

SuMRak 0.9 BETA Manual v1.1

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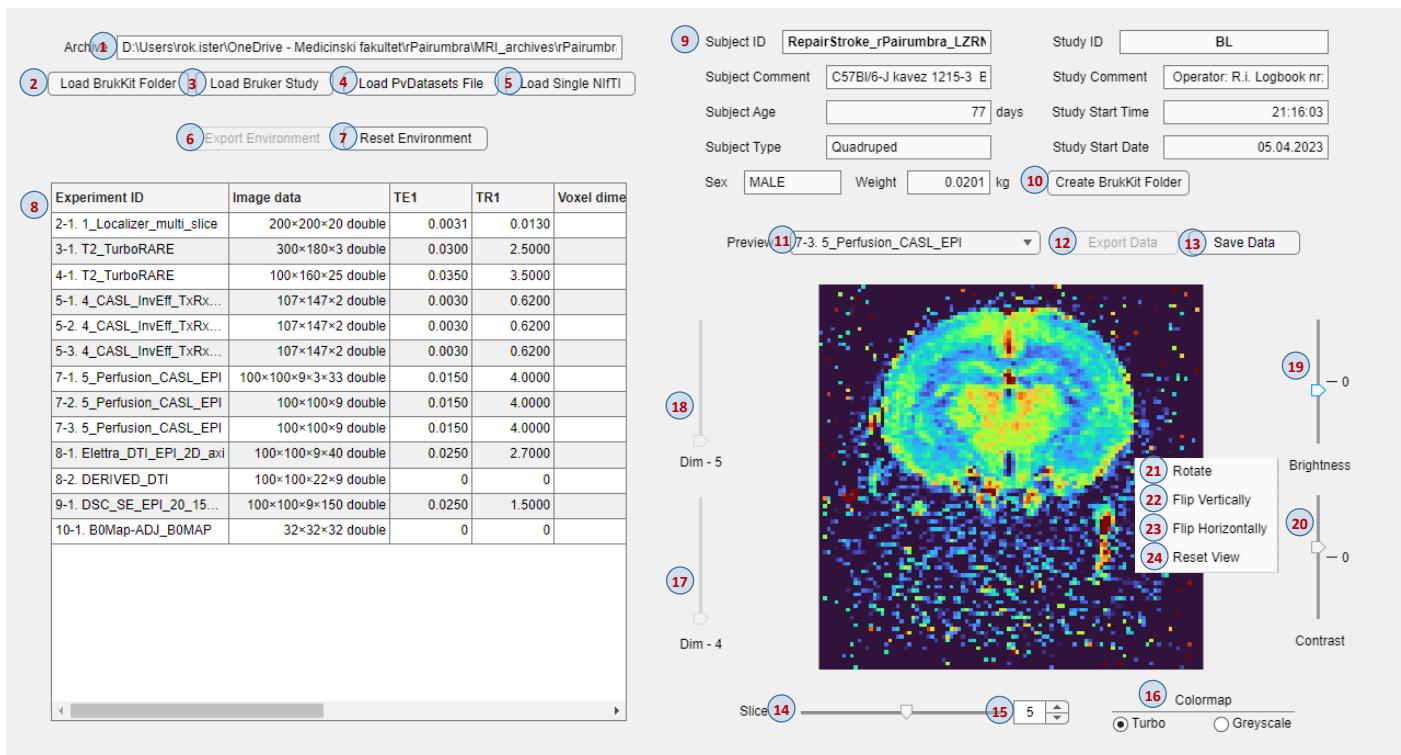
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1. Preview tab



1.1. Archive file text box

Prints the file location of the imported PvDatasets file, loaded SuMRak folder or imported Bruker study folder.

1.2. Load SuMRak folder button

Loads a SuMRak export folder from a previous session. Enables the user to continue data analysis where it has been left off or trace back steps in data analysis pipeline. After a SuMRak folder is chosen, the application loads all originally imported experiments from raw Bruker study folder or PvDatasets Bruker archive file with their respective image data and metadata (1.8)(1.9), as well as experiments derived from original data (segmented data, registered data...).

1.3. Load Bruker study button

Loads a standard Bruker study folder obtained either directly from Bruker console or extracted from a PvDatasets archive file. After a study is selected, recursively loads all experiments in the study and populates the experiment table (1.8) and study/subject info fields (1.9). Also updates the dropdowns in "Preview", "Segmenter" and "Parameter Maps" tabs.

1.4. Load PvDatasets file button

First, deletes all temporary files in %temp%\SuMRak folder. Resets the workspace and prompts the user to select a Bruker archive file with *.PvDatasets extension. Unpacks the contents of the archive to %temp%\SuMRak folder. In case of a subject archive file, prompts the user again to select a desired study folder to load. After a study is selected, recursively loads all experiments in the study and populates the experiment table (1.8) and study/subject info fields (1.9). Also updates the dropdowns in "Preview", "Segmenter" and "Parameter Maps" tabs.

1.5. Load singe NifTI

Loads a single NifTI file into application memory and puts it into experiment table (1.8). Doesn't reset the current environment thus enabling the user to include a single custom experiment in the current working study. User is advised to manually input experiment properties (voxel dimensions, TE, TR...) into its respective row in the experiment table (1.8) for SuMRak to be able to handle the experiment properly.

1.6. Export environment button

Exports or saves the current environment which consists of all originally imported experiments from raw Bruker study folder or PvDatasets Bruker archive file with their respective image data and metadata (1.8)(1.9), as well as experiments derived from original data (segmented data, registered data...). Meant to be used as a way of saving the current application memory in order to be accessed in a later session using "Load SuMRak folder" button (1.2).

1.7. Reset environment button

Deletes everything in temporary memory, clears the experiment table and all image panels.

1.8. Experiment table

Displays individual experiment properties in a tabular format. Values are editable in case some info needs manual correction.

- Experiment ID – name of the experiment preceded by the experiment and processing number: <exp.nr.> – <proc.nr.>. <exp.ID>
- Image data – structure of the loaded image data.
- TE1 – [seconds] echo time of the experiment. In case of multiple echo times, only first is shown.
- TR1 – [seconds] repetition time of the experiment. In case of multiple repetition times, only first is shown.
- Voxel dimensions X, Y and Slice thickness – dimensions of a voxel in the experiment.
- Slice gap – gap between slices in case of a multislice experiment.
- Dimension units – units in which “Voxel dimensions”, “Slice thickness” and “Slice gap” are shown.
- Rotation matrix – 3x3 rotation matrix of the imaged volume for proper exporting to NifTI header metadata.

1.9. Study/Subject info fields

Info fields directly imported from Bruker imageObj metadata. The fields are populated from the last experiment in the loaded study.

1.10. Create export folder button

Prompts the user to select a folder in which an export folder will be created with subject and study IDs (<subjectID>_<studyID>). Automatically exports the experiment table to a Microsoft Excel file “data_info.xlsx” and subject/study info to plaintext “info.txt” file. Prerequisite for exporting NifTI images in SuMRak. In case there are selected experiments in any of experiment selection dropdowns, their respective export buttons will be enabled upon creation of the export folder.

1.11. Preview dropdown

Dropdown select an image to preview. Linked to original imported data from experiment table.

1.12. Export data button

Exports the selected image data as a singular NifTI file to previously created export folder. NifTI image is named as experiment ID from which image is exported. Disabled by default, requires user to create export folder (1.10) first.

1.13. Save data button

Saves the selected image to application memory. Used for image data selection on “Volumetry” and “Registration” tabs in case the user does not wish to segment the image beforehand.

1.14. Slice slider

Discrete slider used to scroll through 3rd dimension of the selected image data (usually Z dimension a.k.a. slice selection). Automatically updates the Slice spinner (1.15). User can use left and right arrow keys to scroll to previous and following slices, respectively.

1.15. Slice spinner

Spinner used to scroll through 3rd dimension of the selected image data (usually Z dimension a.k.a. slice selection). Automatically updates the Slice slider (1.14). User can use left and right arrow keys to scroll to previous and following slices, respectively.

1.16. Colormap radio buttons

Allows the user to change the color lookup table of the selected experiment. Currently implemented a classic “Greyscale” view and a “Turbo” view which maps image intensities to a color heat-gradient.

1.17. 4th dimension slider

Discrete slider used to scroll through 4th dimension of the selected image data. Only enabled if the selected image data size in the 4th dimension is higher than 1.

1.18. 5th dimension slider

Discrete slider used to scroll through 5th dimension of the selected image data. Only enabled if the selected image data size in the 5th dimension is higher than 1.

1.19. Brightness slider

Continuous slider which controls the brightness of the displayed image. Defaults to 0. Can be reset using “Reset view” button available via image panel context menu (right click on the image).

1.20. Contrast slider

Continuous slider which controls the contrast of the displayed image. Defaults to 0. Can be reset using “Reset view” button available via image panel context menu (right click on the image).

[1.21. Rotate context button](#)

Context menu button which rotates the image 90 degrees clockwise.

[1.22. Flip vertically context button](#)

Context menu button which flips the image around the vertical axis.

