CONSENSUS CLUSTERING FOR BAYESIAN MIXTURE MODELS

Stephen Coleman[1]
stephen.coleman@mrc-bsu.cam.ac.uk

Paul D.W. Kirk[1,2,*]
paul.kirk@mrc-bsu.cam.ac.uk

Chris Wallace[1,2,*]
cew54@cam.ac.uk

[1] MRC Biostatistics Unit
[2] Cambridge Institute of Therapeutic Immunology & Infectious Disease
University of Cambridge, U.K.
[*] These authors provided an equal contribution.

January 15, 2021

ABSTRACT

Cluster analysis is an integral part of precision medicine and systems biology, used to define groups of patients or biomolecules. However, problems such as choosing the number of clusters and issues with high dimensional data arise consistently. An ensemble approach, such as consensus clustering, can overcome some of the difficulties associated with high dimensional data, frequently exploring more relevant clustering solutions than individual models. Another tool for cluster analysis, Bayesian mixture modelling, has alternative advantages, including the ability to infer the number of clusters present and extensibility. However, inference of these models is often performed using Markov-chain Monte Carlo (MCMC) methods which can suffer from problems such as poor exploration of the posterior distribution and long runtimes. This makes applying Bayesian mixture models and their extensions to 'omics data challenging. We apply consensus clustering to Bayesian mixture models to address these problems.

Consensus clustering of Bayesian mixture models successfully finds the generating structure in our simulation study and captures multiple modes in the likelihood surface. This approach also offers significant reductions in runtime compared to traditional Bayesian inference when a parallel environment is available. We propose a heuristic to decide upon ensemble size and then apply consensus clustering to Multiple Dataset Integration, an extension of Bayesian mixture models for integrative analyses, showing consensus clustering can be applied to any MCMC-based clustering method, not just mixture models. We from an integrative analysis of three 'omics datasets for budding yeast and find clusters of co-expressed genes with shared regulatory proteins. We validate these clusters using data external to the analysis. We also uncover novel biology, finding evidence for a more direct role for the GAS3 gene in DNA replication. This demonstrates the potential of using consensus clustering in multi-omics studies.

The code and data from this paper are available at
https://github.com/stcolema/ConsensusClusteringForBayesianMixtureModels.

1 Introduction

From defining a taxonomy of disease to creating molecular sets, grouping items can help us to understand and make decisions using complex biological data. For example, grouping patients based upon disease characteristics and personal

omics data may allow the identification of more homogeneous subgroups, enabling stratified medicine approaches. Defining and studying molecular sets can improve our understanding of biological systems as these sets are more interpretable than their constituent members (Hejblum et al., 2015), and study of their interactions and perturbations may have ramifications for diagnosis and drug targets (Bai et al., 2013; Emmert-Streib et al., 2014). The act of identifying such groups is referred to as "cluster analysis". Traditional methods such as K-means clustering (Lloyd, 1982; Forgy, 1965) or hierarchical clustering condition upon a fixed choice of K, the number of clusters. These methods are often heuristic in nature, relying on rules of thumb to decide upon a final model choice. For example, different choices of K are compared under some metric such as silhouette or the within-cluster sum of squared errors (**SSE**) as a function of K. For K-means clustering, its sensitivity to initialisation means multiple runs are often used in practice, with that which minimises SSE used (Arthur and Vassilvitskii, 2006). This problem arises as the algorithm has no guarantees on finding the global minimum of SSE.

In many analyses quantifying confidence in the clustering can be of interest. Returning to the stratified medicine example of clustering patients, there might be individuals with almost equal probability of being allocated between several clusters which might influence decisions made. However, many clustering algorithms provide only a point clustering.

Ensemble methods offer a solution to the problems of sensitivity to initialisation and the lack of measure of uncertainty. These approaches have had great success in supervised learning, most famously in the form of Random Forest (Breiman, 2001) and boosting (Friedman, 2002). In clustering, consensus clustering (Monti et al., 2003) is a popular method which has been implemented in R (Wilkerson et al., 2010) and to a variety of methods (John et al., 2020; Gu et al., 2020) and been applied to problems such as cancer subtyping (Lehmann et al., 2011; Verhaak et al., 2010) and identifying subclones in single cell analysis (Kiselev et al., 2017). Consensus clustering uses W runs of some base model or learner (such as K-means clustering) and compiles the W proposed partitions into a *consensus matrix*, the $(i, j)^{th}$ entries of which contain the proportion of model runs for which the ith and j^{th} individuals co-cluster (for this and other definitions see section 1 of the Supplementary Material). This proportion represents some measure of confidence in the co-clustering of any pair of items. Furthermore, ensembles can offer reductions in computational runtime. This is as the individual learners can be weaker (and thus use either less of the available data or stop before full convergence) and because the learners in most ensemble methods are independent of each other and thus enable use of a parallel environment for each of the quicker model runs (Ghaemi et al., 2009).

Monti et al. (2003) proposed some methods for choosing K using the consensus matrix, but this remains a problem in the methods mentioned so far. An alternative clustering framework, model-based clustering or *mixture models*, embeds the cluster analysis within a formal, statistical framework (Fraley and Raftery, 2002). This means that models can be compared formally, and problems such as the choice of K can be addressed as a model selection problem with all the associated tools. Mixture models are also attractive, as they have great flexibility in the type of data they can be applied to due to different choice of densities.

Furthermore, *Bayesian mixture models* can treat K as a random variable that is inferred from the data. The final clustering is not conditional upon a user chosen value, but K is jointly modelled along with the clustering. Such inference can be performed through use of a Dirichlet Process (Ferguson, 1973), a mixture of finite mixture models (Richardson and Green, 1997; Miller and Harrison, 2018) or an over-fitted mixture model (Rousseau and Mengersen, 2011). These models and their extensions have a history of successful application to a diverse range of biological problems such as finding clusters of gene expression profiles (Medvedovic and Sivaganesan, 2002), cell types in flow cytometry (Chan et al., 2008; Hejblum et al., 2019) or scRNAseq experiments (Prabhakaran et al., 2016), and estimating protein localisation (Crook et al., 2018). Bayesian mixture models can be extended to jointly model the clustering across multiple datasets (Kirk et al., 2012; Gabasova et al., 2017) (section 2 of the Supplementary Material).

Variational inference (**VI**, Blei et al., 2006) may be used to perform approximate inference of Bayesian mixture models (Martin et al., 2020). However, while VI is powerful, "it is not yet well understood" (Blei et al., 2017), can struggle with multi-modality, underestimates the variance in the posterior distribution (Turner and Sahani, 2011) and it has been shown to have a very computationally heavy initialisation cost to have good results (Wang and Dunson, 2011). Implementation is difficult, requiring either complex derivations (see the Appendix Supplementary Methods of Argelaguet et al., 2018, for an example) or black-box, approximate solutions (Kucukelbir et al., 2017).

However, it is Markov chain Monte Carlo (MCMC) methods that remain the most popular method for Bayesian inference. In Bayesian clustering methods, MCMC methods are used to construct a chain of clusterings, and then an assessment of the convergence of this chain is made, to determine if its behaviour aligns with the expected asymptotic theory. This chain of samples will converge to the posterior distribution of the Bayesian model and explore its entire support given an infinite runtime. However, in practice problems arise. Individual chains often fail to explore the full support of the posterior distribution (an example of different chains becoming trapped in a single mode of the likelihood surface can be seen in the Supplementary Materials of Strauss et al., 2020) and experience slow runtimes. Some

84 MCMC methods make efforts to overcome the problem of exploration, often at the cost of increased computational cost
85 per iteration. See, e.g., Robert et al. (2018); Yao et al. (2020) for examples of problems and attempted solutions for
86 MCMC methods.

