Subject: Re: fitting after rebinning

Posted by biophys on Fri, 07 Dec 2007 00:17:53 GMT

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Yes. Using /sample with compression is "morally" wrong in most cases. It makes sense only when you have a need for speed and don't care about the details. The fitting you are doing gives you absolutely the right answer. But how to understand the results. Well I do this kinda fitting almost everyday with CCD images. If you can imagine each data point of the image array as the readout of a CCD array, you will understand this almost immediately. In other words, the data represents the readout from the center of a pixel. Now psf\_gaussian is on the other hand centered on the corner of four neighboring pixels which gives you always the .5 pixel offset. Let's take a look:

```
IDL>a=psf_gaussian(npix=512,fwhm=90)
IDL>print, a[254:257,254:257]
  0.998461
             0.999145
                         0.999145
                                    0.998461
  0.999145
             0.999829
                         0.999829
                                    0.999145
  0.999145
             0.999829
                         0.999829
                                    0.999145
  0.998461
             0.999145
                         0.999145
                                    0.998461
IDL>b=rebin(a,64,64)
IDL>print, b[30:33,30:33]
  0.903193
                         0.943497
             0.943497
                                    0.903193
  0.943497
             0.985599
                         0.985599
                                    0.943497
  0.943497
             0.985599
                         0.985599
                                    0.943497
  0.903193
             0.943497
                         0.943497
                                    0.903193
IDL> c=rebin(a,64,64,/sample)
IDL> print,c[30:33,30:33]
  0.848341
             0.903490
                         0.920975
                                    0.898555
  0.903490
             0.962224
                         0.980846
                                    0.956968
  0.920975
             0.980846
                         0.999829
                                    0.975489
  0.898555
              0.956968
                         0.975489
                                    0.951742
IDL> t=gauss2dfit(a,p1,/tilt)
Compiled module: GAUSS2DFIT.
Compiled module: GAUSSFIT.
```

Program caused arithmetic error: Floating divide by 0 Program caused arithmetic error: Floating underflow

IDL> print,p1

2.19443e-008 0.999914 38.2195 38.2195 255.500

255.500 0.000000 IDL>t=gauss2dfit(b,p2,/tilt)

Compiled module: POLY\_FIT. Compiled module: CURVEFIT.

CURVEFIT: Failed to converge- CHISQ increasing without bound.

Program caused arithmetic error: Floating divide by 0 Program caused arithmetic error: Floating illegal operand

IDL> print,p2 1.54614e-007 0.990991 4.78601 4.78601 31.5000 31.5000 0.000000

As you can see after rebin(w/o /sample), the center is still located at the corner of a pixel. It makes sense that if you think pixel No 0 is located at [-0.5,0.5]x[-0.5x0.5] and so on so that [255.5,255.5] or [31.5,31.5] is exactly what you would expect where the center should be. To proper scale the results before and after rebin you just have to get rid of the half pixel "offset" and do the scale and add back the half pixel back after scaling. e.g. 255.5+0.5=(31.5+0.5)\*(512/64)=(7.5+.5)\*(512/16)

Cheers, BP

On Dec 6, 1:53 pm, Greg Hennessy <greg.henne...@localhost.localdomain> wrote:

>>> The offsets go away. Hmm, I need to think on this.

>

- >> I would consider your assumptions on what happens when
- >> you rebin. :-)

>

- > Yea. If I call A the big image, B a rebin image not using sample, and
- > C the rebin,/sample image, when I plotimage the three A and B look
- > the most alike, with C having an offset, but the fitted parameters
- > of A and C seem more alike. Like i said, I need to think.