. A Bayesian Mallows Model for Complete Rankings

Assume we have a set of n items, labelled $\mathcal{A} = \{A_1, A_2, \dots, A_n\}$. We first assume that each of N assessors ranks all items individually with respect to a considered feature. The ordering provided by assessor j is represented by \mathbf{X}_j , whose n components are items in \mathcal{A} . The item with rank 1 appears as the first element, up to the item with rank n appearing as the n th element. The observations $\mathbf{X}_1, \dots, \mathbf{X}_N$ are hence N permutations of the labels in \mathcal{A} . Let $R_{ij} = \mathbf{X}_j^{-1}(A_i)$, $i = 1, \dots, n$, $j = 1, \dots, N$ denote the rank given to item A_i by assessor j , and let $\mathbf{R}_j = (R_{1j}, R_{2j}, \dots, R_{nj})$, $j = 1, \dots, N$, denote the full set of ranks given to the items by assessor j . Letting \mathcal{P}_n be the set of all permutations of $\{1, \dots, n\}$, we have $\mathbf{R}_j \in \mathcal{P}_n$, $j = 1, \dots, N$. Finally, let $d(\cdot, \cdot) : \mathcal{P}_n \times \mathcal{P}_n \rightarrow [0, \infty)$ be a distance measure on the space of n -dimensional permutations.

The Mallows model (Mallows, 1957) is a class of non-uniform joint distributions for \mathbf{R} on \mathcal{P}_n , of the form $P(\mathbf{R}|\alpha, \rho) = Z_n(\alpha, \rho)^{-1} \exp\{-(\alpha/n)d(\mathbf{R}, \rho)\}1_{\mathcal{P}_n}(\mathbf{R})$, where $\rho \in \mathcal{P}_n$ is the latent

consensus ranking, α is a positive scale parameter, $Z_n(\alpha, \rho)$ is a normalizing constant (or partition function), and $1_S(\cdot)$ is the indicator function of the set S . We assume that the N observed rankings $\mathbf{R}_1, \dots, \mathbf{R}_N$ are conditionally independent given α and the latent ranking ρ , and that each of them follows the Mallows model with these parameters. The likelihood takes then the form

$$P(\mathbf{R}_1, \dots, \mathbf{R}_N | \alpha, \rho) = Z_n(\alpha, \rho)^{-N} \exp \left\{ \frac{-\alpha}{n} \sum_{j=1}^N d(\mathbf{R}_j, \rho) \right\} \prod_{j=1}^N \{1_{\mathcal{P}_n}(\mathbf{R}_j)\}. \quad (1)$$

2.1 Distance Measures and Normalizing Constants

Right-invariant distances (Diaconis, 1988, p. 112) play an important role in the Mallows models.

Definition 1 *Right-invariant distance.* Let $\eta : \mathcal{A} \rightarrow \mathcal{A}$ be a one-to-one map which describes a relabelling of the items. A distance $d(\cdot, \cdot)$ is right-invariant, if $d(\rho_1, \rho_2) = d(\rho_1 \eta, \rho_2 \eta)$ for all η and $\rho_1, \rho_2 \in \mathcal{P}_n$.

A right-invariant distance is unaffected by a relabelling of the items. This is a reasonable assumption in many situations. All distances considered in this paper are right-invariant. For any right-invariant distance it holds that $d(\rho_1, \rho_2) = d(\{1, 2, \dots, n\}, \rho_2 \rho_1^{-1})$, and therefore the partition function $Z_n(\alpha, \rho)$ is independent on the latent consensus ranking ρ , as it can be centered in $\{1, 2, \dots, n\}$, or in any other arbitrary permutation $\mathbf{P} \in \mathcal{P}_n$, and we write $Z_n(\alpha) = Z_n(\alpha, \rho) = \sum_{\mathbf{R} \in \mathcal{P}_n} \exp\{-(\alpha/n)d(\mathbf{R}, \mathbf{P})\}$.

For a given α , the maximum likelihood estimate of the latent consensus ranking is obtained by computing

$$\underset{\rho \in \mathcal{P}_n}{\operatorname{argmax}} \sum_{j=1}^N d(\mathbf{R}_j, \rho),$$

which is NP-hard because of the factorial dimension of \mathcal{P}_n in n . The computation of the partition function for any given α is also prohibitive, for even moderate values of n , since it involves a sum of $n!$ terms. With an important exception, the Kendall distance $d(\mathbf{R}, \mathbf{P})$, which measures the minimum number of pairwise adjacent transpositions which convert \mathbf{R} into \mathbf{P} . The Mallows model with Kendall distance has a partition function that can be analytically computed as $Z_n(\alpha) = \prod_{i=1}^n \sum_{j=0}^{i-1} e^{-\alpha j/n}$, which is computationally feasible also when n is large. For this reason, most applications of Mallows models have been restricted to Kendall distance (Lu and Boutilier, 2014; Meilă and Chen, 2010), except for cases in which the number of items is very small (Murphy and Martin, 2003). However, several other distances have been suggested: important right-invariant distances are the footrule distance, $d(\mathbf{R}, \mathbf{P}) = \sum_{i=1}^n |R_i - P_i|$, and the Spearman distance $d(\mathbf{R}, \mathbf{P}) = \sum_{i=1}^n (R_i - P_i)^2$. Other examples are the Hamming distance, the Ulam distance and the Cayley distance (Marden, 1995, pp. 23–27). The computation of the partition function in the Mallows model when using these distances is NP-hard, as no exact form is known which avoids the summation over $n!$ terms. An interesting asymptotic approximation, when $n \rightarrow \infty$, has been studied in Mukherjee (2013), and we apply it in an example with $n = 200$ items (see Section 5.5). For situations where the number of items is not large enough to justify asymptotic approximations, we suggest an importance sampling scheme which efficiently approximates $Z_n(\alpha)$ to an arbitrary precision. Importantly, since the partition function $Z_n(\alpha)$ does not depend on the latent consensus ρ , it can be approximated off-line over a grid for α , given n . Other ways to work with approximate normalizing constants are possible, including pseudo-marginal approaches (Andrieu and Roberts, 2009).

2.2 Prior Distributions

The Bayesian framework allows incorporation of prior knowledge about the consensus ranking ρ and the parameter α , when available. For example, it is possible to assume a priori that an item A_i is expected to have a high rank in the consensus, say to be the most preferred item, through a prior of the form $\pi(\rho_i) \propto \exp\{-\beta(\rho_i - 1)^2\}$, for some positive β . When no relevant prior knowledge exists about ρ , an obvious choice is the uniform distribution over \mathcal{P}_n , $\pi(\rho) = (1/n!)1_{\mathcal{P}_n}(\rho)$, which we assume in this paper.

To specify the prior distribution for α , we proceed as follows. In the Mallows model we have terms of the form $\exp\{(-\alpha/n)d(R_{ij}, \rho_i)\}$ contributing multiplicatively to the likelihood. To get some idea of what numerical values of α would seem reasonable a priori, we can consider how likely it could be that the rank R_{ij} given by some assessor j to item A_i deviates from the consensus rank ρ_i by $n/2$. Using the footrule distance, this would correspond to $d(R_{ij}, \rho_i) = n/2$, and the likelihood contribution from such an observation would be $\exp\{(-\alpha/n)d(R_{ij}, \rho_i)\} = \exp\{-\alpha/2\}$. We can then calibrate the prior for α so that the prior predictive probability that an assessment is off by $n/2$ ranks is equal to, say, 0.01. For this purpose, we evaluate this likelihood contribution at the prior mean and solve $\exp\{-E(\alpha)/2\} = 0.01$. Using the exponential prior distributions of the form $\pi(\alpha) = \lambda \exp(-\lambda\alpha)1_{[0,\infty)}(\alpha)$, with hyperparameter λ , we find that $E(\alpha) = 10$, so that $\lambda = 1/10$ will be appropriate. Since the footrule distance d_F and Kendall distance d_K are related by the inequality $d_K \leq d_F \leq 2d_K$ (Diaconis and Graham, 1977, Th. 2), we use the same argument when working with the Kendall distance as well. For the Spearman distance, similar reasoning leads to $d(R_{ij}, \rho_j) = n^2/4$, so we can set for example $\lambda = n/20$. We show in Section A.4 of Appendix A that for some of the applications considered in this paper, the results are reasonably robust with respect to small changes of the hyperparameter λ .

2.3 Inference

Given the prior distributions $\pi(\rho)$ and $\pi(\alpha)$, and assuming prior independence of these variables, the posterior distribution for ρ and α is

$$P(\rho, \alpha | \mathbf{R}_1, \dots, \mathbf{R}_N) \propto \frac{\pi(\rho) \pi(\alpha)}{Z_n(\alpha)^N} \exp \left\{ -\frac{\alpha}{n} \sum_{j=1}^N d(\mathbf{R}_j, \rho) \right\}. \quad (2)$$

Typically, one is interested in computing posterior summaries of this distribution, like the posterior mode (the maximum a posteriori, or MAP) or more complex functions, like the posterior probability that a certain item has consensus rank lower than a given level. Another useful example of such more complex summary measures of the posterior distribution is to compute the probability that the consensus rank of a certain item is higher than the consensus rank of another item. These probabilities cannot be easily obtained within the maximum likelihood approach, while the Bayesian setting allows answering these questions in a very natural way by means of a Markov Chain Monte Carlo algorithm, which at convergence samples from the posterior distribution (2), allowing us to approximate all posterior summaries of interest.

2.3.1 BASIC METROPOLIS-HASTINGS ALGORITHM FOR COMPLETE RANKINGS

In order to obtain samples from the posterior in equation (2), we iterate between two steps. In one step we update the consensus ranking. Starting with $\alpha \geq 0$ and $\rho \in \mathcal{P}_n$, we first update ρ by proposing ρ' according to a symmetric distribution which is centred around the current rank ρ .

Definition 2 *Leap-and-Shift Proposal.* Fix an integer $L \in \{1, \dots, \lfloor n/2 \rfloor\}$ and draw a random number $u \sim \mathcal{U}\{1, \dots, n\}$. Define, for a given $\boldsymbol{\rho}$,

$$\mathcal{S} = \begin{cases} \{\rho_u - L, \dots, \rho_u + L\} \setminus \{\rho_u\}, & \text{if } L+1 \leq \rho_u \leq n-L \\ \{1, \dots, 2L\} \setminus \{\rho_u\}, & \text{if } \rho_u \leq L \\ \{n-2L+1, \dots, n\} \setminus \{\rho_u\}, & \text{if } \rho_u \geq n-L+1, \end{cases}$$

and draw a random number r uniformly in \mathcal{S} . Let $\boldsymbol{\rho}^* \in \{1, 2, \dots, n\}^n$ have elements $\rho_u^* = r$ and $\rho_i^* = \rho_i$ for $i \in \{1, \dots, n\} \setminus \{u\}$. The probability mass function for this leap step is given by

$$\begin{aligned} P_L(\boldsymbol{\rho}^* | \boldsymbol{\rho}) &= \sum_{u=1}^n P_L(\boldsymbol{\rho}^* | U=u, \boldsymbol{\rho}) P(U=u) \\ &= \frac{1}{2nL} \sum_{u=1}^n \left\{ 1_{\{L+1, \dots, n-L\}}(\rho_u) \cdot 1_{\{\rho_u - L, \dots, \rho_u + L\} \setminus \{\rho_u\}}(\rho_u^*) + 1_{\{1, \dots, L\}}(\rho_u) \right. \\ &\quad \left. \cdot 1_{\{1, \dots, 2L\} \setminus \{\rho_u\}}(\rho_u^*) + 1_{\{n-L+1, \dots, n\}}(\rho_u) \cdot 1_{\{n-2L+1, \dots, n\} \setminus \{\rho_u\}}(\rho_u^*) \right\} \cdot 1_{\{\boldsymbol{\rho}_{-u}\}}(\boldsymbol{\rho}_{-u}^*), \end{aligned}$$

where $\boldsymbol{\rho}_{-u} = (\rho_i; i \neq u)$. Define $\Delta = \rho_u^* - \rho_u$ and $\boldsymbol{\rho}'$ with elements

$$\rho'_i = \begin{cases} \rho_i - 1 & \text{if } \rho_u < \rho_i \leq \rho_u^* \text{ and } \Delta > 0 \\ \rho_i + 1 & \text{if } \rho_u < \rho_i \leq \rho_u^* \text{ and } \Delta < 0 \\ \rho_i & \text{else,} \end{cases}$$

for $i = 1, \dots, n$, constituting the shift step.

Proposition 1 The leap-and-shift proposal $\boldsymbol{\rho}' \in \mathcal{P}_n$ is a local perturbation of $\boldsymbol{\rho}$, separated from $\boldsymbol{\rho}$ by a Ulam distance 1 .

Proof From the definition and by construction, $\boldsymbol{\rho}^* \notin \mathcal{P}_n$, since there exist two indices $i \neq j$ such that $\rho_i^* = \rho_j^*$. The shift of the ranks by Δ brings $\boldsymbol{\rho}'$ back into \mathcal{P}_n . The Ulam distance $d(\boldsymbol{\rho}, \boldsymbol{\rho}')$ is the number of edit operations needed to convert $\boldsymbol{\rho}$ to $\boldsymbol{\rho}'$, where a single edit operation involves deleting a character and inserting it in a new place. This is equal to 1 in our case, following Gopalan et al. (2006). ■

The acceptance probability for the first step in the Metropolis-Hastings algorithm, is then given by

$$\min \left\{ 1, \frac{\pi(\boldsymbol{\rho}')}{\pi(\boldsymbol{\rho})} \exp \left[\frac{-\alpha}{n} \sum_{j=1}^N \{d(\mathbf{R}_j, \boldsymbol{\rho}') - d(\mathbf{R}_j, \boldsymbol{\rho})\} \right] \right\}. \quad (3)$$

The parameter L is used for tuning this acceptance probability.

The second step of the algorithm updates the value of α . We sample a proposal α' from $\mathcal{N}(\alpha, \sigma_\alpha^2)$, and accept it with probability

$$\min \left\{ 1, \frac{Z_n(\alpha')^{-N} \pi(\alpha')}{Z_n(\alpha)^{-N} \pi(\alpha)} \exp \left[\frac{-(\alpha' - \alpha)}{n} \sum_{j=1}^N d(\mathbf{R}_j, \boldsymbol{\rho}) \right] \right\}, \quad (4)$$

where σ_α^2 can be tuned to obtain a desired acceptance probability. All previously described steps are summarized in Algorithm 1.

Algorithm 1: Basic MCMC Algorithm for Complete Rankings

```

input :  $\mathbf{R}_1, \dots, \mathbf{R}_N; \lambda, \sigma_\alpha, L, d(\cdot, \cdot), Z_n(\alpha), M$ 
output: Posterior distributions of  $\rho$  and  $\alpha$ 

Initialization of the MCMC: randomly generate  $\rho_0$  and  $\alpha_0$ 
for  $m \leftarrow 1$  to  $M$  do
    Update  $\rho$ :
        sample:  $\rho' \sim$  leap-and-shift distribution centred at  $\rho_{m-1}$ 
        compute:  $ratio \leftarrow$  equation (3) with  $\rho \leftarrow \rho_{m-1}$  and  $\alpha \leftarrow \alpha_{m-1}$ 
        sample:  $u \sim \mathcal{U}(0, 1)$ 
        if  $u < ratio$  then
            |  $\rho_m \leftarrow \rho'$ 
        else
            |  $\rho_m \leftarrow \rho_{m-1}$ 
        end

    Update  $\alpha$ :
        sample:  $\alpha' \sim \mathcal{N}(\alpha_{m-1}, \sigma_\alpha^2)$ 
        compute:  $ratio \leftarrow$  equation (4) with  $\rho \leftarrow \rho_m$  and  $\alpha \leftarrow \alpha_{m-1}$ 
        sample:  $u \sim \mathcal{U}(0, 1)$ 
        if  $u < ratio$  then
            |  $\alpha_m \leftarrow \alpha'$ 
        else
            |  $\alpha_m \leftarrow \alpha_{m-1}$ 
        end
    end

```

Proposition 2 *Convergence of the MCMC algorithm for known $Z_n(\alpha)$. The MCMC Algorithm 1 computes (ρ_m, α_m) at step m , which converges in distribution to the Mallows posterior in equation (2), as the number M of iterations tends to infinity.*

Proof Because of reversibility of the proposals, detailed balance holds for the Markow chain. Ergodicity follows by aperiodicity and positive recurrence. A negative α can be proposed, but it is accepted with zero probability because it is outside the support of the prior $\pi(\alpha)$. ■

2.3.2 OFF-LINE IMPORTANCE SAMPLING FOR $Z_n(\alpha)$

For Kendall's distance, the partition function $Z_n(\alpha)$ is computable for large values of n , but this is not the case for other distances. Note also that, for fixed α , there is no need to compute $Z_n(\alpha)$ when sampling ρ , because the partition functions are cancelled from the Metropolis-Hastings ratio (3). We now propose an approximation based on an importance sampling algorithm of the partition function for a given α : the approximation is performed on a grid of α values and then interpolated to yield an estimate over a continuous range.

For rank vectors $\mathbf{R}^1, \dots, \mathbf{R}^K$ sampled from an importance sampling auxiliary distribution $q(\mathbf{R})$, the unbiased importance sampling estimate of $Z_n(\alpha)$ is given by

$$\hat{Z}_n(\alpha) = K^{-1} \sum_{k=1}^K \exp\{-(\alpha/n)d(\mathbf{R}^k, \rho)\} q(\mathbf{R}^k)^{-1},$$

where we set $\rho = \mathbf{1} = \{1, \dots, n\}$. The more $q(\mathbf{R})$ resembles the Mallows likelihood (1), the smaller is the variance of $\hat{Z}_n(\alpha)$. On the other hand, it must be computationally feasible to sample from

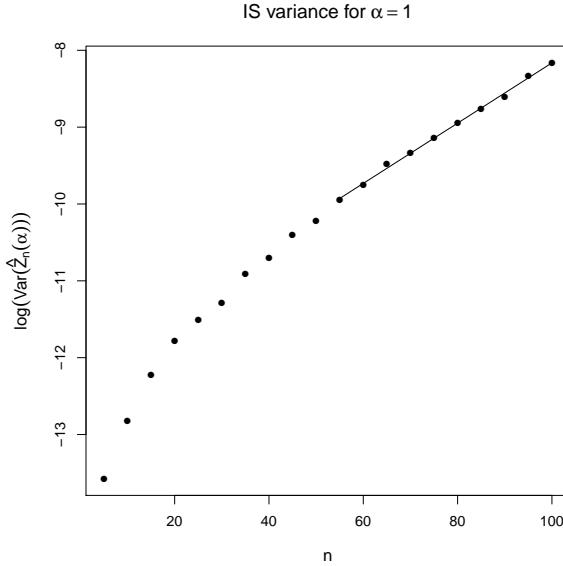


Figure 1: Empirical variance (in log scale) of the partition function estimate computed from 1000 independent runs with importance sampling sample size $K = 10^5$, as a function of the number n of items, with $\alpha = 1$. For large n a linear fit is added, with slope 0.04.

$q(\mathbf{R})$. We use the following pseudo-likelihood approximation of the target (1):

$$P(\mathbf{R}|\mathbf{1}) = P(R_1|R_2, \dots, R_n, \mathbf{1})P(R_2|R_3, \dots, R_n, \mathbf{1}) \cdots P(R_{n-1}|R_n, \mathbf{1})P(R_n|\mathbf{1}),$$

with the conditional distributions given by

$$\begin{aligned} P(R_n|\mathbf{1}) &= \frac{\exp\{-(\alpha/n)d(R_n, n)\} \cdot 1_{[1, \dots, n]}(R_n)}{\sum_{\tilde{\rho}_n \in \{1, \dots, n\}} \exp\{-(\alpha/n)d(\tilde{\rho}_n, n)\}}, \\ P(R_{n-1}|R_n, \mathbf{1}) &= \frac{\exp\{-(\alpha/n)d(R_{n-1}, n-1)\} \cdot 1_{[\{1, \dots, n\} \setminus \{R_n\}]}(R_{n-1})}{\sum_{\tilde{\rho}_{n-1} \in \{1, \dots, n\} \setminus \{R_n\}} \exp\{-(\alpha/n)d(\tilde{\rho}_{n-1}, n-1)\}}, \\ &\vdots \\ P(R_2|R_3, \dots, R_n, \mathbf{1}) &= \frac{\exp\{-(\alpha/n)d(R_2, 2)\} \cdot 1_{[\{1, \dots, n\} \setminus \{R_3, \dots, R_n\}]}(R_2)}{\sum_{\tilde{\rho}_2 \in \{1, \dots, n\} \setminus \{R_3, \dots, R_n\}} \exp\{-(\alpha/n)d(\tilde{\rho}_2, 2)\}}, \\ P(R_1|R_2, \dots, R_n, \mathbf{1}) &= 1_{[\{1, \dots, n\} \setminus \{R_2, \dots, R_n\}]}(R_1). \end{aligned}$$

Each factor is a simple univariate distribution. We sample R_n first, and then conditionally on that, R_{n-1} and so on. The k -th full sample \mathbf{R}^k has probability $q(\mathbf{R}^k) = P(R_n^k|\mathbf{1})P(R_{n-1}^k|R_n^k, \mathbf{1}) \cdots P(R_2^k|R_3^k, \dots, R_n^k, \mathbf{1})$. We observe the similarity of this pseudo-likelihood construction with the sequential representation of the Plackett-Luce model with a Mallows parametrization of its probabilities.