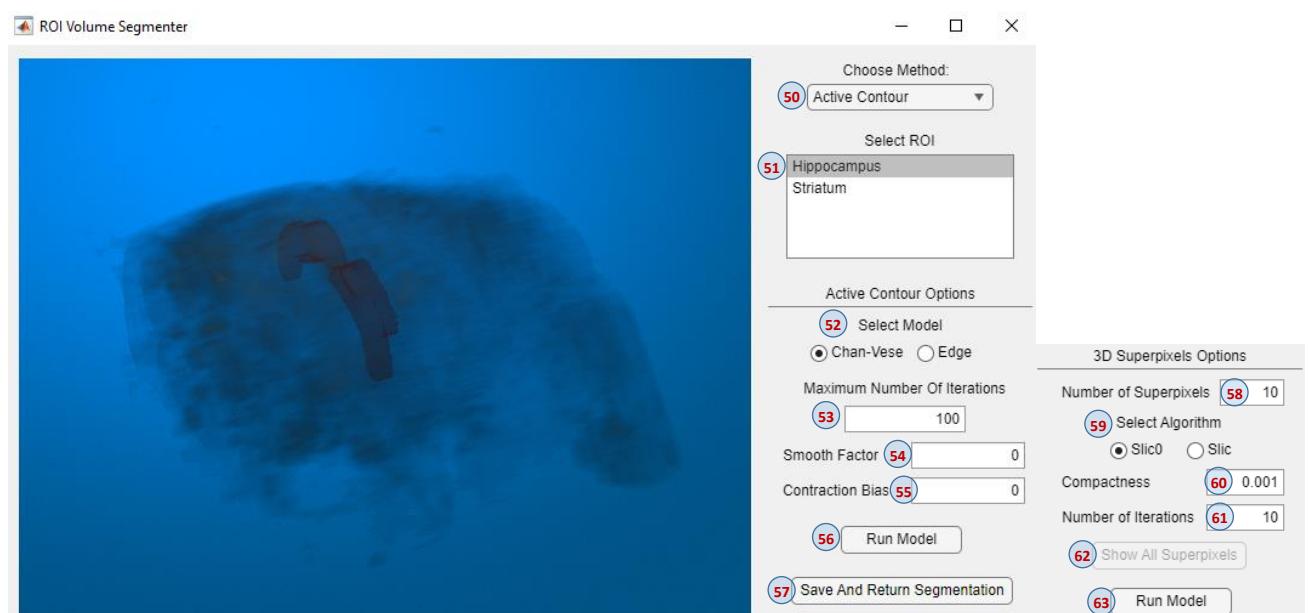
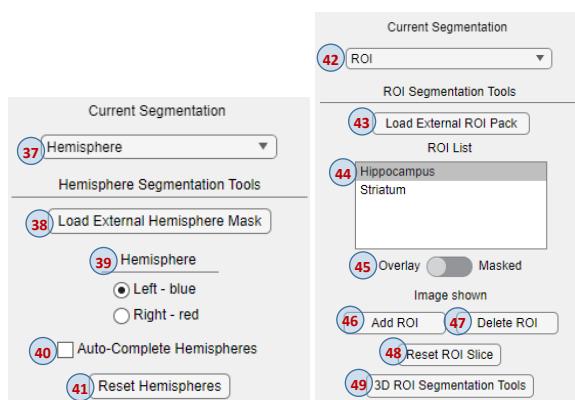
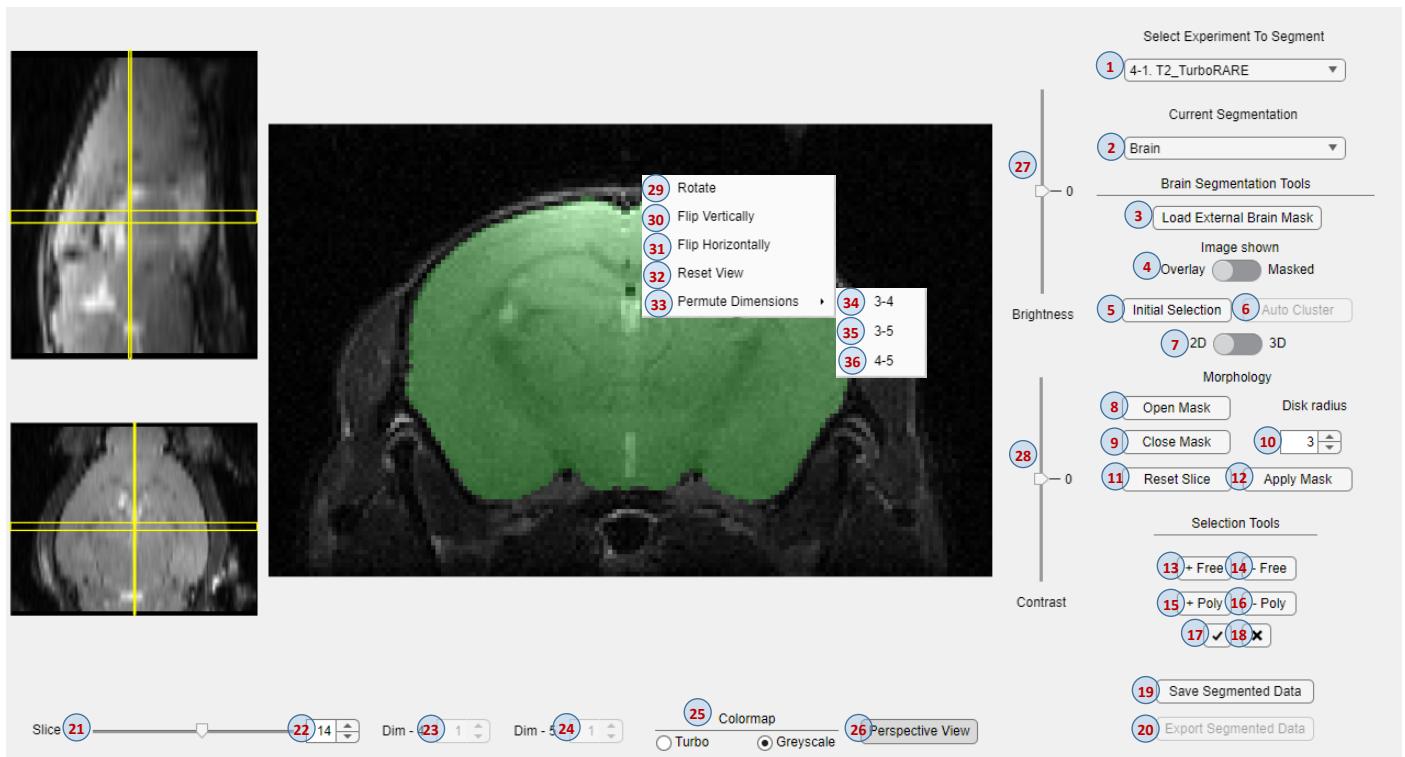
[1.23. Flip horizontally context button](#)

Context menu button which flips the image around the horizontal axis.

[1.24. Reset view context button](#)

Context menu button which resets image zoom (currently not available on “Preview” tab), brightness and contrast of the displayed image data.

2. Segmenter tab



2.1. Segmenter dropdown

Dropdown select an image to segment. Linked to original imported data from experiment table.

2.2. Segmentation strategy dropdown

Dropdown that lets the user decide what approach to use when segmenting. Currently available options are “Brain”, “Hemisphere” and “ROI”. “Hemisphere” option is enabled only after brain segmentation. “ROI” option is a general segmentation strategy which can be used for storing any other regions of interest.

2.3. Load external mask button

Enables user to provide an existing brain mask in NifTI file format. Used brain mask gets automatically applied.

2.4. Image shown switch

Switches between different display methods of current image data. In “Overlay” mode, currently active ROI is overlaid over the original image as a colored transparent area, with color differing across different segmentation strategies. In “Masked” mode, currently active ROI is applied onto the original image as an image mask.

2.5. Initial selection button

First step in brain segmentation pipeline. Using free-hand tool, the user is supposed to roughly outline the brain area on the currently displayed image. After the initial brain selection is made, the “Auto Cluster” button (2.6) is enabled and it is the next step in this segmentation strategy.

2.6. Auto cluster button

Second step in brain segmentation pipeline. After the user makes the initial selection using the “Initial Selection” button (2.5), the “Auto Cluster” button is used to apply a k-means clustering algorithm on the chosen area and take the cluster with the highest mean intensity as the ROI for manual correction in the further steps of this segmentation strategy. If “2D/3D segmentation switch” (2.7) is set to 3D, user is prompted for slice range to perform 3D auto clustering on and then performs 3D k-means clustering on the selected volume.

2.7. 2D/3D segmentation switch

When using “Brain” segmentation strategy, by putting the switch to “3D”, user can use the current initial selection to perform auto clustering and morphological opening/closing operations on a volume consisting of multiple adjacent slices. Disabled when segmenting single-slice experiments. Switching the “Brain” segmentation strategy to 3D, “Auto cluster” (2.6), “Open mask” (2.8), “Close mask” (2.9), “Reset slice” (2.11) and “Apply slice” (2.12) buttons transform into their respective 3D variants.

2.8. Open mask button

Recommended third step in brain segmentation pipeline. The “Open mask” button applies morphological opening of the currently active ROI. Morphological opening operation is an erosion followed by dilation using the same structuring element chosen to be a disk with radius defined in “Disk radius” edit field (2.10). If “2D/3D segmentation switch” (2.7) is set to 3D, morphological opening operation is performed on the whole mask volume.

2.9. Close mask button

Recommended fourth step in brain segmentation pipeline. The “Close mask” button applies morphological closing of the currently active ROI. Morphological closing operation is a dilation followed by erosion using the same structuring element chosen to be a disk with radius defined in “Disk radius” edit field (2.10). If “2D/3D segmentation switch” (2.7) is set to 3D, morphological closing operation is performed on the whole mask volume.

2.10. Disk radius edit field

Customization option that changes the disk radius for operations of dilation and erosion used in “Open mask” (2.8) and “Close mask” (2.9) functions of the segmenter tab.

2.11. Reset slice button

Pressing the “Reset slice” button clears all ROI data for currently displayed image slice, effectively undoing all segmentation progress for the chosen slice. If “2D/3D segmentation switch” (2.7) is set to 3D, button is renamed to “Reset all” signifying that pressing it resets the brain mask for the whole loaded experiment volume.

2.12. Apply mask button

Applies the currently active ROI as the chosen brain mask on the currently displayed slice only. Pressing this button enables the “Hemisphere” segmentation strategy in the “Segmentation strategy” dropdown (2.2). If “2D/3D segmentation switch” (2.7) is set to 3D, button is renamed to “Apply all” signifying that pressing it applies the brain mask for the whole loaded experiment volume.

2.13. Add free-hand ROI button

Enables the user to add an area to the currently active ROI regardless of the current segmentation strategy used. After single-stroke selection, the segmenter fits a spline with arbitrary number of points which can be clicked and dragged to further refine

the selection made. If the selection is satisfactory, user can confirm addition using “Confirm ROI” button (2.17) or cancel it using “Cancel ROI” button (2.18).

[2.14. Subtract free-hand ROI button](#)

Enables the user to subtract an area from the currently active ROI regardless of the current segmentation strategy used. After single-stroke selection, the segmenter fits a spline with arbitrary number of points which can be clicked and dragged to further refine the selection made. If the selection is satisfactory, user can confirm subtraction using “Confirm ROI” button (2.17) or cancel it using “Cancel ROI” button (2.18).

[2.15. Add polygon ROI button](#)

Enables the user to add an area to the currently active ROI regardless of the current segmentation strategy used. After multi-click selection, drawn polygon points can be clicked and dragged to further refine the selection made. If the selection is satisfactory, user can confirm addition using “Confirm ROI” button (2.17) or cancel it using “Cancel ROI” button (2.18).

[2.16. Subtract polygon ROI button](#)

Enables the user to subtract an area from the currently active ROI regardless of the current segmentation strategy used. After multi-click selection, drawn polygon points can be clicked and dragged to further refine the selection made. If the selection is satisfactory, user can confirm subtraction using “Confirm ROI” button (2.17) or cancel it using “Cancel ROI” button (2.18).

