
Subject: something (wrong?) with CONGRID?

Posted by [JP](#) on Mon, 02 May 2011 02:10:45 GMT

[View Forum Message](#) <> [Reply to Message](#)

Hi IDLers,

I think I came across a bug with CONGRID, but I'll be happy to be shown wrong.

in the following example all goes as expected:

```
a = lindgen(95, 74)
b = congrid(a, 95*10, 74*10)
Histo_b = Histogram(b, BINSIZE=1)
help, b
minmax, Histo_b
```

I get:

```
B          LONG      = Array[950, 740]
    100      100
```

so far, so good, b is an array 10 times larger and wider than a and all the elements of a are repeated 100 times in b.

now I change the size of the array a:

```
a = lindgen(958, 745)
b = congrid(a, 958*10, 745*10)
Histo_b = Histogram(b, BINSIZE=1)
help, b
minmax, Histo_b
```

This time I get:

```
B          LONG      = Array[9580, 7450]
    90      120
```

the size of b is OK, but there are some elements repeated 90 times and some others repeated 120 times!!?? I was expecting again 100 and 100.

If I go a bit further and do:

```
Histo_b = REFORM(histo_b, 958, 745)
cgIMAGE, histo_b, SCALE=1
```

I can see that the values of a repeated 90 times (instead as 100 as expected) are in two columns to the right and the values repeated 120 times are in the last column to the right...

Is there anything wrong with CONGRID or I am missing something there?

This is happening in IDL 8.0 and also in IDL 6.1

cheers

JP
