

KIM Software GUI Interface

Usyd Instructions

KIM start window:

Choose:
- **Folder:** For offline run
- **Watch folder:** Online KIM run

kV image directory

kV FOV

KIM tolerance
(i.e., KIM shows “Warning” if
the motion is 3 mm in any
direction for 5 secs, and then
shows “BEAM OFF”.)

KIM learning arc length

KG KIM Gating Clinical Trial Settings

Images

Source: Folder (dropdown) Frames to average: 1 (spinner) Discard accumulated frames: ☒

Directory: E:\LARK PAT15\KIM-KV\ (text) Browse (button)

Patient Centroid Directory

Starting Directory: (text) Browse (button)

Filed of view

AP (mm): 100 (spinner) SI (mm): 100 (spinner)

Machine Parameters

Linac Type: Varian TrueBeam (dropdown) Image Angle = KV: ☐ Enable ADI (TrueBeam Only): ☐

Frames per second: 15.0 (spinner) KIM Log Directory: E:\LARK PAT15\ (text)

Thresholds

Warning at (mm): 3 (spinner) Pause at (mm): 5 (spinner) Baseline Average (seconds): 15 (spinner) Shift Couch to Baseline: ☐

Marker Analysis

Learning Arc (deg): 90 (spinner) Pretx Arc Mode: Fluoro (dropdown) ☒ Invert image

UDP Connection

Select Comm Mode: (dropdown)

Image and Dynalog Transfer

☐ Check box for automatic files transfer at end of session

Images Destination Directory: (text) Browse (button)

Dynalog Source Directory: (text) Browse (button)

Dynalog Destination Directory: (text) Browse (button)

Patient List (text file): (text) Browse (button)

About (button) Continue (button) Cancel (button)

Frame Averaging = 3 for BH patients

Frame Averaging = 1 for FB patients

Choose your linac

Frames per second

Same as the kV image directory

KIM shows ‘Beam OFF’ straight away

KIM provides UDP output (3D or 6D) in DoseTracker format

Press ‘Continue’

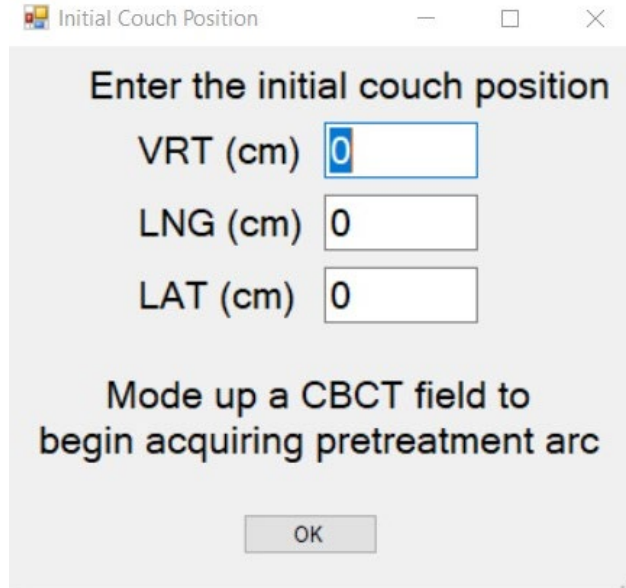
Next: Choose the patient coordinate file (in .txt format)

Patient coordinate file format (Dicom coordinate system):

```
123456(MRN)
KIM1(last name), KIM2(first name)
SUP SEED, X= -12.11, Y=  2.95, Z= -6.60
MID SEED, X=  -8.20, Y= -3.30, Z= -7.75
INF SEED, X=  -6.42, Y= -5.23, Z= -7.74
ISOCENTER (cm), X=  -7.85, Y= -1.16, Z= -6.60
```

- Does not matter which order you add the seeds in this file.
- In principle, you can add as many number of seeds as you want in this file. For LARK, we have tracked 2 seeds and 3 seeds as required, for NINJA we have tracked only one seed as well.

Enter your initial couch position after the initial CBCT match and press “OK”



A screenshot of a software dialog box titled "Initial Couch Position". The dialog box has a title bar with a small icon, the text "Initial Couch Position", and standard window controls (minimize, maximize, close). The main content area is light gray and contains the text "Enter the initial couch position" in bold. Below this text are three input fields: "VRT (cm)" with a blue border and the value "0", "LNG (cm)" with a white border and the value "0", and "LAT (cm)" with a white border and the value "0". Below the input fields is the text "Mode up a CBCT field to begin acquiring pretreatment arc". At the bottom center is an "OK" button. In the bottom right corner, there is a small version number "v1.0.0".