[2.17. Confirm ROI button](#)

Confirms the selection made using general ROI editing tools (2.13-2.16) and either add or subtracts the selection from the currently active ROI, depending on the tool previously chosen by the user.

[2.18. Cancel ROI button](#)

Cancels the selection made using general ROI editing tools (2.13-2.16). Currently active ROI remains unchanged.

[2.19. Save segmented data button](#)

Saves the selected image and its respective masks to application memory. Updates dropdown menus on “Volumetry” and “Registration” tabs. Necessary step for volumetry calculations and a recommended step in image registration pipelines.

[2.20. Export segmented data button](#)

Exports the selected image data and its respective masks as individual NifTI files to previously created export folder. NifTI segmented image is named after experiment ID from which image is segmented. NifTI masks have *_Brain, *_Hemisphere and *_<customROI> suffixes added to file names for brain, hemisphere and custom ROI masks, respectively. Disabled by default, requires the user to create an export folder (1.10) on preview tab first.

[2.21. Slice slider](#)

Discrete slider used to scroll through 3rd dimension of the selected image data (usually Z dimension a.k.a. slice selection). Automatically updates the Slice spinner (2.22). User can use left and right arrow keys to scroll to previous and following slices, respectively.

[2.22. Slice spinner](#)

Spinner used to scroll through 3rd dimension of the selected image data (usually Z dimension a.k.a. slice selection). Automatically updates the Slice slider (2.21). User can use left and right arrow keys to scroll to previous and following slices, respectively.

[2.23. 4th dimension spinner](#)

Spinner used to scroll through 4th dimension of the selected image data. Only enabled if the selected image data size in the 4th dimension is higher than 1.

[2.24. 5th dimension spinner](#)

Spinner used to scroll through 5th dimension of the selected image data. Only enabled if the selected image data size in the 5th dimension is higher than 1.

[2.25. Colormap radio buttons](#)

Allows the user to change the color lookup table of the selected experiment. Currently implemented a classic “Greyscale” view and a “Turbo” view which maps image intensities to a color heat-gradient.

[2.26. Perspective view state button](#)

When pressed, draws a crosshair over GUI for user to select the desired X and Y position where the active experiment should be resliced. After selection, the main segmentation view panel is resized to accommodate for 2 smaller helper screens showing orthogonally resliced experiment with yellow crosshairs depicting current Z and X or Z and Y locations in the active volume.

Thickness of the yellow crosshair arms depicts the relative slice thickness in each dimension. Button stays pressed until user clicks it again to hide helper screens.

[2.27. Brightness slider](#)

Continuous slider which controls the brightness of the displayed image. Defaults to 0. Can be reset using “Reset view” button available via image panel context menu (right click on the image).

[2.28. Contrast slider](#)

Continuous slider which controls the contrast of the displayed image. Defaults to 0. Can be reset using “Reset view” button available via image panel context menu (right click on the image).

[2.29. Rotate context button](#)

Context menu button which rotates the image 90 degrees clockwise.

[2.30. Flip vertically context button](#)

Context menu button which flips the image around the vertical axis.

[2.31. Flip horizontally context button](#)

Context menu button which flips the image around the horizontal axis.

[2.32. Reset view context button](#)

Context menu button which resets image zoom (currently not available on “Preview” tab), brightness and contrast of the displayed image data.

[2.33. Permute dimensions context submenu](#)

Context submenu which opens the available dimension permutations (2.34 – 2.36) on mouse hover.

[2.34. 3-4 permute dimensions context button](#)

Context button available through “Permute dimensions context submenu” (2.33). Permutes the 3rd and 4th dimensions of the currently selected image data and automatically updates the limits on respective sliders and spinners.

[2.35. 3-5 permute dimensions context button](#)

Context button available through “Permute dimensions context submenu” (2.33). Permutes the 3rd and 5th dimensions of the currently selected image data and automatically updates the limits on respective sliders and spinners.

[2.36. 4-5 permute dimensions context button](#)

Context button available through “Permute dimensions context submenu” (2.33). Permutes the 4th and 5th dimensions of the currently selected image data and automatically updates the limits on respective sliders and spinners.

[2.37. Segmentation strategy dropdown](#)

Same as 2.2. After “Hemisphere” strategy is selected from the dropdown menu, hemisphere segmentation tools become available (2.39 – 2.41).

[2.38. Load external hemisphere mask button](#)

Allows the user to load hemisphere masks from a NifTI file. NifTI image needs to have 4th dimension length equal to 2, for left and right hemisphere, respectively.

[2.39. Hemisphere selection radio buttons](#)

Let the user decide if following selections are to be added or subtracted from left or right hemisphere.

[2.40. Auto-complete hemisphere selection checkbox](#)

When checked, the contralateral hemisphere will be automatically selected as the remaining non-selected area.

[2.41. Reset hemisphere button](#)

Pressing this button clears all hemisphere ROIs from the currently selected slice.

[2.42. Segmentation strategy dropdown](#)

Same as 2.2 After “ROI” strategy is selected from the dropdown menu, custom ROI segmentation tools become available (2.44 – 2.48).

[2.43. Load external ROI pack button](#)

Allows the user to load ROI masks from a NifTI file. Each 4th dimension page of the provided image is used to import separate ROIs.

[2.44. ROI list](#)

Displays all custom ROIs user has previously added with the currently selected one being highlighted. When a custom ROI is selected on the list, user can add or subtract area from ROI on the currently displayed slice by using general ROI editing tools (2.13 – 2.16).

[2.45. Image shown switch](#)

Same as 2.4

[2.46. Add ROI button](#)

First step when using custom ROI segmentation strategy. User is presented with a prompt in a popup asking the user to name the new custom ROI. After pressing “OK”, the newly named ROI is made available for selection in the “ROI list” (2.44).

[2.47. Delete ROI button](#)

Deletes the currently selected ROI on the “ROI list” (2.44).

[2.48. Reset ROI slice button](#)

Clears all area from the currently selected ROI on the currently selected image slice only. This action does not delete the currently selected ROI.

[2.49. 3D ROI segmentation tools button](#)

When clicked, opens a new window used for 3D ROI segmentation. Displays the volume of the currently selected experiment as a gradient opacity volume. When a ROI is selected from the list (2.44), it's displayed as a label overlay over the experiment volume.

[2.50. Volume segmentation method dropdown](#)

Selects the desired 3D ROI segmentation method to use. “Active contour” is a deformable model method which requires a seed ROI to be selected before running the model in order to grow it. It uses the Sparse-Field level-set method similar to that described in [1]. “3D superpixels” divides the volume into predefined number of 3D superpixels which can later be joined and selected to use as a seed for “Active contour” method or returned to main SuMRak interface for manual corrections. For more information, refer to official MATLAB documentation.

[2.51. ROI list](#)

Inherits and displays all custom ROIs created in the main SuMRak window interface.

[2.52. Active contour model selection radio buttons](#)

Selects between “Chan-Vese” and “Edge” models for use with “Active contour” 3D ROI segmentation method. “Chan-Vese” is a region-based energy model described in [2] and “Edge” is an implementation of the original geodesic active contour model described in [3]. For more information, refer to official MATLAB documentation.

[2.53. Maximum number of iterations edit field](#)

Specifies the maximum number of iterations of “Chan-Vese” model to run.

[2.54. Smooth factor edit field](#)

Parameter of “Chan-Vese” model which controls the amount of regularities in boundaries of the segmented ROI volume. Default is 0.

[2.55. Contraction bias edit field](#)

Parameter of “Chan-Vese” model which controls the model’s bias toward expanding or shrinking the ROI volume. Accepted values range from -1 to 1, with positive number biasing the volume to shrink and negative biasing the volume to expand.

[2.56. Run model button](#)

When clicked, runs the selected method with displayed parameters. “Active contour” method requires the user to previously select a ROI from the list (2.44) to be used as a seed. Run model takes the previous result ROI as an input for the next run, enabling the user to use the segmentation method iteratively.

[2.57. Save and return segmentation button](#)

When a user is satisfied with displayed results of 3D ROI segmentation, by clicking this button, all result ROIs are mirrored to SuMRak memory and user is returned back to the main SuMRak interface to continue manual segmentation or proceed with analysis pipeline. If “3D superpixels” method was used, the user is prompted to select desired superpixels to add together and the new ROI name by which to name them.

[2.58. Number of 3D superpixels edit field](#)

Specifies the number of 3D superpixels to generate in the currently active experiment volume.

[2.59. Select 3D superpixels algorithm](#) radio buttons

Selects the algorithm to use for generating 3D superpixels. “Slic0” uses SLIC0 algorithm to iteratively refine compactness, while “Slic” keeps the compactness constant during superpixel generation.

[2.60. Compactness edit field](#)

Parameter of the “3D superpixel” method that controls the shape of the generated superpixels. Higher value makes the shape of generated superpixels more regular (rectangular).

[2.61. Number of iterations edit field](#)

Number of iterations of “3D superpixel” generation method.

