Subject: Re: indexing over structure tags
Posted by Paul van Delst on Thu, 19 Apr 2001 18:08:29 GMT
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Randall Skelton wrote:
>
> Thanks Tom... I did think of that. However, in this particular case there
> is some merit in having the name of the structure be a useful and human
> readable tag. Nobody would be happy trying to remember yet another
> arbitrary numbering scheme for molecules when they'd rather just type the
> name ;) My suspicion is that there isn't an easy way to do what I want...

Maybe more context is needed to solve your problem .... the user of the code *shouldn't* have to remember the (not so) arbitrary numbering scheme - the user would type in a molecule name (or names). How your code deals with searching the human readable tagnames is a different matter, no?

e.g.

```
  ; define the basic structure for each
  sm_struc = {basic_struct, comment: ' ', values: fltarr(nlev)}

  ; define the large structure
  data = {big_struct, so4: sm_struc, co2: sm_struc, hcl: sm_struc}

  ; get the names of the tags
  names = tag_names(data)
```

so that names = [so4, co2, hcl].

Say the user requests data for 'so4' and 'hcl' so how about

```
  user_request = ['so4', 'hcl']
  n_requests = N_ELEMENTS( user_request )

  FOR i = 0, n_requests - 1 DO BEGIN
    tag_number = (WHERE( user_request[i] EQ names ))[0]  ; <-- assume this always succeeds
    data_to_get = data.(tag_number).values
    IF ( i EQ 0 ) THEN $
      data_to_return = data_to_get $
    ELSE $
      data_to_return = [ [ data_to_return ], [ data_to_get ] ]
  ENDFOR

  RETURN, data_to_return
```

or something like that? As it is above might not work for plucking out structures, but

that's a detail. So is the concatenation build of the data_to_return. Should be o.k. for small arrays tho'.

paulv

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A little learning is a dangerous thing;
Drink deep, or taste not the Pierian spring;
There shallow draughts intoxicate the brain,
And drinking largely sobers us again.
Alexander Pope.