Step by step for MicMac:

1_Introduction:

Micmac is based on principles of photogrammetry (and photogrammetric data acquisition*), with 3 theoretical steps:
- Tie points recognition and matching between images.
- Calibration > recognition of camera's internal parameters (correction of lens distortion) AND Orientation > relationships between viewpoints and objects.
- Correlation > dense matching for 3D scene reconstruction.

* More information TAPEnADe
http://www.tapenade.gamsau.archi.fr/TAPEnADe/Protocols.html
http://www.int-arch-photogramm-remote-sens-spatial-inf-sci.net/XL-5-W2/421/2013/isprs archives-XL-5-W2-421-2013.pdf
** More information will be post in the next few month for the Culture 3D Cloud project with new tutorials optimized for C3DC pipeline
http://c3dc.fr/

Basically, keep in mind that photographs is paramount in photogrammetric processing. Good pictures are the guaranty of a good processing. Most of issues in processing is caused by a bad (or not good enough) acquisition protocols. Here is some advices to assess the quality of your raw data :
- the camera is moving not the object
- no material with reflection, refraction, translucency
- avoid homogenous chromatic surface (a white wall is nothing more than a bunch of white pixels)
- pictures are framed to encompass maximum surface of the object
- pictures overlapping must be at least 50%, but 60-80% is better to be on the safe side
- don't change the focal length (avoid zoom and prefer prime lens)
- fix manually (even arbitrary) the white balance
- prefer low ISO, pictures must not be noisy
- calculate a "good" depth of field (and keep in mind the best image quality is around f8)
- avoid (motion) blurred picture (shutter speed)
- prefer vertical AND horizontal, better with some transition pictures in between (one at 45° or two at 30° and 60°)

INSTALL:
Micmac is available on all platform (Windows, Osx and Linux) using source code (need to be compiled and all dependencies has to be correctly installed), or precompiled binaries (ready to use).

For getting started quickly it's recommended to use precompiled binairies, for advanced uses it's better to compile source code. Binairies are updated every 3/3 month, when you can benefit of weekly development using source code. It's important to note that MicMac work better on Linux, as an example some bugs could remains on binairies version (SaisieMasqQT and C3DC), usually this kind of problems is corrected the next version.

Go to Micmac IGN website and download the last precompiled binaries version:
http://logiciels.ign.fr/?-Micmac,3-
Extract the "micmac" folder to the root of your system or use the setup for Windows.

2_Micmac:

Sorry, there is no efficient and up to date GUI for Micmac, it means we need run it using command lines. Anyhow, a new interface trial has been started by the CEREMA, it's a python based interface quite well documented, and will be improved even if it doesn't give a full access to all Micmac commands.
Basically the process with MicMac follows these steps :
   - Tie points and matching using the command called Tapioca
   - Bundle adjustment (calibration and orientation) on the recognized matching points using the command called Tapas
   - At this point it's possible to generate a sparse point cloud to check the result using the command called AperiCloud
   - If you create one, it's possible to use the result PLY to draw a 3D masq (region) to calculate only the object of interest using the command called SaisieMasqQT
   - Finally the automatic dense matching is computed using a command called C3DC.
   - A lot of additional features are available in MicMac for GCP, UAV or meshing/texturing (in development) and orthophoto generation. To see the list of commands and have a quick description type : mm3d -help

Beware:
Micmac needs basics shell (UNIX) or CMD (Windows) language to execute workflows. We need to respect to the letter codes, conventions and syntax. So, one missing or extra character, digits will create an error message.
(In UNIX Shell) > It might be fun to create your folder using 'mkdir MyFolder' , but be careful if 'rm' means remove and '*' means all, thus 'rm*' will erase all contents in your current folder.
So if you are at Root, 'rm*' will erase your entire hard-disc!
(In Windows CMD) > It might be fun to create your folder using 'MD MyFolder' , but be careful if 'DSRM' means remove all contents in your current folder.
So if you are at Root, it will erase your entire hard-disc!

In case of emergency Crtl+C (or Cmd C in OSX) will stop a running command.

2.1_Command prompt (Windows) / Terminal (UNIX):

Two file paths are required:

- The directory containing images > we need to be placed inside
- The directory containing micmac's binaries > we need to indicate the path to the mm3d executable.

