

# Applying AI to real world data

### Problems, Pitfalls, Solutions – A tutorial

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### ... running AI models is easy? Right?

Most models where developed in Python

Some models are distributed in "containers"

Most models don't work out of the box

Most models don't work on data different from training data



# Examples for DL applications







### Examples for DL applications

- DeepImageJ
- Nvidia Clara integration in Slicer
- HD Bet for brain extraction
- FatSegNet















# Building up a toolbox for Running Models





#### WSL 2 ARCHITECTURE Toolbox for running DL models Lightweight Linux Utility VM GNU/Linux Usermode Windows Usermode Windows Subsystem for Linux -Python conda -Windows NT Kernel Docker -Git -CONDA **ANACONDA** MINICONDA = miniconda = conda +150 modules +Python.exe + user interface +base modules docker



### Windows Subsystem for Linux

- WSL brings Linux kernel to Windows
- WSL1: translation layer translating every Linux command to Windows API (Almost feels like Linux, but wasn't)
- WSL2: virtual machine with actual Linux Kernel (Full System call capability including docker ...)



https://fossbytes.com/what-is-windows-subsystem-for-linux-wsl/



### Python is easy, right?



MY PYTHON ENVIRONMENT HAS BECOME SO DEGRADED THAT MY LAPTOP HAS BEEN DECLARED A SUPERFUND SITE.

https://xkcd.com/1987/



### Conda to the rescue





### Virtual Machines VS Containers





### Git

Repository

Contains version controlled source code

Git command to use code:

Clone



https://www.javatpoint.com/git-remote



# Repository URL

📢 File Edit Selection View Go Run Terminal Help		Welcome - Visual Studio Code		- 0	×
SOURCE CONTROL X Welcome X	Provide reposito	ory URL.		۵	D
In order to use ait features, you can					
A tour in the wonde	rland of math with python.				
fractals penrose-tili	gs polytopes hopf-fibration re	action-diffusion coxeter-groups	hopcroft domino-shuffling-algorithm		
coupling-from-the-past	uniform-spanning-tree todd-coxete	r uniform-tilings hyperbolic-tilir	gs hyperbolic-honeycombs		
- 396 commits	ິ 1 branch	10 packages 🔊 0 relea	es <b>85</b> contributors	ata MIT	
	• • • • • • • • •	• • • • • • • • • • • • • • • • • • •			
Recently another				Class as developed	
Branch: master 👻	ew pull request		Find file		
neozhaoliang upo	ate galley image		Clone with HTTPS 💿		
src	add code t	for drawing vertices on coxeter pla	Use Git or checkout with SVN usin	g the web URL.	
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🗈 .travis.yml	remove py	thon 3.5 test in travis yaml			





### Examples for DL applications

- DeepImageJ
- Nvidia Clara integration in Slicer
- HD Bet for brain extraction
- FatSegNet



A user-friendly plugin to run deep learning models in ImageJ



### DeepImageJ

- user-friendly plugin
- enables use of pre-trained deep learning models in <u>ImageJ</u> and <u>Fiji</u>.
- runs image-to-image operations on a standard CPU-based computer

nome | news | docs | download | plugins | resources | list | links

#### Download

#### Platform Independent

To install ImageJ on a computer with Java pre-installed, or to upgrade to the latest full distribution (including macros, plugins and LUTs), download the ZIP archive (6MB) and extract the ImageJ directory. Use the *Help>Update ImageJ* command to upgrade to newer versions.

#### Mac OS X

Download ImageJ bundled with Java 1.8.0\_172 (may need to work around Path Randomization). Instructions.

Linux Download ImageJ bundled with Java 1.8.0\_172 (82MB). Instructions.

Windows Download ImageJ bundled with 64-bit Java 1.8.0\_172(70MB). Instructions.

#### Documentation

Tiago Ferreira's comprehensive ImageJ User Guide is available as an 8MB PDF document and as a ZIP archive. The online JavaDoc API documentation is also available as a ZIP archive.

#### Source Code

The ImageJ Java source consists of 132,000 lines of code in 348 files. It is available online and as zip archives.

