Cytosplore Simian Viewer Technical Document

viewer.cytosplore.org
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Contents

1 Introduction

Cytosplore Simian Viewer is a desktop software application designed for comparative visual exploration of multi-species transcriptomic datasets[1] from the Allen Institute in Seattle. The data displayed in this viewer is downloaded from the Allen Cell Types Data and is available from the Allen Cell Types Database.

Cytosplore Simian Viewer was developed in close collaboration between the Allen Institute for Brain Science, the Division of Image Processing and the Computational Biology Center at Leiden University Medical Center, and the Computer Graphics and Visualization Group at the TU Delft in the Netherlands.

This comprehensive visualization system uses multiple visualizations and linked interactions to compare complex transcriptomic datasets of the middle temporal gyrus across various primate species. Medical experts can analyze data on a single screen, perform real-time computations, and gain valuable insights into the molecular basis of cognitive abilities in humans and primates.

2 System Requirements

2.1 Windows System Requirements

- Operating System: Windows 10 (64-bit)

- Processor: Intel Core i5 2.5GHz or equivalent

- Memory: 8 GB RAM

- Graphics: DirectX 11 compatible graphics card with 2GB VRAM

- Storage: 500MB available space

For optimal performance, it is recommended to use a powerful system, as configurations with lower specifications may result in longer wait times for data loading and computing. To ensure compatibility, it is important to update the graphics card drivers to the latest version before installing the Cytosplore Simian Viewer. However, remote operation through Remote Desktop is not supported. Additionally, the software requires recent graphics hardware and OpenGL 3.3 or newer.

3   User Interface

The Cytosplore Simian Viewer User Interface has been developed with the aim of meeting the needs of various analytic tasks. The software is implemented using C++ application and D3js technology and offers a comprehensive system with multiple linked views to facilitate the visual exploration and comparison of multi-species cortical cells.

Figure 1: Cytosplore Simian Viewer Main Screen

The User Interface as seen in Figure 1 consists of four linked views.

3.1   Distance map (Figure 1 A)

The Distancemap View is a vital component of the Cytosplore Simian Viewer, enabling users to compare the distances between cell clusters across different brain regions with ease. Users can select different species and neighborhoods from the dropdown menu to explore a distance map that displays in-species cluster distances of two different species being compared. The viewer uses a sequential color scale to represent the distance between cluster centroids, allowing users to quickly identify similarities and differences in cluster distances. Furthermore, the viewer provides detailed information about each cluster for the two species in a tooltip, including cell counts, layer distribution, and other pertinent details. By serving as a central controller of the viewer, the Distancemap View allows users to select regions of interest (cross-species cluster groups) for further analysis and exploration.

3.2 Differential expression (Figure 1 B)

The Differential Expression View in the Cytosplore Simian Viewer is a powerful tool for analyzing the differences in gene expression values between two selected species for a given cross-species cluster. With the ability to easily select cross-species clusters from the distance map view or the gene expression view, users can view differences in expression values between the selected species as a table with gene names, differential expression values, and mean expression values. To help users explore these results in more detail, the viewer includes filtering and sorting options based on differential expression and expression values. Additionally, the viewer highlights the HAR and HCondel associations of human-specific genes, providing valuable insights into the genetic differences between species. With the counts of HAR and HCondel values associated with human comparisons displayed at the bottom of the view, users can easily assess the number of genes with HAR and HCondel values. Furthermore, by selecting rows representing genes in the table, users can compare gene expression values across cross-species clusters in the gene expression viewer. These powerful features enable users to gain a deeper understanding of the differential gene expression patterns between species, facilitating the discovery of new insights and hypotheses.

3.3 Expression comparison(Figure 1 C)

The Expression Comparison View presents gene and differential expression values of cross-species clusters within the chosen neighborhood for the selected gene, as viewed in the differential expression viewer(Figure 2).

The gene expression analysis in the tool includes three distinct views for pairwise and multi-species comparisons. The first view called the Multi-Species gene expression view (Figure 2A), displays the average gene expression of all species as a set of bar charts. The second view, the Pairwise gene expression view (Figure 2B), compares the mean gene expression of selected species through back-to-back histograms. Finally, the Differential expression with human view (Figure 2C) highlights the differences in gene expression between the other species and humans.

