

RNA-Seq as a Relative Abundance Measure: oportunities afforded by a compositional analysis framework.

Dominic LaRoche Dean Billheimer Shripad Sinari Kurt Michels
Bonnie LaFleur

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1 Introduction

The rapid rise in the use of RNA sequencing technology (RNA-seq) for scientific discovery has led to its consideration as a clinical diagnostic tool. However, as a new technology, the analytical accuracy and reproducibility of RNA-seq must be established before it can realize its full clinical utility [24, 27]. Recent studies evaluating RNA-seq have found generally high intra-platform and inter-platform congruence across multiple laboratories [Li2013, 25, 24]. Despite these promising results, there remains a need to establish reliable diagnostics and quality control metrics to improve the reproducibility of RNA-seq data. Understanding, and capatilizing on, the relative frequency nature of RNA-Seq data provides tools for creating quality control metrics and identifying batch effects leading to improved reproducibility.

Relative frequency measures are characterized as a vector of proportions of some whole. These proportions are necessarily positive and sum to a constant which is determined by the measurement system and not the measurand. As an illustrative example, suppose we take a large bag of marbles of different colors and pour them over a shallow bowl. The bag holds many more marbles than the bowl so most of the marbles spill out and remain unmeasured. Since we measure an unknown portion of the marbles in the bag we cannot know the total number of each marble color that was contained in the bag. However, we can estimate the relative frequencies of each marble color in the bag. The total number of marbles we observe is a function of the measurement, i.e. the size of the bowl. A large bowl and a small bowl yeild exactly the same information about the relative abundances of the marbles in the bag; a property known as scale invariance.

Suppose we repeat this experiment a second time with a new bag to which we double the number of red marbles but keep the same number of all other colored marbles. Again, we expect the number of marbles of each color captured by the bowl to be proportional to the (unknowable) absolute number of marbles in the bag. Since the bowl is fixed in size, as we capture more red marbles, proportional the thier increase in the bag, the number of other colors in the bowl must then decrease even though the absolute number of the other colors in the bag remains constant. Since we are interested in making inference about the marbles in the bag, it is important to recognize that the decrease in the number of non-red colors does not represent a decrease in the absolute abundance of these colors in the bag.

Similarly, targeted and whole transcriptome RNA-Seq measurements from NGS-based instruments provide only relative frequencies of the measured transcripts. The measurment technology, along with sample preparation, preclude the measurement of absolute abundance. High-throughput RNA-Seq instruments have a maximum number of reads available per run. For example, the Roche 454 GS Junior ^(TM) claims approximately 100,000 reads per run for shotgun sequencing and 70,000 reads per run for amplicon sequencing. The Illumina Mi-Seq, with shorter read lengths, is limited to 25 million reads per sequencing run. These reads are distributed across all of the samples included in a sequencing run and, therefore, impose a total sum constraint on the data. This constraint cascades down to each probe or tag within a sample which is, in turn, constrained by the total number of reads allocated to the sample thereby creating a natural hierarchical structure to RNA-Seq data.

Previous authors have identified the relative abundance nature of RNA-Seq data [21, 6, 22, 13, 15]. For example, Robinson and Smyth (2007) [21] consider counts of RNA tags as relative abundances in their development of a model for estimating differential gene expression implemented in the Bioconductor package edgeR. Similarly, Robinson and Oshlack (2010) explicitly acknowledge the mapped-read constraint when developing their widely used Trimmed-Mean of M-values (TMM) normalization method for RNA-Seq data. Finally, the commonly used \log_2 Counts per Million (CPM) re-scaling transformation proposed by Law et al. (2014) [13] divides each sequence count by the total number of reads allocated to the sample thereby transforming the data for each sample into a vector of proportions.

The positivity and summation constraint complicate the analysis of relative frequency data. As early

as 1896 Karl Pearson [20] identified the spurious correlation problem associated with compositions. John Aitchison observed that relative frequency data is compositional and developed a methodology based on the geometric constraints of compositions [1]. Recent authors have argued that ignoring the sum constraint can lead to unexpected results and erroneous inference [16]. Despite the evidence that RNA-Seq data are compositional in nature, few researchers have extended the broad set of compositional data analysis theory and operations for use in RNA-Seq analysis problems. We provide a brief background on compositional methods. We then extend existing compositional data methodology to develop a simple quality control metric and improve batch effect detection for RNA-Seq data. Finally, we show how compositional properties can be exploited to facilitate exploration of high-dimensional RNA-Seq data.

