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User Guide

Voronoi Health Analytics Inc.

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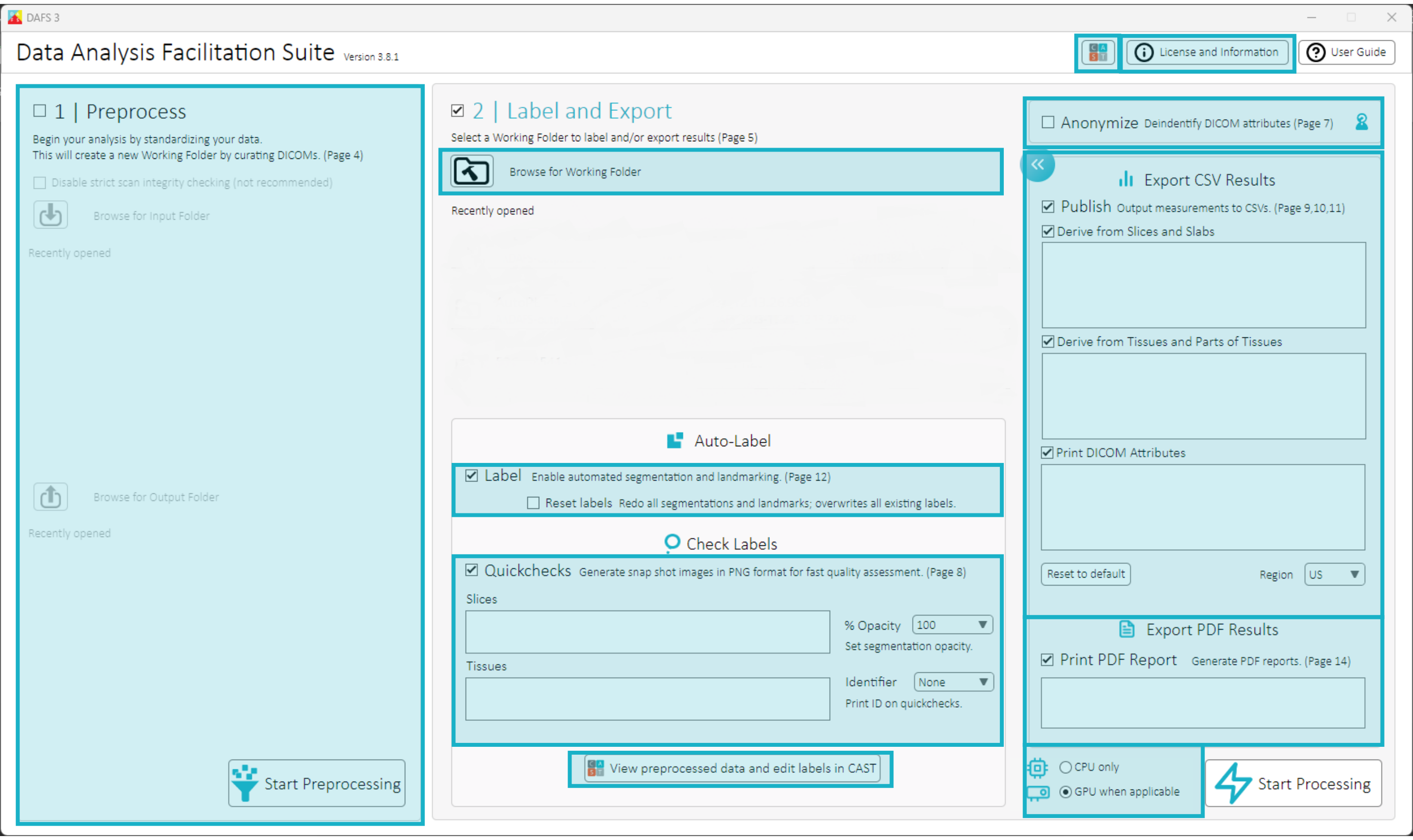
Home

This is an interactive user guide. Click on the blue boxes to learn more about each part of DAFS or click on a menu item on the right.
You can return here anytime to check out other features by clicking the 🏠 icon.



DAFS 3

Data Analysis Facilitation Suite Version 3.8.1

☐ 1 | Preprocess

Begin your analysis by standardizing your data.
This will create a new Working Folder by curating DICOMs. (Page 4)

☐ Disable strict scan integrity checking (not recommended)

☑ 2 | Label and Export

Select a Working Folder to label and/or export results (Page 5)

☑ Label Enable automated segmentation and landmarking. (Page 12)

☐ Reset labels Redo all segmentations and landmarks; overwrites all existing labels.

☑ Quickchecks Generate snap shot images in PNG format for fast quality assessment. (Page 8)

Slices

Tissues

% Opacity: 100
Set segmentation opacity.

Identifier: None
Print ID on quickchecks.

☐ Anonymize Deidentify DICOM attributes (Page 7)

☑ Publish Output measurements to CSVs. (Page 9,10,11)

☑ Derive from Slices and Slabs

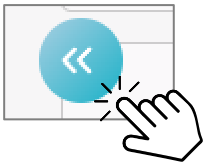
☑ Derive from Tissues and Parts of Tissues

☑ Print DICOM Attributes

Region: US

☑ Print PDF Report Generate PDF reports. (Page 14)

○ CPU only
● GPU when applicable



Use these buttons to
open helpful menus!

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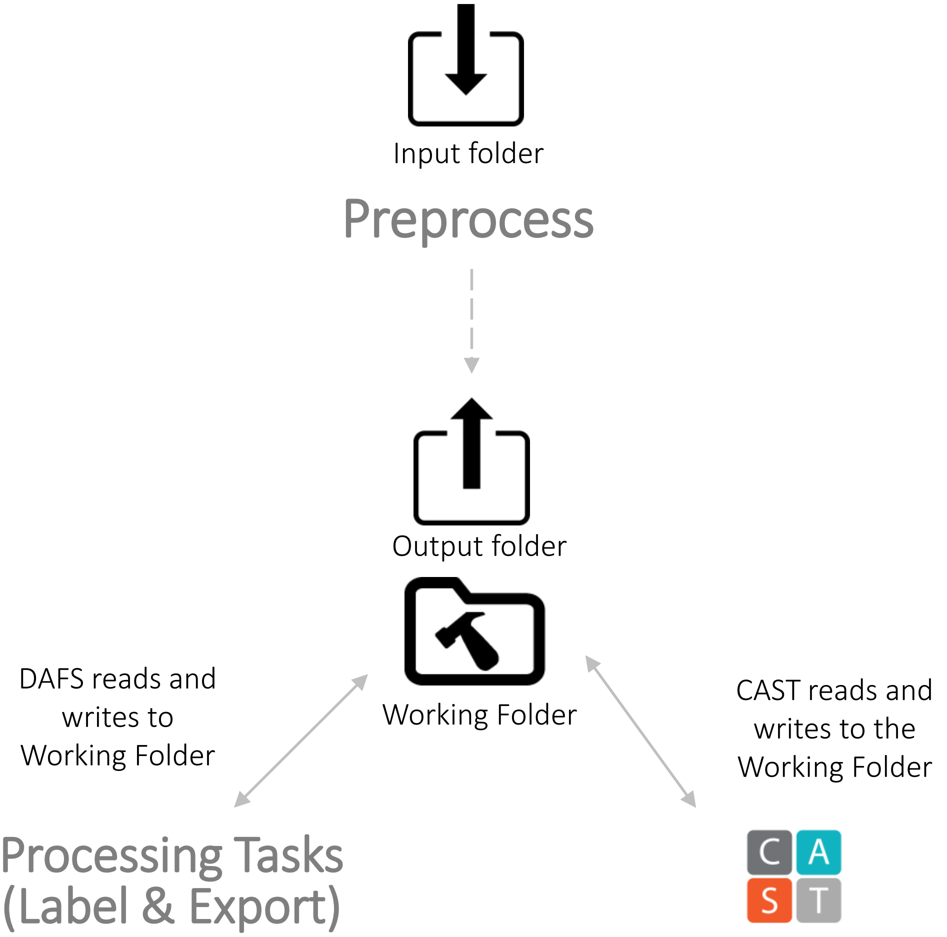
Overview



