Subject: Re: contouring the CT slice

Posted by anne.martel on Tue, 06 May 2003 16:09:51 GMT

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\> Murat Maga wrote:
\>> Hi All,
\>> I have serial cross sections of some long bones, which I would like to
\>> calculate centroids and mass moments of inertia for each slice.
\>> The steps I have managed to do so far:
\>> 1.) Read the stack as a three dimensional volume:
\>> 2.) Calculate a threshold for segmenting the data
\>> 3.) Get the internal and external contours with contours function.
\>>

I'm not sure you need to use contours for this. You can calculate the centre of mass of an image using the following routine (it's not very pretty but it does the job):

```
; PURPOSE:
; returns intensity weighted centre of image
;
; CATEGORY:
; image processing
;
; CALLING SEQUENCE:
; cog_pos=cog(image)
;
; INPUTS:
; image
; OUPUT:
; returns position as a structure {x:xpos,y:ypos}
; EXAMPLE:
; cpos=cog(image)
;
Function cog,image

s = size(image)
tot  = total(image)
if(tot gt 0) then begin
    xtotal=0
    ytotal=0
    xmax = s(1)-1.0
    ymax = s(2)-1.0
    for i = 0.0 , xmax do xtotal = xtotal + total(image(i,*)*i)
    for i = 0.0 , ymax do ytotal = ytotal + total(image(*,i)*i)

    cog_pos = {x: xtotal/tot, $
  y: ytotal/tot}
```

```
endif else cog_pos={x:0,y:0}

return,cog_pos
end
```

Why not just threshold the image and apply CoG to each thresholded slice? You could used a single seed point together with search_3d to make sure that you just had a single connected bone region. If you needed information about the pixels around the inner and outer edges of the bone then you could use morphology - just dilate the bone region once then subtract off the undilated image.

Anne