This research is focused on developing diagnostics for targeted RNA-Seq. Targeted sequencing allows researchers to efficiently measure transcripts of interest for a particular disease by focusing sequencing efforts on a select subset of transcript targets. Targeted sequencing offers several benefits over traditional whole-transcriptome RNA-Seq for clinical use including the elimination of amplification bias, reduced sequencing cost, and a simplified bioinformatics workflow. However, traditional RNA-Seq and targeted RNA-Seq data share many of the same properties so the methods described here should be easily extensible to traditional RNA-Seq.

Extraction-free sequencing technologies, such as HTG EdgeSeq, permit the use of very small sample volumes but create the need for additional quality control metrics since poor quality samples, which would likely be removed after unsuccessful RNA extraction in extraction-based technologies, can be sequenced.

2 Methods

2.1 Compositional Data

We begin with a brief introduction to compositional data, its properties, and some established analytical methods. Compositional data is defined as any data in which all elements are non-negative and sum to a fixed constant [1]. For RNA-seq data, the total sum constraint is imposed by the limited number of available reads in each sequencing run. Since this total differs between sequencing platforms we will refer to the total number of available reads as T . These reads are distributed among the D samples in a sequencing run such

that:

$$\sum_{i=1}^D t_i = \mathbb{T} \quad (1)$$

where t_i represents the total reads for sample i . Because of the total sum constraint, the vector \mathbf{t} is completely determined by $D-1$ elements since the D^{th} element of \mathbf{t} can be determined from the other $d = D-1$ elements and the total \mathbb{T} :

$$t_D = \mathbb{T} - \sum_{i=1}^d \mathbf{t}_i \quad (2)$$

In 2, any of the elements can be chosen for t_D with the remaining elements labeled $1, \dots, d$ in any order [1]. Similarly, the total reads for each sample (t_i) are distributed among the P transcript targets in the assay such that $\sum_{j=1}^P p_{ij} = t_i$, where p_{ij} is the total reads allocated to target j in sample i . We highlight the hierarchical structure of RNA-Seq data as it leads to useful properties when developing quality control metrics.

From equations 1 and 2 it is clear that the total reads allocated to each of the D samples represent a $D-1 = d$ dimensional simplex (\mathcal{S}^d). This leads to a difficulty in interpreting the traditional $D \times D$ covariance structure. In particular, it is clear that for a D -part composition \mathbf{x} , $\text{cov}(x_1, x_1 + \dots + x_D) = 0$ since $x_1 + \dots + x_D$ is a constant. Moreover, the sum constraint induces negativity in the covariance matrix,

$$\text{cov}(x_1, x_2) + \dots + \text{cov}(x_1, x_D) = -\text{var}(x_1). \quad (3)$$

Equation 3 shows that at least one element of each row of the covariance matrix must be negative. Aitchison refers to this as the “negative bias difficulty” (although ‘bias’ is not used in the traditional sense; [1], p. 53). The structurally induced negative values create problems for the interpretation of the covariance matrix.

Because of the difficulties outlined above, standard statistical methodology is not always appropriate [1] and can produce misleading results [15]. To overcome these obstacles, Aitchison [2] proposed working in ratios of components. We focus on the Centered Log-Ratio (CLR) which treats the parts of the composition symmetrically and provides an informative covariance structure. The CLR transformation is defined for a D -part composition \mathbf{x} as:

$$y_i = \text{CLR}(x_i) = \log \left(\frac{x_i}{g(\mathbf{x})} \right), \quad (4)$$

where $g(\mathbf{x})$ is the geometric mean of \mathbf{x} . The $D \times D$ covariance matrix is then defined as:

$$\Gamma = [\text{cov}(y_i, y_j) : i, j = 1, \dots, D] \quad (5)$$

I think it might be better to leave out the details of this and instead reference the paper and give a brief reason why it is beneficial. Original version:

To avoid numerical difficulties arising from sequence targets with 0 reads, Martin-Fernandez et al. [18] suggest an additive-multiplicative hybrid transformation. This transformation is additive on the zero components but multiplicative on the non-zero components. It has several advantages over the simple additive transformation since it preserves several important compositional properties. Martin-Fernandez et al. [18] recommend using $0.55 \times$ the smallest detectable value as originally suggested by Sandford et al. [12, 23]. The threshold value for RNA-seq data must account for read depth since a 0 in a sample with a library size of 1 thousand reads would potentially not be 0 if the total number of reads was increased to 1 million. Therefore, we define the threshold value for a sample as $\delta = \frac{0.55}{\text{Total Reads}}$. The Martin-Fernandez transformation then becomes,

$$v_i = \frac{x_i}{\sum_{i=1}^D x_i} \quad (6)$$

$$u_i = \begin{cases} \delta & \text{if } v_i = 0 \\ v_i \times \left[1 - \left(\sum_{i=1}^D \mathcal{I}_{(v_i=0)} \right) \times \delta \right] & \text{if } x_i \neq 0. \end{cases} \quad (7)$$

Second option:

To avoid numerical difficulties arising from sequence targets with 0 reads, Martin-Fernandez et al. (2000) [18] suggest an additive-multiplicative hybrid transformation. If zeros are present in the data We recommend using the Martin-Fernandez transformation with a threshold value of $\delta = \frac{0.55}{\text{Total Reads}}$ to account for differences in library size. The CLR transformation is then applied to the Martin-Fernandez transformed data which contains no zeros.

