

Combinatorial Mixture Models for Single Cell Assays with Application to Vaccine Studies

Greg Finak¹, SC De Rosa², Mario Roederer³, and Raphael Gottardo¹

¹Vaccine and Infectious Disease Division, Fred Hutchinson Cancer Research Center (FHCRC), Seattle, WA

²HIV Vaccine Trials Network, Fred Hutchinson Cancer Research Center (FHCRC), Seattle, WA

³Vaccine Research Center, NIAID, NIH, 40 Convent Drive, Rm 5509, Bethesda, MD 20892

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Abstract

Most biological samples (*e.g.*, blood and tissue) are composed of many functionally distinct cell subsets that can only be measured accurately using single cell assays. The characterization of these small cell subsets is crucial to decipher system level biological changes. For this reason, an increasing number of studies rely on single-cell assays to provide single-cell measurements of multiple genes and proteins from bulk cell samples. A common problem in the analysis of such data is to identify markers (or combinations of markers) that are differentially expressed between two biological conditions (*e.g.*, before/after vaccination), where expression is defined as the proportion of cells expressing that marker (or marker combination) in the cell subset(s) of interest. Here we present a Bayesian hierarchical framework based on beta-binomial mixture models for testing for differential marker expression using such single-cell assays. Our model allows the inference to be subject specific, while borrowing strength across subjects¹ through common prior distributions. We propose two approaches for parameter estimation: an empirical-Bayes approach using an Expectation-Maximization algorithm and a fully Bayesian one based on a Markov chain Monte Carlo algorithm. We compare our method against Fisher's exact test, a likelihood ratio test, and basic log-fold changes. Using several experimental immunological assays measuring proteins or genes at the single-cell level, we find that our method has higher sensitivity and specificity than alternative methods. Using a simulation study we show that our framework is also robust to model misspecification. Finally, we also demonstrate how our approach can be extended to testing multivariate differential expression across multiple marker combinations using a multinomial-Dirichlet model.

¹Should we use subject, individuals or something else? What about animal studies?

1 Introduction

Cell populations, particularly in the immune system, are never truly homogeneous; individual cells may be in different biochemical states that define functional but measurable differences between them. This single-cell heterogeneity is informative, but lost in assays that measure cell mixtures. For this reason, endpoints in vaccine and immunological studies are measured through a variety of assays that provide single-cell measurements of multiple genes and proteins. In the 1970s, single-cell analysis was revolutionized with the development of fluorescence-based flow cytometry (FCM). Since then, instrumentation and reagent advances have enabled the study of numerous cellular processes via the simultaneous single cell measurement of multiple surface and intracellular markers (up to 17 markers). More recent technological development have drastically extended the capabilities of single-cell cytometry to measure dozens of simultaneous parameters per cell [1]. Although cells sorted using well-established surface markers may appear homogeneous, mRNA expression of other genes within these cells can be heterogeneous [2, 3] and could further characterize and subset these cells. A new technology based on microfluidic arrays combined with multiplexed polymerase chain reactions (PCR) can now be used to perform thousands of PCRs in a single device, enabling simultaneous, high-throughput gene expression measurements at the single-cell level across hundreds of cells and genes [4]. While classic gene expression microarrays sum the expression from many individual cells, the intrinsic stochastic nature of biochemical processes results in relatively large cell-to-cell gene expression variability (add references). This heterogeneity may carry important information, thus single cell expression data should not be analyzed in the same fashion as cell-population level data. Special treatment of single cell level data, which preserves information about population heterogeneity, is warranted in general. For this reason, single-cell assays are an important tool in immunology, providing a functional and phenotypic snapshot of the immune system at a given time. These assays typically measure multiple markers simultaneously on individual cells in a heterogeneous mixture such as whole blood or peripheral blood cell mononuclear cells (PBMC), and are used for immune monitoring of disease, vaccine research, and diagnosis of haematological malignancies [5–7].

During analysis, cell level marker intensities are typically thresholded as positive or negative so that subsets with different multivariate $+/-$ combinations can be obtained as Boolean combinations. For some assays (*e.g.*, flow cytometry), the positivity thresholds are set based on prior biological knowledge while for others thresholds are given by the assay technology. This is the case for the Fluidigm technology where genes are recorded as absent (not expressed) or present (expressed) at the single cell level. After this thresholding step, we obtain a Boolean matrix of dimension $N \times K$ where N is the number of cells recorded and K is number of markers. Using this matrix, one can form 2^K putative cell subsets. When K is large there is a combinatorial explosion of the number of subsets, and many of these might be small or even empty. A common statistical problem is, for a given marker combination, to identify individuals for whom the proportion of cells expressing that com-

bination is significantly different between two experimental conditions (*e.g.*, before and after vaccination). A motivating example from vaccine research is the flow cytometric intracellular cytokine staining (ICS) assay, which is used to identify and quantify individuals' immune responses to a vaccine. Upon vaccination, antigen in the vaccine is taken up and presented to CD4 or CD8 T-cells via antigen presenting cells. While not all T-cells can recognize all antigens, those that recognize antigens in the vaccine become *activated* and produce a variety of cytokines, further promoting the immune response. After activation, this antigen-specific subpopulation proliferates and can persist in the immune system for some time providing *memory* that can more rapidly recognize the same antigen again in the future [8]. These antigen-specific T-cell subpopulations constitute a very small fraction of the total number of CD4 and CD8 T-cells. The ICS assay measures the number of antigen-specific T-cells in PBMC or whole blood by measuring cytokine production in response to activation following stimulation by an antigen that closely matches what was present in the original vaccine. Individual cells are labelled using fluorescently conjugated antibodies against phenotypic markers (CD3, CD4, and CD8), used to subset T-cells, and functional markers (cytokines) used to define antigen specific T-cells [6, 9, 10]. A sufficiently large number of cells must be collected to ensure that the rare cell populations can be detected. Subsequently, each individual cell is classified as either positive or negative for each marker based on predetermined thresholds, then the number of cells matching each subpopulation phenotype is counted. These counts are compared between antigen stimulated and unstimulated samples from an individual to identify significant differences. individuals who generate a response after stimulation are called *responders* whereas individual that do not show any differences are called *non-responders*. In many immunological studies, the size of the functionally distinct subpopulations (*i.e.*, the number of positive cells) is very low (relative to the total number of cells), and real biological differences might be difficult to detect.