87 We propose that applying consensus clustering to Bayesian mixture models can overcome some of the issues endemic
88 in high dimensional Bayesian clustering. Monti et al. (2003) suggest this application as part of their original paper, but
89 no investigation has been attempted to our knowledge. This ensemble approach sidesteps the problems of convergence
90 associated MCMC methods and offers computational gains through using shorter chains run in parallel. Furthermore,
91 this approach could be directly used on any existing MCMC based implementation of Bayesian mixture models or their
92 extensions and would avoid the re-implementation process that changing to newer MCMC methods or VI would entail.

93 We propose a heuristic for deciding upon the ensemble width (the number of learners used, W) and the ensemble depth
94 (the number of iterations run within each chain, D), inspired by the use of scree plots in Principal Component Analysis
95 (**PCA** Wold et al., 1987).

96 We show via simulation that ensembles consisting of short chains can be sufficient to successfully recover generating
97 structure. We also show that consensus clustering explores as many or more modes of the likelihood surface than either
98 standard Bayesian inference or `Mclust`, a maximum likelihood method, all while offering improvements in runtime to
99 traditional Bayesian inference.

100 We go on to perform an integrative analysis of cell cycle data from *Saccharomyces cerevisiae*. The cell cycle is the
101 process by which a growing cell divides into two daughter cells. This involves virtually all cellular processes and
102 diverse regulatory events (Granovskaia et al., 2010). The cell cycle is crucial to biological growth, repair, reproduction,
103 and development (Tyson et al., 2013; Chen et al., 2004; Alberts et al., 2002). The regulatory proteins of the cell cycle
104 are so highly conserved among eukaryotes that many of them function perfectly when transferred from a human cell to
105 a yeast cell (Alberts et al., 2002). This conservation means that a relatively simple eukaryote such as *Saccharomyces*
106 *cerevisiae* can provide insight into a variety of cell cycle perturbations including those that occur in human cancer
107 (Ingalls et al., 2007; Chen et al., 2004) and ageing (Jiménez et al., 2015). Budding yeast is particularly attractive for
108 genetic analysis as large numbers of cells may be synchronised in a particular stage of the cell cycle (Juanes, 2017). We
109 apply consensus clustering to an extension of Bayesian mixture models, Multiple Dataset Integration (**MDI**), a multiple
110 dataset clustering method. We determine the ensemble size using our proposed stopping rule. We use this ensemble to
111 infer clusters of genes across datasets and validate these clusters using knowledge external to the analysis.

2 Material and methods

2.1 Consensus clustering for Bayesian mixture models

114 We apply consensus clustering to MCMC based Bayesian clustering models using the method described in algorithm
115 1. Our application of consensus clustering has two main parameters at the ensemble level, the chain depth, D, and
116 ensemble width, W. We infer a point clustering from the consensus matrix using the `maxpear` function (Fritsch et al.,
117 2009) from the R package `mcclust` (Fritsch, 2012) to (section 3 of the Supplementary Material for details).

2.1.1 Determining the ensemble depth and width

119 As our ensemble sidesteps the problem of convergence within each chain, we need an alternative stopping rule for
120 growing the ensemble in chain depth, D, and number of chains, W. We propose a heuristic based upon the consensus
121 matrix to decide if a given value of D and W are sufficient. We suspect that increasing W and D might continuously
122 improve the performance of the ensemble, but we observe in our simulations that these improvements will become
123 smaller and smaller for greater values, approaching some asymptote for each of W and D. We notice that this behaviour
124 is analogous to PCA in that where for consensus clustering some improvement might always be expected for increasing
125 chain depth or ensemble width, more variance will always be captured by increasing the number of components
126 used in PCA. However, increasing this number beyond some threshold has diminishing returns, diagnosed in PCA
127 by a scree plot. Following from this, we recommend, for some set of ensemble parameters, $D' = \{d_1, \ldots, d_I\}$ and
128 $W' = \{w_1, \ldots, w_J\}$, find the mean absolute difference of the consensus matrix for the d_i^{th} iteration from w_j chains to
129 that for the $d_{(i-1)}^{th}$ iteration from w_j chains and plot these values as a function of chain depth, and the analogue for
130 sequential consensus matrices for increasing ensemble width and constant depth.

131 If this heuristic is used, we believe that the consensus matrix and the resulting inference should be stable (see, e.g.,
132 Von Luxburg and Ben-David, 2005; Meinshausen and Bühlmann, 2010), providing a robust estimate of the clustering.
133 In contrast, if there is still strong variation in the consensus matrix for varying chain length or number, then we believe

Data: $X = (x_1, \ldots, x_N)$
Input:
The number of chains to run, W
The number of iterations within each chain, D
A clustering method that uses MCMC methods to generate samples of clusterings of the data $Cluster(X, d)$
Output:
A predicted clustering, $\hat{Y}$
The consensus matrix $\mathbf{M}$
begin

    /* initialise an empty consensus matrix   */
    $\mathbf{M} \leftarrow \mathbf{0}_{N \times N}$;
    for $w = 1$ **to** W **do**

        /* set the random seed controlling initialisation and MCMC moves   */
        $set.seed(w)$;
        /* initialise a random partition on X drawn from the prior distribution   */
        $Y_{(0,w)} \leftarrow Initialise(X)$;
        for $d = 1$ **to** D **do**

            /* generate a markov chain for the membership vector   */
            $Y_{(d,w)} \leftarrow Cluster(X, d)$;

        end
        /* create a coclustering matrix from the Dth sample   */
        $\mathbf{B}^{(w)} \leftarrow Y_{(D,w)}$;
        $\mathbf{M} \leftarrow \mathbf{M} + \mathbf{B}^{(w)}$;

    end
    $\mathbf{M} \leftarrow \frac{1}{W}\mathbf{M}$;
    $\hat{Y} \leftarrow$ partition X based upon $\mathbf{M}$;
end

Algorithm 1: Consensus clustering for Bayesian mixture models.

that the inferred clustering is influenced significantly by the random initialisation and that the inferred partition is unlikely to be stable for similar datasets or reproducible for a random choice of seeds.

2.2 Simulation study

We use a finite mixture with independent features as the data generating model within the simulation study. Within this model there exist "irrelevant features" (Law et al., 2003) that have global parameters rather than cluster specific parameters. The generating model is

$$p(X, c, \theta, \pi | K) = p(K)p(\pi | K)p(\theta | K) \prod_{i=1}^{N} p(c_i | \pi, K) \prod_{p=1}^{P} p(x_{ip} | c_i, \theta_{c_i p})^{\phi_p} p(x_{ip} | \theta_p)^{(1-\phi_p)}$$

for data $X = (x_1, \ldots, x_N)$, cluster label or allocation variable $c = (c_1, \ldots, c_N)$, cluster weight $\pi = (\pi_1, \ldots, \pi_K)$, K clusters and the relevance variable, $\phi \in \{0, 1\}$ with $\phi_p = 1$ indicating that the pth feature is relevant to the clustering. We used a *Gaussian* density, so $\theta_{kp} = (\mu_{kp}, \sigma_{kp}^2)$. We defined three scenarios and simulated 100 datasets in each (Figure 1 and Table 1) Additional details of the simulation process and additional scenarios are included in section 4.1 of the Supplementary Materials.

Table 1: Parameters defining the simulation scenarios as used in generating data and labels. $\Delta\mu$ is the distance between neighbouring cluster means within a single feature. The number of relevant features (P_s) is $\sum_p \phi_p$, and $P_n = P - P_s$.