The CLR transformation is similar to the familiar Counts per Million (CPM) transformation [13] defined as, $\log_2 \left(\frac{r_{gi} + 0.5}{t_i + 1} \times 10^6 \right)$, where r_{gi} is the number of sequence reads for each probe (g) and sample (i), (scaled to avoid zero counts), adjusted for the number of mapped reads (library count) for each sample t_i (scaled by

a constant 1 to ensure the proportional read to library size ratio is greater than zero). The primary difference between the CLR and log(CPM) transformations is in the use of the geometric mean in the denominator of the CLR transformation. The use of the geometric mean results in subtracting the mean of the log transformed values from each element thereby centering the vector of log-ratio transformed read counts. The difference appears minor but has important implications for the application of several common statistical methods.

The compositional geometry must be accounted for when measuring the distance between two compositions or finding the center of a group of compositions [3]. Aitchison [4] outlined several properties for any compositional difference metric which must be met: scale invariance, permutation invariance, perturbation invariance (similar to translation invariance for Euclidean distance), and subcompositional dominance (similar to subspace dominance of Euclidean distance). The scale invariance requirement is ignorable if the difference metric is applied to data on the same scale (which is generally not satisfied in raw RNA-seq data due to differences in read depth). The permutation invariance is generally satisfied by existing methods such as Euclidean distance [19]. However, the perturbation invariance and subcompositional dominance are not generally satisfied [19].

Aitchison [1, 4] suggests using the sum of squares of all log-ratio differences. Billheimer, Guttorp, and Fagan [8] use the geometry of compositions to define a norm which, along with the perturbation operator defined by Aitchison [1], allow the interpretation of differences in compositions. Martin-Fernandez et al. [19] showed that applying either Euclidean distance or Mahalanobis distance metric to CLR transformed data satisfies all the requirements of a compositional distance metric. Euclidean distance on CLR transformed compositions is referred to as Aitchison distance:

$$d_A(x_i, x_j) = \left[\sum_{k=1}^D \left(\log \left(\frac{x_{ik}}{g(x_i)} \right) - \log \left(\frac{x_{jk}}{g(x_j)} \right) \right)^2 \right]^{\frac{1}{2}}$$

or

$$d_A(x_i, x_j) = \left[\sum_{k=1}^D (clr(x_{ik}) - clr(x_{jk}))^2 \right]^{\frac{1}{2}}.$$

Up to this point we have referred to the total reads available per sequencing run, T . However, it is more

typical to work with the aligned reads in practice. The total aligned reads, T , is always a fraction of the total reads available for a sequencing run, \mathbb{T} . The fraction of the total reads aligned can be affected by multiple factors, including the choice of alignment algorithm, which we do not address here. We assume that T imposes the same constraints on the data as outlined above for \mathbb{T} and will refer exclusively to T hereafter.

3 Sample Quality Control

Problems with sample quality, library preparation, or sequencing may result in a low number of reads allocated to a given sample within a sequencing run. The Percent Pass Filter (% PF) metric provided on Illumina sequencers provides a subjective measure that can identify problems with sequencing that result in a low number of reads allocated to a sample. However, % PF will not necessarily catch problems associated with poor sample quality or problems with sample pre-processing since these processes may affect cluster generation, and not just cluster quality. This is particularly important for extraction-free RNA-Seq technologies, such as the HTG EdgeSeq^(tm), which allow for the use of smaller input amounts but lack the intermediate steps for checking sample quality. There is currently no objective way to evaluate sample quality based on the total number of reads attributed to a sample. We propose a method for objectively identifying problematic samples based on the total number of reads allocated to the sample.

For most experimental designs we expect the number of reads allocated to each sample in a sequencing run to arise from the same general data generating mechanism, namely the chemistry of the NGS-based measurement system, regardless of experimental condition. The objective is then to determine which samples arise from a different mechanism. Outlier detection is well suited for discovering observations that deviate so much from other observations that they are likely to have arisen from a different mechanism [11]. We base our method off Tukey’s box-plots [26], which is a well used and robust method for detecting outliers [7].

