**3-D Modular MBIR-CT System Specification**

Version: 2.2

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**Overview:**

This document contains specifications for the parameter and data files for OpenMBIR I/O. It also specifies the command-line structure for reconstruction code.

**Parameter Files and their contents:**

*File types:*

<sino-fname>.sinoparams - Sinogram parameters file

<sino-fname>.2Dsinodata - 2D Sinogram data file

<wght-fname>.2Dweightdata - 2D weight matrix data file

<image-fname>.imgparams - Image parameter file

<image-fname>.2Dimgdata - 2D image data file

<reconparams-fname>.reconparams - Reconstruction parameters file

< system-matrix-fname>.2Dsysmatrix - 2D system matrix file in sparse matrix format

<ViewAngleList.txt> - Text file containing all view angles in radians

*Sinogram parameters file:*

File: <sino-fname>.sinoparams

Files Contents:

Geometry: 3DPARALLEL

NChannels: <integer> /\* Number of channels in detector \*/

NViews: <integer> /\* Number of view angles \*/

NSlices : <integer> /\* Number of Slices \*/

DeltaChannel: <double> /\* Detector spacing (mm) \*/

CenterOffset: <double> /\* Offset of center-of-rotation (Computed from center of detector) \*/

/\* Units is the number of channels, which can be fractional\*/

DeltaSlice: <double> /\* Spacing between slices (mm) \*/

FirstSliceNumber: <integer> /\* Index of first slice\*/

ViewAngleList: <char string> /\* path/name of ViewAngleList file (path relative to sinoparams location) \*/

*Sinogram data file specification:*

Sinogram parameter files may have associated data files in the same directory

Data stored one file per slice

File names:

Data stored one file per slice

For SliceIndex = FirstSliceIndex to FirstSliceIndex+NSlices-1

<sino-fname>\_slice<SliceIndex>.2Dsinodata

// <SliceIndex> contains leading zeros, and no spaces

File contents:

Binary IEEE single precision floating point format

for i=0 to Nviews-1

for k=0 to Nchannels-1

Sino[i\*Nchannels + k]

*Image parameters*

Center of first pixel is assumed to be at ( -((Nx-1)/2.0)\*Deltaxy mm, -((Ny-1)/2.0)\*Deltaxy mm).

Center of rotation (without any offset) is assumed to be at (0mm, 0mm).

File: <image-fname>.imgparams

Files Contents:

Nx: <int> /\* Number of pixels along x axis (fast variable in storage) \*/

Ny: <int> /\* Number of pixels along y axis (slow variable in storage) \*/

Nz: <int> /\* Number of Slices \*/

FirstSliceNumber: <int> /\* Index of first slice; this and Nz specify reconstruction slice range \*/

Deltaxy: <float> /\* Spacing between pixels within a single slice in x and y direction (mm) \*/

DeltaZ: <float> /\* Spacing between slices (mm) \*/

ROIRadius: <double> /\* (mm); pixels outside radius disregarded in initialization/reconstruction \*/

*Image data file specification:*

Image parameter files may have associated data files in the same directory

File names:

Data stored one file per slice

For SliceIndex = FirstSliceIndex to FirstSliceIndex+NSlices-1

<image-fname>\_slice<SliceIndex>.2Dimgdata

// <SliceIndex> contains leading zeros, and no spaces

Files Contents:

Binary IEEE single precision floating point format

Xaxis[0,Nx-1] (fastest), Yaxis[0,Ny-1] (slowest)

*2D Sparse System Matrix data file:*

File: <system-matrix-fname>.2Dsysmatrix

Files Contents:

Binary IEEE single precision floating point format

for i= 0 to Ncolumns-1

(int) Nnonzero[i] (int) RowIndex[j=0 to Nnonzero[i]] (float) Value[j=0 to Nnonzero[i]] ;

*Reconstruction parameters:*

File: <reconparams-fname>.reconparams

PriorModel: <string> /\* Options: “QGGMRF”. (Other options to follow) \*/

InitImageValue: <double> /\* Initial image Pixel Value. Unit is mm-1\*/

p: <double> /\* q-GGMRF p parameter [default = 1.2] \*/

q: <double> /\* q-GGMRF q parameter [default = 2] \*/

T: <double> /\* q-GGMRF T parameter [default = 0.1] \*/

SigmaX: <double> /\* q-GGMRF sigma\_x parameter (mm^-1) [suggested = 0.02 mm-1] \*/