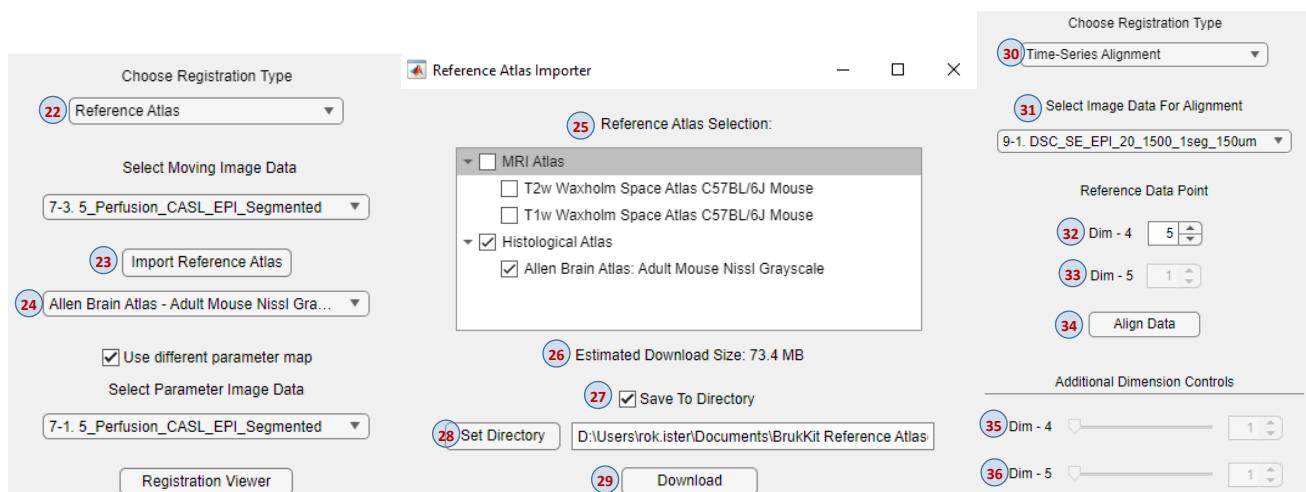
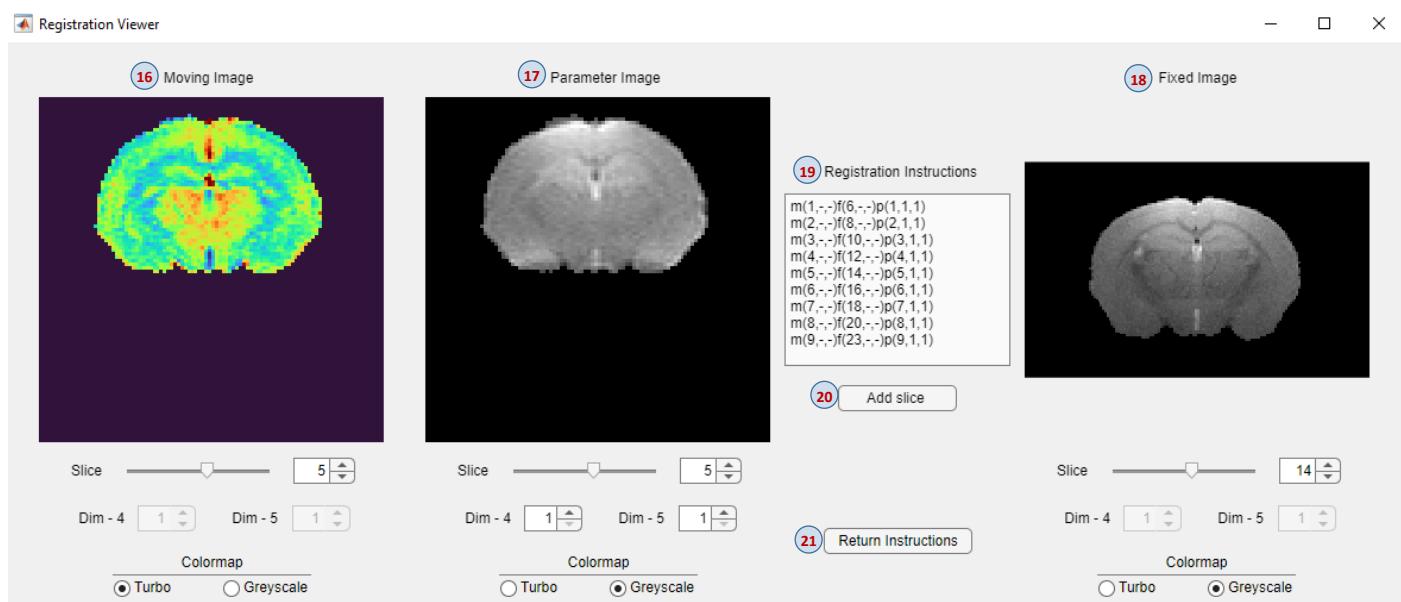
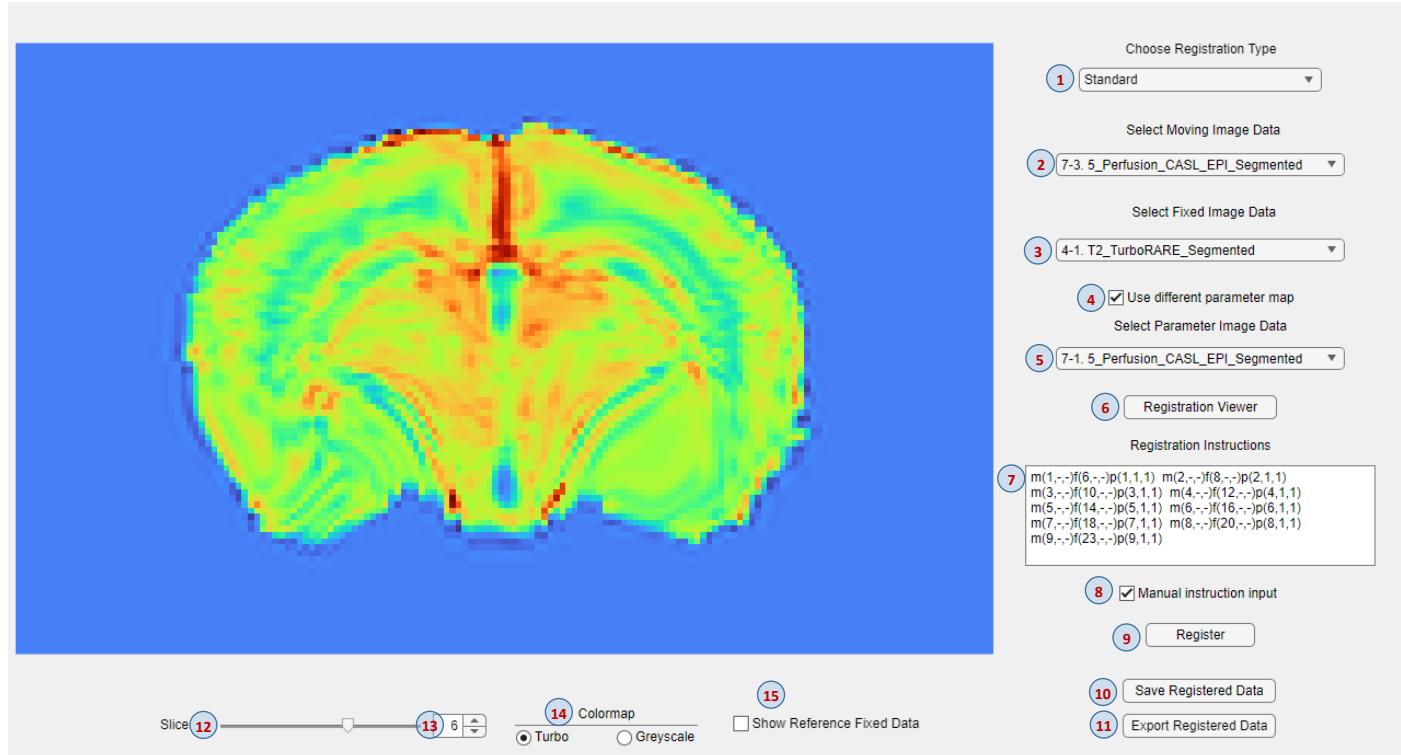
[2.62. Show all superpixels button](#)

When pressed, displays all 3D superpixels overlayed on the currently active experiment volume in arbitrary rainbow coloring.

[2.63. Run model button](#)

Runs the selected 3D ROI segmentation method with currently displayed parameters. After “3D superpixel” segmentation method finishes, all generated superpixels are overlayed on the currently active experiment volume in arbitrary rainbow coloring. ROI list (2.44) is then populated with all generated 3D superpixels, allowing the user to select to preview each one of them individually.

3. Registration tab



3.1. Registration type dropdown

Selects the desired registration style. Currently implemented options are “Standard” where user can register an experiment to another, “Reference Atlas” where user can download or import a reference atlas to register an experiment to, or “Time-series alignment” where the user can rigidly align an experiment acquired as a time sequence of volumes to account for movement artefacts.

3.2. Moving image data dropdown

Selects an image data to be registered, a.k.a. the moving image.

3.3. Fixed image data dropdown

Selects an image data to register the moving image (3.2) to, a.k.a. fixed image.

3.4. Separate parameter map checkbox

When checked, allows the user to pool registration parameters from separate image data. Useful when moving image is a non-magnitude image (i.e. when registering T₁ or T₂ maps, using calculated map as the moving image and its raw image as the parameter image data). Unchecked by default, checking this option enables “Parameter image data” dropdown (3.5).

3.5. Parameter image data dropdown

Selects parameter image data to use for calculation of registration parameters applied to the moving image, instead of the moving image itself, which is the default option (3.4). Useful when moving image is a non-magnitude image (i.e. when registering T₁ or T₂ maps, using calculated map as the moving image and its raw image as the parameter image data).

3.6. Registration viewer button

When clicked, presents the user with a new “Registration Viewer” window. Here, the user can scroll through selected moving, fixed and (optionally) parameter image data. After choosing the equivalent 3rd, 4th and 5th dimensions with respective spinners under “Moving image” (3.16), “Parameter image” (3.17) and “Fixed image” (3.18) viewers, user can add the selection to “Registration instructions list” (3.19) using “Add slice button” (3.20).

3.7. Registration instructions list

Contains all registration instructions separated with blank space, either added via “Add slice” button (3.7) or by manually editing the list by checking “Manual instruction input” checkbox (3.8). Instruction format is as follows: m(x,y,z)f(x,y,z)p(x,y,z) where m is moving image, f is fixed image, p is parameter image data and x,y,z are slice, 4th and 5th dimension indexes, respectively.

3.8. Manual instruction input checkbox

When checked, allows the user to manually input instructions in the “Registration instructions” list (3.7), save them for future reference or paste in previously used set of instructions.

3.9. Register button

Takes the combined image data from “Moving image”, “Fixed image” and “Parameter image data” dropdowns together with complete instruction list in “Registration instructions” list and passes it over to SimpleElastix, an extension of SimpleITK python module. During registration, the user is presented with a “loading” popup window. After registration finishes, the image data is automatically loaded into the image panel of the “Registration” tab. In case of multiple instructions, image data becomes a 3-dimensional volume, thus enabling the “Slice spinner” (3.13).

3.10. Save registered data button

Prompts the user to choose if fixed image mask is to be saved together with registered image data. Useful when user wishes to do volumetry on the registered image data. Saves the registered image data with fixed image mask (if chosen) to temporary application memory and adds it to dropdown menus on “Segmenter” and “Volumetry” tabs. Saved image data is named “Registered data X.”, where X is the current number of registration attempts.

3.11. Export registered data button

Exports the selected image data as a single NifTI file to previously created export folder. NifTI registered image is named “Registered data X.”, where X is the current number of registration attempts. Disabled by default, requires the user to create an export folder (1.10) on preview tab first.

3.12. Slice slider

Slider used to scroll through 3rd dimension of the selected image data (usually Z dimension a.k.a. slice selection). Disabled by default. Gets enabled when registered data with multiple instructions gets loaded into the image panel in “Registration” tab after registration successfully finishes (3.9).