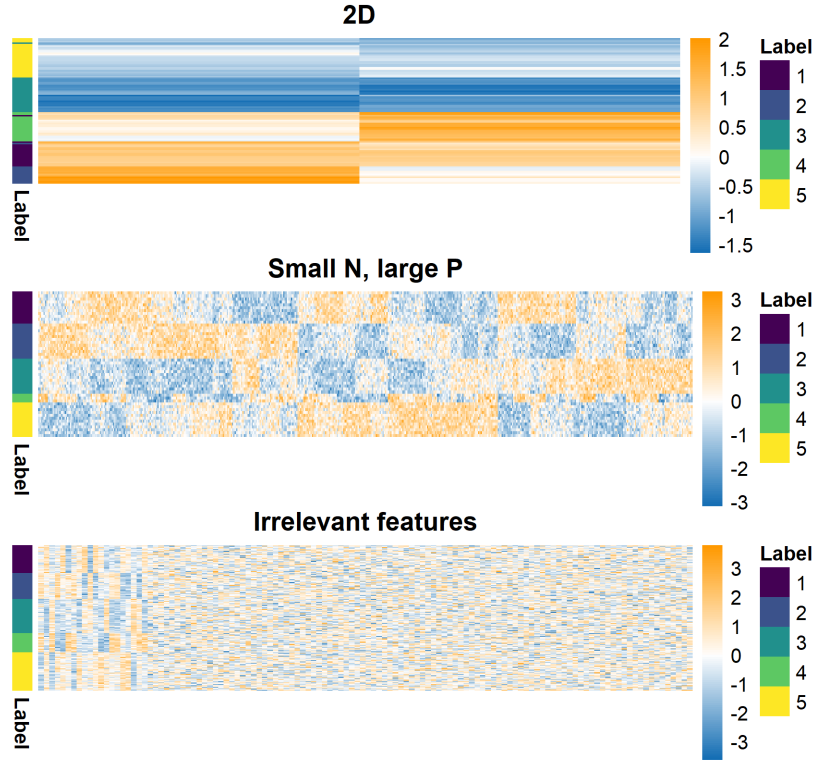| Scenario	N	P_s	P_n	K	$\Delta\mu$	σ^2	π
2D	100	2	0	5	3.0	1	$(\frac{1}{5}, \frac{1}{5}, \frac{1}{5}, \frac{1}{5}, \frac{1}{5})$
Small N, large P	50	500	0	5	1.0	1	$(\frac{1}{5}, \frac{1}{5}, \frac{1}{5}, \frac{1}{5}, \frac{1}{5})$
Irrelevant features	200	20	100	5	1.0	1	$(\frac{1}{5}, \frac{1}{5}, \frac{1}{5}, \frac{1}{5}, \frac{1}{5})$

Figure 1: Example of generated datasets. Each row is an item being clustered and each column a feature of generated data. The 2D dataset (which is ordered by hierarchical clustering here) should enable proper mixing of chains in the MCMC. The small N, large P case has clear structure (observable by eye). This is intended to highlight the problems of poor mixing due to high dimensions even when the generating labels are quite identifiable. In the irrelevant features case, the structure is clear in the relevant features (on the left-hand side of this heatmap). This setting is intended to test how sensitive each approach is to noise.

In each of these scenarios we apply a variety of methods (listd below) and compare the inferred point clusterings to the generating labels using the Adjusted Rand Index (**ARI**, Hubert and Arabie, 1985).

- `Mclust`, a maximum likelihood implementation of finite mixture models (for a range of modelled clusters, K),

- 10 chains of 1 million iterations, thinning to every thousandth sample for the overfitted Bayesian mixture model, and

- A variety of consensus clustering ensembles defined by inputs of W chains and D iterations within each chain (see algorithm 1) with $W \in \{1, 10, 30, 50, 100\}$ and $D \in \{1, 10, 100, 1000, 10000\}$.

The ARI is a measure of similarity between two partitions,c_1, c_2, corrected for chance, with 0 indicating c_1 is no more similar to c_2 than a random partition would be expected to be and a value of 1 showing that c_1 and c_2 perfectly align. Details of the methods in the simulation study can be found in sections 4.2, 4.3 and 4.4 of the Supplementary Material.

2.2.1 `Mclust`

`Mclust` (Scrucca et al., 2016) is a function from the R package `mclust`. It estimates Gaussian mixture models for K clusters based upon the maximum likelihood estimator of the parameters. it initialises upon a hierarchical clustering of the data cut to K clusters. A range of choices of K and different covariance structures are compared and the "best" selected using the Bayesian information criterion, (Schwarz et al., 1978) (details in section 4.2 of the Supplementary Material).

2.2.2   Bayesian inference

To assess within-chain convergence of our Bayesian inference we use the Geweke Z-score statistic (Geweke et al., 1991). Of the chains that appear to behave properly we then asses across-chain convergence using $\hat{R}$ (Gelman et al., 1992) and the recent extension provided by Vats and Knudson (2018). If a chain has reached its stationary distribution the Geweke Z-score statistic is expected to be normally distributed. Normality is tested for using a Shapiro-Wilks test (Shapiro and Wilk, 1965). If a chain fails this test (i.e., the associated p-value is less than 0.05), we assume that it has not achieved stationarity and it is excluded from the remainder of the analysis. The samples from the remaining chains are then pooled and a posterior similarity matrix (**PSM**) constructed. We use the `maxpear` function to infer a point clustering. For more details see section 4.3 of the Supplementary Material.

2.3   Analysis of the cell cycle in budding yeast

2.3.1   Datasets

We aim to create clusters of genes that are co-expressed, have common regulatory proteins and share a biological function. To achieve this, we use three datasets that were generated using different 'omics technologies and target different aspects of the molecular biology underpinning the cell cycle process.

- Microarray profiles of RNA expression from Granovskaia et al. (2010), comprising measurements of cell-cycle-regulated gene expression at 5-minute intervals for 200 minutes (up to three cell division cycles) and is referred to as the **time course** dataset. The cells are synchronised at the START checkpoint in late G1-phase using alpha factor arrest (Granovskaia et al., 2010). We include only the genes identified by Granovskaia et al. (2010) as having periodic expression profiles.
- Chromatin immunoprecipitation followed by microarray hybridization (**ChIP-chip**) data from Harbison et al. (2004). This dataset discretizes p-values from tests of association between 117 DNA-binding transcriptional regulators and a set of yeast genes. Based upon a significance threshold these p-values are represented as either a 0 (no interaction) or a 1 (an interaction).
- Protein-protein interaction (**PPI**) data from BioGrid (Stark et al., 2006). This database consists of of physical and genetic interactions between gene and gene products, with interactions either observed in high throughput experiments or computationally inferred. The dataset we used contained 603 proteins as columns. An entry of 1 in the $(i, j)^{th}$ cell indicates that the ith gene has a protein product that is believed to interact with the jth protein.

The datasets were reduced to the 551 genes with no missing data in the PPI and ChIP-chip data, as in Kirk et al. (2012).

2.3.2   Multiple dataset integration

We applied consensus clustering to MDI for our integrative analysis. Details of MDI are in section 2.2 of the Supplementary Material, but in short MDI jointly models the clustering in each dataset, inferring individual clusterings for each dataset. These partitions are informed by similar structure in the other datasets, with MDI learning this similarity as it models the partitions. The model does not assume global structure. This means that the similarity between datasets is not strongly assumed in our model; individual clusters or genes that align across datasets are based solely upon the evidence present in the data and not due to strong modelling assumptions. Thus, datasets that share less common information can be included without fearing that this will warp the final clusterings in some way.

The datasets were modelled using a mixture of Gaussian processes in the time course dataset and Multinomial distributions in the ChIP-chip and PPI datasets.

3   Results

3.1   Simulated data

We use the ARI between the generating labels and the inferred clustering of each method to be our metric of predictive performance. In Figure 2, we see `Mclust` performs very well in the 2D and Small N, large P scenarios, correctly identifying the true structure However, the irrelevant features scenario sees a collapse in performance, `Mclust` is blinded by the irrelevant features and identifies a clustering of $K = 1$.

