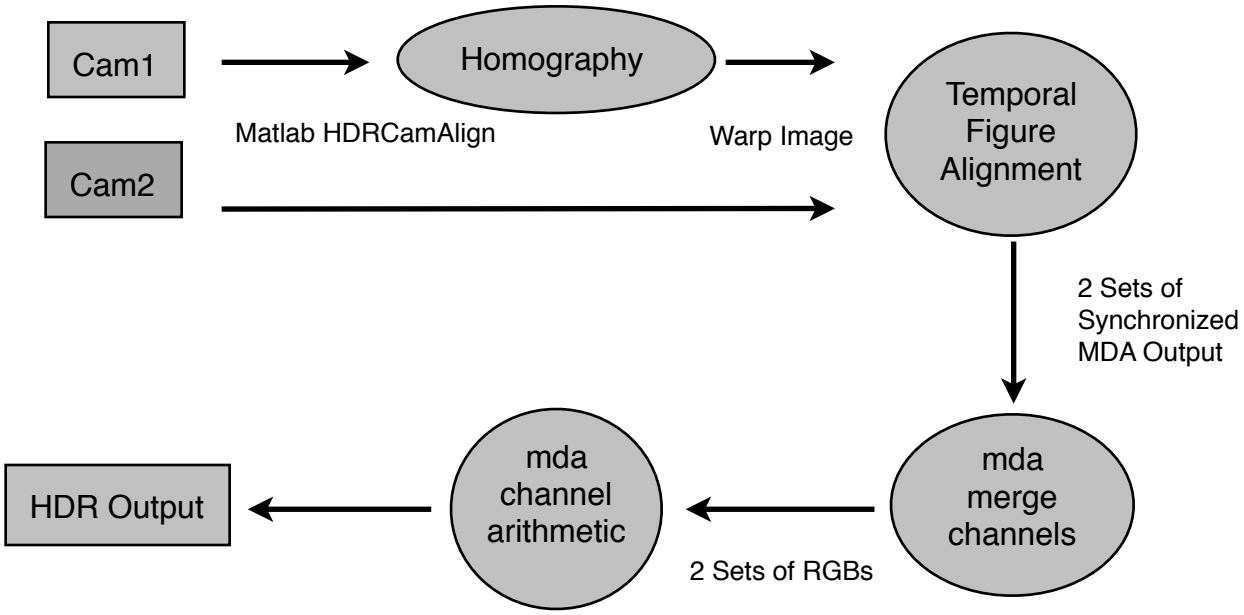
HDRCamera Project

1) Pipeline Diagram:



2) Details on the implementation of Simple Homography:

Files: (1) mda-homography.C (2) SimpleHomography.hh (3) SimpleHomography.C

Basic mda-homography Usage:

mda-homography [Options] metadata.xml < input.mda > output.mda

mda-homography reads both multi-dimensional array stream from input mda file and homography matrix from metadata, then passes the stream to SimpleHomography to do warping. The SimpleHomography is resolution-independent and the homography matrix is normalized, so before using it in rational resampling, mapping image from original dimension to [-1.. 1] and then back to output dimension is necessary. Here's how it's computed:

$$\begin{bmatrix} X_o/2 & 0 & X_o/2 \\ 0 & Y_o/2 & Y_o/2 \\ 0 & 0 & 1 \end{bmatrix} * H_N * \begin{bmatrix} 2/X_i & 0 & -1 \\ 0 & 2/Y_i & -1 \\ 0 & 0 & 1 \end{bmatrix} * \begin{bmatrix} X \\ Y \\ Z \end{bmatrix}$$

Note: (X_o, Y_o): output dimensions
(X_i, Y_i): input dimensions
H_N: normalized homography matrix

Once we have the matrix computed, then it's ready to do resampling. However, resampling is only done horizontally, so we do it first on X and then transpose the whole images and then do it horizontally again (Y of the original image) and transpose it back. Simple Homography will resample one frame after another, first to the last, from bottom to top on each frame.

3) Instructions on how to use mda-homography:

First, get one photo or video from each camera. The original file should be in MTS. Extract one frame from each of them, rename them to cam1.jpg and cam2.jpg. (The checkerboard has to be included in the image) You can either run mts2mda on MTS and mda-toimage to get single frame, or you can try "ffmpeg -i input.MTS -s hd1080 -f image2 cam-%03d.png" to convert frame to images (You can terminate the process once the frame you need is extracted). Run Matlab, put both images in the same folder with HDRCamAlign scripts, enter "hdrcamalign" in Matlab. (You might need to manually set the path in Matlab before you're able to run it) Homography matrix will be automatically computed once it's done and written to metadata.xml. (See the current left directory panel to find where the file is) Locate the metadata, move it to where you store cam1.mda. Run "mda-homography metadata.xml < cam1.mda > cam1_out.mda". cam1_out.mda is transformed, the output we need.

Note: If you see the error: " *** glibc detected *** corrupted double-linked list " while running mda-homography, it's likely that the homography matrix you're using is somehow incorrect. Verify and try again.