Input folder

Preprocess

Output folder

Working Folder

DAFS reads and
writes to
Working Folder

CAST reads and
writes to the
Working Folder

Processing Tasks (Label & Export)

Label

Quickchecks

Anonymize

Publish

Reports

Quality Control

View and edit segmentations

View and edit axial slice landmarks

Preprocessing

Preprocess

Preprocessing will detect all DICOMs within an Input Folder and use the embedded DICOM metadata information to *sort* and *copy* each unique scan into its own folder. It is integral to perform Preprocessing before proceeding with any other processing.

Input Folder – Select any top-level folder containing DICOMs.

- All DICOMs, including those in subfolders within the designated Input Folder will be preprocessed.
- Ensure that no DAFS System Folders (what's this?) are in the Input Folder path.

Output Folder – Select any folder. DAFS will create a new folder known as the Working Folder (what's this?) within the Output Folder (date & time stamped) and the curated scans will be inside, copied from the Input Folder.

- DAFS will create a Working Folder inside the Output Folder.
- Ensure that no DAFS System Folders are in the Output Folder path.

☑ Disable strict scan integrity checking – DAFS has strict checking for the integrity of the 3D scan reconstructed from the DICOMs. Enable this to override strict checking for slice orthogonality, heterogeneous acquisition numbers and heterogeneous slice orientations.

Preprocessing may take some time depending on the size of the Input folder. For an Input folder containing ~10000 files, curation will take ~12.5 minutes.

Where can I find out which scans did not get preprocessed? Learn more

Preprocess: Configuring CT/PT Mapping Rules

CT and PET mapping rules can be configured in:

%LOCALAPPDATA%\Voronoi Health Analytics\DAFS\dafs_config.json

Example:

```
{
   "version": "0.0.2",
   "match_attrs": ["PatientID", "StudyInstanceUID"],
   "match_regex": {"SeriesDescription": ".*[^N]AC.*"}
}
```

"match_attrs”: Mapping based on matching attributes: Specify a list of attributes that must be exactly matching between the CT and PET.

“match_regex”: Regex matching: Specify a list of attributes which values must match specific regular expressions. We recommend using this in conjunction with “match_attrs”, not on its own.

After Preprocessing is run and there are both valid CT scans and PT scans in your dataset, a CT to PT mapping csv will be made in the Working Folder with matching CT-PT pairs according to the mapping rules. This csv can be manually edited if required.

Processing and Exporting

Working Folder

A Working Folder is generated within the Output Folder following Preprocessing and is the location in which DAFS and CAST will both read and write. A Working Folder will be generated with a date & time stamp. DAFS will update the Working Folder each time Start Processing is clicked.

Working Folder – Select a folder generated by Preprocessing. This folder will likely have a date and time stamp if the name has not been modified.
Generated after preprocessing is complete.

- DAFS and CAST will read and write to this folder.

What's inside a Working Folder?

Learn more

Click to see a full map of a Working Folder.

Curated Scans

These are folders, each containing a unique scan that has been curated via Preprocessing.

DAFS-report_date_time folders

These are folders that store processing information and reports from each DAFS run. A DAFS-report folder that is date and time stamped will be generated each time DAFS is run on the same Working Folder, acting as a historical record of DAFS processes. Each DAFS-report may include one or more of the following subfolders depending on the options chosen.

logs

Contains logs on errors that may have occurred during processing. The contents in this folder may help with troubleshooting if the DAFS output was not as expected. Generated every run - **It is highly recommended to check this folder after processing**.

csvs

Contains results from Preprocessing, Anonymization and Publish in csv format.

quickchecks

Contains visual media to aid with quality assessment in PNG format.

reports

Contains results from enabling PDF reports

Representation of a folder structure after three DAFS runs following a suggested workflow.

For more suggested workflows… Learn more

Output Folder

- Working Folder
  - csvs
    - *DICOM Curation.csv*
  - logs
    - *****-failures-log.txt*
  - DAFS-report_2022-00-01_00.00.00.000
    - logs
      - ******-failures-log.txt*
    - quickchecks
    - csvs
      - *Anonymization csv*
    - reports
  - DAFS-report_2022-00-02_00.00.00.000
    - logs
      - ******-failures-log.txt*
    - csvs
      - *Publish csvs*
  - scan_1
  - scan_2
  - scan_3
  - scan_4
  - scan_5
  - scan_6

1st run DAFS-report
- Preprocessing

Preprocessing must always be run first.

Find the curated ID to original file path map here.

Any processing failures can be found in the logs folder.

2nd run DAFS-report
- Anonymize
- Segment Tissues
- Annotate slices
- Quickchecks

You may also choose to directly Publish without quality control in this run.

Find quickchecks here for quality assessment.

Find an anonymization report here.

Find PDF reports here.

3rd run DAFS-report
- Publish

You may choose to run Publish and Quickchecks in multiple runs to generate the most up-to-date results after segmentation and/or annotation quality control.

Find measurement results here for all scans in the Working Folder.

These are folders each containing a unique, curated scan generated by Preprocessing in the 1st run.

Auto-Label

Enable automated segmentation and landmarking.

Reset Labels

Enabling this checkbox will prompt DAFS to replace existing segments. If manual corrections have been done in CAST, it is likely that you should NOT use this feature. Segmentations that are replaced cannot be recovered. Please use with caution.

Quickchecks

Generate visual media for efficient quality checking of segmentations in the Working Folder. Run before, during and/or after segmentation quality control to update quickchecks with the most recent changes. Find results in the quickchecks folder.

