Method Choice in Gene Set Analysis Has Important Consequences for Analysis Outcome

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Abstract: Gene set enrichment analysis is a well-established approach for gaining biological insight from expression data. With many gene set analysis methods available, a question is raised about the consistency of the results of these methods. In this paper, we answer this question with a systematic analysis of ten commonly used gene set analysis methods when applied to microarray data. The statistical analysis suggests that there is a significant difference between the results of these methods. Comparison of the 20 most statistically significant gene sets reported by these methods showed little to no agreement regardless of the dataset being used. This observation suggests that the outcome of a study can be highly dependent on the choice of the gene set analysis method. Comparing the 100 most statistically significant gene sets also led to the same conclusion. Furthermore, biological evaluation using a juvenile idiopathic arthritis dataset agreed with the results of the statistical analysis. The 20 most statistically significant gene sets for some methods showed relevance to the biology of juvenile arthritis, supporting their utility, while most methods led to results that were irrelevant or marginally relevant to the known biology of the disease.

1 INTRODUCTION

High-throughput technologies have made it possible to study the expression activity of a large number of genes in a single experiment. These technologies are commonly used to investigate the effect of different stimuli on the expression activity of genes and detect differential expression. A typical gene expression study may lead to reporting several hundred genes as being differentially expressed. Biological interpretation of such an extensive list of genes is difficult. Gene set analysis, also referred to as gene set enrichment analysis, has been widely used to alleviate this problem by detecting a concordant change in the expression pattern of groups of genes that are known to be related to particular functions, processes, or cellular components. Such groups of genes are known as gene sets.

Due to the lack of gold standard datasets where the enrichment status of gene sets are *a priori* known, evaluation of gene set analysis methods is challenging. In the absence of such gold standard datasets, researchers have used artificial datasets to evaluate the sensitivity and specificity of gene set analysis methods. These datasets often rely on simplifying assumptions about the distribution of gene expression measures. Also, they either ignore the complex gene-gene correlation pattern among genes within gene sets or model it using a constant value (Efron and Tibshirani, 2007; Nam and Kim, 2008; Ackermann and Strimmer, 2009), even though gene-gene correlation has been reported to have a profound impact on the results of enrichment analysis methods (Tamayo et al., 2012). Real expression datasets have also been used to evaluate the sensitivity and specificity of gene set analysis methods (Tarca et al., 2013). Since the true enrichment status of gene sets are not *a priori* known in real datasets, relying on unverified assumptions about the differential enrichment of gene sets in these datasets does not provide an authentic framework for the evaluation of gene set analysis methods (Mathur et al., 2018). Consequently, there is no consensus among researchers about the method to use for a given experimental design.

Many gene set enrichment analysis methods are available. These methods vary in their underlying statistical model and the way they quantify a change in the expression pattern of genes within a gene set. A natural question that arises is whether the results of gene set analysis are comparable across methods. In

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this research, we compare the results of 10 widely used gene set analysis methods to test if the choice of gene set analysis method significantly affects the result of a gene expression study. In addition, since the most statistically significant gene sets are of more value to researchers, we statistically and biologically assess the agreement of the most significant gene sets for all methods under study.

In the rest of the paper, Section 2 describes the data and methodology used. Section 3 presents the experimental results. The biological evaluation of the results of gene set analysis methods are presented in Section 4. Section 5 offers insight gained from the experiments and provides suggestions for further research. Finally, Section 6 ends the paper with a short summary and conclusions.

2 DATA AND METHODOLOGY

2.1 Data

In this study, four large case-control experiments in humans from the Affymetrix GeneChip Human Genome U133 Plus 2.0 microarray platform were selected for evaluation of gene set analysis methods. These datasets originated from 1) renal cell carcinoma tissue and healthy controls (77 controls and 77 cases, GSE53757) (Von Roemeling et al., 2014), 2) skin from patients with psoriasis and healthy control tissue (64 controls and 58 cases, GSE13355) (Swindell et al., 2011), 3) gingival tissues from healthy and diseased individuals (64 controls and 183 cases, GSE10334) (Demmer et al., 2008), and 4) blood samples from individuals with rheumatoid factor (RF)-negative polyarthritis and healthy individuals (23 controls and 35 cases, GSE26554) (Thompson et al., 2012).

The raw data were preprocessed by first reading the CEL files into R using the *GEOquery* version 2.46.15 R package, and generating the normalized expression table using the *affy* version 1.56.0 package and *justRMA* normalization (Irizarry et al., 2003), which have been widely used for normalizing Affymetrix data (Neely and Anderson, 2017; West and Ali, 2017; Zyla et al., 2016). Probe IDs were converted to their corresponding Entrez gene identifiers using the *hgu133plus2.db* version 3.2.3 R package. To avoid over-emphasizing genes with a large number of probes on the arrays, it is a common practice in gene set analysis to collapse duplicate IDs. This was accomplished by using *collapseRows* from *WGCNA* version 1.61 with the *MaxMean* method. *MaxMean* selects the probe that has the maximum average value across samples when multiple probes map to the same gene. Collapsing the probes resulted in 20,514 genes in each experiment from an initial 54,675 probes.

