Subject: Re: Matching 2 lists
Posted by David Baker on Sun, 22 Aug 2010 07:06:05 GMT
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On Aug 21, 8:48 pm, Jeremy Bailin <astroco...@gmail.com> wrote:
> On Aug 21, 11:11 am, David Baker <de...@le.ac.uk> wrote:
>
>> Hi there,
>>          I'm wondering if someone can help me. I'm trying to match
>> two lists of stars together. Where I differ from the standard 1-1
>> match that match_2d.pro does so well is that I would like to be able
>> to compute a 1-many match. I.e find any star in list B that is a
>> possible match to a single star in list A not just the closest.
>
>> Many thanks for any help that someone can provide
>
>> David
>
> This is going to be in the next JBIU release, whenever I have half a
> second to run idldoc on it and tar it all up... it's based heavily on
> match_2d, obviously!
>
> -Jeremy.
>
> ;+
> ; NAME:
> ;   MATCHALL_2D
> ;
> ; PURPOSE:
> ;   Determines which of a set of 2D coordinates are a given distance
> from
> ;   each of a vector of points. Based on JD's MATCH_2D and my
> WITHINSPHRAD_VEC3D
> ;   (in fact, it's basically WITHINSPHRAD_VEC3D tuned back down to a
> ;   Euclidean surface).
> ;
> ; CATEGORY:
> ;   Astro
> ;
> ; CALLING SEQUENCE:
> ;   Result = MATCHALL_2D(X1, Y1, X2, Y2, Distance, Nwithin)
> ;
> ; INPUTS:
> ;   X1:    Vector of X coordinates.
> ;
> ;   Y1:    Vector of Y coordinates.
> ;
> ;   X2:    Vector of X coordinates.
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> ;
> ;    Y2:     Vector of Y coordinates.
> ;
> ;    Distance:  Maximum distance.
> ;
> ; OUTPUTS:
> ;    The function returns the list of indices of X2, Y2 that lie
> within
> ;    Sphrad of each point X1,Y1. The format of the returned array is
> ;    similar to the REVERSE_INDICES array from HISTOGRAM: the indices
> ;    into X2,Y2 that are close enough to element i of X1,Y1 are
> ;    contained in Result[Result[i]:Result[i+1]-1] (note, however, that
> ;    these indices are not guaranteed to be sorted). If there are no
> matches,
> ;    then Result[i] eq Result[i+1].
> ;
> ; OPTIONAL OUTPUTS:
> ;    Nwithin: A vector containing the number of matches for each of
> X1,Y1.
> ;
> ; EXAMPLE:
> ;    Note that the routine is similar to finding
> ;      WHERE( (X2-X1[i])^2 + (Y2-Y1[i])^2 LE Distance^2, Nwithin)
> ;    for each element of X1 and Y1, but is much more efficient.
> ;
> ;    Shows which random points are within 0.1 of various coordinates:
> ;     FIXME
> ;
> ;    seed=43
> ;    nrandcoords = 5000l
> ;    xrand = 2. * RANDOMU(seed, nrandcoords) - 1.
> ;    yrand = 2. * RANDOMU(seed, nrandcoords) - 1.
> ;    xcoords = [0.25, 0.5, 0.75]
> ;    ycoords = [0.75, 0.5, 0.25]
> ;    ncoords = N_ELEMENTS(xcoords)
> ;    matches = MATCHALL_2D(xcoords, ycoords, xrand, yrand, 0.1,
> nmatches)
> ;    PLOT, /ISO, PSYM=3, xrand, yrand
> ;    OPLOT, PSYM=1, COLOR=FSC_COLOR('blue'), xcoords, ycoords
> ;    OPLOT, PSYM=3, COLOR=FSC_COLOR('red'), xrand[matches[ncoords
> +1:*]], $
> ;      yrand[matches[ncoords+1:*]]
> ;
> ; MODIFICATION HISTORY:
> ;    Written by:    Jeremy Bailin
> ;    10 June 2008   Public release in JBIU as WITHINSPHRAD
> ;    24 April 2009  Vectorized as WITHINSPHRAD_VEC
> ;    25 April 2009  Polished to improve memory use
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> ;    9 May 2009     Radical efficiency re-write as WITHINSPHRAD_VEC3D
> borrowing
> ;                 heavily from JD Smith's MATCH_2D
> ;    13 May 2009    Removed * from LHS index in final remapping for
> speed
> ;    6 May 2010     Changed to MATCHALL_2D and just using Euclidean 2D
> coordinates
> ;                  (add a bunch of stuff back in from MATCH_2D and
> take out a bunch
> ;                  of angle stuff)
> ;    25 May 2010    Bug fix to allow X2 and Y2 to have any dimension.