The pooled samples from multiple long chains performs very well across all scenarios and appears to act as an upper bound on the more practical implementations of consensus clustering.
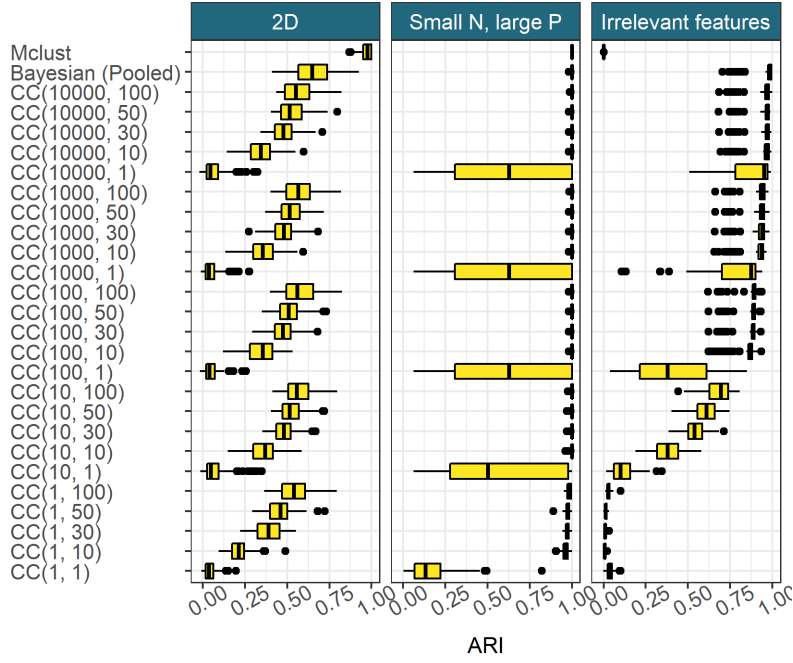
Figure 2: Model performance in the 100 simulated datasets for each scenario, defined as the ARI between the generating labels and the inferred clustering. $CC(d, w)$ denotes consensus clustering using the clustering from the dth iteration from w different chains.

Consensus clustering does uncover some of the generating structure in the data, even using a small number of short chains. With sufficiently large ensembles and chain depth, consensus clustering is close to the pooled Bayesian samples in predictive performance. It appears that for a constant chain depth increasing the ensemble width used follows a pattern of diminishing returns. There are strong initial gains for a greater ensemble width, but the improvement decreases for each successive chain. A similar pattern emerges in increasing chain length for a constant number of chains (Figure 2).

We see very little difference between the similarity matrix from the pooled samples and the consensus clustering (Figure 3). Similar clusters emerge, and we see comparable confidence in the pairwise clusterings. For the PSMs from the individual chains, all entries are 0 or 1. This means only a single clustering is sampled within each chain, implying very little uncertainty in the partition. However, three different modes emerge across the chains showing that the chains are failing to explore the full support of the posterior distribution of the clustering and are each unrepresentative of the uncertainty in the final clustering. This shows that consensus clustering is exploring more possible clusterings than any individual chain and, as it explores a similar space to the pooled samples which might be considered more representative of the posterior distribution than any one chain, it suggests it better describes the true uncertainty present than any single chain. It also shows that pooling chains offers robustness to multi-modality (as expected for an ensemble) and the ARI for the pooled samples is an upper bound on the performance for the individual long chains.

Figure 4 shows that chain length is directly proportional to the time taken for the chain to run. This means that using an ensemble of shorter chains, as in consensus clustering, can offer large reductions in the time cost of analysis when a parallel environment is available compared to standard Bayesian inference. Even on a laptop of 8 cores running an ensemble of 1,000 chains of length 1,000 will require approximately half as much time as running 10 chains of length 100,000 due to parallelisation, and the potential benefits are far greater when using a large computing cluster.

Additional results are in section 4.4 of the Supplementary Material.

3.2   Multi-omics analysis of the cell cycle in budding yeast

We use the stopping rule proposed in 2.1.1 to determine our ensemble depth and width. In Figure 5, we see that the change in the consensus matrices from increasing the ensemble depth and width is diminishing in keeping with results in the simulations. We see no strong improvement after $D = 6,000$ and increasing the number of learners from 500
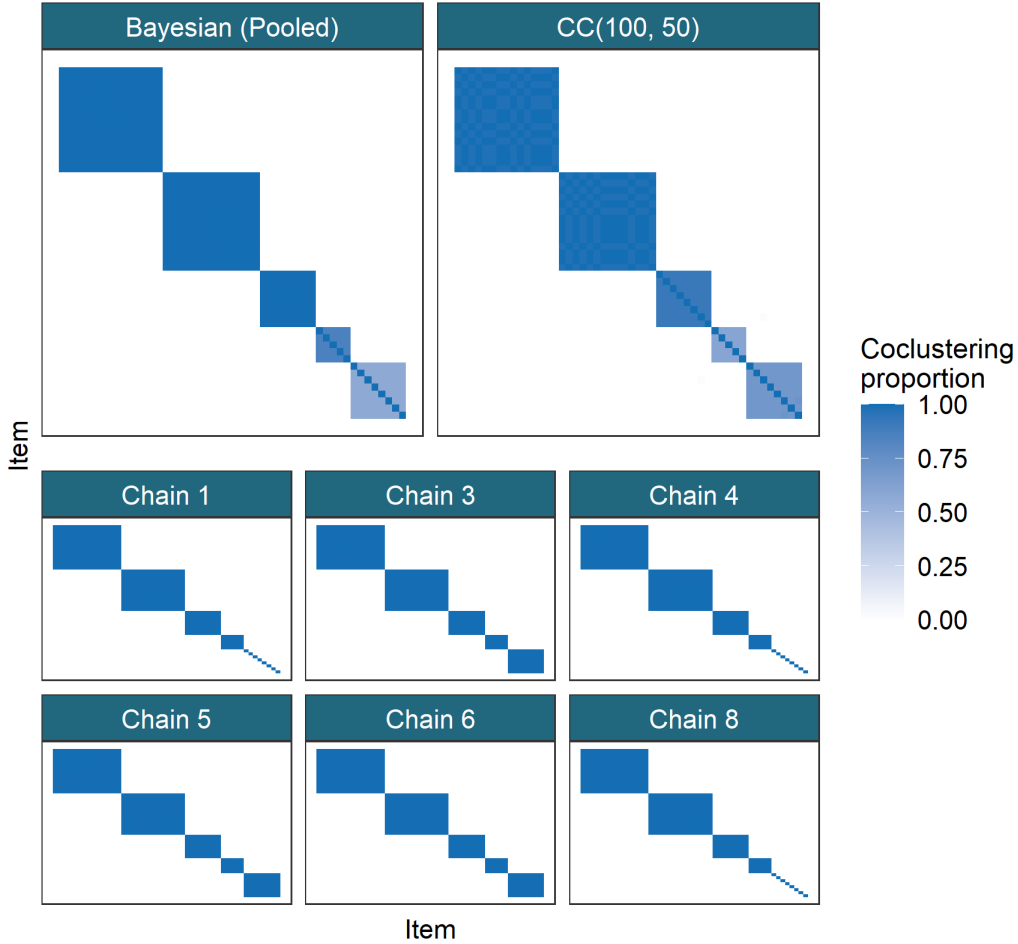
Figure 3: Comparison of similarity matrices from a dataset for the Small N, large P scenario. In each matrix, the $(i, j)^{th}$ entry is the proportion of clusterings for which the ith and j^{th} items co-clustered for the method in question. In the first row the PSM of the pooled Bayesian samples is compared to the CM for CC(100, 50), with a common ordering of rows and columns in both heatmaps. In the following rows, 6 of the long chains that passed the tests of convergence are shown.

to 1,000 has small effect. We therefore use the largest ensemble available, a depth $D = 10001$ and width $W = 1000$, believing this ensemble is stable (additional evidence in section 5.1 of the Supplementary Material).