Although there is no standard approach to analyzing single-cell assays current methods range from ad-hoc rules based on log-fold changes, to permutation tests based on Hotelling's T^2 statistics, to exact tests of 2x2 contingency tables (*e.g.*, Fisher's exact test and χ^2 test²) [9, 11–14]. All of these methods analyze each individual separately, and no information is shared across individuals even though one could expect some similarities across responders (*resp.* non-responders). In addition, these methods generally test one marker at a time or pairwise combinations of markers, raising questions of appropriate multiple testing adjustments, or they perform global tests of significance on multiple markers resulting in decreased power to detect small changes in subsets of cytokines [13, 15]³.

The framework developed in this paper addresses these issues explicitly. In our model, cell counts are modeled via a binomial (or multinomial in the multivariate case) distribution and information is shared across individuals by mean of a prior distribution placed on

²make sure there is a reference for that. Added ref for the HVTN054 trial and the ICS standardization paper from Horton

³What are we trying to say here? Let's update this sentence later

the unknown proportion(s) of the binomial (or multinomial) likelihood. In order to discriminate between responders and non-responders, the prior is written as a mixture of two beta (or Dirichlet in the multivariate case) distributions where the hyper-parameters for each mixture component are shared across individuals. This sharing of information across individuals helps regularize proportion estimates when the cell counts are small, which is typical with single-cell⁴ assays, and increase sensitivity and specificity when detecting responders. Because our framework is multivariate in nature, multiple cell subsets can be model simultaneously, which could help detect small biological changes that are spread out across multiple cell subsets [13].

2 Data structure and notation

In this paper we consider two types of immunological single-cell assays: flow cytometry and single-cell gene expression, as described below.

Flow cytometry: The primary ICS data set is from a trial testing the GeoVax DNA and MVA vaccines in a prime-boost regimen with 120 individuals (98 vaccines and 20 placebo recipients, see supplementary material S.1.1). The goal of this data set was to assess the immune response to the vaccine across multiple stimulations, time points, cytokines and T-cell subsets. Here, we analyze a subset of the data consisting of 98 individual from the vaccinee group at two time points, day 0 and day 182. Samples on day 0 were taken just before vaccination and no response is expected there. The corresponding samples can be used as negative controls. Conversely, day 182 (26 weeks) should be close to the immunogenicity peak, and many individuals are expected to respond, for some cytokines at least.

Fluidigm single-cell gene expression: This is a single-cell gene expression data set of sorted CD8+ T-cells from sixteen individuals. T-cells isolated by flow cytometry from sixteen individuals were stimulated in blocks of four individuals with four different antigens (HIV Gag, HIV Nef, CMV pp65 tm10, CMV pp65 nlv5) and gene expression post-stimulation measured at the single-cell level using the BioMark system (Fluidigm) 96×96 well arrays. The expression from the simulated samples was compared to paired, unstimulated controls.⁵

In the remainder of the paper, we use the following notation to describe our model. From this point on, we assume that we observe cell counts from I individuals in two conditions: stimulated and un-stimulated. Each cell can either be positive or negative for a marker. Given a set of K markers, the measured cells can be classified into 2^K positive/negative marker combinations. We denote by n_{sik} and n_{uik} , $k = 1 \dots 2^K$, the observed counts for the 2^K combinations in the stimulated and un-stimulated samples. We denote by $N_{si} = \sum_k n_{sik}$ and $N_{ui} = \sum_k n_{uik}$ the total number of cells measured for

⁴Let's replace all single cell by single-cell

⁵Add a bit more info here, how many genes, tetramer sorted, etc, Mario et al. could you fill this in?

individual i in each sample. For ease of notations, we will denote by \mathbf{y}_i the vector of observed counts for individual i , *i.e.* $\mathbf{y}_i = (\mathbf{n}_{si}, \mathbf{n}_{ui})$ where $\mathbf{n}_{si} = \{n_{sik} : k = 1, \dots, 2^K\}$ and $\mathbf{n}_{ui} = \{n_{uik} : k = 1, \dots, 2^K\}$. Finally, we define $\mathbf{y} = (\mathbf{y}_1, \dots, \mathbf{y}_I)$.

3 Differential expression with one marker

Datasets like the ones presented here are usually analyzed one marker at a times to avoid being underpowered due to the large number of combinations and the potential for very small cell counts in many of the combinations. As a consequence, we first consider the one marker case (*i.e.* $K = 1$) where marginal cell counts are analyzed separately. In this case, for a given individual, the data can be summarized in a contingency table of $+/ -$ cell counts across the un-stimulated and stimulated samples as depicted in Table 1.

Table 1: 2 x 2 contingency table of counts for marker positive and negative cells between stimulated (s) and unstimulated (u) conditions for a given individual i .

	Marker	
	Negative	Positive
Stimulated	$N_{si} - n_{si}$	n_{si}
Unstimulated	$N_{ui} - n_{ui}$	n_{ui}

For a given individual and stimulation, we consider a marker to be differentially expressed if the proportion of positive cells in the stimulated samples is different from the number of positive cells in the un-stimulated sample. Individuals that show differential expression for a given marker will be called responders for that marker. In this section, we shall be concerned with identifying differential expression one marker at a time, using a beta-binomial mixture model as described in what follows.

3.1 Beta-binomial model

For a given individual i , the positive cell counts for the stimulated and un-stimulated samples are jointly modeled as follows,

$$(n_{si}|p_{si}) \sim \text{Bin}(N_{si}, p_{si}) \quad \text{and} \quad (n_{ui}|p_{ui}) \sim \text{Bin}(N_{ui}, p_{ui}) \quad (1)$$

where p_{si} , p_{ui} are the unknown proportions for the stimulated and un-stimulated paired samples. In order to detect responding individuals we consider two competing models:

$$\mathcal{M}_0 : p_{ui} = p_{si} \quad \text{and} \quad \mathcal{M}_1 : p_{ui} \neq p_{si}. \quad (2)$$

Under the null model, \mathcal{M}_0 , there is no difference between the stimulated and un-stimulated samples, and the proportions are equal. Under the alternative model, \mathcal{M}_1 , there is a

difference in proportions between the two samples and the individual i is a responder. In some study, such as the ICS studies used here, the proportion of positive cells is expected to only increase after stimulation, in which case the alternative model should be defined as $p_s > p_u$. This alternative parametrization is described in Web Supplementary material⁶, and we refer to it as the one-sided model.

