The SuperCOSMOS data processing guides: Pairing

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1 Introduction

Note: If you have not already done so, please read the Beginner's and Introductory Guides to familiarise yourself with SuperCOSMOS data before proceeding.

Plate pairing is a fundamental part of astronomy from plate scans. Multiple measurements of the same object from different plates provides a means of measuring time–dependent phenomena (*eg.* variability, proper motion) while plates in different wavebands provide colour information. Plate pairing can be approached in different ways, but in order for pairing to be achieved quickly and efficiently, the two datasets being paired must be sorted on position. This Guide describes a simple procedure for plate pairing. The process consists of three stages:

- choosing a 'master' and 'slave' plate, then transformation of the xy system of the slave to that of the master;
- sorting both master and transformed slave into the same order, at the same time, purging unwanted image records;
- pairing the two datasets.

Throughout these Guides, the concept of an 'index' is used extensively. An index in this context is simply a binary file of pointers to images in an IAM file. The advantage of using direct access files of pointers is that quick access can be gained to any image in a large IAM dataset, and all 32 parameters for that image are then available. No decision has to be made concerning which parameters to keep from master and slave in a combined file. The pairing routine described herein creates a binary file of pointers (a pair index) containing a pointer record for every record in the master IAM file. If a corresponding image is paired from the slave, then the pointer is simply the record number, in the direct access IAM file, of that slave image. If no image pair exists, then the pointer is written as zero. Any number of slave plates can be paired to the master in this way; subsequently the indices can be accessed to obtain multi–epoch and/or multi–colour information for any image (a simple example of this is given at the end of this Guide).

The choice of master plate is somewhat arbitrary. In most situations it is probably worth choosing the 'best' plate as the master, where 'best' means the deepest (*ie.* the plate containing the most images) in any given set being paired.

2 Transformation of the slave co-ordinate system to that of the master

Code `slavexfrm` carries out a transformation of slave xy co-ordinates to the system defined by the master images. The inputs are simply the master and slave IAM files; the output is a copy of the input slave IAM file with parameters 11 and 12 overwritten with transformed xy co-ordinates. The program uses RA and DEC to associate objects to define the transformation (note that it is of course possible to pair plates using the RA and DEC of images). The global transformation is a six–coefficient linear fit of the form

$$x' = a + bx + cy,$$

$$y' = d + ex + fy.$$

The code has a generalised fit option hard–wired in parameter ITYPE(=6) — other options are available (consult the source code comments in `slavexfrm.f`) but it is recommended that the full 6–coefficient fit is used in general. An iterative least–squares fit is carried out, and the results are output before the transformed slave copy is created, as in the following example:

```
% ./slavexfrm
 Master IAM file?
I16468/iam.srtrd
 Slave IAM file?
I16464/iam.srtrd
 Output file for transformed slave IAM data?
I16464/iam.srtrd.16468
 Pairing master and slave images.
 No. of images read from slave file:        4733
 using image step of          100
 Number of records read from master IAM file:      733740
 No. of pairs for least squares fit (at start):        3067
 Solution converged after          20 iterations.
 No. of pairs in final fit:         1981
 Details of linear fit:
 Zero points: in X (um)   -798.611782655170
                Y          386.634598259123
 Scale factors: in X   0.999988166533708
                  Y   0.999999718978122
 Non-perpendicularity of axes (shear) in degrees   4.536112824109535E-003
 Rotation (degrees):   0.143064370115887

 RMS error: X (um)    2.94658498264357
           Y          2.58235544870825
        Total         3.91802536023107

 Coefficients of fit:
 -7.976192124049131E-004
  0.999985147263717
  2.536525920009728E-003
  3.885956966598325E-004
 -2.457327696580677E-003
  0.999996501990172
 No. of slave images transformed and written:      473535
%
```

Note that the coefficients in the equations above are output by the code in alphabetical order if you wish to perform any operations using them. Note also the RMS residuals per star of the fit are output: take note of these as they are relevant to the matching tolerance when pairing. The RMS values will typically be a few microns when comparing modern plates of similar type; values up to a few tens of microns may be obtained when pairing, for example, old Palomar plates with modern plate data. The RMS errors will rise if the fit type has fewer coefficients; *eg.* they may be a factor of ~ 10 larger for a solid body (*ie.* scale-less) translation and rotation only model (ITYPE=3) when compared with the full six coefficient default, which consists of translation, rotation, independent scale factors in x and y, and also shear.