Initial Couch Position

Enter the initial couch position

VRT (cm) 0

LNG (cm) 0

LAT (cm) 0

Mode up a CBCT field to begin acquiring pretreatment arc

OK

v1.0.0

Fraction Gating Limit

Choose Treatment Type for Gating Limit

Symmetrical threshold

High Dose Fx
Gate at 2 mm

Standard/Breath-hold Fx
Gate at 3 mm

MLC Tracking
Gate at 10 mm

Use preset limit
Only for physicists

Asymmetrical threshold

Browse patient margin file

	<u>Upper</u>	<u>Lower</u>
X (mm)	3	-3
Y (mm)	3	-3
Z (mm)	3	-3

Confirm Threshold Values and Continue

Choose this for 3 mm for 5 secs
KIM tolerance

Choose patient margin file for
FB patients (described in the
next page)

Add here manually for 5 mm 5
sec tolerance or add them in the
patient margin file

Choose the patient margin file for FB patients only (in .txt format)

Patient margin file format:



Gating Thresholds_Pat10.txt - Notepad

File Edit Format View Help

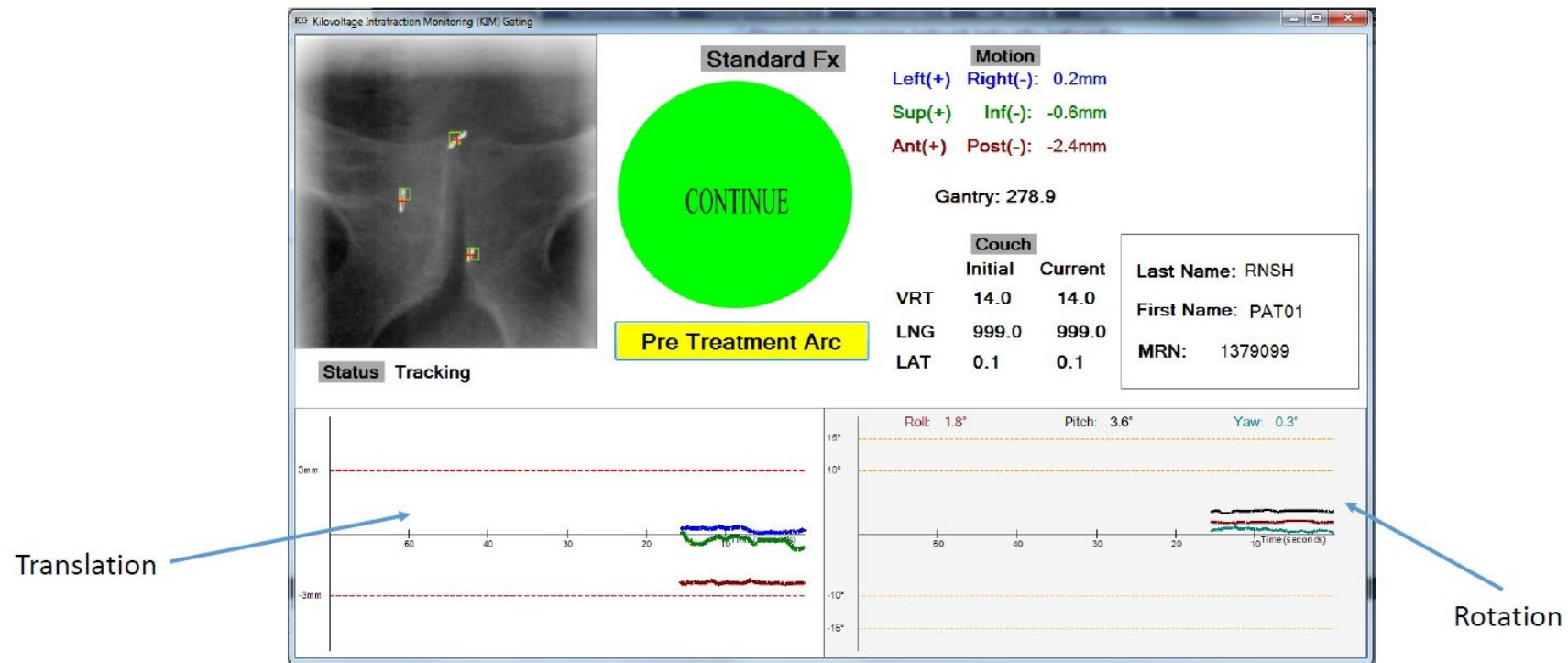
PAT10

Upper Limit(cm), X= 0.3, Y= 0.3, Z= 0.2

Lower Limit(cm), X= -0.3, Y= -0.8, Z= -2.0

			Marker 1	Marker 2	Marker 3							
			CT 50									
			Exhale Point									
		X [cm]	-11.48	-11.26	-8.5							
		Y [cm]	-6.97	-6.96	-7.07							
		Z [cm]	3	1.09	-0.63							
			CT0									
			Inhale Point									
		X [cm]	-11.6	-11.4	-8.27							
		Y [cm]	-7.5	-7.5	-7.75							
		Z [cm]	1	-0.68	-2.5							
											This is assumed to be the baseline exhale position	
						ITV		ITV-PTV				
						Average Motion of markers [cm]		Margin to apply [cm]			Upper KIM limits [cm]	Lower KIM limits [cm]
	Lat	X motion	-0.12	-0.14	0.23	0.0		0.5			0.3	-0.3
	Ant-Post	Y Motion	-0.53	-0.54	-0.68	-0.6		0.5			0.3	-0.8
	Sup-Inf	Z Motion	-2	-1.77	-1.87	-1.9		0.5			0.3	-2.1
						Pat coordinate system						
						*negative values indicate expansions in the following directions						
						Inferior						
						right						
						Anterior						