2.3.3 TESTING THE IMPORTANCE SAMPLER

We study the convergence of the importance sampler with a series of experiments. We first investigate the variance of $\hat{Z}_n(\alpha)$, we then demonstrate the quality of the approximation, and finally

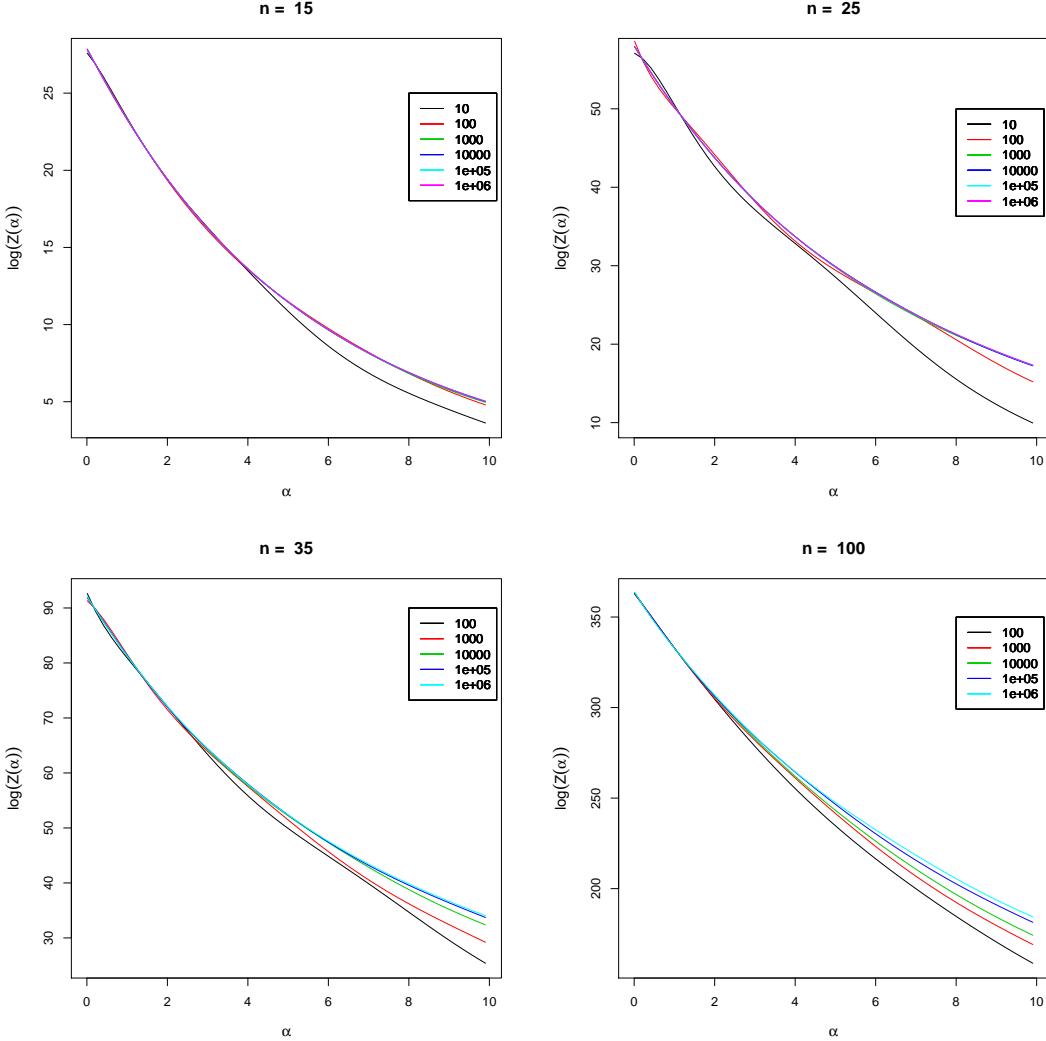


Figure 2: Estimates of the partition function as a function of α (in log scale) for the footrule distance using five different dimensions of the importance sampling sample, as specified by the legend.

study the effect of the approximation on the convergence of the MCMC algorithm. We show results using the footrule distance, but similar results were obtained for the Spearman distance.

The variance of $\hat{Z}_n(\alpha)$ grows with the number of items n . We fixed α and the number of importance sampling samples K , and computed 1000 independent approximations of the partition function via importance sampling for various choices of n , and estimated the associated variance. Results for $K = 10^5$ and $\alpha = 1$ are shown in Figure 1. For $n > 50$, the logarithm of the variance grows approximately linearly with n , with an estimated slope of 0.04. Nevertheless, even when $n = 100$, the variance is around 10^{-4} , several orders of magnitude smaller than the actual value of the partition function. Different values of α do not change the quality of the approximation. For large values of n we do not need to compute the importance sampling approximation, but rather rely on the asymptotic approximation provided in Mukherjee (2013).

Next we investigated the number of importance sampling samples necessary to obtain a sufficiently accurate estimate $\hat{Z}_n(\alpha)$ of $Z_n(\alpha)$. We experimented by increasing the number of importance samples in powers of ten, over a discrete grid of 100 equally spaced α values between 0.01 and 10. Finally, we produced a smooth normalizing function simply using a polynomial of degree ten, see Figure 2. For $n = 15$ the curves based on 10^3 and 10^4 importance sampling samples are already indistinguishable, and the relative error

$$\epsilon = \max_{\alpha} \left[\frac{\left| \log\{\hat{Z}_n(\alpha)\}_{more} - \log\{\hat{Z}_n(\alpha)\}_{less} \right|}{\left| \log\{\hat{Z}_n(\alpha)\}_{less} \right|} \right] \quad (5)$$

is equal to 0.07. Here “more” corresponds to $K = 10^4$ and “less” to $K = 10^3$. Increasing K to 10^5 gives $\epsilon = 0.02$, and the final estimate is very good. For comparison, computing the exact value of the normalizing constant would require summation of $15! \approx 10^{12}$ terms. For $n = 25$, $\epsilon = 0.04$ for K between 10^5 and 10^4 samples. In order to obtain $\epsilon < 0.01$, we need $K = 10^6$, still much less than $25! \approx 10^{25}$. For $n = 100$ items, the approximations are less precise, but still very good for the range of α which turns to be relevant in all our applications, that is $\alpha < 5$. See Table 1. The computations shown here were performed on a desktop computer, and the off-line computation with $K = 10^6$ samples for $n = 35$ took 53 minutes, with no efforts for parallelizing the algorithm, which would be easy and beneficial. $K = 10^6$ samples for $n = 100$ where obtained on a 64-cores computing cluster in 12 minutes.

K , importance samples	Max relative error, ϵ			
	$n = 15$	$n = 25$	$n = 35$	$n = 100$
10	-	-	-	-
10^2	15.51	70.67	-	-
10^3	0.12	3.94	1.63	1.60
10^4	0.07	0.04	0.21	0.21
10^5	0.02	0.04	0.04	0.07
10^6	0.007	0.008	0.007	0.09

Table 1: Approximation of the partition function via the importance sampling for the footrule model with respect to K , the number of samples used in the importance sampling. Each row shows the increment in the maximum relative error between the current and the previous K , as specified by (5).

How does the approximation of $Z_n(\alpha)$ affect MCMC convergence? It is easy to see that a convergence is still achieved.

Proposition 3 *Assume we approximate the partition function $Z_n(\alpha)$ with $\hat{Z}_n(\alpha)$. Then the MCMC in Algorithm (1) computes (ρ_m, α_m) at step m , which converges in distribution to an approximation of the posterior distribution (2), where the prior for α is proportional to*

$$\left(\frac{Z_n(\alpha)}{\hat{Z}_n(\alpha)} \right)^N \pi(\alpha).$$

More on the quality of the approximation used in the MCMC in Section 5.1.1 and Appendix A.3.

3. Extensions to Partial Rankings and Heterogeneous Assessor Pool

We now relax two assumptions of the previous section, namely that each assessor ranks all n items and that the assessors are exchangeable, all sharing a common consensus ranking. This allows us to treat the important situation of pairwise comparisons and of multiple classes of assessors, within the same Bayesian Mallows framework.

3.1 Ranking of the Top Ranked Items

Frequently in applications only a subset of the items is ranked: ranks can be missing at random, or the assessors may only have ranked, say, the in-their-opinion top-5 items. These types of situations can be handled conveniently in our Bayesian framework, by applying data augmentation techniques. We explain our method for the case of the top ranks, while it can easily be extended to any subsets of ranks.

Suppose that each assessor j has ranked the subset of items $\mathcal{A}_j \subseteq \{A_1, A_2, \dots, A_n\}$, giving them top ranks from 1 to $n_j = |\mathcal{A}_j|$. Let $R_{ij} = \mathbf{X}_j^{-1}(A_i)$ if $A_i \in \mathcal{A}_j$, while for $A_i \in \mathcal{A}_j^c$, R_{ij} is unknown, except for the constraint $R_{ij} > n_j$, $j = 1, \dots, N$, and follows a symmetric prior across the permutations of $(n_j + 1, \dots, n)$. We define augmented data vectors $\tilde{\mathbf{R}}_1, \dots, \tilde{\mathbf{R}}_N$ by assigning ranks to these non-ranked items randomly, using an MCMC algorithm, and do this in a way which is compatible with the rest of the data. Let $\mathcal{S}_j = \{\tilde{\mathbf{R}}_j \in \mathcal{P}_n : \tilde{R}_{ij} = \mathbf{X}_j^{-1}(A_i) \text{ if } A_i \in \mathcal{A}_j\}$, $j = 1, \dots, N$, be the set of possible augmented random vectors, i.e. the original partially ranked items together with the allowable ‘‘fill-ins’’ of the missing ranks. Our goal is to sample from the posterior distribution

$$P(\alpha, \rho | \mathbf{R}_1, \dots, \mathbf{R}_N) = \sum_{\tilde{\mathbf{R}}_1 \in \mathcal{S}_1} \dots \sum_{\tilde{\mathbf{R}}_N \in \mathcal{S}_N} P(\alpha, \rho, \tilde{\mathbf{R}}_1, \dots, \tilde{\mathbf{R}}_N | \mathbf{R}_1, \dots, \mathbf{R}_N).$$

Our algorithm alternates between sampling the augmented ranks given the current values of α and ρ , and sampling α and ρ given the current values of the augmented ranks. For the latter, we sample from the posterior $P(\alpha, \rho | \tilde{\mathbf{R}}_1, \dots, \tilde{\mathbf{R}}_N)$ as in Section 2.3.1, where we replace the original data $\mathbf{R}_1, \dots, \mathbf{R}_N$ with the current augmented data vectors. For the former, fixing α and ρ and the observed ranks $\mathbf{R}_1, \dots, \mathbf{R}_N$, we see that $\tilde{\mathbf{R}}_1, \dots, \tilde{\mathbf{R}}_N$ are conditionally independent, and moreover, that each $\tilde{\mathbf{R}}_j$ only depends on the corresponding \mathbf{R}_j . This enables us to consider the sampling of new augmented vectors $\tilde{\mathbf{R}}'_j$ separately for each $j, j = 1, \dots, N$. Specifically, given the current $\tilde{\mathbf{R}}_j$ (which embeds information contained in \mathbf{R}_j) and the current values for α and ρ , $\tilde{\mathbf{R}}'_j$ is sampled in \mathcal{S}_j from the leap-and-shift proposal distribution centred at $\tilde{\mathbf{R}}_j$, as described in Section 2.3.1, meaning that the highest ranks from 1 to n_j have been reserved for the items in \mathcal{A}_j , while compatible ranks are randomly drawn for items in \mathcal{A}_j^c by perturbing $\tilde{\mathbf{R}}_j$. The proposed $\tilde{\mathbf{R}}'_j$ is then accepted with probability

$$\min \left\{ 1, \exp \left[-\frac{\alpha}{n} \left(d(\tilde{\mathbf{R}}'_j, \rho) - d(\tilde{\mathbf{R}}_j, \rho) \right) \right] \right\}. \quad (6)$$

The MCMC algorithm described above and used in the case of partial rankings is given in Algorithm 2. A simple extension of our algorithm can also handle the situation where assessors assign items to a fixed set of ranks, not necessarily representing the top (or bottom) of their preferences.

3.1.1 EFFECTS OF UNRANKED ITEMS ON CONSENSUS RANKING

In applications in which the number of items is large there are often items which none of the assessors included in their top-list. What is the exact role of such ‘‘left-over’’ items in the top- k consensus ranking of all items for different values of k ? How do such results relate to results

Algorithm 2: MCMC Algorithm for Partial Rankings or Pairwise Preferences

input : $\{\mathcal{S}_1, \dots, \mathcal{S}_N\}$ or $\{\text{tc}(\mathcal{B}_1), \dots, \text{tc}(\mathcal{B}_N)\}$; $\lambda, \sigma_\alpha, L, d(\cdot, \cdot), Z_n(\alpha), M$
output: Posterior distributions of ρ , α and $\tilde{\mathbf{R}}_1, \dots, \tilde{\mathbf{R}}_N$

Initialization of the MCMC:randomly generate ρ_0 and α_0 **if** $\{\mathcal{S}_1, \dots, \mathcal{S}_N\}$ among inputs **then**

```

for  $j \leftarrow 1$  to  $N$  do
| randomly generate  $\tilde{\mathbf{R}}_j^0$  in  $\mathcal{S}_j$ 
end
```

else

```

for  $j \leftarrow 1$  to  $N$  do
| randomly generate  $\tilde{\mathbf{R}}_j^0$  compatible with  $\text{tc}(\mathcal{B}_j)$ 
end
```

end**for** $m \leftarrow 1$ **to** M **do****Update ρ :**sample: $\rho' \sim$ leap-and-shift distribution centred at ρ_{m-1} compute: $\text{ratio} \leftarrow$ equation (3) with $\rho \leftarrow \rho_{m-1}$ and $\alpha \leftarrow \alpha_{m-1}$ sample: $u \sim \mathcal{U}(0, 1)$ **if** $u < \text{ratio}$ **then**| $\rho_m \leftarrow \rho'$ **else**| $\rho_m \leftarrow \rho_{m-1}$ **end****Update α :**sample: $\alpha' \sim \mathcal{N}(\alpha_{m-1}, \sigma_\alpha^2)$ compute: $\text{ratio} \leftarrow$ equation (4) with $\rho \leftarrow \rho_m$ and $\alpha \leftarrow \alpha_{m-1}$ sample: $u \sim \mathcal{U}(0, 1)$ **if** $u < \text{ratio}$ **then**| $\alpha_m \leftarrow \alpha'$ **else**| $\alpha_m \leftarrow \alpha_{m-1}$ **end****Update $\tilde{\mathbf{R}}_1, \dots, \tilde{\mathbf{R}}_N$:****for** $j \leftarrow 1$ **to** N **do****if** $\{\mathcal{S}_1, \dots, \mathcal{S}_N\}$ among inputs **then**| sample: $\tilde{\mathbf{R}}'_j$ in \mathcal{S}_j from the leap-and-shift distribution centred at $\tilde{\mathbf{R}}_j^{m-1}$ **else**| sample: $\tilde{\mathbf{R}}'_j$ from the leap-and-shift distribution centred at $\tilde{\mathbf{R}}_j^{m-1}$ and compatible with $\text{tc}(\mathcal{B}_j)$ **end**compute: $\text{ratio} \leftarrow$ equation (6) with $\rho \leftarrow \rho_m$, $\alpha \leftarrow \alpha_m$ and $\tilde{\mathbf{R}}_j \leftarrow \tilde{\mathbf{R}}_j^{m-1}$ sample: $u \sim \mathcal{U}(0, 1)$ **if** $u < \text{ratio}$ **then**| $\tilde{\mathbf{R}}_j^m \leftarrow \tilde{\mathbf{R}}'_j$ **else**| $\tilde{\mathbf{R}}_j^m \leftarrow \tilde{\mathbf{R}}_j^{m-1}$ **end****end****end**

where only the items explicitly ranked by at least one assessor would have been included in the analysis? In the following we first show that these left-over items have no effect on any a posteriori consensus top- k ranking, in the sense that only items explicitly ranked by the assessors appear in top positions of the consensus ranking. We then show that, when considering the MAP consensus ranking, excluding the left-over items from the ranking procedure already at the start has no effect on how the remaining ones will appear in such consensus ranking.

For a precise statement of these results, we need some new notation. Suppose that assessor j has ranked a subset \mathcal{A}_j of n_j items. Let $\mathcal{A} = \bigcup_{j=1,\dots,N} \mathcal{A}_j$, and denote $n = |\mathcal{A}|$. Let n^* be the total number of items, including left-over items which have not been explicitly ranked by any assessor. Denote by $\mathcal{A}^* = \{A_i; i = 1, \dots, n^*\}$ the collection of all items, and by $\mathcal{A}^c = \mathcal{A}^* \setminus \mathcal{A}$ the left-over items. Each rank vector \mathbf{R}_j for assessor j contains, in some order, the ranks from 1 to n_j given to items in \mathcal{A}_j . In the original data the ranks of all remaining items are left unspecified, apart from the fact that implicitly, for assessor j , they would have values which are at least as large as $n_j + 1$.

The results below are formulated in terms of the two different modes of analysis, which we need to compare and which correspond to different numbers of items being included. The first alternative is to include in the analysis the complete set \mathcal{A}^* of n^* items, and to complement each data vector \mathbf{R}_j by assigning (originally missing) ranks to all items which are not included in \mathcal{A}_j ; their ranks will then form some permutation of the sequence $(n_j + 1, \dots, n^*)$. We call this mode of analysis *full analysis*, and denote the corresponding probability measure by P_{n^*} . The second alternative is to include in the analysis only the items which have been explicitly ranked by at least one assessor, that is, items belonging to the set \mathcal{A} . We call this second mode *restricted analysis*, and denote the corresponding probability measure by P_n . The probability measure P_n is specified as before, including the uniform prior on the consensus ranking $\boldsymbol{\rho}$ across all $n!$ permutations of $(1, 2, \dots, n)$, and the uniform prior of the unspecified ranks R_{ij} of items $A_i \in \mathcal{A}_j^c$ across the permutations of $(n_j + 1, \dots, n)$. The definition of P_{n^*} is similar, except that then the uniform prior distributions are assumed to hold in the complete set \mathcal{A}^* of items, that is, over permutations of $(1, 2, \dots, n^*)$ and $(n_j + 1, \dots, n^*)$, respectively. In the posterior inference carried out in both modes of analysis, the augmented ranks, which were not recorded in the original data, are treated as random variables, with values being updated as part of the MCMC sampling.

Proposition 4 Consider two latent consensus rank vectors $\boldsymbol{\rho}$ and $\boldsymbol{\rho}'$ such that

- (i) in the ranking $\boldsymbol{\rho}$ all items in \mathcal{A} have been included among the top- n -ranked, while those in \mathcal{A}^c have been assigned ranks between $n + 1$ and n^* ,
- (ii) $\boldsymbol{\rho}'$ is obtained from $\boldsymbol{\rho}$ by a permutation, where the rank in $\boldsymbol{\rho}$ of at least one item belonging to \mathcal{A} has been transposed with the rank of an item in \mathcal{A}^c .

Then, $P_{n^*}(\boldsymbol{\rho}|\text{data}) \geq P_{n^*}(\boldsymbol{\rho}'|\text{data})$, for the footrule, Kendall and Spearman distances in the full analysis mode.

Proof Having assumed the uniform prior across all permutations of latent consensus ranks, the desired result will hold if and only if $\sum_{j=1,\dots,N} d(\mathbf{R}_j, \boldsymbol{\rho}) \leq \sum_{j=1,\dots,N} d(\mathbf{R}_j, \boldsymbol{\rho}')$. This is true if $d(\mathbf{R}_j, \boldsymbol{\rho}) \leq d(\mathbf{R}_j, \boldsymbol{\rho}')$ holds separately for each assessor j , for $j = 1, \dots, N$. We consider first the footrule distance d , and then show that the result holds also for the Kendall and Spearman distances. This proof follows Proposition 4 in Meilă and Bao (2010).

Suppose first, for simplicity, that all assessors have ranked the same n items, i.e., $\mathcal{A}_1 = \mathcal{A}_2 = \dots = \mathcal{A}_N = \mathcal{A}$. Later we allow the sets \mathcal{A}_j of ranked items to be different for different assessors. Thus there are $n^* - n$ items, which nobody ranked in the original data.

We now introduce synthetic rankings for all these items as well, that is, we augment each \mathbf{R}_j as recorded in the data by replacing the missing ranks of the items $A_i \in \mathcal{A}^c$ by some permutation of their possible ranks from $n+1$ to n^* . We then show that the desired inequality holds regardless of how these ranks $\{R_{ij}, A_i \in \mathcal{A}^c\}$ were assigned. The proof is by induction, and it is carried out in several steps.

For the first step, let $\boldsymbol{\rho}$ be a rank vector where the ranks from 1 to n , in any order, have been assigned to the items in \mathcal{A} , and the ranks R_{ij} between $n+1$ and n^* are given to items in \mathcal{A}^c . Let $\boldsymbol{\rho}'$ be a rank vector obtained from $\boldsymbol{\rho}$ by a transposition of the ranks of two items, say, of $A_{i_0} \in \mathcal{A}^c$ and $A_{i_1} \in \mathcal{A}$, with $\rho_{i_0} = \rho'_{i_1} \geq n+1$ and $\rho_{i_1} = \rho'_{i_0} \leq n$. Fixing these two items, we want to show that $d(\mathbf{R}_j, \boldsymbol{\rho}) \leq d(\mathbf{R}_j, \boldsymbol{\rho}')$. For the footrule distance we have to show that $\sum_{i=1}^n |R_{ij} - \rho_i| \leq \sum_{i=1}^n |R_{ij} - \rho'_i|$. Since $\boldsymbol{\rho}$ and $\boldsymbol{\rho}'$ coincide for all their coordinates $i \neq i_0, i_1$, it is enough to compare here the terms $|R_{i_0j} - \rho_{i_0}|$ and $|R_{i_1j} - \rho_{i_1}|$ on the left to the corresponding terms $|R_{i_0j} - \rho'_{i_0}|$ and $|R_{i_1j} - \rho'_{i_1}|$ on the right. We need to distinguish between two situations:

- (i) Suppose $R_{i_1j} \leq \rho_{i_1}$. Then, $\rho'_{i_1} - R_{i_1j} > \rho_{i_1} - R_{i_1j}$. On the other hand, $\rho_{i_0} \geq n+1$ implies that $A_{i_0} \in \mathcal{A}^c$, and it is therefore ranked by assessor j with $R_{i_0j} \geq n+1$. Therefore, $|R_{i_0j} - \rho'_{i_0}| \geq |R_{i_0j} - \rho_{i_0}|$. By combining these two results we get that $|R_{i_0j} - \rho_{i_0}| + |R_{i_1j} - \rho_{i_1}| \leq |R_{i_0j} - \rho'_{i_0}| + |R_{i_1j} - \rho'_{i_1}|$.
- (ii) Now, suppose that $R_{i_1j} > \rho_{i_1}$. Then, $R_{i_1j} - \rho_{i_1} \leq n - \rho_{i_1} \leq R_{i_0j} - \rho'_{i_0}$. Moreover, since $|R_{i_0j} - \rho_{i_0}| \leq |R_{i_1j} - \rho_{i_0}| = |R_{i_1j} - \rho'_{i_1}|$, we have that again $|R_{i_0j} - \rho_{i_0}| + |R_{i_1j} - \rho_{i_1}| \leq |R_{i_0j} - \rho'_{i_0}| + |R_{i_1j} - \rho'_{i_1}|$ holds.

The same reasoning holds also for the Kendall distance, since the Kendall distance between the two rank vectors, which are obtained from each other by a transposition of a pair of items, is the same as the footrule distance. For the Spearman distance, we only need to form squares of the distance between pairs of items, and the inequality remains valid.

For the general step of the induction, suppose that $\boldsymbol{\rho}$ has been obtained from its original version with all items in \mathcal{A} ranked to the first n positions, via a sequence of transpositions between items originally in \mathcal{A} and items originally in \mathcal{A}^c . Let $\boldsymbol{\rho}'$ be a rank vector where one more transposition of this type from $\boldsymbol{\rho}$ to $\boldsymbol{\rho}'$ has been carried out. Then the argument of the proof can still be carried through, and the conclusion $d(\mathbf{R}_j, \boldsymbol{\rho}) \leq d(\mathbf{R}_j, \boldsymbol{\rho}')$ holds. This argument needs to be complemented by considering the uniform random permutations, corresponding to the assumed prior of the ranks originally missing in the data, across their possible values from $n+1$ to n^* . But this is automatic, because the conclusion holds separately for all permutations of such ranks.

