MITK Hands-On Tutorial Exercises

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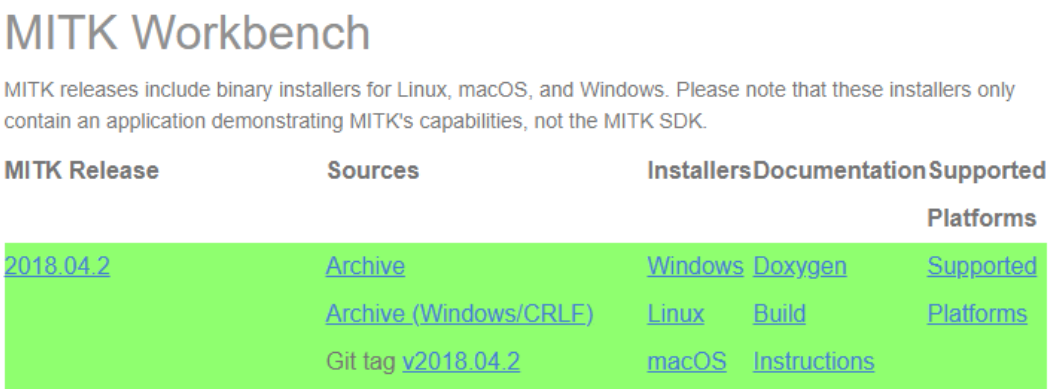
Abstract. This document offers some exercises to get familiar with the MITK workbench. Please make sure you received the data that we handed out together with this document. You will need to use this data during the exercises. The exercises are designed to deepen and practice the information given in MITK introduction talk yesterday. All actions you need to complete the exercises are summarized in the **MITK Hands-On Documentation**. If you have any questions, we are happy to answer them.

Keywords: MITK

1 Introduction

1. Go to **mitk.org/wiki/downloads** and download the most recent version of the MITK workbench (2018.04.2). You can also use the installer provided on the USB flash drive.



MITK Workbench

MITK releases include binary installers for Linux, macOS, and Windows. Please note that these installers only contain an application demonstrating MITK's capabilities, not the MITK SDK.

MITK Release	Sources	Installers	Documentation	Supported Platforms
2018.04.2	Archive	Windows	Doxygen	Supported
	Archive (Windows/CRLF)	Linux	Build	Platforms
	Git tag v2018.04.2	macOS	Instructions	

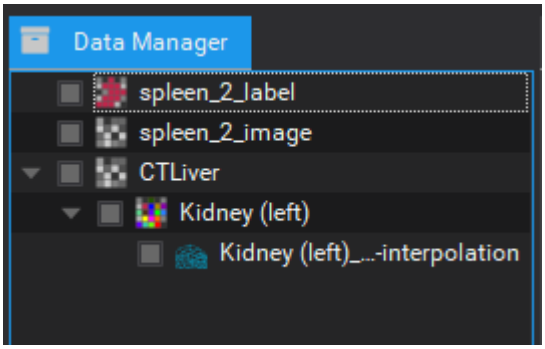
2. After downloading, install the application on your system.
3. Open the MITK workbench.

2 Dataloading and –saving

1. Using the **Open File** dialog, open the image **Data\CTLiver.nrrd**.
2. Using **drag & drop**, open the image **Data\Spleen\spleen_2_image.nii.gz**.
3. Save the MITK scene and then close the project (see chapter 2).
4. Using the **Open File** button, reopen the project by loading the saved MITK scene.
5. Save the **CTLiver** under a different name.
6. Remove the **CTLiver** from the data manger. What are the different ways to remove a node from the Data Manager?
7. Open the file saved at step 5.
8. Close the project.

3 Visualization and Interaction

1. Open the **Data\example.mitk** project. (*Caution: This file is quite big. Therefor loading might take a while.*)
    a. You should see the following data in the Data Manager



