Subject: Re: array convol optimizationv slow now
Posted by Chris[6] on Mon, 13 Jul 2009 23:53:53 GMT
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On Jul 13, 1:26 pm, David Fanning <n...@dfanning.com> wrote:
> newerjazz writes:
>> each particle is a single molecule of protein; we need to visualize
>> all the proteins to get meaningful interpretation.
>
> How does that work? If I put 100 million dots on my screen, things
> get a little blurry. (Of course, my eyes aren't what they used to
> be, admittedly.)
>
>> do you have any suggestions of getting the x,y locations on the image
>> w/ an array operation instead of a for loop?
>
> No, I can't think of any way to do this an an array. :-(
>
> Cheers,
>
> David
> --
> David Fanning, Ph.D.
> Coyote's Guide to IDL Programming (www.dfanning.com)
> Sepore ma de ni thui. ("Perhaps thou speakest truth.")

I've written a routine called densitymap which makes smoothed surface density maps based on the position of 2d sources. You might want to check it out (it has been moderately debugged)

http://www.ifa.hawaii.edu/users/beaumont/code/

It uses a different smoothing scheme (it uses the distance to each pixel's n-th nearest neighbor to estimate the surface density).

If you use it, you should probably download the IDL astronomy user's library, as well as
http://www.ifa.hawaii.edu/~beaumont/code/beaumont_library.ta r
to avoid dependency issues.

Otherwise, you could use hist_2d to pixellate the locations of each point, and then convolve the histogram with a gaussian

Chris