We focus upon the genes that tend to have the same cluster label in both the time course and ChIP-chip datasets as being of the most interest for an integrative analysis. 261 genes (nearly half of the genes present) in this pair of datasets have a common label in most chains, whereas only 56 genes have a common label across all three datasets. Thus, we focus upon this pairing of datasets as they appear to share much common signal. More formally, we analyse the clustering structure among genes for which $\hat{P}(c_{nl} = c_{nm}) > 0.5$, where c_{nl} denotes the cluster label of gene n in dataset l. We show the gene expression and regulatory proteins of these genes separated by their cluster in Figure 6. In Figure 6, the clusters in the time series data have tight, unique signatures (having different periods, amplitudes, or both) and in the ChIP-chip data clusters are defined by a small number of well-studied transcription factors (**TFs**) (see Table 2 of the Supplementary Material for details of these TFs, many of which are well known to regulate cell cycle expression, Simon et al., 2001).

As an example, we briefly analyse clusters 9 and 16 in greater depth. Cluster 9 has strong association with MBP1 and some interactions with SWI6, as can be seen in Figure 6. The Mbp1-Swi6p complex, MBF, is associated with DNA replication (Iyer et al., 2001). The first time point, 0 minutes, in the time course data is at the START checkpoint, or the
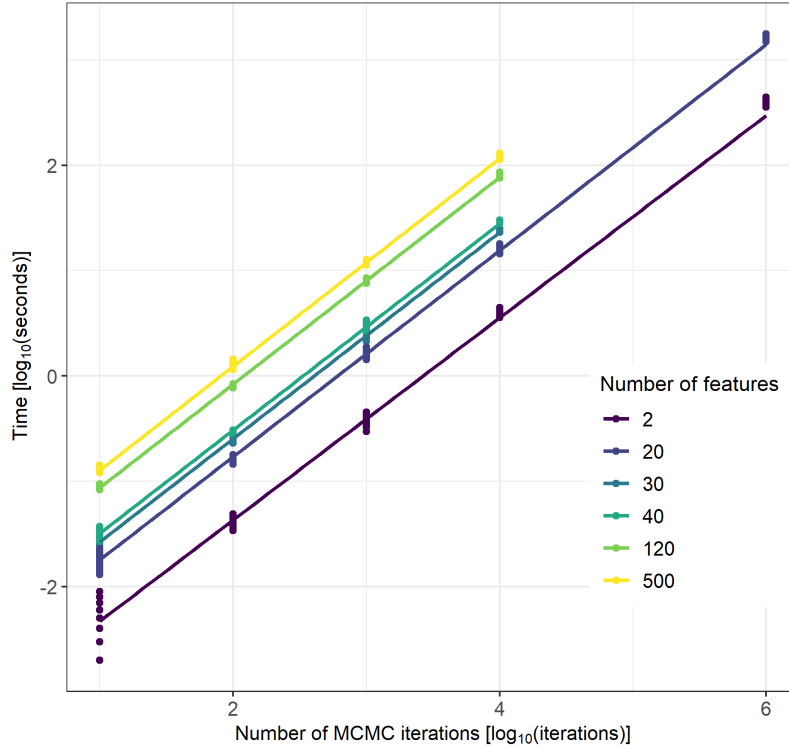
Figure 4: The time taken for different numbers of iterations of MCMC moves in $\log_{10}(seconds)$. The relationship between chain length, D, and the time taken is linear (the slope is approximately 1 on the $\log_{10}$ scale), with a change of intercept for different dimensions. The runtime of each Markov chain was recorded using the terminal command `time`, measured in milliseconds.

G1/S transition. The members of cluster 9 begin highly expressed at this point before quickly dropping in expression (in the first of the 3 cell cycles). This suggests that many transcripts are produced immediately in advance of S-phase, and thus are required for the first stages of DNA synthesis. These genes' descriptions (found using `org.Sc.sgd.db`, Carlson et al., 2014, and shown in Table 3 of the Supplementary Material) support this hypothesis, as many of the members are associated with DNA replication, repair and/or recombination. Additionally, TOF1, MRC1 and RAD53, members of the replication checkpoint (Bando et al., 2009; Lao et al., 2018) emerge in the cluster as do members of the cohesin complex. Cohesin is associated with sister chromatid cohesion which is established during the S-phase of the cell cycle (Tóth et al., 1999) and also contributes to transcription regulation, DNA repair, chromosome condensation, homolog pairing (Mehta et al., 2013), fitting the theme of cluster 9.

Cluster 16 appears to be a cluster of S-phase genes, consisting of GAS3, NRM1 and PDS1 and the genes encoding the histones H1, H2A, H2B, H3 and H4. Histones are the chief protein components of chromatin (Fischle et al., 2003) and are important contributors to gene regulation (Bannister and Kouzarides, 2011). They are known to peak in expression in S-phase (Granovskaia et al., 2010), which matches the first peak of this cluster early in the time series. Of the other members, NRM1 is a transcriptional co-repressor of MBF-regulated gene expression acting at the transition from G1 to S-phase (de Bruin et al., 2006; Aligianni et al., 2009). Pds1p binds to and inhibits the Esp1 class of sister separating proteins, preventing sister chromatids separation before M phase (Ciosk et al., 1998; Tóth et al., 1999). GAS3, is not well studied. It interacts with SMT3 which regulates chromatid cohesion, chromosome segregation and DNA replication (among other things). Chromatid cohesion ensures the faithful segregation of chromosomes in mitosis and in both meiotic divisions (Cooper et al., 2009) and is instantiated in S-phase (Tóth et al., 1999). These results, along with the very similar expression profile to the histone genes in the time course data, suggest that GAS3 may be more directly involved in DNA replication or chromatid cohesion than is currently believed.

We attempt to perform a similar analysis using traditional Bayesian inference of MDI, but after 36 hours of runtime there is no consistency or convergence across chains. Each chain provides different parameter distributions and clustering estimates, leaving no clear clustering solution. For details of this analysis, see section 5.2 of the Supplementary Material.
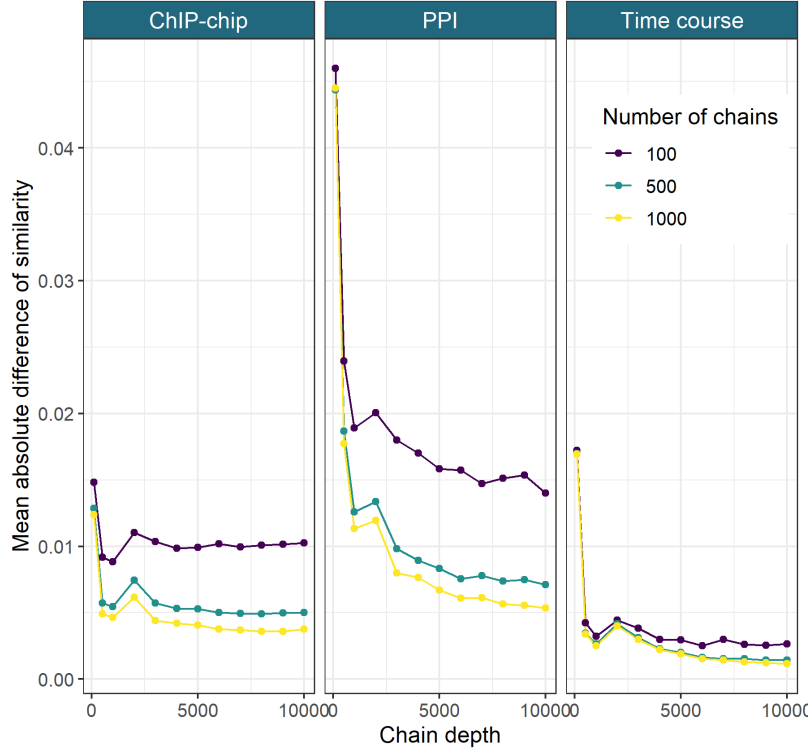
Figure 5: The mean absolute difference between the sequential Consensus matrices. For a set of chain lengths, $D' = \{d_1, \ldots, d_I\}$ and number of chains, $W' = \{w_1, \ldots, w_J\}$, we take the mean of the absolute difference between the consensus matrix for (d_i, w_j) and (d_{i-1}, w_j) (here $D' = \{101, 501, 1001, 2001, \ldots, 10001\}$ and $W' = \{100, 500, 1000\}$).