[3.13. Slice spinner](#)

Spinner used to scroll through 3rd dimension of the selected image data (usually Z dimension a.k.a. slice selection). Disabled by default. Gets enabled when registered data with multiple instructions gets loaded into the image panel in “Registration” tab after registration successfully finishes (3.9).

[3.14. Colormap radio buttons](#)

Allows the user to change the color lookup table of the selected experiment. Currently implemented a classic “Greyscale” view and a “Turbo” view which maps image intensities to a color heat-gradient.

[3.15. Show reference fixed data checkbox](#)

Checking this box, a combined registered-fixed image is displayed in the Registration tab’s image container. The combined image is an algebraic multiplication between registered and fixed image data and is supposed to help the user inspect and evaluate the results of registration.

[3.16. Moving image view and selection](#)

Using the display and the underlying controls, user can select the desired equivalent slice from the moving image data to use for registration after adding it to “Registration instructions list” (3.19) using “Add slice button” (3.20).

[3.17. Parameter image view and selection](#)

Using the display and the underlying controls, user can select the desired equivalent slice from the parameter image data to use for registration after adding it to “Registration instructions list” (3.19) using “Add slice button” (3.20).

[3.18. Fixed image view and selection](#)

Using the display and the underlying controls, user can select the desired equivalent slice from the fixed image data to use for registration after adding it to “Registration instructions list” (3.19) using “Add slice button” (3.20).

[3.19. Registration instructions list](#)

Inherits and displays the registration instruction list from main SuMRak interface (3.7). The syntax of the listed commands is the same as the original one. The list is not manually editable in the “Registration viewer” window.

[3.20. Add slice button](#)

Saves the current selected dimension numbers from the spinners under “Moving image” (3.16), “Parameter image” (3.17) and “Fixed image” (3.18) viewers to “Registration instruction” list (3.19). Each next input to the list is separated with blank space from the previous. Refer to 3.7 for more info on the instruction format.

[3.21. Return instructions button](#)

Returns all added instructions from the registration instruction list in “Registration Viewer” (3.19) windows to the main SuMRak interface (3.7).

[3.22. Registration type dropdown](#)

When user selects “Reference atlas” option from the “Registration type” dropdown, the fixed image dropdown selection gets substituted by “Import reference atlas” button (3.23) and “Reference atlas selection” dropdown (3.24).

[3.23. Import reference atlas button](#)

When clicked, prompts the user to select to download a new reference atlas from the list of supported reference atlases or to import a reference atlas used in a previous SuMRak registration session. If users select the option to download the atlases, a new window is presented to the user named “Reference atlas importer”.

[3.24. Reference atlas selection dropdown](#)

Allows the user to select a downloaded/imported reference atlas to use for registration as a fixed image.

[3.25. Available reference atlases checkbox list](#)

If option to download new reference atlases has been chosen after clicking on “Import reference atlas” button (3.23), user is presented with new “Reference atlas importer” window which lists all reference atlases currently supported for use in SuMRak. User can check the adjacent checkboxes to select which atlases to download and import into SuMRak.

[3.26. Estimated download size label](#)

Shows the sum of the data sizes of the atlases checked for download and import.

[3.27. Save to directory checkbox](#)

When checked, enables the “Set directory” button (3.28) which lets the user select a preferred location for reference atlas download.

[3.28. Set directory button](#)

Prompts the user for a directory in which “SuMRak Reference Atlases” directory should be created. When imported, all atlases will be placed in that directory under separate subdirectories for each atlas imported.

[3.29. Download button](#)

Downloads the selected reference atlases on from the checkbox list (3.25) and, if “Save to directory” checkbox is checked, saves atlases into provided directory. If not, atlases are saved to temporary directory which get purged on application close.

[3.30. Registration type dropdown](#)

When registration type dropdown is set to “Time-series alignment”, registration settings elements change to a single experiment dropdown (3.31) which allows the user to select an experiment for rigid alignment throughout the 4th dimension of the image data. Reference time point can be set using reference data point spinners (3.32) (3.33).

[3.31. Image data selection for time alignment dropdown](#)

Selects an experiment that user wishes to rigidly align in time dimension. Therefore, selected experiment’s image data needs to have time points set as 4th dimension pages. Reference time point can be set using reference data point spinners (3.32) (3.33).

[3.32. 4th dimension reference data point selection spinner](#)

Selects the desired reference data point page in the 4th dimension of the selected experiment.

[3.33. 5th dimension reference data point selection spinner](#)

Selects the desired reference data point page in the 5th dimension of the selected experiment.

[3.34. Align data button](#)

On click, transfer the selected experiment with its selected reference data point over to SimpleElastix for rigid registration. Be aware that this is a time-intensive procedure which effectively runs $Z * n - 1$ number of individual rigid registration processes, where Z is the number of slices and n is the number of collected time points in the selected experiment.

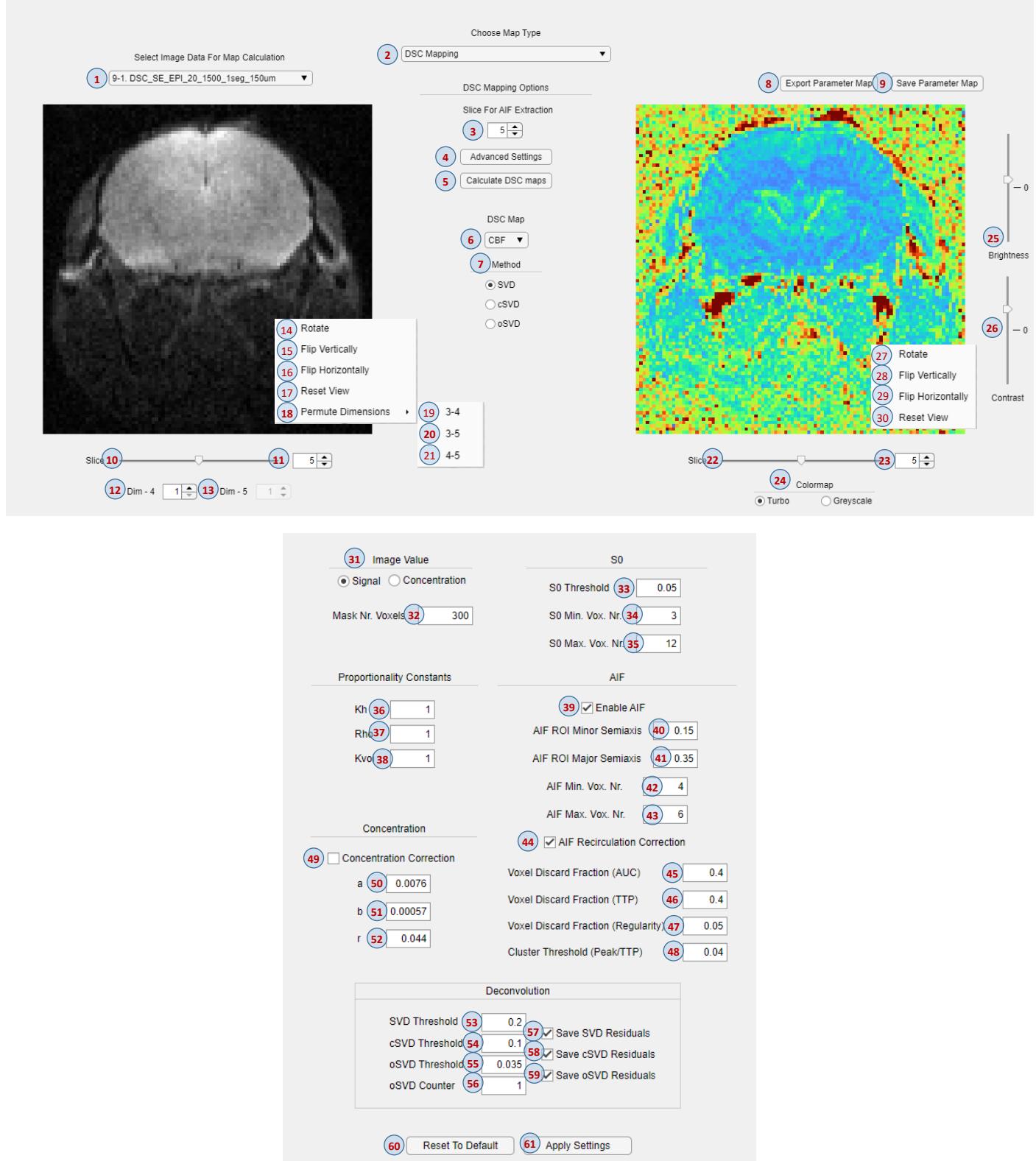
[3.35. 4th dimension additional controls \(slider and spinner\)](#)

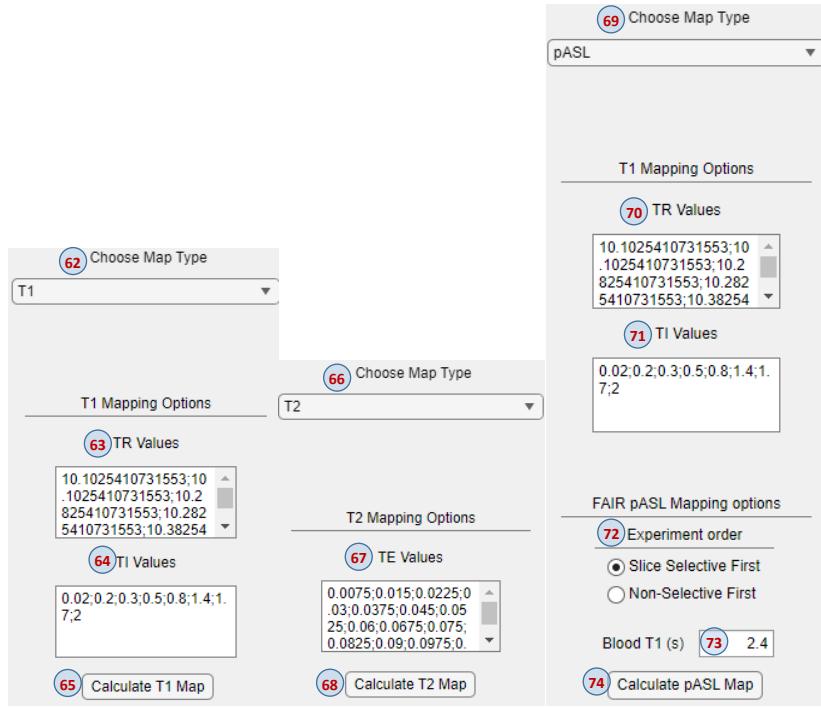
Disabled by default, gets enabled after a successful time-series alignment. Enables the user to scroll through 4th dimension of the result image data.

