Subject: Re: something (wrong?) with CONGRID?
Posted by JP on Mon, 02 May 2011 03:35:39 GMT
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By the way, what I am trying to do is to create an array that groups pixels of my original array ARRAY of dims ns, nl in areas of size x, x.

For example, my array is of size (ns, nl) and x=10 I do:

```
  x= 10
  a = lindgen(ns/x, nl/x)    ; makes array of dims / x
  b = congrid(a, (ns/x)*x, (nl/x)*x)     ; resizes a to original size
  c = lonarr(ns, nl)        ; new array the size I want
  c[0:(ns/x)*x-1, 0:(nl/x)*x-1] = b          ; fills the array I want with b (leaves 0 in the bottom and right
borders which don't add to 10 pixels
  undefine,  a, b            ; gets rid of a and b

  histo_c = Histogram(c, BINSIZE=1, REVERSE_INDICES=ri)
```

then I use the array c (via reverse_indices) to do my processing of ARRAY in areas of 10x10 (in the example above).

If there is a simpler, better way to do that I'll be happy to know.

JP

Subject: Re: something (wrong?) with CONGRID?
Posted by David Fanning on Mon, 02 May 2011 04:13:41 GMT
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JP writes:

```
>  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?

I don't know exactly why this is happening. But I have seen enough of this kind of thing over the years to feel confident that it is yet another (although interesting) variation of the "sky is falling" phenomenon.

http://www.idlcoyote.com/math_tips/sky_is_falling.html

In other words, when the replication isn't exact, interpolation has to play a role and computers just cannot represent every number exactly. Some numbers must fall on the "razor's edge" and this fact results in some slight imbalancing of the number of repeats.

http://www.idlcoyote.com/math_tips/razoredge.html

I don't think there is anything particularly alarming about this. It is really no different then learning that even mathematical theories cannot be complete. It just means that whatever we do, there is mystery in the world. I happen to think that is *exactly* the way it should be. :-)

Cheers,

David
--
David Fanning, Ph.D.
Fanning Software Consulting, Inc.
Coyote's Guide to IDL Programming: http://www.idlcoyote.com/
Sepore ma de ni thui. ("Perhaps thou speakest truth.")

Subject: Re: something (wrong?) with CONGRID?
Posted by JP on Mon, 02 May 2011 04:36:57 GMT

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thanks David...
I may try to find a different way to create my c array in the example above.

JP