The multidimentional scaling (MDS) plots visualizing the case and control samples from each dataset are shown in Figure 1. These plots were produced using *cmdscale* from the *stats* R package version 3.4.4 with default parameters.

2.2 Methodology

In this research, we compare 10 gene set analysis methods: PAGE (Kim and Volsky, 2005), GAGE (Luo et al., 2009), Camera (Wu and Smyth, 2012), ROAST (Wu et al., 2010), FRY (from the *limma* package) (Ritchie et al., 2015), GSEA (Subramanian et al., 2005), ssGSEA (Barbie et al., 2009), GSVA (Hänzelmann et al., 2013), PLAGE (Tomfohr et al., 2005), and over-representation analysis (ORA) (Drăghici, 2016).

The following R packages are utilized in this study: *GSVA* package version 1.18.0 is used for GSVA, PLAGE, and ssGSEA; the *phyper* method from the *stats* package version 3.4.4 is utilized to implement ORA; the *GSEA.1.0.R* script downloaded from the Broad Institute software page for GSEA provides GSEA; the *limma* package version 3.34.9 is used to run Camera, ROAST, and FRY; the *gage* package version 2.20.1 is used for PAGE and GAGE.

In addition to a gene expression dataset, gene set analysis requires a database of gene sets as input. In this research, we used the GO gene sets—hereafter referred to as $\mathbb{G}$—extracted from *MSigDB* version 6.1 (Subramanian et al., 2005). The GO database is widely used for gene set analysis.

For each gene expression dataset D_i and method ψ_j, gene set analysis is conducted using the default parameters proposed by the authors of ψ_j. To adjust for multiple comparisons, the Benjamini-Hochberg adjustment (Benjamini and Hochberg, 1995) with a false discovery rate of 0.05 is applied. The resulting adjusted p-values are denoted by a vector $R_{D_i}^{\psi_j}$, where $R_{D_i}^{\psi_j}(n)$—the n^{th} element of this vector—represents the adjusted p-value resulting from gene set analysis of the n^{th} gene set in the gene set database $\mathbb{G}$ using method ψ_j.

For a significance level $\alpha = 0.05$, we define a vector $E_{D_i}^{\psi_j}$ as follows:

$$E_{D_i}^{\psi_j}(n) = \begin{cases} 1, & \text{if } R_{D_i}^{\psi_j}(n) < \alpha \\ 0, & \text{otherwise} \end{cases} \quad (1)$$

where $E_{D_i}^{\psi_j}$ represents the predicted differential enrichment status of gene sets in $\mathbb{G}$—1 for differentially

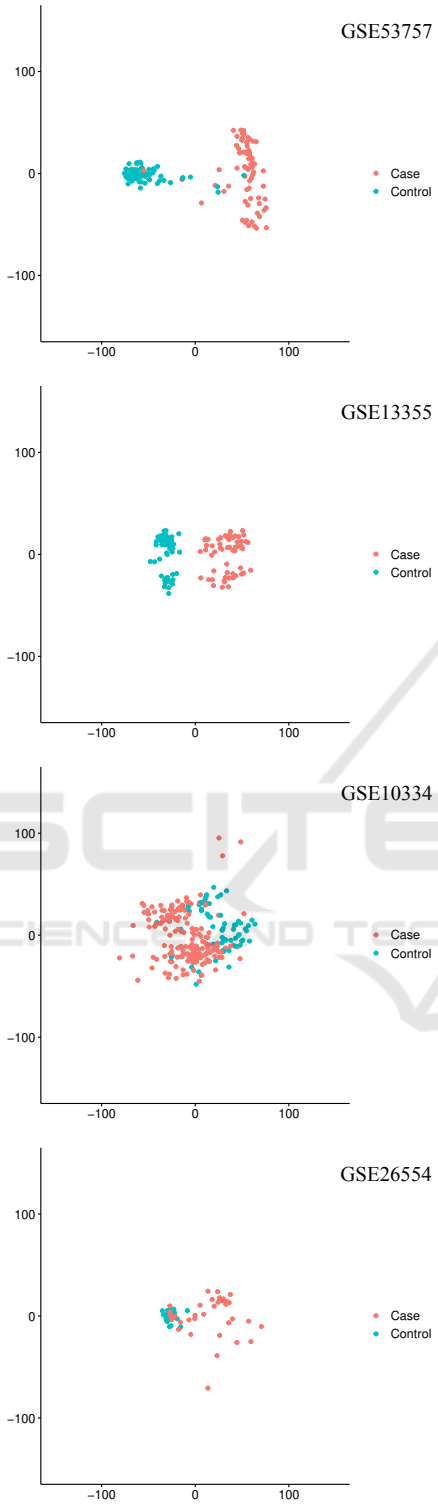

Figure 1: MDS plots for samples from the datasets under study. The MDS plots from top to bottom are for datasets with GEO IDs GSE35757, GSE13355, GSE10334, and GSE26554, respectively.

enriched and 0 for non-differentially enriched—and $E_{D_i}^{\Psi_j}(n)$ is the n^{th} element of $E_{D_i}^{\Psi_j}$. This is accomplished using *cochran.qtest* method from the *RVAideMemoire* R package version 0.9.69.3.