3 Sorting the IAM files

As stated before, sorting greatly speeds up the pairing process, the timing of which generally goes as $\sim N^2$ for unsorted files compared with $\sim N$ for sorted files (when N is large — *eg.* typically ~ 200000 images in master and slave IAM files — this is a huge improvement). The approach taken in code `iamsort` is to sort the plate data into a series of lanes corresponding to the scanning of the plate (consult the Beginner's Guide for more information). Within a lane, the images are sorted in order of increasing y co-ordinate; note also that `iamsort` expunges images of poor quality (quality flag > 65535); parent images of deblends; and also images outside the requested area (this is particularly useful if the data have been xy transformed as in the case of slave data — see the previous Section). Run `iamsort` on both master and slave IAM files as follows (continuing from the example shown in the previous Section):

```
% ./iamsort
 Input IAM file?
I16468/iam.srtrd
 Output IAM file?
I16468/iam.srt.srtrd
 Area to retain: xmin, xmax, ymin, ymax (in mm)?
16.22 338.78 16.22 338.78
 Lane width (in mm)?
11.52
 Number of lanes to be sorted:           28
 Number of records read from IAM file:       713345
            - parent images discarded:        15243
      - poor quality images discarded:         2045
      - images outside requested area:            0

       Images to be sorted and output:       696057
 Completed lane            1; images output:       33452
 Completed lane            2; images output:       60936
     .
     .
     .
 Completed lane           28; images output:      696057
 Finished sorting.
% ./iamsort
 Input IAM file?
I16464/iam.srtrd.16468
 Output IAM file?
I16464/iam.16468.srtrd
 Area to retain: xmin, xmax, ymin, ymax (in mm)?
16.22 338.78 16.22 338.78
 Lane width (in mm)?
11.52
 Number of lanes to be sorted:           28
 Number of records read from IAM file:       473535
            - parent images discarded:        14277
      - poor quality images discarded:         1887
      - images outside requested area:         2270
```

```
      Images to be sorted and output:       455101
 Completed lane           1; images output:       43122
 Completed lane           2; images output:       85616
     .
     .
     .
 Completed lane          27; images output:      440936
 Completed lane          28; images output:      455101
 Finished sorting.
%
```

Note that the area for pairing would normally be the entirety of the master area. This is defined in the house–keeping file in parameters `AXMIN`, `AXMAX` etc. in units of 0.01μm. If you wish to examine the overlap of a pair of plates and/or want to choose a reduced area for pairing, codes `ibrisel` and `briplot` (both described in the Beginner's Guide) plot the 1000 brightest images on each which can be helpful in selecting the required common area for pairing. Finally, the default lane width for scanning is currently 11.52mm (this is also available from the house–keeping file) and it is recommended this be used when sorting IAM files.

4 Pairing two sorted IAM files

Code `npair2` takes a master and transformed slave, both having previously been sorted, and pairs up images within a given search radius. The straight–forward approach here is that the nearest image on the slave, within the search radius, is identified as the one corresponding to a master image; a pointer to the record of the slave IAM file containing that image is written to the output index. The following example illustrates this (again, continuing from the previous examples):

```
% ./npair2

 Master file name?
I16468/iam.srt.srtrd

 Secondary file name?
I16464/iam.16468.srtrd

 Output file name?
I16468/pairs.16464.idx

 Input minimum X (mm), lane width (mm), number
 of lanes & search radius (mm):
16.22 11.52 28 0.05

  No. of objects on slave plate =    455101
Lane:   1 Paired:     30777
Lane:   2 Paired:     63152
            .
            .
```

```
              .
Lane:  23 Paired:    278151
Lane:  24 Paired:    296329

  no. of images paired up  =    307561
 No. of master images:      694073
%
```

Note that the minimum x value, lane width and number of lanes should correspond with those at the sorting stage (see previous Section). Also, the search radius should not be too small when compared with the residuals in the slave transformation (it should be $> 5\sigma$, say) but it should not be so large as to produce many confusing pairings between isolated, spurious features on single plates. The tolerance used above, 50μm, is a good working figure in most situations.