The bars in the views can be selected or deselected to highlight or hide the corresponding clusters in the other views. Additionally, hovering over the bars shows the exact expression values. This view provides a quick and easy way to assess the expression levels of a gene across multiple species and clusters, and how they vary between different regions of the brain.
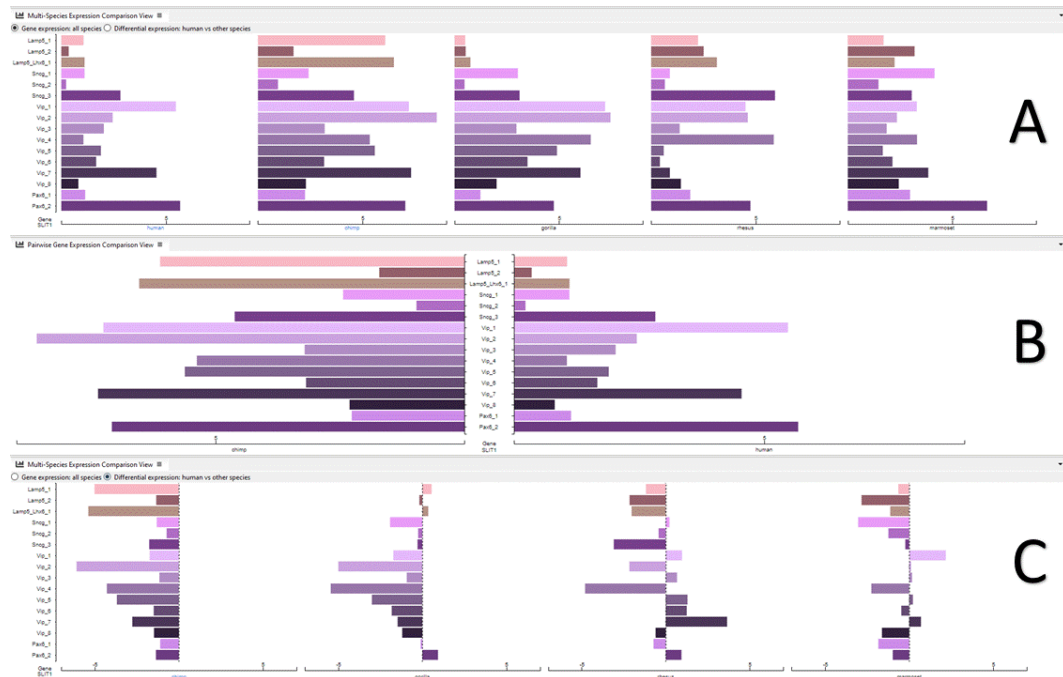
Figure 2: Expression comparison view: A) Multi-Species gene expression, B) Pairwise gene expression and C) Differential expression with human

3.4 Scatterplot (Figure 1, D and E)

The Scatterplot View in the Cytosplore Simian Viewer provides an intuitive and interactive display of low-dimensional UMAP embeddings that correspond to different species being compared. Each point in the scatterplot represents a single cell and is color-coded based on its cross-species cluster. With this view, users can quickly identify cross-species clusters that are specific to each species and investigate the similarities and differences between them. Additionally, the viewer includes various customization options, such as point size, opacity, and color mapping, which allow users to adapt the visualization to their specific needs. This enables users to gain deeper insights into the relationships between cell types and species and discover new patterns and trends.

Overall, these views provide an intuitive and efficient way to explore and compare single-cell datasets. The interactive features and linkage between views enable users to effectively navigate and analyze large datasets, identify species-specific and cross-species clusters, explore gene expression and differential expression and visualize the distances between clusters in different regions of the brain. The default sizes of the views can be easily customized,

allowing for a tailored analysis experience. We also accommodate view isolation(click F3) in order to focus on a specific part of the cross-species visualization. This means that the view of interest is the only view shown, and the other views are hidden. These views facilitate the exploration and interpretation of complex biological datasets by providing a comprehensive visual analysis system.

4   Troubleshooting

If you encounter any problems while using our software, please follow the troubleshooting guide below for assistance.

4.1   Software does not open

If the software fails to open, please ensure that your system meets the minimum requirements for running the software. Check that your system is up-to-date, and that any necessary software updates have been installed. If the problem persists, try restarting your computer and attempting to open the software again.

4.2   Software crashes or freezess

If the software crashes or freezes, try closing other applications and running only the software to free up system resources. Ensure that you are using the latest version of the software, and that your system meets the minimum requirements. If the issue persists, try restarting your computer and running the software again.