Slices

Entries
Head;C1;C2;C3;C4;C5;C6;C7;T1;T2;T3;T4;T5;T6;T7;T8;T9;T10;T11;T12;L1;L2;L3;L4;L5;L6;LSTV;Sacrum;Femur;Knee;Tibia;Feet

Make Quickchecks with slice levels selected in the text area. Defining Slices will create sagittal and coronal .pngs that display the annotated slices in the image. Axial images will also be sampled from selected Slice levels. If Slices are selected in conjunction with Tissues, Slices will take priority in axial quickcheck sampling. Leave empty for equal sampling throughout the scan.

Tissues Tissue Dictionary

Make Quickchecks with Tissues selected in the text area. Using tissues will create sagittal and coronal .pngs that are sampled within the ROI of the tissue. Axial images will also be sampled within the ROI of the tissue **if no Slices are selected**. If Slices are selected in conjunction with Tissues, Slices will take priority in axial quickcheck sampling.

Opacity Control

Control the level of opacity level of segmentation displayed on quickchecks.

Identifier

Enable printing of an image identifier on the quickcheck.

- Options include None, PatientID, PatientName, SeriesNumber, StudyID, AccessionNumber and MRN.
- If the selected identifier does not exist for a scan, no identifier will be printed on the quickcheck.

PNG files naming convention

- annotation-coronal/annotation-sagittal – images displaying annotated slices.
- tissues_and_annotations-axial – images displaying tissues and annotated slices, with annotated slices taking priority in sampling if selected.
- tissues-coronal/tissues-sagittal – images displaying tissues.

Anonymize

Find the anonymization report in the csvs folder.

Attribute	Method of anonymization
InstanceCreatorUID	remove
InstitutionAddress	remove
ReferringPhysicianAddress	remove
ReferringPhysicianTelephoneNumbers	remove
StationName	remove
StudyDescription	remove
SeriesDescription	remove
InstitutionalDepartmentName	remove
PhysiciansOfRecord	remove
NameOfPhysiciansReadingStudy	remove
OperatorsName	remove
AdmittingDiagnosesDescription	remove
DerivationDescription	remove
PatientBirthTime	remove
OtherPatientIDs	remove
OtherPatientNames	remove
PatientAge	remove
PatientSize	remove
PatientWeight	remove
PatientAddress	remove
MedicalRecordLocator	remove
EthnicGroup	remove
Occupation	remove
AdditionalPatientHistory	remove
PatientComments	remove
ProtocolName	remove
ImageComments	remove
RequestAttributesSequence	remove
ContentSequence	remove
StorageMediaFileSetUID	remove

Attribute	Method of anonymization
SOPInstanceUID	change
AccessionNumber	change
InstitutionName	change
ReferringPhysicianName	change
PerformingPhysicianName	change
ReferencedSOPInstanceUID	change
PatientName	change
PatientID	change
PatientBirthDate	change
PatientSex	change
StudyInstanceUID	change
StudyID	change
FrameOfReferenceUID	change
SynchronizationFrameOfReferenceUID	change
UID	change
ReferencedFrameOfReferenceUID	change
RelatedFrameOfReferenceUID	change

Non-anonymizable attributes (3D scan integrity)

SeriesInstanceUID
AcquisitionNumber
SeriesNumber
AnatomicalOrientationType
ImageOrientationPatient
ImagePositionPatient
PixelData
Rows
Columns

PixelSpacing
SliceLocation
SliceThickness
RescaleIntercept
RescaleSlope
PhotometricInterpretation
BitsAllocated
BitsStored
HighBit

Publish

Compile information derived from DICOMs, segmentations and landmarks into csv files. Multiple entries in textboxes are possible by delimiting each entry with a semicolon. See the Publish CSV Dictionary for column definitions. **Cross sectional areas for volumetric slabs are averaged across all slices within the slab*.

Region-Of-Interest (ROI) Constructor

Derive from Slices and Slab(s)

Use anatomical locations to derive tissue measurements by defining vertebral level Slice Annotations (inputs are case insensitive).

Examples:

- FULL_SCAN - use measurements from the entire scan.
- L3mid - use measurements from L3mid slice only (cross-sectional area only).
- T1start-to-L5end – use measurements from the top of T1 vertebrae to bottom of L5 vertebrae.
- avg-T12mid[3] – use measurements at T12mid averaged across 3 slices above and below.
- L1start-to-L1end – use measurements from the top of L1 to bottom of L1 vertebrae.
- L1 – equivalent to L1start-to-L1end.
- ScanStart – defined as the top of the scan; the first slice. ScanEnd is defined as the bottom of the scan; the last slice.

Derive from Tissues and Parts of Tissues

Tissue Dictionary

Select tissues and HU ranges to derive measurements from.

Examples:

- ALLSKM – derive measurements from total skeletal muscle within the scan.
- ALLSKM[-29,150] – derive measurements from total skeletal muscle within the range of -29 to 150 HU only found within the scan.
- VAT[-150,-50]-U-SAT[-190,-30] – derive measurements from VAT within -150 to -50 HU and SAT within -190 to -30 HU combined (unionized) as one segment. Multiple ROIs can be unionized separated by -U-.
- LIV – derive measurements from liver segmentation.
- SPL – derive measurements from spleen segmentation.
- LKID – derive measurements from the left kidney segmentation.

Print DICOM Attributes – Choose DICOM header information to include in the CSV

Define a set of DICOM attributes to be printed as columns in the csv. This is useful if you wish to sort scans by certain DICOM attributes when viewing the csv report. Anonymized attributes will print as NA.

How do I view EUR format in MS Excel? Learn more

My data has leading zeroes and is not being displayed correctly in Excel. Learn more

Tissue Dictionary p1

Muscle Group

Colour	Entry	Anatomical ROI
⬜	ALLSKM	Total skeletal muscle within the scan
	ALLSKM_NOARMS	Total skeletal muscle excluding arms
🟪	LPECMJR	Left pectoralis major
🟪	RPECMJR	Right pectoralis major
🟦	LPECMNR	Left pectoralis minor
🟧	RPECMNR	Right-pectoralis-minor
🟧	LTEMPORALIS	Left temporalis
🟨	RTEMPORALIS	Right temporalis
🟨	LMASSETER	Left masseter
🟥	RMASSETER	Right masseter
🟦	LILIOPSOAS	Left iliopsoas
🟩	RILIOPSOAS	Right iliopsoas
🟪	LUPLGSKM	Left upper leg skeletal muscle
🟪	RUPLGSKM	Right upper leg skeletal muscle
🟪	LLWLGSKM	Left lower leg skeletal muscle
🟪	RLWLGSKM	Right lower leg skeletal muscle
🟫	LASKM	Left arm skeletal muscle
🟫	RASKM	Right arm skeletal muscle

Ventral Adipose Tissue Group

Colour	Entry	Anatomical ROI
🟨	VAT	Visceral adipose tissue
🟩	EpAT	Epicardial adipose tissue
🟦	PaAT	Paracardial adipose tissue
🟨	ThAT	Thoracic adipose tissue

