Antelope Toolbox for Matlab:

Version 1.1

User's Manual and Tutorial

Kent Lindquist
Lindquist Consulting

Introduction

This document describes an Antelope Software toolbox for Matlab. Matlab is a product of Mathworks, Inc. Antelope is a product of Boulder Real-Time technologies, Inc. Included in Antelope is the Datascope relational database system. The major strengths of this Matlab toolbox include those of the Antelope package itself, such as schema-independent relational database support, a generalized and powerful parameter-file management architecture, and a number of tools useful to seismologists.

This toolbox follows closely the interfaces to Datascope and Antelope built into other scripting environments such as Perl and TCL/Tk. This toolbox was developed under Solaris 2.6 on Sun Ultra computers, using Matlab version 5.3, and has since been upgraded for consistency with Solaris 2.8, Linux, and Matlab 6.5.

Installation

The Antelope Toolbox for Matlab is intended to be installed in

$ANTELOPE/data/matlab/antelope

The source code for the package is available via the Antelope contributed-code web site, http://www.indiana.edu/~aug.. The Antelope toolbox should compile into the correct place along with the rest of the contributed code. The $MATLAB environment variable should be set correctly before compilation.

In addition, the paths to the Matlab commands need to be made available to the users. There are several ways this can be done. A simple way for users to do this for themselves is to run the Matlab command

>> **run([getenv('ANTELOPE'),'/data/matlab/antelope/scripts/setup_antelope.m'])**

A system-wide strategy to do this is to modify the file

$MATLAB/toolbox/local/pathdef.m.

to have three more entries[1]:

1. Note the assumption that the ANTELOPE environment variable is correctly set. Note also that the old utility *install_matlab_antelope_links* is deprecated and out of date. With Matlab 6.1 and higher, no links should be necessary.

```
p = [...
        getenv('ANTELOPE'),'/data/matlab/antelope/antelope:',...
        getenv('ANTELOPE'),'/data/matlab/antelope/scripts:',...
        getenv('ANTELOPE'),'/data/matlab/antelope/examples:',...
        matlabroot,'/toolbox/matlab/general:',...
        matlabroot,'/toolbox/matlab/ops:',...
```

There are three directories that get included in the path. The *$ANTELOPE/data/matlab/antelope/antelope* directory is for the main routines of the Antelope Toolbox for Matlab. The *$ANTELOPE/data/matlab/antelope/examples* directory is for the example scripts for each command, discussed below. The *$ANTELOPE/data/matlab/antelope/scripts* directory is a common location for scripts that are written using the Antelope Toolbox for Matlab. Users that write scripts of general utility may want to put them in this directory.

Finally, there is an additional directory *$ANTELOPE/data/matlab/antelope/html* with the html versions of all the documentation, plus a copy of this tutorial. This path should be added to the file

$MATLAB/toolbox/local/docopt.m

by changing the docpath option (under the "elseif isunix" clause in docopt.m) to

```
docpath = [getenv('ANTELOPE'),'/data/matlab/antelope/html'];
```

Help

All toolbox commands are documented with the standard Matlab help utilities. To see a list of available commands, type

>> **help antelope**

or (for the Matlab help window)

>> **helpwin antelope**

or (for an HTML index of the help entries in a web browser)

>> **doc antelope**

For a list of examples, type

>> **help antelope/examples**

'For help on individual commands, give the name of the command. For example:

>> **help dbopen**

```
 DBOPEN Open a Datascope Database

      DBPTR = DBOPEN ( FILENAME, OPENTYPE )


      dbopen opens the database specified by the path name
      FILENAME, using the permissions given by opentype. A
      database pointer with the database index filled in is
      returned in DBPTR. The opentype may be either r (for read
      only) or r+ (for reading and writing).   In the latter
      case, the db package will attempt to open tables
      read/write, but if permissions are incorrect, will open
      the table read only.


      Antelope Toolbox for Matlab
            [Antelope is a product of Boulder Real Time Technologies, Inc.]
      Kent Lindquist
      Lindquist Consulting
      1997-2003
```

>>

The other versions of the help system also work for individual commands:

>> **helpwin dbopen**

or

>> **doc dbopen**

For further insight, consult the man pages and manuals provided with the Antelope software and the Matlab software.

Finally, all commands in the Antelope Toolbox for Matlab come with an example demonstrating their use. To see the example in action, precede the command with the prefix "**dbexample_**". For example, to see the **dbopen** command being used, type **dbexample_dbopen**. There is also a script **dbexample_runall** which will run all available examples. This is useful primarily for system testing. There are also a couple example scripts covering special topics, such as **dbexample_joins**, **dbexample_get_hypocenter_vitals**, **dbexample_sort_and_subset**, and **dbexample_writing**.

Opening a Database

Databases are opened with the **dbopen** command, which takes a filename and a permissions flag. For convenience the Matlab Antelope Toolbox contains a demonstration database from the Joint Seismic Program Center. The schema for this database is CSS3.0. The filename of this database is available through the command

```
>> dbexample_get_demodb_path
demodb_path is /opt/antelope/4.2u/data/matlab/antelope/examples/demodb/demo
>>
```

The dbopen command returns a four-element structure called a database pointer:

```
>> db = dbopen(demodb_path,'r')

db =

    database: 0
       table: -501
       field: -501
      record: -501

>>
```

Under normal conditions the user does not modify these fields directly, with the possible exception of the record field. Two tools are provided to aim the database pointer at specific parts of the database (i.e. set the integers correctly). **dblookup** is the most general of the two. A shorthand version of **dblookup**, **dblookup_table**, is provided for the most common operation, aiming the database pointer at a given table of the database:

```
>> db=dblookup_table(db,'origin')

db =

    database: 0
       table: 10
       field: -501
      record: -501

>>
```

Databases may be closed with the dbclose command, which destroys the database pointer:

```
>> dbclose(db)
>>
```

Handling Parametric Data

The following examples show some common database operations. These examples presume you have already opened the database and looked up the origin table, as shown in the steps above. We can subset our database:

```
>>db=dbsubset(db,'mb > 6');
```

Find out how many records we have:

```
>> dbquery(db,'dbRECORD_COUNT')

ans =

   18

>>
```

Ask for a column of values:

```
>> mb=dbgetv(db,'mb')

mb =

   6.4200
   6.4000
   6.2000
   6.2000
   6.2300
   6.4000
   6.3100
   6.0200
   6.2800
   6.5000
   6.5700
   6.1100
   6.0500
   6.2100
```

6.3000
6.3000
6.2700
6.1400

Or ask for several columns of values:

>> **[lat,lon,depth,time] = dbgetv(db,'lat','lon','depth','time');**

Convert the epoch-times (seconds since 1970) for the hypocentral occurrence time to a standard readable format:

>> **strydtime(time)**

ans =

' 5/04/1992 (125) 8:45:10.089'
' 5/12/1992 (133) 18:05:42.600'
' 5/15/1992 (136) 7:05:05.300'
' 5/17/1992 (138) 9:49:19.100'
' 5/17/1992 (138) 9:49:21.689'
' 5/17/1992 (138) 10:15:31.300'
' 5/17/1992 (138) 21:36:00.492'
' 5/19/1992 (140) 14:42:48.813'
' 5/20/1992 (141) 12:20:34.700'
' 5/21/1992 (142) 4:59:57.500'
' 5/21/1992 (142) 5:00:00.399'
' 5/21/1992 (142) 18:05:48.543'
' 5/22/1992 (143) 21:40:36.691'
' 5/25/1992 (146) 2:51:32.311'
' 5/25/1992 (146) 16:55:04.100'
' 5/27/1992 (148) 5:13:38.800'
' 5/27/1992 (148) 5:13:41.635'
' 5/28/1992 (149) 21:24:51.822'

Or we can customize the time-conversion format:

>> **epoch2str(time,'%A %b %d %I:%M %p %Z')**

ans =

'Monday May 04 08:45 AM UTC'
'Tuesday May 12 06:05 PM UTC'
'Friday May 15 07:05 AM UTC'
'Sunday May 17 09:49 AM UTC'
'Sunday May 17 09:49 AM UTC'

```
    'Sunday May 17 10:15 AM UTC'
    'Sunday May 17 09:36 PM UTC'
    'Tuesday May 19 02:42 PM UTC'
    'Wednesday May 20 12:20 PM UTC'
    'Thursday May 21 04:59 AM UTC'
    'Thursday May 21 05:00 AM UTC'
    'Thursday May 21 06:05 PM UTC'
    'Friday May 22 09:40 PM UTC'
    'Monday May 25 02:51 AM UTC'
    'Monday May 25 04:55 PM UTC'
    'Wednesday May 27 05:13 AM UTC'
    'Wednesday May 27 05:13 AM UTC'
    'Thursday May 28 09:24 PM UTC'

>>
```

As an aside, we can go the other way too:

```
>> str2epoch('2/13/98 15:17')

ans =

  887383020

>>
```

or

```
>> str2epoch('now')

ans =

  9.2039e+08

>>
```

We can pick out the first record in our database view (note the indexing convention!):

```
>> db.record=0

db =

    database: 0
       table: 36
       field: -501
      record: 0
```

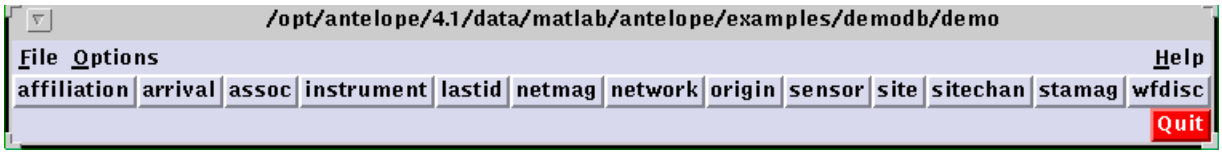
```
>>
```

Find the iasp91 P-phase travel time in seconds from the hypocenter to Fairbanks:

```
>> dbeval(db,'pphasetime(distance(lat,lon,64.836,-147.7048),depth)')

ans =

  780.7877

>>
```

We can launch a spreadsheet tool (*dbe*) on our whole database:

```
>> unix(['dbe ' demodb_path '&'])
[1] 17990

ans =

     0

>>
```



and examine the individual tables by clicking on the buttons.