Finally, the argument needs to be extended to the situation in which the sets \mathcal{A}_j of ranked items can be different for different assessors. In this case we are led to consider, as a by-product of the data augmentation scheme, a joint distribution of the rank vectors $\{\tilde{\mathbf{R}}_j; j = 1, \dots, N\}$. Here, for each j , the n_j items which were ranked first have been fixed by the data. The remaining $n - n_j$ items are assigned augmented random ranks with values between $n_j + 1$ and n , where the probabilities, corresponding to the model P_{n^*} , are determined by the inference from the assumed Mallows model and the data. The conclusion remains valid regardless of the particular way in which the augmentation was done, and so it holds also when taking an expectation with respect to P_{n^*} . ■

Remark. The above proposition says, in essence, that any consensus lists of top- n ranked items, which contains one or more items with their ranks completely missing in the data (i.e., the item was not explicitly ranked by any of the assessors), can be improved *locally*, in the sense of increasing the associated posterior probability with respect to P_{n^*} . This happens by trading such an item in the top- n list against another, which had been ranked but which had not yet been selected to the

list. In particular, the MAP estimate(s) for consensus ranking assign n highest ranks to explicitly ranked items in the data (which corresponds to the result in Meilă and Bao (2010) for Kendall distance). The following statement is an immediate implication of Proposition 4, following from a marginalization with respect to P_{n^*} .

Corollary 1 Consider, for $k \leq n$, collections $\{A_{i_1}, A_{i_2}, \dots, A_{i_k}\}$ of k items and the corresponding ranks $\{\rho_{i_1}, \rho_{i_2}, \dots, \rho_{i_k}\}$. In full analysis mode, the maximal posterior probability $P_{n^*}(\{\rho_{i_1}, \rho_{i_2}, \dots, \rho_{i_k}\} = \{1, 2, \dots, k\} | \text{data})$, is attained when $\{A_{i_1}, A_{i_2}, \dots, A_{i_k}\} \subset \mathcal{A}$.

Another consequence of Proposition 4 is the coincidence of the MAP estimates under the two probability measures P_n and P_{n^*} . For proving this result a further argument, which goes beyond Proposition 4, has to be made explicit.

Corollary 2 Denote by $\boldsymbol{\rho}^{MAP*}$ the MAP estimate for consensus ranking obtained in a full analysis, $\boldsymbol{\rho}^{MAP*} := \operatorname{argmax}_{\boldsymbol{\rho} \in \mathcal{P}_{n^*}} P_{n^*}(\boldsymbol{\rho} | \text{data})$, and by $\boldsymbol{\rho}^{MAP}$ the MAP estimate for consensus ranking obtained in a restricted analysis, $\boldsymbol{\rho}^{MAP} := \operatorname{argmax}_{\boldsymbol{\rho} \in \mathcal{P}_n} P_n(\boldsymbol{\rho} | \text{data})$. Then, $\boldsymbol{\rho}^{MAP*}|_{i:A_i \in \mathcal{A}} \equiv \boldsymbol{\rho}^{MAP}$.

Proof It follows from Proposition 4 that the n top ranks in $\boldsymbol{\rho}^{MAP*}$ are all assigned to items $A_i \in \mathcal{A}$. Therefore, using shorthand $\boldsymbol{\rho}_{\mathcal{A}} = (\boldsymbol{\rho}_i; A_i \in \mathcal{A})$ and $\boldsymbol{\rho}_{\mathcal{A}^c} = (\boldsymbol{\rho}_i; A_i \in \mathcal{A}^c)$ we see that $\boldsymbol{\rho}^{MAP*}$ must be of the form $\boldsymbol{\rho}^{MAP*} = (\boldsymbol{\rho}_{\mathcal{A}}^{MAP*}, \boldsymbol{\rho}_{\mathcal{A}^c}^{MAP*}) = (\boldsymbol{\pi}, \boldsymbol{\pi}')$, where $\boldsymbol{\pi}$ is a permutation of the set $(1, 2, \dots, n)$, and similarly $\boldsymbol{\pi}'$ is some permutation of $(n+1, \dots, n^*)$.

To prove the statement, we show the following: (i) the posterior probabilities $P_{n^*}(\boldsymbol{\rho}_{\mathcal{A}} = \boldsymbol{\pi}, \boldsymbol{\rho}_{\mathcal{A}^c} = \boldsymbol{\pi}' | \text{data})$ and $P_{n^*}(\boldsymbol{\rho}_{\mathcal{A}} = \boldsymbol{\pi} | \boldsymbol{\rho}_{\mathcal{A}^c} = \boldsymbol{\pi}', \text{data})$ are invariant under permutations of $\boldsymbol{\pi}'$, and (ii) the latter conditional probabilities $P_{n^*}(\boldsymbol{\rho}_{\mathcal{A}} = \boldsymbol{\pi} | \boldsymbol{\rho}_{\mathcal{A}^c} = \boldsymbol{\pi}', \text{data})$ coincide with $P_n(\boldsymbol{\rho}_{\mathcal{A}} = \boldsymbol{\pi} | \text{data})$. As a consequence, a list of top- n items obtained from the *full analysis* estimate $\boldsymbol{\rho}^{MAP*}$ qualifies also as the *restricted analysis* estimate $\boldsymbol{\rho}^{MAP}$, and conversely, $\boldsymbol{\rho}^{MAP}$ can be augmented with any permutation $\boldsymbol{\pi}'$ of $(n+1, \dots, n^*)$ to jointly form $\boldsymbol{\rho}^{MAP*}$.

The first part of (i) follows by noticing that the likelihood in the *full analysis*, when considering consensus rankings of the form $\boldsymbol{\rho} = (\boldsymbol{\rho}_{\mathcal{A}}, \boldsymbol{\rho}_{\mathcal{A}^c}) = (\boldsymbol{\pi}, \boldsymbol{\pi}')$, only depends on the observed data via $\boldsymbol{\pi}$. Since the assessors act independently, each imposing a uniform prior on their unranked items, also the posterior $P_{n^*}(\boldsymbol{\rho}_{\mathcal{A}} = \boldsymbol{\pi}, \boldsymbol{\rho}_{\mathcal{A}^c} = \boldsymbol{\pi}' | \text{data})$ will depend only on $\boldsymbol{\pi}$. The second part follows from the first, either by direct conditioning in the joint distribution, or by first computing the marginal $P_{n^*}(\boldsymbol{\rho}_{\mathcal{A}^c} = \boldsymbol{\pi}' | \text{data})$ by summation, and then dividing. (ii) follows then because, for both posterior probabilities, the sample space, the prior, and the likelihood are the same. ■

Remark. The above result is very useful in the context of applications, since it guarantees that the top- n items in the MAP consensus ranking do not depend on which version of the analysis is performed. Recall that a full analysis cannot always be carried out in practice, due to the fact that left-over items might be unknown, or their number might be too large for any realistic computation.

3.2 Pairwise Comparisons

In many situations, assessors compare pairs of items rather than ranking all or a subset of items. We extend our Bayesian data augmentation scheme to handle such data given as partial orderings. Our approach can be seen as an alternative to Lu and Boutilier (2014), who treated preferences by applying their Repeated Insertions Model (RIM). Our approach is simpler, it is fully integrated into our Bayesian inferential framework, and it works for any right-invariant distance.

As an example of paired comparisons, assume assessor j stated the preferences $\mathcal{B}_j = \{A_1 \prec A_2, A_2 \prec A_5, A_4 \prec A_5\}$. Here $A_r \prec A_s$ means that A_s is preferred to A_r , so that A_s has a lower rank

than A_r . Let \mathcal{A}_j be the set of items constrained by assessor j , in this case $\mathcal{A}_j = \{A_1, A_2, A_4, A_5\}$. Differently from Section 3.1, the items which have been considered by each assessor are now not necessarily fixed to a given rank. Hence, in the MCMC algorithm, we need to propose augmented ranks which obey the partial ordering constraints given by each assessor, to avoid a large number of rejections, with the difficulty that none of the items is now fixed to a given rank.

We assume that the pairwise orderings in \mathcal{B}_j are mutually compatible, and define by $\text{tc}(\mathcal{B}_j)$ the transitive closure of \mathcal{B}_j , containing all pairwise orderings of the elements in \mathcal{A}_j induced by \mathcal{B}_j . In the example, $\text{tc}(\mathcal{B}_j) = \mathcal{B}_j \cup \{A_1 \prec A_5\}$. For the case of ordered subsets of items, the transitive closure is simply the single set of pairwise preferences compatible with the ordering, e.g., $\{A_1 \prec A_2 \prec A_5\}$ yields $\text{tc}(\mathcal{B}_j) = \{A_1 \prec A_2, A_2 \prec A_5, A_1 \prec A_5\}$. The R packages **sets** (Meyer and Hornik, 2009) and **relations** (Meyer and Hornik, 2014) can be used to compute transitive closures efficiently.

The main idea of our method for handling such data remains the same as in Section 3.1, and consequently the corresponding algorithm is exactly the same as Algorithm 2. However, the leap-and-shift proposal distribution requires an adjustment in order to propose augmented ranks which are compatible with the partial ordering constraint. Suppose that, from the latest step of the MCMC algorithm, we have a full augmented rank vector $\tilde{\mathbf{R}}_j$ for assessor j , which is compatible with $\text{tc}(\mathcal{B}_j)$. Draw a random number u uniformly from $\{1, \dots, n\}$. If $A_u \in \mathcal{A}_j$, let $l_j = \max\{\tilde{R}_{kj} : A_k \in \mathcal{A}_j, k \neq u, (A_k \succ A_u) \in \text{tc}(\mathcal{B}_j)\}$, with the convention that $l_j = 0$ if the set is empty, and $r_j = \min\{\tilde{R}_{kj} : A_k \in \mathcal{A}_j, k \neq u, (A_k \prec A_u) \in \text{tc}(\mathcal{B}_j)\}$, with the convention that $r_j = n + 1$ if the set is empty. Now complete the leap step by drawing a new proposal \tilde{R}'_{uj} uniformly from the set $\{l_j + 1, \dots, r_j - 1\}$. Otherwise, if $A_u \in \mathcal{A}_j^c$, we complete the leap step by drawing \tilde{R}'_{uj} uniformly from $\{1, \dots, n\}$. The shift step remains unchanged.

3.3 Clustering Assessors Based on their Rankings of All Items

So far we have assumed that there exists a unique consensus ranking shared by all assessors. In many cases the assumption of homogeneity across a large numbers of assessors with respect to an underlying common consensus ranking is unrealistic: the possibility of dividing assessors into more homogeneous subsets, each sharing a consensus ranking of the items, brings the model closer to reality. We solve this using a mixture of Mallows model, again allowing for any right-invariant distance. In the frequentist framework, mixtures of Mallows models have been used to analyze heterogeneous rank data (Busse et al., 2007; Lu and Boutilier, 2014; Murphy and Martin, 2003), while Bayesian approaches have been limited to the Plackett-Luce (Caron et al., 2014) and generalized Mallows models (Meilă and Chen, 2010), the latter using only the Kendall distance. We assume here that the data consist of complete rankings. Clustering based on partial rankings or pairwise preference data is considered in the next section.

Let $z_1, \dots, z_N \in \{1, \dots, C\}$ assign each assessor to one of C clusters. The assessments within each cluster $c \in \{1, \dots, C\}$ are described by a Mallows model with parameters α_c and ρ_c , where ρ_c is called cluster consensus. Assuming conditional independence across the clusters, the augmented data formulation of the likelihood for the observed rankings $\mathbf{R}_1, \dots, \mathbf{R}_N$ is given by

$$P\left(\mathbf{R}_1, \dots, \mathbf{R}_N | \{\rho_c, \alpha_c\}_{c=1, \dots, C}, z_1, \dots, z_N\right) = \prod_{j=1}^N \frac{1_{\mathcal{P}_n}(\mathbf{R}_j)}{Z_n(\alpha_{z_j})} \exp\left\{\frac{-\alpha_{z_j}}{n} d(\mathbf{R}_j, \rho_{z_j})\right\}.$$

For the scale parameters, we assume the prior $\pi(\alpha_1, \dots, \alpha_C) \propto \lambda^C \exp(-\lambda \sum_{c=1}^C \alpha_c)$. We further assume that the cluster labels are a priori distributed according to $P(z_1, \dots, z_N | \tau_1, \dots, \tau_C) = \prod_{j=1}^N \tau_{z_j}$, where τ_c is the probability that an assessor belongs to the c -th subpopulation; $\tau_c \geq$

$0, c = 1, \dots, C$ and $\sum_{c=1}^C \tau_c = 1$. Finally τ_1, \dots, τ_C are assigned the standard symmetric Dirichlet prior $\pi(\tau_1, \dots, \tau_C) = \Gamma(\psi C) \Gamma(\psi)^{-C} \prod_{c=1}^C \tau_c^{\psi-1}$, using the gamma function $\Gamma(\cdot)$.

The number of clusters C is often not known, and the selection of C can be based on different criteria. Here we inspect the posterior distribution of the within-cluster sum-of-squares of the distances of the observed ranks from the corresponding cluster consensus (see Section 5.4 for more details on this criterion), and the Deviance Information Criterion (DIC) for Bayesian model selection (Celeux et al., 2006). The former approach is a Bayesian version of the more classical within-cluster sum-of-squares criterion for model selection, and we expect to observe an elbow in the within-cluster distance posterior distribution as a function of c , identifying the optimal number of clusters. The DIC is a hierarchical modeling generalization of the AIC and BIC, which favors a good fit but also penalizes the effective number of parameters (models with smaller DIC should be preferred). It is difficult to quantify what difference in DIC is significant (Spiegelhalter et al., 2002), but we consider models receiving DIC within 1 or 2 of the “best” as deserving consideration, while models with associated DIC more than 5 above the “best” have considerably less support.

Algorithm 3: MCMC Algorithm for Clustering Complete Rankings

```

input :  $\mathbf{R}_1, \dots, \mathbf{R}_N; C, \psi, \lambda, \sigma_\alpha, L, d(\cdot, \cdot), Z_n(\alpha), M$ 
output: Posterior distributions of  $\rho_1, \dots, \rho_C, \alpha_1, \dots, \alpha_C, \tau_1, \dots, \tau_C, z_1, \dots, z_N$ ,
Initialization of the MCMC:
randomly generate  $\rho_{1,0}, \dots, \rho_{C,0}, \alpha_{1,0}, \dots, \alpha_{C,0}, \tau_{1,0}, \dots, \tau_{C,0}$ , and  $z_{1,0}, \dots, z_{N,0}$ ,
for  $m \leftarrow 1$  to  $M$  do
    Gibbs step: update  $\tau_1, \dots, \tau_C$ 
    compute:  $n_c = \sum_{j=1}^N 1_c(z_{j,m-1})$ , for  $c = 1, \dots, C$ 
    sample:  $\tau_1, \dots, \tau_C \sim \mathcal{D}(\psi + n_1, \dots, \psi + n_C)$ 
    for  $c \leftarrow 1$  to  $C$  do
        Metropolis-Hastings step: update  $\rho_c$ 
        sample:  $\rho'_c \sim$  leap-and-shift distribution centred at  $\rho_{c,m-1}$ 
        compute:  $ratio \leftarrow$  equation (7) with  $\rho_c \leftarrow \rho_{c,m-1}$  and  $\alpha_c \leftarrow \alpha_{c,m-1}$ 
        sample:  $u \sim \mathcal{U}(0, 1)$ 
        if  $u < ratio$  then
            |  $\rho_{c,m} \leftarrow \rho'_c$ 
        else
            |  $\rho_{c,m} \leftarrow \rho_{c,m-1}$ 
        end
        Metropolis-Hastings step: update  $\alpha_c$ 
        sample:  $\alpha'_c \sim \mathcal{N}(\alpha_{c,m-1}, \sigma_\alpha^2)$ 
        compute:  $ratio \leftarrow$  equation (8) with  $\rho_c \leftarrow \rho_{c,m}$  and  $\alpha_c \leftarrow \alpha_{c,m-1}$ 
        sample:  $u \sim \mathcal{U}(0, 1)$ 
        if  $u < ratio$  then
            |  $\alpha_{c,m} \leftarrow \alpha'_c$ 
        else
            |  $\alpha_{c,m} \leftarrow \alpha_{c,m-1}$ 
        end
    end
    Gibbs step: update  $z_1, \dots, z_N$ 
    for  $j \leftarrow 1$  to  $N$  do
        for  $c \leftarrow 1$  to  $C$  do
            | compute cluster assignment probabilities:  $p_{cj} = \frac{\tau_{c,m}}{Z_n(\alpha_{c,m})} \exp \left[ \frac{-\alpha_{c,m}}{n} d(\mathbf{R}_j, \rho_{c,m}) \right]$ 
        end
        sample:  $z_{j,m} \sim \mathcal{M}(p_{1j}, \dots, p_{Cj})$ 
    end
end

```

We sample the resulting posterior distribution using an MCMC algorithm described in Section 3.3.1. Label switching is not explicitly handled inside our MCMC, to ensure full convergence of the chain (Jasra et al., 2005; Celeux et al., 2000). MCMC iterations are re-ordered after convergence is achieved, by using the re-ordering approaches in Papastamoulis (2015).

3.3.1 MCMC ALGORITHM FOR CLUSTERING

The MCMC algorithm used for clustering is sketched in Algorithm 3: it alternates between sampling ρ_1, \dots, ρ_C and $\alpha_1, \dots, \alpha_C$ in a Metropolis-Hastings step, and τ_1, \dots, τ_C and z_1, \dots, z_N in a Gibbs Sampler step. The former is straightforward, since $(\rho_c, \alpha_c)_{c=1, \dots, C}$ are conditionally independent given z_1, \dots, z_N . In the latter, we exploit the fact that the Dirichlet prior for τ_1, \dots, τ_C is conjugate to the multinomial conditional prior for z_1, \dots, z_N given τ_1, \dots, τ_C . Thus,

$$\begin{aligned} P(\tau_1, \dots, \tau_C | \rho_1, \dots, \rho_C; \alpha_1, \dots, \alpha_C; z_1, \dots, z_N) &= P(\tau_1, \dots, \tau_C | z_1, \dots, z_N) \\ &\propto P(z_1, \dots, z_N | \tau_1, \dots, \tau_C) P(\tau_1, \dots, \tau_C) \propto \mathcal{D}(z_1, \dots, z_N; \psi + n_1, \dots, \psi + n_C), \end{aligned}$$

where $\mathcal{D}(\cdot)$ denotes the Dirichlet distribution and $n_c = \sum_{j=1}^N 1_c(z_j)$, $c = 1, \dots, C$. Therefore, in the Gibbs Sampler step for τ_1, \dots, τ_C , we sample from $\mathcal{D}(\psi + n_1, \dots, \psi + n_C)$. In the Metropolis-Hastings step, the proposal ρ'_c for each cluster is sampled from the leap-and-shift distribution centred at ρ_c , and accepted with probability

$$\min \left\{ 1, \frac{\pi(\rho'_c)}{\pi(\rho_c)} \exp \left[\frac{-\alpha_c}{n} \sum_{j:z_j=c} \{d(\mathbf{R}_j, \rho_c) - d(\mathbf{R}_j, \rho'_c)\} \right] \right\}. \quad (7)$$

Next, $\alpha'_c \sim \mathcal{N}(\alpha_c, \sigma_\alpha^2)$, $\forall c = 1, \dots, C$. The proposed value α'_c is accepted with probability

$$\min \left\{ 1, \frac{Z_n(\alpha'_c)^{-n_c} \pi(\alpha'_c)}{Z_n(\alpha_c)^{-n_c} \pi(\alpha_c)} \exp \left[\frac{-(\alpha'_c - \alpha_c)}{n} \sum_{j:z_j=c} d(\mathbf{R}_j, \rho_c) \right] \right\}, \quad (8)$$

for $c = 1, \dots, C$. Finally, in the Gibbs Sampler step for z_j , $j = 1, \dots, N$, we sample from $P(z_j = c | \tau_c, \rho_c, \alpha_c, R_j) \propto \tau_c P(\mathbf{R}_j | \rho_c, \alpha_c) = \tau_c Z_n(\alpha_c)^{-1} \exp\{-(\alpha_c/n)d(\mathbf{R}_j, \rho_c)\}$.

3.4 Clustering of Assessors giving Pairwise Comparisons

It happens frequently in applications that the model extensions described in Sections 3.1, 3.2, and 3.3 occur jointly: the assessors only provide partial rankings or pairwise item comparisons, and they moreover cannot be assumed to form a sample from a homogeneous population. For example, we can think of situations where internet users provide their preferences on some selected movies (see the data experiment described in Section 5.5). In this section we describe how we deal with such complexities straightforwardly in our Bayesian Mallows model.

We cluster the data using the same mixture approach described in Section 3.3. Hence, the structure of the algorithm is the same as described in Section 3.3.1. However, assessors do not provide complete rankings $\mathbf{R}_1, \dots, \mathbf{R}_N$, but they rather give partial rankings described by the sets $\mathcal{S}_1, \dots, \mathcal{S}_N$, or some preferences contained in the sets $\mathcal{B}_1, \dots, \mathcal{B}_N$. Hence, differently from Algorithm 3, we now need to provide these sets as input to the MCMC algorithm, as already sketched in Algorithm 2. Embedded in the new algorithm, after the Gibbs step devoted to the updating of cluster assignments z_1, \dots, z_N , we need to perform the updating of the augmented rankings $\tilde{\mathbf{R}}_1, \dots, \tilde{\mathbf{R}}_N$. For each assessor j , $j = 1, \dots, N$, a new augmented rank vector $\tilde{\mathbf{R}}'_j$ is proposed with

the same strategy used in Algorithm 2: we use the leap-and-shift distribution centred at $\tilde{\mathbf{R}}_j$, and subject to the constraints given by either \mathcal{S}_j or \mathcal{B}_j . Then, the proposed augmented rank vector is accepted with probability

$$\min \left\{ 1, \exp \left[-\frac{\alpha_{z_j}}{n} \left(d(\tilde{\mathbf{R}}'_j, \boldsymbol{\rho}_{z_j}) - d(\tilde{\mathbf{R}}_j, \boldsymbol{\rho}_{z_j}) \right) \right] \right\}, \quad (9)$$

using the current estimates of $\boldsymbol{\rho}_c$ and α_c , for all $c = 1, \dots, C$, and the current cluster assignment of the assessor z_j . This MCMC algorithm used in the case of clustering with partial rankings or pairwise preferences, is sketched in Algorithm 4.

