Manual for RView

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1 Introduction

The following text presents an manual for the RVIEW Program developed by Daniel Rueckert and the Visual Information Processing Group at Imperial College London. It is available to the public: `http://www.doc.ic.ac.uk/~dr/software/`. The following document should provide a short introduction how the most important features works.

RVIEW is an viewer for medical images. It has been developed within the scope of the IRTK Project. The big advantage of this viewer, is that the user can simultaneously work on two images. Several features to compare this images were implemented. Furthermore the program has the ability to apply and modificate transformations on the image. A segmentation can be done in the pictures and can be safed easily. The program can implicitly handle landmarks and can fit in the pictures according to them. RVIEW uses the common medical image format NIfTI.

2 Visualisation

Probably the most important function of the RVIEW tool is the visualisation. It provides the possibility to view 3D NIfTI files in any of the three space directions. To do so just load some NIfTI images by pushing the corresponding button in the menubar as an source or an target image in the RVIEW. To along with the GUI, all the explained parts are highlighted in figure 1.

You can now easily choose your perspective among the three space directions and a combinition of all three by clicking the buttons in the upper right.

Using the slider just over the image area one can zoom in and out. To zoom in increase the slider value by pulling it right to zoom out oull it in the other direction.

The three other bars surrounding the picture are also used to manipulate the view, but in a very different way. To understand the functionality of these bars correctly you have to remember that we are handling 3D pictures. What we are getting displayed are just 2D pictures. So there should be a possibility to move in or out of our current displaying plane. This possibility is provided by the three bars. By turning one of them you move in one space direction out of the drawing plane. You can see the effect on two different
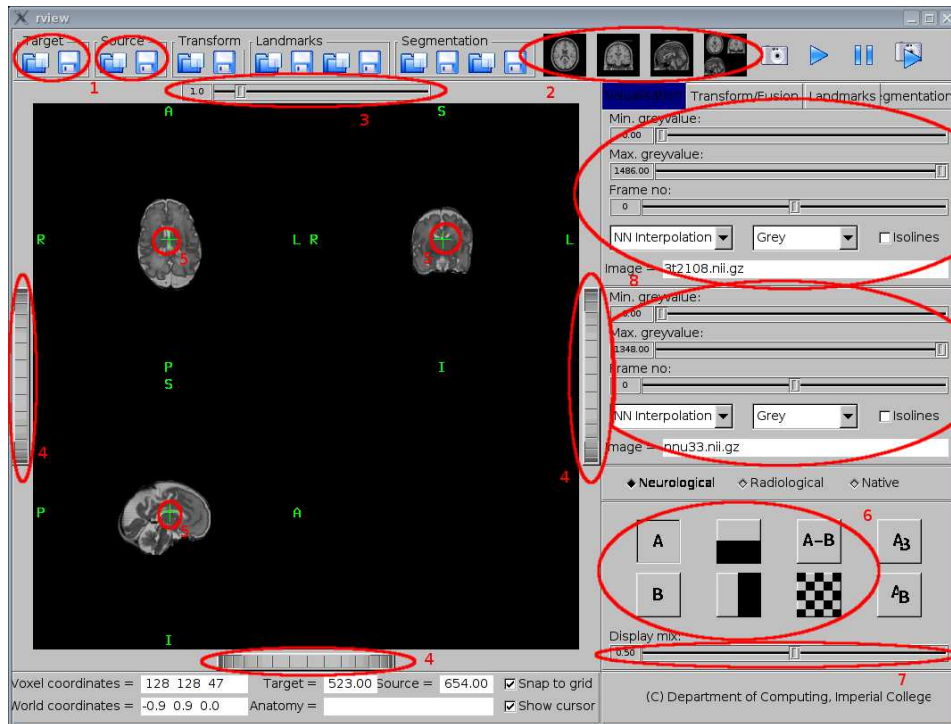
Figure 1: The RVIEW GUI in the visualisation mode.

ways. Firstly the two views, which have the moving direction as a space direction in their plane, will just be translated in this direction. The more interesting effect can be seen in the view, whos drawing plane is perpendicular to the moving direction. As you can see the picture is not only translated, like in the other views, but it changes it shape. That is because you look at different slices along these moving direction. Which slice you currently observe is specified by the green cursor in the center of each view.