#### Example Images

31 downloadable sample images and stacks are available in ImageJ's *File>Open* Samples submenu. These images, and more, are also available as a 8.2MB zip archive.

Download the latest release of the plugin (1.2.1)

The ZIP file is a plugin for <u>ImageJ</u> or <u>Fiji</u>. It contains all the necessary libraries (JAR files) to load and run TensorFlow models on any OS: Windows, Mac OSX, Linux.

One-click Installation: Unzip the ZIP file and drag-and-drop the 5 JAR files into ImageJ or Fiji. Restart Fiji.

- LeepImageJ for CPU
- LeepImageJ for GPU



### **DeepImageJ Bundled Models**

#### **U-Net Pancreatic Segmentation**

Binary segmentation - Phase contrast microscopy



#### Jones Virtual Staining

Virtual labelling - Light transmission microscopy



### **CARE Isotropic Reconstruction**

Isotropic reconstruction - Fluorescence microscopy

### Noise2Void Denoising

Denoising - Fluorescence microscopy

### MT<sub>3</sub> Virtual Staining

Virtual labelling - Light transmission microscopy

### Widefield TxRed Super-resolution

Super-resolution - Fluorescence microscopy







🛓 ImageJ				_		×	
File Edit Image Process Analyze	Plugins Win	dow Help					
$\Box \bigcirc \Box \heartsuit / \measuredangle \ddagger \land \land$	Macros		•	8 🖊		≫	
Nand (tracing) tool	Shortcuts		•[				
	Utilities		۰				
	New		۲				
	Compile and	Run					
	Install	Ctrl+Shift+M					
	3D		۰				
	Analyze		•				
	DeepImageJ	J	•	DeepIn	nageJ F	Run	
	Examples		۲	DeepIn	nageJ E	Explore	
	Filters		•	DeepIn	nageJ B	Build Bu	undledModel
	Graphics		٢				
	Input-Output						
	Scripts		۲				
	Stacks		۲				
	Tools		۲				



#### 실 DeeplmageJ Explore [1.2.1]

Х

C:\tools\IJ153	-~1\ImageJ\	models\	C:\tools\IJ153-~1\ImageJ\models\u-net_pancreatic_segmentation\						
Name	Model	Loadin	Li Net Demorratio Call Serve		Feature	Value			
U-Net Pancreatic .	11.04 Mb	492.9	U-Net Pancreatic Cell Segn	nentation	Tag	tf.saved_model.tag_const			
			DeepimageJ, Ignacio Arganda-Ca	rreras	Signature	tf.saved_model.signature			
			(PhC-C2DL-PSC)		Model size	11.04 Mb			
			URL: https://github.com/deepimagej/models/u-net_p		Graph size	890279			
					Metagraph size	1202106			
	Version: 0.1		Patch policy	8 mini.					
			Date: Jun 23, 2020	Date: Jun 23, 2020		816			
			Reference:		Padding	47			
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		Gómez-de-Mariscal E. et al., biorXi	v 2019;	Slices/Channels	1/1				
			Ulman V. et al., Nature Methods 2017; Roppeberger O. et al. MICCAI 2015		Preprocessing	preprocessing.txt (5 lines)			
			Conneberger O. et al., MICCAI 201	5	Postprocessing	postprocessing.txt (15 line			
			Test		Test input image	exampleImage.tiff (720x57			
			Input size: 720x576		Test output image	resultImage.tiff (720x576)			
			Output size: 720x576		Input name(form)	input(NHWC)			
			Runtime: 2.8 s		Output name(form)	output(NHWC)			
			Pixel Size: 1,60E-04cmx1,60E-04cm						
About	Refresh	Close	Help	Ar	chitecture	Run on Test Image			











### Examples for DL applications

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- HD Bet for brain extraction
- FatSegNet





### **NVIDIA Clara**



https://developer.nvidia.com/clara



### Nvidia Al-assisted annotation (AIAA) for 3D Slicer



https://github.com/NVIDIA/ai-assisted-annotation-client/tree/master/slicer-plugin