3.5 Class and Preference Prediction

Reliable prediction of missing information relating to the assessors is an important aspect in many applications. Often a curated training set is available, including assessors whose information (class assignments, rankings) is complete, and it is of interest to perform personalized predictions concerning the class membership or items ranking of new unknown users, who just provided very few preferences. These tasks are sometimes referred to as *personalized predictions*, being the first step towards personalized recommendation. These situations can be treated within our Bayesian Mallows model, by combining the strategies presented in the previous sections, in the following way.

Assume that assessors in a curated training set $\mathcal{T} \in \{1, \dots, N\}$ have provided a complete ranking of the items and have known class membership, while assessors in the testing set $\mathcal{T}^c := \{1, \dots, N\} \setminus \mathcal{T}$ only give partial information on their preferences (each assessor has left some items unranked), and no class membership is available. The task is to predict (with uncertainty) the missing class membership, and the ranks which assessors would have given to their unranked items. To do so, it is sufficient to use the Bayesian Mallows model extension concerning clustering with partial ranking or pairwise preference data: we run Algorithm 4, where $\{z_j\}_{j \in \mathcal{T}}$ are kept fixed at their true class memberships, while $\{z_j\}_{j \in \mathcal{T}^c}$ are estimated along the MCMC. The algorithm provides not only MAP estimates of the class memberships of assessors belonging to the testing set, which can be used to perform actual class assignments, but also the posterior predictive distribution of these class assignments, which quantify the uncertainties that are involved. This is a semi-supervised version of the unsupervised clustering algorithm described in Section 3.3 and 3.4. Moreover, if rankings provided by assessors in the training set are complete, we do not need to estimate a posterior distribution for $\{\tilde{\mathbf{R}}_j\}_{j \in \mathcal{T}}$; we just need to estimate it for $j \in \mathcal{T}^c$, and this can be used to assess (with uncertainty) the ranks which the assessors would have given to their unranked items.

Another important problem concerns individual prediction of preferences, often named *preference learning*, from observed preference information (Furnkranz and Hullermeier, 2011). In many situations, a training set is constructed from a set of assessors who have made extensive paired comparisons or even provided complete rankings. Based on these, we want to predict the preferences for new assessors, who have made just a small number of paired comparisons, see Francis et al. (2010) and the Netflix competition (netflixprize.com). We can again easily use the Bayesian mixture of Mallows models for prediction of preferences: if assessor j has compared only a subset of items, $P(\tilde{\mathbf{R}}_j | \text{data})$ represents posterior predictive probabilities about his/her full rankings. These posterior probabilities are directly obtained from our MCMC algorithms. For example, if assessor j did not compare A_1 to A_2 , we might be interested in $P(A_1 \prec_j A_2 | \text{data})$, which is readily obtained from $P(\tilde{\mathbf{R}}_j | \text{data})$. Here, ' \prec_j ' denotes a preference of assessor j .

Algorithm 4: MCMC Algorithm for Clustering Partial Rankings or Pairwise Preferences

input : $\{\mathcal{S}_1, \dots, \mathcal{S}_N\}$ or $\{\text{tc}(\mathcal{B}_1), \dots, \text{tc}(\mathcal{B}_N)\}$; $C, \psi, \lambda, \sigma_\alpha, L, d(\cdot, \cdot)$, $Z_n(\alpha)$, M
output: Posterior distributions of $\rho_1, \dots, \rho_C, \alpha_1, \dots, \alpha_C, \tau_1, \dots, \tau_C, z_1, \dots, z_N$, and $\tilde{\mathbf{R}}_1, \dots, \tilde{\mathbf{R}}_N$

Initialization of the MCMC:
randomly generate $\rho_{1,0}, \dots, \rho_{C,0}, \alpha_{1,0}, \dots, \alpha_{C,0}, \tau_{1,0}, \dots, \tau_{C,0}$, and $z_{1,0}, \dots, z_{N,0}$,
if $\{\mathcal{S}_1, \dots, \mathcal{S}_N\}$ among inputs then
 for $j \leftarrow 1$ to N **do**
 | randomly generate $\tilde{\mathbf{R}}_j^0$ in \mathcal{S}_j
 end
else
 for $j \leftarrow 1$ to N **do**
 | randomly generate $\tilde{\mathbf{R}}_j^0$ compatible with $\text{tc}(\mathcal{B}_j)$
 end
end
for $m \leftarrow 1$ to M **do**

Gibbs step: update τ_1, \dots, τ_C
compute: $n_c = \sum_{j=1}^N 1_c(z_{j,m-1})$, for $c = 1, \dots, C$
sample: $\tau_1, \dots, \tau_C \sim \mathcal{D}(\psi + n_1, \dots, \psi + n_C)$

for $c \leftarrow 1$ to C **do**
Metropolis-Hastings step: update ρ_c
sample: $\rho'_c \sim$ leap-and-shift distribution centred at $\rho_{c,m-1}$
compute: $\text{ratio} \leftarrow$ equation (7) with $\rho_c \leftarrow \rho_{c,m-1}$ and $\alpha_c \leftarrow \alpha_{c,m-1}$
sample: $u \sim \mathcal{U}(0, 1)$
if $u < \text{ratio}$ **then**
 | $\rho_{c,m} \leftarrow \rho'_c$
else
 | $\rho_{c,m} \leftarrow \rho_{c,m-1}$
end

Metropolis-Hastings step: update α_c
sample: $\alpha'_c \sim \mathcal{N}(\alpha_{c,m-1}, \sigma_\alpha^2)$
compute: $\text{ratio} \leftarrow$ equation (8) with $\rho_c \leftarrow \rho_{c,m}$ and $\alpha_c \leftarrow \alpha_{c,m-1}$
sample: $u \sim \mathcal{U}(0, 1)$
if $u < \text{ratio}$ **then**
 | $\alpha_{c,m} \leftarrow \alpha'_c$
else
 | $\alpha_{c,m} \leftarrow \alpha_{c,m-1}$
end

end

Gibbs step: update z_1, \dots, z_N
for $j \leftarrow 1$ to N **do**
 for $c \leftarrow 1$ to C **do**
 | compute cluster assignment probabilities: $p_{cj} = \frac{\tau_{c,m}}{Z_n(\alpha_{c,m})} \exp \left[\frac{-\alpha_{c,m}}{n} d(\tilde{\mathbf{R}}_j^{m-1}, \rho_{c,m}) \right]$
 end
 sample: $z_{j,m} \sim \mathcal{M}(p_{1j}, \dots, p_{Cj})$
end

Update $\tilde{\mathbf{R}}_1, \dots, \tilde{\mathbf{R}}_N$:
for $j \leftarrow 1$ to N **do**
if $\{\mathcal{S}_1, \dots, \mathcal{S}_N\}$ among inputs **then**
 | sample: $\tilde{\mathbf{R}}'_j$ in \mathcal{S}_j from the leap-and-shift distribution centred at $\tilde{\mathbf{R}}_j^{m-1}$
else
 | sample: $\tilde{\mathbf{R}}'_j$ from the leap-and-shift distribution centred at $\tilde{\mathbf{R}}_j^{m-1}$ and compatible with $\text{tc}(\mathcal{B}_j)$
end
compute: $\text{ratio} \leftarrow$ equation (9) with $\rho_{z_j} \leftarrow \rho_{z_{j,m}, m}$, $\alpha_{z_j} \leftarrow \alpha_{z_{j,m}, m}$ and $\tilde{\mathbf{R}}_j \leftarrow \tilde{\mathbf{R}}_j^{m-1}$
sample: $u \sim \mathcal{U}(0, 1)$
if $u < \text{ratio}$ **then**
 | $\tilde{\mathbf{R}}_j^m \leftarrow \tilde{\mathbf{R}}'_j$
else
 | $\tilde{\mathbf{R}}_j^m \leftarrow \tilde{\mathbf{R}}_j^{m-1}$
end

end

end

4. Related Work

We briefly review the literature on rank modelling and inference which appears to be most closely connected to our approach, in addition to background references given in Sections 1 and 2. Here we consider papers using the Mallows model, and papers following a fully probabilistic approach.

In terms of focus and aim, one of the proposals closer to ours is Lu and Boutilier (2014). Both this and the present paper develop methods which have the capacity of employing pairwise comparison data, and then of forming clusters of assessors for the purpose of preference learning and prediction. Indeed, two of our key illustrations, described in detail in the later Sections 5.4 and 5.5, are based on data sets considered also in Lu and Boutilier (2014). On the other hand, the approaches differ from each other in several ways, and most notably in the algorithms that are employed. While our MCMC approach uses a combination of data augmentation and leap-and-shift proposal moves for sampling latent complete data vectors based on pairwise comparison data, Lu and Boutilier (2014) construct such vectors, one by one for each assessor and applying sequential conditioning of the selection probabilities, using their basic Repeated Insertions Model (RIM), its generalization (GRIM), or a computationally more feasible version called Approximate Mallows Posterior (AMP). Moreover, like in nearly all papers on the Mallows model, only the Kendall distance is considered explicitly in Lu and Boutilier (2014). The Kendall distance is advantageous not only in the computation of the normalizing constant, but also in choosing the form of the insertion probabilities. In our paper, in addition to Kendall's, also the footrule and the Spearman distances are considered; apart from the computation of the normalizing constant, which is done off-line, the computational complexity remains approximately the same for all three distances. Finally, Lu and Boutilier (2014) target their statistical inference on deriving the Maximum Likelihood (ML) estimate of the consensus rank vector, using a method based on the Expectation Maximization (EM) algorithm, and they thus do not provide any uncertainty quantification for their estimates. Our target is the full posterior distribution of the unknown rank vector. The MCMC sampling algorithm uses again the leap-and-shift proposal moves, but now for updating the latent consensus ranks instead of incompletely specified data vectors. The fact that, for the uniform prior, the Maximum-a-Posterior (MAP) estimates and the ML estimates coincide, establishes a natural link between these inferential targets.

Other proposals based on the Mallows model include Meilă and Chen (2010) and Meilă and Bao (2010). A Dirichlet process mixture model over incomplete rankings is proposed in Meilă and Chen (2010), where two Gibbs sampling inference techniques for estimating the posterior are studied. The model handles clustering of partial rankings, and it is based on the Mallows model with the Kendall distance, thus extending the framework already described in Fligner and Verducci (1986) to handle heterogeneous rankings in a Bayesian setting. This framework is further enriched in Meilă and Bao (2010), where a Mallows model for infinite rankings is proposed: the Generalized Mallows (GM) model of Fligner and Verducci (1986) is further generalized to an infinite set of items, thus deriving the novel Infinite Generalized Mallows (IGM) model. Meilă and Bao (2010) give sufficient statistics and they define algorithms for ML estimation; they also propose a conjugate prior, and show that inference is much harder in a Bayesian framework (with the conjugate model). However, their model is again limited to the Kendall distance.

Among other probabilistic approaches, we find Sun et al. (2012). This promising non-parametric proposal constructs a fully probabilistic model on preferences, by also handling heterogeneous preference information. It gives clear statistical estimation procedures for the prediction of item rankings, the discovery of association rules, and the estimation of probabilities of interesting events. This work extends the non-parametric density estimation approaches over rankings (Lebanon and Mao, 2008) to include ranking data of arbitrary incompleteness and tie structure. However, from

a practical perspective, the approach is based on a random-censoring assumption, which could be easily violated in practice: people tend to rate items that they feel strongly about more frequently than those for which they do not have strong feelings. The robustness of the method to departures from the assumptions has not been considered extensively.

Another interesting proposal, which is close to ours more in the possibility to handle different data sources than in the method itself, is Volkovs and Zemel (2014): they use the Multinomial Preference Model (MPM), and the method is score-based. It can deal with pairwise preferences, even inconsistent ones, and it estimates via ML assessor-specific α 's. The approach also extends to supervised problems. Other issues related to this proposal are the of use gradient optimization on a non-convex problem (which can lead to local optima), and the somewhat arbitrary way of imputing missing ranks.

5. Experiments

The examples in this section illustrate the use of our approach in the various situations corresponding to different data structures. We start with the basic model and full data.

5.1 The Potato Experiment

To illustrate the method, we first consider an experiment where the true value of ρ is known. We bought a bag of potatoes, with a total weight of approximately 1.5 kilograms. The $n = 20$ potatoes were picked out from the bag one at a time at random, and marked by letter codes A, B,...,T. We then spread the potatoes on a table, and asked 12 assessors to rank them according to their weight twice: first just by visual inspection, and then he/she was allowed to feel the weight of the potatoes by holding them. The assessors acted independently. Afterwards we weighed each potato, thus deriving the true ranking ρ_{true} . Based on Section 2.2, we chose the exponential prior with rate $\lambda = 1/10$ when using the footrule and Kendall distance, and $\lambda = n/20$ when using the Spearman distance.

The heat plots in Figure 3 show the posterior probabilities, for all potatoes, for being ranked as the k -th heaviest, plotted against their true ranks. The trace is the sum of the posterior probabilities that each potato is ranked correctly, namely $\sum_{i=1}^n P(\rho_i = \rho_{true,i} | \text{data})$. The Kullback-Leibler distance between the posterior marginal probability $P(\rho_i | \text{data})$ and the density with all mass on the true value $\rho_{true,i}$ could also be used. In the visual inspection experiment, the Spearman distance had the largest trace, while the Kendall distance had the smallest. In the weighing experiment, the footrule distance performed slightly better than the Kendall distance, and both provided much more accurate results than the Spearman distance. The middle range potatoes were ranked less accurately by the assessors than those at the extremes, especially in the visual inspection experiment. Figure A3 in the Appendix shows posterior histograms for the latent ranks for selected potatoes. The different distance measures performed varyingly in the different situations, but overall the Mallows model with the footrule distance seemed to be the best in order to maximize the expected number of correctly ranked potatoes.

5.1.1 IMPORTANCE SAMPLING APPROXIMATION OF THE PARTITION FUNCTION IN THE POTATO EXPERIMENT

We use the potato experiment to study the effect of the importance sampling approximation of the normalising constant on the convergence of the MCMC. We performed such a test on the potato weighing experiment with full data, by running the MCMC for different choices of the number M of MCMC iterations, and using a \hat{Z} estimated with importance sampling with a varying number K of

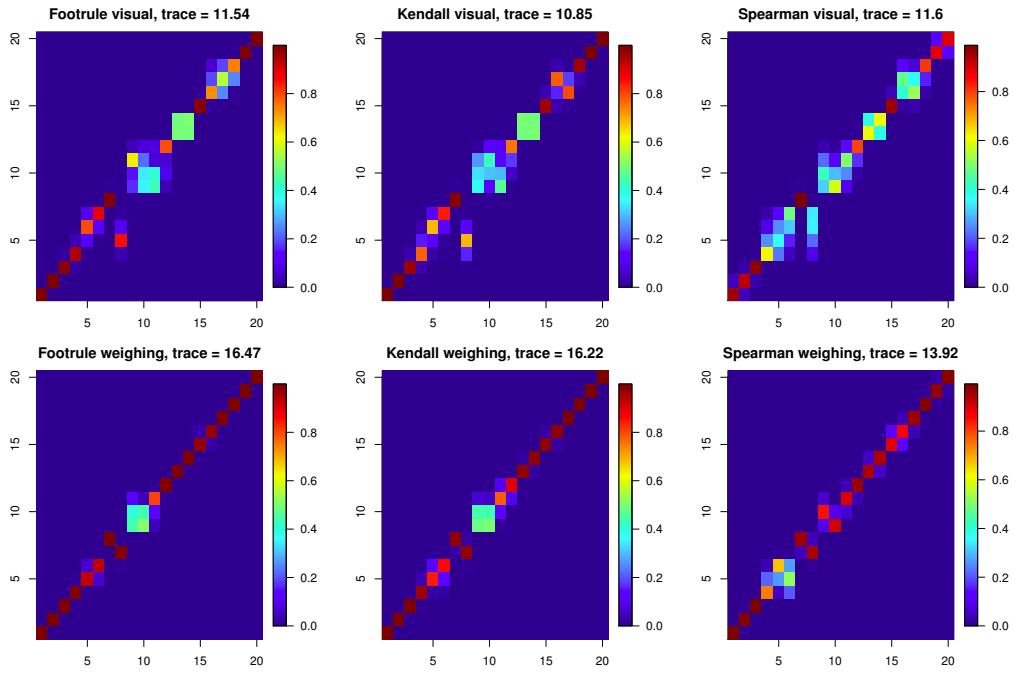


Figure 3: Results of the potato experiment. Heat plots of the latent ranks (vertical axis) versus the true rank (horizontal axis).

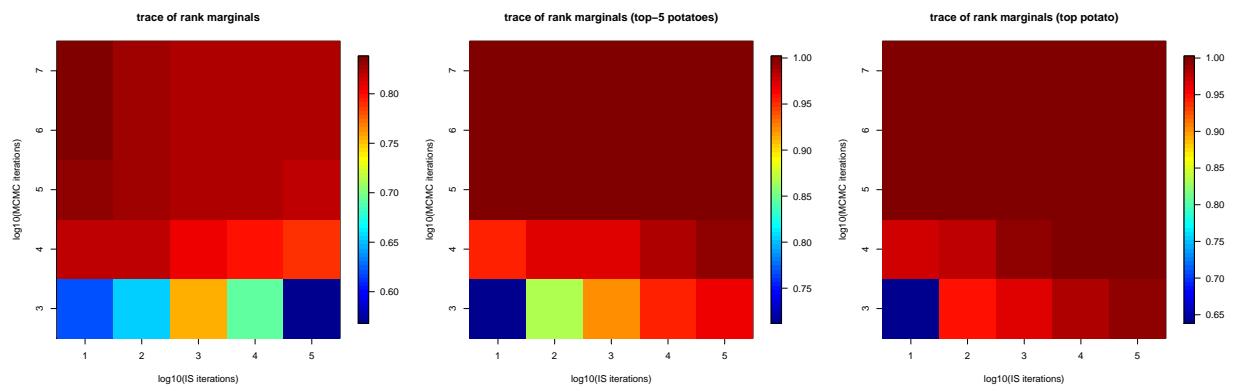


Figure 4: Results of the potato experiment. Posterior MCMC estimation with full ranking with the footrule distance, varying the number of IS (on x-axis in log scale) and MCMC iterations (on y-axis in log scale). Left: posterior expectation of the proportion of correctly ranked potatoes. Center: same posterior expectation for the top-5 potatoes. Right: posterior probability for correctly ranking the top potato.

Method Distance	Visual experiment						
	PerMallows Kendall	Rankcluster -	RankAggreg*		Bayesian Mallows*		
			Spearman	Kendall	Footrule	Spearman	Kendall
# of correctly estimated potatoes**	13	10	6	1	13	13	12
$d(\rho, \rho_{true})$	4	10	38	62	5	4	7
comp. time (sec)	0	276	3.54	1304.4	12.75	13.67	143.39

Method Distance	Weighing experiment						
	PerMallows Kendall	Rankcluster -	RankAggreg*		Bayesian Mallows*		
			Spearman	Kendall	Footrule	Spearman	Kendall
# of correctly estimated potatoes**	14	15	9	5	18	14	16
$d(\rho, \rho_{true})$	3	3	19	66	1	3	2
comp. time (sec)	0.1	257	3.76	3212.9	13.28	16	141.89

Table 2: Results of the potato experiment. Top, visual experiment; bottom: weighing experiment.

Comparison of performance of various methods for ranks estimation; $d(\rho, \rho_{true})$ refers to the Kendall distance between the true and the estimated ranking. *The RankAggreg and Bayesian Mallows method allow for different distances. **For the Rankcluster and Bayesian Mallows methods, which are probabilistic, the # of correctly estimated potatoes and $d(\rho, \rho_{true})$ refer to the MAP.

iterations. Our aim was to check whether a weaker approximation of the normalizing constant can prevent the MCMC from converging to a close approximation of the correct posterior distribution, or, on the other hand, whether our MCMC is sufficiently robust to small perturbations in \hat{Z} .

The results were evaluated by computing the posterior expectation of the proportion (out of the $n = 20$ potatoes) of correctly ranked potatoes. Results are shown in Figure 4 (left): a large number of MCMC iterations was always sufficient for convergence, even when the normalizing constant was badly estimated. Somewhat surprisingly, the results corresponding to a large number of MCMC iterations appear better when the estimates of \hat{Z} are worse. This was due to the 7th and 8th heaviest potatoes being almost always ranked in the wrong order by the assessors, apparently because of the somewhat unusual shape of the latter (see Figure A1). Understandably, this reversal of ranks no longer influences the results concerning the top-5 potatoes (Figure 4, center), nor those on the identification of the heaviest potato (Figure 4, right): in both cases the estimates became consistently better the more MCMC iterations were performed, and this happened faster when the normalizing constant was estimated more accurately. We conclude that the importance sampling approximation of \hat{Z} does not disturb significantly the convergence of the MCMC to the right limit.

5.1.2 COMPARISON WITH OTHER METHODS IN THE POTATO EXPERIMENT

We use the potato experiment also to compare the performance of our method with other existing approaches to the analysis of rank data. We compare the performance of our Bayesian method with two distance-based approaches, which are based on the Mallows model and which allow for some flexibility in the choice of the distance, and with one probabilistic approach. To our knowledge there is no approach, apart from ours, for performing model-based probabilistic inference when using a distance-based rank model with the possibility of using distances other than the Kendall's.

The PerMallows R package includes functions to perform ML estimation in the Mallows model with the Kendall's-tau, Cayley, Hamming and Ulam distances, and inference is based on the EM. RankAggreg (Pihur et al., 2014) formulates the rank aggregation as a distance-based optimization problem, allowing for both the Kendall and the Spearman distances to be used, and it solves it via either a CrossEntropy method or a Genetic Algorithm. It does not quantify the uncertainty associated to the results, and it does not guarantee convergence to a global optimum. Rankcluster (Jacques et al., 2014) proposes both modeling and clustering tools for partial ranking data, by using the Insertion Sorting Rank (ISR) model, parametrized by a central ranking and a dispersion

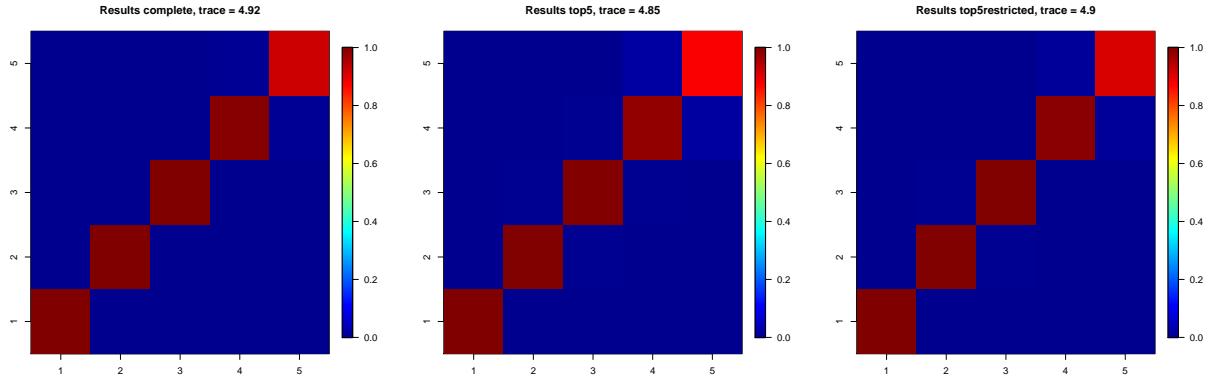


Figure 5: Results of the potato experiment. Heat plots of the latent ranks (vertical axis) versus the true rank (horizontal axis) of the five heaviest potatoes. Left: situation 1, complete rankings. Center: situation 2a, only the top-5 rankings for each assessor. Right: situation 2b, only the five heaviest potatoes.

parameter. It is a probabilistic approach, and it thus provides full uncertainty quantification, but it is not based on the Mallows model. The RMallows package (Murphy and Martin, 2003) could not be used, because it allows only for 2 or more clusters, which was unreasonable for the potato experiment.