3.2 Priors

Our model shares information across all individuals using exchangeable Beta priors on the unknown proportions, as follows,

$$(p_{ui}|z_i = 0) \sim \text{Beta}(\alpha_u, \beta_u) \quad (3)$$

$$(p_{si}|z_i = 1) \sim \text{Beta}(\alpha_s, \beta_s) \quad \text{and} \quad (p_{ui}|z_i = 1) \sim \text{Beta}(\alpha_u, \beta_u) \quad (4)$$

where z_i is an indicator variable equal to one if individual i is a responder, i.e. \mathcal{M}_1 is true, and zero otherwise, and $\alpha_u, \beta_u, \alpha_s, \beta_s$ are unknown hyper-parameters shared across all individuals. Note that the parameters α_u, β_u are explicitly shared across the two models, whereas α_s, β_s are only present in the alternative model. Finally, we assume that the z_i 's are independent and identically distributed Bernoulli with probability w , where w represents the (unknown) proportion of responders. It follows that marginally, *i.e.* after integrating z_i , p_{ui} and p_{si} are jointly distributed as a mixture of a one dimensional and a two dimensional Beta distributions with mixing parameter w . Treating the z_i 's as missing data, the unknown parameter vector $\boldsymbol{\theta} \equiv (\alpha_u, \beta_u, \alpha_s, \beta_s, w)$ can be estimated in an Empirical-Bayes fashion using and Expectation-Maximization [16] algorithm as described in Section 3.3. As an alternative, we also describe a fully Bayesian model where the hyperparameters α_u, β_u and α_s, β_s are given vague exponential priors with mean 10^3 , and w is assumed to be drawn from a uniform distribution between 0 and 1. In this case, all parameters will be estimated via a Markov Chain Monte Carlo algorithm as described in Section 3.3.

3.3 Parameter estimation

Our estimation algorithms make direct use of the marginal likelihoods, L_0 and L_1 , obtained after integrating out the $p_{\{s,u\}i}$'s for the null and alternative models, which greatly simplify our calculations. Given the conjugacy of the priors, the marginal likelihoods L_0 and L_1 are available in closed forms (Web Supplementary material), and are given by,

$$L_0(\alpha_u, \beta_u|\mathbf{y}) = \prod_{i=1}^P \binom{N_{ui}}{n_{ui}} \binom{N_{si}}{n_{si}} \frac{B(n_{si} + n_{ui} + \alpha_u, N_{si} - n_{si} + N_{ui} - n_{ui} + \beta_u)}{B(\alpha_u, \beta_u)} \quad (5)$$

⁶let's make sure we use the proper format for referencing the supplementary material

and

$$L_1(\alpha_u, \beta_u, \alpha_s, \beta_s | \mathbf{y}) = \prod_{i=1}^P \binom{N_{ui}}{n_{ui}} \binom{N_{si}}{n_{si}} \frac{B(n_{ui} + \alpha_u, N_{ui} - n_{ui} + \beta_u)}{B(\alpha_u, \beta_u)} \frac{B(n_{si} + \alpha_s, N_{si} - n_{si} + \beta_s)}{B(\alpha_s, \beta_s)}. \quad (6)$$

Assuming that the missing data, the z_i 's, are known, we define the complete data log-likelihood as follows,

$$l(\boldsymbol{\theta} | \mathbf{y}, \mathbf{z}) = \sum_i z_i l_0(\alpha_u, \beta_u | \mathbf{y}_i) + (1 - z_i) l_1(\alpha_u, \beta_u, \alpha_s, \beta_s | \mathbf{y}_i) + z_i \log(w) + (1 - z_i) \log(1 - w) \quad (7)$$

where l_0 and l_1 are the log marginal-likelihoods and $\boldsymbol{\theta} \equiv (\alpha_u, \beta_u, \alpha_s, \beta_s, w)$ is the vector of parameters to be estimated. In the one-sided case, the alternative prior specification must satisfy the constraint $p_s > p_u$, and the marginal likelihood derivation involves the calculation of a normalizing constant that is not available in closed form but can easily be estimated. All calculations for the one-sided case are described in Supplementary Web material.

3.3.1 EM algorithm

Given an estimate of the model parameter vector $\tilde{\boldsymbol{\theta}} = \{\tilde{\alpha}_u, \tilde{\beta}_u, \tilde{\alpha}_s, \tilde{\beta}_s, \tilde{w}\}$ and the data \mathbf{y} , the E step consists of calculating the posterior probabilities of differential expression, defined by

$$\tilde{z}_i \equiv \Pr(z_i = 1 | \mathbf{y}, \tilde{\boldsymbol{\theta}}) = \frac{\tilde{w} \cdot L_1(\tilde{\alpha}_u, \tilde{\beta}_u, \tilde{\alpha}_s, \tilde{\beta}_s | \mathbf{y}_i)}{(1 - \tilde{w}) \cdot L_0(\tilde{\alpha}_u, \tilde{\beta}_u | \mathbf{y}_i) + \tilde{w} \cdot L_1(\tilde{\alpha}_u, \tilde{\beta}_u, \tilde{\alpha}_s, \tilde{\beta}_s | \mathbf{y}_i)}.$$

The M-step then consist of optimizing the complete-data log-likelihood over $\boldsymbol{\theta}$ after replacing z_i by \tilde{z}_i in (7). Straightforward calculations lead to $\tilde{w} = \sum_i \tilde{z}_i / I$, but unfortunately no closed form solutions exist for the remaining parameters. We use numerical optimization as implemented in R's *optim* function to estimate the remaining parameters. Starting from some initial values, the EM algorithm iterates between the E and M steps until convergence. In our case, we initialize the z_i 's using Fisher's exact test to assign each observation to either the null or alternative model components. We then use the estimated z_i 's to estimate the p_{ui} 's and p_{si} 's and use these to set the hyper-parameters to their method-of-moments estimates.

3.3.2 MCMC algorithm

Realizations were generated from the posterior distribution via MCMC algorithms [17]. All updates were done via Metropolis-Hastings sampling except for the z_i 's and w that were done via Gibbs samplings. Details about the algorithms are given in supplementary

material. We used the method of Raftery and Lewis [18, 19] to determine the number of iterations, based on a short pilot run of the sampler. For each dataset presented here, this suggested that a sample of no more than about 1,000,000 iterations with 50,000 burn-in iterations was sufficient to estimate standard posterior quantities. Guided by this, and leaving some margin, we used 2,000,000 iterations after 50,000 burn-ins for each dataset explored here.

4 Results

In this section, we apply our MIMOSA model to the data described in Section 2, and present the results of a simulation study based on the ICS data.