SAT (Subcutaneous Adipose Tissue) Group

Colour	Entry	Anatomical ROI
🟦	SAT	Subcutaneous adipose tissue
🟦	LASAT	Left arm SAT
🟦	RASAT	Right arm SAT

IMAT (Intra-muscular Adipose Tissue) Group

Colour	Entry	Anatomical ROI
⬜	ALLIMAT	Intramuscular adipose tissue
	ALLIMAT_NOARMS	Total scan IMAT excluding the arms
🟩	LUPLGIMAT	Left upper leg IMAT
🟩	RUPLGIMAT	Right upper leg IMAT
🟩	LLWLGIMAT	Left lower leg IMAT
🟩	RLWLGIMAT	Right lower leg IMAT
🟩	LAIMAT	Left arm IMAT
🟩	RAIMAT	Right arm IMAT

More tissues on the next page

Tissue Dictionary p2

Fluid Buildup

Colour	Entry	Anatomical ROI
⬜	ASCITES	Ascites; abdominal fluid
🟦	LUNGEFFUSION	Lung effusion; pleural effusion

Cardiovascular

Colour	Entry	Anatomical ROI
⬜	AOC-U-CAAC	enables AOC-CAAC-based agatston score
🟪	AOC	enables AOC-based agatston score
🟥	CAAC	enables CAAC-based agatston score

Organs

Colour	Entry	Anatomical ROI	Colour	Entry	Anatomical ROI
🟥	LIV	Liver	🟪	AO	Aorta
🟧	SPL	Spleen	🟪	AOC	Aortic calcification
🟪	LKID	Left kidney	🟥	CAAC	Cardiac aggregate calcium
🟩	RKID	Right kidney	🟥	LLUNG	Left lung
🟦	GB	Gallbladder	🟦	RLUNG	Right lung
🟨	HRT	Heart	⬜	TRACH	Trachea
🟥	PANC	Pancreas	🟩	BLADDER	Bladder
🟨	BRAIN	Brain	🟫	PROSTATE	Prostate

Bone Group

Colour	Entry	Anatomical ROI
⬜	ALLBONE	Total bone within the scan
	ALLBONE_NOARMS	Total bone within the scan excluding the arms
🟩	LFMRHEAD	Left femoral head
🟧	RFMRHEAD	Right femoral head
🟦	LFMRNECK	Left femoral neck
🟦	RFMRNECK	Right femoral neck
🟧	LFMRSHAFT	Left femoral shaft
🟧	RFMRSHAFT	Right femoral shaft
🟨	LHPBONE	Left hip bone
🟨	RHPBONE	Right hip bone
🟫	TRBCLR	Trabecular bone
⬜	LABONE	Left arm bone
🟦	RABONE	Right arm bone

Reports

Body Composition Reports

Ensure that you have your annotations ready for your scans before running PDF report generation.

Outputs will be sent to a DAFS Report folder in your working folder under the folder name “reports”.

Specify one or more landmarks with each entry separated by a semicolon. The entries are case insensitive.

Examples:

- L3mid (the middle slice of L3).
- avg-L3mid[5] (average cross sectional area 5 slices above and below L3 middle annotation).
- T4start (the top slice marked as T4).
- L5end (the bottom slice marked as L5).
- T12mid;L3mid;avg-L5mid[2] (print reports for T12mid, L3mid and L5mid averaged across 2 slices above and below).
- FULL_SCAN - use measurements from the entire scan.
- T1start-to-L5end – use measurements from the top of T1 vertebrae to bottom of L5 vertebrae.
- L1start-to-L1end – use measurements from the top of L1 to bottom of L1 vertebrae.
- L1 – equivalent to L1start-to-L1end.
- L4start-to-scanend – use measurements from the top of L4 to bottom of scan. “scanend” is used to define the lowest slice of the scan.
- L4start-to-scanstart – use measurements from the top of L4 to top of scan. “scanstart” is used to define the highest slice of the scan.

Organ Reports

Outputs will be sent to a DAFS Report folder in your working folder under the folder name “reports”.

Specify one or more organs with each entry separated by a semicolon. The entries are case insensitive.

Possible entries:
LIV;SPL;LKID;RKID;HRT;CAAC;GB;AO;AOC;LLUNG;RLUNG;TRACH;PANC;BRAIN;BLADDER;PROSTATE

CAST: Segmenter

Select the Working Directory

Toggle blending of the CT/PT (if both are available)
100% CT | 50/50 CT/PT | 100% PT

Toggle maximized viewport

Toggle crosshair (hover on viewport while pressing shift)

Link dual views to scroll and zoom together

Save changes

Change windows of the CT volume

Choose the layout of the Viewport

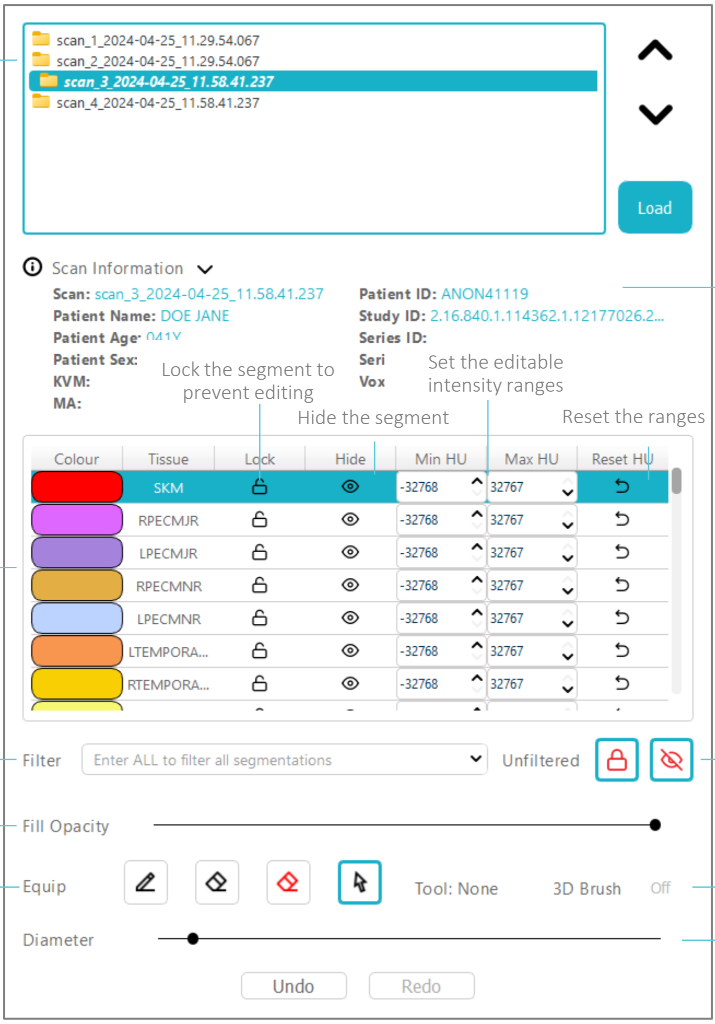
Center the Volume

Toggle slice intersections

Toggle segmentation outline

Change editor

List of scans in the Working Directory; Double-click to load



- scan_1_2024-04-25_11.29.54.067
- scan_2_2024-04-25_11.29.54.067
- ***scan_3_2024-04-25_11.58.41.237***
- scan_4_2024-04-25_11.58.41.237

