Subject: Re: Need Some Advice on Seperating Out Some Data
Posted by JD Smith on Wed, 09 Aug 2006 22:17:18 GMT
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On Wed, 09 Aug 2006 13:13:12 -0700, rdellsy wrote:

> Thanks for that. I took it, and played around with it a bit to get it
> to work. [Errors I found were: x and y don't concatinate in the line
> 'array=transpose([[x],[y]])' and I found I had to comment away the
> /ISOTROPIC in the plotting.) Unfortunately, it seems that cluster
> seperates on a purely 1 dimensional basis. I tried discarding the
> histogram related code in favor of a much simpler system in case that
> was the problem, and it still didn't work. If you look at the data set
> I provided, the problem should be self evident.

Probably your x,y are column vectors. I can't parse that data set;
please repost in plain ASCII. I'm not sure why you say it works
1-dimensionally. Did you try the example as given with the fake cluster
data?

> Incidentally, I replaced everything from
> h=histogram(c,reverse_indices=ri) down to the second to last line with:
> --
> plot,x,y,psym=2
> bmax=max(array[0,*],maxsubsc)
> goodc=c[maxsubsc]
> keep=where(c[*] eq goodc)
> --
> I feel that my code may be a tad more efficient, though I don't know
> how efficient the WHERE command is.

HISTOGRAM is more efficient than WHERE, but then again if it's not slowing
you down, it's a bit harder to parse, and you're only searching on a few
cluster index values. You don't need c[*] above: that just slows things
down unnecessarily.

> Anywho, I'm looking CLUSTER_TREE right now, which shows some more
> promise. If I understand it correctly, it works using distance appart,
> not coordinates which is a bit more useful, I think, for my problem.
> I'm just not sure how I can take the output and turn it into a set of
> clusters.

I think CLUSTER does similar, it just doesn't build a "tree" of
cluster membership.

JD