Handling Waveform Data

The database contains data for one earthquake. We can get the data for the P wave in one of two ways. First we need to get the correct database pointer:

```
>> db=dblookup_table(db,'wfdisc');
>> dbt=dblookup_table(db,'arrival');
>> db=dbjoin(dbt,db);
>> db= dbsubset(db,'arrival.chan == wfdisc.chan');
>> dbt=dblookup_table(db,'assoc');
>> db=dbjoin(dbt,db);
```

```
>>dbt=dblookup_table(db,'origin');
>> db=dbjoin(dbt,db);
>> db=dbsubset(db,'sta == "CHM" && chan == "BHZ"');
>> [time,endtime]=dbgetv(db,'time','endtime')

time =

    7.061397100070000e+08


endtime =

    7.061398415000000e+08

>>
```

Now we have a couple options for getting data. We can use **trload_css** to load the database waveform contents into a trace-object, another database pointer that includes information on waveforms loaded into memory; or we can use **trgetwf**. The former, which is the preferred method, requires us to call **trextract_data** to get the actual waveform data. Further detail on these commands is provided in their descriptions below, especially in the text for the **trload_css** command.

```
>> tr=trload_css(db,time,endtime);
>>data1=trextract_data(tr);
```

Or we can go directly to the waveform data from the database pointer:

```
>> [data2,nsamp,t0,t1]=trgetwf(db,time,endtime);
```

Response information

Response information stored in a database may be loaded into a *dbresponse* object for evaluation. We precede our demonstration of this with an extraction of the correct filename from the database:

```
>> db=dblookup_table(db,'sensor');
>> dbinst=dblookup_table(db,'instrument');
>> db=dbjoin(db,dbinst);
>> db.record=dbfind(db,'sta == "CHM" && chan == "BHZ"');
>> respfile = dbfilename(db)
```

```
respfile =

/opt/antelope/4.2u/data/matlab/antelope/examples/demodb/response/sts2_vel_RT72A.1

>>
```

Now we use this filename to construct a *dbresponse* object:

```
>> resp=dbresponse(respfile)
resp =

        dbresponse object: 1-by-1

>>
```

Next we use the **eval_response** command to evaluate the response curve at 5 Hz, noting the conversion to radians/sec:

```
>> eval_response(resp, 5 * 2 * pi)

ans =

   0.9969 - 0.0749i

>>
```

The returned value is in general complex. Next we evaluate the response for several frequencies at once:

```
>> myvals = eval_response(resp,[0.1; 1; 10]*6.28)

myvals =

   0.9968 - 0.0502i
   0.6239 - 0.7815i
  -0.0115 - 0.0053i

>>
```

These results are of course amenable to standard Matlab processing:

```
>> abs(myvals)

ans =

    0.9980
```

```
   1.0000
   0.0126

>>angle(myvals)*180/pi

ans =

  -2.8853
 -51.3982
-155.2421

>>
```

When we are done with the *dbresponse* object, we remove it with the **free_response** command:

```
>> free_response(resp)
>>
```

Parameter files

Antelope parameter files allow the specification of ASCII-text parameter files. For complete documentation, see the Antelope manuals.

As an example, here's a small text file in my current working directory:

```
nordic% cat /home/kent/temp/test.pf
cat /home/kent/temp/test.pf

# Test parameter file

number_of_things 3
string_thing Dr. Seuss Lives
myboolean True

thing_names &Tbl{
ball
chew-toy
toy mouse
}

thing_owners &Arr{
      ball          Kirby
```

```
        chewtoy         Rover
        mouse           Jasmine
    }
    on_the_fly &ask What is a convenient value for this
    nordic%
```

To open this as a parameter file, type the following:

```
>> pf=dbpf('test')

pf =

        dbpf object: 1-by-1

>>
```

The returned object is called a parameter-file (*dbpf*) object. This one was actually constructed from the single file shown above. However, the PFPATH environment variable specifies all the locations which may contain parameter files, and all files of the specified name are read. Repeated parameters are overwritten in the order in which they are read, allowing users to override default settings of software packages with subsets of parameter files in their own directories and with correct settings of PFPATH.

To see which existent, readable files will contribute to a *dbpf* object, use **pffiles**:

```
>> pffiles('test')

ans =

    './test.pf'

>>
```

To see all the possibilities that are investigated, regardless of whether they exist or are readable, use the 'all' option:

```
>> pffiles('test','all')

ans =

    '/opt/antelope/4.2u/data/maps/site/test.pf'
    '/opt/antelope/4.2u/data/pf/test.pf'
    '/opt/antelope/4.2u/data/pf/site/test.pf'
    '/home/kent/data/pf/test.pf'
    './test.pf'
```

```
>>
```

Now, to see the parameter names in the parameter-file object, use **pfkeys**:

```
>> pfkeys(pf)

ans =

    'number_of_things'
    'string_thing'
    'thing_names'
    'thing_owners'

>>
```

To convert the entire object to a string, use **pf2string**:

```
>> pf2string(pf)

ans =

myboolean True
number_of_things        3
on_the_fly &ask What is a convenient value for this
string_thing    Dr. Seuss Lives
thing_names     &Tbl{
ball
chew-toy
toy mouse
}
thing_owners    &Arr{
ball    Kirby
chewtoy Rover
mouse   Jasmine
}

>>
```

To extract a single numeric parameter out of the *dbpf* object, use **pfget_num**. This actually retrieves the parameter as a string, then applies the Matlab **str2num** function.

```
>> pfget_num(pf,'number_of_things')

ans =

     3
```

```
>>
```

To get string values, use **pfget_string**:

```
>> pfget_string(pf,'string_thing')

ans =

Dr. Seuss Lives

>>
```

To get boolean values, use **pfget_boolean**. This returns -1 (which evaluates to true in an **if** statement) for affirmative values ('true','yes', etc.) in the parameter file, and 0 for negative values.

```
>> pfget_boolean(pf,'myboolean')

ans =

   -1

>>
```

Lists of things may be retrieved from the parameter file with **pfget_tbl**:

```
>> pfget_tbl(pf,'thing_names')

ans =

   'ball'
   'chew-toy'
   'toy mouse'

>>
```

Also, the parameter file may contain associative arrays of key--value pairs. Notice that such an entity is really just like a nested parameter file, so these are returned as subsidiary *dbpf* objects, as shown by this return from the **pfget_arr** command:

```
>> pfget_arr(pf,'thing_owners')

ans =

        dbpf object: 1-by-1
```

```
>>
```

Of course, Matlab has a built-in strategy for dealing with blocks of key-value pairs, namely the structure. Therefore there is a command **pf2struct** to convert a *dbpf* object to a Matlab *struct*. There is a caveat here, however. Matlab structure-field names are limited in length, and are not allowed to contain any strange characters. The underlying parameter-file implementation is much more tolerant. Therefore if you have long names or weird names with dots and hashes in them, **pf2struct** will fail and you will need to use **pfget_string** or other appropriate functions on the subsidiary *dbpf* object.
With reasonable parameter files, however, **pf2struct** will work fine:

```
>> mystruct=pf2struct(ans)

mystruct =

      ball: 'Kirby'
   chewtoy: 'Rover'
     mouse: 'Jasmine'

>>
```

In order to simplify reading complex, nested parameter files, the **pfget_arr**, **pfget_tbl**, **pf2struct**, **pfget**, and **pfresolve** commands (the latter are described below) allow a 'recursive' option:

```
>> pfget_arr(pf,'thing_owners','recursive')

ans =

      ball: 'Kirby'
   chewtoy: 'Rover'
     mouse: 'Jasmine'

>>
```

The **pfget** routine is generic, exercising its discretion on what datatype to return. String entries that are interpretable as numbers by Matlab's **str2double** function are returned as numbers [note that this is a change from the original behavior of the Antelope Toolbox for Matlab]:

```
>> pfget(pf,'thing_names')

ans =

   'ball'
   'chew-toy'
   'toy mouse'
```

```
>>
```

If a parameter-file entry is specified with the *&ask* tag, as is the parameter named on_the_fly above, the user will be queried directly. This is based on the Matlab INPUT command, which means that answer may be given using the full-fledged Matlab interpreter:

```
>> pfget(pf,'on_the_fly')
What is a convenient value for this : 27 + 13*pi

ans =

  67.8407

>>
```

Repeated calls are dynamically re-queried:

```
>> pfget(pf,'on_the_fly')
What is a convenient value for this : 'a string value'

ans =

a string value

>>
```

Next, we will look at a more complex example. Real-time operations at the Alaska Earthquake Information Center are managed in part by a parameter-file specifying real-time system setup. This is actually one of several files, helping administrators track the multiple *Antelope Seismic Information Systems* that are running.

```
>> setup=dbpf('aeic_rtsys')

setup =

      dbpf object: 1-by-1

>>
```

Again, we will use the **pffiles** command to see the filenames contributing to this *dbpf* object:

```
>> pffiles('aeic_rtsys')

ans =

    '/opt/antelope/4.2u/data/pf/site/aeic_rtsys.pf'
```

>>

As an interlude to help the reader understand the following demonstration of parameter file commands, here is the aeic_rtsys.pf parameter file itself:

nordic% **cat /opt/antelope/4.2u/data/pf/site/aeic_rtsys.pf**

```
primary_system op

processing_systems &Arr{

        op &Arr{
                system_name             Operation
                host                    earlybird
                site_database           /iwrun/op/params/Stations/worm
                archive_database        /iwrun/op/db/archive/archive
        }

        dev &Arr{
                system_name             Development
                host                    nordic
                site_database           /iwrun/dev/params/Stations/worm
                archive_database        /iwrun/dev/db/archive/archive
        }

        bak &Arr{
                system_name             Backup
                host                    ice
                site_database           /iwrun/bak/params/Stations/worm
                archive_database        /iwrun/bak/db/archive/archive
        }
}

rtexec_run_dirs &Arr{
        nordic          /iwrun/dev/run
        earlybird       /iwrun/op/run
        ice             /iwrun/bak/run
        fk              /home/bbanddat/run
        beam            /iwrun/acq/run
        marvin          /home/uafarr/run
        megathrust      /home/beeper/run
        strike          /export/mitch/run
        ugle            /Seis/ugle1/run
}
nordic%
```

Again, the **pfkeys** command names the component parameters:

```
>> pfkeys(setup)

ans =

    'primary_system'
    'processing_systems'
    'rtexec_run_dirs'
```

We will take three approaches to answering the question "where is the primary acquisition system currently putting continuous waveform data." The first mechanism of asking this from the parameter file is deliberately long-winded, for instructional purposes:

```
>> sys=pfget(setup,'processing_systems')

sys =

        dbpf object: 1-by-1

>> pfkeys(sys)

ans =

    'bak'
    'dev'
    'op'

>>
>> op = pfget(sys,'op')

op =

        dbpf object: 1-by-1

>>
>> pfkeys(op)

ans =

    'archive_database'
    'host'
    'site_database'
    'system_name'
```

```
>> pfget_string(op,'archive_database')

ans =

/iwrun/op/db/archive/archive

>>
```

Now let's speed that up a bit:

```
>> nestedanswer = pf2struct(setup,'recursive');
>> nestedanswer.processing_systems.op.archive_database

ans =

/iwrun/op/db/archive/archive

>>
```

In addition to the parameter-file reading interface described above, there is an alternative interface through the **pfresolve** command. This allows square-brackets in the parameter name to index list (Tbl) entries, and curly braces to index associative-array entries. We will combine these with a nested **pfget** inquiry to find the name of the primary system:

```
>> name=[ 'processing_systems{' pfget(setup,'primary_system')  ...
'}{archive_database}'];
>> pfresolve(setup,name)

ans =

/iwrun/op/db/archive/archive

>>
```

Note that this setup allows system maintainers to smoothly transition between operational and backup Antelope systems. By switching the primary system from Operation to Backup, operators can preserve continuous, transparent service to user processes while installing new disk drives etc.