As an alternative to these three bars, you can simply click into one of the views. The cursor position will be aligned to the pixel you have clicked on. By clicking into different views you can change the perspective in different directions.

The green cursor and the space direction in the views can also be deactivated. To do this, simply deactivate the "Show cursor" checkbox at the bottom of the GUI. You can also toggle the cursor on or off by pressing the space bar.

But so far we were just able to deal with the target picture. For dealing with the target picture or even both pictures at once you need the buttons in the lower right corner.

Let's work through this button group. The first button labeld with an "A", is for displaying the traget image alone. Similarly the "B"-button displays just the target image. No matter which of these displaying modes are selected you can manipulate it on the same way using the bars and the slider.

A nice feature to compare the source and the target images can be applied by one of the buttons in the second raw of the button image. These buttons are used to display parallel one part of each picture. The upper button shows the upper part of the target

picture upon the lower part of the source picture. The lower button displays the left part of the target image next to the right part of the source image. By moving the slider "Display mix" you can move the border between the two parts up and down or left and right, depending on the displaying mode you are using. A "Display mix" slider value of 1 displays 100% of the target image and nothing of the source image, a slider value of 0 displays only the source image and 0% of the target image. If the slider value is 0.5 the program will display a half of both of the pictures.

A further very useful displaying mode can be accessed by pressing "A-B". The grey-value of the resulting picture equals at each pixel the difference of the greyvalues of the corresponding pixels in the source and the target image. This mode is very useful for comparing the images. Assume you have an source image and a second image registered to this source, in this case you are certainly interested in how similiar these two pictures are to each other. You can find this easily out using the diffence displaying mode. Every greyvalue which is not equal 0 indicates an difference from the source to the target image in this pixel. Notice that the greyvalue zero is not displayed black, because the greyvalues of the difference will range from the negative maximum of the source plus the minimum of the target to the positiv maximum of the target minus the minimum of the source. Thats why the greyvalue of 0 will be displayed in most cases as some medium gray. Every pixel which is lighter indicates that there is something in the target which doesn't appear in the source and vice versa. By setting the minimum or the maxium displayed greyvalue to zero, you can determine just to display meanderings on the source and on the target side respectively. How to set these minimum and maximum greyvalues will be explained later.

The last displaying mode which should be mentioned in this manual is represented by this checked pattern. The resulting image is an overlaying of the source and the target. By using the slider under the button group you can specify the intensity with which the two pictures are weighted. If the value of the "Display mix" slider is 0 then the target is weighted with 0 and you can only see the source image. But if the slider value is 1 the weight of the target is one and you can only see the target image. The next part of the GUI we want to study is in the right side. There are two labels containg three sliders, a textfield and a checkbox which should look almost the same. The upper one is to configure the properties of the target image and the lower one is used for the source. They work identically so only one of them will be explained. Notice in advance that if you use the difference displaying mode, you set the properties of the resulting image in the upper of these two panels. The first slider is labeld with "Minimum greyvalue:", using that slider you can specify a lower bound for the greyvalues in this picture. If you set the slider for example on 100, than every greyvalue which is smaller then 100 will be set to this. Similar you can specify a upper bound to the size of the greyvalues using the second slider. A important displaying option can be activated by checking the "Isoline" box. You will see some yellow lines in the picture. These lines are the so called "Isolines" and they indicate the edge of areas with the minimum occuring greyvalue. So in the inside of these lines every pixel has an greyvalue greater than the minimum and in the outside every pixel's greyvalue is the specified minimum value. With increasing the minimum greyvalue using the first slider more and more pixels will take this minimum
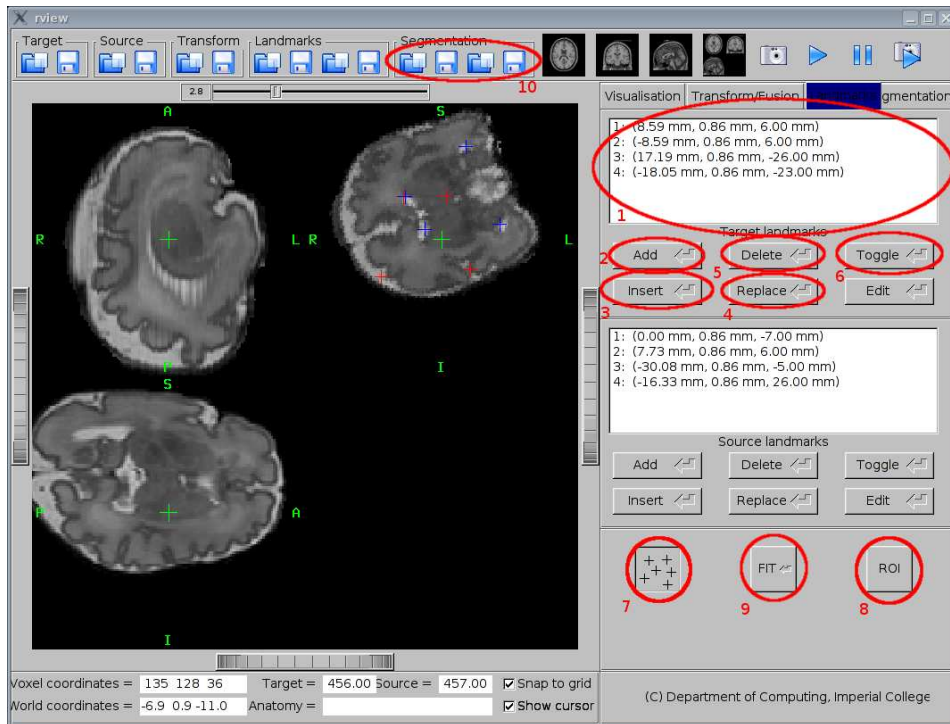
Figure 2: The RVIEW GUI in the landmarks mode.