We expect the total number of reads allocated to each sample, t_i , to be equivalent notwithstanding random variation. For a given sequencing run with D samples we define the vector of total reads allocated to each sample as \mathbf{t} . Since the D dimensional vector \mathbf{t} is a composition we have $\mathbf{t} \in \mathcal{S}^{D-1}$, the $D-1$ -dimensional simplex. As noted above, traditional statistical methods may not be appropriate for data in the simplex. Therefore, we map $\mathbf{t} \in \mathcal{S}^{D-1} \rightarrow \mathbf{x} = CLR(\mathbf{t}) \in \mathcal{R}^D$ using the Centered Log Ratio transformation 4. We

then apply Tukey’s method for detecting outliers to \mathbf{x} , which simply identifies those observations which lie outside 1.5 times the inter-quartile range.

Definition 1. x_i is a quality control sample failure if $x_i < \text{lower-quartile} - 1.5 \times \text{IQR}$ or $x_i > \text{upper-quartile} + 1.5 \times \text{IQR}$, where IQR is the interquartile range of \mathbf{x} .

We demonstrate the utility of our sample quality control measure using two sets of targeted RNA-Seq data: 1) 120 mRNA technical replicate universal-RNA samples prepared with the HTG EdgeSeq Immuno-Oncology assay and sequenced in 5 different equally sized runs, and 2) 105 miRNA technical replicate samples of human plasma, FFPE tissue, and Brain RNA prepared with the HTG EdgeSeq Whole Transcriptome miRNA assay. These two data sets differ in both the type of RNA (mRNA versus miRNA) and the number of sequence targets in each assay (558 versus 2,280 targets, for the mRNA and miRNA assays respectively). All samples were prepared for sequencing using the HTG EdgeSeq Processor and sequenced with an Illumina Mi-Seq sequencer.

4 Batch Effects and Normalization

Batch effects arising from differing laboratory conditions or operator differences have been identified as a problem in high-throughput measurement systems [14, 9]. Identifying and controlling for batch effects is a critical step in the transition of RNA-Seq from the lab to the clinic. Batch effects are typically identified with a hierarchical clustering (HC) method or principal components analysis (PCA). For both methods, the multivariate distance between the samples is visualized, either in a biplot for PCA or a dendrogram for HC, to check for the existence of clusters of samples related to batch. The compositional nature of RNA-Seq data has important implications for the detection of batch effects because of the difficulty of interpreting the covariance matrix [1] and the incompatibility with standard measures of distance between compositions as noted above [1, 19].

The next generation sequencing process results in arbitrary differences in scale among samples as some samples will receive more total reads than others. Principle components analysis is sensitive to differences in scale among the variables, failure to remove these difference can mask potential batch effects and leave unwanted technical variation in the data. Most normalization methods use a scaling factor calculated for each sample to rescale the read count for each gene within the sample [10]. The CLR transformation can also

be viewed as a scaling factor (the inverse of the geometric mean $1/g(x)$), which is multiplied to each gene read count in the sample. Unlike other normalization methods, the CLR transformation has the added benefit of being applied at the individual sample level, not experiment wise. This makes it particularly suited for the clinic where there are generally no reference samples to normalize to.

Aitchison demonstrated that the CLR transformation has several other useful properties in addition to rescaling the data [1], particularly with respect to PCA biplots [5]. Most notably for the detection of batch effects, the distance between any two points representing samples in the form-biplot approximates the Euclidean distance between the two samples. The CLR transformation retains the property that this distance is at least as great as the distance between any corresponding subset of these two compositions (subspace dominance). Other scaling methods do not necessarily satisfy this property when used with compositions, and therefore batch effects may be masked.

- I thought I would put a toy example here of problems with subcompositional dominance when measuring distance between compositions. I want to demonstrate why it matters to have a proper distance metric represented in the PCA.

We demonstrate the use of the compositional biplot to detect batch effects using technical replicates of three sample types: brain, plasma, and fresh frozen paraffin embedded (FFPE). Each sample is replicated 8 times in each of 5 sequencing runs for a total of 120 samples. Samples were prepared using the EdgeSeq Whole Transcriptome miRNA assay which measures 2,280 targets including including 11 control probes and 2,269 unique miRNA probes. All sequencing was performed on an Illumina Mi-seq^(tm) sequencer.

We create a second data set, by re-scaling the original data, to better illustrate the effects of changes in read depth on batch effect detection. To re-scale the samples from the original we multiply every read count in a given sample by a factor, ranging from 0.5 to 1.5, randomly generated from the uniform distribution. We then obtain a new data set in which the proportions between the read counts remains unchanged but the variance in the total number of reads among the samples is increased.