4 Discussion

Our proposed method has demonstrated good performance on simulation studies, uncovering generating structure and approximating Bayesian inference when the Markov chain is exploring the full support of the posterior. However, we have shown that if a finite Markov chain fails to describe the full posterior and is itself only approximating Bayesian inference, our method has better ability to represent several modes in the data than individual chains and thus offers a more consistent and reproducible analysis. Furthermore, consensus clustering is significantly faster in a parallel environment than inference using individual chains, while retaining the ability to robustly infer K, the number of occupied components present.

We proposed a method of assessing ensemble stability and deciding upon ensemble size which we used when performing an integrative analysis of yeast cell cycle data using MDI, an extension of Bayesian mixture models that jointly models multiple datasets. We uncovered many genes with shared signal across several datasets and explored the meaning of some of the inferred clusters, using data external to the analysis. We found sensible results as well as signal for possibly novel biology.

The results of our simulations and the multi-omics analysis show that consensus clustering can be successfully used in a broad context, being applicable to any MCMC based clustering method. It offers computational gains and greater applicability to these methods as a result and, attractively, it can be applied to existing implementations, unlike improvements to the underlying MCMC methods or alternative methods for Bayesian inference such as VI which would require re-writing software. However, consensus clustering does lose the theoretical framework of true Bayesian inference. We attempt to mitigate this with our assessment of stability in the ensemble, but this diagnosis is heuristic and subjective, and while there is empirical evidence for its success, it lacks the formal results for the tests of model convergence for Bayesian inference.

We expect that researchers interested in applying some of the Bayesian integrative clustering models such as MDI and Clusternomics (Gabasova et al., 2017) will be enabled to do so, as consensus clustering overcomes some of the
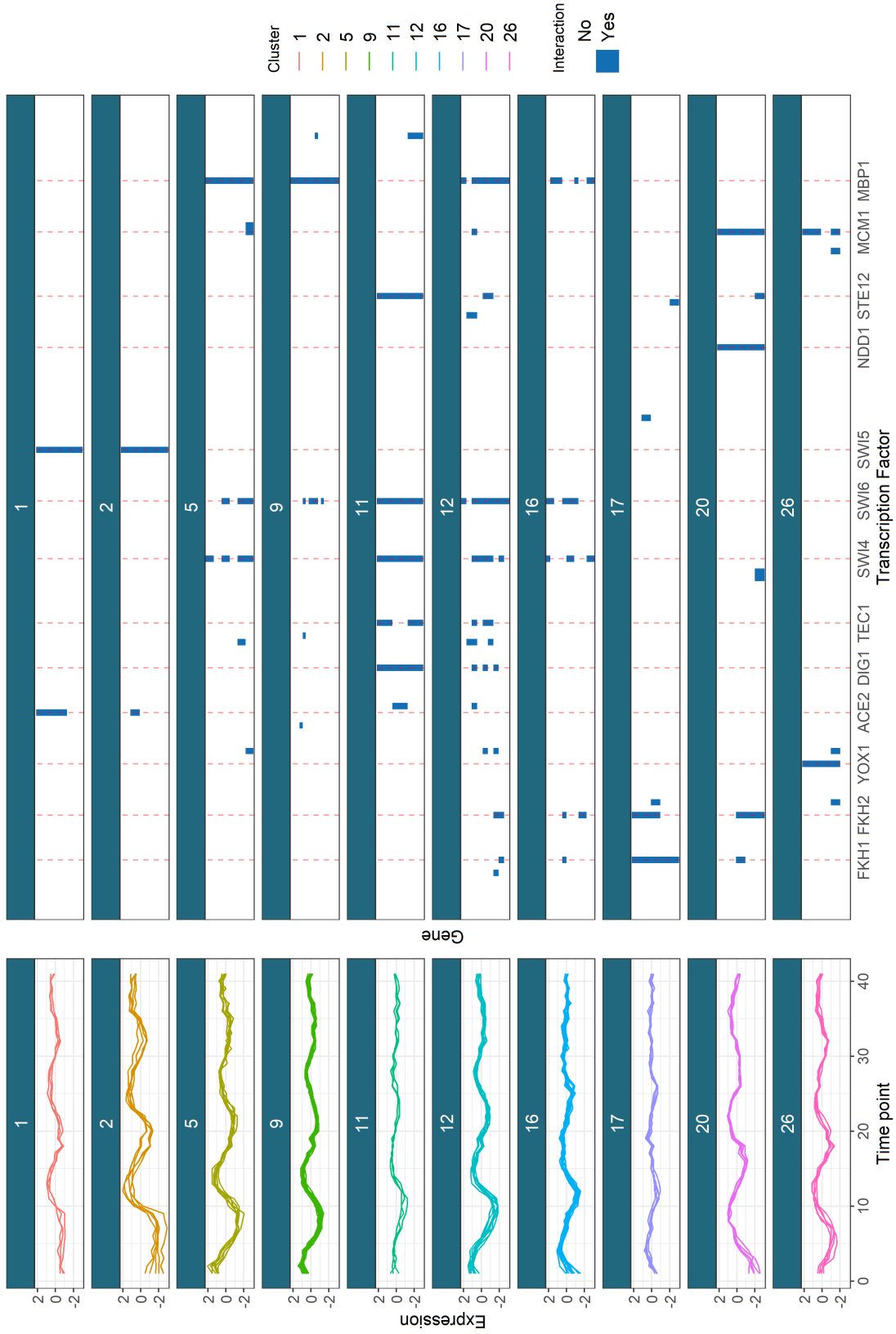
Figure 6: The gene clusters which tend to have a common label across the time course and ChIP-chip datasets, shown in these datasets. We include only the clusters with more than one member and more than half the members having some interactions in the ChIP-chip data. Red lines for the most common transcription factors are included.

unwieldiness of these large, joint models. More generally, we expect that our method will be useful to researchers performing cluster analysis of high-dimensional data where the runtime of MCMC methods becomes too onerous and multi-modality is more likely to be present.

Funding

References

Bruce Alberts, Alexander Johnson, Julian Lewis, Martin Raff, Keith Roberts, and Peter Walter. The cell cycle and programmed cell death. *Molecular biology of the cell*, 4:983–1027, 2002.

Sofia Aligianni, Daniel H Lackner, Steffi Klier, Gabriella Rustici, Brian T Wilhelm, Samuel Marguerat, Sandra Codlin, Alvis Brazma, Robertus AM de Bruin, and Jürg Bähler. The fission yeast homeodomain protein Yox1p binds to MBF and confines MBF-dependent cell-cycle transcription to G1-S via negative feedback. *PLoS Genet*, 5(8):e1000626, 2009.

Ricard Argelaguet, Britta Velten, Damien Arnol, Sascha Dietrich, Thorsten Zenz, John C Marioni, Florian Buettner, Wolfgang Huber, and Oliver Stegle. Multi-omics factor analysis—a framework for unsupervised integration of multi-omics data sets. *Molecular systems biology*, 14(6):e8124, 2018.

David Arthur and Sergei Vassilvitskii. k-means++: The advantages of careful seeding. Technical report, Stanford, 2006.

Jane PF Bai, Alexander V Alekseyenko, Alexander Statnikov, I-Ming Wang, and Peggy H Wong. Strategic applications of gene expression: from drug discovery/development to bedside. *The AAPS journal*, 15(2):427–437, 2013.