First we need to be placed inside pictures folder;
type 'cd'
then drag and drop the folder inside the window
type enter

Then for each command we need to indicate the path to reach mm3d as follows;
File/Path/To/Micmac/bin/mm3d

So, to run a command you need to type a command line such as this template;
File/Path/To/Micmac/bin/mm3d CommandName Argument Option

For Windows precompiled version it's possible to add the filepath in environment variable it means you'll just need to type 'mm3d' to launch it.
For Unix system you need to add the filepath in your bashrc (google is your friend) for using this easier command launching.

2.2_QT graphical interface:

Instead of writing a command line it's possible to open a parameter window in order to configure easily a command line. For source code, QT need to be compiled before and linked using the Cmake template.
To launch this windows just type 'v' before the command.
.../mm3d vTapioca
It shows all mandatory arguments needed by the command and all options we can add.
To get more information about arguments and options type '-help' after the command:
.../mm3d Tapioca MulScale -help

3.0_MM3D pipelines:

3 MicMac pipeline for dense matching coexists, a fully automatic (new and in development called C3DC), a semi-automatic (called Malt still working perfectly and actually C3DC commands are just some of Malt parametrisation) and a manual one (out dated but still efficient called MICMAC).
It's possible to mix these workflows to create an improved hybrid one corresponding more precisely to the peculiar aim of your photogrammetric data processing.

Example of manual process (because the two last commands needs you to draw a masq and select master/secondaries images relationship):
- Tapioca > Tapas > AutoCal > Apericloud > SaisieMasqQT > Micmac or Malt

Example of manual semi-automatic process:
- Tapioca > Tapas > AperiCloud > AperoChImSecMM > MMInitial Model

Example of fully automatic process:
- Tapioca > Tapas >   C3DC

Examples of hybrids process:
- Tapioca > Tapas > AperiCloud > AperoChImSecMM >   Malt
- Tapioca > Tapas > AperiCloud > SaisieMasqQT> C3DC

3.0.1_DicoCamera and metadata:

Micmac needs at least two information, focal length (automatically found in EXIF if existing) and sensor size. In case of missing EXIF, launch command SetExif :

mm3d SetExif –help > to know how to change metadata

mm3d SetExif ".*JPG" Cam="Nikon D3100" F=50 F35=75 > Example
This command will change/add all the metadata of JPG files contained in the current folder, adding the name of the camera, the focal length and it's equivalent in full frame (use the correct crop factor !).

If an error occurred at the first step (with a log relative to exif and the name of the camera) we need to check if the camera used is in the database "DicoCamera.xml". This file is located here:
micmac > include > XML_User.

If needed add your camera using this template:

<CameraEntry>
        <Name> SONY NEX-7 </Name>
        <SzCaptMm>   16 24   </SzCaptMm>
        <ShortName> NEX7   </ShortName>
    </CameraEntry>

NB : The name need to be exactly the same shown in the metadata.

3.0.2_Batch processing :

Once an efficient pipeline defined for a dataset, it's possible to repeat it on a similar one. You just need to create an all-in-one command, to launch one command after another with '&&' in between. As an example:

mm3d Tapioca MulScale ".*JPG" 600 1600 && mm3d Tapas FraserBasic ".*JPG" Out=All && mm3d AperiCloud ".*JPG" All RGB=0 && mm3d C3DC QuickMac ".*JPG" All

Let explain literally a little bit this command line :
Call mm3d to launch Tapioca (tie points and matching) in MulScale mode on every JPG files in the current folder using a first fast matching on 600px wide resized pictures and a final matching on 1600px wide resized picture THEN call mm3d to launch Tapas

(calibration and orientation) using FraserBasic model on every JPG and place the result in a folder called All THEN call mm3d to launch AperiCloud (sparse pointcloud) for every oriented JPG using the orientation inside All without RGB coloring (faster) THEN finally call mm3d to launch C3DC (automatic dense matching) in QuickMac mode (not dense but fast similar to lowest resolution in PhotoScan) on every oriented JPG located inside the orientation folder called All.

3.0.3_My Rename:

.../mm3d MyRename "(.*).EXT" "F\$2_\$1.EXT" AddFoc=1 Exe=1

My Rename is an optional tool to rename files using their metadata (EXIF), such as focal length. This command is interesting when we have to deal with a complex dataset using different focal length. Thus, it's convenient to structure the pipeline (as many calibration is required as different focal length). It allows to check an unwanted focal length variation in case of zoom lens use.

