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syngo.PET&CT Oncology CT Tutorial

Storyboard
VA30

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1 What's New in the Latest Upgrade of syngo.PET&CT Oncology?



The license name *syngo.PET&CT Oncology* corresponds to the clinical workflow of *syngo.via MM Oncology*, the CT part of which will be presented in this Tutorial. In the following, we will only use the license name.

This table provides you with an overview of the latest software upgrade of *syngo.PET&CT Oncology* with regard to CT.

Click a Play button in the far right column to view the corresponding training movie of this Tutorial.

CT Feature	Description	Link to Training Movie
Layout of the Case Navigator	Get an overview of the new Case Navigator layout in the CT Oncology workflow compared to the VA20 CT Oncology workflow layout.	2.4 (→ Page 8 <i>Layout of the Case Navigator</i>)
LungCAD mini toolbar	View LungCAD findings from a mini toolbar at the bottom of the MPR segments and accept or reject them.	3.7 (→ Page 22 <i>Step 6: Showing LungCAD Results</i>)
Arterial enhancement fraction (AEF)	Comfortably assign data roles to the segments.	3.9 (→ Page 25 <i>Introduction to Arterial Enhancement Fraction (AEF)</i>)
Initial Layout Rules	Configure the default layout loaded for specific data sets by selecting an Assignment Object, followed by an Assignment Condition.	3.11 (→ Page 27 <i>Step 9: Configuring initial layout rules</i>)

2 Introduction

2.1 Prerequisites

Before starting to work with *syngo*.PET&CT Oncology **Prefetching** and **Prior Rules** as well as **Workflow Mapping Rules** need to be set up in the **Administrator Portal**.

Depending on your service contract, please contact your Clinical IT Administrator or Siemens Application Specialist to set them up for you.

Prior to loading a lung data set into *syngo*.PET&CT Oncology, please make sure the series of the CT lung data set available fulfill the prerequisites listed here in order to start the **Computer Aided Detection LungCAD** during pre-processing.

2.2 Introduction to CT Liver and CT Lung

syngo.PET&CT Oncology is a powerful tool designed to handle complex workflows, such as **CT liver** and **CT lung** workflows, within daily oncology reading.

It combines findings in multi-phase data sets **within** and **between** time points as well as a full PACS integration in order to support pre-fetching of images, etc.

This Tutorial describes a simple CT Oncology workflow based on a liver multiphase dataset consisting of a **prior** and a **follow-up** study and highlights particularities of a CT lung workflow.

2.3 Loading of Data Sets

With *syngo*.PET&CT Oncology, you can load data sets with a single click.

- 1 Move your mouse over the **Read QuickWorklist** icon to see the patient data currently included in the QuickWorklist.

- 2 Click the patient whose data you would like to view, process, or read, which should already be mapped to the MM Oncology workflow.

The data set of the patient is instantly loaded in an appropriate layout.



syngo.PET&CT Oncology automatically loads both baseline and follow-up examinations of your patient.