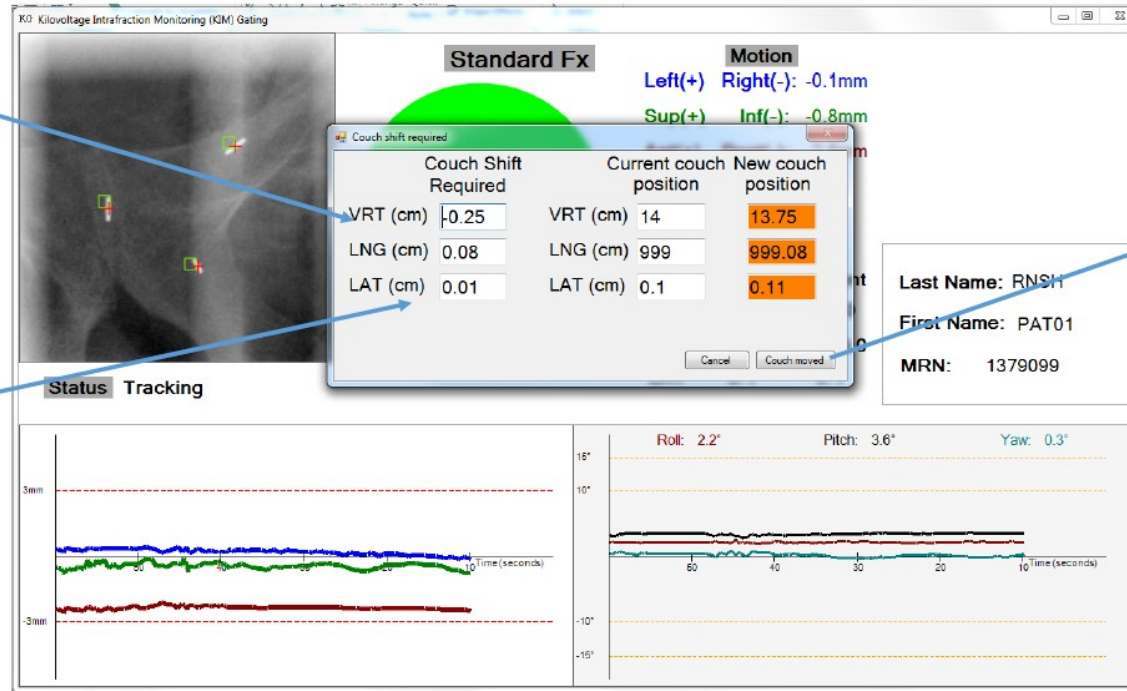
KIM interface



Couch shift in higher precision for TrueBeam

The couch shift required is now in linac coordinate to simplify the workflow on TrueBeam

KIM now allow the user to enter the couch position.



Unlike previous versions. KIM will not automatically log the couch shift positions. New couch position will only be logged when user click "Couch moved"

Always match final KIM couch shift with the final linac couch shift.

KIM settings file located in\KIM\DefaultSettings\

- For Truebeam:
 - machine_offsetsx = 0, 0, 0
 - machine_offsetsy = 0, 0, 0

For Elekta, get the flexmap correction.

- Add SAD, SID, Pixellengthatdetector.
- Add kV image machine_xcenterPixel, machine_ycenterPixel

KIM search region:

For BH patients,

-method_segmentationsearchregionwidth = 41
-method_segmentationsearchregionlength = 41

For FB patients of peak to peak magnitude of 10 - 18 mm,

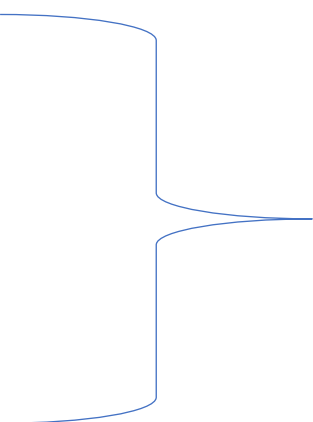
-method_segmentationsearchregionwidth = 41
-method_segmentationsearchregionlength = 71

For FB patients of peak to peak magnitude of 18 - 25 mm,

-method_segmentationsearchregionwidth = 51
-method_segmentationsearchregionlength = 91 - 101

For FB patients of peak to peak magnitude of >25 mm,

-method_segmentationsearchregionwidth = 51
-method_segmentationsearchregionlength = 111 - 121



These numbers are approximate. You may have to tweak them a little to get the best tracking.