5 Results

5.1 Sample Quality Control

We compare the utility of our method to evaluation of the untransformed total counts. Figure 1 shows a boxplot and heatmap of the total number of reads allocated to each sample for each of 5 sequencing runs. Figure 2 shows the same data after CLR transformation. After transformation the poor samples become much more visually evident in the heat maps. Additionally, the ability to detect outlying values increases and the number of poor samples detected increases from 1 to 6.

how would we demonstrate the increase in power mathematically?

5.2 Batch Effects and Normalization

We perform a PCA on log-transformed and CLR transformed data. We then construct form-biplots of the first two principle components for each transformed data set (Fig. 5.2). The differences between the 3 samples types (brain, plasma, and FFPE) dominate the first two principle componenets for both data sets. However, the CLR transformed data provides tighter clusters, relative to the distance between the clusters, than the log-transformed raw data. There is also a single FFPE sample which is closer to the brain samples than the other samples. It is worth noting that this sample would have been removed using our proposed quality control metric.

Since the sample type differences overwhelm the potential batch effects we performed a second PCA on only the brain samples for both transformed data sets (Fig. 5.2). Both biplots exhibit clustering by batch but the CLR transformed data shows better separation between the batches, although batches are still overlapping.

Some of the batch effects detected in the log-transformed data may be attributable to the differnces in total reads between batches. By randomly re-scaling each sample by a constant we are able to break the realtionship between batch and the total reads in a sample. Figure ?? gives the biplots for log-transformed and CLR-transformed randomly re-scaled data. The sample type clusters in the log-transformed data become more diffuse while the CLR-transformed biplot remains unchanged. Most notably, the batch effects previously visible in the log-transformed brain samples become completely obscured in the randomly re-scaled data but remain unchanged in the CLR-transformed data (Fig. 5.2).