Results of the comparison are summarized in Table 2, in terms of number of correctly estimated rankings, distance from the truth, and computational time. From an inspection of the table we conclude that the Rankcluster method is extremely inefficient (very high computational time in both experiments), while the RankAggreg is not giving reliable estimates (the distance from the true ranking is much larger than the one obtained with other methods). The PerMallows and our Bayesian Mallows are somehow comparable, even though our proposal outperforms PerMallows in the weighing experiment. Note that a long computational time is the price that has to be paid when using probabilistic approaches, which on the other hand allow for much more insightful results.

5.1.3 TOP- k ESTIMATION IN THE POTATO EXPERIMENT

In many applications, the main interest lies in estimating the top- k items, for some number $k < n$. Collecting complete ranks is more demanding than asking for only the top items, thus in the planning of experiments, and when collecting data, it is important to decide how many top ranks each assessor should identify. We aim here at providing a small illustration of these matters.

We investigate this in the case of our potato weighing experiment, leaving all settings unchanged and using the footrule distance, which proved to be best in this case (see results in Figure 3). We aim at correctly ranking the top-5 potatoes, and we consider the following three situations, using the notation introduced in Section 3.1.1:

1. complete data: $n_j = n = n^* = 20$, $j = 1, \dots, 12$;
- 2a. only the top-5 rankings for each assessor, all potatoes included in the analysis (*full analysis*): $n_j = 5$, $j = 1, \dots, 12$; $n = 8$, $n^* = 20$;
- 2b. only the top-5 rankings for each assessor, only the ranked potatoes included in the analysis (*restricted analysis*): $n_j = 5$, $j = 1, \dots, 12$; $n = n^* = 8$;

Rank	Gene	$P(\rho \leq \text{Rank})$	$P(\rho \leq 10)$	$P(\rho \leq 25)$
1	HPN	0.05	0.34	0.61
2	AMACR	0.07	0.27	0.54
3	NME1	0.07	0.23	0.51
4	GDF15	0.09	0.23	0.5
5	EEF2	0.1	0.19	0.42
6	FASN	0.13	0.21	0.45
7	KRT18	0.13	0.18	0.4
8	UAP1	0.13	0.17	0.4
9	CANX	0.12	0.14	0.34
10	SLC25A6	0.15	0.15	0.33
11	NME2	0.17	0.16	0.36
12	MTHFD2	0.19	0.16	0.38
13	OACT2	0.2	0.16	0.36
14	PPIB	0.19	0.14	0.34
15	ALCAM	0.2	0.13	0.34
16	STRA13	0.21	0.13	0.32
17	GRP58	0.22	0.13	0.32
18	SLC19A1	0.23	0.13	0.32
19	RPS13	0.24	0.12	0.31
20	SND1	0.25	0.12	0.3
21	MARCKS	0.26	0.12	0.3
22	TMEM4	0.27	0.11	0.31
23	MRPL3	0.27	0.12	0.3
24	PCDHGC3	0.28	0.12	0.3
25	CCT2	0.32	0.12	0.32

Table 3: Results of the meta-analysis experiment: finding a consensus of genes across studies (with a *restricted analysis*). The table shows the top-25 genes in the MAP consensus ranking estimated from five different studies of prostate cancer, comprising a total of 89 genes. The cumulative probability of each gene in the top-25 positions in the MAP of being in that position, or higher, is shown in the third column of the table ($P(\rho \leq \text{Rank})$). The probabilities of being among the top-10 and top-25 are also shown for each gene.

Note that $n = 8$ in the situations 2a and 2b because exactly 8 out of 20 potatoes had been ranked among the top-5 by at least one assessor. All 20 potatoes were included in the analysis 2a (*full analysis*), whereas in 2b the 12 unranked potatoes were discarded at the beginning (*restricted analysis*). Figure 5 shows heat plots of the estimated five heaviest potatoes in these three situations. We observe that reducing the amount of information did not result in a significant loss in accuracy of the estimates, and that in particular the ranking order between the top-5 potatoes remained the same in the MAP. This latter property is consistent with the statement of Corollary 2 in Section 3.1. In Section 5.2 we consider a situation in which both n and n^* are much larger, where a ranking following the *restricted analysis* mode is still doable, but where performing a *full analysis* would be both extremely laborious and, in view of Corollary 2, not worth the effort.

5.2 Meta-Analysis of Differential Gene Expression

Studies of differential gene expression between two conditions produce a list of genes, ranked according to their level of differential expression as measured by, e.g., p -value. There is often little overlap between gene lists found by independent studies comparing the same conditions, and it is interesting to find a consensus list over all available studies. We handle this situation in our Bayesian Mallows model by considering each study $j \in \{1, \dots, N\}$ to be an assessor, providing a top- n_j list of differentially expressed genes, which are the ranked items. This problem has been studied by DeConde et al. (2006); Deng et al. (2014); Lin and Ding (2009), who all used five studies comparing prostate cancer patients with healthy controls (Dhanasekaran et al., 2001; Luo et al., 2001; Singh et al., 2002; True et al., 2006; Welsh et al., 2001). We consider the same five studies, and we aim at estimating a final consensus with focus on the associated uncertainty. Data consist of the top-25 lists of genes from each study, in total 89 genes. Here we can only perform a restricted analysis, and in this case $n_j = 25$ for all $j = 1, \dots, 5$, and $n = 89$. We could not establish the exact

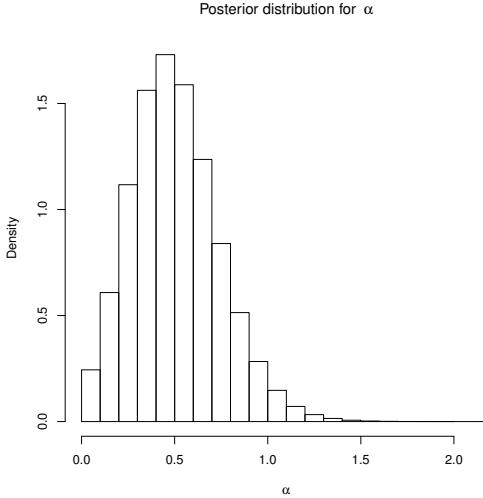


Figure 6: Results of the meta-analysis experiment. Posterior distribution for α in the meta analysis of gene lists.

total number n^* of genes appearing in all original studies together. However, it must be at least 7567, which was the largest number of genes included in any of the five original studies (DeConde et al., 2006).

Table 3 shows the result of analyzing the five gene lists with the Mallows footrule model. Like DeConde et al. (2006); Deng et al. (2014); Lin and Ding (2009), our method ranks the genes HPN and AMACR first and second in the MAP consensus ranking, but otherwise there is little agreement. The low level of agreement between the studies is also illustrated by the posterior distribution for α , shown in Figure 6: α is small, with a mean around 0.5, indicating a low level of agreement between the studies. Following Section 2.2, this means that the likelihood contribution of a ranking R_i deviating from ρ_i by $n/2$, is about 78%. Notice also the low posterior probability for each gene to be among the top-10. In the hypothetical situation in which we had included in our analysis all n^* genes following a *full analysis* mode, this would have had the effect of making the posterior probabilities in Table 3 even smaller. On the other hand, because of Corollary 2, the ranking order obtained from such a hypothetical analysis based on all n^* genes would remain the same as in Table 3. We thus conclude that these five studies of prostate cancer jointly have led to quite incompatible evidence.

5.3 A Premier League Season

The English football Premier League consists of 20 teams, which all play two games against each other in every season. To illustrate the use of paired comparisons, we let the Mallows model with footrule distance give an alternative ranking of the teams, by considering each matchday as an assessor, and each match as a pairwise comparison between the two teams (items) involved. Each game not ending in a draw is considered as a fixed pairwise comparison, giving preference to the winning team. Games resulting in a draw are uniformly randomized to a preference inside the MCMC algorithm. The results of the games during the 2010/11 season are all used to estimate a final ranking of the teams based on the Mallows model. Note that a predictive model for betting would take into account a large number of other factors (home/away games, players, time during

Official League Table			Mallows Footrule Table		
Team	Points	GD	Team	Cum. prob.	90 % HPD Int.
1 Man. United	80	+41	1 Man. United	0.21	(1,7)
2 Chelsea	71	+36	2 Man. City	0.30	(1,10)
3 Man. City	71	+27	3 Chelsea	0.36	(1,11)
4 Arsenal	68	+29	4 Tottenham	0.43	(1,12)
5 Tottenham	62	+9	5 Arsenal	0.52	(1,12)
6 Liverpool	58	+15	6 Everton	0.45	(1,14)
7 Everton	54	+6	7 Liverpool	0.47	(1,15)
8 Fulham	49	+6	8 Fulham	0.46	(1,16)
9 Aston Villa	48	-11	9 Aston Villa	0.36	(3,19)
10 Sunderland	47	-11	10 Sunderland	0.42	(5,20)
11 West Bromwich	47	-15	11 Newcastle	0.45	(5,20)
12 Newcastle	46	-1	12 West Bromwich	0.49	(6,20)
13 Stoke City	46	-2	13 Bolton	0.55	(6,20)
14 Bolton	46	-4	14 Wigan	0.62	(6,20)
15 Blackburn	43	-13	15 Stoke City	0.64	(6,20)
16 Wigan	42	-21	16 Birmingham	0.67	(6,20)
17 Wolverhampton	40	-20	17 Blackburn	0.75	(7,20)
18 Birmingham	39	-21	18 Blackpool	0.78	(9,20)
19 Blackpool	39	-23	19 Wolverhampton	0.87	(10,20)
20 West Ham	33	-27	20 West Ham	1.00	(10,20)

Table 4: Results of the Premier League experiment. Right: official final Premier League table for season 2010/11. Left: Premier League teams arranged according to the CP consensus ranking in the Mallows model with footrule distance, together with the corresponding 90% highest posterior density intervals.

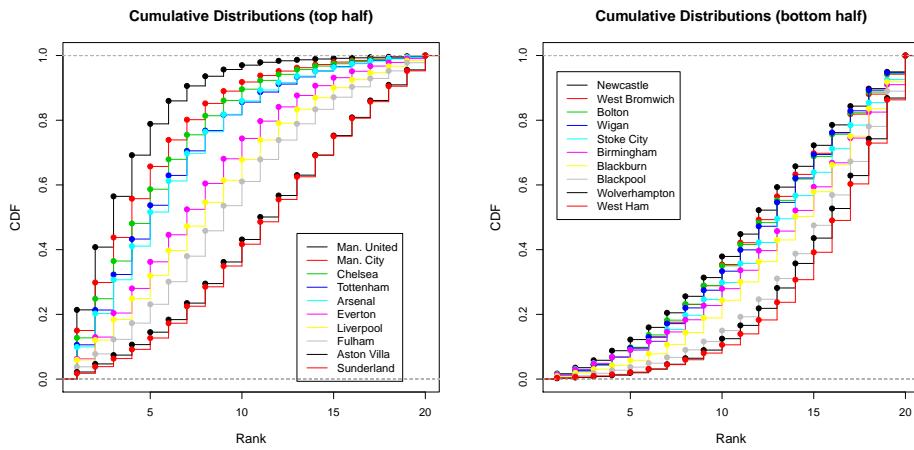


Figure 7: Results of the Premier League experiment. Posterior cumulative distribution functions obtained with the Mallows model with footrule distance, for the ranks of the teams in the Premier League in the 2010/11 season.

the season, etc.), which we have not included at this point. Our aim in using this data is rather to illustrate the potentiality of the Mallows model, and its ability to estimate a good ranking.

To summarize the joint posterior distribution for the ranks of all teams, we first identified the team with highest marginal posterior probability for having rank 1, then the team with the highest marginal posterior probability for having rank 1 or 2 (excluding the first), and so on. In the following, we will denote this ranking strategy cumulative probability (CP) consensus ranking (see Table 4). The numbers in parentheses show the 90 % highest posterior density intervals (HPDI) for the ranks of each team, representing the posterior uncertainty in the ranking based on the actual game results. Table 4 agrees very well with the official final league table of that season, especially in the top and bottom of the table. The HPDIs are very wide, because there is considerable variability

	$c = 1$	$c = 2$	$c = 3$	$c = 4$	$c = 5$
τ_c (%)	27.56 (26.28,28.73)	12.65 (11.96,13.39)	13.67 (12.93,14.42)	16.02 (15.21,16.86)	30.1 (29.06,31.26)
α_c	3.57 (3.46,3.68)	3.16 (2.87,3.45)	2.82 (2.62,3.02)	3.9 (3.74,4.05)	1.9 (1.82,1.99)
fatty tuna	sea urchin	shrimp	fatty tuna	fatty tuna	fatty tuna
sea urchin	sea eel	squid	tuna	sea eel	tuna
salmon roe	shrimp	egg	tuna roll	salmon roe	salmon roe
tuna	salmon roe	sea eel	shrimp	shrimp	tuna roll
shrimp	squid	cucumber roll	squid	squid	squid
sea eel	egg	tuna	egg	egg	egg
tuna roll	fatty tuna	tuna roll	sea eel	sea urchin	sea urchin
squid	tuna	fatty tuna	cucumber roll	cucumber roll	cucumber roll
egg	tuna roll	salmon roe	salmon roe	salmon roe	salmon roe
cucumber roll	cucumber roll	sea urchin	sea urchin	sea urchin	sea urchin

Table 5: Results of the Sushi experiment. Sushi items arranged according to the CP consensus ranking found from the posterior distribution of ρ_c , $c = 1, \dots, 5$. At the top of the table, corresponding MAP estimates for τ (in %) and α , with 95% HPDIs (in parenthesis).

in the outcomes of individual games, and because the data are fairly sparse, as each pair of teams meet only twice per season. Interestingly, most other sports have more games in the final rounds.

Figure 7 shows the posterior cumulative distribution functions for the ranks of the Premier League teams. The plots indicate that most teams are stochastically ordered: we say that team A_i dominates A_j , in the sense of stochastic ordering, if $P(\rho_i \leq r | \text{data}) \geq P(\rho_j \leq r | \text{data})$, $\forall r \in \{1, \dots, n\}$. The posterior CDFs for the rankings of all twenty teams, shown in Figure 7, reveal perfect stochastic orderings between most of the teams, with Manchester United stochastically dominating all others, and West Ham being stochastically dominated by all others. Supplementary Table A4 shows an indicator matrix for all the stochastic orderings.

5.4 Sushi Data

We illustrate clustering based on full rankings using the benchmark dataset of sushi preferences collected across Japan (Kamishima, 2003), see also Lu and Boutilier (2014). $N = 5000$ people were interviewed, each giving a complete ranking of $n = 10$ sushi variants. Cultural differences among Japanese regions influence food preferences, so we expect the assessors to be clustered around different preferences. We analyzed the sushi data using mixtures of Mallows models with the footrule distance. In the Dirichlet prior for τ , we set $\psi = N/C$, thus favoring high-entropy distributions (note that this parameter is updated during the MCMC by adding the number of assessors within each cluster).

For each candidate $C \in \{1, \dots, 10\}$, we used a thinned subset of MCMC samples to compute the posterior footrule distance between ρ_c and the ranking of each assessor assigned to cluster c , for $c = 1, \dots, C$. The posterior of the sum of squares of such within-cluster distances over all assessors and cluster centers, i.e., of $\sum_{c=1}^C \sum_{j:z_j=c} d(\mathbf{R}_j, \rho_c)^2$, was used for choosing an appropriate value for C , see Figure 8 (top, left). We found an elbow at $C = 5$, which was then used to further inspect results. We also inspect the DIC of each model, shown in the top right panel of Figure 8: the DIC also points to $C = 5$ as the optimal and most parsimonious choice, since all models with $C \geq 5$ have comparable DIC, significantly different from the DIC obtained when $C < 5$.

Table 5 shows the results when the number of clusters is set to $C = 5$: the maximum a posteriori (MAP) estimates for τ and α , together with their 95% HPDIs, are shown at the top of the table. The table also shows the sushi items, arranged in cluster-specific lists according to the CP consensus ranking; this is the same strategy as that employed in Section 5.3. These lists are very similar to the results of Lu and Boutilier (2014), Section 5.3.2, with $C = 6$ clusters: their sushi items lists characterizing clusters 5 and 6 are very similar to each other, and both are very well represented

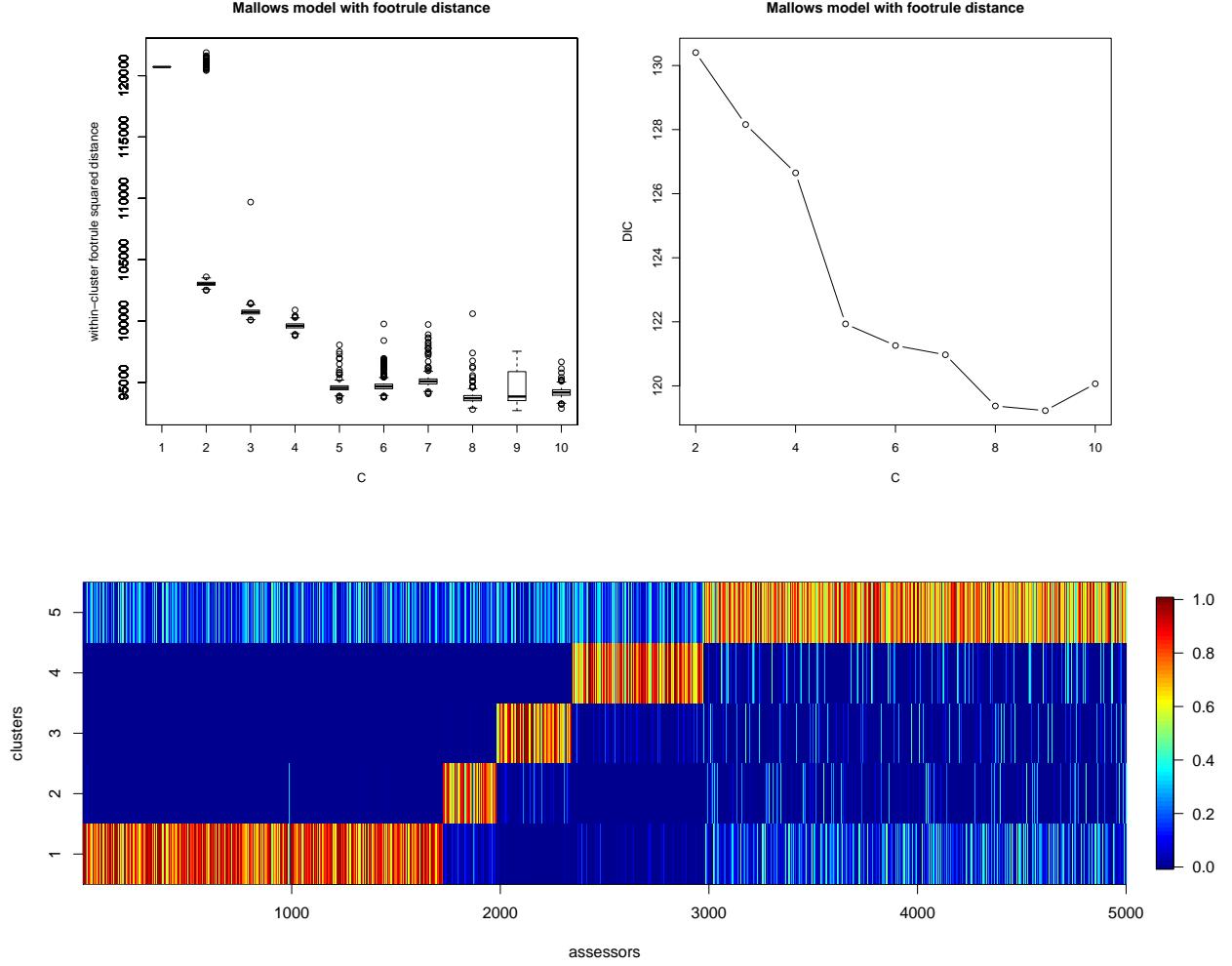


Figure 8: Results of the Sushi experiment. Top, left: boxplots of the posterior distributions of the within-cluster sum-of-squares distances of assessors from the corresponding cluster center for different choices of C . Top, right: DIC index for different choices of C . Bottom: heatplot of posterior probabilities for all 5000 assessors (on the x-axis) of being assigned to each cluster ($c = 1, \dots, 5$ from bottom to top).

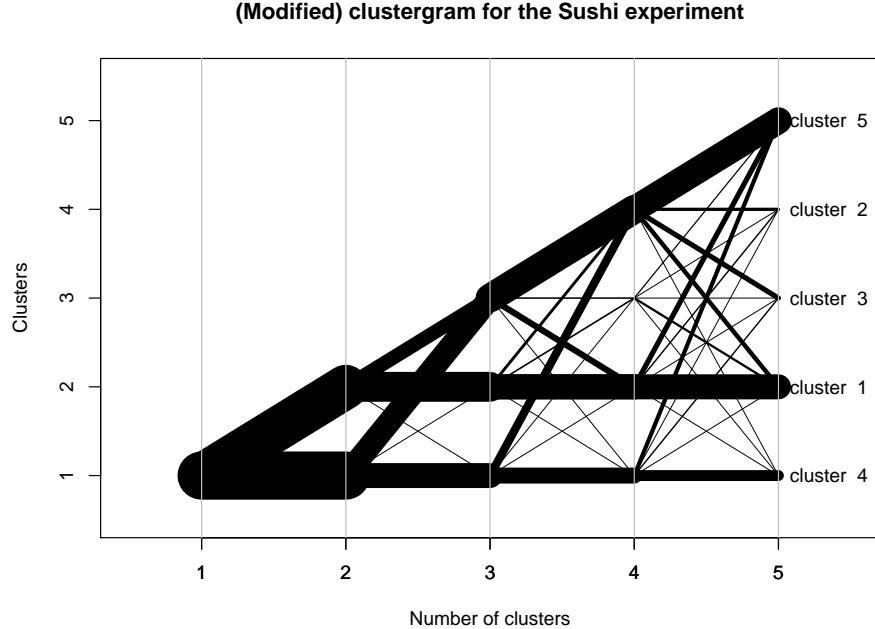


Figure 9: Results of the Sushi experiment. Clustergram of cluster assignments for $C = 1, \dots, 5$.

by the list corresponding to ρ_1 , cluster 1 in Lu and Boutilier (2014) can correspond to ρ_5 , cluster 2 to ρ_3 , cluster 3 to ρ_2 , and cluster 4 to ρ_4 .