Scan: scan_3_2024-04-25_11.58.41.237
Patient Name: DOE JANE
Patient Age: 041Y
Patient Sex:
KVM:
MA:
Patient ID: ANON41119
Study ID: 2.16.840.1.114362.1.12177026.2...
Series ID:
Seri
Vox

DICOM Information panel for the loaded scan

Lock the segment to prevent editing

Set the editable intensity ranges

Hide the segment

Reset the ranges

Colour	Tissue	Lock	Hide	Min HU	Max HU	Reset HU
🟥	SKM	🔓	👁	-32768	32767	↺
🟪	RPECMJR	🔓	👁	-32768	32767	↺
🟪	LPECMJR	🔓	👁	-32768	32767	↺
🟧	RPECMNR	🔓	👁	-32768	32767	↺
🟦	LPECMNR	🔓	👁	-32768	32767	↺
🟧	LTEMPORA...	🔓	👁	-32768	32767	↺
🟨	RTEMPORA...	🔓	👁	-32768	32767	↺

List of segmentations; click to enable editing.

Filter for segments in the Segment list.
Use "ALL" to show all segments

Lock and/or hide filtered out segments (prevent overwriting and visualization)

Adjust segmentation fill opacity

Change editing tool;
Shortcuts: 1, 2, 3, 4
Pen, Erase, Erase All, Pointer

Toggle 3D brush

Adjust brush diameter

Filtering the Segment list

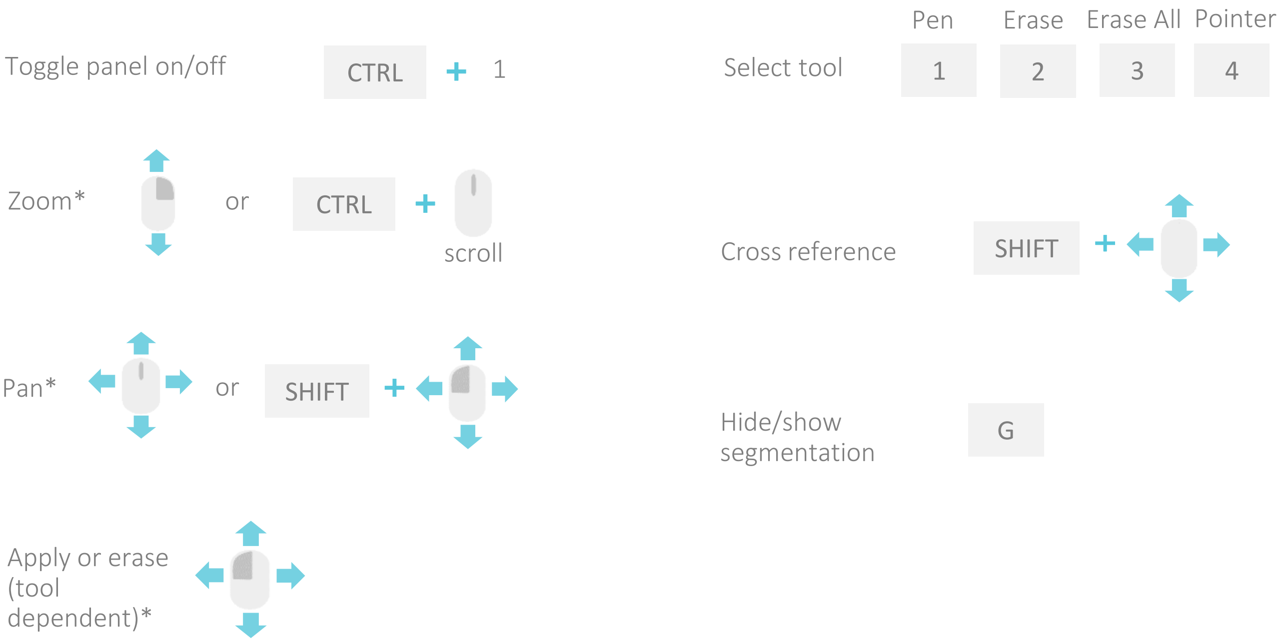
Type in tissue names separated by semi-colon or hyphen and press Enter to display them in the Segment list, thereby, narrowing the focus of segmentation QC to only segments you wish to see and edit. Examples:

- ALL will display all available segments for the scan.
- SKM;VAT will display SKM and VAT segments only.
- SKM-VAT will display all segments between SKM and VAT.

For Unfiltered segments:

🔒	👁	Segments not in the Segment list cannot be overwritten or seen.
🔓	👁	Segments not in the Segment list can be overwritten but not seen.
🔓	👁	Segments not in the Segment list can be overwritten and seen.

Keyboard and mouse shortcuts
(* requires mouse cursor to be on Viewport)



CAST: Annotator

Annotator is a unique tool that enables editing of annotations generated by AVA or creation of manual annotations without AI assistance. While there is a small learning curve, the next three pages will help you get familiar with Annotator and its functions.

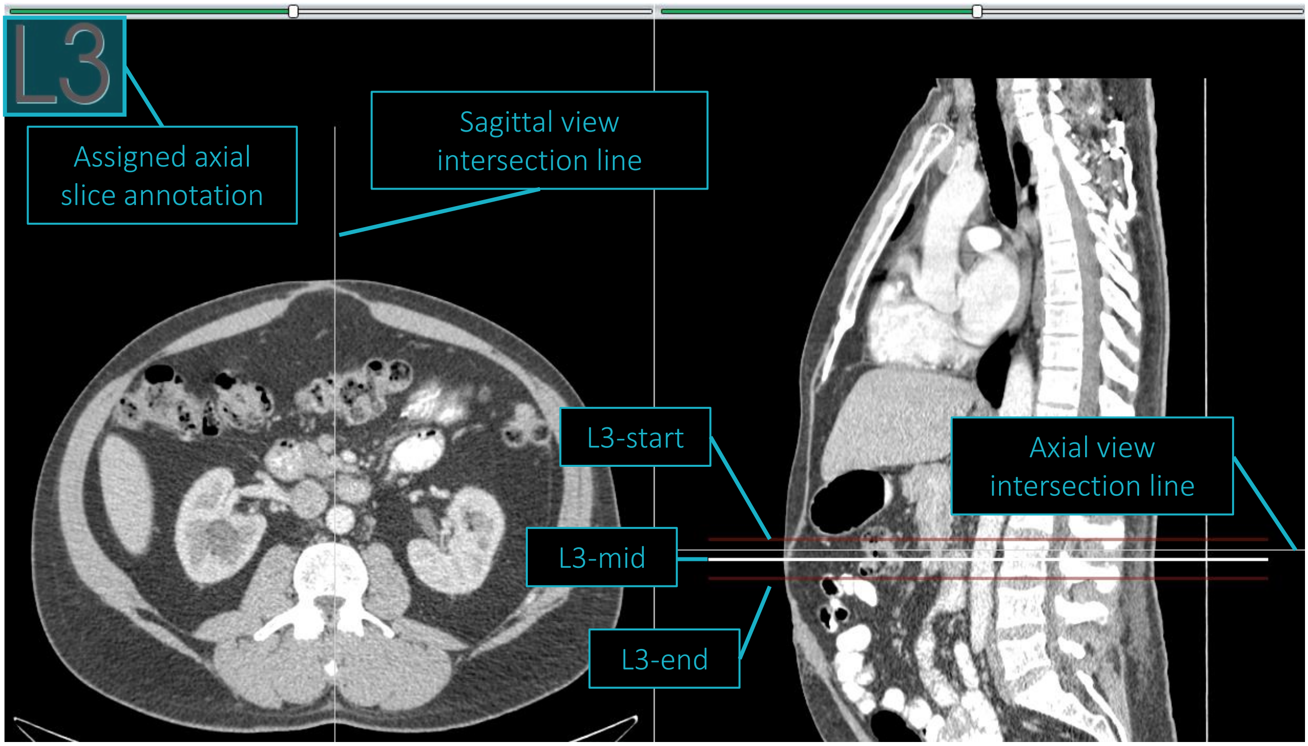
DICOM Information panel for the loaded scan