Use:
- Change .EXT with your file extension (.jpg/ .JPG / .DNG / …)
  -      (.*)   Means the command will be applied to all file corresponding to the filetype .EXT. Thus, '.*' means all before.

3.1_Tie Points computation using Tapioca:

.../mm3d Tapioca Mode "FilePattern" Arguments Options

.../mm3d Tapioca Line ".*EXT" 1500 5
.../mm3d Tapioca MulScale ".*EXT" 300 1500
.../mm3d Tapioca All ".*EXT" 1500

Tapioca runs Pastis program (for tie points matching) using SIFT algorithm and transforms the pictures (creating .tif files in grayscale) to make them usable for the different steps of micmac.
As in other photogrammetry software, different methods are available:
- Line = Generic > means the research will be compute on a certain numbers of adjacent images, but in MicMac you can set the number of overlapped pictures
- All or MulScale = Disabled > means that for each image the research will be compute on every others
- File is a mode that enable to to predefine your own methodology using an xml file (expert use)
- Graph is a mode that allows to compute research according to GPS external data.

A resolution parameter is also needed, not explicitly like in PhotoScan with High, Middle and Low but by setting the scale by specifying the size en pixel of the larger dimension. Notice that MicMac enable you to search for tie points in the full resolution of pictures using the parameter -1 (minus one), generally its not necessary to use this time consuming parameter until there is not enough overlapping between images.

To use the command:
- change the .EXT on the extension of your file (.JPG/ .DNG/ ...)
-        ".*EXT"   means that the command will consider all the files of the .EXT type which are located inside the working folder. So pay attention if you are working with .tif, because the masks are created as well in .tif format in the same working folder. In case of resampling, you need to change the command or isolate the masks temporary.
-        300 1500   Corresponds to "MulScale". Because of this command Tapioca effects a sampling on a set of pictures, working in several scales. This command is going to format the set of pictures in a low pass (300) and in a high pass (1500), corresponding to the large side of the picture. It's possible to optimize the result increasing the match (500 2000), or decrease the calculation time by lowering the match (200 1000). In an unpredictable set of pictures (bad calibration or orientation problems), increasing the sampling helps sometimes to solve problems or to obtain a better result, but with much longer calculation time. Theoretically you can work therefore up to the full resolution of the file by entering the longest pixel high value, otherwise you can type "-1", which means that the high pass will not be resized.
-        1500 5   Corresponds to "Line". The first parameter indicate the size on the pass and the second one the numbers of adjacent images in which detection and matching will be processed.
-        Circ=1   Specifying this option is useful to also matching the end of the sequence with the beginning (to close the loop), for example for a circular acquisition
-        Pat2=   This option is used to specify a second file pattern. It will search only the matches in between the two patterns.
-        Detect=   Is a option to change the path to the algorithm of features extraction, MicMac is using an implementation of SIFT called sift++, but other could be used like SURF, ASIFT…
-        NoMin/Max= Could be used to set the min and max numbers of matches.

NB: So as there are different styles of the Tapioca its means that we need to choose the good method. program, "MulScale" (multi-scale) is the one that may be appropriate in most cases of the surveys, but it can be good to know that there is also a command "Tapioca Line", especially optimized for linear surveys. It is highly recommended to use this option in case of linear surveys, because the command will only search for corresponding points in adjacent pictures and not on the whole set of pictures, which can save a lot of time. It might help as well to fix the number of adjacent pictures that the command should consider for the calculation as a preset of pairs related to the overlap you choose.
There is also a basic command "Tapioca All" for not taking in calculation different sampling passes, but allowing a unique resizing. This command allows very good results for the sets of pictures containing few pictures, because the calculation times are longer. Look at the Micmac documentation to use these functions (3.2) ore tape vTapioca.

3.3_Tapas:

Like for the Tapioca command, there are different modes for the calibration/orientation command called Tapas. Their uses for the bundle adjustement depend of the material,

the set of pictures or the type of the process. They are sorted by the number of constraints they impose. The more the constraints are, more accurate the calibration will be, but it will be even more "difficult" to get a good calibration.