About this time, when one gets multiple *dbpf* objects constructed and needs to keep track of them, it is useful to be able to identify the type of each dbpf object. This is done with the **pftype** command:

```
>> pftype(sys)

ans =
```

PFARR

>> **pftype(setup)**

ans =

PFFILE

>>

Top-level *dbpf* objects will be of type PFFILE. Subsidiary arrays are indicated with PFARR. The names under which PFFILE-type *dbpf* objects were launched may be obtained with the **pfname** command:

>> **pfname(pf)**

ans =

test

>> **pfname(setup)**

ans =

aeic_rtsys

>>

When one is done with a Matlab *dbpf* object, one can call **pffree** or **clear**() on it in order to remove the object. Note, however, that subsidiary parameter-file objects will no longer be useful once the parent is cleared, so it is important to get all the information one wants out of a parameter file object before freeing or clearing it.

>> **pffree(setup)**
>>
>> **clear(op)**
>> **clear(sys)**
>>

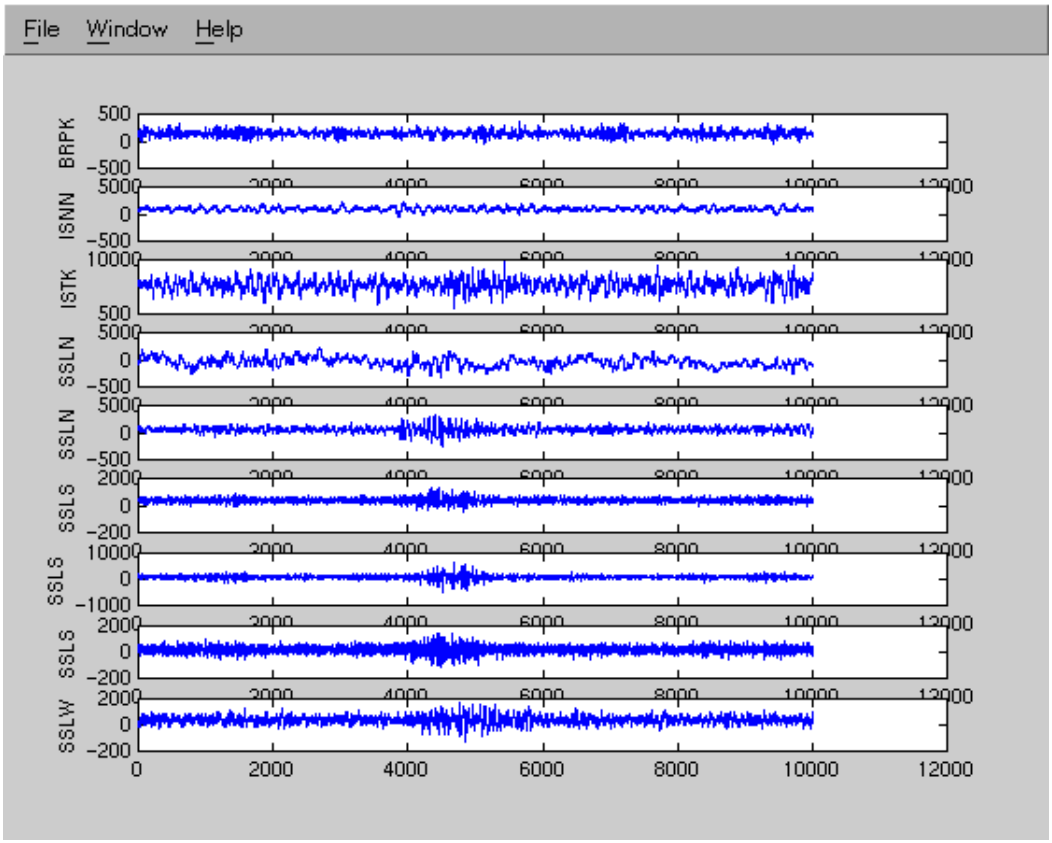
Values may also be written to parameter files with the **pfput** series of command, or with the **dbpf** command used to compile strings into parameter files. This is explained in the documentation for the individual commands below. If a parameter file is changing from the outside as your Matlab program runs, the **pfupdate** command may be used to keep up with any changes to the parameter file.

Advanced Example

Get 100 seconds of data that occurred 10 minutes ago on the network of stations at Shishaldin volcano:

```
pf=dbpf('aeic_rtsys');

% Get the name of the current archive database from our local parameter file
primary = pfget(pf,'primary_system');
dbname = pfresolve(pf,['processing_systems{' primary '}{archive_database}']);

db = dbopen( dbname, 'r' );

db = dblookup_table( db, 'affiliation' );

net = 'Shshldn';
db = dbsubset(db, ['net == "' net '"']);

dbw = dblookup_table( db, 'wfdisc');
db=dbjoin(db, dbw);

% Get data from 10 minutes ago:
st = str2epoch('now') - 600;
et = st + 100;

tr = trload_css( db, st, et );

nrecs = dbquery( tr, 'dbRECORD_COUNT');

for i=1:nrecs,
      subplot( nrecs, 1, i )
      tr.record=i-1;
      data=trextract_data(tr);
      plot(data)
      ylabel(dbgetv(tr,'sta'));
end

trdestroy( tr );
dbclose( db );
```

Channel names are not labelled. One station has three components, and another has both a vertical component and a pressure sensor, explaining the repetition of names in this figure.


File Window Help
BRPK
ISNN
ISTK
SSLN
SSLN
SSLS
SSLS
SSLS
SSLW
0
2000
4000
6000
8000
10000
12000

Examples of each command

Many of these presume you have run the command **dbexample_get_demodb_path**, which sets the variable *demodb_path* to the name of a sample database. An attempt was made to make each of these examples self-sufficient. Hence there are usually a number of setup commands to make the example call possible. Some of the examples may be a bit contrived. Note that in practice, it is not necessary to keep reopening a database or a parameter-file object! The parameter-file routines use the dbloc2.pf and the rtexec.pf parameter files as examples. They should be available on any properly installed Antelope system. There are also Matlab .m files showing examples of each command in use. These example files should be in $ANTELOPE/data/matlab/antelope/examples on a properly configured system. For a list of available examples, type **help antelope/examples**.

arr_slowness

The **arr_slowness** command calculates the slownesses of all known seismic phases, given the distance delta in degrees to the earthquake and the depth of the earthquake in kilometers. The default travel-time model is IASPEI ‘91, however this may be modified with the TAUP_TABLE environment variable. The returned slowness values are in seconds/km.

```
>> delta = 20;
>> depth = 10;

>> [slowness, phasenames] = arr_slowness( delta, depth );

>> space(1:length(slowness),1) = ' ';

>> [num2str(slowness) space char(phasenames)]

ans =

 0.097873 P
  0.10638 Pn
 0.097967 pP
 0.097943 sP
  0.10668 pPn
 0.082873 P
   0.1066 sPn
 0.082883 pP
  0.08288 sP
  0.12307 PnPn
  0.17998 S
  0.21628 Sn
   0.2027 S
```

```
  0.21256 S
  0.18023 sS
  0.21638 sSn
  0.20348 sS
  0.21217 sS
  0.14975 S
  0.14986 pS
  0.14981 sS
  0.22062 SnSn
 0.016438 PcP
 0.021013 ScP
 0.021017 PcS
 0.030333 ScS
0.0039843 PKiKP
0.0039835 pPKiKP
0.0039837 sPKiKP
0.0042026 SKiKP
-0.0040705 PKKPdf
-0.0038634 SKKPdf
-0.0038632 PKKSdf
-0.0036761 SKKSdf
-0.0053076 P'P'df
 -0.039783 P'P'ab
-0.0041508 S'S'df

>>
```

arrtimes

The **arrtimes** command calculates the travel-times of all known seismic phases, given the distance delta in degrees to the earthquake and the depth of the earthquake in kilometers. The default travel-time model is IASPEI '91, however this may be modified with the TAUP_TABLE environment variable. The returned travel-time values are in seconds. In this example, we feed the result to **strtdelta** to produce a more readable result.

```
>> delta = 20;
>> depth = 10;

>> [times, phasenames] = arrtimes( delta, depth );

>> [char(strtdelta(times)) char(phasenames)]

ans =

  4:33 minutes       P
```

4:34 minutes	Pn
4:36 minutes	pP
4:37 minutes	sP
4:37 minutes	pPn
4:38 minutes	P
4:39 minutes	sPn
4:41 minutes	pP
4:42 minutes	sP
4:49 minutes	PnPn
8:18 minutes	S
8:20 minutes	Sn
8:20 minutes	S
8:21 minutes	S
8:23 minutes	sS
8:24 minutes	sSn
8:25 minutes	sS
8:25 minutes	sS
8:27 minutes	S
8:30 minutes	pS
8:32 minutes	sS
8:36 minutes	SnSn
8:48 minutes	PcP
12:25 minutes	ScP
12:26 minutes	PcS
16:07 minutes	ScS
16:37 minutes	PKiKP
16:41 minutes	pPKiKP
16:42 minutes	sPKiKP
20:08 minutes	SKiKP
31:47 minutes	PKKPdf
35:18 minutes	SKKPdf
35:19 minutes	PKKSdf
38:50 minutes	SKKSdf
40:17 minutes	P’P’df
42:47 minutes	P’P’ab
54:25 minutes	S’S’df

>>

cggrid

The **cggrid** command creates a Matlab object with references an Antelope computational-geomegry grid. This command may be given one argument or three. A single argument will be interpreted as a filename, out of which a previously saved grid will be retrieved. If three arguments are given, they should be matrices of X,Y, and Z coordinate values for the grids, in the style of the Matlab **mesh** command.

```
>> [X,Y] = meshgrid(-2:0.2:2,-3:0.3:3);
>> Z = exp( -X.^2 - Y.^2 );
>> cgg = cggrid( X, Y, Z )

cgg =

      cggrid object: 1-by-1

>>
```

cggrid_dx

This command returns the grid-spacing of a computational-geometry grid in the x direction:

```
>> [X,Y] = meshgrid(-2:0.2:2,-3:0.3:3);
>> Z = exp( -X.^2 - Y.^2 );
>> cgg = cggrid( X, Y, Z );

>> dx = cggrid_dx( cgg )

dx =

   0.2000

>>
```

cggrid_dy

This command returns the grid-spacing of a computational-geometry grid in the y direction:

```
>> [X,Y] = meshgrid(-2:0.2:2,-3:0.3:3);
>> Z = exp( -X.^2 - Y.^2 );
>> cgg = cggrid( X, Y, Z );

>> dx = cggrid_dy( cgg )

dy =

   0.3000
```

```
>>
```

cggrid_free

The **cggrid_free** command removes a previously created cggrid object, freeing all underlying references to the Antelope cgeom(3) library. This is equivalent to the (overloaded) **clear** command for the cggrid object.

```
>> [X,Y] = meshgrid(-2:0.2:2,-3:0.3:3);
>> Z = exp( -X.^2 - Y.^2 );
>> cgg = cggrid( X, Y, Z );
>> cggrid_free( cgg )
>>
```

cggrid_get

The **cggrid_get** command returns a two-dimensional array of x,y, and z values for the specified grid. The second and third return values are the number of points in the x and y directions, respectively (useful if one wishes to call the **reshape** command on the result).