Mark or unmark a slice as the "middle" of the landmark

Buttons to add or modify slab endpoints (heights of slabs)

Deletes all annotations

Deletes the slab that corresponds with the current axial slice shown in the viewport

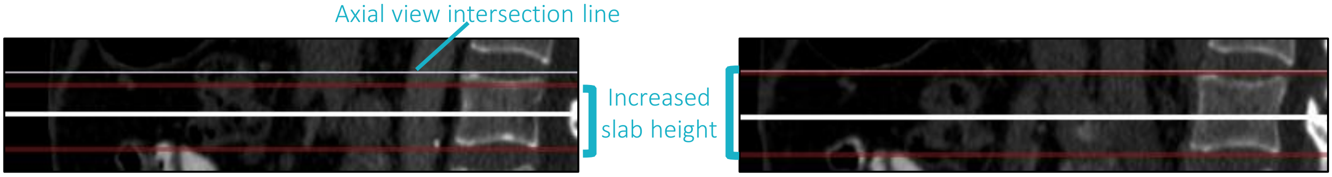


Annotator enables assignment and editing of vertebral annotations to DICOM slices. The tool works by adjusting landmark "slab" heights. Slab heights can range from 1 slice to N number of slices in the image. The -start and -end indicate the top and bottom boundaries of the slab and every slice between the two boundaries are annotated as the same landmark. There is also a -mid suffix which indicates the slice annotated as a middle slice of that landmark; this annotation is displayed in white in the ViewPort.

To begin, first try placing your mouse cursor on the sagittal viewport. Hold SHIFT + move your mouse up and down. Notice that the axial view intersection line is following your cursor and that the axial view is changing rapidly.

Next, place the axial view intersection line a few slices above a –start boundary. Then, click the button of the landmark you are working on. Notice that the –start boundary has moved and the height of the slab is increased. Similarly, placing the intersection line below the boundary will decrease the height and contract the slab. Try this with the –end boundary, but this time placing above the boundary will contract slab, and below will expand the slab.

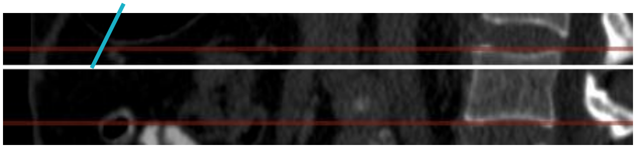
Annotator will always edit the boundary that is closest to the Axial view intersection line.



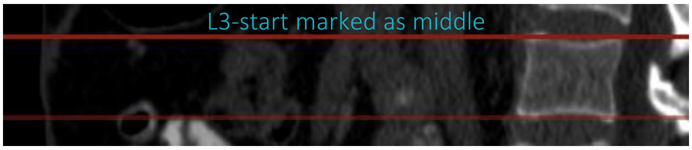
To assign middle slices, both boundaries for a given landmark must be present. You cannot assign a middle slice on a slab with thickness = 1 (only 1 DICOM is annotated). To reassign a different DICOM as the middle slice, simply place axial slice intersection line within a landmark's slab boundary and click "Mark as middle slice".

Axial view intersection line

Reposition middle slice annotation



You may also mark –start and –end slices as middle slices. Notice that the boundary marked as middle will appear slightly brighter.


L3-start marked as middle

You may choose to unmark a middle slice for a given vertebra. Locating the axial view intersection line within the landmark's slab will enable you to reassign slices to the middle slice or remove the middle slice annotation for that vertebrae.

Appendix

Preprocessing Error Logs in Detail

Preprocessing failures will occur if the following errors are detected. You can find a curation failures log in the DAFS-report and logs folder. See page 6 to learn more about where to find reports and logs.

heterogeneous_series_numbers – Corrupted or empty DICOM header.

heterogeneous_acquisition_numbers – Corrupted or empty DICOM header.

heterogeneous_series_uids – Corrupted or empty DICOM header.

invalid_anatomy_type – Corrupted or empty DICOM header.

invalid_image_orientation_patient – Corrupted or empty DICOM header.

invalid_image_position_patient – Corrupted or empty DICOM header.

heterogeneous_slice_orientations – Corrupted or empty DICOM header.

duplicate_slice – Corrupted scan containing 2 or more of the same DICOM file.

no_valid_dicom_slices - Only .asg files are present in the Input folder.

non_anonymized – PHI fields detected.

non_axial_orthogonal_orientation – There are non-axial slices present.

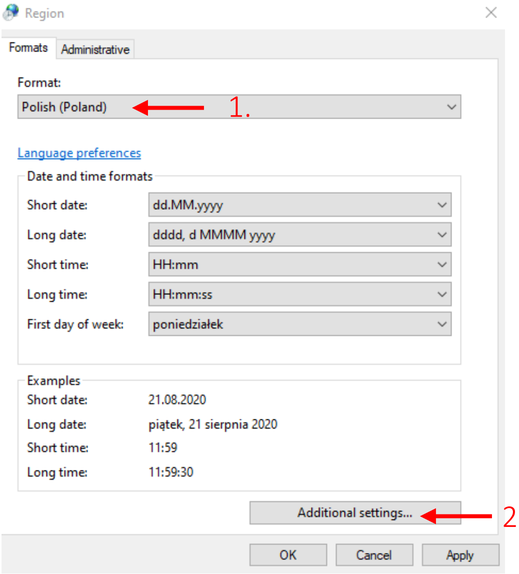
missing_slices – There are DICOMs missing and disrupting 3D scan integrity.

3D_scan_loading_failure – Issue with 3D scan.