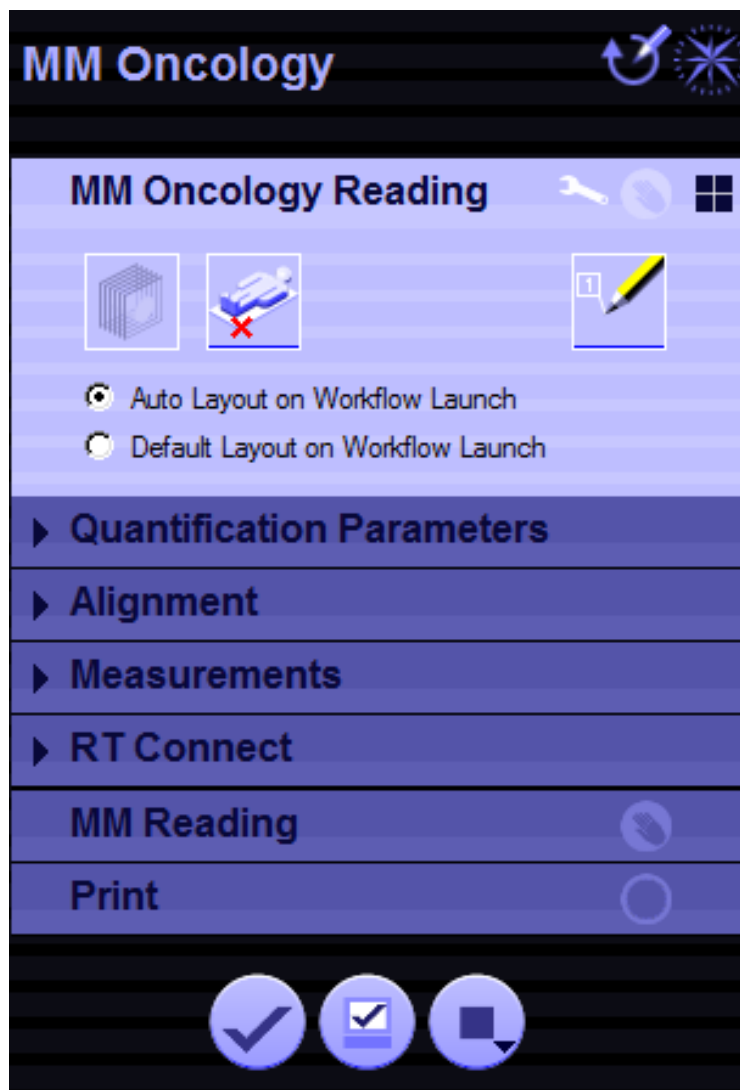
Prior findings such as markers, segmentation objects, pdf reports, etc. are also prefetched, loaded and even displayed along with your current study.

2.4 Layout of the Case Navigator

In VA30, the Case Navigator layout of the **CT Oncology** workflow has been simplified to a great extent.

The new Case Navigator layout is intended to be more workflow-oriented. In this section the modifications to the new CT Oncology workflow layout will be briefly explained.

Layout in VA20:



Layout in VA30:



You'll find the functions of the Step **MM Oncology Reading** in the following places:

- Select **Auto layout** and **Default layout** via the Configuration for MM Oncology Reading.
- The other functions (**DE FOV**, **Table Removal** and **Review Marker**) are now located in the corner menus of the segments.

The **Alignment** and **Measurements** steps have been taken out of the Case Navigator. Their icons and functions have moved to the following places:

- **Automatic Alignment** is now in the upper left corner menu of segments.
- **Manual Alignment** icons are now available in the Common Tools area.
- You will find the **ROI tools** in the upper right corner menu of the segments.
- All other functions of the **Measurements** step are now in the **MM Oncology Reading** workflow step.

The **Quantification Parameters**, **RT Connect** and **Print** steps will appear, as soon as you need them:

- **Quantification Parameters** is only displayed, if data containing attenuation-corrected PET is loaded.
- The **RT Connect** step appears as soon as proper GTV segmentation has been performed.

The **Print** step will be displayed if you send the first item to printing.

3 *syngo*.PET&CT Oncology Clinical Workflow CT

3.1 Overview Sheet Clinical Workflow CT

As a recommendation, this overview sheet provides you with the order and individual steps of the CT clinical workflow of *syngo*.PET&CT Oncology:

1 **Aligning Images**

Before starting your viewing and reading, you can adjust the alignment of data sets in several different ways. Alignment enables you to see the same anatomical structure at the same position in multiple images, such as multimodality images or images from multiple time points or contrast phases.

2 **Performing Manual Measurements**

Perform a manual measurement based on either RECIST or WHO standards. And for a better judgement of the current tumor response according to the Choi response criteria, perform a combined RECIST and ROI (region of interest) measurement.

3 **Performing Automatic Segmentation**

Automatic segmentation algorithms for lung, liver, lymph node and generic segmentation make the comparison of prior findings with current findings quick and easy.

4 **Measuring Lesions**

Measure and modify lesions and view their environment in 3D by using corresponding tools from the in-segment corner menus, mini toolbar and Measurement Details window.