- The mode Fraser is the most demanding, because it is the one with the largest spectrum, taking into account 12 parameters as degree of freedom (Focal, principal point, center of distorsion, radial, tangent..).

- The mode FraserBasic is a restricted version with 10 parameters.

- The mode RadialExtended handles 10 parameters (less "accurate" and without decentering), it should be the most generic or medium mode that suits in most cases.

- The mode RadialBasic (5 parameters) allows sometimes to obtain a calibration when the Extended mode does not work.

- In case of a equirectangular fisheye   (also called diagonal), wich look like a full frame fisheye, you have to use the mode "FishEyeEqui".

- In the specific case of a circular fisheye (180° circular frame outlined in black), you should use the command "HemiEqui" that will consider only this hemispherical image and its black mask.

- As it can be quite hard to correctly, to calibrate a fisheye lens and to orient those pictures, a more robust model is FishEyeBasic.

- It's possible to apply afterwards AutoCal or Figee without applying any of the previous models, to refine a result. While using Radial distorsion models, it's better use this refinement step. These two modes, only process the orientation, it means that a previous calibration on few pictures must have been done before. AutoCal reevaluates the results while Figee freezes them. This way to compute the calibration then the orientation, is more interesting and less time consuming for large dataset processing.

All of this modes are well documented and explained in the micmac documentation PDF.

(http://logiciels.ign.fr/IMG/pdf/docmicmac.pdf)

3.3.1_Tapas RadialExtented:

.../mm3d Tapas RadialExtended ".*(0[12345]).EXT" Out=Calib

This command allows to run both the calibration and the orientation steps. You don't get necessarily better results by doing a calibration for all the pictures of the survey. The goal is only to recognize the internal parameters of the camera and to correct the intrinsic deformations of the optical composition (distortion etc.). So you can better get a good calibration with a low number of pictures rather than an average calibration with a much larger set.

To obtain a good calibration, you generally carry out a small dataset to calibrate the camera (extended convex or concave fields on a corner while rotating AND moving your device). This generally gives good results for a number of 5 – 10 pictures.

To use the command:

- Change .EXT to the extension of your file (.JPG / .DNG / …)

- You can use several syntax systems to select the calibration pictures:

".*EXT"   > to perform a calibration on all the pictures

".*(01|02|03|04|05).EXT"   > to perform a calibration on a reduced set of pictures (by changing the photo numbering accordingly)

Calibration of the pictures from 01 to 05

To calibrate the pictures from 01 to 09 the command becomes: ".*(01|02|03|04|05|06|07|08|09).EXT"

If the numbering is composed by 3 or 4 digits, you can use the abbreviated selection.

".*(0[12345]).EXT"   > a type of abbreviated selection.

Calibration on the pictures starting with 0 and ending with the numbers going from 1 to 5

To calibrate the pictures from 01 to 09 the command becomes: ".*(0[123456789]).EXT"

To calibrate the pictures from 1234 to 1243:

".*(123[456789]|124[0123]).EXT"

To calibrate the pictures from 1234 to 1243 without the pictures 1236 and 1239: ".*(123[4578]|124[0123]).EXT"

ETC…

".*(0[1-5]).EXT"   > another type of abbreviated selection.

Calibration of the pictures starting with 0 and finishing with the digits going from 1 to 5

To calibrate the pictures from 01 to 09 the command becomes: ".*(0[1-9]).EXT"

To calibrate the pictures from 1234 to 1243: ".*(123[4-9]|124[0-3]).EXT"

Remember you can launch the vTapas, in order to select more easily your file pattern.

-        Out=Calib   Means that the results of the calibration will be placed in the folder "Calib" created automatically. For convenience we generally use Out=All.

It is possible to change the name of the folder to organize its set of pictures or to use or test several calibrations.

For example "Calib28", to place it inside a specific calibration folder for the calibration of a 28 mm lens.

To optimize the calibration:

The purpose of this command is to achieve an optimal bundle ajustment. You can check the results during and at the end of the operation by looking at the average residual or the residual value of each picture. A calibration is more successful, the lower the residual is, but to obtain a perfect calibration with 0 residual value doesn't exist. An excellent result is less than 0,5 (which is very rare), a good result is between 0,5 and 1, beyond the result is average. It might be interesting to try to do a calibration with more or less pictures to improve the error of reprojection. To continue the calculations with a residue higher than 1,5 is possible, but there might be problems afterwards. You will obtain most often residues around 1 which won't be any problem afterwards. The calculation starts with a more or less high value and this value decreases with the interactions (Iter x) and/or the steps (ETAPE X). So the final residual value at the end of the calculation will predominate, the analysis of the previous results will only be necessary if the final result is not optimal!