Note that the dispersion parameter α in our Bayesian Mallows model is connected to the dispersion parameter ϕ in Lu and Boutilier (2014) by the link $\alpha = -\log(\phi)$. Hence, we can also observe that the estimated dispersion around the cluster lists reported in Table 5 is much lower than in Lu and Boutilier (2014) results, there represented by the corresponding estimates of $\{-\log(\phi_0), -\log(\phi_1), \dots, -\log(\phi_5)\}$.

We can also investigate the stability of the clustering. Figure 8 (bottom) shows a heatplot of posterior probabilities, for all 5000 assessors (shown on the x-axis), for being assigned to each of the $C = 5$ clusters identified in Table 5 (clusters $c = 1, \dots, 5$ from bottom to top in Figure 8). As shown by the heatplot, most of these individual probabilities were concentrated on some particular preferred value of c among the five possibilities, indicating a reasonably stable behavior in the cluster assignments.

Finally, since our Bayesian Mallows mixture is not a hierarchical clustering method, we can inspect how consistent the clustering obtained for different values of C actually is. Figure 9 shows a clustergram (Schonlau, 2002), which is a graphical representation of the flow in the assignment of assessors to different clusters when a new cluster is added to the mixture. The figure is based on the MAP estimates of cluster assignments for $C \in \{1, \dots, 5\}$. The thickness of each line represents the proportion of assessors in the cluster who moved along that route. The labels were arranged so that larger flows did not cross too much, and that the clusters could be compared easily to the results reported in Table 5 and Figure 8. The clustergram in Figure 9 shows good stability in the cluster memberships for different values of C , especially for bigger clusters.

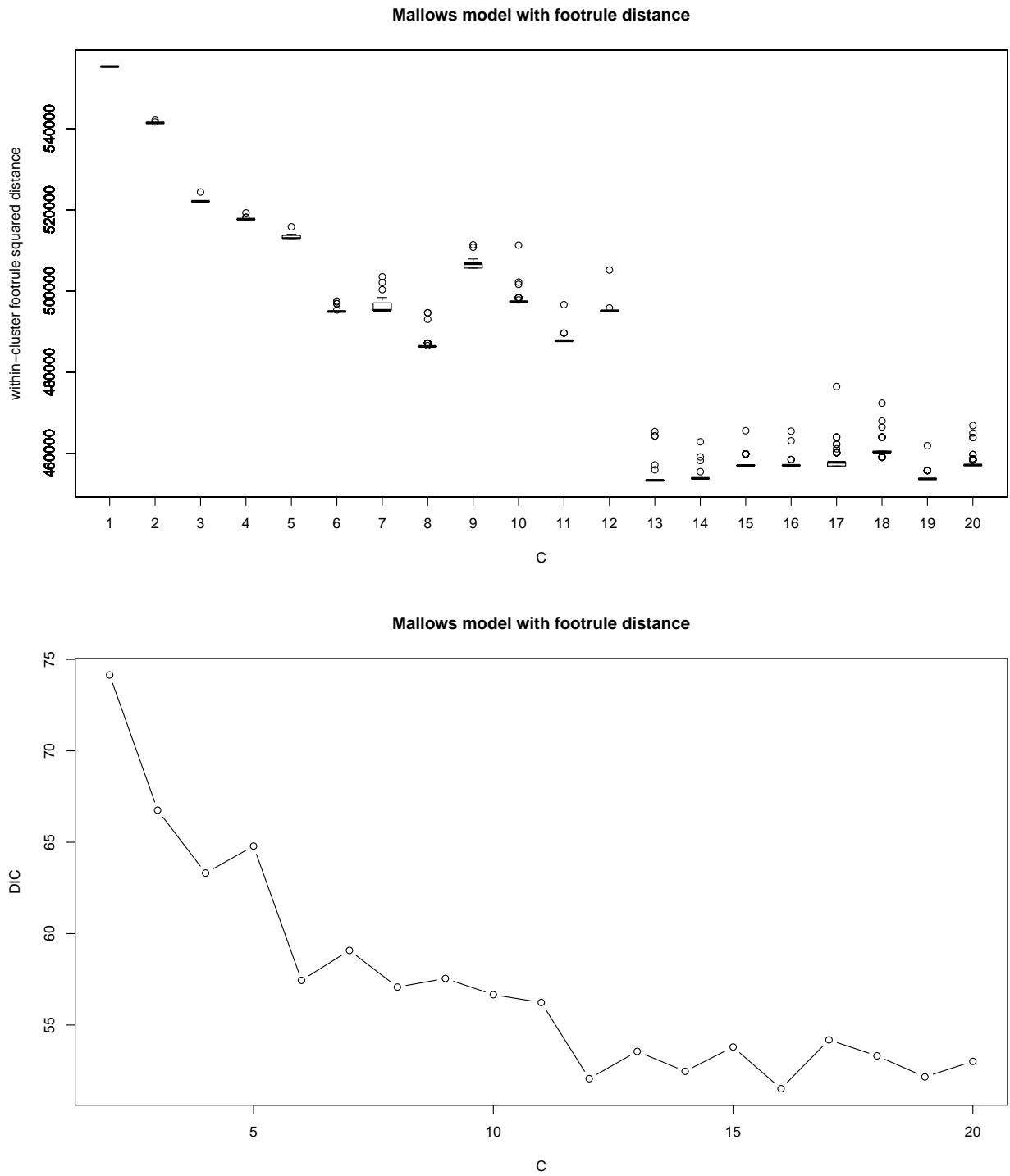


Figure 10: Results of the MovieLens experiment. Top: boxplots of the posterior distributions of the within-cluster sum-of-squares distances of assessors from the corresponding cluster center for different choices of C . Bottom: DIC index for different choices of C .

5.5 MovieLens Data

The MovieLens dataset (www.grouplens.org/datasets/) contains movie ratings from 6040 users. In this illustrative example, we focused on the $n = 200$ most rated movies, and on the $N = 5989$ users who rated at least 3 of these movies¹. Each user had considered only a subset of the n movies (30.2 on average). We then converted the ratings given by each assessor from a 1-5 scale to pairwise preferences as described in Lu and Boutilier (2014): each movie was preferred to all movies which the assessor in question had rated strictly lower. For simplicity, movies whose rating coincided for an assessor were randomized to a preference at the beginning: for each pair of movies with the same rating, a preference was created by sampling one of the two possible outcomes with equal probability. Preference inconsistencies, which could be generated in the tie randomization, were then automatically removed when computing the transitive closure. Note that the Bayesian Mallows model easily allows to randomize the ties also within the MCMC, but we decided not to do so in the present application in order to reduce the computational burden of the procedure.

We applied for these data the Mallows model with the footrule distance. With $n = 200$, the importance sampling scheme for $Z_n(\alpha)$ was not converging, and we implemented the asymptotic approximation described in Mukherjee (2013). Since we expected preference heterogeneity among assessors, due to age/gender/social factors/education, we applied our clustering scheme for pairwise comparisons. We kept all settings described in Section 3.3. Note that the label switching problem only affects inference on cluster-specific parameters, but it does not affect predictive distributions (Celeux et al., 2006). We varied the number C of clusters in the set $\{1, \dots, 20\}$, and inspected the posterior sum of squares of the within-cluster distances together with the DIC in order to select the optimal C . Results are shown in Figure 10. The posterior within-cluster distance shows two elbows: one at $C = 6$ and one at $C = 13$. The same behavior can be observed in the DIC plot. Hence, according to these criteria, both choices seemed initially conceivable.

In order to select one of these two models, we examined their predictive performance. Before converting ratings to preferences, we discarded for each assessor j one of the rated movies at random. Then, we randomly selected one of the movies used to obtain preferences, and used it to create a pairwise preference involving the discarded movie. This preference was then not used for inference. After running the Bayesian Mallows model, we were able to compute, for each assessor, the predictive probabilities $P(\mathbf{R}_j|\text{all data})$, and thereby the probabilities for correctly predicting the discarded preference. The median, across all assessors, of these probabilities was 0.9505 for the model with $C = 6$ clusters, and 0.7349 for $C = 13$ clusters. Moreover, for $C = 6$, 80 % of these probabilities were higher than 0.5. These are very positive results, and they suggest that the predictive performance of the model with 6 clusters is much better than the one with 13 clusters. It appears that the larger number of clusters in the latter model leads to a deteriorating precision of the corresponding cluster centers estimates, and this is likely to be the main cause of the loss in the predictive success.

Figure 11 shows boxplots of the posterior distribution of the probability for correct preference prediction of the left out comparison, stratified with respect to the number of preferences stated by the assessor. The histogram on the right shows the marginal posterior probability for correctly predicting the discarded preference for all assessors for the model with $C = 6$, regardless of how many preferences they had expressed (the median is 0.9505). By inspection of the figure it is evident that the model has a very good predictive power, which becomes better and better the more preferences are available for a given assessor. When the assessors have more than 150 preferences,

1. The selected users had rated at least 3 movies, two of which needed to create at least a pairwise movie comparison, and a third one needed for prediction purposes, as explained in the following.

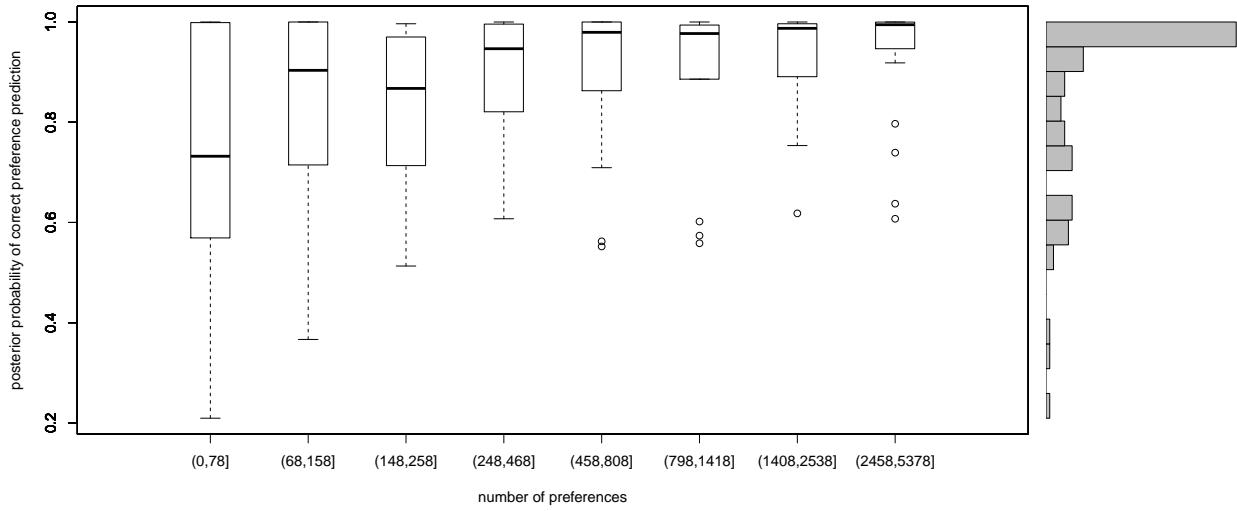


Figure 11: Results of the Movielens experiment. Boxplots of the posterior probability for correctly predicting the discarded preference conditionally on the number of preferences stated by the assessor, for the model with $C = 6$. The histogram on the right shows the marginal posterior probability for correct preference prediction.

	$c = 1$	$c = 2$	$c = 3$
τ_c (%)	17.14 (12.2,21.02)	14.20 (9.69,18.62)	19.97 (14.49,26.14)
α_c	2.09 (2.01,2.16)	2.11 (2.03,2.17)	2.14 (2.09,2.17)
	Ghostbusters (1984) Shakespeare in Love (1998) Fargo (1996) Star Wars: Return of the Jedi (1983) The Matrix (1999) Star Wars: The Empire Strikes Back (1980) Raiders of the Lost Ark (1981) Braveheart (1995) Star Wars: A New Hope (1977) E.T. the Extra-Terrestrial (1982)	The Sixth Sense (1999) Back to the Future (1985) The Princess Bride (1987) Star Wars: The Phantom Menace (1999) Schindler's List (1993) Raiders of the Lost Ark (1981) Being John Malkovich (1999) Ghostbusters (1984) American Beauty (1999) Terminator 2: Judgment Day (1991)	The Godfather (1972) American Beauty (1999) Forrest Gump (1994) Star Wars: The Empire Strikes Back (1980) Star Wars: Return of the Jedi (1983) Jurassic Park (1993) Star Wars: A New Hope (1977) Groundhog Day (1993) Back to the Future (1985) The Princess Bride (1987)
	$c = 4$	$c = 5$	$c = 6$
τ_c (%)	11.67 (7.92,15.84) 1.12 (1.00,1.23)	21.34 (15.68,27.99) 1.97 (1.79,2.07)	15.68 (11.53,19.48) 2.05 (1.92,2.13)
	Star Wars: The Phantom Menace (1999) Saving Private Ryan (1998) Raiders of the Lost Ark (1981) Braveheart (1995) Fargo (1996) Shakespeare in Love (1998) E.T. the Extra-Terrestrial (1982) Back to the Future (1985) The Sixth Sense (1999) Schindler's List (1993)	Raiders of the Lost Ark (1981) Back to the Future (1985) Terminator 2: Judgment Day (1991) Forrest Gump (1994) The Silence of the Lambs (1991) Ghostbusters (1984) Toy Story (1995) Jurassic Park (1993) Saving Private Ryan (1998) Men in Black (1997)	Pulp Fiction (1994) Terminator 2: Judgment Day (1991) American Beauty (1999) Schindler's List (1993) Men in Black (1997) Star Wars: The Empire Strikes Back (1980) E.T. the Extra-Terrestrial (1982) Shakespeare in Love (1998) Being John Malkovich (1999) The Princess Bride (1987)

Table 6: Results of the Movielens experiment. Movies arranged according to the CP consensus ranking, from the posterior distribution of ρ_c , $c = 1, \dots, 6$.

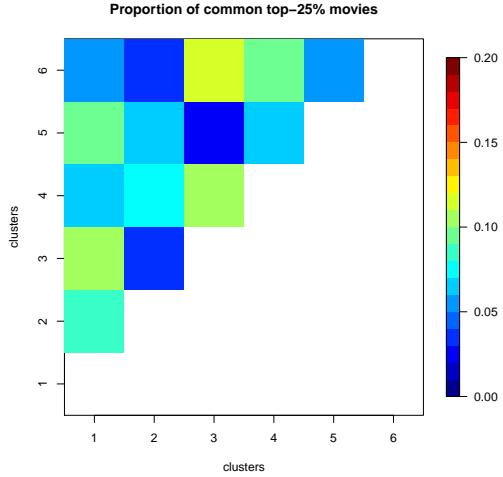


Figure 12: Results of the MovieLens experiment. Discrepancy of the CP consensus rankings: row i and column j in the matrix correspond to the proportion of movies which appear in the top-50 consensus lists of both cluster i and j , for $i, j \in \{1, \dots, 6\}$.

the distribution support is in the interval $(0.5, 1]$. This figure can guide personal recommendation algorithms, which should not be used for users who have given just few ratings.

In Table 6 the maximum a posteriori (MAP) estimates for τ and α , together with their 95% HPDIs, are shown at the top. The table also shows a subset of the movies, arranged in cluster-specific top-10 lists according to the CP consensus ranking, from the posterior distribution of ρ_c , $c = 1, \dots, 6$. We note that all α values correspond to a reasonable within-cluster variability, much lower than the one observed in the results of Lu and Boutilier (2014). Moreover, if compared to the final movie lists in Lu and Boutilier (2014), the lists reported in Table 6 are more specific, and characterize the assessors belonging to the same cluster as individuals sharing a reasonably well understood preference profile. These lists show very little overlap, and this is true not only for the top-10 movies: Figure 12 shows the discrepancy among the same movie lists, now considering the first 50 movies. Row i and column j in the matrix in Figure 12 correspond to the proportion of movies which appear in the top-50 lists of both cluster i and j , for $i, j \in \{1, \dots, 6\}$: the values are very low, all below 12%.

Since in the MovieLens dataset additional information on the assessors is available, we were able to compare the estimated cluster assignments with the age, gender, and the occupation of the users. This exercise helped interpreting the lists shown in Table 6: while occupation showed no interesting patterns, the first cluster is mostly composed by females under 25 years old, the third is a mix of both sexes in the age range 18–25, and the fifth is 80% males over 35.

6. Discussion

In this paper, we have developed a fully Bayesian hierarchical framework for the analysis of rank data. An important advantage of the Bayesian approach is that it offers coherently propagated and directly interpretable ways to quantify posterior uncertainties of estimates of any quantity of interest. Earlier Bayesian treatments of the Mallows rank model are extended in many ways: we develop an importance sampling scheme for $Z_n(\alpha)$ allowing use of other distances than Kendall's,

and our MCMC algorithm efficiently samples from the posterior distribution for the unknown parameters. We also develop various extensions of the model, motivated by particular applications.

The Mallows models perform very well with a large number of assessors N , as we show in the Sushi experiment of Section 5.4, and in the Movielens experiment of Section 5.5. On the other hand, they may not be computationally feasible when the number of items is extremely large, e.g. $n \geq 10^4$, which is common for search engines and in ranking of players in online games (Volkovs and Zemel, 2014). For the footrule and Spearman distances, there exist asymptotic approximations for $Z_n(\alpha)$ as $n \rightarrow \infty$ (Mukherjee, 2013), which we used in Section 5.5, but the MCMC algorithm converges slowly in such large spaces. Maximum likelihood estimation of ρ runs into the same problem when n gets large (Aledo et al., 2013; Ali and Meilă, 2012). Volkovs and Zemel (2014) developed the multinomial preference model (MPM) for cases with very large n , which can be efficiently computed by maximizing a concave log-likelihood function. The MPM thus seems a useful choice when n is very large and real time performance is needed.

All methods presented have been implemented in C++, and run efficiently on a desktop computer, with the exception of the Movielens experiment, which needed to be run on a cluster. Obtaining a sufficiently large sample from the posterior distribution takes from a few seconds for the full potato data to several minutes in the examples involving massive data augmentation, e.g., the Premier League data.

Many of the extensions we propose for solving specific problems (clustering, preference prediction, pairwise comparisons, ...) are needed jointly in real applications, as we illustrate for example in the case of the Movielens data. Our general framework is flexible enough to handle such extensions.

There are many situations in which rankings vary over time, as in political surveys (Regenwetter et al., 1999) or book bestsellers (Caron and Teh, 2012). We are currently working on extending our approach to this setting. We assume to observe ranks at discrete timepoints indexed by $t = 0, 1, \dots, T$ and let $\rho^{(t)}$ and $\alpha^{(t)}$ denote the parameters of the Mallows model at time t . An interesting task is the prediction of rankings in future time instances.

In certain applications, one might want to weight differently the distances of specific items, leading to metrics involving given weights, like in $\sum_{i=1}^n w_i |\rho_i - \rho'_i|$, which is not right-invariant. For these distances, the normalizing constant cannot be precomputed off-line. Then it may be possible to usefully adopt a version of the pseudo-marginal MCMC (Andrieu and Roberts, 2009).

Acknowledgments

Øystein Sørensen and Valeria Vitelli contributed equally to this paper and are joint first authors. The authors thank Tyler Lu and Craig Boutilier for their help with the Movielens data, and Magne Thoresen for helpful discussions.



Figure A1: Left: The 20 potatoes labeled by letters A-T. Right: Assessors in action.

Assessor	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T
1	10	18	19	15	6	16	4	20	3	5	12	1	2	9	17	8	7	14	13	11
2	10	18	19	17	11	15	6	20	4	3	13	1	2	7	16	8	5	12	9	14
3	12	15	18	16	13	11	7	20	6	3	8	2	1	4	19	5	9	14	10	17
4	9	17	19	16	10	15	5	20	3	4	8	1	2	7	18	11	6	13	14	12
5	12	17	19	15	7	16	2	20	3	9	13	1	4	5	18	11	6	8	10	14
6	10	15	19	16	8	18	6	20	3	7	11	1	2	4	17	9	5	13	12	14
7	9	16	19	17	10	15	5	20	3	8	11	1	2	6	18	7	4	14	12	13
8	14	18	20	19	11	15	6	17	4	3	10	1	2	7	16	8	5	12	9	13
9	8	16	18	19	12	13	6	20	5	3	7	1	4	2	17	10	9	15	14	11
10	7	17	19	18	9	15	5	20	3	10	11	1	2	6	16	8	4	13	12	14
11	12	16	19	15	13	18	7	20	3	5	11	1	2	6	17	10	4	14	8	9
12	14	15	19	16	12	18	8	20	3	4	9	1	2	7	17	6	5	13	10	11
True rank	11	17	19	16	10	15	5	20	3	4	9	1	2	6	18	7	8	14	12	13
True weight	73	56	50	59	77	62	87	46	95	89	78	115	99	86	54	85	80	68	72	71

Table A1: Ranks given by the 12 assessors (rows) to the 20 potatoes (columns) in the visual inspection experiment. The true ranks, and the true weights in grams, are given in the two bottom rows.

Appendix A. Additional Results for the Potato Experiment

A.1 Data Collection

Figure A1 (left) shows the 20 potatoes laid out on a plate, marked by letters from A to T, and Figure A1 (right) shows some of the assessors performing the visual inspection part of the experiment. Table A1 shows the ranks given by the 12 assessors in the visual inspection experiment, and Table A2 shows the ranks given in the weighing experiment.

Assessor	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T
1	10	17	19	15	6	16	4	20	2	5	11	1	3	7	18	8	9	14	12	13
2	13	18	19	16	10	15	5	20	4	3	12	1	2	6	17	8	7	11	9	14
3	11	16	20	15	10	14	6	19	9	4	7	1	3	2	18	5	8	17	12	13
4	10	17	19	16	11	15	5	20	3	4	9	1	2	6	18	8	7	12	14	13
5	11	17	19	16	6	15	4	20	2	8	12	1	3	5	18	10	7	13	9	14
6	9	16	18	15	10	17	8	19	3	7	11	2	1	4	20	5	6	14	12	13
7	9	17	19	16	11	15	5	20	3	8	10	1	2	7	18	6	4	14	12	13
8	12	17	19	18	9	15	5	20	3	4	10	1	2	8	16	7	6	14	11	13
9	9	16	19	18	12	14	6	20	5	2	8	1	4	3	17	10	7	15	13	11
10	10	17	19	16	7	15	4	20	3	9	11	1	2	5	18	8	6	13	12	14
11	11	16	18	15	12	17	7	20	3	4	10	1	2	6	19	8	5	14	9	13
12	12	16	19	15	10	17	8	20	3	4	9	1	2	6	18	5	7	14	11	13
True rank	11	17	19	16	10	15	5	20	3	4	9	1	2	6	18	7	8	14	12	13
True weight	73	56	50	59	77	62	87	46	95	89	78	115	99	86	54	85	80	68	72	71

Table A2: Ranks given by the 12 assessors (rows) to the 20 potatoes (columns) in the weighing experiment. The true ranks, and the true weights in grams, are given in the two bottom rows.