5 **Using Advanced HU Statistics**

Visualize and identify hypodense areas, for example necrotic areas, or hyperdense areas within a segmented lesion by using Advanced HU Statistics.

6 **Showing LungCAD Results**

Even though LungCAD calculations are done as a pre-processing step whenever the prerequisites are fulfilled, you can easily start them manually by clicking the corresponding tool on the upper right corner of any MPR Segment.

7 Using the Findings Navigator

Easily navigate through markers, measurements and snapshots in the Findings Navigator, get an overview of all different findings and evaluate tumor progression in detail by using the Findings Details window.

8 Introduction to Arterial Enhancement Fraction

The CT arterial enhancement fraction is considered to indirectly reflect the ratio of hepatic arterial perfusion to that of total perfusion. The CT AEF also indicates small regional misbalances before they become morphologically visible.

9 Opening a Report

After performing *syngo*.PET&CT Oncology, open a Report, for example to send a PDF file to the referring physician.

10 Configuring initial layout rules

Configure the default layout loaded for specific data sets by selecting an Assignment Object, followed by an Assignment Condition.

11 Finalizing *syngo*.PET&CT Oncology

Several options are available to finalize your Clinical Workflow of *syngo*.PET&CT Oncology, including Complete with archiving, Complete and Suspend.

3.2 Step 1: Aligning images

3.2.1 Introduction

You can perform image alignment in order to see the same anatomical structure at the same position in multiple images, such as multimodality images or images from multiple time points or contrast phases.

When data is loaded into the **MM Oncology** workflow, the system first performs an alignment during the pre-processing phase.

The application identifies and matches corresponding characteristics between data sets by considering intensities. The best matches between the images are calculated based on a set of statistical parameters. Large areas of similar intensity, such as organs, can have a greater influence on calculations than focal areas.

If the data sets are only slightly misaligned, you can perform an automatic alignment. If there is a large misalignment, you should first adjust the data manually and then run an automatic alignment.



The **MM Oncology** workflow uses a rigid alignment process for automatic and manual alignment of data.

Alignment is achieved by rotating and translating one data set in 3D in relation to the other. There is no change in the size or shape of the image.

3.2.2 Image alignment process

A simple image alignment process goes as follows:

■ Alignment during pre-processing

You have started the application and images are loaded into a certain layout, depending on the type of data. The application creates a scanner alignment set. If the scans are not co-acquired, then automatic alignment starts. This is based on statistical measures, and concludes with a first custom alignment set.

■ Assessing and correcting automatic alignment

You can check and adjust the images according to your needs.

You have the following options:

– **Aligning manually**

If images are poorly aligned, or cover different extents of the body, the manual method may provide better results. You can use this rough alignment as a starting point for automatic alignment.

– **Aligning Automatically**

Assess the initial alignment of the data sets. If data sets are only slightly misaligned, you can use the automatic method. You can align using fused or separate segments.

■ Resetting the alignment

You can discard any alignments you have made and reset to the initial alignment set, or to the scanner alignment.

3.2.3 Automatic volume alignment

Certain volumes can be automatically aligned. The pre-processing alignment is calculated for all series available for the patient. However, this may be suboptimal if you are only interested in the best alignment for a subset of the series.

Aligning separate segments or time points automatically

- 1 Make sure you have oriented the data sets and performed a rough visual alignment.
- 2 Make sure you have loaded two or more volumes.
- 3 Select an appropriate layout, press the **Ctrl** key and click on the relevant segments of different volumes or views of the timepoints accordingly.
- 4 From the upper left corner menu, select **Automatic Registration**.

The data in the segments will be updated to show the automatic alignment result. The result will overwrite the custom alignment set.

3.2.4 Manual alignment

You can align images side by side, so that the same anatomical body part is shown in the segments.

Locking or unlocking alignments between time points

✓ You have loaded a layout that displays more than one time point.

You can easily move one time point with respect to another, as the misalignment between time points can be large. By unlocking time points, you can change the alignment links between time points without changing the alignment within the volumes in the individual time points. You can use this method to quickly align a number of data sets at the same time.