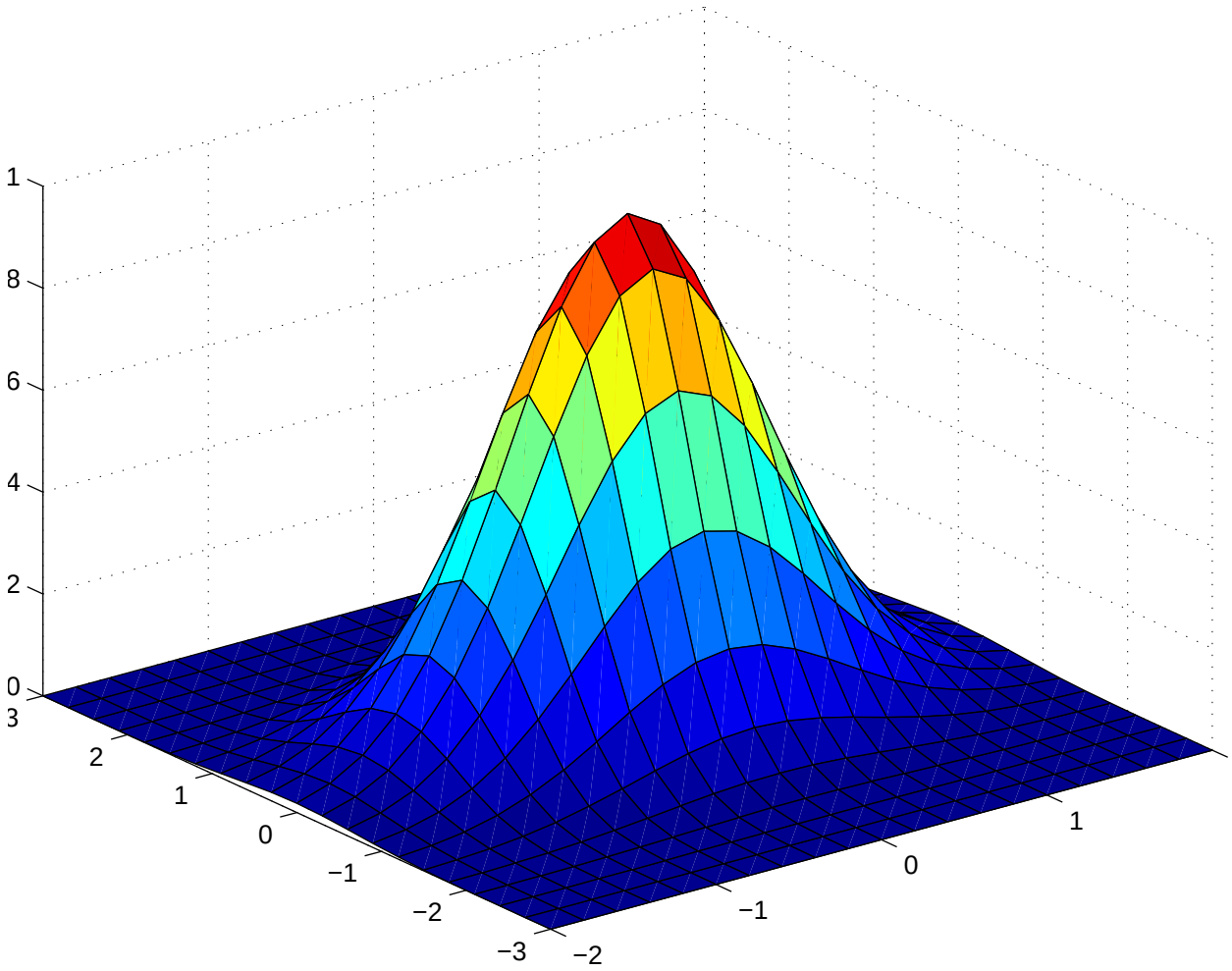
```
>> [X,Y] = meshgrid(-2:0.2:2,-3:0.3:3);
>> Z = exp( -X.^2 - Y.^2 );
>> cgg = cggrid( X, Y, Z );

>> [mytriplets, nx, ny] = cggrid_get( cgg );

>> whos mytriplets
  Name           Size                Bytes  Class

  mytriplets     441x3                 10584  double array

Grand total is 1323 elements using 10584 bytes

>> nx

nx =

    21

>> ny

ny =

    21
```

>>

cggrid_getmesh

The **cggrid_getmesh** command formats a cggrid object into three arrays of X,Y, and Z coordinate values, suitable for direct use with the Matlab **mesh**, **surf**, and related commands.

```
>> [X,Y] = meshgrid(-2:0.2:2,-3:0.3:3);
>> Z = exp( -X.^2 - Y.^2 );
>> cgg = cggrid( X, Y, Z );
>> [myx, myy, myz] = cggrid_getmesh( cgg );

>> surf( myx, myy, myz )
>>
```



cggrid_nx

This command returns the number of points for a computational-geometry grid in the x direction:

```
>> [X,Y] = meshgrid(-2:0.2:2,-3:0.3:3);
>> Z = exp( -X.^2 - Y.^2 );
>> cgg = cggrid( X, Y, Z );

>> nx = cggrid_nx( cgg )

nx =

   21

>>
```

cggrid_ny

This command returns the number of points for a computational-geometry grid in the y direction:

```
>> [X,Y] = meshgrid(-2:0.2:2,-3:0.3:3);
>> Z = exp( -X.^2 - Y.^2 );
>> cgg = cggrid( X, Y, Z );

>> ny = cggrid_ny( cgg )

ny =

   21

>>
```

cggrid_probe

This command returns the value of a cggrid at a specified test point, or NaN if the test point is outside the grid. If the test point does not lie exactly on a grid node, bilinear interpolation is used to extract the grid value.

```
>> [X,Y] = meshgrid(-2:0.2:2,-3:0.3:3);
>> Z = exp( -X.^2 - Y.^2 );
>> cgg = cggrid( X, Y, Z );

>> x_test = 1.138;
>> y_test = -2.045;
```

```
>> a_value = cggrid_probe( cgg, x_test, y_test )

a_value =

   0.0047

>>
```

cggrid_write

The **cggrid_write** command sends a cggrid object to a filename in the specified format. The format is indicated by a two-letter string, such as ‘as’ or ‘t4’, as documented in the Unix man-page cggrid(5).

```
>> [X,Y] = meshgrid(-2:0.2:2,-3:0.3:3);
>> Z = exp( -X.^2 - Y.^2 );
>> cgg = cggrid( X, Y, Z );
>> outfile = ['/tmp/mycggrid_' getenv('USER')];

>> cggrid_write( cgg, 't4', outfile )
>>
```

cggrid2db

The **cggrid2db** command assumes the specified grid is associated with an earthquake. The database-pointer provided must be aimed at a row containing the origin-time (‘time’) and origin-id (‘orid’) for the hypocenter. The database must also contain a ‘qgrid’ table as in the gme1.0 database schema, to hold a reference to the output qgrid file. The arguments to **cggrid2db** in the example below are, respectively, the input grid; the database pointer containing information on the corresponding earthquake; the name of the recipe used to create the grid; the name of the grid itself; a formatting string for the filename in which to save the grid; the format of the grid; and the units of the grid (acceleration in g):

```
>> % Construct a contrived grid:

>> [X,Y] = meshgrid(-2:0.2:2,-3:0.3:3);
>> Z = exp( -X.^2 - Y.^2 );
>> cgg = cggrid( X, Y, Z );

>> % Save this to a fake database as though it belonged
>> % to an earthquake:

>> output_dir = ['/tmp/exampledir_' getenv('USER')];
>> unix( ['/bin/rm -rf ' output_dir] );
>> unix( ['mkdir ' output_dir] );
```

```
>> output_dbname = [output_dir '/newdb'];
>> fid = fopen( output_dbname, 'w' );
>> fprintf( fid, '#\nschema rt1.0:gme1.0\n' );
>> fclose( fid );

>> db=dbopen( output_dbname,'r+' );
>> db=dblookup( db,'','origin','','' );

>> orid = dbnextid( db, 'orid' );
>> db.record = dbaddv( db, 'lat', -116, ...
                'lon', 34, ...
                'depth', 0, ...
                'time', str2epoch( '12/31/2002' ), ...
                'orid', orid );

>> cggrid2db( cgg, db, 'dbexample_fake', 'testgrid', ...
        '%Y/%j/%{gridname}_%{recipe}.%{qgridfmt}', ...
        't4', 'g', 'pga', 'matlab_demo' );
>>
```

clear_register

Most of the toolbox routines are pretty good about complaining of problems when they occur. However, if you suspect the package is caching a useful error message, this is the way to bring them to the surface.

```
>> clear_register('print')
>>
>> % [...if there were error messages accumulated, this would have flushed them out...]
```

compare_response

The compare_response command may be used to compare the coefficients for two response objects, returning a true value if they differ. In the following contrived example, two arbitrarily chosen response structures are loaded and compared:

```
>> db = dbopen(demodb_path,'r');
>> db=dblookup_table(db,'instrument');
>> db.record=0;
>> file1=dbfilename(db);
>> resp1 = dbresponse(file1);
>> db.record=1;
>> file2=dbfilename(db);
>> resp2 = dbresponse(file2);>>
```

```
>> compare_response( resp1, resp2 )
1
>>
```

db2struct

This is probably one of the more useful commands in the toolbox. It can operate on a database table or on a view that contains only one table (for example, it will work on a view showing a sub-set of the origin table, but not a view that was made by joining the origin and assoc tables).

```
>> db = dbopen(demodb_path,'r');
>> db = dblookup_table( db, 'origin' );
>> db.record=0;
>>
>> % Example 1:
>> db2struct(db)

ans =

          lat: 40.0740
          lon: 69.1640
        depth: 155.1660
        time: 7.0437e+08
        orid: 1
        evid: -1
        jdate: 1992118
        nass: 7
        ndef: 7
        ndp: -1
        grn: 715
        srn: 48
        etype: '-'
        review: ''
       depdp: -999
       dtype: 'f'
        mb: 2.6200
        mbid: 1
        ms: -999
        msid: -1
        ml: -999
        mlid: -1
    algorithm: 'locsat:kyrghyz'
      auth: 'JSPC'
      commid: -1
      lddate: 790466871
```

```
>>
>>
>> % Example 2:
>> db=dblookup(db,'','','','dbALL');
>> db2struct(db)

ans =

1x1351 struct array with fields:
    lat
    lon
    depth
    time
    orid
    evid
    jdate
    nass
    ndef
    ndp
    grn
    srn
    etype
    review
    depdp
    dtype
    mb
    mbid
    ms
    msid
    ml
    mlid
    algorithm
    auth
    commid
    lddate

>>
>>
>> % Example 3:
>> db.record=0;
>> db2struct(db,'lat','lon','depth','mb')

ans =

      lat: 40.0740
```

```
        lon: 69.1640
      depth: 155.1660
      mb: 2.6200

>>
```