value. As a result the "Isolines" will change. So if you want to surround an specific level of the greyvalues by the Isolines, all you have to do is setting the value of the first slider to this level.

As the bars beside the image area were used to display everything of an 3D picture, one could roughly say that the third slider in the panel is used to display 4D pictures. These pictures are not only depending on the three space directions but also varies in time. With the slider called "Frame number" you can change the timepoint, at which you want to study the picture.

Last but not least there is a textfield in each of the panels. The textbox simply contains the name of the target and the source image respectively. So if you load an image, as described above you can check in this box, whether you have loaded the right file.

3 Landmarks

A Registration algorithm has been implemented in this GUI as well. It is based on some landmarks which can be manually placed by the user in the traget and the source image. The algorithm will try to fit these two sets of landmarks as close as it's possible to each other. As usual all steps can be compared to the figure 2.

To make use of this function, please change to the "Landmarks" tab. You can now see three panels. The upper two, containing a list box and six buttons, are used for

manipulating the sets of landmarks for the target and the source image respectively. The third panel is used for applying different functions on these sets. Since the upper two panels work identically only one will be descriped below.

Before we will create our own set of landmarks please make sure that you are observing the image, for which you want to set the landmarks. That means if you are using the first panel, please make sure that the target image is displayed and if you are using the second panel, the source image should be displayed. You can now add a landmark at the cursors position by clicking the "Add" button. The position of the landmark will be then listed in the box. Instead of adding the landmark to the end of the list you can insert it before an existing item. To do so select the item and click "Insert" and a landmark with the current cursor position will be placed right before the selected item.

Please note that the order of the landmarks is significant, because the algorithm tries to align the first target landmark with the first source landmark and the second target landmark with the second source landmark and so on. Even if you specify the same landmarks at the same anatomic features in different pictures, a worng order will probably prevent the algorithm from working correctly.

By selecting a landmark and pressing "Replace" it is replaced by a landmark with the currently focused position. You can also delete landmarks by selecting them in the list and clicking "Delete".

By clicking on "Toggle" the landmark which is in the list right after the currently selected one, will be selected and the cursor will be aligned to its position. If the last landmark in the list is selected, the first one will be chosen. If no landmark is selected, the functionality will also be applied to the first one of the list.

You can easily get your landmarks displayed by clicking on the button labeld with several "+"s. The target landmarks will be displayed red, whereas the source landmarks will be displayed blue.

To stay in the region of interest with your landmarks, you can get this displayed in a semitransparent yellow, just by clicking the "ROI" in the third panel.