1 In the Common Tools area, click the **Adjust Spatial Alignment between Time Points** icon.

The volumes will now be unlocked. You can scroll and pan independently.

2 Change slice positions by navigating and panning, as necessary.

3 Click the **Adjust Spatial Alignment between Time Points** icon a second time to re-lock segments.

The result will overwrite the custom alignment set.

Locking or unlocking alignments between volumes

You can easily adjust the alignment between all volumes, even if they belong to the same time point.



1 In the Common Tools area, click the **Adjust Spatial Alignment** icon.

2 Change the slice positions in the segments by navigating and panning, as necessary.

3 Click the **Adjust Spatial Alignment** icon a second time to re-lock the data sets.

The result will overwrite the custom alignment set.

In **MM Oncology**, if you unlock spatial alignment, segments displaying the same orientation and the same volume will scroll synchronously.

For information on adjusting spatial alignment, see the section on **Correcting the synchronized navigation** in the *syngo*.via Application Basics Operator Manual.

3.2.5 Reset alignments

Setting scanner alignments ♦ From the upper left corner menu, select **Scanner Alignment**.

The alignment of the selected segments is reset to the base alignment that is obtained from the scanner.



The **Scanner Alignment** menu item is only enabled if you have selected at least two co-acquired volumes.

Resetting alignment You can return to the initial alignment used when the volume was loaded.

♦ From the upper left corner menu, select **Reset Alignment**.

The selected series are reset to the initial alignment. The initial alignment can either be the scanner alignment, a previously saved registration, or a robust initial alignment registration.

3.3 Step 2: Performing Manual Measurements

3.3.1 Performing Manual RECIST/WHO Measurements

In syngo.via MM Oncology, you can perform a manual measurement based on either **RECIST** or **WHO** standards.

1 To start measuring, click the **RECIST/WHO Ruler** icon in the **Case Navigator**

– or –

you can switch on the RECIST/WHO Ruler tool in the upper right corner of any MPR segment.

2 Then go to a lesion of interest and perform a manual measurement:

For a **measurement according to RECIST standards**, simply left-click, hold the mouse button down, drag the mouse through the lesion, and release the mouse button.

For a **measurement according to WHO standards**, draw the two WHO cross lines while pressing the **Shift** key.

The RECIST or WHO measurement value will appear in an **annotation box** and a corresponding finding will be created in the **Findings Navigator**.

You can continue with further measurements as long as the RECIST/WHO Ruler is switched on.

3.3.2 Performing Combined RECIST and ROI Measurement

For a better judgement of the current **tumor response** according to the **Choi response criteria**, you can perform a **combined RECIST and ROI (region of interest) measurement**:

1 Start with the RECIST measurement

Click the **RECIST/WHO Ruler** icon in the **Case Navigator** or

In the upper right corner menu of any MPR segment, switch on the **RECIST/WHO Ruler** tool.

Then go to the lesion of interest and perform a manual measurement.

2 Perform the ROI measurement next

In the upper right corner menu of any segment, choose the **ROI Circle** tool.

The cursor shape changes to a circle.

Draw the ROI circle. Click at the start point and drag until the circle is the desired size.

The RECIST and ROI measurements' values will appear in separate **annotation boxes** and corresponding findings will be created in the **Findings Navigator**.

3.4 Step 3: Performing Automatic Segmentation

Automatic segmentation makes the comparison of prior findings with current findings quick and easy.

Four segmentation algorithms are available: lung, liver, lymph node and generic segmentation.

1 To switch on liver segmentation, for example, click the **Liver Segmentation** icon in the **Case Navigator**.

– or –

select the algorithm in the upper right corner menu of any MPR segment.

- 2 To segment the lesion, simply left-click outside the suspicious lesion, hold the mouse button down, drag the mouse through the lesion, and release the mouse button outside the suspicious lesion.

The segmentation performed will be indicated by a **contour line** in the image.



To segment **small lesions**, just left-click the suspicious lesion.