### Install Slicer And add plugin:









### Sample data -> Brain Tumor







# Go to Segment Editor

٩,	📓 Annotations 🛛 🔻		÷	٠			Ŵ	۲	<b>A</b>	* **	<u>(</u>	
	🔣 Annotations											
	📒 Data											
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	Models											
	I Scene Views											
	👍 Segment Editor											
it sup y Marl	🦄 Segmentations		cene. ns are	fiducia	l poin	its, ru	ilers, a	nd regi	ons of i	interest	t (ROIs	).
<u>e docu</u>	Transforms											
	腸 View Controllers											
	🌍 Volume Rendering											
	🖤 Volumes											
	Welcome to Slicer											
	Wizards	Þ										
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	Segmentation	×	👍 s	Gegmen	t Edit	tor						
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	Diffusion	►	S	pecializ	ed						►	
	Filtering	Þ										



### Create new Segment





### Click "Nvidia AIAA" effect





In "Segment from boundary points" section, select "annotation\_mri\_brain\_tumors\_t1ce\_tc" (model trained to segment tumor on contrast-enhanced brain MRI)

Nvidia AIAA				
NVIDIA AI-A	assisted Annotation for automatic and boundary points based	segmentation <u>Show details.</u>		
NVidia AIAA	server: enter server address or leave empty to use default			- C
🔻 Auto-se	egmentation			
Model: seg	gmentation_ct_spleen		•	🥯 Start
- Segmer	nt from boundary points (DExtr3D)			
Model:	annotation_mri_brain_tumors_t1ce_tc		• 7	Start
Boundary:	\$	Ì	. 👤	Start
▶ DeepGr	ow			



### Click "Place markup point" button,

Ividia AIAA								
NVIDIA AI-A	NVIDIA AI-Assisted Annotation for automatic and boundary points based segmentation Show details.							
NVidia AIAA	server: enter server address or leave empty to use default		- C					
▼ Auto-se	egmentation							
Model: seg	gmentation_ct_spleen	•	Start 🕺					
🔻 Segmer	nt from boundary points (DExtr3D)							
Model:	annotation_mri_brain_tumors_t1ce_tc		Start					
Boundary:		i j						
▶ DeepGrow								
	S Undo							



# and click near the edge of the tumor on all 6 sides in slice views, then click "Start"



NVIDIA AI-A	ssisted Annotation for automatic and boundary points based	segmentation Show details.	
NVidia AIAA	server: enter server address or leave empty to use default		- C
▼ Auto-se	egmentation		
Model: seg	gmentation_ct_spleen		👻 🥯 Start
🔻 Segmer	nt from boundary points (DExtr3D)		
Model:	annotation_mri_brain_tumors_t1ce_tc		T Start
Boundary:	\$	Ū.	, 🖉
▶ DeepGr	ow		





# click "Show 3D" button above the segment list.

▶ н	elp & A	cknowledgement					
Segme	ntatior	n: Segmentation					•
Master	volum	e: MRBrainTumor1				-	
		🕂 Add	Remove	is Show 3D	r 🌖	Segmentations	•
• •				Name			P
÷		Segment_1					1
- 77							





### Go to Sample Data module and load "CTACardio" data set




### Go to Segment Editor





### Create a new segment

Segme	ntatior	n: Segmentation	Segmentation						
Master volume:		ne: CTACardio	CTACardio						
		🕂 Add	- Remove	(ĝi Show 3D	🔹 🌖 Se	gmentations			
				Name		2			
4		Segment_1				0			



### Rename to liver

Segmentation: Segmentation								
4astei	r volum	e: CTACardio	CTACardio 👻					
		🕂 Add	Remove	Show 3D	•	Segmentations	-	
~ •				Name			P	
•		liver					0	



# Click "Nvidia AIAA" effect, "Segment from boundary points" section





# Select "annotation\_ct\_liver" (model trained to segment liver in portal-venous-phase CT image)

T FIGHT FILEFOR							
NVIDIA AI-Assisted Annotation for automatic and boundary points based segmentation Show details.							
NVidia AIAA server: enter server address or leave en	npty to use default		- C				
<ul> <li>Auto-segmentation</li> </ul>							
Model: segmentation_ct_spleen	Model: segmentation_ct_spleen						
<ul> <li>Segment from boundary points (DExtr3D)</li> </ul>							
Model: annotation_ct_liver							
Boundary:		<u>İ</u>	Start				
▶ DeepGrow							