4.1 ICS

HVTN065

Using the ICS data, an ROC (receiver operator characteristic) analysis was performed to assess the sensitivity and specificity of the one-sided MIMOSA model compared to a one-sided Fisher’s exact test, ranked log fold change, and a likelihood ratio test based on the MIMOSA model for identifying vaccine responders and non-responders. Observations at the day 0 time point were treated as true negatives, while observations at the day 182 time point were treated as true positives (potentially underestimating the sensitivity due to non-responders). We examined the CD4+ T-cell cytokine responses for ENV-1-PTEG and GAG-1-PTEG stimulated samples⁷. The MIMOSA model has higher sensitivity and specificity than Fisher’s exact test, the likelihood ratio test, or ranked log fold change for discriminating vaccine responders and non-responders when the magnitude of response was small (i.e. ENV-1-PTEG stimulation) (Figure 1 A), (AUC=0.954 for MIMOSA vs. 0.923 for Fisher’s exact test vs. 0.827 for LRT vs. 0.775 for ranked fold change). When the magnitude of response was larger (GAG-1-PTEG stimulation), MIMOSA performed as well as Fisher’s exact test, and better than other competing methods (Figure 1 C) (AUC=0.982 for MIMOSA vs. 0.978 for Fisher’s exact test vs. 0.877 for LRT vs. 0.784 for ranked fold change). Irrespective of the magnitude of the response to stimulation, MIMOSA gave better estimates of the observed false discovery rate than competing methods (Figure 1 B,D). These results are consistent for other cytokines (see supplementary material S.1.3, supplementary figure 1)⁸.

⁷Were these stimulations described in the data section

⁸Perhaps we could only keep the Env stimulation

HVTN054

4.2 Single-cell gene expression

We applied the MIMOSA model to Fluidigm single-cell gene expression data from CD8+ T-cells from 16 individuals, under four different stimulation conditions, as well as unstimulated samples. This time we used the two-sided MIMOSA model because genes could be up or down regulated upon stimulation. In order to detect stimulation specific changes of expression, our model was fit to each gene within each stimulation. The results presented in Figure 2 A-C show that MIMOSA identifies stimulation-specific differences in the proportions of cells expressing each gene, while preserving inter-individual variability (Figure 2). These patterns are evident in the posterior probabilities (Figure 2 A), and preserved in the posterior estimates of the differences of proportions and the posterior log fold changes of proportions (Figure 2 B,C). A similar analysis using a two-sided Fisher’s exact test (Figure xx) does not reveal any stimulation specific changes of expression.⁹

4.3 Simulation Studies

We examined the performance of the constrained ($p_s > p_u$) and unconstrained ($p_s \neq p_u$) beta-binomial mixture models via simulations. Using hyper parameters estimated from a one-sided MIMOSA model fit to data from Gag1-stimulated, CD4-positive, IL2-expressing T-cells from day 28 post-vaccination of the HVTN054 trial [14]. We simulated data from this constrained model with 500 observations, a response rate of 60%, an N of 10K, 20K, 30K, 50K, 75K, 100K, and 150K events, with ten independent realizations of data for each N . The one-sided MIMOSA model was fit to this data and the sensitivity and specificity of the model’s ability to correctly identify observations from the “responder” and “non-responder” groups was evaluated through analysis of ROC curves, and compared against Fisher’s exact test, the likelihood ratio test, and ranked log fold change. This procedure was repeated for the two-sided models fit to two-sided data (Figure 3 A-D). In addition, the nominal *vs.* observed FDR¹⁰ was also examined to assess the ability of each method to properly estimate the FDR (Figure 3 E-F).

For both the constrained and unconstrained simulations, MIMOSA out-performed competing methods, including Fisher’s exact test, with respect to sensitivity and specificity at all values of N (Figure 3 A, D). Additionally, the estimated FDR for MIMOSA more closely reflected the nominal FDR compared to Fisher’s exact test (Figure 3 E, F).

To assess the sensitivity of the model to deviations from model assumptions, we repeated the simulations with the cell proportions drawn from truncated normal distributions on $(0, 1)$, rather than beta distributions. The means and variances of the truncated normal distributions were set to the maximum likelihood estimates of the beta distributions defined by the α, β hyper parameters estimated from the HVTN065 data set (Supplementary

⁹Perhaps it would be good to compare the number of differentially expressed genes

¹⁰Need to define this earlier

Figure 2). Even under these departures from the model assumptions, the unconstrained MIMOSA model outperformed Fisher’s exact test and performed about as well as the constrained MIMOSA model fit to one-sided data.

5 Differential expression across marker combinations

Our beta-binomial model described in Section 3.1 can be generalized to a Dirichlet-multinomial model to assess differential expression across multiple marker combinations. As described in the data section, we now have counts for each marker combination, denoted by $\mathbf{n}_{si} = \{n_{sik} : k = 1, \dots, 2^K\}$ and $\mathbf{n}_{ui} = \{n_{uik} : k = 1, \dots, 2^K\}$.¹¹

5.1 Model

In our multivariate model, the beta distribution is replaced by a multinomial distribution, as follows,

$$(\mathbf{n}_{ui} | \mathbf{p}_{ui},) \sim \mathcal{M}(N_{ui}, \mathbf{p}_{ui}) \quad \text{and} \quad (\mathbf{n}_{si} | \mathbf{p}_{si}) \sim \mathcal{M}(N_{si}, \mathbf{p}_{si}) \quad (8)$$

where $N_{\{s,u\}i} = \sum_{k=1}^{2^K} n_{\{s,u\}ik}$ are the number of cells collected and \mathbf{p}_{ui} and \mathbf{p}_{si} are the unknown proportions for the un-stimulated and stimulated samples.

5.2 Prior

As in the one-marker case, we share information across individuals using an exchangeable prior on the unknown proportions. This time the beta priors are replaced by Dirichlet priors, as follows,

$$\begin{aligned} (\mathbf{p}_{ui} | z_i = 0) &\sim \text{Dir}(\boldsymbol{\alpha}_u) \\ (\mathbf{p}_{ui} | z_i = 1) &\sim \text{Dir}(\boldsymbol{\alpha}_u) \quad \text{and} \quad (\mathbf{p}_{si} | z_i = 1) \sim \text{Dir}(\boldsymbol{\alpha}_s) \end{aligned} \quad (9)$$

where the indicator variable z_i is as defined in (2), i.e. $z_i \sim \text{Be}(w)$ where w is the proportion of responders. As in the beta-binomial case both an EM and MCMC algorithms can be used for parameter estimation. When using a fully Bayesian approach via MCMC, we use the same priors for $\boldsymbol{\alpha}_{\{u,s\}}$ and w as for the beta-binomial model.

