



## Step by Step tutorial to transfer man model to XFDTD format

Matlab files needed : change.m, cnt.m, fliphd.m, xchange.m, head.m, mm.m

Other files needed: man1.mod, man2.mod, ... man6.mod, read223.f

Note : Be sure to load the appropriate files each time before running any of the matlab codes.

1. Start by choosing the portion of the man model (Ask Dr. Furse for the graphs - lateral and frontal view of the manmodel) that needs to be transferred to XFDTD from the figure. Note down the coordinates of the desired portion.
2. Using file read223.f (ask Dr. Furse for it) select the slices of the man model that would cover the desired portion. This is done by comparing the k axis values in the file with that in the y-axis of the graph (frontal view of man model).
3. The desired slices of the man model are concatenated using the cat command. For example if the desired slices are man1.mod and man2.mod then the two slices are concatenated using the cat command as follows.  
cat man1.mod man2.mod >man  
Note: Before concatenating them make sure you delete the 999's for the end of the file.  
Now "man" is the file that contains the desired portion of the man model.
4. In the next step we need to count the number of cells of the different tissue types present in the desired portion of the man model i.e. data in the "man" file. This is done using the matlab function file cnt.m. (e.g. cnt('filename'))  
(A table containing the tissue number and corresponding tissue type is given at the end of this tutorial)
5. The output obtained from the cnt.m is a column of numbers containing either finite values or zero. Write down these values and number this values as 1, 2, 3... n. These numbers would indicate the tissue numbers.

- a. The tissues are then rearranged so that all the tissues that are not present in the desired portion are eliminated. (This is indicated by zeros in the output of cnt.m)
  - b. This is done by moving the tissues that are present upward, replacing the tissues that are not present. (This is done for you)
  - c. Also, the first value in the column i.e. row 1 is shifted to occupy the position below the last tissue. (This step is done since material type 1 in XFDTD represents metal.)
  - d. This procedure is implemented using the program change.m. To use this function you need to first load the file from Step 3 into matlab. This is done by typing, load filename. (Ex. From step 3 the filename is man so we type: load man) Once the file is loaded set 'x' equal to the file by typing x=filename (man in this case). Now you are ready to use the change.m command by typing change.
  - e. After the new model file is created, the cnt.m program is run again using the new model to make sure the changes were made correctly and that number of tissues, and the number of cells in each tissue remains the same (the tissue number might be the same or different).
6. After the position of the tissues is changed, the file fliphd.m is run. This file normalizes the locations of the tissues, which in essence moves the model closer to the origin. This is done to reduce the size of the grid needed in XFDTD to hold the model. This program also flips the head over so that when it is loaded into the XFDTD program it isn't upside down. (The file man.flp is created by fliphd.m )
  7. The next step would be to find the maximum and minimum value along the x,y,z coordinates and also the size of the file. This is done by using the function mm. (mm('filename') gives the desired result.) Use man.flp as the filename.
  8. Using the program xch.m the position of the model in the grid is altered, so that it is centered in the grid. ( The file h is created )
    - a. This is obtained by making the resultant of the minimum values of x,y,z axis to be 10.
    - b. The above change is verified using the function mm with the file that stores the resultant model.
    - c. Now use the program bdry.m to create a boundary around the model. In the matlab code be sure to change the tissue number to one not

being used in the model. Then once the model is loaded into XFDTD use 2/3 muscle for the boundary tissue type. (The file h1 is created by using bdry.m )

9. The final program, but not the final step, is used to add the remaining two tissue types needed in XFDTD. The XFDTD program requires three tissue definitions for each point, where the model created by Dr. Furse only contains one. This final program, head.m (maybe named headtest.m), adds the other two onto the array. It also manipulates the y directed tissue type to create a smoother model. The x directed tissue is not manipulated because the processing time was increased dramatically when this was attempted. (The file head is created from head.m)
  
10. The size, max & min of the 3 coordinates for file where the resultant data is stored is found using the mm ( mm('head') ) function, and the maximum values obtained along the three coordinates are noted.
  
11. The final step in preparing the model for the XFDTD program was to place the header file on the top of the tissue file. The header file (header.id) was created using the XFDTD program by creating a new geometry file that has a grid whose maximum values are the values noted in the previous step. The header file is concatenated with the resultant file obtained in step 10. This was done using the cat command, as discussed in step1 and the concatenated file is named with extension .id (e.g. man.id). The file is now ready to be loaded into the XFDTD program. Once the file is loaded, the tissue dielectric properties need to be specified.

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Table : Tissue Number and Type

Number	Material
0	Air
1	Muscle
2	Fat
3	Bone Combined
3a	Soft Bone
3b	Hard Bone

4	Cartilage
5	Skin
5a	Wet Skin
5b	Dry Skin
6	Nerve
7	Intestine
8	Spleen
9	Pancreas
10	Heart
11	Blood
12	Parotid Gland
13	Liver
14	Kidney
15	Inflated Lung
16	Bladder
17	CSF
18	Humor of the Eye
19	Sclera
20	Lens
21	Stomach
22	Erectile Tissue
23	Prostrate Gland
24	Sperm Cord
25	Testicle
26	Compact Bone
27	Ligament
28	
29	Pineal Gland
30	Pituitary Gland
31	Brain
31a	White matter
31b	Grey Matter