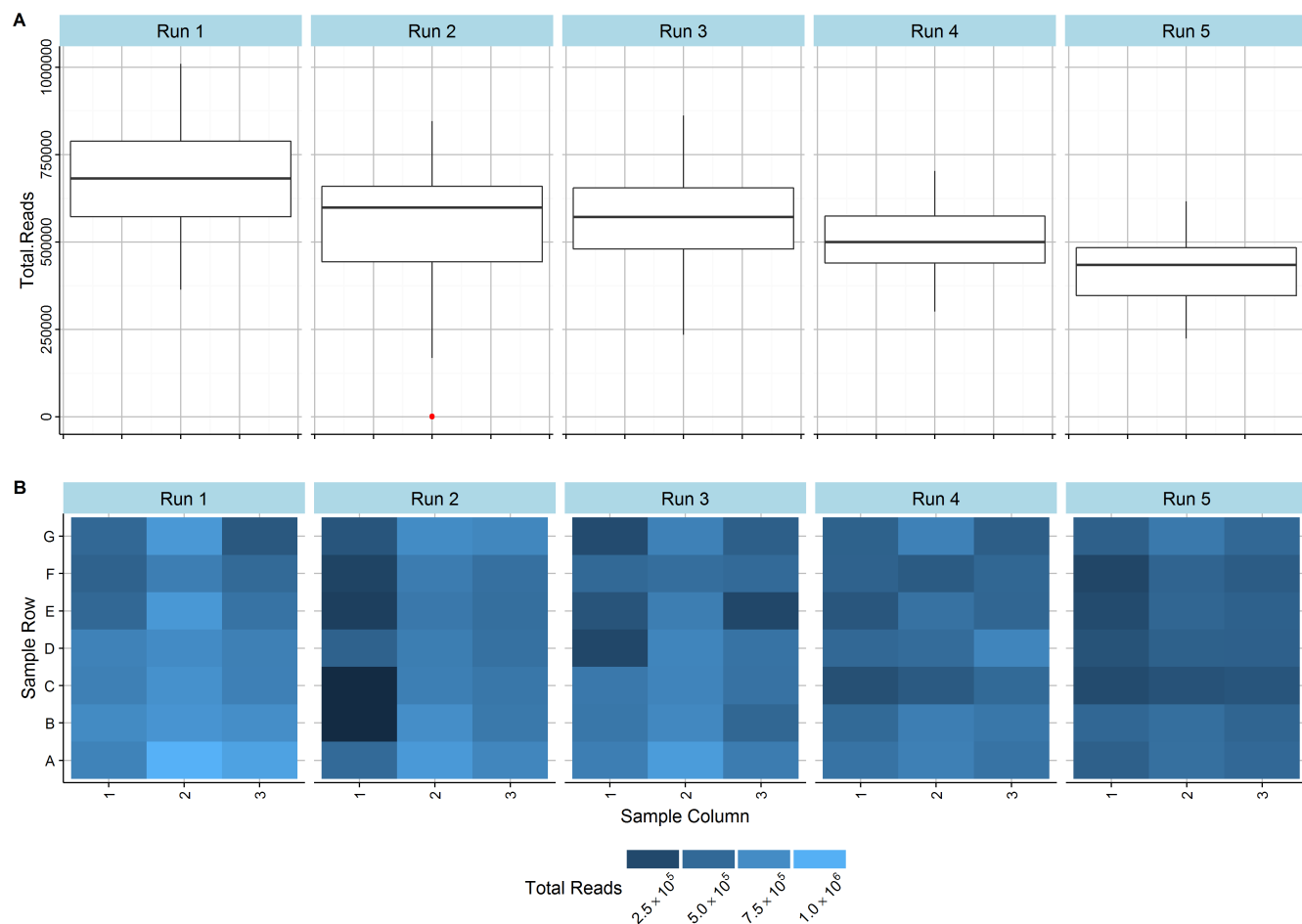


Figure 1: A) Distributions of total reads allocated to each sample in 5 runs on an Illumina Mi-Seq sequencer. Only 1 sample is identified as a problematic sample. B) Heatmaps showing the relative totals for each sample within each run. The darker heatmaps for runs 4 and 5 reflect the generally lower number of total reads in those sequencing runs as compared to runs 1 and 2. This is caused by normal variation in the number of reads available in a sequencing run.