4.3   Warning message: "HDPS requires OpenGL 3.3 or newer"

If you see the warning message "HDPS requires a graphics card with support for OpenGL 3.3 or newer. The currently used card supports version..." and the application crashes, there are a few things you can try to resolve the issue.

First, check whether your graphics drivers are up to date. An outdated driver may prevent the graphics card from supporting OpenGL 3.3 or newer. Updating the driver may upgrade the OpenGL version and fix the issue.

Another possible cause of the error is that the program is not running on high-performance dedicated graphics hardware, instead, it is using integrated graphics hardware. This could explain why the application is complaining about the OpenGL version.

To ensure that the application is running on high-performance hardware, try the following steps:

- Right-click the application icon and select "Run with graphics processor".

- Select "High-performance NVIDIA processor" or "High-performance AMD processor", depending on your graphics card.

- If the option to run with a high-performance graphics processor is not available, you can force the application to use the dedicated GPU by following the steps in the link.

By ensuring that the application is using high-performance dedicated graphics hardware and updating your graphics drivers, you can resolve the OpenGL version issue and prevent the application from crashing due to the "HDPS requires OpenGL 3.3 or newer" error.

4.4   Windows Defender SmartScreen prevents installation

If a Windows dialog box appears before installation, containing the message "Windows Defender SmartScreen prevented an unrecognized app from starting," you should click on "More info" and then click on the "Run anyway" button that appears at the bottom. This will allow you to continue with the installation.

If the "Run anyway" option does not appear, you can try the following troubleshooting steps:

- Open Windows Defender and go to "App & Browser Control".

- Under "Check apps and files," select the "Warn" option instead of the "Block" option.

- Relaunch the installation file and click the "See more" option.

- This will reveal the "Run Anyway" button that you can click to run the app in question.

If none of the above troubleshooting options solve the issue that you are facing, please contact our support team for further assistance.

5 Frequently Asked Questions

5.1 What operating systems are the software compatible with?

Our software is compatible with Windows.

5.2 What are the minimum requirements to run the software?

The minimum requirements to run the software on Windows are a 64-bit processor and operating system, 4GB RAM, and 500 MB of free disk space. Please refer to our section on minimum system requirements.

5.3 How to download the software?

You can download the software directly from our Cytposplore website.

5.4 Is it possible to install the software if there is no internet connection?

Yes, we have an offline version of the installation file which can be used to complete the installation process without an internet connection. However, the online installation version requires a stable internet connection to install Cytosplore Simian Viewer in your system.

5.5 How to install the software?

To install the software, follow these steps:
- Download the installation file from our website or the provided link.
- Open the file and follow the instructions in the installation wizard.
- Choose the folder where you want to install the software.
- Review and accept the license agreement.
- Select any additional options presented during installation.
- Wait for the installation to complete, then click "Finish" to exit the wizard.

If you encounter any issues, consult our troubleshooting guide or contact our support team. Note that it is recommended to uninstall any previous version of HDPS Simian Viewer before installing the new one to avoid file mismatch.

5.6   How to uninstall the software?

To uninstall the software, follow these steps:

- Go to the Control Panel and select "Programs and Features" or "Add or Remove Programs", depending on your operating system.

- Locate the software in the list of installed programs and select it.

- Click "Uninstall".

- Follow the instructions in the uninstallation wizard.

- Wait for the uninstallation process to complete.

If you encounter any issues during the uninstallation process or if you need to reinstall the software in the future, consult our installation guide or contact our support team for assistance.

6   Contact Information

Thank you for using our software. We value your feedback. If you have any questions or suggestions about our software, please don't hesitate to contact us on our Cytposplore website.

7   Acknowledgements

Cytosplore simian Viewer was developed in close collaboration between the Allen Institute for Brain Science in Seattle, the Division of Image Processing and the Computational Biology Center at Leiden University Medical Center, and the Computer Graphics and Visualization Group at the TU Delft, the Netherlands.

Cytosplore Simian Viewer makes use of the following open-source software:

- QT

- D3 - Data-Driven Documents

- d3-context-menu

- d3-scale-chromatic

8 References

[1] Nikolas L Jorstad et al. "Comparative transcriptomics reveals human-specific cortical features". In: *bioRxiv* (2022), pp. 2022–09.