5.3 Parameter estimation

Again, to simplify the estimation problem, we make use of the marginal likelihoods that can be obtained in closed forms (see Supplementary Material). For the null component,

¹¹At some point we should say that such multivariate models are not appropriate for one sided models.

the marginal likelihood L_0 is given by,

$$L_0(\boldsymbol{\alpha}_u | \mathbf{n}_s, \mathbf{n}_u) = \prod_{i=0}^I \frac{B(\boldsymbol{\alpha}_u + \mathbf{n}_{ui} + \mathbf{n}_{si})}{B(\boldsymbol{\alpha}_u)} \cdot \frac{N_{si}!}{\prod_k n_{sik}!} \cdot \frac{N_{ui}!}{\prod_k n_{uik}!} \quad (10)$$

where B is the 2^K -dimensional Beta function defined as $B(\boldsymbol{\alpha}) = \prod_k \Gamma(\alpha_k) / \Gamma(\sum_k \alpha_k)$. Similarly the marginal likelihood for the alternative model is given by

$$L_1(\boldsymbol{\alpha}_u, \boldsymbol{\alpha}_s | \mathbf{n}_s, \mathbf{n}_u) = \prod_{i=0}^I \frac{B(\boldsymbol{\alpha}_u + \mathbf{n}_{ui})B(\boldsymbol{\alpha}_s + \mathbf{n}_{si})}{B(\boldsymbol{\alpha}_s)B(\boldsymbol{\alpha}_u)} \cdot \frac{N_{si}!}{\prod_k n_{sik}!} \cdot \frac{N_{ui}!}{\prod_k n_{uik}!}. \quad (11)$$

The estimation procedures (both EM and MCMC based) for the multinomial-Dirichlet are the same as for the beta-binomial model except that the number of parameters to be estimated is larger. In our experience, the performance of the EM algorithm greatly deteriorates when K becomes larger than 2. It becomes highly dependent on the initial values and can even fail to converge when good initial values are provided. Although our MCMC algorithm is slightly more computational, it does not suffer from this problem and can be used even when K is large. More details about both algorithms are given in supplementary material.

5.4 Polyfunctionality in Fluidigm Single Cell Gene Expression Data

As a proof-of-concept, we fitted our multivariate MIMOSA model looking at two specific genes in the Fluidigm data, namely BIRC3 and CCL5. In this case, $K = 2$ and we have four possible combinations. In Figure 4 we show heatmaps of the counts of cells expressing all combinations of the BIRC3 and CCL5 genes in unstimulated and stimulated samples (Figure 4 A,B). Only CCL5 positive cells express BIRC3, and the expression of BIRC3 increases upon stimulation. The typical approach to analyzing poly-functional populations from intracellular cytokine staining data (summing the counts over all possible poly-functional cell populations) would not be appropriate in this case, since changes in the counts of these different cell populations occur in both directions. That is to say, the number of BIRC3-/CCL5+ cells decreases upon stimulation and the number of BIRC3+/CCL5+ cells increases. There is no difference in the marginal counts for any sample (Figure 4 C). In contrast, multivariate MIMOSA tests all cell subpopulations simultaneously, and identifies a significant difference between stimulated and unstimulated conditions in 13 of the 16 samples (Figure 4 D). Testing all combinations simultaneously is an advantage over performing multiple univariate tests on the individual combinations, which requires multiplicity adjustment and a potential loss of power.

Since the Fluidigm data has a limited number of observations (100 cells and 16 samples), we could not look at more than two makers at once. Therefore, we performed simulations in eight dimension to assess the power of the multivariate MIMOSA model compared to

Fisher’s exact test on the resulting 2x5 tables, Fisher’s exact test performed marginally on each dimension of the data and p-values combined through Fisher’s method ($\chi^2 = -2 \sum_{i=1}^k \log(p_i)$), as well as the likelihood ratio test (Figure 5 A-C). These results show that multivariate MIMOSA has significantly increased power to detect true differences in multivariate data, even with small counts and small effect sizes, and the model is a better fit to the data than other standard approaches tested for analyzing such multivariate count data (Figure 5 B).

6 Discussion

The variety of single-cell assays being adopted by the immunology community is increasing. Flow cytometry, mass cytometry, ELISPOT, Fluidigm, and other single-cell assays can all be analyzed as single-cell count data. Development of effective statistical methods to detect differences in gene or protein expression at the single cell level is becoming increasingly important. Current approaches rely on asymptotic approximations (t-test, or χ^2 test), empirical or ad-hoc methods (2-fold change), or exact tests (Fisher’s exact test) where model assumptions are generally not satisfied, all of which can lead to invalid conclusions about the data [9, 11, 12, 15, 20]. Most importantly, existing classical methods do not share information across samples, resulting in less power to detect true differences than empirical-Bayes and hierarchical modelling approaches, which are widely applied in the microarray literature [21–23].

The MIMOSA model presented here uses a mixture model framework of Beta-Binomial or Multinomial-Dirichlet distributions to model counts in experimental units (i.e. individuals) across multiple conditions (i.e. vaccine responders and non-responders). Information is shared across non-responder individuals and across responders individuals through exchangeable Beta or Dirichlet priors, increasing the power to detect true differences between treatment and control conditions compared to Fisher’s exact test, even when model assumptions are violated (Figures 3 and Supplementary Figure 2). The MIMOSA model based on the Beta-Binomial distribution allows us to constrain the alternative hypothesis to the case $p_s > p_u$, where the proportion of cells in the stimulated sample is strictly greater than the proportion of cells in the matched unstimulated sample.

Importantly, the analysis of real-world ICS data from vaccine trials demonstrated that the constrained MIMOSA model performs as well or better than Fisher’s exact test or other non-Bayesian alternatives for identifying vaccine responders across multiple antigen stimulations and multiple cytokines (Figure 1). Although the MIMOSA model was fit within each antigen stimulation \times cytokine combination, the model is naive to vaccine time point. Despite this, MIMOSA demonstrated a higher sensitivity and specificity to discriminate between vaccine responders and non-responders on days 0 (pre-vaccination) and 182 (post-vaccination) than the current standard approach (Fisher’s exact test), or non-Bayesian alternatives such as the likelihood ratio test or ranking by log-fold change

(Figure 1 A,C). Our approach treats all day 0 observations as true negatives and all day 182 observations as true positives, yet we know that not all vaccine recipients are likely to exhibit a vaccine response on day 182. None the less, this shortcoming, at worst, leads us to underestimate the true sensitivity of MIMOSA, and does not negatively impact the comparison. Additionally, MIMOSA was found to be a better fit to real-world ICS data from vaccine trials than other analysis approaches, as evidenced by more accurate estimates of true false discovery rate (Figure 1 B,D).

