Towards unified quality verification of synthetic count data with *countsimQC*

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Abstract

Summary: Statistical tools for biological data analysis are often evaluated using synthetic data, designed to mimic the features of a specific type of experimental data. The generalizability of such evaluations depends on how well the synthetic data reproduce the main characteristics of the experimental data, and we argue that an assessment of this similarity should accompany any synthetic data set used for method evaluation. We describe *countsimQC*, which provides a straightforward way to generate a stand-alone report that shows the main characteristics of (e.g., RNA-seq) count data and can be provided alongside a publication as verification of the appropriateness of any utilized synthetic data.

Availability and implementation: *countsimQC* is implemented as an R package (for R versions ≥ 3.4) and is available from https://github.com/csoneson/countsimQC under a GPL (≥ 2) license.

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1 Introduction

The analysis of biological data, for example those coming from high-throughput sequencing applications, is often highly dependent on sophisticated statistical tools and algorithms. Each such tool aims to extract a specific type of biologically relevant information from data, and its ability to perform the intended task is usually evaluated at the time of publication. Although the ultimate aim is to develop methods that give accurate results for real, experimental data, this is often difficult to assess in practice due to the lack of an independently validated ground truth. Thus, most statistical data analysis tools are (at least partly) evaluated on synthetic data, obtained either via parametric simulation or via sampling from experimental data. The synthetic data are assumed to share important characteristics with experimental data, but the signal of interest as well as other, potentially confounding, signals are completely controlled in the data generation. In such cases, the usefulness of any performance evaluation ultimately comes down to how realistic the synthetic data are. Thus, we argue that any evaluation relying on synthetic data sets should take care to verify that these reflect the most important characteristics of the data type of interest. Currently, many studies whose conclusions crucially depend on synthetic data do not provide extensive evidence of such similarity. We hypothesize that one reason for this is a lack of general guidelines regarding the set of aspects that should be investigated, as well as a straightforward way to easily generate a quality evaluation report for synthetic data, which exists for other aspects of high-throughput sequencing data analysis (e.g., FastQC [http://www.bioinformatics.babraham.ac.uk/projects/fastqc/], MultiQC [Ewels et al., 2016]).

To fill this gap, we developed *countsimQC*, an R package that allows the user to quickly explore and compare a variety of characteristics across one or more count data sets and generate a summary report for evaluation and dissemination. For example, a user can visualize the characteristics of a synthetic data set (e.g., a simulated RNA-seq count matrix) side by side with those of an experimental data set of the type that it is intended to mimic. However, the package is not limited to such comparisons, and can be used to summarize and compare the properties of any collection of one or more count data sets.

2 Methods

To run *countsimQC*, the user provides a count matrix and information about the experimental design for each data set. The software then calculates a set of characteristics for each data set and generates a stand-alone pdf or html report, which can be used to assess the properties of,
Fig. 1. Example illustrations from a countsimQC report, comparing characteristics of three datasets: one real single-cell RNA-seq data set (Original) and two data sets simulated using the real data set as the underlying source of population parameters (powsim, splat). A. BCV (biological coefficient of variation) as a function of average expression level, both calculated by edger (Robinson et al., 2010). B. Distribution of library sizes (total count sum) across all cells. C. Distribution of average expression levels (log count per million) across all genes. D. Distribution of the fraction of zeros across all genes. E. Relationship between the average expression level (log count per million) and the fraction of zeros for all genes.

3 Results

To illustrate the output generated by countsimQC, we use two recently published R packages (the ‘splat’ framework from splatter (v1.0.2) (Zappia et al., 2017) and powsim (v1.0.1) (Vieith et al., 2017)) to generate synthetic single-cell RNA-seq count matrices from an underlying, experimentally obtained count matrix (GSE48968-GPL13112 (Shalek et al., 2014)), downloaded from the conquer repository (http://imlspenticton.uzh.ch:3838/conquer (Soneson and Robinson, 2017)). Figure 1 shows a subset of the figures that are included in the countsimQC report. From these plots, it is clear that a single evaluation criterion is not enough to fully capture the degree of similarity between data sets, and that the simulation that is most similar to the underlying real data in one aspect can be far from it when another criterion is considered. Thus, having a comprehensive report illustrating the level of similarity from different aspects is useful not only for the synthetic data generator but also for the reader interested in judging the degree of generalizability of conclusions based on the synthetic data. The full report of the comparison summarized in Figure 1, as well as additional example reports for various types of real and synthetic count data sets can be accessed from https://github.com/csoneson/countsimQC.

4 Conclusions

With the countsimQC package, we wish to spark a discussion about the importance of evaluating the suitability of synthetic data. We encourage researchers who use synthetic data to draw conclusions to provide a report, such as that generated by countsimQC, as evidence that the synthetic data mimic real data, since this is not always easy to assess from a text description of a simulation model. We note that it is not the first effort in this direction; the compcodeR package (Soneson, 2014) as well as powsim (Vieith et al., 2017) contain functions for summarizing the characteristics of a single data set, and the splatter package (Zappia et al., 2017) also provides the opportunity to generate figures comparing various aspects of a collection of single-cell RNA-seq data sets. However, to our knowledge it is the first independent, “one-stop” solution to generate an extensive, publishable report comparing multiple count data sets, optionally including the code that was used to generate the plots.

There are of course situations where a high degree of similarity between the synthetic data and real data is less critical. For example, synthetic data are often used to illustrate the ability of algorithms and tools to correctly estimate hyperparameters of underlying data distributions, or to illustrate the influence of changing particular features of a data set, possibly out of the realistic range, for better understanding of the advantages, disadvantages and sensitivities of the methodology. However, even in such situations we argue that it can be useful, both for the analyst and for the reader, to understand the characteristics of the generated data and how it compares to what would be seen in practice.

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