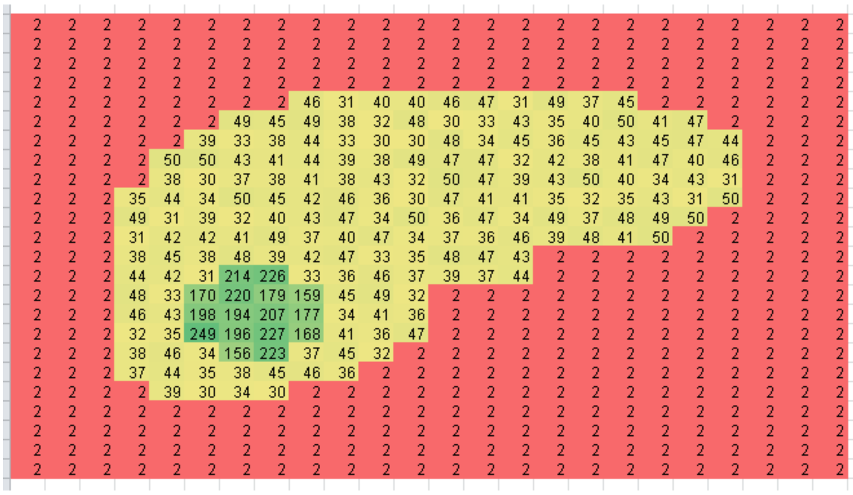
iDUG SIRT workshop BNMS

Worked example tab

On the Worked Example tab is a simulated 2D liver slice of a SPECT scan with one liver lesion.



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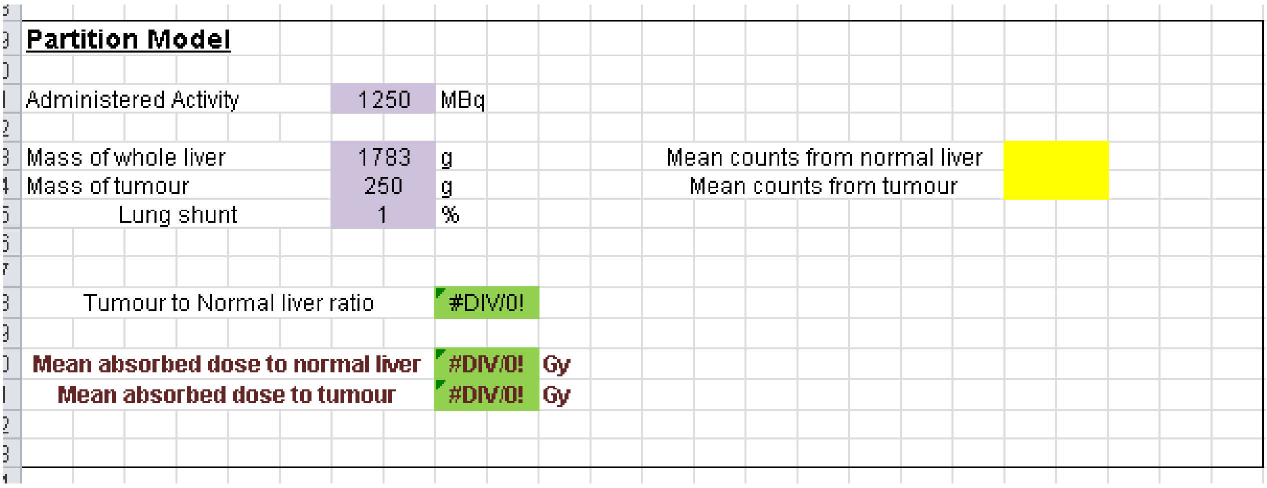
Partition Model

$$\boxed{D_{normalliver} = \frac{A_0\left[49.58\left(1 - L/100\right)\right]}{\left(TNR.M_{tumour} + M_{normalliver}\right)}}$$

$$\boxed{D_{tumour} = TNRxD_{normalliver}}$$



Partition Model

Administered Activity 1250 MBq

Mass of whole liver 1783 g

Mass of tumour 250 g

Lung shunt 1 %

Mean counts from normal liver

Mean counts from tumour

Tumour to Normal liver ratio #DIV/0!