Although ICS is the motivating example for the MIMOSA model, it can be applied any type of single-cell assay where cells are dichotomized into positive and negative sets, counted and compared across different conditions. To date, the typical approach to Fluidigm single cell gene expression analysis has been focused on identifying differences in the continuous part of the signal, corresponding to the C_t values and the “missing” data from cells that don’t express a given gene has generally been ignored, or used as part of ad-hoc pre-filtering[3]. The ability of MIMOSA to identify stimulation-specific expression patterns in single-cell gene expression data demonstrates not only the broader utility of the method, but importantly, also demonstrates that biologically relevant signal is present in the proportion of cells expressing each gene under different conditions (Figure 2 A-C). MIMOSA explicitly models and performs inference on the observed positive cell counts between different conditions. Additionally, extending the model to take into account multiple conditions is straightforward.

Detecting differences in polyfunctional cell populations (i.e. identifying changes in cell populations that co-express multiple proteins, cytokines, or genes), is important in vaccine research, since it allows the identification of more precisely defined, more homogeneous cell populations [24]. These polyfunctional cell populations may be correlated with differential vaccine response or efficacy and have the potential to inform vaccine development and trial design. What’s more, changes in these polyfunctional cell populations are not always detectable when looking at the marginal populations (Figure 4 A-C). Existing methods for identifying polyfunctional cytokine profiles from ICS data either separately test individual combinations of cytokines, or perform global tests between groups of individuals even when the populations under study are known to be heterogeneous (i.e. mixtures of responders and non-responders). Sometimes these tests are entirely empirical in nature (i.e. thresholds based on fold change or some factor over background), and these methods generally do not share information across observations [9, 11–13, 15, 20]. As others have pointed out, in order to have the most power to detect a true difference, the statistical test should be selected taking into account the cytokine combinations of interest [13]. Here we have shown that MIMOSA has higher sensitivity and specificity than these competing methods to identify true differences between conditions in multivariate count data (Figure 4 A, and Figure 5 A,C), and the model generally provides a better fit to the single-cell assay count data arising from studies with these types of experimental designs (Figure 5 B).

7 Conclusions

We have developed a mixture model framework that we call MIMOSA .for identifying differences between treatment conditions in paired observations of cell counts from a variety of single-cell assays that frequently arise in the context of vaccine trials and immunological studies. Our model can be applied in a univariate or multivariate fashion, and we have shown that it has greater sensitivity and specificity than other typical approaches used to analyze the type of count-based data derived from single cell assays, including Fisher’s exact test, the non-Bayesian likelihood ratio test, or ad-hoc rank based approaches. The software is implemented in R and C++, and is freely available from GitHub (<http://www.github.org/finak/MIMOSA>).

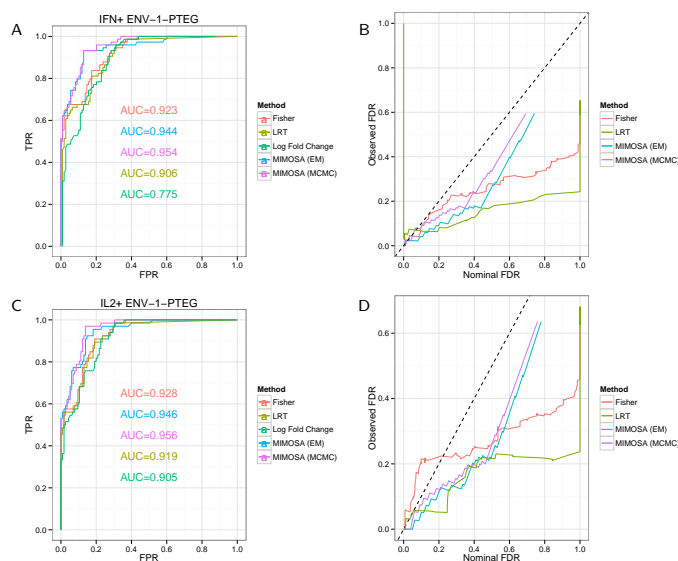


Figure 1: Performance of MIMOSA (EM and MCMC implementations, one-sided model) and competing methods on ICS data from HVTN065. Sensitivity and specificity (ROC analysis) as well as observed and nominal false discovery rates for positivity calls from CD4+ T-cells stimulated with A–B) ENV-1-PTEG and expressing IFN γ or C–D) ENV-1-PTEG and expressing IL2. ROC and FDR plots of other cytokine combinations can be found in the supplementary material.

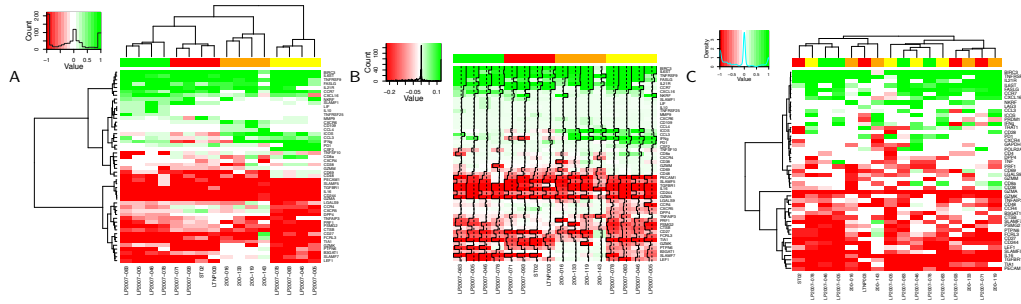


Figure 2: Signed posterior probability, difference and log-odds ratio of the proportion of single cells expressing each gene on a 96x96 Fluidigm array. The posterior probability of response times the sign of the change in expression is shown in A) (red indicates a decrease, green an increase, relative to the control). Columns and rows are clustered based on these signed posterior probabilities. B) The posterior differences in proportion of cells expressing a gene in the stimulated vs. control samples. Rows and columns are ordered as in A) for comparison. The traces show the deviations of each cell from zero. Colors along the columns denote different stimulations (green: CMV pp65 nlv5, red: HIV Gag, orange: HIV Nef, yellow: CMV pp65 tm10). C) Genes selected from Fisher's exact test at the 10% FDR level. Clustering of the maximum likelihood estimates of difference in proportions of cells expressing a gene in stimulated vs. control samples with significant genes selected using Fisher's exact test.

