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BIOINFORMATICS

Vol. 00 no. 00 2015-2016
Pages 1–2

# MicroScope: magnifying interactive gene expression heatmaps with RShiny and JavaScript

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Received on XXXXX; revised on XXXXX; accepted on XXXXX

Associate Editor: XXXXXXX

**ABSTRACT**

**Motivation:** Large gene expression heatmaps ($\geq$ 200 genes) are difficult to read: while general expression level patterns may be observed via hierarchical clustering, the identities of specific gene names become entirely unreadable at large scale. More importantly, current state-of-the-art heatmaps are entirely static and require programming skills to produce.

**Results:** We create a user-friendly web app to create heatmaps that are both dynamic and interactive. A few mouse clicks allows a user to generate a heatmap based on an input .csv file and proceed to dynamically navigate to any sector of the heatmap via zooming in and out to any specific region, cluster, or even single gene. In addition to magnification, MicroScope also allows users to hover the mouse pointer over any specific gene to show precise expression level details, as well as create row and column dendrograms with colored branches using simple button clicks. As such, MicroScope presents a significant advance in heatmap visualization technology over current standard protocols.

**Availability and implementation:** MicroScope is hosted online as an RShiny web app based on the D3 JavaScript library: https://microscope.shinyapps.io/microscope. The methods are implemented in R, and are available as part of the MicroScope project at: https://github.com/Bohdan-Khomtchouk/Microscope.

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## 1 INTRODUCTION

Currently existing heatmap software produce static heatmaps [1-5], with no features available to dynamically interact with and explore the landscape of a heatmap. Such a feature would allow the user to interact with the data in a visual manner in real-time, thereby allowing for a deeper data exploration experience. An interactive, non-reproducible heatmap tool was previously employed in the study of the transcriptome of the *Xenopus tropicalis* genome [6]. However, no open-source, dynamic and interactive heatmap software has yet been proposed to explore an arbitrary user-specified input dataset.

**Fig. 1.** MicroScope user interface showcasing the magnification feature as well as features such as: file input, multiple heatmap color schemes, hierarchical clustering, row/column dendrogram branch coloring, row/column font size, and a download file utility.

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## 2 APPROACH

In this paper, we leverage R's d3heatmap [7], shiny [8], htmlwidgets [9], and RColorBrewer [10] libraries to create a dynamic, interactive heatmap web app called MicroScope, in recognition of the software's magnification utility (described in Results section). All heatmaps produced are generated within the R environment on the server-side, thereby obviating the need for any programming skills on the client-side.

## 3 RESULTS

MicroScope is an RShiny and JavaScript (D3.js) software program designed to produce dynamic, interactive heatmaps in a web browser. Figure **??** shows the UI in action. MicroScope allows you to magnify any portion of a heatmap by a simple click-and-drag feature to zoom in, and a click-once feature to zoom out. MicroScope is designed with large heatmaps in mind (e.g., gene expression heatmaps with thousands of genes), where individual entries quickly become unreadable as more and more add up. However, MicroScope allows you to repeatedly zoom in to any sector of the heatmap to investigate a region, cluster, or even a single gene. You can scroll up and down the page of your web browser to see more genes than automatically fit your window. MicroScope also allows you to hover the mouse pointer over any specific gene to show precise expression level details. Some of the user-friendly features of MicroScope include:

- User-specified file input widget
- Multiple heatmap color schemes widget
- Hierarchical clustering widget
- Row/column dendrogram branch coloring widget
- Row/column font size widget
- Download widget

## 4 CONCLUSION

We provide access to a user-friendly web app designed to produce dynamic and interactive heatmaps within the R programming environment, without any prerequisite programming skills required of the user. Our software tool aims to enrich the genomic data exploration experience by allowing for the ability to magnify any portion of a gene expression heatmap and thereby exploring specific gene regions along with their respective expression level details.

## ACKNOWLEDGEMENTS

BBK wishes to acknowledge the financial support of the United States Department of Defense (DoD) through the National Defense Science and Engineering Graduate Fellowship (NDSEG) Program: this research was conducted with Government support under and awarded by DoD, Army Research Office (ARO), National Defense Science and Engineering Graduate (NDSEG) Fellowship, 32 CFR 168a.

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