Mean absorbed dose to normal liver #DIV/0! Gy

Mean absorbed dose to tumour #DIV/0! Gy

Purple cells are known quantities:

- administered activity,
- liver mass,
- tumour mass,
- lung shunt

Green cells have formulas in:

- tumour to normal liver ratio
- Mean absorbed dose to normal liver
- Mean absorbed dose to tumour

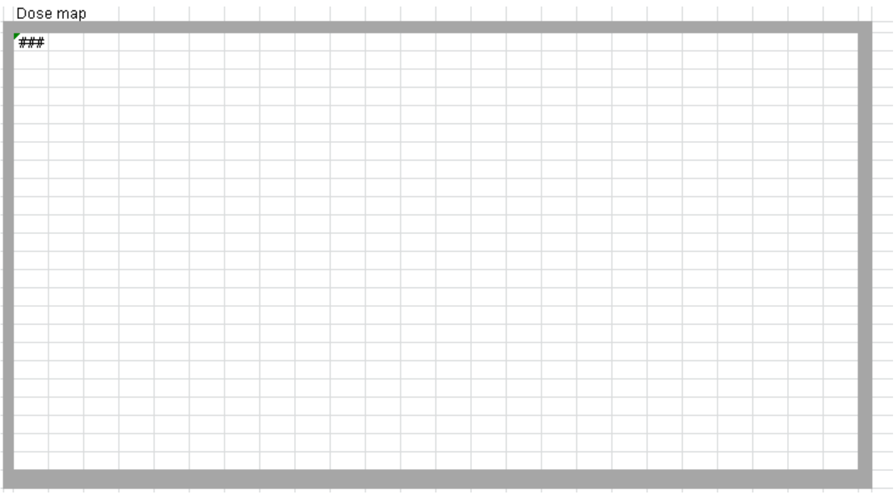
Yellow cells are values to be entered:

- Mean counts from normal liver
- Mean counts from tumour

Define the mean counts in the yellow cells for tumour and normal liver, you can use the Excel AVERAGE() function and the Ctrl key.

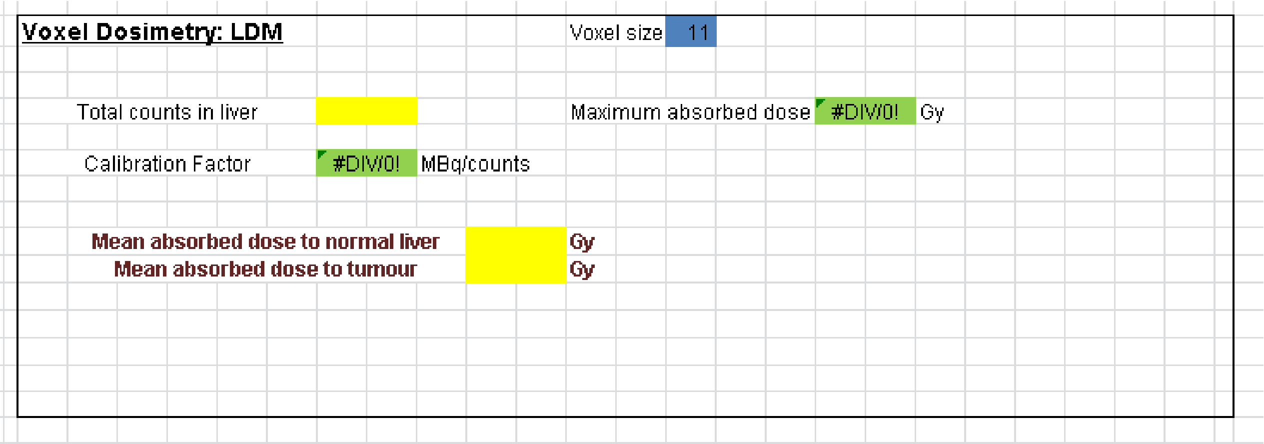
Local deposition method

$$D_{voxel}(Gy) = counts_{voxel}x\left(\frac{49.58\ x\ A_0(MBq)}{m_{voxel}(g)x\ counts_{liver}}\right)$$



Calculate the total counts within the liver using the excel Sum() function – this and the administered activity (from cell G31) give the calibration factor

The formula in the dose map region in the top left-hand cell should be copied to all cells in the grey box. Copy the cell (Ctrl + C) highlight all of the cells in the grey box and paste (Ctrl + V).