SigmaY: <double> /\* Scaling constant for weight matrix (W<-W/SigmaY^2); [default = 1] \*/

b\_nearest: <double> /\* Relative nearest neighbor weight [default = 1] \*/

b\_diag: <double> /\* Relative diagonal neighbor weight in (x,y) plane [default = 1/sqrt(2)] \*/

b\_interslice: <double> /\* Relative inter-slice neighbor weight [default=1; suggest = DeltaXY/DeltaZ] \*/

StopThreshold: <double> /\* Stopping threshold in percent [suggested = 1; 0=run max iterations] \*/

MaxIterations: <integer> /\* Maximum number of iterations, [default = 20] \*/

Positivity: <int> /\* Positivity constraint: 1=yes, 0=no \*/

Specify default values by leaving field blank

Note certain reconstruction parameters are implicit in the image param file:

imgparams/{Nz,FirstSliceNumber} specifies the slice range to reconstruct

imgparams/ROIRadius specifies radius of reconstruction

**Prior model parameterization:**

Standard prior model (QGGMRF):

In this case, the reconstructions use a prior model with the form:

where is specified by SigmaX and is specified by T. Also, we assume that for any given pixel, *s*, that

with the relative value of nearest neighbor, diagonal, and -neighbor weights proportional to the values specified in the .reconparams file.

Proximal map prior model:

In this case, the reconstructions use a prior model with the form:

where is specified by SigmaX in the .reconparams file, and is the input proximal map image (or volume) specified as the argument to the -p flag (see below).**Programs and their command structure:**

The program call for generating the sparse system matrix should have the following syntax:

./<GenerateSystemMatrix3DParallel>

-i <InputFileName>[.imgparams]

-j <InputFileName>[.sinoparams]

-m <OutputFileName>[.2Dsysmatrix]

Description: This function generates a system matrix in sparse column format. It determines the geometry from the image parameters and the sinogram parameters. It need only be run once for a specific geometry.

Inputs:

InputFileName[.imgparams] - Input file containing parameters of reconstructed image

InputFileName[.sinoparams] - Input file containing sinogram parameters

Outputs:

OutputFileName[.2Dsysmatrix] - Output file containing the sparse system matrix

Note: The necessary extensions for certain input files are mentioned above within a "[ ]" symbol. However, they are NOT to be included as part of the file name in the command line arguments.

The program call for3D MBIR reconstruction should have the following syntax:

./<MBIR\_3DCT>

-i <InputFileName>[.imgparams] // note: omit extension in command line

-j <InputFileName>[.sinoparams]

-k <InputFileName>[.reconparams]

-m <InputFileName>[.2Dsysmatrix]

-s <InputProjectionsBaseFileName>

-w <InputWeightsBaseFileName> // weights computed internally if –w unspecified

-r <OutputImageBaseFileName>

-t <InitialImageBaseFileName> // Optional: initial image input

-p <ProxImageBaseFileName> // Optional: Image input to proximal map

-v // Optional: verbose output

Description: This function performs 3DMBIR reconstruction using following inputs and outputs. It is designed to reconstruct in units of mm-1 without any initialization. However, an option is provided to provide an initial reconstruction.

Inputs:

InputFileName[.imgparams] - Input file containing image parameter file

InputFileName[.sinoparams] - Input file containing sinogram parameters

InputFileName[.reconparams] - Input file containing sinogram reconstruction parameters

InputFileName[.2Dsysmatrix] - Input file containing sparse system matrix data

InputProjectionsBaseFileName - Base Name for list of input files containing projection data slice by slice

InputWeightsBaseFileName - Base Name for list of input files containing weight data slice by slice

Optional Inputs:

InitialImageBaseFileName - Base Name for list of input files containing initial image data slice by slice (mm-1)

ProxImageBaseFileName - Base Name for proximal map input files

Outputs:

OutputImageBaseFileName - Base Name for list of output files containing reconstructed image data slice by slice (mm-1)

Note: The necessary extensions for certain input files are mentioned above within a "[ ]" symbol. However, they are NOT to be included as part of the file name in the command line arguments.