

SORT

:- Sort command sort the current table and outputs the sorted data to a new table.

Syntax:-

`SORT ON <field1> [/A | /D] ,<field2> [/A | /D] TO <file> [ascending]
[descending][scope][for <expL>][while<expL>]`

when a table is sorted a new table is created <on> <field1> you must include a name of a field [/A | /D] for each field you include in the sort you can specify an ascending or descending sort order. ASCENDING | DESCENDING You can specify a sort order for all sort fields not followed by /A or /D <scope> The scope clauses are: All, NEXT <expN>, REOCD <expN> and REST

e.g.

To sort the current table on field name and store it to temp table

Use stud

Sort on name /a to temp

To sort the current table on field name and store it to temp table but in descending order

Use stud

Sort on name /d to temp

To sort current table on Title and include only selected fields to it

Use lib

Sort on title fields title, author, cost to temp

Index:-

This command is used to arrange the records in ascending or descending order. There are two types of indexing compound indexing (.cdx) containing multiple entries called tag and simple index (idx) containing single index entry.

Syntax

`Index on <field exp>[to <idx file>]/[tag <tag name>][for <expL>][compact]
[ascending | descending]`

include fields on which you want to index file (not allowed different data type fields if you want to use then first convert its data type using function.)

e.g

use lib

index on name, dtoc(dofp) to a

to index file on name in ascending order

use abc

index on name to a

What is structural compound index file?

A compound index file can hold more than one index file in a single file. Each index file within a compound index file is called index tag. The compound index file given a extension .CDX It is also called

Structural Compound

index file. It has same name as the opened .DBF file with extension .CDX .You can also create separate compound index file which is called

Independent Compound

index file(with extension .CDX) but this file will not open automatically when DBF file open. The records can notreindex whenever you will not open the independent compound index file.For e.g

.USE STUD

INDEX ON NAME TAG NAME

It create structural compound index file with name STUD.CDX