### Click "Place markup point" button, and click near the edge of the liver on all 6 sides in slice views, then click "Start"







### DeepGrow model requires own GPU server ...

▼ DeepGrow					
Model:		-			
Foreground (+ve) Points:		, in the second se			
Background (-ve) Points:	\$				

#### Setup steps:

- 1. https://github.com/NVIDIA/nvidia-docker
- 2. https://docs.nvidia.com/clara/tlt-mi/clara-train-sdk-v3.0/nvmidl/installation.html#installation
- 3. <u>https://docs.nvidia.com/clara/tlt-mi/clara-train-sdk-v3.0/aiaa/installation.html#installation</u>
- 4. https://docs.nvidia.com/clara/tlt-mi/clara-train-sdk-v3.0/aiaa/quickstart.html#running-aiaa
- 5. <u>https://docs.nvidia.com/clara/tlt-mi/clara-train-sdk-v3.0/aiaa/tutorial/deepgrow.html</u>



### ngc registry model list nvidia/med/\*

#### root@3ee2ce48b8fc:/opt/nvidia# ngc registry model list nvidia/med/\*

Name	Repository	Latest Version	Application	Framework	Precision	Last Modified	Permission
classification_chest	nvidia/med/classific	1	Classification	Medical	FP32	Sep 25, 2020	locked
_xray clara_ct_seg_spleen_   amp	nvidia/med/clara_ct_	1	Segmentation	   Medical 	   FP32 	   Sep 25, 2020 	unlocked     I I
clara_ct_seg_spleen_	nvidia/med/clara_ct_	1	Segmentation	Medical	FP32	Sep 25, 2020	unlocked
no_amp clara_ct_seg_liver_a   nd_tumor_amp	seg_spleen_no_amp nvidia/med/clara_ct_ seg_liver_and_tumor_ amp	1	Segmentation	   Medical 	   FP32 	   Sep 25, 2020   	unlocked   
clara_ct_seg_liver_a   nd_tumor_no_amp	nvidia/med/clara_ct_ seg_liver_and_tumor_	1	Segmentation	Medical   	,   FP32 	,   Sep 25, 2020   	unlocked   
clara_mri_seg_brain_   tumors_br16_full_amp	nvidia/med/clara_mri _seg_brain_tumors_br 16_full_amp	1	Segmentation	Medical	FP32	Sep 25, 2020	unlocked   



### After installation of docker + nvidia docker + SSH tunnel

export dockerImage=nvcr.io/nvidia/clara-train-sdk:v3.0 sudo docker pull \$dockerImage

sudo docker run -it --rm --gpus all --shm-size=1G --ulimit memlock=-1 --ulimit stack=67108864 -p 80:80 -v /mnt/ResearchFS/steffen/clara-experiments:/workspace/clara-experiments \$dockerImage /bin/bash

ngc registry model download-version nvidia/med/clara\_train\_deepgrow\_aiaa\_inference\_only:1

start\_aas.sh --workspace /clara-experiments/aiaa-1



lvidia AIAA							
NVIDIA AI-Assisted Annotation for automatic and boundary points based segmentation Show details.							
NVidia AIAA server: http://127.0.0.1:8080/							
Auto-segmentation							
Segment from boundary points (DExtr3D)							
TeepGrow							
Model:							
Foreground (+ve) Points:	2	<u> </u>					
Background (-ve) Points:		Ť.					