[3.36. 5th dimension additional controls \(slider and spinner\)](#)

Disabled by default, gets enabled after a successful time-series alignment. Enables the user to scroll through 4th dimension of the result image data.

4. Parameter maps tab





4.1. Image data for map calculation dropdown

Selects an image data to be used for parameter map calculation and displays it on the image panel beneath the dropdown for user to preview. Listed experiments to choose are original imported experiments only at the current state.

4.2. Map type selection dropdown

Selects the category of parameter map user wishes to calculate for selected image data (4.1) and presents the accompanying options for that map category.

4.3. Slice for AIF extraction spinner

Spinner with which user can manually determine which slice of the selected image data to use for AIF (arterial input function) extraction (usually the center slice of the selected image data).

4.4. Advanced settings button

Opens up a new window with all settings supported for fine tweaking of the DSC map model used for map calculation. After manual input in the “Advanced settings” window, user can save the settings using “Apply settings” button (4.61) or reset all values to default using “Reset to default” button.

4.5. Calculate DSC maps

Button which compiles the selected image data with its imported TE and TR and associated settings for DSC mapping in order to pass it over properly to “DSC-mri-toolbox”, a MATLAB script publicly available on GitHub made by @peruzzod and @marcocastellaro ([marcocastellaro/dsc-mri-toolbox: Dynamic Susceptibility Contrast MRI toolbox - AIF selection, deconvolution and leakage correction \(github.com\)](https://github.com/marcocastellaro/dsc-mri-toolbox)). AIF extraction tool used is made by Perruzzo *et al.* [7]. User can select the preferred deconvolution model to use for map calculation with “Deconvolution method” radio buttons (4.7). Available deconvolution methods are SVD(singular value decomposition), cSVD(circular-block singular value decomposition) and oSVD(circular-block singular value decomposition with oscillation index). Leakage correction is implemented in accordance with Boxerman *et al.* [8]. Please refer to the provided GitHub repository’s readme or relevant cited work for more information.

4.6. DSC map dropdown

Dropdown for selection of the desired parameter map to display on the right-hand image panel. Available parameter maps are CBF(cerebral blood flow), CBV(cerebral blood volume) and MTT(median transfer time). Disabled by default, becomes available after DSC map calculation exits successfully and the default CBF map gets displayed on the right-hand image panel. The values displayed on parameter maps depend on the advanced settings of the DSC mapping tool (4.4). Absolute values will be displayed only if “Proportionality constants” (4.36 – 4.38) have been set to values lower than 1 prior to DSC map calculation. (Set to 1 by default, which defaults the parameter maps to rCBF, rCBV and rMTT to be exact).

4.7. Deconvolution method radio buttons

Implied to be set before “Calculate DSC maps” button is pressed. Defaults to SVD(singular value decomposition). Other available options are cSVD(circular-block singular value decomposition) and oSVD(circular-block singular value decomposition with oscillation index). Please refer to GitHub repository’s readme or relevant cited work provided in 4.5 for more information.

[4.8. Export parameter map button](#)

Exports the parameter map image data displayed on the right-hand image panel as a single NifTI file to the previously created export folder. NifTI parameter map image is named after experiment ID from which image is segmented with map name added as suffix (<experimentID>_<mapname>.nii). Disabled by default, requires the user to create an export folder (1.10) on preview tab first.

[4.9. Save parameter map button](#)

Saves the parameter map image data displayed on the right-hand image panel to temporary application memory. Updates dropdown menus on “Segmeter”, “Volumetry” and “Registration” tabs. This way, the user can continue to segment the new parameter map or use it for registration purposes.

[4.10. Slice slider](#)

Discrete slider used to scroll through 3rd dimension of the selected image data for map calculation (usually Z dimension a.k.a. slice selection). Automatically updates the Slice spinner (4.11).

[4.11. Slice spinner](#)

Spinner used to scroll through 3rd dimension of the selected image data for map calculation (usually Z dimension a.k.a. slice selection). Automatically updates the Slice slider (4.10).

[4.12. 4th dimension spinner](#)

Spinner used to scroll through 4th dimension of the selected image data. Only enabled if the selected image data for map calculation size in the 4th dimension is higher than 1.

[4.13. 5th dimension spinner](#)

Spinner used to scroll through 5th dimension of the selected image data. Only enabled if the selected image data for map calculation size in the 5th dimension is higher than 1.

[4.14. Rotate context button](#)

Context menu button which rotates the image 90 degrees clockwise.

[4.15. Flip vertically context button](#)

Context menu button which flips the image around the vertical axis.

[4.16. Flip horizontally context button](#)

Context menu button which flips the image around the horizontal axis.

[4.17. Reset view context button](#)

Context menu button which resets image zoom (currently not available on “Preview” tab), brightness and contrast of the displayed image data.

[4.18. Permute dimensions context submenu](#)

Context submenu which opens the available dimension permutations (4.19 – 4.21) on mouse hover.

[4.19. 3-4 permute dimensions context button](#)

Context button available through “Permute dimensions context submenu” (4.18). Permutes the 3rd and 4th dimensions of the currently selected image data and automatically updates the limits on respective sliders and spinners.

[4.20. 3-5 permute dimensions context button](#)

Context button available through “Permute dimensions context submenu” (4.18). Permutes the 3rd and 5th dimensions of the currently selected image data and automatically updates the limits on respective sliders and spinners.

[4.21. 4-5 permute dimensions context button](#)

Context button available through “Permute dimensions context submenu” (4.18). Permutes the 4th and 5th dimensions of the currently selected image data and automatically updates the limits on respective sliders and spinners.

[4.22. Slice slider](#)

Discrete slider used to scroll through 3rd dimension of the displayed parameter map image data (usually Z dimension a.k.a. slice selection). Automatically updates the Slice spinner (4.23).

[4.23. Slice spinner](#)

Spinner used to scroll through 3rd dimension of the selected displayed parameter map image data (usually Z dimension a.k.a. slice selection). Automatically updates the Slice slider (4.22).

[4.24. Colormap radio buttons](#)

Allows the user to change the color lookup table of the displayed parameter map image. Currently implemented a classic “Greyscale” view and a “Turbo” view which maps image intensities to a color heat-gradient.

[4.25. Brightness slider](#)

Continuous slider which controls the brightness of the displayed parameter map image. Defaults to 0. Can be reset using “Reset view” button available via image panel context menu (right click on the image).

[4.26. Contrast slider](#)

Continuous slider which controls the contrast of the displayed parameter map image. Defaults to 0. Can be reset using “Reset view” button available via image panel context menu (right click on the image).

[4.27. Rotate context button](#)

Context menu button which rotates the image 90 degrees clockwise.

[4.28. Flip vertically context button](#)

Context menu button which flips the image around the vertical axis.

[4.29. Flip horizontally context button](#)

Context menu button which flips the image around the horizontal axis.

[4.30. Reset view context button](#)

Context menu button which resets image zoom (currently not available on “Preview” tab), brightness and contrast of the displayed image data.

[4.31. Image value type radio buttons](#)

Tells the algorithm for DSC map calculation if the provided image data for map calculation contains either raw signal intensities or tracer contrast concentration values.

[4.32. Number of voxels for image mask](#)

Not in use since SuMRak has its own dedicated “Segmenter” tab for segmentation purposes.

[4.33. \$S_0\$ threshold edit field](#)

Threshold used to choose the instant of tracer appearance.

[4.34. \$S_0\$ minimal scan number edit field](#)

Minimum number of initial scans on which to calculate S_0 .

[4.35. \$S_0\$ maximal scan number edit field](#)

Maximum number of initial scans on which to calculate S_0 .

[4.36. \$K_h\$ edit field](#)

Proportionality constant “ K_h ”. Accepted value range is [0 – 1]. 1 by default which makes the final measurements relative (rCBF, rCBV and rMTT).

[4.37. \$Rho\$ edit field](#)

Proportionality constant “ Rho ”. Accepted value range is [0 – 1]. 1 by default which makes the final measurements relative (rCBF, rCBV and rMTT).

[4.38. \$Kvo\$ edit field](#)

Proportionality constant “ Kvo ”. Accepted value range is [0 – 1]. 1 by default which makes the final measurements relative (rCBF, rCBV and rMTT).

[4.39. Enable AIF checkbox](#)

Checking the box enables the automatic AIF (arterial input function) extraction tool which is critical for getting perfusion measurements. AIF gets extracted from a ROI which is hardcoded to be an ellipse positioned a bit off-center to the bottom of the slice selected for AIF extraction (4.3). Enabled by default. User can, however, change the length of ROI’s minor and major semiaxis with 4.40 and 4.41, respectively. AIF extraction tool used is made by Perruzo *et al.* [7].

[4.40. AIF ROI minor semiaxis edit field](#)

Changing this value the user can change the length of the minor semiaxis length in ROI used for AIF extraction tool (4.39).

[4.41. AIF ROI major semiaxis edit field](#)

Changing this value the user can change the length of the minor semiaxis length in ROI used for AIF extraction tool (4.39).

[4.42. AIF minimal voxel number edit field](#)

Changing this value affects the minimal voxel number to be sampled from ROI used when extracting AIF.

[4.43. AIF maximal voxel number edit field](#)

Changing this value affects the minimal voxel number to be sampled from ROI used when extracting AIF.

[4.44. AIF recirculation correction checkbox](#)

Enables the AIF(arterial input function) correction for the effects of tracer recirculation. Enabled by default.

[4.45. Voxel discard fraction due to AUC edit field](#)

Sets the fraction of voxels to be discarded from the AIF(arterial input function) extraction tool due to AUC(area under curve) criterion.

[4.46. Voxel discard fraction due to TTP edit field](#)

Sets the fraction of voxels to be discarded from the AIF(arterial input function) extraction tool due to TTP(time to peak) criterion.

[4.47. Voxel discard fraction due to regularity edit field](#)

Sets the fraction of voxels to be discarded from the AIF(arterial input function) extraction tool due to regularity criterion.

[4.48. Cluster selection threshold edit field](#)

Sets the threshold to decide whether to select the cluster based on peak or TTP.

[4.49. Concentration correction checkbox](#)

When checked, employs correction factors (4.50 –4.52) to correct the concentration values for different properties of the applied tracer. Relevant when image data provided for DSC map calculation contains concentration data instead of usual signal intensities. Disabled by default.

[4.50. Correction factor "a" edit field](#)

Factor "a" used for concentration correction function. Not used when "Concentration correction" checkbox (4.49) is disabled.

[4.51. Correction factor "b" edit field](#)

Factor "b" used for concentration correction function. Not used when "Concentration correction" checkbox (4.49) is disabled.

[4.52. Correction factor "r" edit field](#)

Factor "r" used for concentration correction function. Not used when "Concentration correction" checkbox (4.49) is disabled.