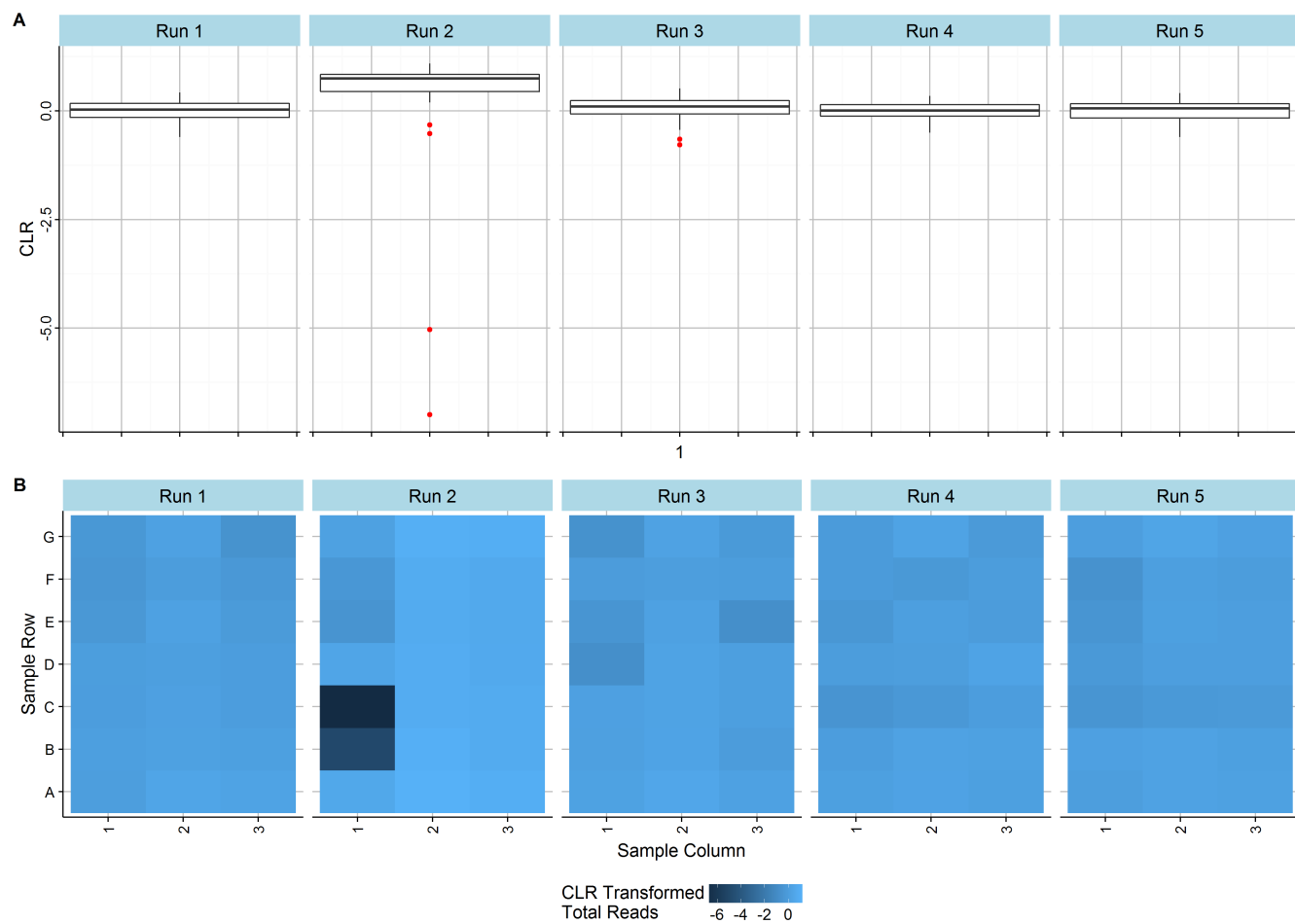


Figure 2: A) Distributions of CLR tranformed total reads allocated to each sample in 5 runs on an Illumina Mi-Seq sequencer. After CLR transformation, 6 samples are identified as a problematic. B) Heatmaps showing the relative CLR transformed totals for each sample within each run.

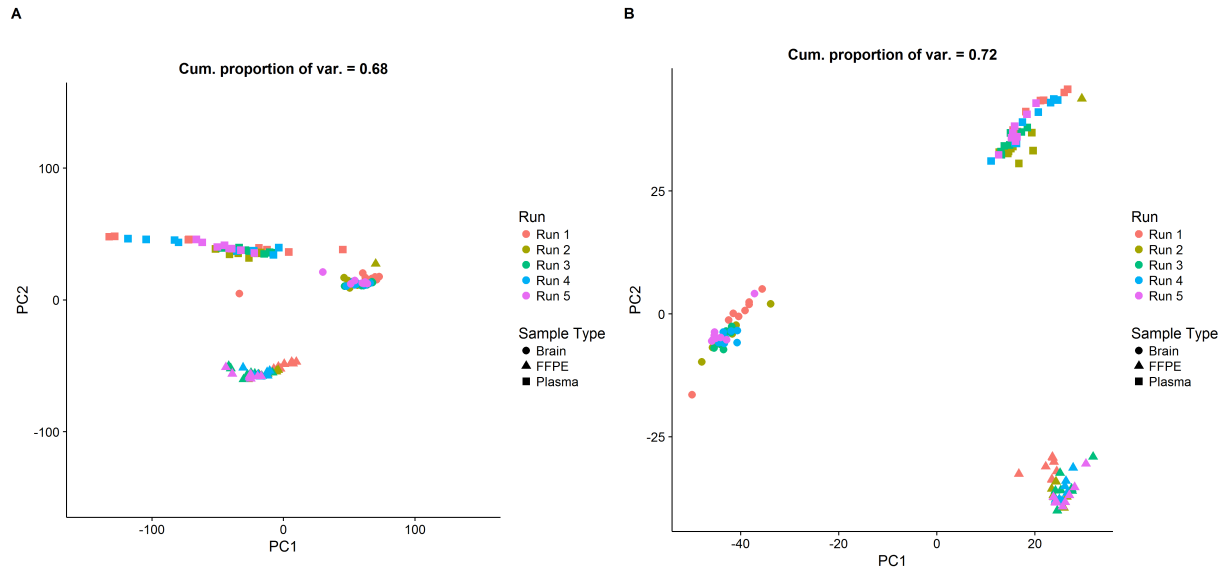


Figure 3: Principle component analysis of A) log-transformed and B) CLR-transformed read count data. The differences between sample types is much greater than the batch effects in both transformation. The CLR transformation results in tighter sample type clusters resulting from less variation along the first principle component.