5 Testing the pairing process

It is a good idea to test the above procedure to check that the pairing is working as required. Code `testpairs` is a version of `ncharts` (see the Beginner's Guide) that makes ellipse plots of a small specified region. The six plots show all images, all paired images, and all unpaired images from both master and slave IAM files. Run the code as in the following example:

```
% ./testpairs
Master IAM filename:
I16468/iam.srt.srtrd
Slave IAM filename:
I16464/iam.16468.srtrd
Pair index filename:
I16468/pairs.16464.idx
Co-ordinates of test region:
03 44 0.0 22 57 0.0
Equinox (0=1900, 1=B1950, 2=J2000):
1
Size of plot on a side (arcmin):
10
Graphics device/type:
xwindows
%
```

The corresponding output plot is shown in Figure 1. Note that pairing two plates will greatly reduce spurious images from single plates (due to, for example, emulsion flaws, image structure around bright stars and satellite trails) in the paired dataset.

6 Example of the use of a pair index

As an example of the use of image pairing, code `cmdiag` takes (sorted) master and slave IAM files plus a pair index and plots a colour–magnitude diagram of all paired objects. The magnitudes can be on the raw instrumental scale, or on a calibrated scale from another image parameter record (*eg.* photoelectrically calibrated magnitudes from parameter 32 as described