[4.53. SVD threshold edit field](#)

Determines the threshold used for classic SVD(singular value decomposition) deconvolution method. Default is 0,2. Only used when SVD is the selected deconvolution method (4.7)

[4.54. cSVD threshold edit field](#)

Determines the threshold used for cSVD(circular-block singular value decomposition) deconvolution method. Default value is 0,1 and is based on measurements obtained at 1,5T. Only used when cSVD is the selected deconvolution method (4.7)

[4.55. oSVD threshold edit field](#)

Determines the threshold used for oSVD(circular-block singular value decomposition with oscillation index) deconvolution method. Default value is 0,035 which is supposedly an optimal threshold given TR=1s and SNR=20 according to Wu et al. [9]. Can be defined as an array of thresholds in which case "oSVD counter" edit field (4.56) determines the index of the threshold to use. Only used when oSVD is the selected deconvolution method (4.7)

[4.56. oSVD counter edit field](#)

Specifies the index of the value in "oSVD threshold" edit field (4.55). Mostly used for scripted testing of different threshold values on a data set.

[4.57. Save SVD residuals checkbox](#)

When checked, the toolbox produces a 4-D matrix of residuals. Only used if enabled and SVD is the chosen deconvolution method in 4.7. Currently not implemented as an output so it's discarded anyway.

[4.58. Save cSVD residuals checkbox](#)

When checked, the toolbox produces a 4-D matrix of residuals. Only used if enabled and cSVD is the chosen deconvolution method in 4.7. Currently not implemented as an output so it's discarded anyway.

[4.59. Save oSVD residuals checkbox](#)

When checked, the toolbox produces a 4-D matrix of residuals. Only used if enabled and oSVD is the chosen deconvolution method in 4.7. Currently not implemented as an output so it's discarded anyway.

[4.60. Reset to default button](#)

Resets all of "Advanced settings" window (4.4) values to default.

[4.61. Apply settings button](#)

Applies all displayed settings in the "Advanced settings" window (4.4).

[4.62. Map type selection dropdown](#)

When selected to "T1", user gets presented with imported TR and TI values list (4.63) (4.64) which are freely editable.

[4.63. TR values list](#)

Lists all imported TR values for the selected experiment. List is freely editable and needs to have same number of element as the size of the selected experiment's image data 4th dimension size (number of echoes).

[4.64. TI values list](#)

Lists all imported TI values for the selected experiment. List is freely editable and needs to be empty or have same number of element as the size of the selected experiment's image data 4th dimension size (number of echoes). In case where is empty, SuMRak assumes it's a variable TR experiment type. If not, inversion recovery experiment is assumed.

[4.65. Calculate T1 map button](#)

Starts the T1 map calculation on button click. In case where TI values list (4.64) is empty, SuMRak assumes it's a variable TR experiment type. If not, inversion recovery experiment is assumed.

[4.66. Map type selection dropdown](#)

When selected to "T2", user gets presented with imported TE values list (4.67) which is freely editable.

[4.67. TE values list](#)

Lists all imported TE values for the selected experiment. List is freely editable and needs to be empty or have same number of element as the size of the selected experiment's image data 4th dimension size (number of echoes).

[4.68. Calculate T2 map button](#)

Starts the T2 map calculation on button click.

[4.69. Map type selection dropdown](#)

When selected to "pASL", user is presented with imported TR and TI values list (4.63) (4.64), as well as additional FAIR pASL settings. Like with T1 mapping, the selected experiment needs to have number of TR and TI values equal to 4th dimension size of the selected experiment (number of echoes).

[4.70. TR values list](#)

Same as 4.63.

[4.71. TI values list](#)

Same as 4.64.

[4.72. Experiment order radio buttons](#)

Describes the order of the interleaved pASL experiments. The default setting is slice-selective experiment first in the interleaved order.

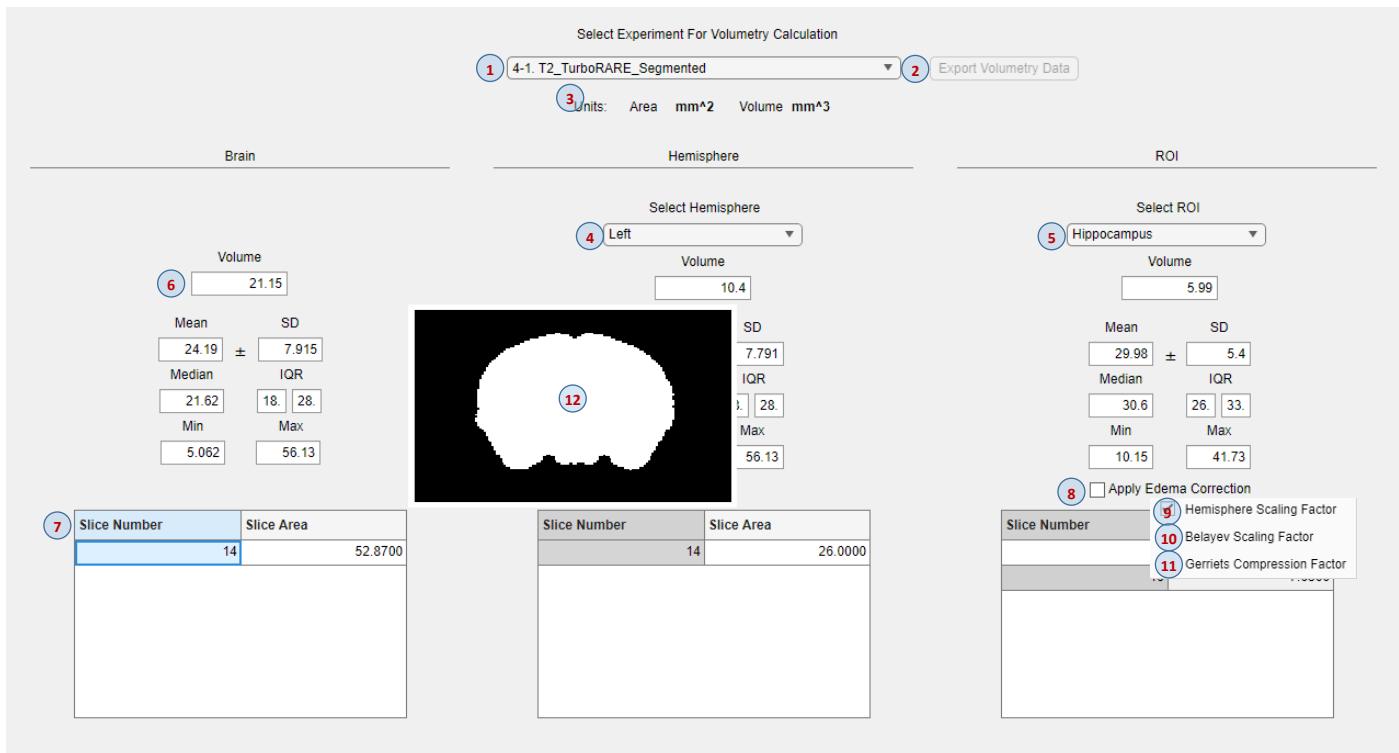
[4.73. Blood T1 edit field](#)

Blood T1 constant, used for pASL CBF map calculation purpose.

[4.74. Calculate pASL map button](#)

Starts the pASL map calculation on button click.

5. Results tab



5.1. Volumetry image dropdown

Lets the user decide on which sequence to calculate ROI volumetry on. List contains only experiments saved to temporary application data. For instance, after saving segmented image data with 2.19.

5.2. Export volumetry data button

Exports the volumetry data into a Microsoft Excel file as <experimentID>_Volumetry.xlsx file in the previously selected export location. Disabled by default. Requires user to create an export folder first using "Create export folder" (1.10).

5.3. Units of measurement

Prints out the spatial units of measurement for the respective image data selected for volumetric calculations (5.1).

5.4. Hemisphere selection dropdown

Selects the hemisphere to display in the "Hemisphere" section of the "Volumetry" tab.

5.5. ROI selection dropdown

Selects the ROI to display in the "ROI" section of the "Volumetry" tab.

5.6. Segmented region statistics display

General statistic of the respective segmented region for the currently selected image data. Volume is calculated on base of slice thickness of the experiment selected together with estimated slice gap volume. Slice gap volume is estimated as an average surface of adjoining slices multiplied by the slice gap thickness. All data is printed in units displayed in "Units of measurement" (5.3).

5.7. Slice breakdown table

Table displaying all slices where user has segmented the respective region ("Brain", "Hemisphere" or "ROI") together with its area size for that particular slice. Area size values are printed in units displayed in "Units of measurement" (5.3).

5.8. Edema correction checkbox

Checking this box, application recalculates all volume statistics with the chosen edema correction method in the context menu. Used when studying phenomena commonly associated with brain edema (stroke, brain trauma, etc.). Currently available edema correction methods can be selected in the context menu by right-clicking on the checkbox or its text description. Default edema correction method is "Hemisphere scaling factor" (5.9).

5.9. Hemisphere scaling factor selection

Available via context menu of the "Edema correction checkbox" (5.8). Employs "Hemisphere scaling factor" calculated as a ratio of contralateral and ipsilateral hemisphere areas for each segmented slice of the active custom ROI.

$$A_{corrected} = A_{original} \times \frac{A_{contralateral}}{A_{ipsilateral}}$$

Formula is displayed in the tooltip visible on mouse hover over the selection. [4]

[5.10. Belayev scaling factor selection](#)

Available via context menu of the “Edema correction checkbox” (5.8). Employs “Belayev scaling factor” calculated as a complement of a ratio of hemisphere area difference and contralateral hemisphere area for each segmented slice of the active custom ROI.

$$A_{corrected} = A_{original} \times \left(1 - \frac{A_{ipsilateral} - A_{contralateral}}{A_{contralateral}} \right)$$

Formula is displayed in the tooltip visible on mouse hover over the selection. [5]

[5.11. Gerriets compression factor selection](#)

Available via context menu of the “Edema correction checkbox” (5.8). Employs “Gerriets compression factor” for each segmented slice of the active custom ROI. Tooltip of this selection refers to this manual chapter for the formula.