Go back to Preprocessing

Generating EUR csv format

Windows Control Panel -> Clock and Region -> Region



Region

Formats | Administrative

Format: Polish (Poland)

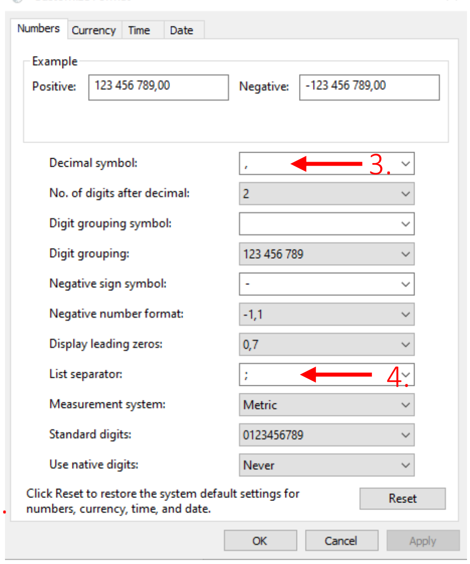
Language preferences

Date and time formats

Short date: dd.MM.yyyy
Long date: dddd, d MMMM yyyy
Short time: HH:mm
Long time: HH:mm:ss
First day of week: poniedziałek

Examples

Short date: 21.08.2020
Long date: piątek, 21 sierpnia 2020
Short time: 11:59
Long time: 11:59:30



Customize Format

Numbers | Currency | Time | Date

Example

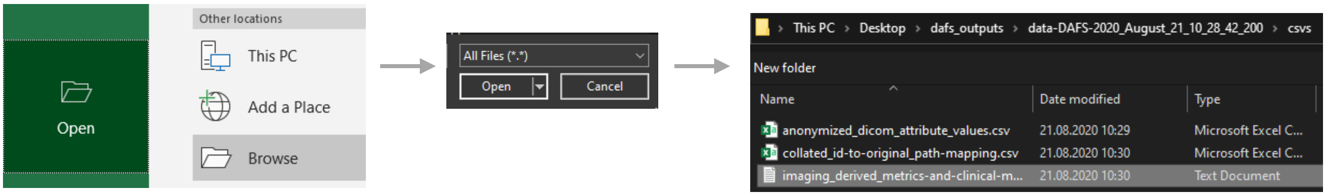
Positive: 123 456 789,00 Negative: -123 456 789,00

Decimal symbol: ,
No. of digits after decimal: 2
Digit grouping symbol:
Digit grouping: 123 456 789
Negative sign symbol: -
Negative number format: -1,1
Display leading zeros: 0,7
List separator: ;
Measurement system: Metric
Standard digits: 0123456789
Use native digits: Never

Click Reset to restore the system default settings for numbers, currency, time, and date.

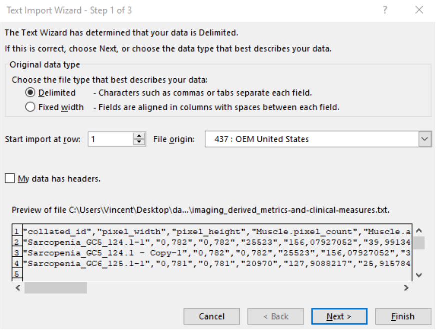
1. Check the Format option to confirm a European country.
2. Click on Additional settings…
3. Check to make sure Decimal symbol is a comma.
4. Check to make sure List separator is a semicolon.

Open Excel, and click Open -> Browse -> select All files (*.*) and navigate to the Output folder ‘csvs’ subfolder to find the *Publish.txt* and open.



Name	Date modified	Type
anonymized_dicom_attribute_values.csv	21.08.2020 10:29	Microsoft Excel C...
collated_id-to-original_path-mapping.csv	21.08.2020 10:30	Microsoft Excel C...
imaging_derived_metrics-and-clinical-m...	21.08.2020 10:30	Text Document

A Text import Wizard will appear.



Text Import Wizard - Step 1 of 3

The Text Wizard has determined that your data is Delimited.
If this is correct, choose Next, or choose the data type that best describes your data.

Original data type

Choose the file type that best describes your data:

● Delimited - Characters such as commas or tabs separate each field.
○ Fixed width - Fields are aligned in columns with spaces between each field.

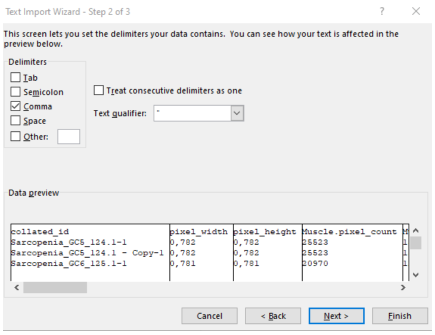
Start import at row: 1 File origin: 437 : OEM United States

☐ My data has headers.

Preview of file C:\Users\Vincent\Desktop\da...\imaging_derived_metrics-and-clinical-measures.txt.

```
1 "collated_id","pixel_width","pixel_height","Muscle.pixel_count","Muscle.a
2 "Sarcopenia_GC5_124.1-1","0,782","0,782","25523","156,07927052","39,99134
3 "Sarcopenia_GC5_124.1 - Copy-1","0,782","0,782","25523","156,07927052","3
4 "Sarcopenia_GC6_125.1-1","0,781","0,781","20970","127,9088217","25,915784
5
```

1. Choose file type that best describes your data. It should say Delimited by default. Click Next.



Text Import Wizard - Step 2 of 3

This screen lets you set the delimiters your data contains. You can see how your text is affected in the preview below.

Delimiters

☐ Tab
☐ Semicolon
☑ Comma
☐ Space
☐ Other:

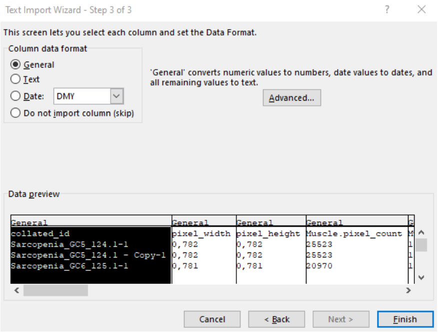
☐ Treat consecutive delimiters as one

Text qualifier: "

Data preview

```
collated_id                   pixel_width pixel_height Muscle.pixel_count M
Sarcopenia_GC5_124.1-1        0,782       0,782        25523              1
Sarcopenia_GC5_124.1 - Copy-1 0,782       0,782        25523              1
Sarcopenia_GC6_125.1-1        0,781       0,781        20970              1
```

2. Select Comma as the only Delimiter. Click Next.



Text Import Wizard - Step 3 of 3

This screen lets you select each column and set the Data Format.

Column data format

● General
○ Text
○ Date: DMY
○ Do not import column (skip)

'General' converts numeric values to numbers, date values to dates, and all remaining values to text.