For a given dataset D_i, we statistically assess whether there is a significant difference between these predictions across different methods or not. Since the enrichment status is a dichotomous variable and there are paired data for each gene set (enrichment status for the same gene set across methods), we conduct Cochran's Q test for $E_{D_i}^{\Psi_j}$ across all values of Ψ_j, i.e. all methods. As post hoc analysis, Wilcoxon sign test is conducted for pairwise comparisons if the Cochran's Q test suggests a significant difference across methods.

Moreover, given the result of two gene set analysis methods Ψ_j and Ψ_k, we compare the similarity of their results when analyzing dataset D_i using the Jaccard index (Bakus, 2007) as follows:

$$J(S_{D_i}^{\Psi_j}, S_{D_i}^{\Psi_k}) = \frac{S_{D_i}^{\Psi_j} \cap S_{D_i}^{\Psi_k}}{S_{D_i}^{\Psi_j} \cup S_{D_i}^{\Psi_k}} \quad (2)$$

where $S_{D_i}^{\Psi_j}$ is the set of all statistically significant gene sets—i.e. gene sets with an adjusted p-value less than α—when analyzing dataset D_i using Ψ_j. A Jaccard index of 1 corresponds to the highest similarity, i.e. $S_{D_i}^{\Psi_j} = S_{D_i}^{\Psi_k}$, while a Jaccard index of 0 represents no similarity. Also, we define the Jaccard index to be 1 if $S_{D_i}^{\Psi_j}$ and $S_{D_i}^{\Psi_k}$ both are empty sets. In this paper, we interchangeably refer to the Jaccard index as overlap score.

In addition, since the most statistically significant results—i.e. gene sets predicted as being differentially enriched with the lowest p-values—are of the most interest to researchers, we investigate the agreement among the methods regarding their most significant results. In this regard, we define $S(D_i, \Psi_j, t)$ to be the set of up to t statistically most significant gene sets predicted as being differentially enriched—with an adjusted p-value less than α—when analyzing dataset D_i using Ψ_j. It should be noted that in cases where the number of differentially enriched gene sets is less than t, $S(D_i, \Psi_j, t)$ is equal to the entire set of differentially enriched gene sets resulting from analysis of D_i using Ψ_j. After determining $S(D_i, \Psi_j, t)$ for each method Ψ_j, we quantify the agreement of different methods for their most significant results using an overlap score of $J(S(D_i, \Psi_j, t), S(D_i, \Psi_k, t))$. In this research, we investigate agreement between the top 20 (and also the top 100) most significant results reported by each method.

3 EXPERIMENTAL RESULTS

First, each of the four datasets was analyzed using the ten methods under study. Next, $E_{D_i}^{\Psi_j}$, i.e. the differential enrichment status of gene sets in $\mathbb{G}$, were determined. For each dataset D_i a Cochran's Q test with a significance level $\alpha = 0.05$ was used to statistically assess if there is a significant difference between the differential enrichment status of gene sets in $\mathbb{G}$ across the methods under study. The Cochran's Q test for all datasets showed a statistically significant difference between the results of the methods under study (see Tables 2 to 6 in the Appendix for test results and the post hoc analysis).

Figure 2, using a series of triangular heat maps, illustrates the extent of overlap between the results of the 10 gene set analysis methods for the four datasets and three different scenarios: 1) when overlap is measured from the top 20 most significant gene sets predicted by each method, 2) when overlap is measured from the top 100 most significant gene sets predicted by each method, and 3) when overlap is measured from all the significant gene sets predicted by each method. Each cell in these heat maps represents the overlap score between the results of two methods. A blue hue of a cell indicates low overlap and a red hue indicates high overlap in enriched gene sets between two methods. The heat maps in Figure 2 show that, regardless of the datasets being used, the consistency—as measured by overlap score—between the results of different gene set analysis methods is generally low. However, as we move from scenario 1 to 3, the overlap between the results of some of the methods increases. In some instances, such as ROAST and FRY, the amount of overlap remains consistently high across scenarios. The consistency among methods when considering the top 20 most statistically significant results is much lower than the consistency when considering all significant results. This pattern is also observed when comparing the top 100 most statistically significant gene sets to all gene sets predicted as being differentially enriched. Also, Camera and GSEA have little consistency with all other methods under study.

Table 1 shows the total number of differentially enriched gene sets reported for all the datasets and all ten methods. GSEA, Camera, and ORA predict a smaller number of gene sets as differentially enriched compared to the other methods.

Figure 3 visualizes the distribution of the size of the top 20 and the top 100 most significant gene sets predicted as being differentially enriched for each method. These box plots further highlight the difference between the results of the gene set analysis methods. GAGE, ORA, and ssGSEA tend to report larger gene sets, i.e. gene sets that contain higher numbers of genes, in comparison to the other methods regardless of the dataset being analyzed.

Table 1: Number of gene sets predicted as being differentially enriched by each method for each dataset.