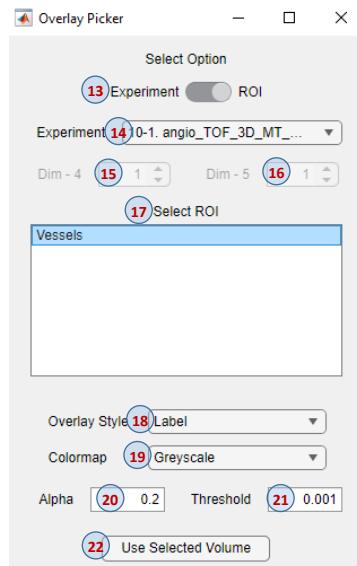
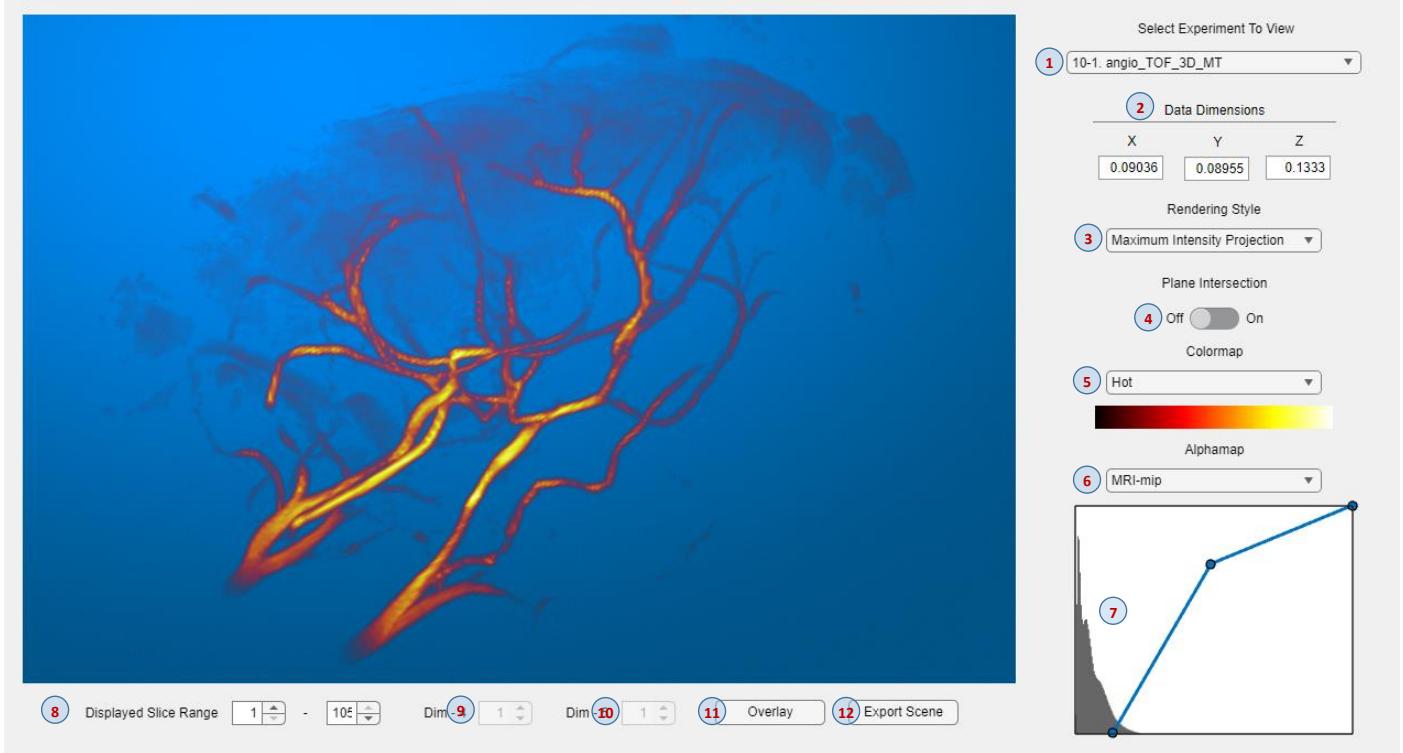
$$A_{corrected} = A_{contralateral} + A_{ipsilateral} - (A_{contralateral} + A_{ipsilateral} - A_{original}) \times \frac{A_{contralateral} + A_{ipsilateral}}{2 \times A_{contralateral}}$$

[6]

[5.12. Floating mask display](#)

When the user selects a segmented slice from the currently selected experiment in one of the “Slice breakdown” tables (5.7), a new floating display opens with the current brain/hemisphere/ROI mask shown as a binary image. User can hide the floating display by clicking anywhere outside the range of the floating mask display.

6. 3D Viewer



6.1. 3D viewer experiment selection dropdown

Selects the experiment to use for 3D volume viewer. The available list is combined list of the original imported experiments as well as modified saved image data.

6.2. Data aspect dimensions edit fields

On experiment selection via dropdown (6.1), data aspect dimension edit fields get populated from imported or inherited voxel dimension size data. Fields are freely editable should the user need to correct values to properly display the selected volume.

6.3. Rendering style dropdown

Type of volume rendering to use for 3D preview. All available MATLAB rendering styles are implemented and include: Volume, Maximum intensity projection, Minimum intensity projection, Slice planes, Gradient opacity and Isosurface. Maximum intensity projection, minimum intensity projection and isosurface styles are not compatible with overlay function.

6.4. Plane intersection switch

When this switch is set to “On”, only intersecting or overlapping regions of all present clipping planes are clipped (logical AND). By default, this setting is turned off (logical OR).

6.5. Colormap dropdown

Lets the user decide colormap to map the volume's intensity data values to a color gradient. All available options are default MATLAB colormaps and include: Greyscale (default), Turbo, Hot, Jet, Parula, Sky, Cool, Copper, Bone. After colormap selection, user can inspect the whole colormap gradient in the underlying color bar.

6.6. Alphamap dropdown

Lets the user select from one of the pre-defined alphamaps. All alphamaps plot each intensity value 0-255 to a transparency setting (alpha). Starting from one of the pre-defined options, user can modify the alphamap voluntarily using polyline displayed over the underlying histogram plot (6.7).

6.7. Histogram with alphamap polyline

Displays the selected experiment image data value histogram. A polyline is drawn over the histogram depending on the chosen preset (6.6). User can add or drag and drop individual vertices of the polyline in order to customize the applied alphamap of the 3D volume view.

6.8. Displayed slice range spinners

Control of the rendered slice range of the selected experiment image volume.

6.9. 4th dimension spinner

Scrolls through pages in the 4th dimension of the selected experiment image volume.

6.10. 5th dimension spinner

Scrolls through pages in the 5th dimension of the selected experiment image volume.

6.11. Overlay state button

On click, opens up the overlay picker tool window for user to choose an experiment or a ROI to display over the initial selected volume in the 3D volume viewer. Regardless of the overlay type chosen, overlay volume needs to have identical dimension sizes in order to be loaded properly in the 3D volume viewer.

6.12. Export scene button

On click, prompts the user to choose a file name for the scene image export. The exported scene image is effectively a screenshot confined to boundaries of the 3D viewer scene container. Therefore, resolution of the exported image is determined directly as the size of the actual on-screen resolution of the user's graphical interface.

6.13. Overlay option switch

Using this switch, user can choose between types of the overlay volume to preview, either whole experiment volume or a custom ROI from an experiment (created in Segmenteer tab).

6.14. Overlay experiment dropdown

Selects the desired experiment to use as an overlay volume, either as a whole or one of its custom ROIs created in Segmenteer tab.

6.15. 4th dimension spinner

Scrolls through pages in the 4th dimension of the selected experiment overlay volume.

6.16. 5th dimension spinner

Scrolls through pages in the 5th dimension of the selected experiment overlay volume.

6.17. ROI selection list

Disabled by default. Gets enabled if overlay option switch (6.13) is set to "ROI" and the selected experiment contains at least one custom ROI which can be used as a volume overlay. User can directly select and highlight the ROI to use as an overlay.

6.18. Overlay style dropdown

Rendering style to use when displaying the chosen overlay volume. All the MATLAB options available are implemented and are as following: Label, Volume and Gradient. Label option is recommended when displaying ROI masks or any other logical or categorical volume matrices.

6.19. Overlay colormap dropdown

Colormap to use for displaying the overlay volume. Same as in 6.5.

6.20. Overlay alpha edit field

For sake of simplicity, alpha values for the overlay volume is not being input into 3D viewer as a alphamap, but rather as a singular value applied for whole selected overlay volume.

6.21. Overlay threshold edit field

Threshold for the overlay volume voxel value inclusion. All voxels with values lower than this threshold get rejected during 3D viewer overlay rendering process.

6.22. Use selected volume button

Applies all shown overlay options to the 3D volume viewer of the main SuMRak interface and displays the chosen overlay on top of the initial selected experiment volume. Be advised that maximum intensity projection, minimum intensity projection and isosurface rendering styles are not compatible with the overlay function.

About

suMRak is an open-source tool developed in MATLAB for the analysis of MRI data for research purposes. It is provided "AS IS" and is a non-commercial research-only program package not meant to be sold or distributed to a third party. suMRak is a pre-clinical experimental tool and it is not to be used in a clinical setting. The authors of suMRak provide no warranty or support for any alleged or actual damage, arising in any way out of the use of suMRak. suMRak source code, along with the provided manual and test data, are protected under a public license.

suMRak was developed as a part of the doctoral study of Ister Rok, MD, PhD candidate in Neuroscience at University of Zagreb School of Medicine, Šalata 3, 10000 Zagreb, Croatia. The work of doctoral student Ister Rok has been fully supported by the "Young researchers' career development project – training of doctoral students" project of the Croatian Science Foundation funded by the European Union from the European Social Fund.

BRUKER pvmatlab is integrated and provided, alongside its respective manual, with suMRak under written consent from Bruker BioSpin MRI GmbH, Rudolf-Plank Str. 23, 76275 Ettlingen. suMRak uses BRUKER pvmatlab solely to import reconstructed image data and metadata by initializing objects of its ImageDataObject class. Bruker reserves all rights on the use and distribution of the pvmatlab package. Its source code and test data are protected under copyright. For additional info, refer to the "Legal Matters" section of the pvmatlab manual. Bruker is a registered trademark of BRUKER-PHYSIK AG.

Dynamic Susceptibility Contrast (DSC) MRI toolbox is an open source MATLAB toolbox used to analyze DSC-MRI data authored by Peruzzo Denis and Castellaro Marco. It is used in suMRak solely for DSC map calculation. DSC MRI toolbox source code is available at: <https://github.com/marcocastellaro/dsc-mri-toolbox>.

Registration of image data is implemented using SimpleElastix. SimpleElastix is an extension of SimpleITK that offers a user-friendly API to the popular image registration algorithms of the elastix C++ library. SimpleElastix source code is available at: <https://github.com/SuperElastix/SimpleElastix>

The 3D viewer screen export is implemented using the Screen Capture tool by Yair Altman, openly available via MATLAB Central's File Exchange.

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