Having build up two sets of landmarks using the methods described above we can now apply the registration algorithm on it. Before doing this please make sure that you have specified the same number of landmarks for the target and the source image. Due to reasons of the uniqueness of a solution you have to specify at least four landmarks in each picture. Please note that two landmarks assigned to the same position are handled as one. If you have met this restriction and click on the "FIT" button the program will automatically transform your source image, on such a way that the difference of the landmarks position is minimized.

The set of landmarks of the target and the source can be both saved and loaded. The corresponding functions can be selected in the menubar. The sets will be stored in .vtk node file. It is recommended to save the set of landmarks if you deal with the same picture several times, because the landmarks will be not stored implicity in the NIfTI-Image.

But be careful with using the landmarks with transformations. The source landmarks you attach to the image will be transformed, as well! That means, if you place a source landmark somewhere in the picture and a transformation, which is not the identity, is

Figure 3: The RView GUI in the segmentation mode.

assigned before, the landmark will not appear at the cursors position. Instead they will be transformed and appear at the transformation of the cursors' position. You can illustrate this process, by thinking of a different order. First the landmarks are placed on the not transformed source image. So the coordinates of the landmarks are stored, as there would be no transformation. And then the tranformation is applied to both the source image and the source landmarks. That's why the landmarks won't neither appear at the cursors position nor at the position corresponding to the cooridnates in the list.

By using the landmark registration with a predefined transformation, the transformation is simply ignored. The algorithm just fits in the traget image with the not transformed source image and replaces the predefined transformation, with the result of the algorithm.

4 Segmentation

As mentioned above, RView provides some functions to do perform segmentation on the images. To make this explanation more comprehensible figure 3 shows the GUI of RView with the buttons for the following steps highlighted. To use them switch to the tab called "Segmentation". You can now easily create some labels to save different parts of your segmentation in them. Just push the "Add" button to do so.

Usually the first inserted Label, the one with the ID "0", is assigned as the background. So if you display this label 0 by activating the checkboxes "Labels" and "Display label" you'll see the entire image in the specified color, because the background is now displayed. To avoid this just deactivate the Checkbox "Display label" for the label 0.

You can now add more labels and use them to save your own segmentation. For each label you can choose a color and type in a name. The slider named transparency, provides another possibility to change the appearance of the label. A value of 1 will make the filled areas of the label completly non-transperent while a value of 0 makes it transparent. Please make sure that the "Display label" box is checked for every label you create, except the background label.

To add an segmentation to the labels you can use two types of drawing. The first one is the open region. To use this push the left one of the two buttons showing the green pencil. To draw hold the "Shift" key and press down the left mouse button. You can now draw a line by moving the mouse inside of one of the views. After releasing the mouse button you can press enter to assign the drawn line to one of the labels. Don't draw in different views without pressing enter in between, this would lead to some errors. Pressing shift and the right mouse button you can fill some closed regions of the picture. With using the open draw mode, please make sure that you have completely enclosed an region, otherwise the shift and the right mouse click will fill out the entire image.

To overcome this problem a second drawing mode has been implemented. The closed region drawing can be selected by pressing the right of the two buttons showing a green pencil. It works exactly like the open drawing mode, with the slight different that with releasing the left mouse key after drawing it will automatically close the path.

If you have created your own segementation there are two types of saving it. The first type is to save the segementation itself. That means the selected areas will be stored as an own NIfTI image. To tell the different labels appart a gray value according to the label ID is assigned to every region of this segementation. You can open this segementation as a own picture using RView. What you will see is the different areas you have specified, with different brightnesses, one for each label. To open the segementation as a segmentation and not as an image you additionally need a look up table. RView uses this tables to reassociate the regions to labels and to their color and transperancy specification. So the second type to save the segmentation is saving the lookup table.

If you want to reuse your segmentation you can just load it clicking the corresponding buttons in the menubar. After loading the segmentation stored as a NIfTI image you can decide wheter you want to load your old lookup table or to specify a new one. In the second case it is necessary for a correct displaying, that you use the same label IDs as in the original lookup table.

The big advantage of seperation between the NIfTI image segmentation and the lookup table is that you can apply every image manipulating tool for NIfTI images also on the segmentation. Assume you have several images showing the same object but under different circumstances, so that you have to do registration on them. Moreover you want the same segmentation of this object shown in every picture. Instead of assigning the segmentation for each picture you could simply assign it for one and then apply a suitable transformation on it. This suitable transformation you can easily get as an

output of the registration process between the pictures.