Example of the end of the process with a good residu at 0,7 :

|| RESIDU LIAISON MOYENS = 0.696993 for Id_Pastis_Hom

--- End Iter 4 ETAPE 2

Besides this optimization by the average value you can also detect if one or several pictures, for different reasons, are found problematic for the calibration. Therefore you can control the residue value of each picture (ER2 X.xxxxxx). If a picture presents an abnormal peak in the middle of the set (as below), it could be interesting to relaunch the calculation without this picture. An other way to see if something goes wrong is the second value corresponding to the percentage of tie-points recognized, generally due to a lack of overlapping.

RES:[F019_DSC_01.ARW] ER2 0.765652 Nn 99.6018 Of 15820 Mul 10059 Mul-NN 10016 Time 0.921944

RES:[F019_DSC_02.ARW] ER2 6.681986 Nn 67.8253 Of 13739 Mul 5889 Mul-NN 5882 Time 1.831963

RES:[F019_DSC_03.ARW] ER2 0.739195 Nn 99.6952 Of 15749 Mul 8978 Mul-NN 8953 Time 0.880865

3.3.2_Tapas AutoCal:

Tapas AutoCal ".*EXT" InCal=Calib Out=All

This command only realizes the global orientation by providing an overall view of the scene, to obtain a spatial coherence between the purpose of the survey and the different points of view. It means that we need to use a calibration result called by the argument InCal. Thus AutoCal might be used when you want to add new pictures taken by the same camera and focal, you already calibrated (and placed in this exemple in the floder called Calib). AutoCal will reuse the calibration model found in your InCal.

If a Tapas in mode Fraser or Radial is already succesfull on all the pictures, there is no mandatory need to call AutoCal, because pictures are already calibrated and oriented.

To use the command:

- Change .EXT to the extension of your file (.JPG / .DNG / …)

- You can use a different syntax selection if you want to try only on a part of the set of pictures, but generally you launch this command on the entire set of the survey with this formulation ".*EXT". Note that the command will fail if you have not done ALL the necessary calibrations (multiples sensors and/or focal lenght).

-     InCal=Calib   Means that the command will use the calibration files in the folder "Calib".

                                    If you changed the name of the folder in the previous command, you will have to change to the name you used.

-     InOri=All   Means that the command will use the orientation files from a previous Tapas and placed in the folder "All".

-     Out=All   Means that the results of the orientation will be placed in the folder named "Ori-All" created automatically by the command.

-     FrozenPoses=   This option enable to freeze some pictures, it means that those pictures will not move during this new orientation.

3.3.3_FraserBasic:

In the automated process it's better to use the mode FraserBasic (more accurate than RadialExtended) to perform a calibration – orientation on the set of pictures (thus

AutoCal becomes superfluous). Actually, depending to the quality of the bundle adjustement you can be sure about the metric accuracy of your model but you can also increase the density of the dense matching. As an example, with a reprojection error below 0,5 its possible to reach a very fine pointcloud using the full resolution of the picture :

../mm3d Tapas FraserBasic ".*EXT" Out=All

To use the command:

- Change .EXT to the extension of your file (.JPG / .DNG / …)

- It performs the calibration and the orientation on the set of pictures:

".*EXT"   > to perform a calibration on all the pictures (if the set of pictures is small)

-        All   Means that the calibration – orientation results will be placed in the folder named "Ori-All" created automatically.

In case of emergency, when there is no way to succeed Tapas, you should at first consider to check to your images quality, then call the old version of Tapas. By default, the new Tapas is launched, this new version is a very high polynomial approach refining itself at very steps, iterations, and sub iterations. So when something seems to be wrong with a good dataset, retry using OldTapas instead of Tapas.

