

#####Two step to use FIRT:

\*\*\*\*\*Step 1. Reconstruct Tomogram slice by slice using FIRT(mpi version)--generate serial 2D reconstruction named mid\*\*\*\*\*.mrc

```
mpirun -n $THREADNUM ./FIRTmpi $projectionFile $tiltFile $resultPath
$sliceNumber_begin $sliceNumber_end $FIRT_iteration_time $ART_iteration_time
$ART_Lambda $NAD_iteration_time $NAD_Lambda $NAD_K
```

#####The parameters of FIRTmpi

```
(1)$projectionFile -- projection to be reconstructed;
(2)$tiltFile -- tilt file;
(3)$resultPath -- the folder where 2D reconstructions goes(It should exists before FIRT
starts);
(4)$sliceNumber_begin -- the index of the first slice to be reconstructed (start from 0);
(5)$sliceNumber_end -- the index of the last slice to be reconstructed (start from 0);
(6)$FIRT_iteration_time -- the total iteration time of FIRT; (15~20 is an appropriate range);
(7)$ART_iteration_time -- the number of ART iteration during one FIRT iteration (1 is an
appropriate choice);
(8)$ART_Lambda -- the step for ART to update (1 is an appropriate choice);
(9)$NAD_iteration_time -- the number of NAD iteration during one FIRT iteration (200 is
an appropriate choice);
(10)$NAD_Lambda -- the step for NAD to update (0.2 is an appropriate choice);
(11)$NAD_K -- the threshold value to control diffusion intensity, it varies from
different images.
```

Notice:

(A) a certain amount of ART iterations (controlled by "\$ART\_iteration\_time") will be executed before FIRT start, thus if "\$FIRT\_iteration\_time" is set to 0, then FIRTmpi will only perform "\$ART\_iteration\_time" times of ART;

(B) one FIRT iteration = a certain amount of NADs + a certain amount of ARTs (controlled by "\$NAD\_iteration\_time" and "\$ART\_iteration\_time")

(C) 6 parameters control the performance of FIRT, including \$FIRT\_iteration\_time, \$ART\_iteration\_time,\$ART\_Lambda,\$NAD\_iteration\_time,\$NAD\_Lambda,\$NAD\_K .

According to our experience, 5 parameters can be set to appropriate values to generate a satisfactory reconstruction (mentioned above), user should adjust \$NAD\_K to generate such satisfactory reconstruction. Since a proper \$NAD\_K is important for a good reconstruction, we suggest users to find a proper \$NAD\_K by reconstructing and analysing one slice before reconstructing the whole tomogram.

\*\*\*\*\*Step 2. Copy program "MRCCatch" to resultPath and combine all 2D reconstructions into a 3D reconstruction

```
./MRCCatch $sliceNumber_begin $sliceNumber_end $cutSize $outputFile"
```

#####The parameters of MRCCatch

```
(1)sliceNumber_begin -- the index of the first slice to be combined (Corresponding to
*****" in "mid*****.mrc");
(2)sliceNumber_end -- the index of the last slice to be combined (Corresponding to
*****" in "mid*****.mrc");
(3)cutSize -- the size of Z axis after cutting
(4)outputFile -- output file
```