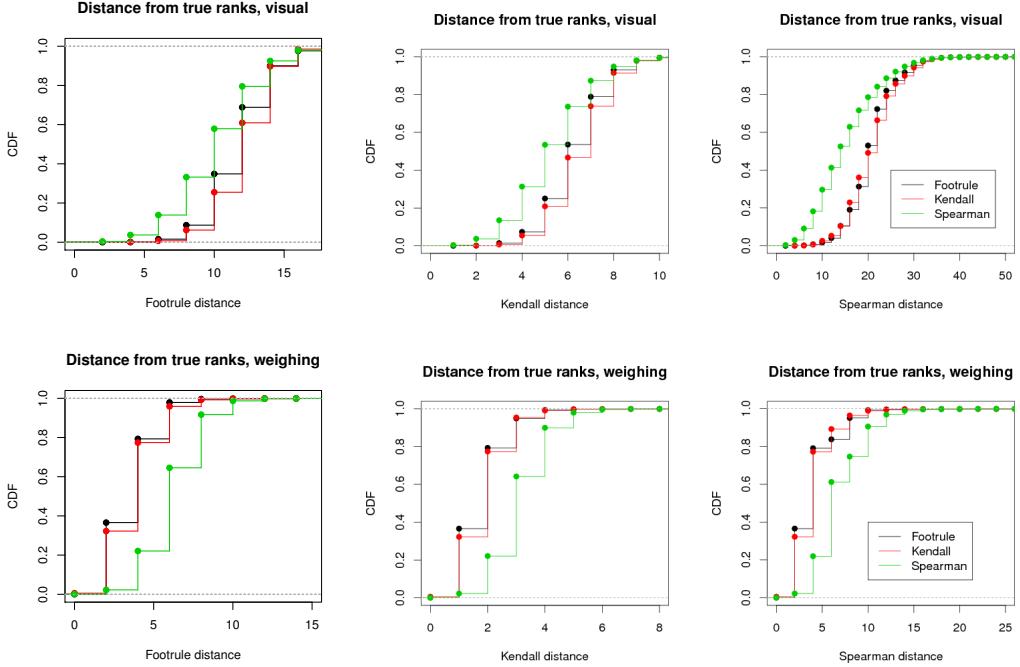


Figure A2: The posterior distributions, expressed in terms of the CDFs for the total distance between the latent and true ranks. The blue curves represent the posterior distributions for the latent ranks in the Mallows model with the footrule distance, the red curves with the Kendall distance, and the green curves with the Spearman distance.

A.2 Posterior Distributions for Ranks

Figure A2 shows the cumulative distribution functions for the total distance between the latent ranks and the true ranks, as measured by the footrule, Kendall and Spearman distances. The Mallows model with the footrule and Kendall distances turned out best in the weighing experiment, while the Mallows model with the Spearman distance performed best in the visual inspection experiment. Figure A3 shows a selection of results from the potato visual experiment (an analogous plot can be made for the weighing experiment, showing improved precision). The true rank of the heaviest and lightest potatoes had strongly peaked distributions, while the distributions of the potatoes closer to middle in weight, had a larger spread, representing a greater uncertainty about their true rank.

We now consider estimating the set of top-5 potatoes, neglecting their order, still using the full data. For each of the three models, the posterior probability of being among the top-5 was computed for each potato, and is shown in the columns in Table A3. The potatoes are listed according to their true rank, and the mean ranking provided by the assessors is presented in the right column. The numbers in the columns for each model show, for each potato, the posterior probability that it is among the top-5. Defining the estimated top-5 set as the five potatoes with highest value of this posterior probability, we see from Table A3 that the Spearman model is the only one which identified the correct set of potatoes in the visual inspection experiment. (Both the footrule and the Kendall model gave potato Q, whose true rank was 8, a high probability of being among the top-5. The high posterior ranking given to potato Q can also be seen in the top left and

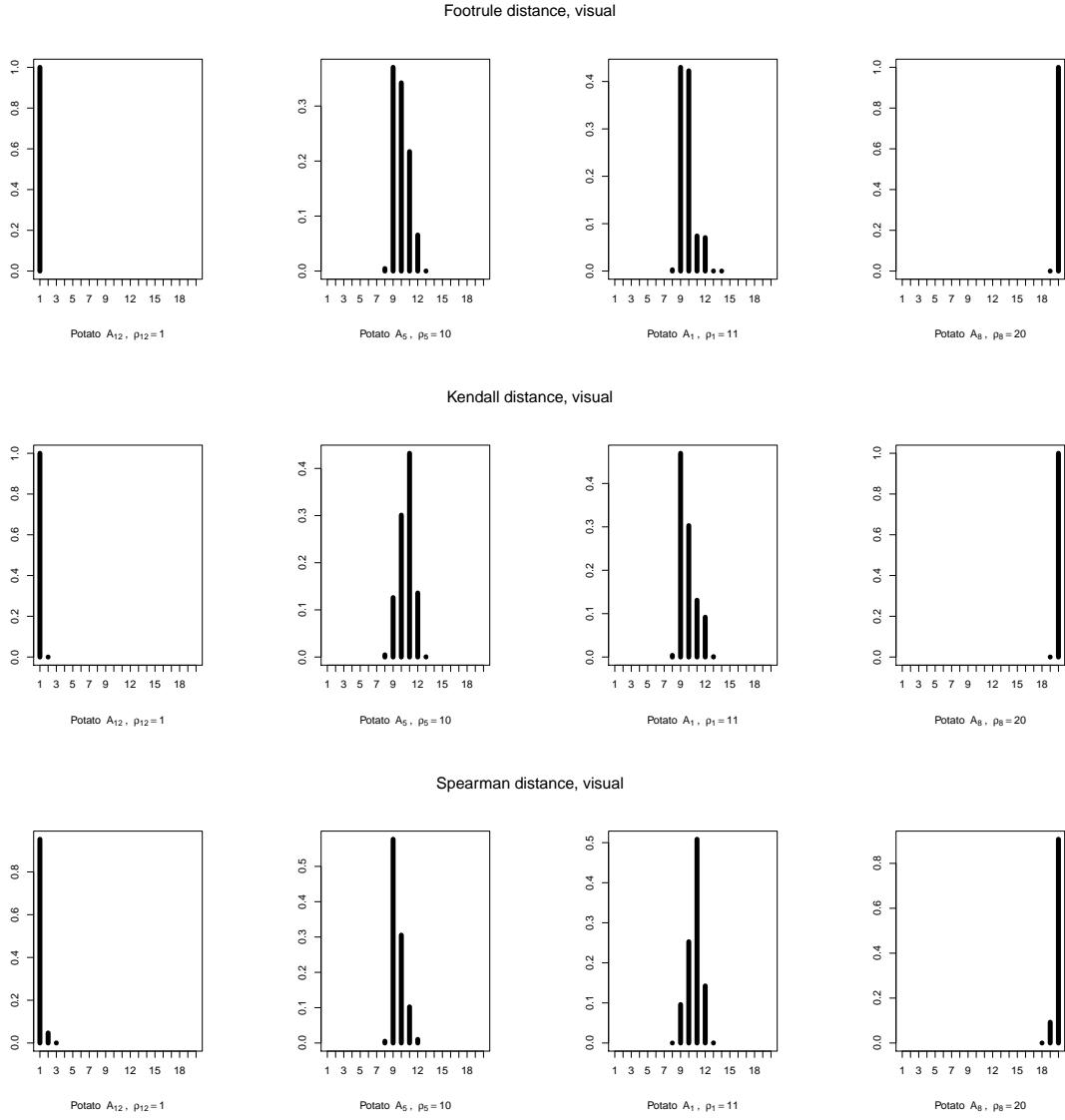


Figure A3: Posterior probabilities of the true ranks from the Mallows models in the visual inspection experiment, for the potatoes with true ranks 1 (heaviest), 10, 11 (middle), and 20 (lightest).

Rank	Potato	Visual				Weighing			
		Footrule	Kendall	Spearman	Mean	Footrule	Kendall	Spearman	Mean
1	L	1.00	1.00	1.00	1.08	1.00	1.00	1.00	1.08
2	M	1.00	1.00	1.00	2.25	1.00	0.999	1.00	2.33
3	I	1.00	1.00	1.00	3.58	1.00	1.00	1.00	3.58
4	J	0.997	0.961	0.882	5.33	1.00	0.997	0.960	5.17
5	G	0.107	0.173	0.603	5.58	0.936	0.866	0.315	5.58
6	N	0.006	0.013	0.206	5.83	0.065	0.138	0.725*	5.42
7	P	0.000	0.000	0.000	8.42	0.000	0.000	0.000	7.33
8	Q	0.890*	0.852*	0.310	5.75				
9	K	0.000	0.000	0.000	10.33				
:	:	:	:	:	:	:	:	:	:
20	H	0.000	0.000	0.000	19.75	0.000	0.000	0.000	19.83

Table A3: The posterior probability of being among the top-5 for each potato. Numbers in boldface indicate credibility level of 95 % or higher, while asterisks indicate potatoes which were wrongly assessed to be top-5.

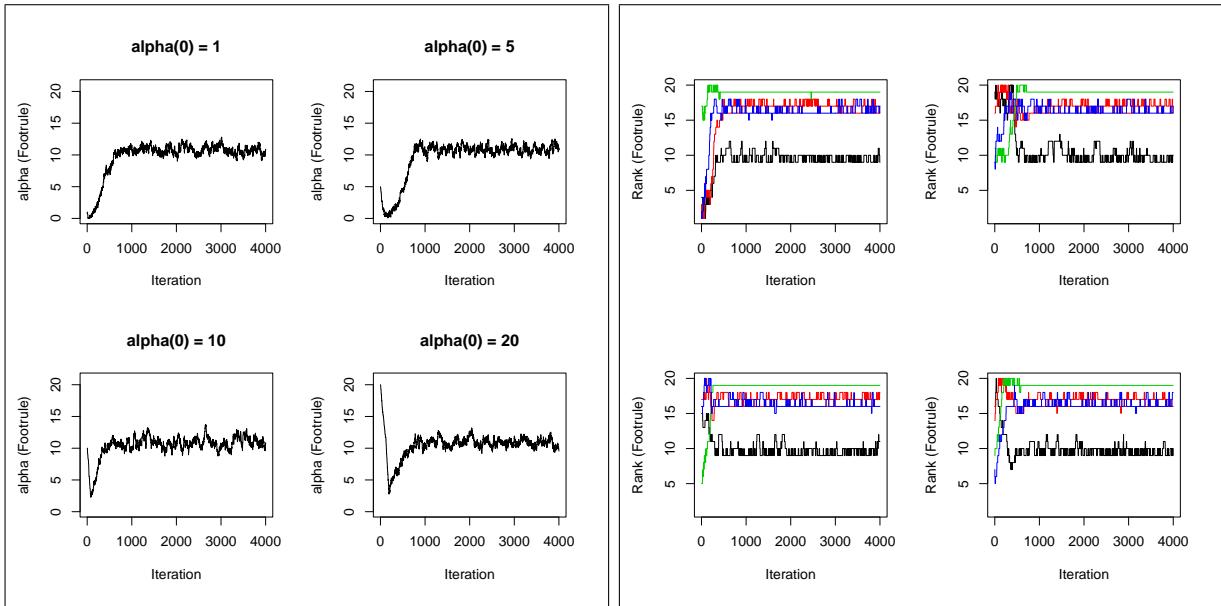


Figure A4: Convergence in the Mallows model with footrule distance. Left: Trace plots from four different initial values for α . Right: Trace plots for potatoes A (black line), B (red line), C (blue line), and D (green line) using four different random starting points for the rank vector.

center heat plots in Figure 3 of the main paper, as the red/yellow square which stands out below the diagonal at position 8 on the horizontal axis.) In the weighing experiment, both the footrule and Kendall model correctly identified the top-5, while the Spearman model included potato N (true rank 6) instead of potato G (true rank 5).

Table A3 and Figure A3 illustrate how the Bayesian framework easily allows for a quantification of the uncertainty in the estimates. In addition, we can compare the results obtained when using different distance measures, in contrast to most earlier work which have only used the Kendall distance. Here, the best results from the weighing experiment were obtained by applying the footrule distance, while use of the Spearman distance gave best results in the visual experiment.

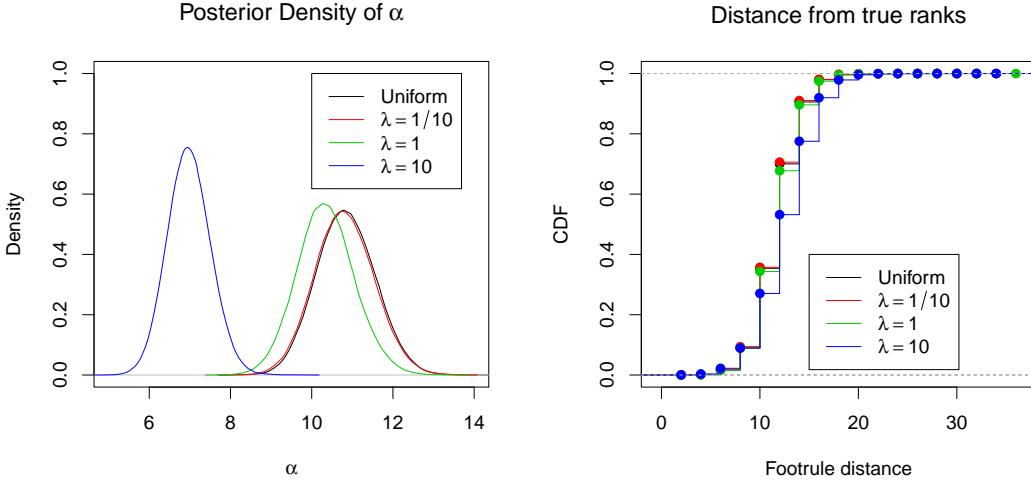


Figure A5: Impact of the prior distribution in the potato experiment with full data. Results are shown for the Mallows model with the footrule distance in the visual inspection experiment.

A.3 Convergence of Metropolis-Hastings Algorithm with Full Data

Here we describe how to assess convergence of our Metropolis-Hastings algorithm, using examples from the potato experiment. Similar convergence assessments were performed for all the experiments presented in the paper. Figure A4 (left) shows trace plots of the first 4000 iterations of the MCMC algorithm using the footrule model and the data from the visual inspection experiment. The four plots show the traces for four different starting points. We see that after about 1000 iterations, α had converged to the same distribution in all cases. In each of the four runs, the starting points for the ranks were sampled uniformly from \mathcal{P}_n . Figure A4 (right) shows the corresponding trace plots for potatoes A , B , C , and D . Also here we see that the impact of the initial configuration was negligible after about 1000 iterations. The trace plots of the 16 remaining potatoes gave very similar results (not shown). Keeping in mind that Figure A4 shows traces of different parameters sampled from the same Markov chain, it is interesting to note that only one of the two plots is sufficient to assess convergence. When the algorithm starts, ρ has little agreement with the data, and therefore α is drawn towards zero, regardless of the starting point. Eventually, after some hundreds of iterations, ρ reaches configurations which agree more with the data, and α therefore increases again. We hence recommend trace plots of α as a simple tool for assessing convergence. In producing these plots, α' was sampled for $\mathcal{N}(\alpha, \sigma_\alpha^2)$, with $\sigma_\alpha = 0.04$, and ρ' from the leap-and-shift distribution with $L = 1$. The same plots can be obtained for the Mallows model with the Kendall distance and for the Spearman distance (not shown).

A.4 Sensitivity to the Choice of Prior Distribution

In the potato experiment with full data, described in Section 5.1 of the main paper, we used an exponential prior for α with rate $\lambda = 1/10$ for the footrule and Kendall distances, and $\lambda = n/20$ for the Spearman distance. Here we investigate the sensitivity to the choice of this prior distribution for the Mallows model with the footrule distance in the visual experiment. Additional

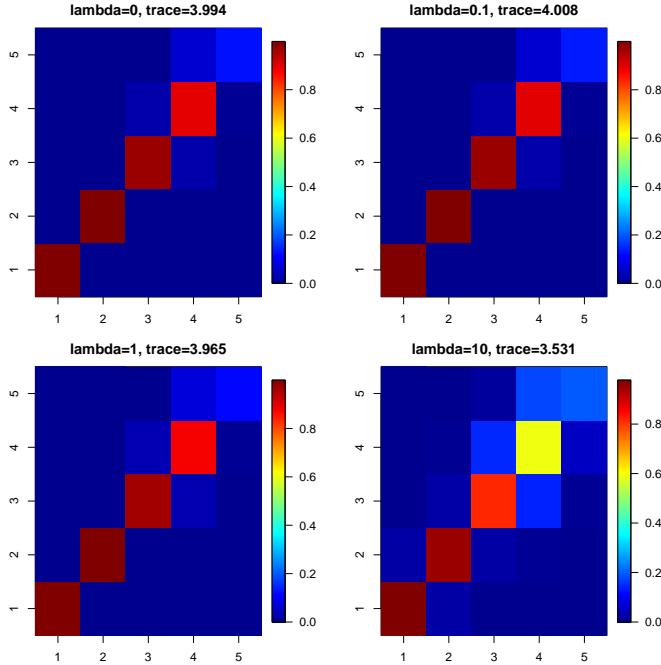


Figure A6: Impact of the prior distribution for α in the potato experiment, when the top-5 rankings of each assessor in the visual inspection part of the potato experiment were used, for the Mallows model with the footrule distance.

experiments of this type were also performed for the other Mallows models, as well as in the weighing experiment, and the results were similar. An exponential distribution with rate λ has mean $1/\lambda$, and variance $1/\lambda^2$, so a large value of λ implies a strong prior assumption that α is close to zero, and a correspondingly low precision in the measurements made by the assessors.

Figure A5 shows how the prior distribution for α influences the result. “Uniform” denotes the uniform improper prior distribution on the positive half line, $\pi(\alpha) = \mathcal{U}(0, \infty)$. We see that the uniform prior and the exponential prior with $\lambda = 1/10$ gave nearly identical posterior distributions for α , as well as posterior distributions for the distance from the estimated ranks to the true ranks. Setting $\lambda = 1$ resulted in a shift in the posterior distribution for α , but the distance to the true ranks was nearly unchanged. On the other hand, setting $\lambda = 10$ gave a strong shift to the left of the posterior distribution for α , and a clearly larger distance from the estimated ranks to the true ranks. We conclude that the model seems robust to small variations in the choice of λ in this case. Both $\lambda = 1$ and $\lambda = 10$ imply a very strong prior assumption that α is close to zero, and the model still produced reasonable results in these situations, with quite modest sample size.

In the top- k experiment described in Section 5.1.3, we used less data than in the full data experiment. One could therefore suspect that the prior distribution is more important in this case. We thus repeated the top-5 experiment for the *restricted* analysis (i.e., we put ourselves in the situation 2b described in Section 5.1.3), and Figure A6 shows the resulting heat plots for the four different prior distributions for the Mallows model with the footrule distance, using the top-5 rankings of each assessors in the visual inspection experiment. Again we see that the results were essentially equal for the choices $\lambda = 1/10$ and $\lambda = 1$, as well as when the uniform prior was assumed. The extreme value $\lambda = 10$, on the other hand, yielded considerably worse performance.

	West Ham																			
	Wolverhampton																			
	Blackpool																			
Man. United	0	0.59*	0.64*	0.68*	0.77*	0.78*	0.84*	0.9*	0.91*	0.92*	0.93*	0.93*	0.94*	0.97*	0.97*	0.98*	0.98*	0.97*	0.97*	
Man. City	0	0.54*	0.54*	0.58*	0.69*	0.69*	0.72*	0.78*	0.78*	0.87*	0.87*	0.88*	0.88*	0.89*	0.92*	0.92*	0.92*	0.95*	0.95*	0.95*
Chelsea	0.36	0.46	0	0.53	0.54*	0.66*	0.68*	0.74*	0.83*	0.84*	0.86*	0.86*	0.87*	0.87*	0.89*	0.92*	0.92*	0.92*	0.94*	0.94*
Tottenham	0.32	0.42	0.47	0	0.5	0.6*	0.65*	0.72*	0.8*	0.81*	0.84*	0.85*	0.85*	0.86*	0.88*	0.88*	0.88*	0.91*	0.92*	0.93*
Arsenal	0.32	0.41	0.46	0.5	0.61*	0	0.61*	0.63*	0.68*	0.78*	0.8*	0.82*	0.83*	0.84*	0.85*	0.86*	0.86*	0.89*	0.89*	0.93*
Everton	0.23	0.31	0.34	0.4	0.39	0	0.54*	0.61*	0.71*	0.72*	0.73*	0.74*	0.75*	0.76*	0.77*	0.78*	0.79*	0.8*	0.89*	0.89*
Liverpool	0.22	0.28	0.32	0.35	0.37	0.46	0	0.55*	0.67*	0.68*	0.69*	0.72*	0.73*	0.75*	0.76*	0.77*	0.78*	0.84*	0.86*	0.87*
Fulham	0.16	0.22	0.26	0.28	0.3	0.39	0.45	0	0.61*	0.62*	0.65*	0.67*	0.67*	0.68*	0.7*	0.72*	0.75*	0.8*	0.82*	0.84*
Aston Villa	0.1	0.16	0.17	0.2	0.22	0.29	0.33	0.39	0	0.5*	0.52*	0.56*	0.56*	0.58*	0.62*	0.63*	0.67*	0.7*	0.73*	0.76*
Sunderland	0.09	0.14	0.16	0.19	0.2	0.28	0.32	0.38	0.5	0	0.52*	0.56*	0.54*	0.56*	0.59*	0.61*	0.63*	0.69*	0.72*	0.74*
Newcastle	0.08	0.13	0.16	0.19	0.18	0.27	0.31	0.35	0.48	0	0.52*	0.53*	0.52*	0.58*	0.61*	0.68*	0.71*	0.72*	0.74*	0.75*
West Bromwich	0.07	0.13	0.14	0.16	0.17	0.26	0.28	0.33	0.44	0.44	0.48	0	0.51	0.55	0.56	0.59	0.66*	0.69*	0.7*	0.71*
Bolton	0.07	0.12	0.15	0.15	0.17	0.24	0.27	0.33	0.44	0.46	0.48	0	0.49	0	0.51	0.54	0.56	0.66*	0.68*	0.71*
Wigan	0.07	0.12	0.14	0.16	0.16	0.24	0.29	0.32	0.44	0.44	0.47	0.5	0.49	0	0.54	0.56	0.58*	0.65*	0.69*	0.69*
Stoke City	0.07	0.11	0.14	0.16	0.15	0.21	0.25	0.3	0.42	0.41	0.45	0.46	0.46	0	0.53*	0.54*	0.61*	0.63*	0.67*	0.67*
Birmingham	0.07	0.11	0.13	0.14	0.14	0.2	0.24	0.28	0.38	0.39	0.42	0.44	0.44	0.47	0	0.52	0.59*	0.61*	0.64*	0.64*
Blackburn	0.06	0.08	0.09	0.12	0.11	0.18	0.22	0.25	0.37	0.37	0.39	0.41	0.41	0.42	0	0.48	0.46	0.48	0.58*	0.61*
Blackpool	0.03	0.06	0.07	0.09	0.08	0.13	0.16	0.2	0.3	0.31	0.32	0.34	0.34	0.35	0	0.41	0.42	0	0.52*	0.56*
Wolverhampton	0.02	0.05	0.05	0.08	0.07	0.11	0.14	0.18	0.27	0.28	0.29	0.31	0.32	0.31	0.37	0.39	0.48	0	0.53	0.53
West Ham	0.03	0.05	0.06	0.07	0.07	0.11	0.13	0.16	0.24	0.26	0.28	0.3	0.29	0.31	0.33	0.36	0.44	0.47	0	0

Table A4: Stochastic orderings in the Premier League example. Each matrix element (i, j) denotes the posterior probability that team A_i has a lower rank than team A_j . If the number is marked with an asterisk, it means that A_i stochastically dominates A_j .