3.4_AperiCloud:

.../mm3d AperiCloud ".*EXT"   All

This command allows to obtain a point cloud in .ply format in low density, containing all the tie points recognized. This command locates also the position of the cameras. The command is optional, but allows finally to verify and to validate visually the results of all the proceeding steps after all the previous calculations. Thanks to the visualization of this point cloud, it is possible to control the accuracy of the reconstruction of the scene and therefore it should be well restituted in the dense point cloud. This step allows to verify the global orientation of the scene and it gives you also some indications for the correlation phase. Indeed the areas of the point cloud where you can see a lower density, will be the areas where the correlation will be more difficult. If there is a spatial coherence problem, it will be necessary to re-launch some commands differently parametrized whose possibilities are:

- Increase the sampling of Tapioca, to obtain more tie points and therefore it is possible that some errors of geometric correspondence might be corrected.

- Try to obtain a better internal calibration changing the "ModeCalib" (from Radial to Fraser), verifying the residual values and if needed add or remove some pictures of the calibration.

- Perform an AutoCal on the problematic areas to verify or to identify the source of the problem.

- Logically, according to the chosen commands to solve the problem, you will generally need to redo all the following commands. "AperiCloud" will use the folder "All", "Autocal" will overwrite the files in the folder "All" and will use the folder "Calib", and so on…

To use the command:

- Change the .EXT to the extension of your file (.JPG / .DNG / …)

- You can use a different syntax selection if you want to try or verify only a part of the set of pictures.

-       All   Means that the command will use the files in the folder "Ori-All".

- You can add "RGB=0", to obtain a colorless file which is very convenient to save computation time, especially if you are working on a large set of pictures.

        Example: AperiCloud ".*DNG" All RGB=0

-       WithCam=0   You can choose to display camera positions or not, using this boolean option (by default is true 1). The same option also exist to display points (WithPoint=1 or 0)

-       SeuilEc=2   Using this option you can filter points with high residu and so it could be use for example to remove outliers.

To visualize the point cloud AperiCloud, you need to use a software that opens files in .ply format. The softwares commonly used are MeshLab or CloudCompare.

3.5_Automated protocol:

Prerequisite: to have a calibrated and orientated set of pictures

3.5.1_C3DC (still in development):

.../mm3d C3DC Mode FilePattern Ori Option1 Option2 OptionN

.../mm3d C3DC QuickMac ".*JPG" All

.../mm3d C3DC Statue".*JPG" All ZoomF=4 Masq3D=AperiCloud_All_polyg3d.xml Out=MyObject_C3DC_Statue_Middle_Masqued.ply

The command Culture 3D Cloud (C3DC) is the first version of a 100% automatic point cloud correlation. It is possible to launch it just after the AperiCloud so the PLY can use the 3D mask. It is based on AperoChImSecMM and MMInitialModel experience.

This command generates automatically masks (using tie points), select best pictures for correlation and prevent certain bad projections at the borders of 2D masks. It will create a colored, oriented .ply file with the normals.

Notice that different mode of correlation are available, while Quick/Mic/BigMac are multistereoscopic, the Statue mode is stereoscopic (with an epipolar geometry approach, better but slower).

To use the command:

- All   Means that the command will use all the files in the folder "Ori-All".

- QuickMac   This is a mode of C3DC with ZoomF=8 (low preset 1pt/64px)

- MicMac   This is a mode of C3DC with ZoomF=4 (medium preset 1pt/16px)

- BigMac   This is a mode of C3DC with ZoomF=2 (high preset 1pt/4px)

- Statue   This is a different mode of C3DC with ZoomF=2 (high preset with less noise)

- PlyCoul   Color of the point cloud (true by défault)

- ZoomF   Useful option to set density of the pointcloud, depends on the mode used but can be changed this way (use 1, 2, 4, 8, 16 where to is the maximum value)

- DownScale   Useful to subsample the pointcloud a DownScale=2 will result a divided by 2 ZoomF but with more a regular density of points

- Masq3D   To add a 3D mask from a file PLY*

        *A 3D mask is an .xml format that has recorded the different operations performed chronologically (kept as a roto-translation matrix). Use SaisieMasqQT on a AperiCloud result (AperiCloud_All_polyg3d.xml)

NB : You can see on the C3DC -help some additional features such as DefCor (threshold to force the matching) or ZReg (regularization factor). These are some interesting tunning parameters described in the Malt (semi-auto processing) documenation. For now, the are not avalaible in precompiled version but will be released sooner or later.

