

INTRODUCTION

Importance of DiVE Visualization Tool

- Visualization tools for tractography are important for displaying complexities of white matter pathways
 - Helps researchers and clinicians understand an individual brain's structural connectivity
 - Display population based findings for neurological and psychiatric conditions
 - Supports statistics-based visualization
 - Create high-quality images
 - Simultaneous visualization of bundle specific meshes, volumes or masks, and streamlines or tracts.
- There is no tool as comprehensive and versatile available.

DiVE Usage

- It allows users to visualize tracts in various formats (TRK, TCK, TRX).
- Binary masks in NIFTI format, can be visualized in specific a color and multi labeled mask.
- Meshes in VTK format using specific colors and colors based on masks.
- Users also have the flexibility to load multiple Regions of Interest (ROIs) in different combinations
- Visualize a single type of data mesh, mask, or tract) or combination of types.
- Users can toggle between 3D visualization using a glass brain 2D brain slices in different orientations and even saving the output by specifying a designated path.

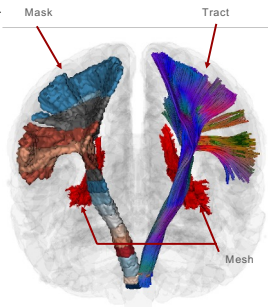


Figure 1. visualization of tracts colored based on their direction, a mask using a threshold and colored based of t-value stats, and meshes in 3D

METHODS

- We have used the Free Unified Rendering library in pPython (FURY) a high-performance scientific visualization library [1] to create the visualization results.
- The user can give a 3D region of interest label image in NIFTI format and the tool will render it as a set of 3D contours. (Figure 2A)
- Tract rendering can be conducted across all common formats (trk, tck, trx, vtk), with user defined coloring options, as well as available defaults. (Figure 2B)
- Each fiber tract is displayed as tubes with a user-defined width.
- The tool applies either the color specified by the user or a random color for single labeled masks and chooses a set of distinct colors for multi-labeled masks using "distinctipy" [2] or uses the colormap specified by the user. (Figure 2C)
- A mesh (vtk) is rendered as a surface mesh using pyVista [3] polydata inherited from Python VTK representing the geometry of 3D objects using a combination of points, vertices, lines, and polygons. (Figure 2D)
- DiVE also allows for the overlay of NIFTI masks and surface meshes on the fiber tracts, which can map scalar values to color or opacity, providing insights into tissue microstructure.
- The tool supports backgrounds using either a 3D glass brain or 2D slices.
- Visualization can be done in any stereotaxic space.

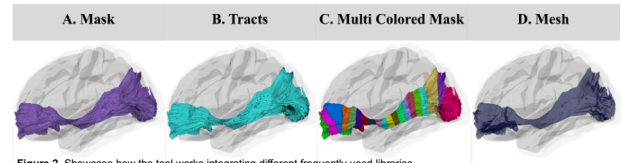


Figure 2. Showcase how the tool works integrating different frequently used libraries

RESULTS

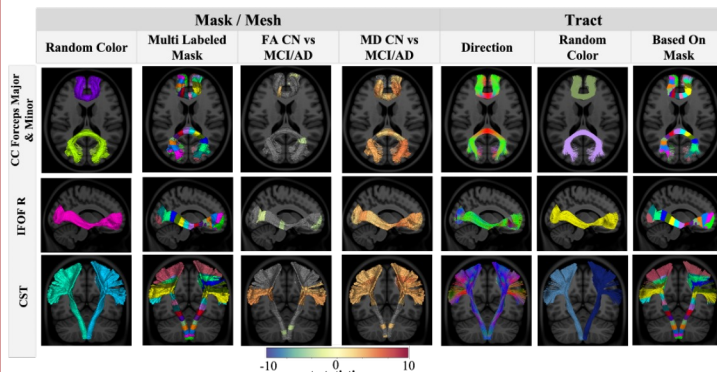




Figure 3. Diverse visualization capabilities within the tool. Random colors can be assigned to mask, mesh, or tract elements. The tool supports the visualization of multi-labeled masks, multi-labeled mesh, and tracts based on a mask and tracts based on their direction. Additionally, t-statistics along tracts are employed for bundles segmented, with colored areas indicating significant associations ($P_{FDR} < 0.05$) with clinical impairment [4].