dbadd

The raw storage format of the Datascope files is fixed-format ASCII rows. Usually, interaction with the database tables is smoother if you avoid handling entire rows at once. However, there are occasions where it is useful to move an entire row around. **dbadd** adds an entire database row to the flat-file table at once. The database pointer for each table contains something called a 'scratch' record for that table. The scratch record is an entire row that is in memory for the sole purpose of scribbling. In this example we add several values to the scratch row of the origin table, then write the scratch row to the database (i.e. in this example that means we've written the fixed-format ASCII row to the end of the file /tmp/newdb.origin).

```
>> db=dbopen('/tmp/newdb','r+');
   >> db=dblookup(db,'','origin','','dbSCRATCH');
   >> dbputv(db,'lat',61.5922,'lon',-149.130,'depth',20,'time',str2epoch('now'));
   >> db.record=dbadd(db,'dbSCRATCH')

   db =

      database: 0
        table: 10
        field: -501
       record: 0

   >>
```

dbadd_remark

The css3.0 schema, plus several other related schemas, have a separate table for comments. This table is infrequently used. The **dbadd_remark** and **dbget_remark** functions encapsulate the operations involved in adding a row to the remark table and linking it to a database row on another table such as the origin table..

```
>> db=dbopen('/tmp/newdb','r+');
>> db=dblookup_table(db,'origin');
>> db.record =  dbaddnull(db);
>> dbputv(db,'lat',61.5922,'lon',-149.130,'depth',20,'time',str2epoch('now'))
>> dbadd_remark(db,'This earthquake occurred under Palmer, Alaska')
>>
```

dbaddnull

Similar to **dbadd**, **dbaddnull** puts into a database table an entire fixed-format ASCII row, with format appropriate for that table. In this case all the fields of the new row are set to their null values.

```
>> db=dbopen('/tmp/newdb','r+');
>> db=dblookup_table(db,'origin');
>> db.record =  dbaddnull(db)

db =

   database: 0
      table: 10
      field: -501
     record: 0

>>
```

dbaddv

This is one of the most commonly used functions in the Datascope libraries. **dbaddv** adds a new fixed-format row to the specified table, setting all fields to their null values. It then modifies the specified fields to contain the more interesting values given in each key-value pair. **dbaddv** checks to make sure none of the primary keys match those for another row of the database, i.e. it takes some steps to keep you from corrupting your database.

```
>> db=dbopen('/tmp/newdb','r+');
>> db=dblookup_table(db,'origin');
>> db.record=dbaddv(db,'lat',61.5922,'lon',-
149.130,'depth',20,'time',str2epoch('now'))

db =

   database: 0
      table: 10
      field: -501
     record: 0

>>
```

dbclose

This routine closes a database pointer, freeing all the associated resources (It does no harm to the underlying database files).

```
>> db = dbopen(demodb_path,'r');
>> dbclose(db)
>>
```

dbcrunch

Removing rows from a database is usually done in two steps. The first is to set all the fields of a row to their null values, but to leave the row in its place. This first step is performed by **dbmark**. The second stage, accomplished by the **dbcrunch** command, is to actually remove the null rows from the database table. This two-step procedure prevents skewing of all the record numbers for a table, often useful if the program is still working on the table.

```
>> db=dbopen('/tmp/newdb','r+');
>> db=dblookup_table(db,'origin');
>> % Add four copies of the same quake, all at slightly different times:
>>db.record=dbaddv(db,'lat',61.5922,'lon',-149.130,'depth',20,'time',str2epoch('now'))
>>db.record=dbaddv(db,'lat',61.5922,'lon',-
149.130,'depth',20,'time',str2epoch('now'));
>>db.record=dbaddv(db,'lat',61.5922,'lon',-
149.130,'depth',20,'time',str2epoch('now'));
>>db.record=dbaddv(db,'lat',61.5922,'lon',-
149.130,'depth',20,'time',str2epoch('now'));
>>
>> db.record=1;
>> dbmark(db)
>> dbcrunch(db)
>> dbquery(db,'dbRECORD_COUNT')

ans =

    3

>>
```

dbdelete

This command immediately deletes a row from a database table.

```
>> db=dbopen('/tmp/newdb','r+');
>> db=dblookup_table(db,'origin');
>> % Add four copies of the same quake, all at slightly different times:
```

```
>> db.record=dbaddv(db,'lat',61.5922,'lon',-
149.130,'depth',20,'time',str2epoch('now'))
>>db.record=dbaddv(db,'lat',61.5922,'lon',-
149.130,'depth',20,'time',str2epoch('now'));
>>db.record=dbaddv(db,'lat',61.5922,'lon',-
149.130,'depth',20,'time',str2epoch('now'));
>>db.record=dbaddv(db,'lat',61.5922,'lon',-
149.130,'depth',20,'time',str2epoch('now'));
>>
>> dbquery(db,'dbRECORD_COUNT')

ans =

    4

>> db.record=1;
>> dbdelete(db)
>> dbquery(db,'dbRECORD_COUNT')

ans =

    3

>>
```

dbeval

This command is a general-purpose calculator which has access to standard math commands, useful seismological functions such as travel-time calculators, and to all the fields of a database view which is fed to the command.

```
>> db = dbopen(demodb_path,'r');
>> db=dblookup_table(db,'origin');
>> dbs=dblookup_table(db,'site');
>> db.record=0;
>> db=dbjoin(db,dbs);
>> db.record=0;
>> dbeval(db,'arrival("PKiKP")-time')

ans =

  982.2883

>>
>> dbeval(db,'distance(site.lat,site.lon,origin.lat,origin.lon)')
```

ans =

27.4124

>>

dbextfile

In the css3.0 schema and related schemas, many times external files are referenced in tables by the two fields *dir* and *dfile*. The **dbextfile** command combines these two fields into a full pathname, resolving all relative pathnames into absolute pathnames as well as adjusting for the actual location of the database table. The dbextfile command requires the name of the base table from which the *dir* and *dfile* fields should come. (Note that in many cases, the simpler **dbfilename** command will suffice instead of **dbextfile**).

>> **db = dbopen(demodb_path,'r');**
>> **db = dblookup_table(db, 'wfdisc');**
>> **dbt = dblookup_table(db, 'sensor');**
>> **db = dbjoin(db, dbt);**
>> **dbt = dblookup_table(db,'instrument');**
>> **db = dbjoin(db, dbt);**

>> **db.record=0;**

>> **dbextfile(db, 'instrument')**

ans =

/usr/local/matlab/toolbox/antelope/examples/demodb/response/sts2_vel_RT72A.1

>> **dbextfile(db, 'wfdisc')**

ans =

/usr/local/matlab/toolbox/antelope/examples/demodb/wf/knetc/1992/138/210426/
19921382155.15.CHM.BHZ

>>

dbfilename

In the css3.0 schema and related schemas, many times external files are referenced in tables by the two fields *dir* and *dfile*. The **dbfilename** command combines these two fields into a full pathname, resolving all relative pathnames into absolute pathnames as well as adjusting for the actual location of the database table.

```
>> db = dbopen(demodb_path,'r');
>> dblookup_table(db,'instrument');
>> db.record=0;
>> dbfilename(db)

ans =

/opt/antelope/4.2u/data/matlab/antelope/examples/demodb/response/sts2_vel_RT72A.1

>>
```

Note that if more than one table with external file references is present in the input view, only the first one will be chosen and returned. This may not always be the intended filename. For cases where the *dir* and *dfile* fields appear multiple times in the input view, use **dbextfile** instead of **dbfilename**.

dbfind

This command is a general-purpose utility to hunt through a database table or view for a record matching a specific criterion. Useful features include the ability to skip the first few matches, or to search backwards through the view.

```
>> db = dbopen(demodb_path,'r');
>> db = dblookup_table( db, 'origin' );
>> db.record = dbfind(db,'mb>6',0)

db =

   database: 0
      table: 10
      field: -501
     record: 80

>>
>> db.record = dbfind(db,'mb>6',0,3)

db =

   database: 0
      table: 10
```

```
       field: -501
      record: 266

>>
>> db.record = dbfind(db,'mb>6','backwards')

db =

   database: 0
      table: 10
      field: -501
     record: 1262

>>
>> dbgetv(db,'mb')

ans =

   6.1400

>>
```

dbfree

This command frees up the resources allocated when a new view is created. The input database pointer must identify a single table, that is db.table and db.database should be valid. Generally, it is only necessary to explicitly free database views when they are very large or many of them are made within the same program.

```
>> db = dbopen( demodb_path,'r' );
>> dbarrival = dblookup_table( db,'arrival' );
>> % Make a temporary view
>> dbtemp = dbsubset( dbarrival, 'sta == "AAK"' );

>> % Get something out of the temporary view
>> dbgetv( dbtemp, 'deltim' )

ans =

   0.0980
   2.1640
   2.2220

>> % Free resources associated with the temporary view
>> dbfree( dbtemp );
```

```
>>
```

dbget

As explained for the **dbadd** command, the underlying storage of database tables is as fixed-format ASCII rows. The **dbget** command can be used to retrieve an entire database row as a string (in fact, it is much more general, allowing the retrieval of entire tables or just specific fields depending on the value of the database pointer). Rather than trying to parse the output of **dbget**, use **dbgetv** to find specific pieces of information in a table or database row.

```
>> db = dbopen(demodb_path,'r');
>> db = dblookup_table( db, 'origin' );
>> db.record=0;
>> dbget(db)

ans =

  40.0740   69.1640  155.1660   704371900.66886       1      -1  1992118    7    7   -1      715
48 -      -999.0000 f    2.62       1 -999.00       -1 -999.00       -1 locsat:kyrghyz  JSPC              -
1   790466871.00000


>>
```

dbget_remark

As explained under **dbadd_remark**, **dbget_remark** eases the retrieval of comments in databases with the css3.0 *remark* table.

```
>> db=dbopen('/tmp/newdb','r+');
>> db=dblookup_table(db,'origin');
>> db.record =  dbaddnull(db);
>> dbputv(db,'lat',61.5922,'lon',-149.130,'depth',20,'time',str2epoch('now'))
>> dbadd_remark(db,'This earthquake occurred under Palmer, Alaska')
>> dbget_remark(db)

ans =

This earthquake occurred under Palmer, Alaska

>>
```

dbgetv

The **dbgetv** command is one of the most frequently used commands in the Antelope programming environment. With **dbgetv** one can get specific fields out of a database row. A unique characteristic of the Matlab-interface **dbgetv** command is the ability to extract entire columns at once out of a database table.

```
>> db = dbopen(demodb_path,'r');
>> db = dblookup_table( db, 'origin' );
>> db.record=0;
>> [lat,lon,auth] = dbgetv(db,'lat','lon','auth')

lat =

   40.0740


lon =

   69.1640


auth =

JSPC

>>
>> db = dbsubset(db,'mb>6');
>> dbgetv(db,'mb')

ans =

    6.4200
    6.4000
    6.2000
    6.2000
    6.2300
    6.4000
    6.3100
    6.0200
    6.2800
    6.5000
    6.5700
    6.1100
    6.0500
    6.2100
    6.3000
    6.3000
```