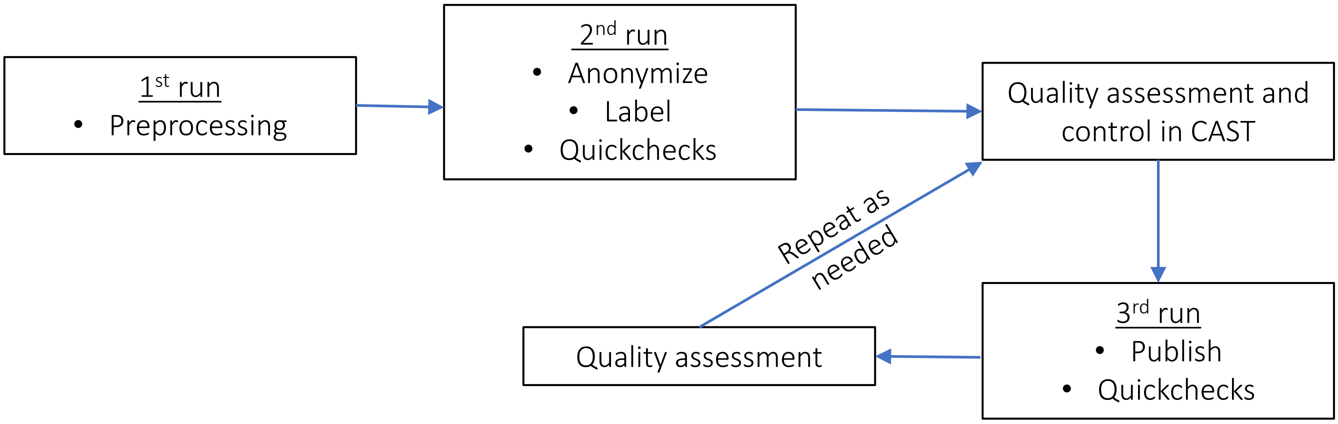
Data preview

```
General                       General     General      General            G
collated_id                   pixel_width pixel_height Muscle.pixel_count M
Sarcopenia_GC5_124.1-1        0,782       0,782        25523              1
Sarcopenia_GC5_124.1 - Copy-1 0,782       0,782        25523              1
Sarcopenia_GC6_125.1-1        0,781       0,781        20970              1
```

3. Click Finish.

Go back to Publish

Suggested Workflow



1st run
- Preprocessing

2nd run
- Anonymize
- Label
- Quickchecks

Quality assessment and control in CAST

3rd run
- Publish
- Quickchecks

Quality assessment

Repeat as needed

Go back to Working Folder

Folders Dictionary

Input Folder – Select any top-level folder containing DICOMs. All DICOMs, including those in subfolders within the designated Input Folder will be processed. Applies to Preprocessing only.

Output Folder – Select any folder. DAFS will create a Working Folder within the Output Folder. Applies to Preprocessing only.

Working Folder – Select any curated folder generated by Preprocessing. This folder will likely have a date and time stamp if the name has not been modified and must only have subfolders inside. All processing by DAFS and edits made in CAST will be saved within the Working Folder. DAFS will automatically designate the Working Folder after Preprocessing is complete.

DAFS System Folders – Folder names that cannot be anywhere in the path of the Input Folder, Output Folder or Working Folder. DAFS will not continue processing if the following keywords are detected in any of these paths (case insensitive). Furthermore, any of these key words followed by an underscore (_) cannot be anywhere in the paths.

- DAFS-report
- logs
- quickchecks
- reports
- csvs
- tmp
- Anonymize
- Tissue Statistics_slicewise
- Tissue Statistics
- Preprocessing
- ABACS 3D
- AVA

Go back to Preprocessing

Go back to Working Folder

Supported GPUs

GPU utilization can be enabled for automated segmentation and annotation processing. Using GPUs may decrease processing time by 10 times or more when compared to CPU.

Recommended GPU: Nvidia GeForce RTX 2070 or higher.

List of supported Nvidia GPU microarchitectures and tested graphics card models:

- Ada Lovelace
    - Nvidia GeForce 4000 series
- Ampere
    - Nvidia GeForce RTX 3060
    - Nvidia GeForce RTX 3060 Ti
    - Nvidia GeForce RTX 3070
    - Nvidia GeForce RTX 3090
    - Nvidia RTX A5000
- Turing
    - Nvidia GeForce RTX 2060
    - Nvidia GeForce RTX 2070
    - Nvidia GeForce RTX 2070 Super
- Volta
- Pascal
    - Nvidia GeForce MX150
    - Nvidia GeForce MX250
    - Nvidia GeForce MX330
    - Nvidia GeForce GTX 1070
    - Nvidia GeForce GTX 1050 Ti

Note: DAFS 3 may also be compatible with other graphics card models not listed above with the supported microarchitectures.

If you think you may have a compatible GPU, but DAFS is not detecting it, please contact us at support@voronoihealthanalytics.com.

Publish CSV Dictionary

Category **General format**

General scan attributes: **scan_folder, orig_path, voxel_size_WxLxH**

Slab attributes: **$slab;num_slices, $slab;img_size_WxLxH, $slab;height_mm**

Slab and Tissue (ROI) attributes: **$slab;$tissue;$tissue_statistic**

- **$tissue_statistic =** cross.sectional_area_pixels, cross_sectional_area_cm2, volume_voxels, volume_cm3, HU_mean, HU_std, HU_min, HU_max

** “$” represents a variable.**

Term	Meaning
defined_slab	(applicable to by_slab csv only) Describes the slab in which the measurements belong.
scan_folder	A unique ID assigned to a scan after curation which also is the folder name of that scan.
orig_path	The original path of the scan or DICOM files.
img_size_WxLxH	Image dimensions in width, length and height.
voxel_size_WxLxH	Voxel dimensions in width, length and height.
height_mm	The vertical anatomical height of the defined.slab in mm.
num_slices	The number of DICOM slices in the defined.slab.
cross.sectional_area_pixels	Cross sectional number of pixels - number of voxels within the region-of-interest.
cross_sectional_area_cm2	Cross sectional area in centimeters squared within the region-of-interest.
volume_voxels	Volume number of voxels - number of voxels within the region-of-interest.
volume_cm3	Volume in centimeters cubed within the region-of-interest.
HU_mean	Mean Hounsfield Unit within the region-of-interest.
HU_std	Hounsfield Unit standard deviation within the region-of-interest.
HU_min	Minimum Hounsfield Unit within the region-of-interest.
HU_max	Maximum Hounsfield Unit within the region-of-interest.
pet_uptake_*	Measurements derived from the PET image
tissue[####,####]	The region-of-interest defined by the tissue name and hounsfield unit range.
tissue[####,###]-U-tissue[####,###]	An ROI defined by multiple region-of-interests unionized defined by the tissue names and Hounsfield unit ranges.

Go back to Publish

License and Information

Expiration date – Date of license expiry.

Scans processed – The number of unique scans that have been processed out of the total number of available scans provisioned in the license.

Scans remaining – The number of available scans left in the license.