Masashige Bando, Yuki Katou, Makiko Komata, Hirokazu Tanaka, Takehiko Itoh, Takashi Sutani, and Katsuhiko Shirahige. Csm3, Tof1, and Mrc1 form a heterotrimeric mediator complex that associates with DNA replication forks. *Journal of Biological Chemistry*, 284(49):34355–34365, 2009.

Andrew J Bannister and Tony Kouzarides. Regulation of chromatin by histone modifications. *Cell research*, 21(3): 381–395, 2011.

David M Blei, Michael I Jordan, et al. Variational inference for Dirichlet process mixtures. *Bayesian analysis*, 1(1): 121–143, 2006.

David M Blei, Alp Kucukelbir, and Jon D McAuliffe. Variational inference: A review for statisticians. *Journal of the American statistical Association*, 112(518):859–877, 2017.

Leo Breiman. Random forests. *Machine learning*, 45(1):5–32, 2001.

M Carlson, S Falcon, H Pages, and N Li. Org. sc. sgd. db: Genome wide annotation for yeast. *R package version*, 2(1), 2014.

Cliburn Chan, Feng Feng, Janet Ottinger, David Foster, Mike West, and Thomas B Kepler. Statistical mixture modeling for cell subtype identification in flow cytometry. *Cytometry Part A: The Journal of the International Society for Analytical Cytology*, 73(8):693–701, 2008.

Katherine C Chen, Laurence Calzone, Attila Csikasz-Nagy, Frederick R Cross, Bela Novak, and John J Tyson. Integrative analysis of cell cycle control in budding yeast. *Molecular biology of the cell*, 15(8):3841–3862, 2004.

Rafal Ciosk, Wolfgang Zachariae, Christine Michaelis, Andrej Shevchenko, Matthias Mann, and Kim Nasmyth. An esp1/pds1 complex regulates loss of sister chromatid cohesion at the metaphase to anaphase transition in yeast. *Cell*, 93(6):1067–1076, 1998.

Katrina F Cooper, Michael J Mallory, Vincent Guacci, Katherine Lowe, and Randy Strich. Pds1p is required for meiotic recombination and prophase I progression in Saccharomyces cerevisiae. *Genetics*, 181(1):65–79, 2009.

Oliver M Crook, Claire M Mulvey, Paul DW Kirk, Kathryn S Lilley, and Laurent Gatto. A Bayesian mixture modelling approach for spatial proteomics. *PLoS computational biology*, 14(11):e1006516, 2018.

Robertus AM de Bruin, Tatyana I Kalashnikova, Charly Chahwan, W Hayes McDonald, James Wohlschlegel, John Yates III, Paul Russell, and Curt Wittenberg. Constraining g1-specific transcription to late g1 phase: the mbf-associated corepressor nrm1 acts via negative feedback. *Molecular cell*, 23(4):483–496, 2006.

Frank Emmert-Streib, Matthias Dehmer, and Benjamin Haibe-Kains. Gene regulatory networks and their applications: understanding biological and medical problems in terms of networks. *Frontiers in cell and developmental biology*, 2: 38, 2014.

Thomas S Ferguson. A Bayesian analysis of some nonparametric problems. *The annals of statistics*, pages 209–230, 1973.

Wolfgang Fischle, Yanming Wang, and C David Allis. Histone and chromatin cross-talk. *Current opinion in cell biology*, 15(2):172–183, 2003.

Edward W Forgy. Cluster analysis of multivariate data: efficiency versus interpretability of classifications. *biometrics*, 21:768–769, 1965.

Chris Fraley and Adrian E Raftery. Model-based clustering, discriminant analysis, and density estimation. *Journal of the American statistical Association*, 97(458):611–631, 2002.

Jerome H Friedman. Stochastic gradient boosting. *Computational statistics & data analysis*, 38(4):367–378, 2002.

Arno Fritsch. *mcclust: process an MCMC sample of clusterings*, 2012. URL https://CRAN.R-project.org/package=mcclust. R package version 1.0.

Arno Fritsch, Katja Ickstadt, et al. Improved criteria for clustering based on the posterior similarity matrix. *Bayesian analysis*, 4(2):367–391, 2009.

Evelina Gabasova, John Reid, and Lorenz Wernisch. Clusternomics: Integrative context-dependent clustering for heterogeneous datasets. *PLoS computational biology*, 13(10):e1005781, 2017.

Andrew Gelman, Donald B Rubin, et al. Inference from iterative simulation using multiple sequences. *Statistical science*, 7(4):457–472, 1992.

John Geweke et al. *Evaluating the accuracy of sampling-based approaches to the calculation of posterior moments*, volume 196. Federal Reserve Bank of Minneapolis, Research Department Minneapolis, MN, 1991.

Reza Ghaemi, Md Nasir Sulaiman, Hamidah Ibrahim, Norwati Mustapha, et al. A survey: clustering ensembles techniques. *World Academy of Science, Engineering and Technology*, 50:636–645, 2009.

Marina V Granovskaia, Lars J Jensen, Matthew E Ritchie, Joern Toedling, Ye Ning, Peer Bork, Wolfgang Huber, and Lars M Steinmetz. High-resolution transcription atlas of the mitotic cell cycle in budding yeast. *Genome biology*, 11 (3):1–11, 2010.

Zuguang Gu, Matthias Schlesner, and Daniel Hübschmann. cola: an R/Bioconductor package for consensus partitioning through a general framework. *Nucleic Acids Research*, 12 2020. ISSN 0305-1048. doi: 10.1093/nar/gkaa1146. URL https://doi.org/10.1093/nar/gkaa1146. gkaa1146.

Christopher T Harbison, D Benjamin Gordon, Tong Ihn Lee, Nicola J Rinaldi, Kenzie D Macisaac, Timothy W Danford, Nancy M Hannett, Jean-Bosco Tagne, David B Reynolds, Jane Yoo, et al. Transcriptional regulatory code of a eukaryotic genome. *Nature*, 431(7004):99–104, 2004.

Boris P Hejblum, Jason Skinner, and Rodolphe Thiébaut. Time-course gene set analysis for longitudinal gene expression data. *PLoS computational biology*, 11(6):e1004310, 2015.

Boris P Hejblum, Chariff Alkhassim, Raphael Gottardo, François Caron, Rodolphe Thiébaut, et al. Sequential Dirichlet process mixtures of multivariate skew t-distributions for model-based clustering of flow cytometry data. *The Annals of Applied Statistics*, 13(1):638–660, 2019.

Lawrence Hubert and Phipps Arabie. Comparing partitions. *Journal of classification*, 2(1):193–218, 1985.

BP Ingalls, BP Duncker, DR Kim, and BJ McConkey. Systems level modeling of the cell cycle using budding yeast. *Cancer informatics*, 3:117693510700300020, 2007.

Vishwanath R Iyer, Christine E Horak, Charles S Scafe, David Botstein, Michael Snyder, and Patrick O Brown. Genomic binding sites of the yeast cell-cycle transcription factors SBF and MBF. *Nature*, 409(6819):533–538, 2001.

Javier Jiménez, Samuel Bru, Mariana Ribeiro, and Josep Clotet. Live fast, die soon: cell cycle progression and lifespan in yeast cells. *Microbial Cell*, 2(3):62, 2015.

Christopher R John, David Watson, Dominic Russ, Katriona Goldmann, Michael Ehrenstein, Costantino Pitzalis, Myles Lewis, and Michael Barnes. M3C: Monte Carlo reference-based consensus clustering. *Scientific reports*, 10(1):1–14, 2020.

M Angeles Juanes. Methods of synchronization of yeast cells for the analysis of cell cycle progression. In *The Mitotic Exit Network*, pages 19–34. Springer, 2017.

Paul Kirk, Jim E Griffin, Richard S Savage, Zoubin Ghahramani, and David L Wild. Bayesian correlated clustering to integrate multiple datasets. *Bioinformatics*, 28(24):3290–3297, 2012.