	GSE53757	GSE13355	GSE10334	GSE26554
FRY	4937	4876	4241	3660
GSEA	19	17	17	33
ORA	1547	573	130	222
Camera	155	73	3	313
ssGSEA	5844	5869	5862	5846
PAGE	1967	1400	1375	1054
GSVA	4730	3847	3819	2988
PLAGE	5900	5830	5242	5698
ROAST	4949	4737	4256	3380
GAGE	3951	3899	3887	2441

4 BIOLOGICAL EVALUATION

Juvenile idiopathic arthritis (JIA) is a class of childhood arthritis with unknown cause developing before the age of 16 years and persisting for at least 6 weeks. JIA comprises seven categories including: 1) systemic arthritis, 2) oligoarthritis, 3) polyarthritis rheumatoid factor (RF)-negative, 4) polyarthritis RF-positive, 5) psoriatic arthritis, 6) enthesitis-related arthritis (ERA), and 7) undifferentiated (Petty et al., 2004). For biological validation of methods under study, a JIA dataset containing RF-negative polyarthritis samples and healthy controls was obtained from the same Affymetrix GeneChip Human Genome U133 Plus 2.0 microarray platform as the other datasets (23 controls and 35 cases, GSE26554).

Expression profiles tend to be distinguishable among JIA categories. Gene expression and genome-wide genotyping have identified genes associated with different JIA subtypes, particularly *HLA* gene complex, *PTPN22*, *PTPN2*, *STAT4*, *ANKRD55*, Interleukin *(IL)2-IL21*, *IL-2RA*, *IL-6*, *SH2B3-ATXN2*, *MIF*, *SLC11A1* (*NRAMP1*), *TNFA*, *TNFAIP3*, *TRAF1/C5*, *VTCN1*, *CCL5*, *CD14*, and *WISP3* (Prahalad, 2004; Phelan et al., 2006; Prahalad and Glass, 2008; Martinez et al., 2008; Yao et al., 2009; Fung et al., 2009). The functions of these genes are chiefly regulating production and function of inflammatory biomarkers and their receptors. For instance, *PTPN2* modulates the expression of *IL-2*, *IL-4*, *IL-6*, and *IFN*. Variants of this gene can cause impairment in the regulation of inflammatory pathways, including joint inflammation (Jorde, 2000; Prahalad, 2006; Prahalad et al., 2000). The inflammatory process is mediated by an array of innate regulators