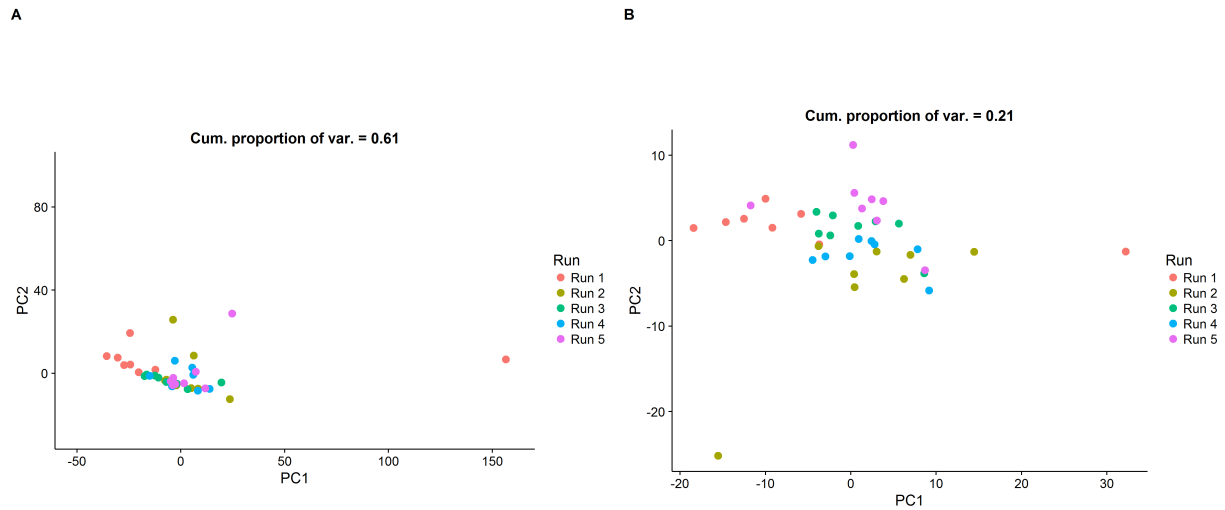
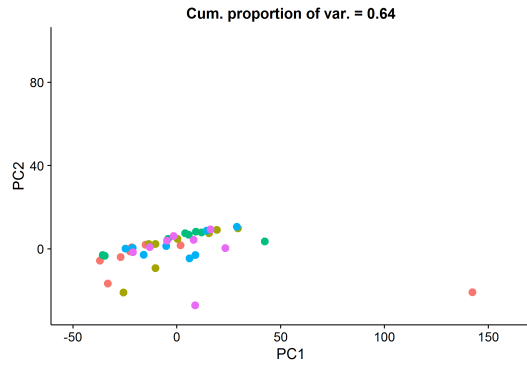


Figure 4: Principle component analysis of only brain samples from A) log-transformed and B) CLR-transformed read count data. The batch effects are more easily identified in the CLR transformed data.

A



B

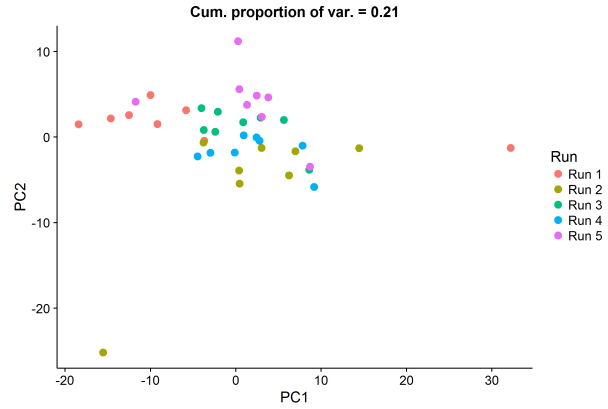


Figure 5: Principle components analysis of the randomly re-scaled brain samples for A) log-transformed and B) CLR-transformed read count data. The batch effects visual in the log-transformed raw data disappear after random re-scaling whereas the batch effects remain identifiable in the CLR transformed data.

6 Discussion

Our sample quality control metric can identify problematic samples which arise from multiple failure modes, e.g. a low quality sample or a sequencing problem. However, it is conceivable that a sample might have an unusually low (or high) number of reads and still provide quality information. In certain experimental designs one might be able to further evaluate these samples with a PCA biplot on the CLR transformed data. In our PCA analysis we identified a FFPE sample which would have failed our quality control and was clearly very different from the other technical replicates. However, if this sample had remained quite similar to the other FFPE replicates this would have provided information that the sample may still be valuable. In this way, the quality control metric and PCA biplot can be used in tandem to provide additional information about the quality of a sample.

The principal components analysis biplot is a well know dimension reduction visualization. For the current data the dimension is reduced from 2,280 probes to 2 principle components. The utility of the data reduction, including the quality of the approximation of the multivariate distance between the samples, is proportional to the amount of variance explained by these two principle components. In our data the first two principle components explain between 72 and 21 percent of the variation in the data. The analysis with

the lowest percent of variation explained by the first 2 components is of the CLR-transformed brain samples. Surprisingly, batch effects are still visible in this plot, in which case they can be removed [17].

As RNA-Seq makes the transition from the research laboratory to the clinic there is a need for robust quality control metrics. The realization that RNA-Seq data are compositional opens the door to the existing body of theory and methods developed by John Atchison and others. We show that the properties of compositional data can be leveraged to develop new metrics and enhance existing methods.

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