To segment **bigger lesions**, it is recommended that you draw a line through the lesion.

Furthermore, you can define the properties of every CT segmentation algorithm more specifically.

Right-click any segmentation algorithm from the upper right corner menu of any MPR segment and select **CT Segmentation Properties** from the drop-down list.

The **CT Segmentation Evaluation** window will open.

Check or uncheck the properties required for your specific segmentation. Then click **OK**.

After the automatic segmentation, evaluated data of the checked properties will be displayed in an **annotation box** close to the contour line of the segmentation.

3.5 Step 4: Measuring Lesions

3.5.1 Using the Segmentation Toolbar

When you have accomplished a CT segmentation, and you have selected only one segmentation, a mini toolbar is shown **at the segment bottom** to edit your segmentation.

From left to right on the mini toolbar, you can perform the following editing functions and advanced HU statistics:

- 1 Correct the segmentation

- 2 Undo the last step
- 3 Delete the segmentation
- 4 Show or hide measurements
- 5 Advanced HU Statistics function
- 6 Open the Measurement Details window

3.5.2 Using the Measurement Details Window

After performing your segmentation, you can edit the finding by using the **Measurement Details** window.

- 1 To open it, click the **Edit Finding** icon in the **Case Navigator** or on the **Segmentation Toolbar**, right-click the segmentation and select **Edit** or press the **Alt + E** keys.

In the **Measurement Details** window, you will find all lesions listed in order based on their proximity to the newly created measurement. The closest lesion is highlighted.

- 2 If you want to create a new measurement, just link to **<new>** on the list. Of course, it is always possible to link your finding to another one in the list.
- 3 In the **Properties** area of the Measurement Details window, you can select, enter or delete the **Organ** affected by the tumor and a **Label** and also select a **Color** for the on-screen color of the measurement.
- 4 Whenever automatic segmentation is used, the lesion is marked as a **Target Lesion** on the lower half of the window and taken into the **tumor burden calculation**. However, you can uncheck this, if necessary.



The tumor burden is displayed in the **Findings** tab of the report.

After clicking **OK**, the existing finding will be **updated** in the **Findings Navigator**.

3.6 Step 5: Using Advanced HU Statistics

After creating a measurement with a CT segmentation tool, use **Advanced HU Statistics** to visualize and identify **hypodense areas**, for example necrotic areas, or **hyperdense areas** within a segmented lesion.

- 1 Click the Advanced HU Statistics button on the CT segmentation mini toolbar.

A threshold slider and two threshold options will be displayed above the button in the mini toolbar.

- 2 Select **Upper Threshold** if you want to see the lower densities, or **Lower Threshold** if you want to see the higher densities.
- 3 Adjust the thresholds according to your needs by dragging the slider on the left **or by typing in the HU value**.



The default HU value is set to 15 HU. A range between 0 and 200 HU can be set.

By changing the thresholds, the volume of the segmentation is immediately recalculated and displayed in its **annotation box**.

If the **upper threshold** is displayed, the **red color** in the segmentation shows **necrotic areas**, for example.

3.7 Step 6: Showing LungCAD Results

LungCAD calculations are done as a pre-processing step whenever the prerequisites are fulfilled.

To learn about them, please see (→ Page 7 *Prerequisites*) in this Tutorial.

After loading the data set, the LungCAD findings are **hidden by default**.

- 1 To display them, click the **Show/Hide LungCAD** icon in the **Case Navigator**

– or –

if LungCAD needs to be started manually, click the corresponding tool in the upper right corner of any MPR Segment.

At the bottom of the segment, a mini toolbar will open displaying the findings.



LungCAD findings are **not** displayed within a radius of 10 mm of a previously performed manual finding.

- 2 Simply click a LungCAD finding in the mini toolbar to navigate directly to it.

All image segments will be updated immediately to show the location of this finding.

- 3 You can accept or delete each finding by clicking the **Accept** icon or **Delete** icon in that finding.