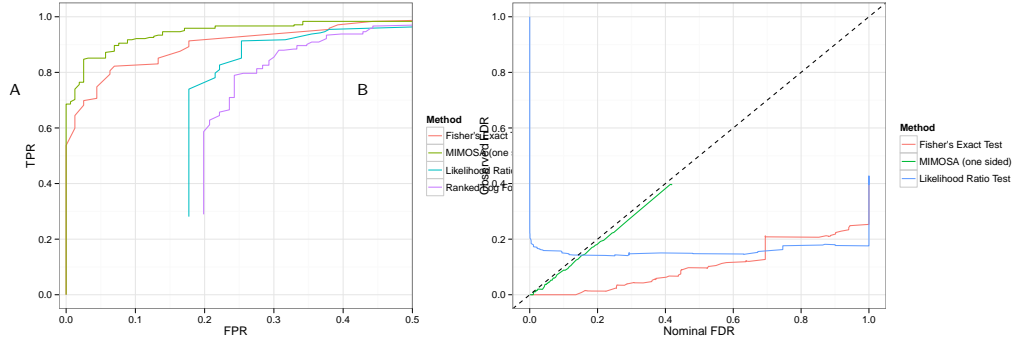


Figure 3: Comparison of positivity detection methods on data simulated from the one-sided model. Ten simulations were generated at an N of 5,000 total counts using hyper-parameter estimates from real ICS data (IFN γ expressing CD4 $^{+}$ T-cells stimulated with ENV-1-PTEG from HVTN065) with a five-fold effect size between responder and non-responder components. A) Average ROC curve over the 10 simulated data sets ($N=5,000$) D) Average observed and nominal false discovery rate over 10 simulated data sets ($N=5,000$). Curves are shown for MIMOSA (one-sided), Fisher's exact test, the likelihood ratio test, and ranked log fold-change. Results for the two-sided model and the MIMOSA fit to a model violating model assumptions, as well as other values of N are in the Supplementary Material.

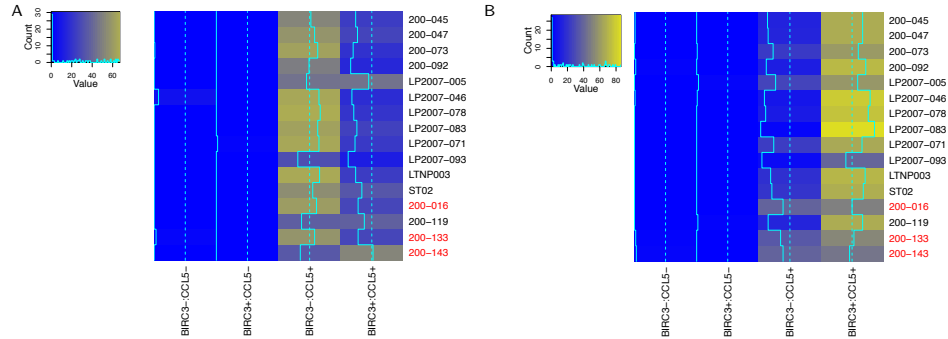


Figure 4: Counts of cells expressing different combinations of BIRC3 and CCL5 genes in the A) unstimulated and B) stimulated conditions. No difference is observed from the marginalized counts, while multivariate MIMOSA detects a difference between stimulated and unstimulated conditions in 13 of 16 samples. Sample names highlighted in red identify those where MIMOSA did not detect a difference.

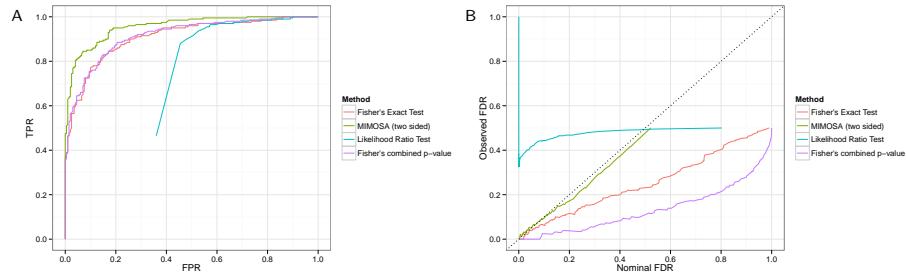


Figure 5: Multivariate simulations from a two-sided model. Ten, eight-dimensional data sets were simulated from a two-sided model with an effect sizes of 2.5×10^{-3} and -2.5×10^{-3} in two of the eight dimensions ($N=1,500$). Multivariate MIMOSA was compared against Fisher's exact test, the likelihood ratio test, and Fisher's combined p-value (combining Fisher's exact test run marginally on each of the five dimensions). A) Average ROC curves for the competing methods over 10 simulations. B) Average observed and nominal false discovery rate for each method over 10 simulations.

Supplementary Information

S.1.1 HVTN065 and HVTN054 Vaccine Trial ICS Data Description

HVTN065 is a phase 1 (safety and immunogenicity) trial of GeoVax HIV/AIDS DNA and MVA vaccine in 120 individuals (100 vaccinees, 20 placebo recipients, parts A and B). CD4 and CD8 T-cell epitope specific immune responses were measured via the ICS assay. Other humoral and cellular immune responses were measured via ELISA, and neutralizing antibody assays. Cytokines measured in the ICS assay included IFNg, TNFa, IL2, and IL4, and antigens included three Env, three Gag, and three Pol peptide pools. Results of the trial have been published [25].

S.1.2 Constrained Beta-binomial model

We can define a model where we constrain the stimulated proportions under the alternative model such that $p_s > p_u$. In this case, the only changes required are for the alternative marginal likelihood L_1 defined in equation (6). The marginal likelihood for the constrained model becomes $L_1 \times C$, where C is a ratio of normalizing constants for the likelihood and the prior.

$$C = \frac{\int_{p_{ui}=0}^1 \left(\frac{1}{B(n_{ui}+\alpha_u, N_{ui}-n_{ui}+\beta_u)} p_{ui}^{n_{ui}+\alpha_u-1} (1-p_{ui})^{N_{ui}-n_{ui}+\beta_u-1} \right) (I_{1-p_{ui}}(N_s^i - n_s^i + \beta_s, n_s^i + \alpha_s)) dp_{ui}}{\int_{p_{ui}=0}^1 \left(\frac{1}{B(\alpha_u, \beta_u)} p_{ui}^{\alpha_u-1} (1-p_{ui})^{\beta_u-1} \right) (I_{1-p_{ui}}(\beta_s, \alpha_s)) dp_{ui}} \quad (12)$$