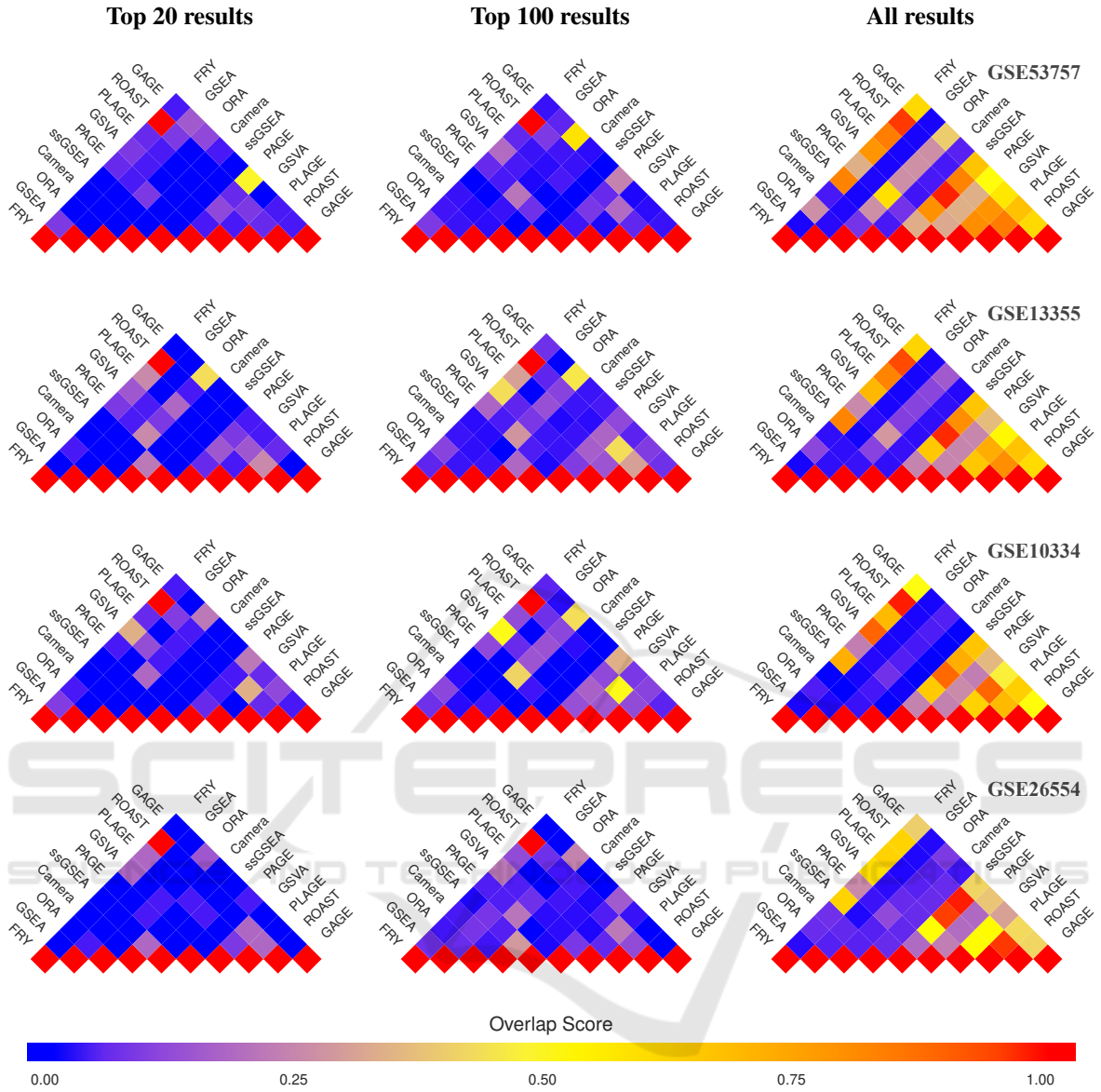

Figure 2: A set of triangular heat maps depicting the consistency of the results of gene set analysis methods—as measured by overlap score—across databases. Each triangular heat map illustrates the overlap score of the results of gene set analysis methods when analyzing a gene expression dataset. The layers in the plot, from top to bottom, correspond to datasets with GEO id of GSE53757, GSE13355, GSE10334, and GSE26554, respectively. Ranging from 0 to 1, the overlap score is represented by color hues from blue to red, separated by yellow in the middle (overlap of 0.5). The plot suggests that there is little consistency between the results of the gene set analysis methods under study. This lack of consistency is more pronounced among the top 20 (left column) and top 100 (middle column) most statistically significant results compared to all differentially enriched gene sets (right column).

including interleukins, chemokines, growth factors, and matrix metalloproteinases (MMPs)(Petty et al., 2015). There has been increasing interest in identifying molecules involved in regulating immune responses related to susceptibility to, and outcome of, JIA.

Biological evaluation of the 10 gene set enrichment analysis methods under study was performed based on the gene sets/pathways that are known to play a role in JIA using the dataset GSE26554 to determine the biological relevance of the gene sets predicted as being differentially enriched.

All of the top 20 gene sets predicted as being differentially enriched by GAGE showed general relevance to JIA. For example, the top 3 gene sets were “immune response” (GO:0006955), “regulation