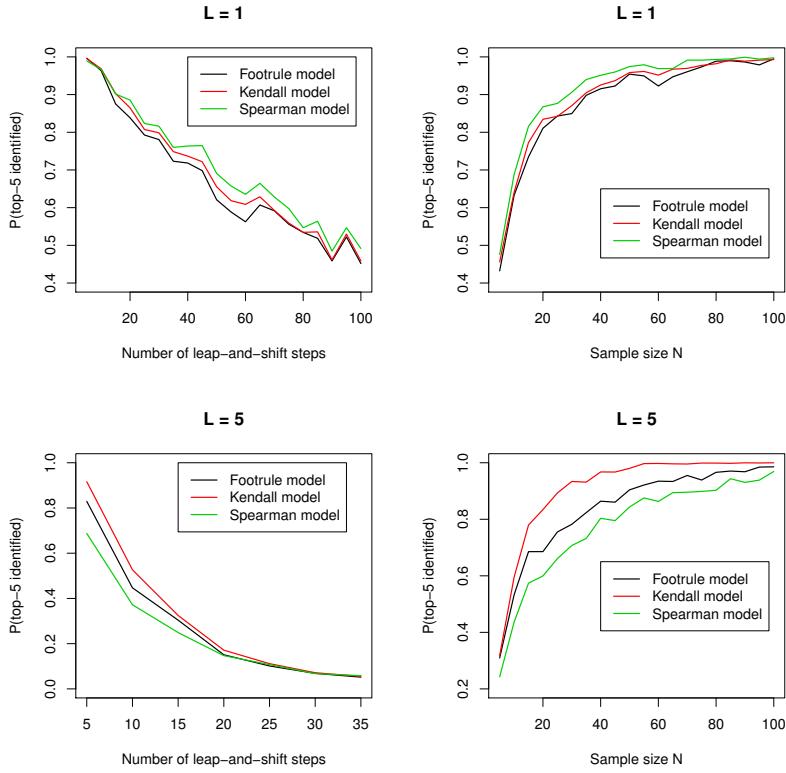


Figure A7: Probability of identifying the top-5 items as the number of leap-and-shift moves used to generate each observation increases (left), and as N increases (right).

Appendix B. Additional Results for the Premier League Teams

The Premier League data were downloaded from
http://clearlyandsimply.com/files/2010/05/premier_league.zip.

Figure 7 in the paper shows the posterior cumulative distribution functions for the ranks of the Premier League teams. We can also consider a stronger mode of ‘pointwise’ ordering between teams and compute the posterior probability that team A_i has a lower rank than A_j , given by $P(\rho_i < \rho_j | \text{data})$. Table A4 summarizes these measures for all the teams. The number in matrix entry (i, j) shows $P(\rho_i < \rho_j | \text{data})$, and if it is marked with an asterisk, team A_i stochastically dominates A_j . Out of the 190 pairs of teams, 182 were stochastically ordered. The remaining 8 pairs had matrix elements very close to 0.5. For example, the probability that Bolton has a higher rank than Newcastle was 0.51, and neither team dominated the other in the sense of stochastic ordering in our assessment.

Appendix C. Simulation Experiments

The results of the potato experiment, where the true ranks were known to us, give some hints about the comparative performances of the Mallows models with footrule, Kendall, and Spearman distances. In order to do a more systematic analysis, we also performed simulation experiments. Define the true ranking $\boldsymbol{\rho} = (1, \dots, n)$. The observations \mathbf{R}_j , $j = 1, \dots, N$, will be generated in two

ways: either by perturbing the true ranking ρ by applying the leap-and-shift proposal recursively a number of times (see results in Section C.1), or by generating observed rankings from the Mallows model (see results in Section C.2).

C.1 Ranks Generated from the Leap-and-Shift distribution

We generated a set of rankings \mathbf{R}_j , $j = 1, \dots, N$ by applying the leap-and-shift proposal recursively N_{leap} independent times starting from the true ranking ρ . This means that each sampled \mathbf{R}_j is a perturbed version of ρ , whose distance from ρ depends on the choices of N_{leap} and L . We used the values $L = 1$ and $L = 5$ for the leap parameter. $L = 1$ implies that in each move of the algorithm, only neighboring items can be shuffled. $L = 5$, on the other hand, means that items which originally are further away from each other also can be interchanged. We first investigated how the noise level in the data influences the results by varying the number of leap-and-shift moves applied in the data generation, while fixing $N = 10$ and $n = 20$. In the $L = 1$ case the number of moves N_{leap} was gradually increased from 5 to 100, and in the $L = 5$ case from 5 to 35, in steps of size 5. Next, we investigated how the number of assessors influences the results, keeping the number of leap-and-shift moves fixed at 50 in the $L = 1$ case and at 10 in the $L = 5$ case, while increasing N from 5 to 100 in steps of size 5. We computed the posterior probability for correctly identifying the top-5 items in each of 200 independent Monte Carlo simulations.

The left plots in Figure A7 show the results for varying numbers of leap-and-shift moves. With $L = 1$, the Spearman distance performed best, followed by the Kendall and footrule distance. In the $L = 5$ case, the Kendall distance showed the best performance. The right plots show how the results varied with the sample size, and not surprisingly, the quality of the results improved with increasing N . Also, the comparative performances of the different Mallows models were very similar to the plots on the left-hand side. When $L = 1$, the Spearman distance was the best, followed by the Kendall and footrule distances, while when $L = 5$, the Kendall distance was best, followed by the footrule and Spearman distances.

We can interpret the differences in performances of the models in Figure A7 by comparing the distance measures. The footrule and Kendall distances are additive, in the sense that perturbing two ranks by one unit off their true value has the same likelihood as perturbing one rank by two units. In other words, if a rank has already been perturbed by one unit, it is as likely to be perturbed by yet another unit off as any other, yet unperturbed rank, by one unit from its true position. In the Spearman distance this is no longer the case, because of the square in the exponent. Thus, if occasional bigger displacements come up in the data, as in the $L = 5$ case, the description given by the Spearman distance is likely to be less fitting. In other words, the inferences provided by the Mallows model with Spearman distance are less robust to larger noise than footrule or Kendall. The Spearman model gives lower posterior probability to latent ranks which are in strong disagreement with some of the assessors, even when the latent rank is in perfect agreement with other assessors.

C.2 Ranks Generated from a Mallows Model

In addition to the previous simulations, where the data were generated by sequences of perturbations from a fixed initial position, we conducted further experiments in which the ranks were generated from the three Mallows models with the footrule, Kendall, and Spearman distance. We set the number of assessors to $N = 10$, and the number of items to $n = 20$. For each value of α in a discrete range, we used the Metropolis-Hastings algorithm with fixed ranks $\rho = (1, \dots, n)$ and fixed α to obtain N simulated samples. This was done by first running the algorithm until convergence, and then taking N observed ranks with a large enough interval between each sample to make them nearly independent. This gave a set $\mathbf{R}_1, \dots, \mathbf{R}_N$ of observed ranks, which was then used

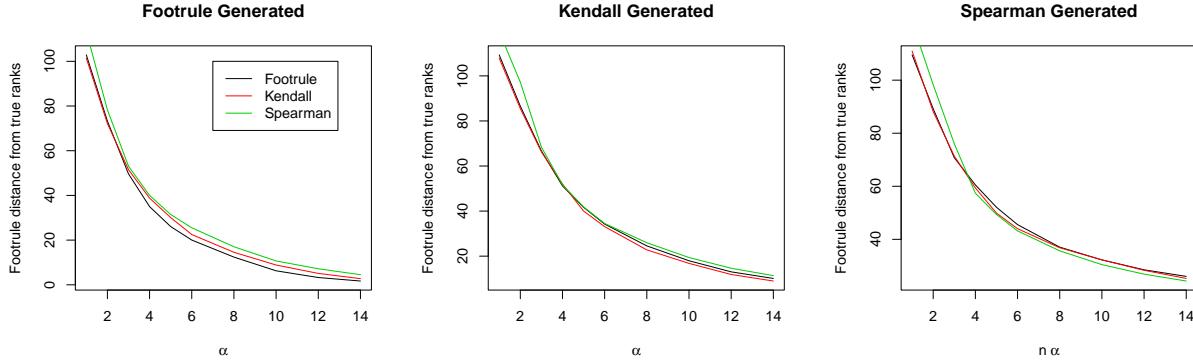


Figure A8: The plots from left to right show the mean distance between the posterior ranks and the true ranks in our simulation experiment, when the observed ranks were *generated* from the Mallows model with the footrule, Kendall, and Spearman distance, respectively. The black curves represent the ranks *estimated* with a Mallows model with the footrule distance, the red curves with the Kendall distance, and the green curves with the Spearman distance.

with the three distance measures, and the prior distributions described in Section 2.2. This gave three posterior distributions for latent ranks, one for each distance measure, and we finally found the mean posterior distance to the true ranks. We thus had a 3×3 design, with three models for generating samples and three for analyzing the observed ranks. The procedure was repeated 100 times for each value of α and each of the 9 settings. The values of α used for generating the observed ranks were 1, 2, 3, 4, 5, 6, 8, 10, 12, 14 with the footrule and Kendall distance, and the equivalent $1/n, 2/n, 3/n, 4/n, 5/n, 6/n, 8/n, 10/n, 12/n, 14/n$ with the Spearman distance.

Figure A8 shows the mean footrule distance from the posterior means to the true ranks over the 100 simulations. The error bars were very narrow, and hence omitted. Similar plots using the Kendall or Spearman distance on the vertical axis gave practically identical results, and are not shown. The left plot in Figure A8 shows the case in which the model with the footrule distance was used to generate the samples. In this case, it is clear that inference with the footrule distance that was used to generate the samples, gave the best results over the whole range of α values considered, although the difference between the models was rather modest. The center plot shows the case in which the model with the Kendall distance was used to generate the samples. Here, it is harder to see any difference between the results obtained from the inference with the different distance measures. For small values of α , the Spearman distance gave poorer results, while the two other distances gave very similar results. For large values of α , on the other hand, the Kendall distance produced slightly better results than the other two. Finally, the right plot shows the results obtained for the samples generated with the Spearman distance. Here, it is interesting to see that inference with the footrule and Kendall distance was better than with the Spearman distance for small values of α , despite the fact that the samples were generated with the latter model. For α in the middle and upper range, on the other hand, inference with the Spearman distance gave slightly better results than the two other models. These experiments suggest that the Spearman distance is at a disadvantage when α is small, i.e., when the ranks are close to being uniformly distributed. For larger values of α , inference with the same model as was used to generate the data is slightly better than inference with any of the other two models.

References

- Bahman Afsari, Ulisses Braga Neto, and Donald Geman. Rank Discriminants for Predicting Phenotypes from RNA Expression. arXiv:1401.1490 [q-bio.GN], 2014.
- Juan A. Aledo, Jose A. Gàmez, and David Molina. Tackling the rank aggregation problem with evolutionary algorithms. *Applied Mathematics and Computation*, 222:632 – 644, 2013.
- Alnur Ali and Marina Meilă. Experiments with Kemeny ranking: What works when? *Mathematical Social Sciences*, 64(1):28 – 40, 2012.
- Mayer Alvo and Philip L.H. Yu. *Statistical Methods for Ranking Data*. Frontiers in Probability and the Statistical Sciences. Springer, New York, NY, USA, 2014.
- Christophe Andrieu and Gareth O. Roberts. The pseudo-marginal approach for efficient Monte Carlo computations. *The Annals of Statistics*, 37(2):697–725, 2009.
- Ludwig M. Busse, Peter Orbanz, and Joachim M. Buhmann. Cluster analysis of heterogeneous rank data. In *Proceedings of the 24th International Conference on Machine Learning*, ICML '07, pages 113–120, New York, NY, USA, 2007. ACM.
- François Caron and Yee W. Teh. Bayesian nonparametric models for ranked data. In F. Pereira, C. J. C. Burges, L. Bottou, and K. Q. Weinberger, editors, *Advances in Neural Information Processing Systems 25*, pages 1520–1528. Curran Associates, Inc., 2012.
- François Caron, Yee Whye Teh, and Thomas Brendan Murphy. Bayesian nonparametric Plackett-Luce models for the analysis of preferences for college degree programmes. *The Annals of Applied Statistics*, 8(2):1145–1181, 2014.
- Gilles Celeux, Merrilee Hurn, and Christian Robert. Computational and inferential difficulties with mixture posterior distribution. *Journal of the American Statistical Association*, 95(451):957–970, 2000.
- Gilles Celeux, Florence Forbes, Christian P. Robert, and D. Michael Titterington. Deviance information criteria for missing data models. *Bayesian Analysis*, 1(4):651–674, 2006.
- Robert P. DeConde, Sarah Hawley, Seth Falcon, Nigel Clegg, Beatrice Knudsen, and Ruth Etzioni. Combining results of microarray experiments: A rank aggregation approach. *Statistical Applications in Genetics and Molecular Biology*, 5(1):Article 15, 2006.
- Ke Deng, Simeng Han, Kate J. Li, and Jun S. Liu. Bayesian aggregation of order-based rank data. *Journal of the American Statistical Association*, 109(507):1023–1039, 2014.
- Saravana M. Dhanasekaran, Terrence R. Barrette, Debashis Ghosh, Rajal Shah, Sooryanarayana Varambally, Kotoku Kurachi, Kenneth J. Pienta, Mark A. Rubin, and Arul M. Chinmaiyan. Delineation of prognostic biomarkers in prostate cancer. *Nature*, 412:822–826, 2001.
- P. Diaconis. *Group representations in probability and statistics*, volume 11 of *Lecture Notes - Monograph Series*. Institute of Mathematical Statistics, Hayward, CA, USA, 1988.
- Persi Diaconis and R. L. Graham. Spearman’s footrule as a measure of disarray. *Journal of the Royal Statistical Society. Series B (Methodological)*, 39(2):262–268, 1977.

- M. A. Fligner and J. S. Verducci. Distance based ranking models. *Journal of the Royal Statistical Society: Series B (Methodological)*, 48(3):359–369, 1986.
- Brian Francis, Regina Dittrich, and Reinhold Hatzinger. Modeling heterogeneity in ranked responses by nonparametric maximum likelihood: how do europeans get their scientific knowledge? *The Annals of Applied Statistics*, 4(4):2181–2202, 2010.
- Johannes Furnkranz and Eyke Hullermeier. *Preference Learning*. Springer, 2011.
- P. Gopalan, T.S. Jayram, R. Krauthgamer, and R. Kumar. Approximating the longest increasing sequence and distance from sortedness in a data stream. Research Microsoft Publications, 2006.
- John Guiver and Edward Snelson. Bayesian inference for plackett-luce ranking models. In *proceedings of the 26th annual international conference on machine learning*, pages 377–384. ACM, 2009.
- David R. Hunter. MM algorithms for generalized Bradley-Terry models. *The Annals of Statistics*, 32(1):384–406, 2004.
- Julien Jacques and Christophe Biernacki. Model-based clustering for multivariate partial ranking data. *Journal of Statistical Planning and Inference*, 149:201–217, 2014.
- Julien Jacques, Quentin Grimonprez, and Christophe Biernacki. Rankcluster: an R package for clustering multivariate partial rankings. preprint submitted to Elsevier, 2014.
- A. Jasra, C.C. Holmes, and D.A. Stephens. Markov chain Monte Carlo methods and the label switching problem in Bayesian mixture modeling. *Statistical Science*, 20(1):50–67, 2005.
- Toshihiro Kamishima. Nantonac collaborative filtering: Recommendation based on order responses. In *Proceedings of the Ninth ACM SIGKDD International Conference on Knowledge Discovery and Data Mining*, pages 583–588, New York, NY, USA, 2003. ACM.
- M.E. Khan, Y.J. Ko, and M. Seeger. Scalable collaborative bayesian preference learning. In *Proceedings of the 17th International Conference on Artificial Intelligence and Statistics*, volume 33, pages 475–483, 2014.
- Guy Lebanon and Yi Mao. Non-parametric modeling of partially ranked data. *Journal of Machine Learning Research*, 9:2401–2429, 2008.
- Shili Lin and Jie Ding. Integration of ranked lists via cross entropy Monte Carlo with applications to mRNA and microRNA studies. *Biometrics*, 65(1):9–18, 2009.
- Tyler Lu and Craig Boutilier. Effective sampling and learning for Mallows models with pairwise-preference data. *Journal of Machine Learning Research*, 15:3783–3829, 2014.
- R. Duncan Luce. *Individual choice behavior: A theoretical analysis*. Wiley, New York, NY, USA, 1959.
- Jun Luo, David J. Duggan, Yidong Chen, Jurga Sauvageot, Charles M. Ewing, Michael L. Bittner, Jeffrey M. Trent, and William B. Isaacs. Human prostate cancer and benign prostatic hyperplasia: Molecular dissection by gene expression profiling. *Cancer Research*, 61(12):4683–4688, 2001.
- C. L. Mallows. Non-null ranking models. I. *Biometrika*, 44(1/2):114–130, 1957.

John I. Marden. *Analyzing and Modeling Rank Data*, volume 64 of *Monographs on Statistics and Applied Probability*. Chapman & Hall, Cambridge, MA, USA, 1995.

Adam A. Margolin, Ilya Nemenman, Katia Bassi, Chris Wiggins, Gustavo Stolovitzky, Riccardo Dalla Favera, and Andrea Califano. ARACNE: An algorithm for the reconstruction of gene regulatory networks in a mammalian cellular context. *BMC Bioinformatics*, 7(Suppl 1):S7, 2006.

Marina Meilă and Le Bao. An exponential model for infinite rankings. *Journal of Machine Learning Research*, 11:3481–3518, 2010.

Marina Meilă and Harr Chen. Dirichlet process mixtures of generalized Mallows models. In *Proceedings of the Twenty-Sixth Conference Annual Conference on Uncertainty in Artificial Intelligence (UAI-10)*, pages 358–367, Corvallis, OR, USA, 2010. AUAI Press.

David Meyer and Kurt Hornik. Generalized and customizable sets in R. *Journal of Statistical Software*, 31(2):1–27, 2009.

David Meyer and Kurt Hornik. relations: Data structures and algorithms for relations. R package version 0.6-3, 2014. URL <http://CRAN.R-project.org/package=relations>.

S. Mukherjee. Estimation of parameters in non uniform models on permutations. arXiv:1307.0978 [math.PR], 2013.

Thomas Brendan Murphy and Donal Martin. Mixtures of distance-based models for ranking data. *Computational Statistics & Data Analysis*, 41(34):645 – 655, 2003.

Panagiotis Papastamoulis. label.switching: An R package for dealing with the label switching problem in MCMC outputs. arXiv:1503.02271v1 [stat.CO], 2015.

Vasyl Pihur, Somnath Datta, and Susmita Datta. Rankaggreg, an R package for weighted rank aggregation. Submitted., 2014.

R. L. Plackett. The analysis of permutations. *Journal of the Royal Statistical Society. Series C (Applied Statistics)*, 24(2):193–202, 1975.

Michel Regenwetter, Jean-Claude Falmagne, and Bernard Grofman. A stochastic model of preference change and its application to 1992 presidential election panel data. *Psychological Review*, 106(2):362–384, 1999.

Matthias Schonlau. The Clustergram: a graph for visualizing hierarchical and non-hierarchical cluster analyses. *The Stata Journal*, 3:316–327, 2002.

Dinesh Singh, Phillip G. Febbo, Kenneth Ross, Donald G. Jackson, Judith Manola, Christine Ladd, Pablo Tamayo, Andrew A. Renshaw, Anthony V. D'Amico, Jerome P. Richie, Eric S. Lander, Massimo Loda, Philip W. Kantoff, Todd R. Golub, and William R. Sellers. Gene expression correlates of clinical prostate cancer behavior. *Cancer Cell*, 1(2):203 – 209, 2002. ISSN 1535-6108.

David G. Spiegelhalter, Nicola G. Best, Bradley P. Carlin, and Angelica van der Linde. Bayesian measures of model complexity and fit. *Journal of the Royal Statistical Society: Series B (Statistical Methodology)*, 64(4):583–639, 2002.

Mingxuan Sun, Guy Lebanon, and Paul Kidwell. Estimating probabilities in recommendation systems. *Journal of the Royal Statistical Society, Series C*, 61(3):471–492, 2012.

Lawrence True, Ilsa Coleman, Sarah Hawley, Ching-Ying Huang, David Gifford, Roger Coleman, Tomasz M. Beer, Edward Gelmann, Milton Datta, Elahe Mostaghel, Beatrice Knudsen, Paul Lange, Robert Vessella, Daniel Lin, Leroy Hood, and Peter S. Nelson. A molecular correlate to the gleason grading system for prostate adenocarcinoma. *Proceedings of the National Academy of Sciences*, 103(29):10991–10996, 2006.

Maksims N. Volkovs and Richard S. Zemel. New learning methods for supervised and unsupervised preference aggregation. *Journal of Machine Learning Research*, 15:1135–1176, 2014.

John B. Welsh, Lissa M. Sapino, Andrew I. Su, Suzanne G. Kern, Jessica Wang-Rodriguez, Christopher A. Moskaluk, Henry F. Frierson, and Garret M. Hampton. Analysis of gene expression identifies candidate markers and pharmacological targets in prostate cancer. *Cancer Research*, 61(16):5974–5978, 2001.