



SMASER

DOCTOR

TRIPsystem
Product Documentation



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About this document

The following document describes the prompts received from the DOCTOR utility and how to respond to them in order to successfully analyze the BAF file of a database.

Conventions used in this document

xyzzzy (x) is a prompt from DOCTOR to the user (where 'x' is the default response provided by DOCTOR and taken if the user simply hits the RETURN key)

IF <condition> ... Else is a block whose entry is determined by the validity of the condition given to the IF clause. If the condition is false, the block following the "ELSE" keyword is to be executed.



What is DOCTOR?

DOCTOR is a utility provided with the TRIP system with the purpose of examining the content of a database's BAF file and check for inconsistencies.

When the DOCTOR runs, it prints a list of the phases that it is going through in checking the integrity of the file. These phases are :

1. Simple file structure analysis

Check that the file is a BAF and that each block that is in the file conforms with, at least minimally, the requirements for file blocks (checksums, etc).

2. Simple internal structure analysis

Check that the free list and the directory track can be found, and that the blocks that make up these entities identify themselves as being free or directory blocks. Also check that the reported size of the BAF is the same as the actual size.

3. Cache defeat file structure analysis

Perform phase 1 again with a cache defeat algorithm that ensures that the physical hardware used to store the BAF is reliable. This can, and has, shown up problems in disk caching software (notably on PCs).

4. Directory track analysis

Read every entry in the directory track and check that it points to a data block that does contain the record that it is supposed to. Also check that the directory track is of the correct size and that it can all be read.

5. Free list analysis

Check that each entry in the free list agrees with the free space entry in the data block to which it is related (this is what the program CHKFREE (now obsolete) did).

6. Exhaustive data analysis

Read every version of every record in the BAF using a different algorithm than TRIPkernel, which can detect a wider range of inconsistencies. This phase will show up errors in the physical structure of the data as it relates to the database design, as well as any data corruption errors.

Using the BAF DOCTOR

The DOCTOR utility program is located in the directory with the same path that is defined as TDBS_EXE in the TRIPsystem configuration file tdbb.conf. Run DOCTOR from the command line:

```
<TDBS_EXE>/doctor
```

To see the arguments of DOCTOR use :

```
doctor --help
```

which will print out a list of the switches that the DOCTOR understands.

Prompts from DOCTOR

If DOCTOR is started without providing the necessary arguments, you will be prompted as follows:

Username :

Specify here your TRIP username.

**Password :**

Specify here your TRIP password.

Database :

Specify here the name of database whose BAF you wish to examine.

“Real world” examples of using DOCTOR

If there is nothing wrong in the BAF file, all six steps will report “Ok”.

```
**** TRIP System Utility BAF DOCTOR - Diagnose faulty BAF's ****
      Version 6.0-0   10-Dec-2008 09:11:12

Username : system
Password :
Database : alice

      1. Performing simple file structure analysis.....[Ok]
      2. Performing simple internal structure analysis.....[Ok]
      3. Performing cache defeat file structure analysis.....[Ok]
      4. Performing directory track analysis.....[Ok]
      5. Performing free list analysis.....[Ok]
      6. Performing exhaustive data analysis.....[Ok]

Elapsed: 00:00:12
```

The example below shows how DOCTOR would react on a BAF file that has been hopelessly mangled.

```
**** TRIP System Utility BAF DOCTOR - Diagnose faulty BAF's ****
      Version 6.0-0   10-Dec-2008 09:14:11

Username : SYSTEM
Password :
Database : ALICE

      1. Performing simple file structure analysis.....[Error]
           Block sequence error in block 1 [538976257]!

           Block sequence error in block 2 [538976258]!
      ...

      2. Performing simple internal structure analysis.....[Error]
           Reported file size is incorrect:
                Reported      : 538976442
                Actual        : 186

Elapsed: 00:00:07
```