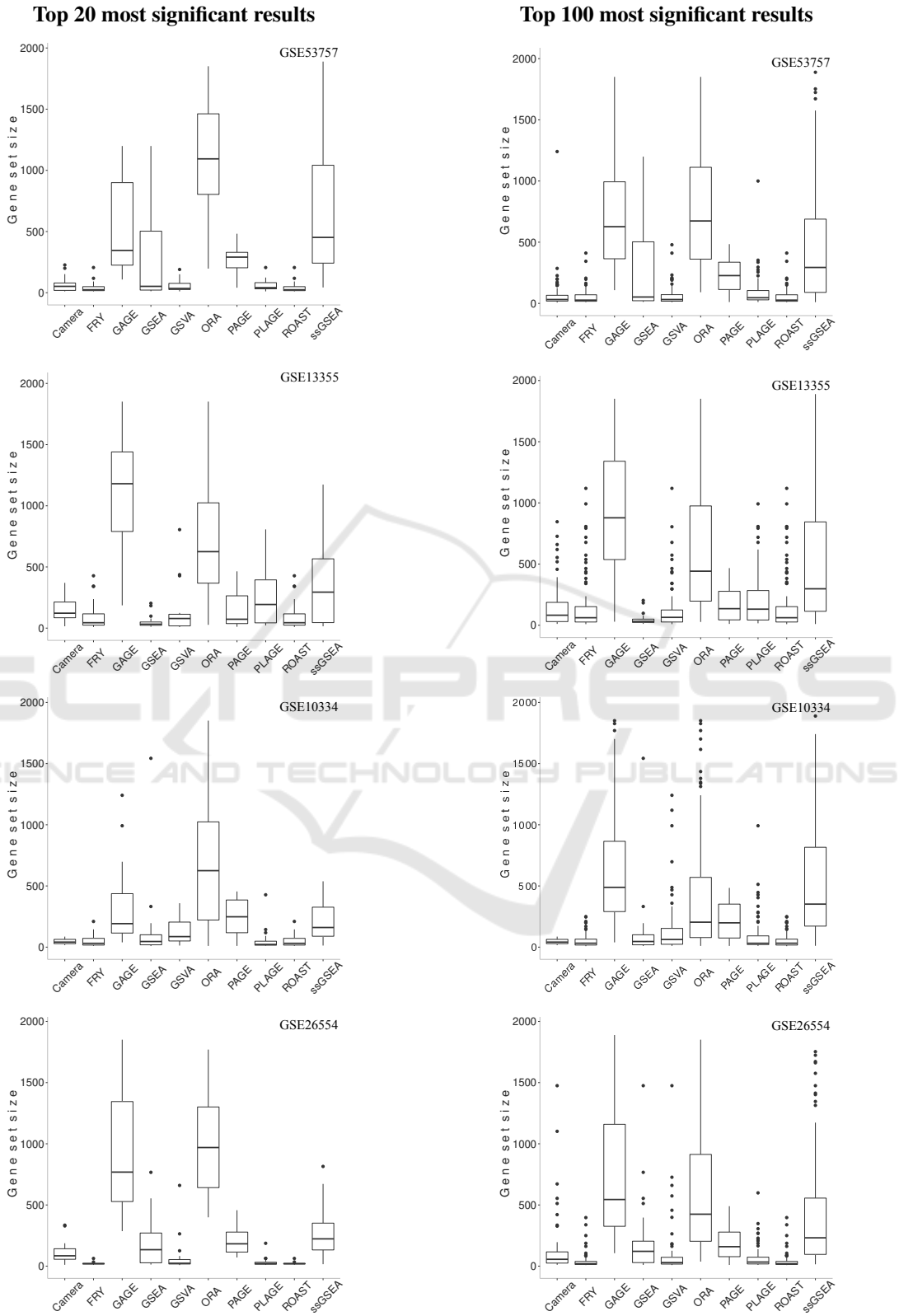

Figure 3: Box plots visualizing the distribution of gene set size among the top 20 (left) and top 100 (right) most statistically significant gene sets reported by each method. The plots, from top to bottom, correspond to datasets with GEO id of GSE53757, GSE13355, GSE10334, and GSE26554 respectively.

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of immune system process" (GO:0002682), and "immune system process" (GO:0002376). All these gene sets are relatively large and nonspecific to the actual disease or related pathways, with sizes approaching or exceeding 1000 genes. Several gene sets contained fewer genes, while still potentially relating to JIA, including "response to cytokine" (GO:0034097) and "inflammatory response" (GO:0006954). Furthermore, many of the gene sets in the top 20 predicted using GAGE had many terms relating to a general immune process or response (8 of the top 20 gene sets predicted as being differentially enriched).

GSEA also predicted a moderate number of gene sets that are thought to play a role in JIA, but unlike GAGE, these gene sets were much smaller and related to more specific processes. The small predicted gene sets related to JIA included the HLA complex in the gene set "trans-Golgi network" (GO:0005802). Other gene sets predicted as differentially enriched included "positive regulation of antigen receptor-mediated signaling pathway" (GO:0050857), which involves the cross-linking of antigen receptors of immune cells, and "cellular response to interferon-beta" (GO:0035458), which involves responses to a particular cytokine.

ORA also predicted a moderate number of gene sets related to cytokines, while PAGE predicted gene sets related to immune response. The few gene sets relevant to JIA reported by ORA and PAGE were also reported by GAGE. This agrees with our observations in Section 3, as the results of these three methods moderately overlap. The other six methods produced few gene sets—among their top results—associated with immune response or inflammation, as shown by the overlap scores (in the triangular heat maps for dataset GSE26554) for the top 20 and top 100 most significant results reported by these methods.

5 DISCUSSION

In this research, we showed that there is a significant difference between the results of ten commonly used gene set analysis methods. We quantified the similarity between the results of the methods using Jaccard index. Since researchers value the most statistically significant results, we studied the distribution of gene set size for the top 20 and top 100 most significant results of each method.

The results showed that ROAST and FRY share the same top 20 and top 100 significantly enriched gene sets. This is expected as FRY was designed to be a computationally efficient approximation of ROAST. Also, there are moderate overlaps between the top 20 (and top 100) most significant results reported by ORA, GAGE, and PAGE. This similarity can be explained as all three of these methods are parametric gene set analysis methods; ORA and GAGE are based on two-sample t-tests, and PAGE is based on a z-score. These observations support the validity of the experimental design in this research.

When considering all gene sets predicted as being differentially enriched, there are moderate to high overlaps between the results of all methods, with the exception of ORA, Camera, and GSEA. These high overlaps appear to be a consequence of the high number of gene sets reported as being differentially enriched. As seen by combining the results in Figure 2 and Table 1, two methods with high overlap between their results also report a high number of gene sets as being differentially enriched. This happens when some methods report a large proportion of gene sets as being differentially enriched. At the extreme, if two methods report all gene sets, the overlap will be its maximum value, i.e. 1. However, as also depicted in Figure 2, there is no or very small overlap between the top 20 (and top 100) differentially enriched gene sets reported by methods that achieve high overlap scores when considering all of their significant results. These observations suggest that the methods under study generally do not agree in the gene sets they reported as most statistically significant.

The high numbers of reported differentially enriched gene sets (for some methods) are not an artifact of the choice of the expression datasets or the preprocessing steps. Single gene expression analysis reported that GSE53757 had 571 differentially expressed genes, GSE13355 had 121, GSE10334 had 12, and GSE26554 had 5 differentially expressed genes. These results were produced using the *limma* package with a log fold change cutoff of ± 2, a Benjamini-Hochberg correction for multiple comparisons, and a significant level $\alpha = 0.05$.

