I. HELICAL TOMOTHERAPY DICOM RT PLAN FILES

In the following, I want to present a brief comparison between the internal structure of Helical Tomotherapy DICOM RT Plan files generated by Hi-Art and RayStation 9A. I will use the following relations provided by ACCURAY in order to extract the quantities which are not contained in the files:

$$CouchTranslation = TargetLength + FieldWidth \tag{1}$$

$$Numberof Rotations = \frac{CouchTranslation}{FieldWidth \times Pitch} \tag{2}$$

$$HelicalGantryPeriod \approx \frac{FractionDose}{DoseRate} \times MF \times Pitch \tag{3}$$

$$HelicalTreatmentTime = Numberof Rotations \times HelicalGantryPeriod \tag{4}$$

A. Hi-Art

The following quantities can be found in Info.BeamSquence.Item_1:

- **300D, 1040:** Tomo Gantry period [s]
- **300D, 1060**: Tomo Treatment Pitch $\frac{\Delta y}{FW}$
- **300D, 1080:** Tomo Couch Speed [mm/s]
- **Beam Description**: it contains pitch and field width values

Considering that each gantry period is subdivided into 51 projections, the number of rotations can be obtained as:

$$Numberof Rotations = \frac{Numberof Projections}{51} \tag{5}$$

Therefore, the CouchTranslation can be obtained from Eq. (2) as follows:

$$CouchTranslation = Numberof Rotations \times FieldWidth \times Pitch \tag{6}$$

Alternatively, the CouchTranslation can be also obtained using the information abouth the HelicalTreatmentTime and couch speed, as:

$$CouchTranslation = CouchSpeed \times HelicalTreatmentTime \tag{7}$$

Considering the definition of the Pitch for Helical Tomotherapy treatments, which is:

$$Pitch = \frac{\Delta y}{FieldWidth} \tag{8}$$

we can derive the distance Δy travelled by the couch during one complete rotation of the gantry. The only missing quantity is the projection time which is not provided in the Hi-Art DICOM file. Assuming that there are no dead time intervals within a gantry period, namely the sum of the duration of the 51 projections gives exactly the HelicalGantryPeriod, we have that:

$$ProjectionTime = \frac{HelicalGantryPeriod}{51} \tag{9}$$

To conclude, based on the previous considerations and the relations provided by ACCURAY all the quantities of interest can be easily computed starting from the variables saved in the DICOM RT Plan file generated by the Hi-Art system.

B. RayStation 9A

Differently from Hi-Art, RayStation 9A DICOM RT Plan files provides the following quantities inside info.BeamSequence.Item_1

- **4001,1053**: Tomo Projection Time [s]
- **BeamDescriptions**: in **our files it's empty.**

Fortunately, in the files I have at the moment, the field width is part of the file names. In order to extract the unknown quantities we can proceed as follows.
Again, assuming the there are no dead time intervals within gantry period, namely the sum of the duration of the 51 projections gives exactly the HelicalGantryPeriod, we have that:

$$HelicalGantryPeriod = ProjectionTime \times 51 \tag{10}$$

It follows, that the HelicalTreatmentTime can be derived using Eq. (4). Since the Pitch is not available in the DICOM file, we can derive it using Eq. (3) as follows:

$$Pitch \approx HelicalGantryPeriod \times \frac{DoseRate}{FractionDose \times MF} \tag{11}$$

The MF is the one calculated from the sinogram, since it's not provided in the DICOM RT Plan file. The DoseRate is provided in [MU/min] and needs to be converted in [Gy/s]. Using this estimation of the Pitch we can extract the last missing quantity, the CouchTranslation, using Eq. (6).

1. Private attributes

In the following, a brief list of the Private attributes of info.BeamSequence.Item_1 is presented.

- **4001,1001**: Treatment Machine Commission Time
- **4001,1020**: Tomo IDMS Machine ID
- **4001,1023**: Tomo Beam Isocenter
- **4001,1025**: Tomo Machine Revision
- **4001,1026**: Tomo Beam Revision
- **4001,1027**: Tomo Intended Back Jaw Position
- **4001,1028**: Tomo Intended Front Jaw Position

2. Other useful attributes

Inside info.FractionGroupSequence.Item_1.ReferencedBeamSequence.Item_1:

- **BeamMeterset**: total MU for the beam