Vladimir Yu Kiselev, Kristina Kirschner, Michael T Schaub, Tallulah Andrews, Andrew Yiu, Tamir Chandra, Kedar N Natarajan, Wolf Reik, Mauricio Barahona, Anthony R Green, et al. SC3: consensus clustering of single-cell RNA-seq data. *Nature methods*, 14(5):483–486, 2017.

Alp Kucukelbir, Dustin Tran, Rajesh Ranganath, Andrew Gelman, and David M Blei. Automatic differentiation variational inference. *The Journal of Machine Learning Research*, 18(1):430–474, 2017.

Jessica P Lao, Katie M Ulrich, Jeffrey R Johnson, Billy W Newton, Ajay A Vashisht, James A Wohlschlegel, Nevan J Krogan, and David P Toczyski. The yeast DNA damage checkpoint kinase Rad53 targets the exoribonuclease, Xrn1. *G3: Genes, Genomes, Genetics*, 8(12):3931–3944, 2018.

Martin H Law, Anil K Jain, and Mário Figueiredo. Feature selection in mixture-based clustering. In *Advances in neural information processing systems*, pages 641–648, 2003.

Brian D Lehmann, Joshua A Bauer, Xi Chen, Melinda E Sanders, A Bapsi Chakravarthy, Yu Shyr, Jennifer A Pietenpol, et al. Identification of human triple-negative breast cancer subtypes and preclinical models for selection of targeted therapies. *The Journal of clinical investigation*, 121(7):2750–2767, 2011.

Stuart Lloyd. Least squares quantization in pcm. *IEEE transactions on information theory*, 28(2):129–137, 1982.

Gael M Martin, David T Frazier, and Christian P Robert. Computing Bayes: Bayesian Computation from 1763 to the 21st Century. *arXiv preprint arXiv:2004.06425*, 2020.

Mario Medvedovic and Siva Sivaganesan. Bayesian infinite mixture model based clustering of gene expression profiles. *Bioinformatics*, 18(9):1194–1206, 2002.

Gunjan D Mehta, Ravinder Kumar, Sanjeeva Srivastava, and Santanu Kumar Ghosh. Cohesin: functions beyond sister chromatid cohesion. *FEBS letters*, 587(15):2299–2312, 2013.

Nicolai Meinshausen and Peter Bühlmann. Stability selection. *Journal of the Royal Statistical Society: Series B (Statistical Methodology)*, 72(4):417–473, 2010.

Jeffrey W Miller and Matthew T Harrison. Mixture models with a prior on the number of components. *Journal of the American Statistical Association*, 113(521):340–356, 2018.

Stefano Monti, Pablo Tamayo, Jill Mesirov, and Todd Golub. Consensus clustering: a resampling-based method for class discovery and visualization of gene expression microarray data. *Machine learning*, 52(1-2):91–118, 2003.

Sandhya Prabhakaran, Elham Azizi, Ambrose Carr, and Dana Pe'er. Dirichlet process mixture model for correcting technical variation in single-cell gene expression data. In *International Conference on Machine Learning*, pages 1070–1079, 2016.

Sylvia Richardson and Peter J Green. On Bayesian analysis of mixtures with an unknown number of components. *Journal of the Royal Statistical Society: series B*, 59(4):731–792, 1997.

Christian P Robert, Víctor Elvira, Nick Tawn, and Changye Wu. Accelerating mcmc algorithms. *Wiley Interdisciplinary Reviews: Computational Statistics*, 10(5):e1435, 2018.

Judith Rousseau and Kerrie Mengersen. Asymptotic behaviour of the posterior distribution in overfitted mixture models. *Journal of the Royal Statistical Society: Series B (Statistical Methodology)*, 73(5):689–710, 2011.

Gideon Schwarz et al. Estimating the dimension of a model. *The annals of statistics*, 6(2):461–464, 1978.

Luca Scrucca, Michael Fop, Brendan T. Murphy, and Adrian E. Raftery. mclust 5: clustering, classification and density estimation using Gaussian finite mixture models. *The R Journal*, 8(1):289–317, 2016. URL https://doi.org/10.32614/RJ-2016-021.

Samuel Sanford Shapiro and Martin B Wilk. An analysis of variance test for normality (complete samples). *Biometrika*, 52(3/4):591–611, 1965.

Itamar Simon, John Barnett, Nancy Hannett, Christopher T Harbison, Nicola J Rinaldi, Thomas L Volkert, John J Wyrick, Julia Zeitlinger, David K Gifford, Tommi S Jaakkola, et al. Serial regulation of transcriptional regulators in the yeast cell cycle. *Cell*, 106(6):697–708, 2001.

Chris Stark, Bobby-Joe Breitkreutz, Teresa Reguly, Lorrie Boucher, Ashton Breitkreutz, and Mike Tyers. Biogrid: a general repository for interaction datasets. *Nucleic acids research*, 34(suppl_1):D535–D539, 2006.

Magdalena E Strauss, Paul DW Kirk, John E Reid, and Lorenz Wernisch. Gpseudoclust: deconvolution of shared pseudo-profiles at single-cell resolution. *Bioinformatics*, 36(5):1484–1491, 2020.

Attila Tóth, Rafal Ciosk, Frank Uhlmann, Marta Galova, Alexander Schleiffer, and Kim Nasmyth. Yeast cohesin complex requires a conserved protein, Eco1p (Ctf7), to establish cohesion between sister chromatids during DNA replication. *Genes & development*, 13(3):320–333, 1999.

Richard Eric Turner and Maneesh Sahani. Two problems with variational expectation maximisation for time-series models. In David Barber, A Taylan Cemgil, and Silvia Chiappa, editors, *Bayesian time series models*, chapter 5. Cambridge University Press, 1 edition, 2011.

446 John J. Tyson, Katherine C. Chen, and Béla Novák. Cell cycle, budding yeast. In Werner Dubitzky, Olaf Wolkenhauer,
447 Kwang-Hyun Cho, and Hiroki Yokota, editors, *Encyclopedia of Systems Biology*, pages 337–341. Springer New
448 York, New York, NY, 2013.

449 Zoé Van Havre, Nicole White, Judith Rousseau, and Kerrie Mengersen. Overfitting Bayesian mixture models with an
450 unknown number of components. *PloS one*, 10(7):e0131739, 2015.

451 Dootika Vats and Christina Knudson. Revisiting the gelman-rubin diagnostic. *arXiv preprint arXiv:1812.09384*, 2018.

452 Roel GW Verhaak, Katherine A Hoadley, Elizabeth Purdom, Victoria Wang, Yuan Qi, Matthew D Wilkerson, C Ryan
453 Miller, Li Ding, Todd Golub, Jill P Mesirov, et al. Integrated genomic analysis identifies clinically relevant subtypes
454 of glioblastoma characterized by abnormalities in pdgfra, idh1, egfr, and nf1. *Cancer cell*, 17(1):98–110, 2010.

455 Ulrike Von Luxburg and Shai Ben-David. Towards a statistical theory of clustering. In *Pascal workshop on statistics
456 and optimization of clustering*, pages 20–26. Citeseer, 2005.

457 Lianming Wang and David B Dunson. Fast Bayesian inference in Dirichlet process mixture models. *Journal of
458 Computational and Graphical Statistics*, 20(1):196–216, 2011.

459 Wilkerson, Matthew D., Hayes, and D. Neil. ConsensusClusterPlus: a class discovery tool with confidence assessments
460 and item tracking. *Bioinformatics*, 26(12):1572–1573, 2010.

461 Svante Wold, Kim Esbensen, and Paul Geladi. Principal component analysis. *Chemometrics and intelligent laboratory
462 systems*, 2(1-3):37–52, 1987.

463 Yuling Yao, Aki Vehtari, and Andrew Gelman. Stacking for non-mixing Bayesian computations: the curse and blessing
464 of multimodal posteriors. *arXiv preprint arXiv:2006.12335*, 2020.