The number of differentially enriched gene sets reported by ORA and Camera, compared to all other methods under study, seem to be more sensitive to the variation between the case and control groups of each dataset (see Figure 1). For the datasets that have more distinct groups, more gene sets are reported as differentially enriched. When the variation is low, ORA—for example—predicts fewer differentially enriched gene sets. One explanation is that the list of genes predicted as being differentially expressed, an input to ORA, is based on a t-test. The t-test statistic denominator represents the variance of expression measures for a gene, and when the sample variation is high, as with GSE10334, the statistic value decreases and the derived p-value increases; this results in a small num-

ber of differentially expressed genes. This, in turn, decreases the number of differentially enriched gene sets reported by ORA.

GSEA and Camera typically report a small number of differentially enriched gene sets for each data set. Since the number of reported differentially enriched gene sets is small, these methods have a very small overlap with the results of other methods and also to each other.

Gene sets extracted from GO are associated with GO terms, where the more general terms usually correspond to larger gene sets, and specific terms correspond to smaller gene sets. As depicted in Figure 3, for the 20—and also top 100—most statistically significant gene sets reported, ORA, GAGE, PAGE, and ssGSEA tend to report gene sets with larger sizes. Although there could be cases where a gene set with a large size is associated with a phenotype of interest, these three methods consistently report larger gene sets across the datasets compared to the other methods. This may be a sign of systematic bias in favour of large gene set sizes, which are usually less informative. With ORA in particular, the amount of variation between gene set sizes tends to be high as well; also, the median gene set size is typically higher than all other methods. On the other hand, reported gene sets by GSEA have a low median size, although variation between sizes is larger than some of the other methods such as Camera, FRY, ROAST, and GSVA. This is because GSEA reports a mixture of small gene sets followed by large gene sets in the top 20 and 100 results. Camera also reports a small number of gene sets, usually with small sizes. PLAGE, FRY, ROAST, and GSVA—on the other hand—report a large number of gene sets as differentially enriched but, like Camera, their most significant gene sets have small sizes. This could suggest that the reported gene sets are very specific to a particular biological process, molecular function, or cellular component. However, this does not necessarily mean these gene sets are biologically informative to the phenotype under study. To assist with interpreting these results, the relevancy of the most significant genes sets for the JIA dataset was explored by biological interpretation.

The biological evaluation in Section 4 suggests that GAGE performed the best followed by GSEA, ORA, and PAGE at predicting the most gene sets that were relevant to the phenotype of interest. This is on par with the overlap scores where GAGE achieved moderate overlap scores with ORA and PAGE. GSEA reports a small number of gene sets as being differentially enriched and therefore achieves low overlap scores with other methods. However, some of its reported gene sets showed relevance to specific immune system processes, which could be more informative compared to some of the more general gene sets reported by GAGE, ORA, and PAGE. We suggest that these results be confirmed further with validation performed on a wide variety of datasets to ensure the results are not dataset or phenotype dependent.

These observations further highlight the lack of agreement between the results of gene set analysis methods. Our results support the utility of methods such as GAGE, GSEA, ORA, and PAGE in gaining biological insight. Drawing a conclusion based on the results of the other methods, even their most significant results, is more challenging and prone to investigator bias toward a hypothesis of interest. This is even a more serious problem for methods that report a large number of gene sets as being differentially enriched. Since it is unlikely for a living organism to undergo such a dramatic change involving several thousand gene sets, this can be interpreted as the lack of specificity, i.e. incorrectly reporting a large number of gene sets as being differentially enriched. We suggest developing methods with higher specificity without sacrificing sensitivity as future research.

Often, it is the case that researchers studying the same phenomenon come up with different results (e.g. different implicated gene sets) even though they appear to have each followed a valid methodology. We are left searching for an explanation for the difference in results. Since our study shows that there is a lack of consistency between the results of gene set analysis methods, part of the explanation could be using different gene set analysis methods, if different gene set analysis methods were used.

6 CONCLUSION

In this paper, we studied the consistency of the results of ten commonly used gene set analysis methods when applied to real expression datasets. The data analysis showed that there is a significant difference between the results of these methods. Our study suggests that not only do these methods differ in the gene sets reported as being differentially enriched, but they also differ in the distribution of the size of the reported gene sets. Further, there is little to no overlap between the results of top 20 (and top 100) most statistically significant gene sets reported, except between FRY and ROAST.

The biological validation of the most significant results using a JIA dataset revealed that GAGE performs the best followed by GSEA, ORA, and PAGE at predicting the most gene sets relevant to the phenotype of interest. The biological evaluation of the

most significant results reported by the gene set analysis methods revealed that the majority of the methods reported gene sets that are not related to the known biology of JIA. GAGE was the only method with all of its top 20 gene sets relevant to the biology of juvenile arthritis. In addition, GSEA, ORA, and PAGE reported relevant gene sets, with GSEA reporting fewer but more specific gene sets. This supports the utility of these methods for gene set analysis. However, any more general conclusion would require a broader study.

