Subject: Re: Read a file

Posted by penteado on Fri, 28 Jan 2011 15:26:03 GMT

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On Jan 28, 12:50 pm, Giovanna <giovanna01.san...@gmail.com> wrote:

> Hello,
>
> Me again....
>
> I'm trying read two files and to save in other file. See my code:http://pastebin.com/GRmNtags
>
> I run a command restore, to restore the file .sav and .cnj.... and
> then saved in 'data.dat' using 'printF'
>
> Is this correct what I did in rows 16 to 23??

Semantically, the code is correct, assuming that you have a structure named modelo with a field name imag, and a structure named conjugado with a field name imag. It is up to you to say if that is correct in the sense of producing the file you wanted.

Though I do not see why do

modelo.imag=[MODELO.imag]
conjugado.imag=[CONJUGADO.imag]

Which does not change these variables.

However, there is an oddity coming before those lines: You first read file.sav as a text file, into a string array. Then you restore it (that is, read it as an IDL savefile). If it is a text file, the restore will fail. And if it is a savefile, the read into a string array, done that way, will probably read some (maybe all) of the file, but the contents of the string array will be the bytes of the (binary) savefile, interpreted as characters, which is going to be hard to make sense of.

Also, you open file2.cnj, and never close it (never even use it). And, as mentioned before, closing the unit opened with /get_lun to openw does not release the unit number back into the pool (which a free_lun would do).

The main question to me is: what do you want to be in the file you are creating? To say it another way: what should the file look like?