Voxel Dosimetry: LDM

Voxel size 11

Total counts in liver

Maximum absorbed dose #DIV/0! Gy

Calibration Factor #DIV/0! MBq/counts

Mean absorbed dose to normal liver **Gy**

Mean absorbed dose to tumour **Gy**

Purple cells are known quantities:

- administered activity – cell G31
- liver mass,
- tumour mass,
- lung shunt

Green cells are formulas in:

- calibration factor
- Maximum absorbed dose

Yellow cells are values to be entered:

- Total counts in liver
- Mean absorbed dose to normal liver
- Mean absorbed dose to tumour

The blue cell gives the voxel size – necessary in the calculation.

Enter the mean absorbed dose to tumour and normal liver in the appropriate yellow cells. *Scroll along and you will see a cumulative dose volume histogram. Reading off this graph gives the percentage of normal liver (or tumour) volume that receives at least a particular dose.*

Exercises

A. MAA example
B. Brem example
C. MAA example: LDM vs VDK
D. Necrotic tumour MAA
E. Necrotic tumour brem
F. Smaller Liver MAA example

A. MAA example

This consists of a ^{99m}Tc-MAA simulated 2D SPECT scan.

Obtain mean counts for normal liver and tumour – using the partition model find values for the mean absorbed dose to normal liver and tumour.

Obtain total counts in the liver – using the local deposition method find values for the mean absorbed dose to normal liver and tumour.

1. Change the administered activity – how does this affect the mean dose value?
2. What will the administered activity need to be to give an absorbed dose of 205 Gy to the tumour? What is the subsequent normal liver absorbed dose?
3. Look at the cumulative dose volume histogram: What is the percentage of normal liver that receives at least 20 Gy?
4. In the partition model how does the tumour and normal liver absorbed dose change when the mean counts (and tumour to normal liver ratio) are changed? i.e., changing the Volumes of interest (VOIs) for a scan.
5. In the partition model: change the lung shunt – how does this affect the absorbed doses?
6. In the local deposition method what is the effect of changing the VOI for the whole liver? That is keeping the tumour VOI constant but changing the total liver VOI, i.e., the total counts for the liver.

B. Brem example

This consists of a ^{90}Y-microsphere simulated 2D SPECT scan – the same original distribution as the MAA example.

Obtain mean counts for normal liver and tumour – using the partition model find values for the mean absorbed dose to normal liver and tumour.

Obtain total counts in the liver – using the local deposition method find values for the mean absorbed dose to normal liver and tumour.

1. In the partition method: Keeping all of the purple parameters the same between the MAA and the Brem example how do the absorbed doses differ?
2. In the local deposition method: how does the maximum tumour absorbed dose differ between the MAA and the Brem example?
3. In the partition method: have the same voxels been defined for tumour and normal liver between the MAA and the Brem examples?
4. In the local deposition method: have the same voxels been defined for total liver counts between the MAA and the Brem examples?

C. MAA example: LDM vs VDK

This example consists of a ^{99m}Tc-MAA simulated 2D SPECT scan with two dose maps – one generated from the local deposition method and one generated from convolution of the scan with a voxel dose kernel.

1. Which method gives the highest mean dose for tumour? And why?
2. Which method do you think gives the most representative dose?

D. Necrotic tumour MAA

This consists of a ^{99m}Tc-MAA simulated 2D SPECT scan with a necrotic tumour. The original distribution can be seen.

1. What is the mean dose to the necrotic tumour?
2. What happens if the tumour has a necrotic centre – what do you include?

E. Necrotic tumour Brem

This consists of a ^{90}Y-microsphere simulated 2D SPECT scan with a necrotic tumour. The original distribution can be seen.

1. What is the mean dose to the necrotic tumour?
2. What difference can be seen between the MAA and the Brem examples of the necrotic tumour?

F. Smaller liver MAA example

This consists of a ^{99m}Tc-MAA simulated 2D SPECT scan with a smaller liver than previously.

1. In the partition method: What is the effect of keeping the administered activity identical, and the tumour mass identical but having the whole liver smaller?