> ;-
> function matchall_2d, x1, y1, x2, y2, distance, nwithin
>
> if n_elements(x2) ne n_elements(y2) then $
>   message, 'X2 and Y2 must have the same number of elements.'
> if n_elements(x1) ne n_elements(y1) then $
>   message, 'X1 and Y1 must have the same number of elements.'
> if n_elements(distance) ne 1 then $
>   message, 'Distance must contain one element.'
>
> n1 = n_elements(x1)
> n2 = n_elements(x2)
>
> gridlen = 2.*distance
> mx=[max(x2,min=mnx2),max(y2,min=mny2)]
> mn=[mnx2,mny2]
> mn-=1.5*gridlen
> mx+=1.5*gridlen
>
> h =  hist_nd([reform(x2,1,n_elements(x2)),reform(y2,1,n_elements( y2))],
> $
>   gridlen,reverse_indices=ri,min=mn,max=mx)
> d = size(h,/dimen)
>
> ; bin locations of 1 in the 2 grid
> xoff = 0. > (x1-mn[0])/gridlen[0] < (d[0]-1.)
> yoff = 0. > (y1-mn[1])/(n_elements(gridlen) gt 1?gridlen[1]:gridlen) <
> (d[1]-1.)
> xbin = floor(xoff) & ybin=floor(yoff)
> bin = xbin + d[0]*ybin   ; 1D index
>
> ; search 4 bins for closets match - check which quadrant
> xoff = 1 - 2*((xoff-xbin) lt 0.5)
> yoff = 1 - 2*((yoff-ybin) lt 0.5)
>
> rad2 = distance^2
>
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>  ; loop through all neighbouring cells in correct order
>  for xi=0,1 do begin
>   for yi=0,1 do begin
>    b = 0l > (bin + xi*xoff + yi*yoff*d[0]) < (d[0]*d[1]-1)
>
>    ; dual histogram method, loop by count in search bins (see JD's
>  code)
>    h2 = histogram(h[b], omin=om, reverse_indices=ri2)
>
>    ; loop through repeat counts
>    for k=long(om eq 0), n_elements(h2)-1 do if h2[k] gt 0 then begin
>     these_bins = ri2[ri2[k]:ri2[k+1]-1]
>
>     if k+om eq 1 then begin ; single point
>      these_points = ri[ri[b[these_bins]]]
>     endif else begin
>      targ=[h2[k],k+om]
>      these_points = ri[ri[rebin(b[these_bins],targ,/sample)]+ $
>       rebin(lindgen(1,k+om),targ,/sample)]
>      these_bins = rebin(temporary(these_bins),targ,/sample)
>     endelse
>
>     ; figure out which ones are really within
>     within = where( (x2[these_points]-x1[these_bins])^2 +
>  (y2[these_points] - $
>      y1[these_bins])^2 le rad2, nwithin)
>
>     if nwithin gt 0 then begin
>      ; have there been any pairs yet?
>      if n_elements(plausible) eq 0 then begin
>       plausible = [[these_bins[within]],[these_points[within]]]
>      endif else begin
>       ; concatenation is inefficient, but we do it at most 4 x N1
>  times
>       plausible = [plausible,[[these_bins[within]],
>  [these_points[within]]]]
>      endelse
>     endif
>
>    endif
>   endfor
>  endfor
>
>  if n_elements(plausible) eq 0 then begin
>   nwithin=replicate(0l,n1)
>   return, replicate(-1,n1+1)
>  endif else begin
>   ; use histogram to generate a reverse_indices array that contains
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>    ; the relevant entries, and then map into the appropriate elements
>    ; in 2
>    nwithin = histogram(plausible[*,0], min=0, max=n1-1,
>  reverse_indices=npri)
>    npri[n1+1] = plausible[npri[n1+1:*],1]
>    return, npri
>  endelse
>
>  end
```

Jeremy thats fantastic thank you so much, already saving me many hours of data processing my supervisor will certainly be happy.

-David