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APPENDIX

Table 2: The results of Cochran's Q test for all datasets.

Dataset	Q Statistic	Degrees of freedom	p-value
GSE53757	32133.2	9	<2.2e-16*
GSE13355	33592.8	9	<2.2e-16*
GSE10334	31661.4	9	<2.2e-16*
GSE26554	29326.9	9	<2.2e-16*

* 2.2e-16 is the smallest p-value reported by *cochran.qtest* method from *RVAideMemoire*

Table 3: The p-values of Wilcoxon sign tests for pairwise comparisons of the results of the methods using dataset GSE53757.

	Camera	FRY	GAGE	GSEA	GSVA	ORA	PAGE	PLAGE	ROAST
FRY	4.94e-324								
GAGE	0.00e+00	2.51e-101							
GSEA	4.47e-28	0.00e+00	0.00e+00						
GSVA	0.00e+00	2.37e-09	1.46e-57	0.00e+00					
ORA	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00				
PAGE	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	1.62e-44			
PLAGE	0.00e+00	5.21e-282	0.00e+00	0.00e+00	0.00e+00	4.94e-324	4.94e-324		
ROAST	0.00e+00	4.41e-01	4.69e-103	0.00e+00	2.47e-10	0.00e+00	0.00e+00	9.51e-277	
ssGSEA	4.94e-324	5.41e-207	0.00e+00	0.00e+00	1.15e-266	0.00e+00	0.00e+00	2.04e-09	1.57e-202

Note that a p-value of 0.00e+00 is smaller than the representable floating-point precision.

Table 4: The p-values of Wilcoxon sign tests for pairwise comparisons of the results of the methods using dataset GSE13355.

	Camera	FRY	GAGE	GSEA	GSVA	ORA	PAGE	PLAGE	ROAST
FRY	0.00e+00								
GAGE	0.00e+00	4.08e-104							
GSEA	1.25e-09	9.88e-324	0.00e+00						
GSVA	0.00e+00	4.66e-159	3.03e-01	0.00e+00					
ORA	2.78e-101	9.88e-324	0.00e+00	1.05e-152	0.00e+00				
PAGE	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	9.55e-152			
PLAGE	9.88e-324	6.49e-233	0.00e+00	9.88e-324	0.00e+00	0.00e+00	0.00e+00		
ROAST	0.00e+00	5.33e-15	6.33e-74	0.00e+00	5.39e-134	0.00e+00	0.00e+00	4.37e-272	
ssGSEA	0.00e+00	7.62e-253	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	1.02e-03	1.81e-295

Note that a p-value of 0.00e+00 is smaller than the representable floating-point precision.

Table 5: The p-values of Wilcoxon sign tests for pairwise comparisons of the results of the methods using dataset GSE10334.

Camera	Camera	FRY	GAGE	GSEA	GSVA	ORA	PAGE	PLAGE	ROAST
FRY	0.00e+00								
GAGE	0.00e+00	1.55e-11							
GSEA	2.70e-03	4.94e-324	0.00e+00						
GSVA	0.00e+00	2.36e-100	2.04e-01	0.00e+00					
ORA	4.41e-37	4.94e-324	0.00e+00	4.44e-23	4.94e-324				
PAGE	0.00e+00	4.94e-324	0.00e+00	0.00e+00	0.00e+00	0.00e+00			
PLAGE	0.00e+00	9.91e-132	6.79e-212	4.94e-324	3.28e-229	0.00e+00	0.00e+00		
ROAST	0.00e+00	5.00e-02	1.93e-12	0.00e+00	1.70e-104	0.00e+00	4.94e-324	7.23e-128	
ssGSEA	0.00e+00	0.00e+00	0.00e+00	4.94e-324	0.00e+00	4.94e-324	4.94e-324	6.10e-145	0.00e+00

Note that a p-value of 0.00e+00 is smaller than the representable floating-point precision.

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Table 6: The p-values of Wilcoxon sign tests for pairwise comparisons of the results of the methods using dataset GSE26554.

	Camera	FRY	GAGE	GSEA	GSVA	ORA	PAGE	PLAGE	ROAST
FRY	0.00e+00								
GAGE	0.00e+00	1.05e-128							
GSEA	3.920e-67	0.00e+00	0.00e+00						
GSVA	0.00e+00	3.78e-60	3.44e-24	0.00e+00					
ORA	5.00e-05	0.00e+00	0.00e+00	5.33e-39	0.00e+00				
PAGE	9.58e-105	0.00e+00	1.90e-320	9.41e-285	0.00e+00	2.07e-173			
PLAGE	4.94e-324	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00		
ROAST	0.00e+00	1.76e-12	1.03e-65	0.00e+00	3.86e-65	0.00e+00	0.00e+00	0.00e+00	
ssGSEA	0.00e+00	0.00e+00	0.00e+00	4.94e-324	0.00e+00	4.94e-324	0.00e+00	3.06e-19	0.00e+00

Note that a p-value of 0.00e+00 is smaller than the representable floating-point precision.

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