- Accepted markers are removed from the LungCAD mini toolbar and saved as findings in the **Findings Navigator**.
- Deleted markers are also removed from the LungCAD mini toolbar, and a colored bar between the thumbnails indicates the deleted finding.



If you need to segment a LungCAD finding with the Lung Segmentation tool, please proceed as described in (→ Page 19 *Step 3: Performing Automatic Segmentation*).

3.8 Step 7: Using the Findings Navigator

3.8.1 Navigating through Findings

All markers, measurements and snapshots will be listed as findings in the **Findings Navigator**, including the finding's **Name**, its **Value**, **Source** and **Key Images**.

- 1 Simply **left-click** a marker or measurement to navigate directly to it.

All image segments will be **updated immediately** to show the location of this finding in the default layout.

- 2 In the column on the far right in the Findings Navigator, an icon indicates **snapshots**. The snapshots are key images that have been automatically created with a finding. To open and view snapshots of a finding, double-click the corresponding icon.

- 3 **Scroll** with the scroll wheel of your mouse to look through the key image stack.

If a **Volume Measurement** has been performed, a histogram will be saved in the key image stack.

- 4 Click the **cross** in the upper right corner of the snapshot to close it.

3.8.2 Using the Findings Details Window

The Findings Details window gives you an overview of all different findings. It also enables you to evaluate tumor progression in detail.

To open the window, click the **Findings Details** icon in the **Findings Navigator**.

- 1 The **Series Details** tab displays the patient data and relevant acquisition information in which different timepoints are considered.

- 2 The **Trending** tab displays tumor information over time.

- Since there are **up to eight timepoints available** in MM Oncology, you can choose which of the prior timepoints you would like to compare with the current timepoint for your report.

Select the desired prior timepoint from the **Baseline** field on the upper right part of the tab.

You can **only select one** of the prior timepoints for comparison in your report.

- All of the tumor information is automatically included into the report.

To get further information about any timepoint, simply move the mouse cursor over a point on the graph. A tooltip will appear showing absolute and percentage change.

Tables and graphs from both tabs can be **exported** as Excel file.

3.9 Introduction to Arterial Enhancement Fraction (AEF)

The **Arterial Enhancement Fraction (AEF)** is considered to indirectly reflect the ratio of hepatic arterial perfusion to that of total perfusion.

As the AEF increases, both for higher arterial enhancement as well as for reduced portal venous enhancement, quantitative 3D display on a standardized color scale should increase the conspicuity of malignant lesions, such as metastases, that go along with a changed balance of normal arterial and portal venous perfusion.

It also indicates small regional misbalances before these become morphologically visible.

The CT AEF is computed in a percentage as the ratio of enhancement in the arterial phase to enhancement in the portal venous phase according to the following equation:

$$\text{AEF} = (A - N) / (V - N) \times 100$$

- **A** is the CT number in the arterial phase
- **N** is the CT number in the unenhanced CT images
- **V** is the CT number in the portal venous phase

In the **late arterial phase**, dominant enhancement is due to the hepatic artery, while parenchymal enhancement is still limited.

In the **portal venous phase**, the portal venous inflow of contrast agent is dominant and the contrast agent still remains in both the hepatic artery and the hepatic vein.

3.9.1 Pre-processing of arterial enhancement fraction

MM Oncology performs arterial enhancement fraction (AEF) pre-processing to facilitate your work. As a prerequisite for pre-processing, additional image information about data roles has to be provided at the scanner when acquiring the images. To successfully trigger the AEF data, the series need to be identified as contrast or non-contrast series.

The series must be acquired at the following phases:

- Before adding a contrast agent
- With a contrast agent during the arterial phase
- With a contrast agent during the portal venous phase

Parameter	Description
on	Describes the workflow name
.pre	Phase before adding contrast agent Example: VIA on.pre
.art	Phase during the arterial phase Example: VIA on.art
.pv	Phase during portal venous phase Example: VIA on.pv

3.9.2 Switching to the CT arterial enhancement fraction layout

If you have configured the CT AEF calculation, the dedicated layout will automatically be chosen when selecting the function.