6.2700
6.1400

>>

dbgroup

The **dbgroup** command takes a sorted view and groups the records into 'bundles', clustering together all those records that have the same values for the group fields. For example, in the operation below we take the arrival table, sort it by station, and group arrivals together by station. This allows us to make an easy count of the number of arrivals at each station, via the 'count()' function in **dbeval**. The input list of group fields should be a cell-array of strings, hence the squiggly brackets in the **dbgroup** call below.

```
>> db = dbopen( demodb_path,'r' );
>> db = dblookup_table( db, 'arrival' );
>> db = dbsort( db, 'sta' );
>> db = dbgroup( db, { 'sta' } );
>> % Find the number of arrivals at each station:
>> for i=1:dbnrecs(db)
db.record=i-1;
sta = dbgetv(db,'sta');
narr = dbeval( db, 'count()' );
sprintf( '%s %d\n', sta, narr )
>> end

ans =

AAK 3

ans =

CHM 2

ans =

EKS2 1

ans =

KBK 2

ans =

KMI 1
```

ans =

TKM 1

ans =

USP 2

dbinvalid

The database-pointer is actually a structure of four integers. There is an 'invalid' value for all of these which is occasionally useful for tests or as the input to some commands.

>> **db = dbinvalid**

db =

database: -102
table: -102
field: -102
record: -102

>>

dbjoin

dbjoin allows the user to construct composite views in a relational database. Information in each table is cross-referenced according to its primary fields to construct a set of the corresponding, joined rows.

>> **db = dbopen(demodb_path,'r');**
>> **dbarrival=dblookup_table(db,'arrival');**
>> **dbwfdisc=dblookup_table(db,'wfdisc');**
>> **db=dbjoin(dbarrival,dbwfdisc)**

db =

database: 0
table: 34
field: -501
record: -501

>>

dbjoin_keys

The standard Datascope join operations between database tables are accomplished by inferring the sensible join keys with which to combine the two tables. **dbjoin_keys** explains which fields were used or will be used to perform a join.

```
>> db = dbopen(demodb_path,'r');
>> dbarrival=dblookup_table(db,'arrival');
>> dbwfdisc=dblookup_table(db,'wfdisc');
>>
>> % Example 1:
>> dbjoin_keys(dbarrival,dbwfdisc)

ans =

    'sta'
    'time == time::endtime'

>>
>> % Example 2:
>> dbjoin_keys(db,'origin','assoc')

ans =

    'orid'

>>
```

dblist2subset

Normally, database views are created with commands such as **dbsubset**, **dbsort**, **dbjoin**, **dbunjoin**, etc., which perform operations on one or more views to create a new view. However, sometimes one encounters situations where one knows the exact row numbers of interest for an existing view and wants to create a new view containing just those rows. For this purpose there is the **dblist2subset** command. Given an array of numbers specifying the row numbers to include, **dblist2subset** will create a new view. The example below shows this in use with the **trload_css** command. Since the **trload_css** command ignores the actual record-number field of the input database pointer, a preceding **dblist2subset** call can restrict the input view to just one or several rows of interest (if several rows are desired, instead of just one as in the example below, the row numbers should be put into a single Matlab vector which is then given to **dblist2subset** as its second argument). The **dblist2subset** can also be called without a second argument, in which case **dblist2subset** assumes the database pointer refers to a group (as created by the **dbgroup** command) and turns the group into a proper view of its own.

```
>> db = dbopen( demodb_path,'r' );
```

```
>> db=dblookup_table( db,'wfdisc' );

>> db.record=3;

>> format long
>> [time,endtime,nsamp,samprate]=dbgetv( db,'time','endtime','nsamp','samprate' )

time =

    7.061397047000000e+08


endtime =

    7.061398015500000e+08


nsamp =

       1938


samprate =

   20

>> % The trload_css command by itself ignores the record number of the
>> % database pointer, loading everything it finds in the input table.
>> % the dblist2subset command below creates a subset view the consists solely
>> % of the record of interest, thus limiting the amount of data loaded by the
>> % command. Note that this strategy assumes all the data of interest
>> % exist in the row being pointed to, which may or may not defeat the strength
>> % of the trload_css command, depending on the application. At the very least
>> % one may wish to include all relevant wfdisc row numbers in the list fed
>> % to dblist2subset, in which case a simple dbsubset command might be less
>> % effort to design.
>>
>> db = dblist2subset( db, 3 );

>> tr = trload_css( db,time,endtime );
>> tr.record = 0;
>> data = trextract_data( tr );
>>
>> % Do something interesting (or, in this case, boring) with the data:
>> mean( data )
```

```
ans =

   -6.830181208053691e+03

>> dbclose( db );
>> trdestroy( tr );
```

dblookup

The four-element dbpointer structure, used as a handle to reference different fields or sections of a relational database, is rarely modified by hand. **dblookup** allows the four elements of the dbpointer structure to be aimed based on human-readable names for the tables and fields. Additionally, several recognized constants such as ‘dbALL’ and ‘dbSCRATCH’ allow further control of the parts of the database to which dblookup aims the database pointer.

```
>> db = dbopen(demodb_path,'r');
>> dblookup(db,'','origin','','dbALL')

ans =

   database: 0
      table: 10
      field: -501
     record: -501

>>
```

dblookup_table

One of the most common operations with **dblookup** is to aim the database pointer at a particular table. **dblookup_table** is an easier-to-type shorthand for this operation.

```
>> db = dbopen(demodb_path,'r');
>> db = dblookup_table(db,'origin')

db =

   database: 0
      table: 10
      field: -501
     record: -501

>>
```

dbmark

This command is the first stage of a two-part process to remove a row from a database table, as explained under **dbcrunch**. For the impatient, see **dbdelete**.

```
>> db=dbopen('/tmp/newdb','r+');
>> db=dblookup_table(db,'origin');
>> % Add four copies of the same quake, all at slightly different times:
>> db.record=dbaddv(db,'lat',61.5922,'lon',-
149.130,'depth',20,'time',str2epoch('now'))
>>db.record=dbaddv(db,'lat',61.5922,'lon',-
149.130,'depth',20,'time',str2epoch('now'));
>>db.record=dbaddv(db,'lat',61.5922,'lon',-
149.130,'depth',20,'time',str2epoch('now'));
>>db.record=dbaddv(db,'lat',61.5922,'lon',-
149.130,'depth',20,'time',str2epoch('now'));
>>
>> db.record=1;
>> dbmark(db)
>>
```

dbnextid

In several of the css3.0-style database tables, entries such as hypocentral solutions ("origin" table) or seismic phase arrivals ("arrival" table) are identified with unique, integer id's. The **dbnextid** command allows the retrieval of the next unused value for any of these integer indices.

```
>> db=dbopen('/tmp/newdb','r+');
>> dbnextid(db,'orid')

ans =

    1

>>
```

dbnojoin

Similar to **dbjoin**, the **dbnojoin** command returns a view showing rows in the first table that have no counterpart in the second.

```
>> db = dbopen(demodb_path,'r');
>> dbarrival=dblookup_table(db,'arrival');
>> dbwfdisc=dblookup_table(db,'wfdisc');
```

```
>> db=dbnojoin(dbarrival,dbwfdisc)

db =

    database: 0
      table: 36
      field: -501
     record: -501

>>
```

dbnrecs

The **dbnrecs** command returns the number of records in a database table or view.

```
>> db = dbopen( demodb_path,'r' );
>> db = dblookup_table( db,'origin' );
>> nrecs = dbnrecs( db )

nrecs =

       1351

>>
```

dbopen

The first step in using Datascope on a relational database is to create a 'handle', called a database pointer, to the ASCII flat files which store the database contents. This step is performed by **dbopen**. Here we have written a small routine to reliably provide the pathname of a sample database for these examples.

```
>> dbexample_get_demodb_path

demodb_path =

/opt/antelope/4.2u/data/matlab/antelope/examples/demodb/demo

>> db = dbopen(demodb_path,'r')

db =

    database: 0
      table: -501
      field: -501
```

```
        record: -501

>>
```

dbpf

Many programs require some form of parameter file to store information about run-time configuration. The Antelope parameter-file utility provides a very powerful mechanism to handle such input files, including boolean, string, and numeric values as well as tables or key-value arrays, all of which can be nested. In the Antelope Toolbox for Matlab, interaction with a parameter file is through a 'handle' called a dbpf object. See the Antelope documentation for more details on the parameter file mechanism.

```
>> pf = dbpf( 'dbloc2' )

pf =

        dbpf object: 1-by-1

>> % Now as a contrived example of the other methods of use,
>> % convert it to a string, then compile it into a new parameter-file object:
>> string_version = pf2string( pf );
>> % Create an empty parameter-file object:
>> newpf = dbpf

newpf =

        dbpf object: 1-by-1

>> % Compile the new string into the empty parameter-file object:
>> % (you can compile into parameter-file objects that aren't empty as well)
>> newpf = dbpf( newpf, string_version)

newpf =

        dbpf object: 1-by-1

>>
```

dbprocess

Dbprocess provides a simplified interface for forming various views. When a sequence of standard database operations (such as subsets, joins, sorts, etc.) need to be performed all in a row, they can be combined into a single block, passed as a list of statements to **dbprocess**.

```
>> db = dbopen( demodb_path,'r' );

>> db = dbprocess( db, { 'dbopen arrival';
                         'dbsubset sta == "AAK"';
                         'dbjoin assoc' } );

>> [iphase, delta] = dbgetv( db,'iphase', 'timeres' )

iphase =

   'P'
   'S'


delta =

  -0.0500
   0.8600


>>
```