### **Examples for DL applications**

- DeepImageJ
- Nvidia Clara integration in Slicer
- HD Bet for brain extraction
- FatSegNet





### HDBET

- Brain extraction is important preprocessing step neuroimaging studies
- Most tools aimed at healthy volunteers and fail in pathologies
- HD-BET is DL based algorithm and outperforms six popular, publicly available brain extraction algorithms (FSL BET, AFNI 3DSkullStrip, Brainsuite BSE, ROBEX and BEaST)



RESEARCH ARTICLE | 🗇 Open Access | 💿 😧 🗐 🏵

### Automated brain extraction of multisequence MRI using artificial neural networks

Fabian Isensee, Marianne Schell, Irada Pflueger, Gianluca Brugnara, David Bonekamp, Ulf Neuberger, Antje Wick, Heinz-Peter Schlemmer, Sabine Heiland, Wolfgang Wick ... See all authors  $\checkmark$ 

First published: 12 August 2019 | https://doi.org/10.1002/hbm.24750 | Citations: 7



BET, BEaST, and MONSTR tend to underestimate the brain mask

3DSkullStrip, BSE, and ROBEX tend to overestimate





### Install

Note that you need to have a python3 installation for HD-BET to work. Please also make sure to install HD-BET with the correct pip version (the one that is connected to python3). You can verify this using the --version command:

(dl\_venv) fabian@Fabian:~\$ pip --version
pip 20.0.2 from /home/fabian/dl\_venv/lib/python3.6/site-packages/pip (python 3.6)

If it does not show python 3.X, you can try pip3. If that also does not work you probably need to install python3 first.

Once python 3 and pip are set up correctly, run the following commands to install HD-BET:

1. Clone this repository:

git clone https://github.com/MIC-DKFZ/HD-BET

2. Go into the repository (the folder with the setup.py file) and install:

cd HD-BET pip install -e .

3. Per default, model parameters will be downloaded to ~/.hd-bet\_params. If you wish to use a different folder, open HD\_BET/paths.py in a text editor and modify folder\_with\_parameter\_files



### Installing Python packages is trivial, right?



MY PYTHON ENVIRONMENT HAS BECOME SO DEGRADED THAT MY LAPTOP HAS BEEN DECLARED A SUPERFUND SITE.

https://xkcd.com/1987/



### Miniconda to the rescue!

https://docs.conda.io/en/latest/miniconda.html

-> Installers for Windows, Linux, Mac ©

Anaconda Prompt (Miniconda3)

base) C:\Users\uqsbollm>





### This sounds easy!

But ... (torch is not available for windows in an updated version)

(base) C:\Github>cd HD-BET

- (base) C:\Github\HD-BET>pip install -e .
- Obtaining file:///C:/Github/HD-BET
- Requirement already satisfied: numpy in c:\users\uqsbollm\miniconda3\lib\site-packages (from HD-BET==1.0)
   (1.19.2)
- ERROR: Could not find a version that satisfies the requirement torch>=0.4.1 (from HD-BET==1.0) (from vers ions: 0.1.2, 0.1.2.post1, 0.1.2.post2)
- ERROR: No matching distribution found for torch>=0.4.1 (from HD-BET==1.0)



### Conda to the rescue again:

(base) C:\Github\HD-BET>conda install pytorch torchvision torchaudio cpuonly -c pytorch Collecting package metadata (current\_repodata.json): \ \_

Installing collected packages: HD-BET Attempting uninstall: HD-BET Found existing installation: HD-BET 1.0 Uninstalling HD-BET-1.0: Successfully uninstalled HD-BET-1.0 Running setup.py develop for HD-BET Successfully installed HD-BET



### Working?

# (base) C:\Github\HD-BET\HD\_BET>hd-bet 'hd-bet' is not recognized as an internal or external command, operable program or batch file.



### Windows Subsystem for Linux to the rescue:

https://docs.microsoft.com/en-us/windows/wsl/install-win10

(base) uqsbollm@uqsbollm-7952:/mnt/c/Github/HD-BET\$ hd-bet -i example.nii

#### \*

If you are using hd-bet, please cite the following paper:

Isensee F, Schell M, Tursunova I, Brugnara G, Bonekamp D, Neuberger U, Wick A, Schlemmer HP , Heiland S, Wick W,Bendszus M, Maier-Hein KH, Kickingereder P. Automated brain extraction of multi-sequence MRI using artificialneural networks. arXiv preprint arXiv:1901.11341, 201 9.