- ◆ In the Case Navigator, click the **Arterial Enhancement Fraction** icon.

The **CT Arterial Enhancement Fraction** will be displayed.

3.9.3 Assigning images to data roles manually

If the automatic AEF mapping failed to work or if there are no PRE, ART, or PV data roles configured, the segments will display appropriate user guidance text. Follow the instructions to manually assign the series to data roles and start the AEF calculation.

As soon as you have assigned all series, the AEF calculation will start.

- 1 In the Case Navigator, click the **Arterial Enhancement Fraction** icon.

The AEF layout will be displayed and the segments will contain information about how to assign the data roles.

- 2 From the Series Navigator, left-click and drag the series into the corresponding segment of the AEF layout.

Data roles are automatically assigned according to the segment the data was dragged into.

- The AEF calculation will start immediately after the assignment is completed.
- After the AEF calculation is finished, the layout will display an AEF image.

3.10 Step 8: Opening a Report

After performing syngo.PET&CT Oncology, you would like to open a Report, for example to send a PDF file to the referring physician.

- 1 First you need to check the boxes of the findings you want to include in your report. You can either do this in the **Findings Navigator** or in the **Findings Details** window.
- 2 Then go to the patient case displayed in the **Access Bar** and click the small down arrow to the far right. Choose the **Starts the Report Editor** button.

The report opens in a floating window on top of the user interface.

3.11 Step 9: Configuring initial layout rules

You can configure the default layout loaded for specific data sets by selecting an Assignment Object, followed by an Assignment Condition. Both Assignment Object and Assignment Condition establish a rule which will automatically select a layout depending on the data loaded. You can select from the following Assignment Objects:

- study description
- protocol name
- body part examined

3.11.1 Adding new layout rules

- 1 From the **Configuration** window, select the **Initial Layouts** tab.
- 2 From the initial layout list, select **My Initial Layouts Rules**.
- 3 Click the **Add New Rule** icon to add a new layout rule.

The **Assign Initial Layout** dialog box opens.

- 4 Select an Assignment Object from the selection menu.
- 5 Select an Assignment Condition relevant to the current study from the selection menu.

The list of Assignment Conditions is populated depending on the Assignment Object selected and can be used to further specify the default layout selection.

- or -

You can type a new Assignment Condition.

- 6 From the **Use this layout** list, select a layout.
- 7 Click **Accept**.

The new layout assignment rule is listed in the **Initial Layouts** tab.

- or -

Click **Cancel** to close the dialog box without accepting changes.

3.11.2 Changing the priority of initial layout rules

You can use priorities to create very specific rules followed by more general rules. By using the up and down arrow icons, you can change the priority of initial layout rules.

- 1 Make sure you have selected an initial layout.
- 2 Click the up or down arrow icons to change the priority of the initial layout selected.

The first rule listed that matches the current data set will be loaded.

You can use priorities to create very specific rules followed by more general rules.

Status of initial layout rules

A plus sign to the left of the layout indicates a new layout rule.

A green bubble to the left of the layout rule indicates that the layout is in use.

A red bubble indicates that the layout is unavailable.

3.11.3 Editing initial layout rules

- 1 Make sure you have selected an initial layout.
- 2 In the **Configuration** window, select the **Initial Layouts** tab.
- 3 Select the layout rule that you wish to edit.

The **Assign Initial Layout** window will open for editing.

3.11.4 Deleting initial layout rules

- 1 In the **Configuration** window, select the **Initial Layouts** tab.
- 2 Select the layout rule you wish to delete.
- 3 Click the **Delete Rules** icon.

You have deleted the selected rule.

3.12 Step 10: Finalizing syngo.PET&CT Oncology

You have reached the end of your Clinical Workflow. Now you would like to finalize it.

- ◆ Click the **Complete with archiving** icon in the Control Area to complete your task, store your results in syngo.via and send them to your archive.

– or –

Click the **Complete** icon to complete your task and store your results in syngo.via.

– or –




Click the **Actions for stopping work item** icon.


