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3Dscript.server: True server-side 3D animation of microscopy images using a natural language-based syntax

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Abstract

Summary: Creating 3D animations from microscopy data is computationally expensive and requires high-end hardware. We therefore developed 3Dscript.server, a 3D animation software that runs as a service on dedicated, shared workstations. Using 3Dscript as the underlying rendering engine, it offers unique features not found in existing software: Rendering is performed completely server-side. The target animation is specified on the client without the rendering engine, eliminating any hardware requirements client-side. Still, defining an animation is intuitive due to 3Dscript’s natural language based animation description. We implemented a new OMERO web app to utilize 3Dscript.server directly from the OMERO web interface; a Fiji client to use 3Dscript.server from Fiji for integration into image processing pipelines; and batch scripts to run 3Dscript.server on compute clusters for large scale visualization projects.

Availability: Source code and documentation is available at https://github.com/bene51/omero_3Dscript, https://github.com/bene51/3Dscript.server and https://github.com/bene51/3Dscript.cluster.

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Supplementary information: Supplementary data are available at Bioinformatics online.

Today, there is an increasing endeavor to enable remote work wherever possible. Still, for creating 3D animations, users need physical access to a dedicated rendering computer, as the only alternative, screen-sharing, often lacks the required responsiveness. To our knowledge, no software exists that runs as a service, to which users can submit animation jobs from remote. The reason for this gap is the way existing software creates 3D animations: The user adjusts the state of the 3D scene, including orientation, color, etc., for different time points, in keyframes. The rendering engine then creates a movie by interpolating between them. Keyframes therefore constitute a necessary input for the animation service. Creating them, however, is interactive and therefore requires the rendering engine and also the corresponding hardware on the client.

Recently, we have presented 3Dscript (Schmid et al., 2019), where textual instructions, written in a natural-language based syntax (“From frame 0 to frame 100 rotate by 70 degrees horizontally”), describe and define arbitrarily complex animations and thereby replace keyframes. 3Dscript fulfills two criteria that make it ideally suited for a rendering framework based on a client-server architecture: Animations are defined as human-readable text that gives a good idea of the rendering result even without rendering engine and preview, and this text is composed without any hardware requirements (as it is text only). We used this fact to develop a framework that for the first time creates 3D animations purely server-side.

Here we introduce 3Dscript.server, which runs a 3D rendering server, implemented as an ImageJ/Fiji plugin (Rueden et al., 2017; Schindelin et al., 2012; Schneider et al., 2012) with 3Dscript as the underlying framework. We present three client implementations. (i) 3Dscript client, a Fiji client for seamless integration into image analysis workflows. (ii) OMERO.3Dscript, a web application for the image management software OMERO (Allan et al., 2012), and (iii) 3Dscript.cluster, to run large-scale 3D animation projects on a high-performance compute cluster (Suppl. Fig. 1).

Closest related to the current work is ClearVolume (Royer et al., 2015), for remotely observing in real-time data acquisition on a volumetric microscope; FPBioimage (Fantham and Kaminski, 2017), for collaborative 3D visualization of biomedical images in a web browser; and BigDataViewer (Pietzsch et al., 2015), for visualizing arbitrarily-sized datasets. In all three applications input datasets are loaded from a server but rendered client-side.

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With the animation text being written in natural English language, it may even be entered conveniently using speech recognition.

### 3Dscript.cluster - Running 3Dscript.server on an HPC cluster

To create 3D animations on a larger scale, 3Dscript.server also runs on compute clusters. Different time points of time-lapse data or different datasets of image collections are processed in parallel on distinct nodes, which reduces processing time significantly. We developed scripts for submitting rendering tasks to the “Emmy” compute cluster of the University of Erlangen-Nuremberg, which includes ten nodes with at least one graphics processing unit (GPU) required for 3Dscript. The provided batch scripts are written for the Tongue job management system (Adaptive Computing Inc.), but are easily adapted to different systems.

With 3Dscript.server, it is finally possible to create high-quality scientific 3D animations “on-the-go”, e.g. on a tablet PC while discussing a poster on a conference, instead of sitting in front of a high-end workstation.

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### References

Allan, C., Burel, J. M., Moore, J., Blackburn, C., Linkert, M., Loyton, S., MacDonald, D., Moore, W. J., Neves, C., Patterson, A., Potter, M., Tarkowska, A., Lorringer, B., Avondo, J., Lasterdi, I., Luaus, L., Leo, S., Hands, K., Hay, R. T., Patwardhan, A., Best, C., Kleywegt, G. J., Zanetti, G., and Swedlow, J. R. (2012). OMERO: Flexible, model-driven data management for experimental biology. *Nature Methods*, 9(3), 245–253.

Bardenbacher, M., Ruder, B., Britzen-Laurent, N., Schmid, B., Wülffner, M., Naschberger, E., Schul, M., Müller, W., Günter, C., Becker, C., Städel, M., and Tripal, P. (2019). Permeability analyses and three dimensional imaging of interferon gamma-induced barrier disintegration in intestinal organoids. *Stem Cell Research*, 35.

Fantham, M. and Kaminski, C. F. (2017). A new online tool for visualization of volumetric data. *Nature Photonics*, 11(2), 69.

Frisch, T., Saalfeld, S., Preibisch, S., and Tomancak, P. (2015). BigDataViewer: visualization and processing for large image data sets. *Nature Methods*, 12(6), 481–483.

Royer, L. A., Weigert, M., Günter, U., Maghelli, N., Jag, F., Shaltarani, I. F., and Myers, E. W. (2015). *ClearVolume*: open-source live 3D visualization for light-sheet microscopy. *Nature Methods*, 12(6), 480–481.

Rueden, C. T., Schindelin, J., Hiner, M. C., DeZonia, B. E., Walter, A. E., Arena, E. T., and Eliceiri, K. W. (2017). *ImageJ2*: ImageJ for the next generation of scientific image data. *BMC Bioinformatics*, 18(1), 529.

Schindelin, J., Arganda-Carreras, I., Frise, E., Kaynig, V., Longair, M., Pietzsch, T., Preibisch, S., Rueden, C., Saalfeld, S., Schmid, B., Timirove, J. Y., White, D. J., Hartenstein, V., Eliceiri, K., Tomancak, P., and Cardona, A. (2012). Fiji: An open-source platform for biological-image analysis. *Nature Methods*, 9(7), 676–682.

Schmid, B., Tripal, P., Faufel, T., Kersten, C., Ruder, B., Grüneboom, A., Huisken, J., and Tripal, P. (2019). 3Dscript: animating 3D/4D microscopy data using a natural-language-based syntax. *Nature Methods*, 16(6), 278–280.

Schneider, C. A., Rasband, W. S., and Eliceiri, K. W. (2012). *NIH Image to ImageJ*: 25 years of image analysis. *Nature Methods*, 9(7), 671–675.

Voigt, F. F., Kirschenbaum, D., Platonova, E., Pagis, S., Campbell, R. A., Kastli, R., Scarratt, E., Egili, L., van der Bong, A., Bethge, F., Haennel, K., Fritz, N., Topiko, T., Perin, P., Hiller, D., Hildebrand, S., Schuur, A., Roebroeck, A., Roska, B., Stoeckli, E. T., Pizzala, R., Renier, N., Zeilhofer, H. U., Karayannis, T., Ziegler, U., Bati, L., Holtmaat, A., Lüscher, C., Aguzzi, A., and Helmchen, F. (2019). The mesoSPIM initiative: open-source light-sheet microscopes for imaging cleared tissue. *Nature Methods*, 16(11), 1105–1108.