\*

Downloading https://zenodo.org/record/2540695/files/0.model?download=1 ...



### At least starting ③

(base) uqsbollm@uqsbollm-7952:/mnt/c/Github/HD-BET\$ hd-bet

#### \*

If you are using hd-bet, please cite the following paper:

Isensee F, Schell M, Tursunova I, Brugnara G, Bonekamp D, Neuberger U, Wick A, Schlemmer HP , Heiland S, Wick W,Bendszus M, Maier-Hein KH, Kickingereder P. Automated brain extraction of multi-sequence MRI using artificialneural networks. arXiv preprint arXiv:1901.11341, 201 9.

usage: hd-bet [-h] -i INPUT [-o OUTPUT] [-mode MODE] [-device DEVICE] [-tta TTA] [-pp PP] [-s SAVE\_MASK] [--overwrite\_existing OVERWRITE\_EXISTING] hd-bet: error: the following arguments are required: -i/--input



### Getting there?

#### (base) uqsbollm@uqsbollm-7952:/mnt/c/Github/HD-BET\$ hd-bet -i example.nii

#### \*

If you are using hd-bet, please cite the following paper:

Isensee F, Schell M, Tursunova I, Brugnara G, Bonekamp D, Neuberger U, Wick A, Schlemmer HP , Heiland S, Wick W,Bendszus M, Maier-Hein KH, Kickingereder P. Automated brain extraction of multi-sequence MRI using artificialneural networks. arXiv preprint arXiv:1901.11341, 201 9.

#### 

No.

RuntimeError: Found no NVIDIA driver on your system. Please check that you have an NVIDIA G PU and installed a driver from http://www.nvidia.com/Download/index.aspx



### Run without GPU:

(base) uqsbollm@uqsbollm-7952:/mnt/c/Github/HD-BET\$ hd-bet -i example.nii -device cpu -mode fast -tta 0

#### \*\*\*\*

If you are using hd-bet, please cite the following paper:

Isensee F, Schell M, Tursunova I, Brugnara G, Bonekamp D, Neuberger U, Wick A, Schlemmer HP , Heiland S, Wick W,Bendszus M, Maier-Hein KH, Kickingereder P. Automated brain extraction of multi-sequence MRI using artificialneural networks. arXiv preprint arXiv:1901.11341, 201 9.

File: example.nii preprocessing... image shape after preprocessing: (171, 160, 117) prediction (CNN id)...



### Working 🙂





### Examples for AI models

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- FatSegNet





### FatSegNet - Adipose Segmentation on Abdominal Dixon MRI

Magnetic Resonance in Medicine / Volume 83, Issue 4

FULL PAPER 🔂 Open Access 💿 😧

## FatSegNet: A fully automated deep learning pipeline for adipose tissue segmentation on abdominal dixon MRI

Santiago Estrada ➡, Ran Lu, Sailesh Conjeti, Ximena Orozco-Ruiz, Joana Panos-Willuhn, Monique M. B. Breteler, Martin Reuter

First published: 21 October 2019 https://doi.org/10.1002/mrm.28022

• segmenting visceral and subcuteneous adipose tissue on fat images from a two-point Dixon sequence.



### Usage

We wrap our tool on a docker image, so there is no need to install any library dependencies or drivers, the only requirement is to have docker (cpu) or nvidia-docker(gpu) installed.

Prerequisites:

- Docker (For running on CPU) (https://docs.docker.com/install/)
- NVIDIA-Docker (For running on GPU ) (https://github.com/nvidia/nvidiadocker/wiki)



### **Tool installation**

- 1. Run on the terminal sudo git clone https://github.com/reuterlab/FatSegNet.git or download .zip file from the github repository
- 2. From the download repository directory run on the terminal:
- bash build\_docker\_cpu.sh for CPU (In case GPU is not available)
- bash build\_docker\_gpu.sh for GPU



### Let's try in WSL (docker in latest windows 10 runs in WSL)

(base) uqsbollm@uqsbollm-7952:~/Github\$ git clone https://github.com/reuter-lab/FatSegNet.git Cloning into 'FatSegNet'... remote: Enumerating objects: 129, done. remote: Counting objects: 100% (129/129), done. remote: Compressing objects: 100% (91/91), done. Receiving objects: 24% (50/208), 32.34 MiB | 3.11 MiB/s