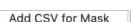
- The associations of fractional anisotropy (FA) and mean diffusivity (MD) with clinical impairments (MCI/AD) compared to cognitively normal (CN) individuals, are derived from the MeTA [4]. T-values for the MeTA 25% core volume along the segmented bundles, including (CST, IFOF_R, and CC major and minor), are presented in (Figure 3). Regions colored in the visualizations indicate significant associations between MCI/AD and CN, while gray regions denote no significant associations.
- DiVE's 3D visualization feature allows users to render complex fiber structures in 3D space
- Enables viewing of fiber bundles from different angles and perspectives, providing a comprehensive understanding of their spatial distribution.
- DiVE is a dynamic open-source initiative, operating across multiple platforms, and we anticipate continuous development and active community engagement.
- Python integration allows for easy scripting, a high degree of flexibility and automation
- DiVE is compatible with various neuroimaging file formats, ensuring seamless integration of existing data.

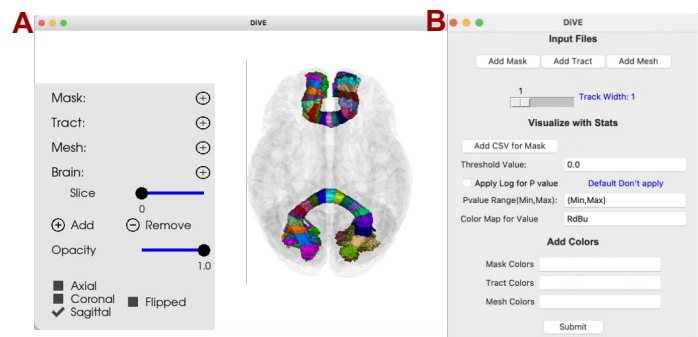
Figure 4A All the options available to a user to adjust what they have visualized. Allowing them flexibility to view and save the results based on their specific needs. B All the options available after to add ROIs. If user wants to load more ROI's or misses something then can add ROIs similar to the command line using the GUI interface. Also they can remove unnecessary ROIs.

User Interface (UI) (Figure 4A)

- Different buttons to change the current selected ROI based on its type (Mask, Tract, Mesh, Background Brain)
- A slider to change the brain slice for 2D brain allowing user to precisely control the slice in view.
- Add button to add more ROIs on the same screen  Add
- Remove button to remove the current selected ROI  Remove
- A slider to change the opacity of the current selected ROI
- Buttons to toggle between different views

User Interface (UI) (Figure 4B)

- Choose which type of ROI the user wants to add a Mask, Tract or Mesh.
- Color the ROI mask using a file with statistical (or other) values of interest using  Add CSV for Mask
- Options to threshold values provided in the CSV, apply a Log10 transformation for P values and set the range for the color map
- Choose any color to apply on the specific files, either by using the name e.g (red) or by hex-code (#FF0000)
- Multiple files (Mask, Tract, Mesh) of either same type or different types can be provided



CONCLUSION

- DiVE is available at <https://github.com/USC-LoBeS/DiVE> or by scanning the QR code
- It complements existing toolboxes with a range of customization options
- It gives users flexibility to work both through command line and using a graphical user interface
- It supports files in multiple tractography formats
- Available open source for integration into commonly used diffusion software packages

Please test for your diffusion visualization needs and give us your valuable feedback!



REFERENCES

1. E. Garyfalidis et al., "FURY: advanced scientific visualization," J. Open Source Softw., vol. 6, no. 64, p. 3384, Aug. 2021.
2. J. Roberts, J. Crall, K.-M. Ang, and Y. Brandt, "alan-turing-institute/distinctipy: v1.2.3. 2023," doi: 10.5281/zenodo.8355862.
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