Known issues :

Sometimes a process suddenly stop with an "End process", by typing Enter you can see some additionnal error message where appears the name of one or multiples pictures. It means that something went wrong before, if you relaunch the command and be aware of any error message, apparently one or more images can't be used but C3DC keep going on until this fatal error. Identity the bad pictures and remove it from your set. This is bug existing only precompiled binaries (OSX and Windows), it will be fix on the next release (hopefully).

3.6_Additional features :

Some additionnal features are available as an example for using scanned pictures, generating an orthophoto, scale and georeference the model using GCP, meshing an texturing

3.6.1_SaisieMasqQT:

../mm3d SaisieMasqQT

The command "SaisieMasqQT" launches a small program from which you can draw the masks for the correlation. The masks allow you to define the correlation zone to calculate only the essential. Or on contrary, it allows to force the correlation on a forgotten area in a manual process. It is important to note that it is possible to create 3D masks starting from a .ply file! Therefore you have to select the correlation volume starting from the file AperiCloud.ply.

NB : Sometimes, the QT windows crash while loading the ply, this seems to be a problem of OpenGL, so you should consider to check your graphic card drivers and parameters.

To use the command:

- File > Open Image

- Left click > Draw the mask

- Right click > Finish the mask

- Dial > Zoom

- Mask Edition > To modify the mask (add subtract, etc…)

- File > Save Mask

3.6.2_PIMs2Mnt:

../mm3d PIMs2Mnt Mode DoOrtho=1

../mm3d PIMs2Mnt MicMac DoOrtho=1

The generation of an orthoimage use to be quite tricky with MicMac, even more when we are working on image geometry (no DTM) and we need to fake measurements system. For few month there is this automatic command to turn the result of a dense matching into an orthophoto. This is a work in progress command, not very efficient for now but still has to be known and it's working nicely on flat surface (wall painting etc…).

As the name of the command is quite explicit, it will turn a result from a Per Image Matching into a Modele Numérique de Terrain (aka DTM) with an option to compute an orthophoto.

To use the command:

-       Mode   Means that the command will use all the files in the folder PIMs-Mode (BigMac, MicMac, QuickMac...)

-       DoOrtho=1   To enable the Orthophoto generation

-       Repere   To add a metric system and define the projection plane (using and xml file > see PDF documentation or forum Micmac)

NB : After this command an other one is needed to create the mosaic. PIMs2Mnt will create a folder PIMs-ORTHO where you'll orthorectified pictures. The command Tawny, will merge them together to create the final orthophotomosaic. To run Tawny :

mm3d Tawny PIMs-ORTHO

3.6.3_TiPunch and Tequila :

../mm3d TiPunch -help

../mm3d Tequila -help

After a dense matching using C3DC its possible to process meshing and texture the mesh directly with micmac. TiPunch is for meshing and use the well known Screened Poisson Surface Reconstruction algorithm. Tequila is for texturing the mesh using the photos as raster images.

As these commands are quit new and still under heavy development, better informations can be found in the micmac documentation in PDF.

3.6.4_GCP :

There are tools for adding GCP, check point or change coordinate system in MicMac (Campari, GCPBascule, GCPControl, SaisieAppuiInitQT...). As it will require an other document like this one, the best way to learn it is to experience and visit MicMac forum, where a the community of MicMac can introduce the basic pipeline.

4.0_Solving the problems:

You should know that 95% of the error messages are generated due to a bad manipulation on the part of the operation. Therefore 95% of the errors can be resolved by an operator or cautioned for the toughest problems. These errors also include in their messages the mention "KIND OF ERR : User's error"

The message FATAL ERROR doesn't mean that there is nothing to do to solve the problem. When an error message occurs, it informs of the cause that has generated the problem and indicates of which nature the error is and at which stage it occurred and with or starting from which file. Trying to understand these indications you can more or less easily find an auto-resolution to the problem. Once again, most of the error messages are wellknown for micmac users, so check the forum, you are not the first one to see it and most of the time somebody know how to fix it !