2. **Toggle** the visibility of the objects in the Data Manager, so that only CTLiver and the corresponding segmentations are visible.
3. Focus the windows in the display area on CTLiver and the corresponding segmentations by applying **Reinit**.
4. Navigate with the crosshair to the kidney center.
5. Select the kidney and the image by checking both in the **Data Manager** so that both are visible.
6. Adjust the level window in a way that highlights the kidneys. (Try using the level window slider, editing the values below the slider and try out some presets).
7. Maximize the axial Display Window (Hint: The following features can all be found in the upper right corner of each of the displays).
8. Hide the crosshair.
9. Set the slice thickness (the slider labelled with **TS** in the **+** section) to different values (5, 10, 15). What changes in the display window?
10. Zoom into the image to maximize the segmented kidney and pan, until the kidney is centred.
11. Minimize the axial Display Window to get back to the Four Window View.
12. Visualize all images and segmentations by applying **Global Reinit**.
    a. What effect does the visibility of the data nodes spleen_2_label and spleen_2_image have? What is the difference between **Reinit**, **Global Reinit** while the data nodes are not visible and **Global Reinit** while the data nodes are visible.
13. Make yourself familiar with the plane rotation, scaling, zooming and translation (you can find information in the other document).

Close the project.

4 Measuring- and Marking-Tools

4.1 Measurement

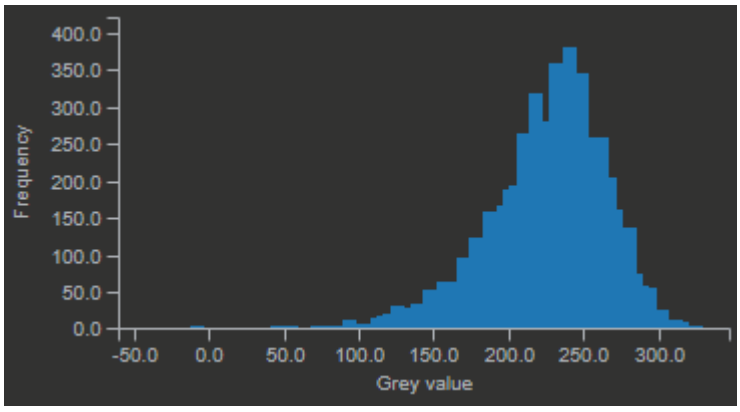
1. Open the **Measurement** plugin.
2. Open the image **Data\CTLiver.nrrd.**
3. Select the Line measurement and measure the largest diameter of the **liver**.
4. **Advanced:** Select some of the other measurement tools and make yourself familiar with them.

Optional: Save the created measurements by right-clicking on the data nodes to store your results. Then "Close project".

4.2 Image Statistics

1. Open image **Data\CTLiver.nrrd.**
2. Segment the right kidney on the axial slice 118.
3. Open the **ImageStatistics** plugin.
4. Select the image and then with CTRL+Click the segmentation.
5. Calculate the statistics for the created segmentation. Compare your results to the following table:

Mean	224.20
Median	231.17
StdDev	42.35
RMS	228.16
Max	353.00
Min	-90.00
NumberOfVoxels	6489
Skewness	-1.27286
Kurtosis	7.28198
Uniformity	0.03436
Entropy	5.16548
MPP	224.74
UPP	0.03436
V [mm³]	1697.57



The results should be similar to the provided values.

5 Segmentation

5.1 Segmentation Task 01

1. Open the **Segmentation** plugin**.**
2. Open the image **Data\Lung\lung_001_image.nii.gz**.
3. Create a new segmentation, name it **lung_tumor** and change the color of the segmentation to **yellow**.
4. Locate the tumor in the upper right lung.
5. Select the **Add** tool and segment the tumor slice by slice.
6. Load the label **Data\Lung\lung_001_label.nii.gz** and compare it with your own segmentation. For an easier comparison, you can change the color of the loaded label by right clicking the data node.
    a. Advanced: Use the **Segmentation Utilities** plugin to compare the two segmentations.

Optional: Save the created segmentation by right-clicking on the data node to store your results. Then "Close project".

5.2 Segmentation Task 02

1. Open the image **Data\Lung\lung_003_image.nii.gz**.
7. Create a new segmentation and change the color of the segmentation to **yellow**.
2. Locate the tumor in the left lung.
3. Segment the tumor using some of the other tools.
4. Load the label **Data\Lung\lung_003_label.nii.gz** and compare it with your own segmentation. For an easier comparison, you can change the color of the loaded label by right clicking the data node in the Data Manager
5. Open the **Image cropper** plugin
6. Select the original image (not the segmentation) in the Data Manager
7. Create a new bounding box
8. Move the bounding box in the 2D widgets so that the tumor is placed inside of the box (you can change the extent of the box by using the handles)
9. Press the **Crop** button.
10. Sometimes it might be useful to have a "safety" area around the tumor. Go to **Segmentation Utilites** and look for the section with morphological operations. Use the tool that increases the size of your segmentation.