In the drop-down list, three other actions for stopping a work item will appear. The first one is the **Suspend** icon: Pause your task for later resume and save your results temporarily.

4 syngo.PET&CT Oncology Tools and Shortcuts

MM Oncology provides specific tools in the Case Navigator and on corner menus. The most frequently used tools are accessible via the context menu of each segment. You can also use the keyboard shortcuts described in the tooltips.



The following table shows available tools and functions and corresponding keyboard shortcuts:

Icon	Description	Available in				Key-board shortcut
		Case Navigator	Corner menu	Context menu	Mini toolbar	
	CT Presets	–	Lower right	–	–	F5 F6 F7 F8
	PET Presets	–	Lower right	–	–	–
	CT Color LUT and PET Color LUT	–	Lower right	Lower right	–	Shift + F5 Shift + F6 Shift + F7 Shift + F8

Icon	Description	Available in				Key-board shortcut
		Case Navigator	Corner menu	Context menu	Mini tool-bar	
	Table Removal	-	Upper left	-	-	-
	Edit Table	-	Upper left	-	Yes	-
	Automatically applying punch	-	-	-	Yes	-
	Perform Punch	-	-	-	-	-
	Units	-	Lower right	-	-	-
	Automatically Place PERCIST Liver Reference Regions	Yes	-	-	-	-
	Automatically Place PERCIST Blood Pool Reference Regions	Yes	-	-	-	-
	Visual Alignment	-	Upper left	-	-	-
	Automatic Registration	-	Upper left	-	-	-
	Reset Alignment	-	Upper left	-	-	-
	Scanner Alignment	-	Upper left	-	-	-

Icon	Description	Available in				Key-board shortcut
		Case Navigator	Corner menu	Context menu	Mini toolbar	
	Global View	–	Lower left	–	–	–
	Result View	–	Lower left	–	–	–
	Edit Result View	–	Upper left	–	–	–
	Reset Result View	–	Upper left	–	–	–
	ROI Circle	–	Upper right	–	–	C
	Dual Energy ROI Circle	–	Upper right	–	–	–
	Pixel Lens	–	Upper right	–	–	L
	VOI Sphere	–	Upper right	–	–	V
	RECIST/WHO Ruler	Yes	Upper right	–	–	Alt + Q
	Lung Lesion Segmentation	Yes	Upper right	–	–	Alt + 1
	Liver Lesion Segmentation	Yes	Upper right	–	–	Alt + 2

Icon	Description	Available in				Key-board shortcut
		Case Navigator	Corner menu	Context menu	Mini toolbar	
	Lymph Node Segmentation	Yes	Upper right	–	–	Alt + 3
	Generic Segmentation	Yes	Upper right	–	–	Alt+ 4
	Evaluate a lesion with RECIST/WHO + VOI isocontour	Yes	Upper right	–	–	Alt + H
	Show/Hide LungCAD results	Yes	–	–	–	–
	Start LungCAD	–	Upper right	–	–	–
	Correct segmentation	–	–	–	Yes	–
	Undo Edit	–	–	–	Yes	–
	Delete segmentation	–	–	–	Yes	–
	Hide Selected Measurement	–	–	–	Yes	–
	Edit Finding	–	–	–	Yes	Alt + E
	Lesion Auto Zoom	Yes	–	–	Yes	Alt + Z

Icon	Description	Available in				Key-board shortcut
		Case Navigator	Corner menu	Context menu	Mini toolbar	
	Marker	–	Upper right	–	–	Alt + M
	Wrench	Yes	–	–	–	–

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Global Business Unit

Siemens AG
Customer Services
Henkestr. 127
91052 Erlangen
Germany
Phone: +49 9131 84-0

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Global Siemens Headquarters

Siemens AG
Wittelsbacherplatz 2
80333 Muenchen
Germany

Global Siemens Healthcare Headquarters

Siemens AG
Healthcare Sector
Henkestr. 127
91052 Erlangen
Germany
Telephone: +49 9131 84-0

Legal Manufacturer

Siemens AG
Wittelsbacherplatz 2
DE-80333 Muenchen
Germany