Detailed explanations of the valid statements available in dbprocess may be found in the unix man-pages for the dbprocess command. For reference, a summary list is provided here:

dbopen table
dbjoin [-o] table [key key ..]
dbgroup key [key ..]
dbleftjoin [-o] table [key key ..]
dbnojoin table [key key ..]
dbselect expr [expr ...]
dbseparate table
dbsever table
dbsort [-ru] key ..]
dbsubset expression
dbtheta table [expression ..]
dbungroup

dbput

This function is similar to **dbput**, however it does not automatically add its own null row. Also, it does not do any consistency checking to make sure the new row makes sense given the contents of the rest of the table. Again, avoid working with entire rows at once unless necessary. Consider using **dbputv** if possible.

```
>> db=dbopen('/tmp/newdb','r+');
>> db=dblookup_table(db,'origin');
>> db.record =  dbaddnull(db);
>> dbputv(db,'lat',61.5922,'lon',-149.130,'depth',20,'time',str2epoch('now'))
>> record = dbget(db)

record =

  61.5922 -149.1300   20.0000   923760231.63253       -1       -1       -1   -1   -1   -1       -1       -1
-  -    -999.0000 - -999.00       -1 -999.00       -1 -999.00       -1 -             -                  -1
923760231.66952


>>
>> db.record =  dbaddnull(db);
>> dbput(db,record)
>>
```

dbputv

The **dbputv** command is used to put individual field values into a database row. This is an extremely important command in the Datascope library. Here, we make a new row with the **dbaddnull** command so we have somewhere to put our values.

```
>> db=dbopen('/tmp/newdb','r+');
>> db=dblookup_table(db,'origin');
>> db.record =  dbaddnull(db);
>> dbputv(db,'lat',61.5922,'lon',-149.130,'depth',20,'time',str2epoch('now'))
>>
```

dbquery

The **dbquery** command is used to request a wide variety of information about a database or one of its component parts. One of the most common uses is to count the number of records in a a table.

```
>> db = dbopen(demodb_path,'r');
>> db = dblookup_table(db,'origin');
>> dbquery(db,'dbRECORD_COUNT')

ans =

        1351
```

```
>>
>> dbquery(db,'dbTABLE_FIELDS')

ans =

    'lat'
    'lon'
    'depth'
    'time'
    'orid'
    'evid'
    'jdate'
    'nass'
    'ndef'
    'ndp'
    'grn'
    'srn'
    'etype'
    'review'
    'depdp'
    'dtype'
    'mb'
    'mbid'
    'ms'
    'msid'
    'ml'
    'mlid'
    'algorithm'
    'auth'
    'commid'
    'lddate'

>>
>> dbquery(db,'dbDATABASE_NAME')

ans =

/opt/antelope/4.2u/data/matlab/antelope/examples/demodb/demo

>>
```

dbread_view

dbread_view is a less common command, used to read a view out of a file (for example, out of the file saved by **dbsave_view**). An example of that straightforward usage is shown in the script **dbexample_dbread_view**.m. For the tutorial we will show a far more unconventional use just to add interest. We will create a named-pipe with the unix *mkfifo*(1) command, then write to that pipe by calling the command-line version of *dbsubset* [Note for the advanced that it's necessary to do that in the background when using the Matlab **unix**() command, since the pipe will not close until the other end is read and flushed]. Then we get the database view out of the pipe and into Matlab with the **dbread_view** command:

```
>> unix('mkfifo /tmp/mypipe');
>> unix(['dbsubset ' demodb_path '.origin "ms > 6.8" > /tmp/mypipe &']);
>> db = dbread_view( '/tmp/mypipe' )

db =

    database: 3
       table: 45
       field: -501
      record: -501

>> dbgetv( db, 'ms' )

ans =

    7.1000
    7.5000
    6.9000
    7.0000

>>
```

dbresponse

The css3.0 schemas and related schemas reference instrument response information in separate files. These response files allow poles-and-zeros format, frequency-amplitude-phase triplet format, FIR format, and more. The **dbresponse** object is a handle to one of these response files, from which response information can be extracted.

```
>> db = dbopen(demodb_path,'r');
>> db=dblookup_table(db,'instrument');
>> db.record=0;
>> file=dbfilename(db)

file =
```

```
/opt/antelope/4.2u/data/matlab/antelope/examples/demodb/response/sts2_vel_RT72A.1

>>
>> resp = dbresponse(file)

resp =

        dbresponse object: 1-by-1

>>
```

dbsave_view

dbsave_view takes a current view into a database and saves it as though it were a base table of the main database. This is useful if a lot of processing was necessary to create the original view. Note that because the Antelope Toolbox for Matlab does not currently support named views, the name of the saved view will default to the name assigned by Datascope. However, once the database is closed the file may be moved to a new name. Also note that saved views are binary files of indexes. The **dbe** program should be used to view them. Views will become stale if any of the component tables change. To make an example of this command, we will copy the necessary parts of the demo database, make a joined view, and save it:

```
>> output_dbname = ['/tmp/newdb_' getenv('USER')];
>> unix( ['cp ' demodb_path '.arrival ' output_dbname '.arrival'] );
>> unix( ['cp ' demodb_path '.wfdisc ' output_dbname '.wfdisc'] );
>> db = dbopen( output_dbname,'r' );

>> dbarrival=dblookup_table( db,'arrival' );
>> dbwfdisc=dblookup_table( db,'wfdisc' );
>> db=dbjoin( dbarrival,dbwfdisc );

>> dbsave_view( db );
>>
```

dbseparate

dbseparate extracts the rows from the specified base table that participate in a given view. For example, we can start with a whole set of wfdisc records, construct a view that joins them ultimately to hypocentral information, subset for a hypocenter of interest, and then extract the resulting wfdisc records which have matched:

```
>> db = dbopen( demodb_path,'r' );
>> db = dbprocess( db, { 'dbopen wfdisc'; ...
     'dbjoin arrival'; ...
     'dbjoin assoc'; ...
```

```
    'dbjoin origin'; ...
    'dbsubset orid == 645' } );
>> db = dbseparate( db, 'wfdisc' );

>> db.record=0;
>> dbextfile( db, 'wfdisc' )

ans =

/opt/antelope/data/db/demo/wf/knetc/1992/138/210426/19921382155.15.CHM.BHZ

>>
```

For brevity, we have only printed one of the resulting file names from the records this retrieved.

dbsever

The **dbsever** command takes an existing view and removes an unwanted or no-longer needed table from that view. The returned value is a view without any fields from the removed table. If necessary, the resulting view is condensed to eliminate any duplicate rows.

```
>> db = dbopen( demodb_path,'r' );
>> dborigin=dblookup_table( db,'origin' );
>> dbstamag=dblookup_table( db,'stamag' );
>> db=dbjoin( dborigin, dbstamag );

>> % Get rid of the stamage values now that we know which orids have stamags:
>> db= dbsever( db, 'stamag' )

db =

   database: 1
      table: 46
      field: -501
     record: -501

>> dbgetv( db, 'orid' )

ans =

  645

>>
```

dbsort

This command takes any database view and returns a view sorted according to the specified expression.

```
>> db = dbopen(demodb_path,'r');
>> db=dblookup_table(db,'origin');
>> db=dbsubset(db,'mb>6.3');
>> db=dbsort(db,'mb');
>> dbgetv(db,'mb')

ans =

   6.3100
   6.4000
   6.4000
   6.4200
   6.5000
   6.5700

>>
```

If one of the arguments to dbsort is 'dbSORT_UNIQUE', the view returned will have only one representative for each unique value of the sort field(s). I.e. rows which have duplicate sort keys will be eliminated. If one of the arguments is 'dbSORT_REVERSE', the sort will be performed in reverse order.

dbsubset

This command, fairly self-explanatory, returns a database view containing only those rows from the input view which match the specified expression.

```
>> db = dbopen(demodb_path,'r');
>> db=dblookup_table(db,'origin');
>> db=dbsubset(db,'mb>6.3');
>> dbgetv(db,'mb')

ans =

   6.4200
   6.4000
   6.4000
   6.3100
   6.5000
   6.5700
```

```
>>
```

dbtheta

In the **dbjoin** command, specified above, the comparison fields ("join keys") used to describe which rows correspond were inferred. The **dbtheta** command allows you to perform the join with full command over whether or not two rows should be associated together or not, based on the supplied test expression.

```
>> db = dbopen(demodb_path,'r');
>> dbassoc = dblookup_table(db,'assoc');
>> dbwfdisc = dblookup_table(db,'wfdisc');
>> db=dbtheta(dbassoc,dbwfdisc,'assoc.sta == wfdisc.sta')

db =

    database: 0
       table: 45
       field: -501
      record: -504

>>
```

dbungroup

The **dbungroup** command is the inverse of the **dbgroup** command. It unpacks a bundle of rows into a view containing the individual rows.

```
>> db = dbopen( demodb_path,'r' );
>> db = dblookup_table( db, 'arrival' );
>> db = dbsort( db, 'sta' );
>> db = dbgroup( db, { 'sta' } );

>> % Subset for one station:
>> db = dbsubset( db, 'sta == "AAK"' );

>> db = dbungroup( db );

>> % Get the arriving phases detected at this station:
>> db = dblookup( db, '', '', '', 'dbALL' );
>> dbgetv( db, 'iphase' )

ans =
```

```
    'S'
    'P'
    'del'

>>
```

dbunjoin

Once a view is created, many database operations can be performed on it which winnow out certain rows of each component table. The resulting view may be split into the component rows from each participating table and written to a new database. This is accomplished with the **dbunjoin** command.

```
>> db = dbopen(demodb_path,'r');
>> dbarrival=dblookup_table(db,'arrival');
>> dbwfdisc=dblookup_table(db,'wfdisc');
>> db=dbjoin(dbarrival,dbwfdisc);
>> dbunjoin(db,'/tmp/newdb');
>> !ls /tmp/newdb*
/tmp/newdb.arrival  /tmp/newdb.wfdisc
>>
```

dbwrite_view

dbwrite_view writes a database view to a file. This can be used in a number of ways, for example to pipe a view to an external command (such as *dbe(1)*) via a named pipe. First we will set up the named pipe, and set up the Antelope *dbe* program (running in the background) waiting for input from the pipe. Then we will create our customized view in Matlab. Finally, we will write our view to the named pipe (which, like everything in unix, just looks like a file). At that point *dbe* will receive its input

```
>> pipe_name = ['/tmp/mypipe_' getenv('USER')];
>> unix( ['mkfifo ' pipe_name] );
>> unix( ['cat ' pipe_name ' | dbe - &'] );

>> db = dbopen( demodb_path,'r' );
>> dbarrival=dblookup_table( db,'arrival' );
>> dbwfdisc=dblookup_table( db,'wfdisc' );
>> db=dbjoin( dbarrival,dbwfdisc );

>> dbwrite_view( db, pipe_name );
>>
```

This causes a *dbe(1)* window to appear, showing the view that was calculated in Matlab.