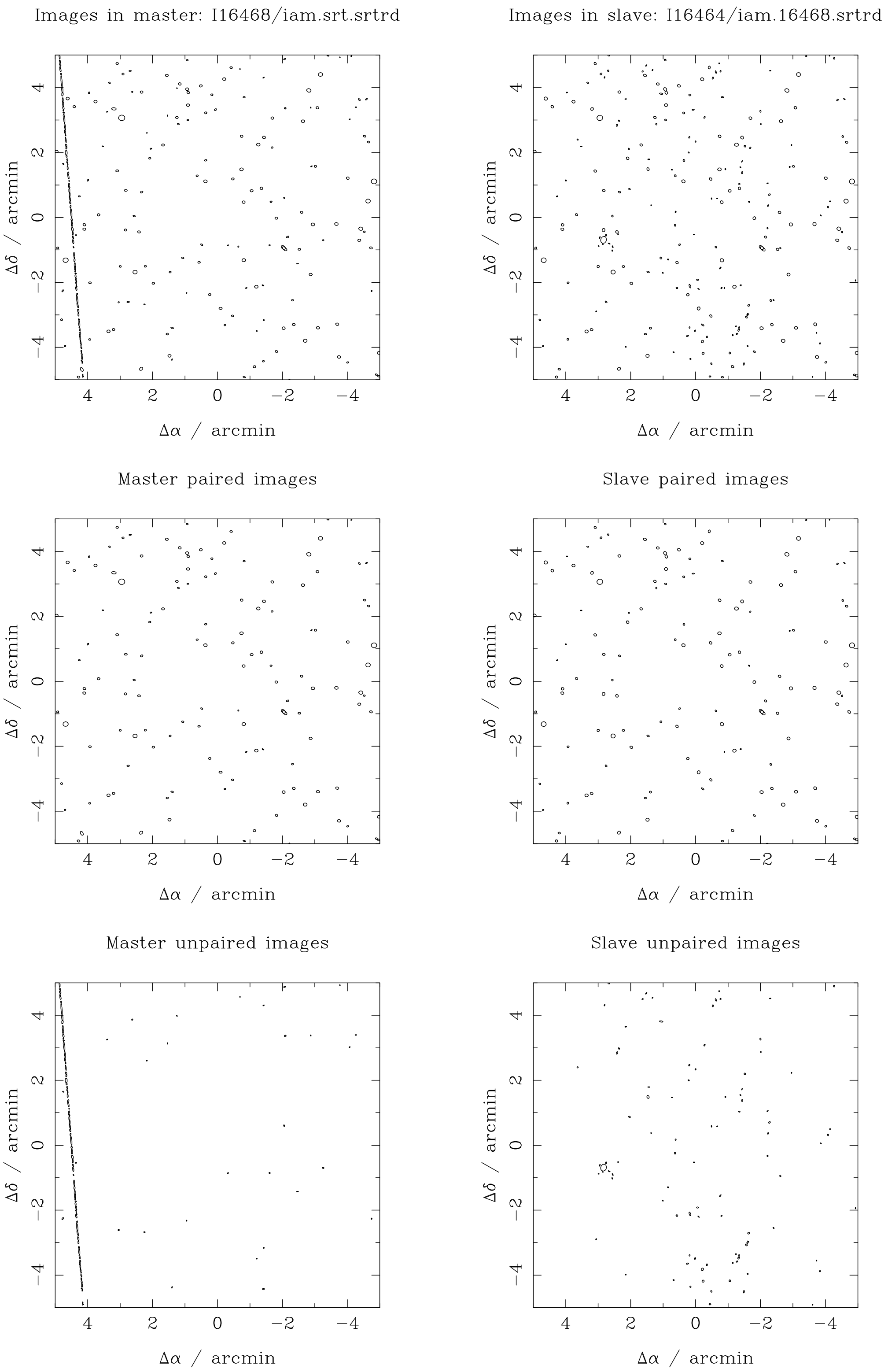

Figure 1: Example of displayed output from **testpairs**.

in the Photometry Guide). Use as in the following example (the corresponding plot is shown in Figure 2):

```
% ./cmdiag
Master IAM filename:
UKJ185/iam.srt.srtrd
Slave IAM filename:
UKR185/iam.J.srtrd
Pair index filename:
UKJ185/pairs.R.idx
Plot raw instrumental magnitudes (y/n)?
y
Image step (1 to plot every image pair):
100
Graphics device/type:
xwindows
%
```

The step input allows a 'quick–look' plot by skipping the specified number of records in the pair index between plotted points. The key lines of code for reading the IAM files and pair index pointers are as follows:

```
       open (unit=1,file=master,recl=32 ... )
       open (unit=2,file=slave,recl=32 ... )
       open (unit=3,file=index,recl=1 ... )
       .
       .
       .
       read (1,rec=i,err=20) mbuff
       read (3,rec=i) pointer
       if (pointer.ne.0) then
        read (2,rec=pointer) sbuff
        .
        .
        .
```

where the master image parameters are read record by record; for each master record the index is read to get the pair pointer in the slave file. If this is non–zero, then a pair exists and the slave parameters are read for that paired image. Note that for reasons described in the photometry Guide the raw instrumental magnitude scale for stars is non–linear with respect to apparent magnitude. This results in the colour–magnitude scatter diagram (*eg.* Figure 2) having an unconventional morphology; nevertheless, objects having extreme colour (for example) can be identified. Fully calibrated magnitudes would yield a 'conventional' morphology.

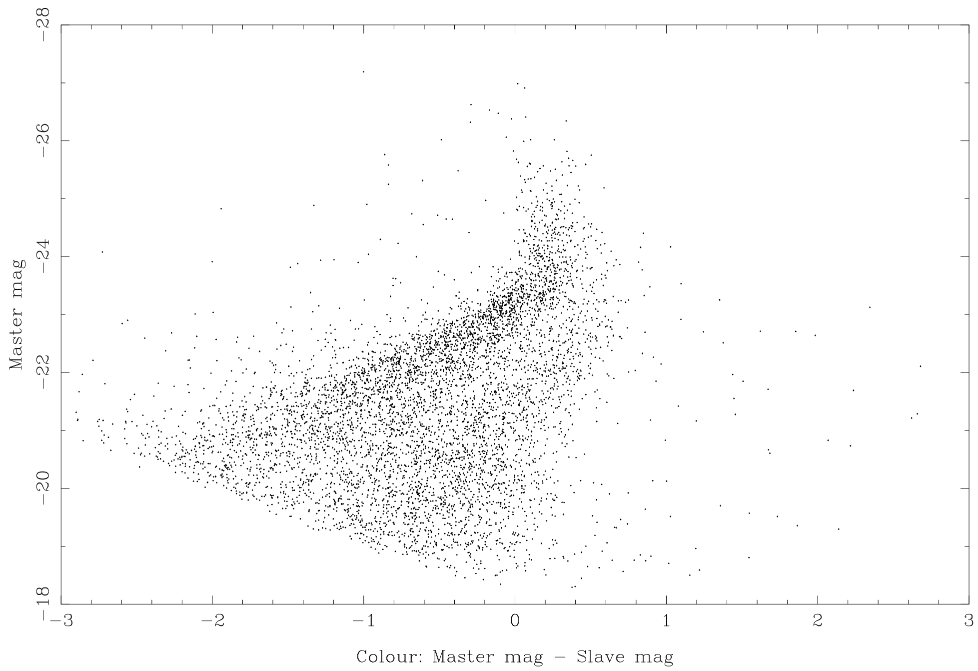

Figure 2: Example of displayed output from **cmdiag**.