### **Running FatSegNet**

docker run -it --rm --name fatsegnet -u \$(id -u) -v \$PWD/data/:/tool/Data -v \$PWD/output:/tool/Output adipose\_tool:cpu\_v1 -loc

Loading participant from file : /tool/Data/participants.csv
Loading Subject subject_1
Loading Fat Image /tool/Data/subject_1/FatImaging_F.nii.gz Volume will be sample from (1.7361, 1.7361, 3.0) to [1.9531, 1.9531, 5.0] Volume will be resize from (256, 208, 74) to [256, 224, 72]
Uoading Water Image /tool/Data/subject_1/FatImaging_W.nii.gz Volume will be sample from (1.7361, 1.7361, 3.0) to [1.9531, 1.9531, 5.0] Volume will be resize from (256, 208, 74) to [256, 224, 72]
Run Abdominal Localization Block
Evaluating coronal



### Worked?

General Contrast	Color Map I	nfo Metadata	3					
Linear Contrast Adjustment:								
Minimum: 0.0	Level:	249.5	Reset					
Maximum: 499.0	Window:	499.0	Auto					
Curve-Based Contrast								
Index Into Color Map	200 Image Int	1000	0 500					
Selected control point Id: 1 x: 0.0	:: у: 0.000		+ -					







# Networks are sensitive to data ranges -> intensity normalization







### For debugging it can help to "de-dockerize"

Dockerfile shows what's in container:

#FROM tensorflow/tensorflow:1.6.0-py3 FROM tensorflow/tensorflow:1.6.0-gpu-py3 #FROM tensorflow/tensorflow:latest-gpu-py3 ##Install custom libraries RUN apt-get update && apt-get install -y --no-install-recommends \ python3-tk # install dependencies from python packages RUN pip3 --no-cache-dir install \ pandas = 0.21.0scikit-learn==0.19.1 \ scipy==1.1.0\ scikit-image==0.15.0 \ SimpleITK==1.1.0 \ nibabel==2.2.1 \ keras==2.2.4 \ numpy = 1.15.4## Copying application code (present working directory) and configuration to docker image COPY ./tool /tool WORKDIR "/tool" RUN bash /tool/bash\_profile

ENTRYPOINT ["python3","./run\_FatSegNet.py"]



### Reproducing the environment of the container

```
(base) C:\Users\uqsbollm>conda install -c conda-forge tensorflow=1.6.0
Collecting package metadata (current_repodata.json): done
Solving environment: failed with initial frozen solve. Retrying with flexible solve.
Collecting package metadata (repodata.json): done
Solving environment: failed with initial frozen solve. Retrying with flexible solve.
Solving environment: |
Found conflicts! Looking for incompatible packages.
This can take several minutes. Press CTRL-C to abort.
failed
```

UnsatisfiableError: The following specifications were found to write the state of the specification of the second to be incompatible with the existing python installation in your environment:

Specifications:

- tensorflow=1.6.0 -> python[version='>=3.5,<3.6.0a0|>=3.6,<3.7.0a0']</pre>

Your python: python=3.8



### Tensorflow versions require specific Python versions:

https://anaconda.org/conda-forge/tensorflow/files?page=2

conda 28.2 (1) | win-64/tensorflow-1.6.0-MB py36\_0.tar.bz2

(base) C:\Users\uqsbollm>conda create -n fatsegnet python=3.6 Collecting package metadata (current\_repodata.json): done Solving environment: done

```
## Package Plan ##
```

environment location: C:\Users\uqsbollm\Miniconda3\envs\fatsegnet

```
added / updated specs:
```

- python=3.6


## Install tensorflow from conda-forge

(base) C:\Users\uqsbollm>conda activate fatsegnet

(fatsegnet) C:\Users\uqsbollm>conda install -c conda-forge tensorflow==1.6.0



## Thank you

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CRICOS code 00025B