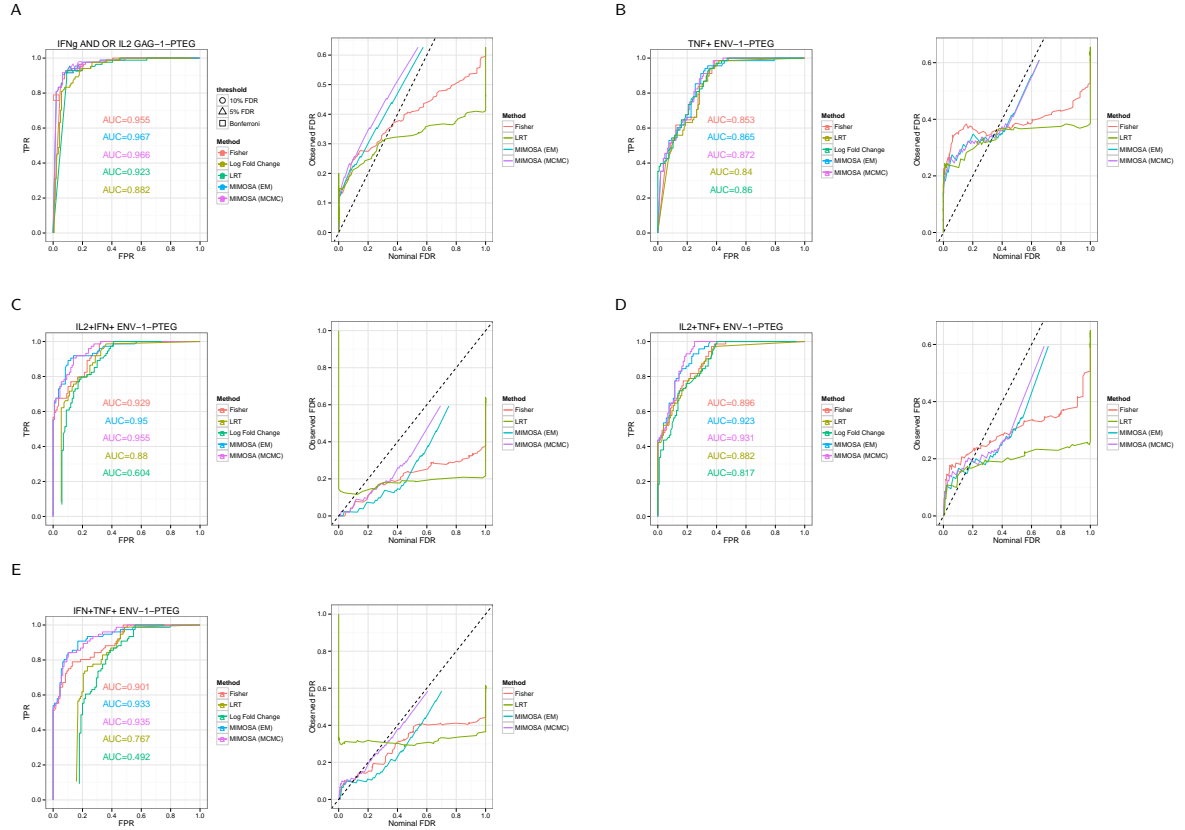
The term $I_{1-p_{ui}}(\beta_s, \alpha_s) = 1 - I_{p_{ui}}(\alpha_s, \beta_s) = Pr(p_{si} > p_{ui}; \alpha_s, \beta_s)$ is the regularized incomplete Beta function, which is just the CDF of a Beta distribution with parameters α_s, β_s , resulting in a 1-dimensional integral that can be computed via Monte-Carlo integration (i.e. in our EM implementation). However, this can be computationally costly in the MCMC framework. In the latter case, we can compute the integral exactly if α_s and β_s are integers by using the identity:

$$I_{1-p_u}(\beta_s, \alpha_s) = \sum_{j=\beta_s}^{\beta_s+\alpha_s-1} \frac{(\beta_s + \alpha_s - 1)!}{j!(\beta_s + \alpha_s - j)!} (1-p_u)^j (p_u)^{\beta_s+\alpha_s-j} \quad (13)$$

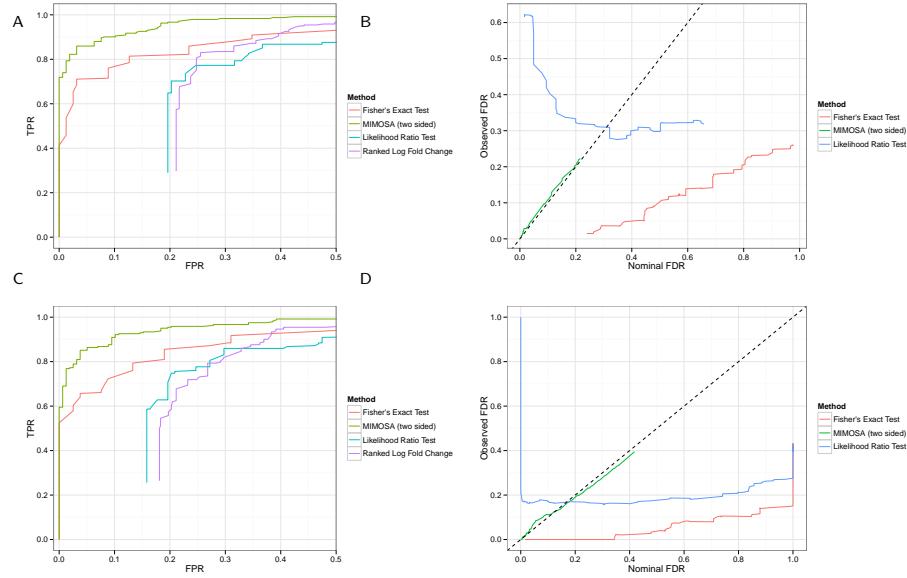
Typically, in ICS data $\beta_s \gg \alpha_s$, leading to relatively few terms in the sum in equation 13. This leads to an exact expression for the normalizing constant:

foo

S.1.3 HVTN065 Results for Other Cytokines



Supplementary Figure 1: Comparison of MIMOSA on other cytokines and cytokine combinations for ENV-1-PTEG stimulated CD4⁺ T-cells from the HVTN065 trial.



Supplementary Figure 2: Unconstrained MIMOSA model fit to two-sided data (A-B) or to data where model assumptions are violated (C-D). Two-sided data were simulated from a standard model. A) Average ROC curves from 10 simulations and B) average observed vs nominal FDR from 10 simulations at $N=5,000$. Unconstrained MIMOSA fit to two-sided data simulated from a model where the proportions were drawn from a truncated normal distribution over $[0, 1]$, rather than a Beta distribution. C) Average ROC curves from 10 simulations and D) average observed vs nominal FDR from 10 simulations at $N=5,000$.

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