## Refined Template Matching – developed by Alex Foden

We have provided an example deck for refined template matching of multiphase materials.

General descriptions of variables:

In the *%% setup* section, you need to set the location of the directories for AstroEBSD and MTEX.

The *%% Inputs* section is where all of the user defined variables are set.

The **InputUser** structure contains information about file I/O.

*InputUser.HDF5\_folder* is the location of the folder containing the HDF5 or BCF file to be indexed

*InputUser.EBSD\_File* is the name of the file you wish to index

*InputUser.Phase\_Input* is the name of the phase file for the phase you are indexing

The **RTM** structure contains information and settings for the template matching.

*RTM.screensize* sets the number of pixels in each side of a square screen used to make the library, making this bigger will cause the time taken to index longer. For the filter settings, this has to be 2n pixels squared.

*RTM.Sampling\_Freq* sets the maximum angular separation of each of the orientations in the library.

*RTM.iterations* is the number of times the refinement step iterates.

*RTM.LPTsize* sets the screen size of the log polar transform used to measure the z rotation for the correction.

The **Settings\_CorX** structure contains settings for EBSP background correction.

Once these are filled in, clicking *Run* will run the code as is.

Results are stored in the *RTM.Output* structure. You can plot IPF maps using *Astro\_IPF\_plot* , which when parsed an input ‘printing’ of 1, will save figures to the current directory.

For information on the workings of specific functions, please email either:

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