Anyway here are some known message error :

- In Tapioca, a message related to Foc-Metadata means that some essential metadata cant be found in the exiv profiles of pictures. You need to check, modify or create your metadata using SetExif command and/or and your camera inside the dico-camera.xml

- In Tapas several error messages could appears, there is 2 kind. Before the bundle adjustement, or during. If something wrong happen before the first step of the first iteration it means somethings goes wrong with the image matching (in Tapioca) or with a previous Tapas. If you used badly InCal or InOri, messages are pretty clear and easy to understand and fix (Cannot determinate internal calibration for, Ori-Name is not an existing folder…). Messages related to a bad Pastis/Tapioca could be, UN-Connected (ie two black of images cannot be linked), A-BestCam=0 (ie not enough tie points), Problem of connection in MST or POINT-HOM out of image (ie original pictures has been rotated…). Except the last one, those problem could be solved by a new Tapioca changing the strategy and/or increasing the size. Errors happening during the bundle adjustement are clearly linked to image quality or bad data acquisition, at this point elements display by the terminal can give good hint (one picture with abnormal high residu, use of a small part of tie-points). Message are like, radial distorsion abnormally high, Very singular value in Gauss, Point behind camera (orientation problem). The first way to resolve it, is to change the calibration model (generally by decreasing is to a less demanding degree), try to remove bad pictures, play with options (using InCal by giving a better initial calibration).The second move is to retry a new Tapioca strategy. If both doesnt work you really should consider redo a better data acquisition…

- In AperiCloud, all error are user's error, just check your command because it seems like you are doing it wrong.

- In C3DC, errors are also often user's. Some bug could remains especially on precompiled binaries (like the Statue mode on Windows). Most of the time, the computation will fail if something is going wrong with Ori folders (missing internal calibration or orientation) and previous PIMs folder (multiples PIMs, etc…).

- One tip to solve most of issue in MicMac processing is actually displayed at the screen, you'll see at the end of a command a template with some advices. The first one is « Take a Pastis », dont take it litteraly, it means you should need to try a new Tapioca strategy (Pastis is a program behind Tapioca for the tie points extraction). It also could be helpful sometime to clean a bit your folder, especially the Tmp-Mm-Dir wich is the temp files folder, just keep in my mind that you new computation will be slower because, MicMac will have to reconvert every single files needed for different steps. Other advices displayed may help you too, like MicMac works better on Linux or at the end contact the forum :

http://forum-micmac.forumprod.com

- One last word about back-up and micmac folder management. If you have the need to archive a folder and keep the chance to recompute it afterward, all mandatory files to relaunch a C3DC command are stored in Homol (not the SRes one) and Ori folders (and PIMs if you want to recompute an orthophote). Thus feel free to remove unwanted data stored in Pastis, Pyram, Tmp and others folders that will appears during differents commands.

4.1_ "Parsing errors"

"Parsing" in computer language defines the mode of the data coding and its syntax system. Its corollary in "human" language is defined in the same way. A "parsing" error, therefore a language error from the operator, results in a lack of understanding by its listener, in this case a computer. The language and syntax errors (parsing) can be at two levels for micmac. There is only one single rule: rigor!

Language mistakes "Shell" or "MS-DOS" occur when the command is incorrect for the terminal and therefore it cannot appeal to the micmac commands. Basically, if you type "Cd" instead of "cd" to be placed in a folder, an error message "No such file or directory" follows. The same if you type "cd.." instead of "cd .." to return to the parent folder. So there is no approximation, the syntax needs to be exact! A block letter, an extra space or the lack of a space and the command will not run. Micmac which is based on this kind of language will not tolerate any deviation as well, for example if the file name you want to use with the command does not match exactly the actual file name (be careful of CAPS extension file .jpg is different to .JPG). But beyond this common language, micmac needs also its own syntax for launching commands. For example:

- "../Saisie Masq" instead of "../SaisieMasq" will lead to the message "Command not found"

- Missing a mandatory unnamed argument (Size in Tapioca) such as writing badly a named option (Incal or zoomF) will create an error message.

- Tapas RadialExtended .*(0[12345]).EXT Out=Calib, instead of Tapas RadialExtended ".*(0[12345]).EXT" Out=Calib (because the double quote indicate that we want to use the relative file path and not the micmac synthax wich can be slighly different).

- The error message; "can't open file : […] (in mode rb)", "no match for this poses name", are resolved by correcting the syntax of the command.

Therefore, before seeking the cause of the problem in more detail (if that is indeed the case), ALWAYS start by checking the syntax of the command. As you have seen, a space, a character, a block letter in excess or a missing character are the main cause of the problems and can be solved easily with a bit of patience!