Optional: Save the created segmentations by right-clicking on the data nodes to store your results. Then "Close project".

5.3 Segmentation Task 03

1. Open image **Data\CTLiver.nrrd**
2. Create new segmentations for left (blue) and right (green) Kidney.
3. Segment the Kidneys using the **2D Region Growing** tool and 3D interpolation (enable checkbox "3D interpolation"). Some hints can be found in the plugin documentation (press F1).
4. Save the created segmentations by right-clicking on the data nodes to store your results. Then "Close project".

5.4 Segmentation correction

1. Open the **Data\example.mitk** project.
2. Check the kidney segmentation on **CTLiver**. You will probably find some issues with this segmentation. Take the segmentation tool of your choice to correct the segmentation.

Optional: Save the segmentation by right-clicking on the data nodes to store your results. Then “Close project”.

6 Result visualization

6.1 Volume visualization

1. Open the segmentation results you created for task 03.
2. Open the **Volume Visualization** plugin.
3. Click on the image **CTLiver** and then check the **Volumerendering** button.
4. Modify the green circles on the histogram and see how the 3D appearance changes.
5. Select the preset to CT bone.
6. Set the opacity of the image to 0.

6.2 Screenshot making

1. Open the **Screenshot Maker** plugin.
2. Create screen shots by either using the 2D screenshot or the 3D screenshot.
3. Change the color of the background to a different color and take another 3D screenshot.

6.3 Movie making

1. Open the **MovieMaker** plugin.
2. Click on the **PLUS** button to add an Orbit sequence (behavior is comparable to the AnimationPane in Microsoft Powerpoint).
3. Set the duration to 10 sec and increase the Orbit to 720° and press the **PLAY** button.
4. You can now still change the orientation of the image in the 3D view.
5. Play around with the sequences / duration / delay.
6. Optional (if installed on your device): Press recording and record your sequence to create a nice video of your results.
7. Close the project.

7 Registration

7.1 Manual registration

1. Load data sets **training_001_ct.mhd** and **training_001_mr_T1.mhd** in the folder **Registration/training001.**
2. Open the **Match Point Registration Evaluator.**
3. Select both images in the Data Manager and press **Start evaluation.**
4. See the differences of the two images by selecting different visualization styles.
5. Press stop evaluation and open the **Match Point Registration Manipulator.**
6. Select the mr_t1 image as moving (first) and the CT image as target image (second) and press **Start Manual Registration**. Try to adjust all the colored sliders to fit the data correctly.
7. When you are satisfied with the result, click on **Confirm+Store**.
8. Open the **Match Point Registration Evaluator.**
9. If not selected, select the registration matrix (called #ManuelRegistration).
10. Go through all of the visualization options and play around which style is the best to compare the result.

7.2 Automatic registration

1. Go to the **MatchPoint Algorithm Browser** and click on the best suited algorithm. (Hint: Remember the properties: Points vs. Images, Modality, Local vs. Global, Type of transformation, if you are still unsure you can ask anytime).
2. Go to the **MatchPoint Algorithm Control** and load the selected algorithm as well as your data. Make sure to select the CT as target and the MR as moving image.
3. Leave the default settings and press on **Start** in the Execution tab.
4. Go to **MatchPoint Registration Evaluator** again and this time select the data and the **Reg #2** you just created. Compare the new results.
5. Optional: Change the settings of the registration.

7.3 Register additional data

1. Load **training_001_pet.mhd** in folder **Data\Registration\pet.**
2. Right-click on the image in the Data Manager and change the color map to **PET color**
3. Go to the **MatchPoint Algorithm Browser** and click on the best suited algorithm.
4. Make sure to select the CT as target and the PET as moving image.
6. Go to the **MatchPoint Algorithm Control** and load the selected algorithm as well as your data.
7. Leave the default settings and press on Execute --> **Start.**
8. Go to **Match Point Registration Evaluator** again and this time select the data and the **Reg #3** you just created. Compare the new results.
5. Right-click on the **Reg #3 mapped moving data** in the Data Manager and adjust the opacity of the image such that the CT and the PET are visualized at the same time.