epoch2str

Most time handling in Antelope (not to mention Unix) is done in terms of Unix epoch seconds, or seconds since 1970. The **epoch2str** command provides a highly flexible method for creating more human-readable time strings from an epoch time.

```
>> now = str2epoch('now')

now =

    9.237062953704129e+08

>> epoch2str( now, '%D %H:%M:%S %Z')

ans =

 4/10/99 01:04:55 UTC

>> epoch2str( now, '%A, %B %d %Y')

ans =

Saturday, April 10 1999

>>
>> epoch2str( now, '%G %l %p')

ans =

1999-04-10  1 AM

>>
```

eval_response

This function allows a **dbresponse** object (ultimately, a file of instrument response information stored as poles and zeroes or frequency-amplitude-phase triplets etc.) to be queried for the complex response at certain frequency values.

```
>> db = dbopen(demodb_path,'r');
>> db=dblookup_table(db,'instrument');
>> db.record=0;
>> file=dbfilename(db);
```

```
>> resp = dbresponse(file);
>> eval_response(resp,6.28)

ans =

   1.0008 - 0.0041i

>>
>> eval_response(resp,transpose([0.01 0.1 1 10])*6.28)

ans =

   0.2550 + 0.8025i
   0.9936 + 0.1116i
   1.0008 - 0.0041i
   0.0000 - 0.0000i

>>
```

free_response

Once the user is done with a dbresponse object, it must be freed with the **free_response** command.

```
>> db = dbopen(demodb_path,'r');
>> db=dblookup_table(db,'instrument');
>> db.record=0;
>> file=dbfilename(db);
>> resp = dbresponse(file);
>> free_response( resp )
>>
```

getpid

Get the system process-id of the Matlab interpreter from which this was called:

```
>> mypid = getpid

mypid =

4764

>>
```

orbafter

This command allows the user to set the beginning time for reading from an Antelope real-time ORB buffer. Note that all the orb examples below require a running orb, for which you have permission to connect.

```
>> % This presumes that you have connect permission to a running
>> %  orb called 'nordic' (you probably don't...)
>> fd = orbopen( 'nordic', 'r' );
>> [result,time, srcname, pktid] = orbget( fd );
>> pktid

pktid =

      2357

>> % Get the next packet with timestamp after the packet we just got:
>> % (note that there's no a-priori requirement that packets arrive on the
>> % orb in time order)
>> orbafter( fd, time )

ans =

  497

>>
```

orbclose

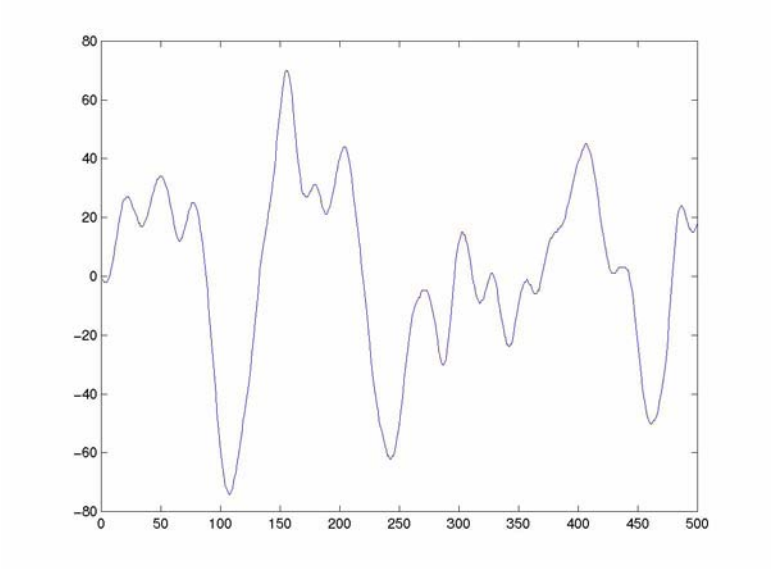
This allows the user to close down an open connection to an Antelope ORB.

```
>> % This presumes that you have connect permission to a running
>> %  orb called 'nordic' (you probably don't...)
>> fd = orbopen( 'nordic', 'r' );
>> orbclose( fd )
>>
```

orbget

The **orbget** command collects the specified packet from an Antelope ORB, unpacks it based on its type, and returns it to the user. Currently the understood types are waveform, parameter-file (you can put an entire parameter file on an ORB), and database-row. Other types of packets are returned as byte vectors. Each packet on an orb has a timestamp and a source-name, which are also returned.

```
>> % This presumes that you have connect permission to a running
>> %  orb called 'nordic' (you probably don't...)
>>
>> % First we'll get a waveform-data object from an orb:
>> fd = orbopen( 'nordic', 'r' );
>> orbreject( fd, '/db/.*|/pf/.*' );
>> [result, time, srcname, pktid, type] = orbget( fd )

result =

    database: 16
       table: 5
       field: -501
      record: 0

time =

   9.4638e+08


srcname =

AT_MID_SHZ

pktid =

      724328

type =

waveform

>> result.record = 0;
>> plot( trextract_data( result ) );
```



>> **trdestroy(result);**
>> **orbclose(fd);**

>> % Now get a database-row object from an orb:
>> **fd = orbopen('megathrust','r');**
>> **orbselect(fd,'/db/.*');**
>> **orbseek(fd,'ORBOLDEST');**
>> **result=orbget(fd)**

result =

database: 0
table: 19
field: -501
record: -504

>> **[lat,lon,mb]=dbgetv(result,'lat','lon','ml')**

lat =

59.8962

lon =

-152.0661

mb =

```
   1.8600

>> % Finally, get a parameter-file object from an orb:
>> orbselect(fd,'/pf/.*');
>> orbseek(fd,'ORBOLDEST');
>> result=orbget(fd)

result =

      dbpf object: 1-by-1

>> pf2string(result)

ans =

cmdstring       "echo hi | mail kent"

>>
```

orbopen

The **orbopen** command allows you to establish a read or write connection to a running Antelope ORB server anywhere on the internet (provided the orbserver maintainers have given you permission to connect to that orb). You may have multiple connections at once to the same ORB.

```
>> % This presumes that you have connect permission to a running
>> %  orb called 'nordic' (you probably don't...)
>> fd = orbopen( 'nordic', 'r' )

fd =

   21

>>
```

orbping

This command is primarily useful to verify that an ORB connection is up and running. It has the side benefit of telling you the version number of the orbserver.

```
>> % This presumes that you have connect permission to a running
>> %  orb called 'nordic' (you probably don't...)
>> fd = orbopen( 'nordic', 'r' );
>> orbping( fd )
```

```
ans =

    6

>>
```

orbreap

This is one of the most common orb commands. Evaluated in a tight loop, it allows you to successively receive packet after packet for the streams you've chosen. Each packet can then be processed as necessary.

```
>> % This presumes that you have connect permission to a running
>> %  orb called 'nordic' (you probably don't...)
>> fd = orbopen( 'nordic', 'r' );
>> for i = 1:3,
[result,time,srcname] = orbreap( fd );
srcname
end

srcname =

AK_MDM_SHZ

srcname =

AK_KTH_SHZ

srcname =

AK_MCK_SHZ

>>
```

orbreject

This command allows the user to reject certain packets from ever coming across a particular orb connection. The specification is by means of regular-expression matching on the source-names of the packets.

```
>> % This presumes that you have connect permission to a running
>> %  orb called 'nordic' (you probably don't...)
>> fd = orbopen( 'nordic', 'r' );
>> % Reject all parameter-file packets, all database-row packets,
```

```
>> % and all waveform packets for the Alaska net whos station-names
>> % start with A,B, or C:
>> % (return the number of sources still available on the connection)
>> orbreject( fd, '/db/.*|/pf/.*|AK_[A-C].*' )

ans =

  276

>>
```

orbseek

For a given read connection to an orbserver, the **orbseek** command allows the user to position the reading point in the stream to a certain packet number or to a specified relative location in the stream (newest packet, oldest packet, next packet, etc.).

```
>> % This presumes that you have connect permission to a running
>> %  orb called 'nordic' (you probably don't...)
>> fd = orbopen( 'nordic', 'r' );
>> orbseek( fd, 'ORBOLDEST' )

ans =

     790548

>> orbseek( fd, 'ORBNEXT' )

ans =

     790549

>> orbseek( fd, 'ORBNEWEST' )

ans =

     321046

>> orbseek( fd, 'ORBPREV' )

ans =

     321045

>> orbseek( fd, 'ORBPREV' )
```

```
ans =

     321044

>> mypktid = orbtell( fd )

mypktid =

     321044

>> orbseek( fd, 'ORBPREV' )

ans =

     321043

>> orbseek( fd, mypktid )

ans =

     321044

>>
```

orbselect

Orbselect is a very useful command which allows the user to filter packets from an orb connection so that only those matching certain source-name criteria get through.

```
>> fd = orbopen( 'nordic', 'r' );
>> % Choose all components of station DIV (Divide, Alaska)
>> % Return the number of selected sources
>> orbselect( fd, 'AK_DIV_.*' )

ans =

    3

>>
```

orbtell

This command returns the packet-identification-number for the current packet on read connection to an orbserver.

```
>> % This presumes that you have connect permission to a running
>> %  orb called 'nordic' (you probably don't...)
>> fd = orbopen( 'nordic', 'r' );
>> % Find the packet-id for the current packet:
>> orbtell( fd )

ans =

    377956

>>
```

parse_response

The parse_response command takes a dbresponse object and expands it into its component filter stages and filter coefficients. The result is returned as a cell array. Each cell in the cell array contains one stage of the filter, represented as a Matlab structure. The field names in the structure vary according to the type of the filter, although all of the structures have a 'type' field listing the type of the filter. For example, a filter stage of type 'paz' (poles and zeroes) will have vectors of the poles and zeros for the filter stage. A filter stage of type 'fap' (frequency-amplitude-phase) will have vectors of the frequency-amplitude-phase triplets.

```
>> db = dbopen( demodb_path,'r' );
>> db=dblookup_table( db,'instrument' );
>> db.record=0;
>> file=dbfilename( db );
>> resp = dbresponse( file );
>> parsed = parse_response( resp )

parsed =

   [1x1 struct]
   [1x1 struct]
   [1x1 struct]
   [1x1 struct]
   [1x1 struct]


>> % Display the results:
>> celldisp( parsed )

parsed{1} =

            type: 'paz'
```

npoles: 2
nzeros: 2
normalization: 1
frequency: 0
poles: [2x1 double]
pole_errors: [2x1 double]
zeros: [2x1 double]
zero_errors: [2x1 double]

parsed{2} =

type: ‘paz’
npoles: 6
nzeros: 0
normalization: 1.5020e+19
frequency: 0
poles: [6x1 double]
pole_errors: [6x1 double]
zeros: []
zero_errors: []

parsed{3} =

type: ‘fir’
nnum: 99
nden: 1
srate: 1000
dec_factor: 5
seed_dec_offset: 0
midpoint: -1
num_coefs: [99x1 double]
num_coef_errors: [99x1 double]
den_coefs: 1
den_coef_errors: 0

parsed{4} =

type: ‘fir’
nnum: 95
nden: 1

```
        srate: 200
        dec_factor: 2
        seed_dec_offset: 0
        midpoint: -1
        num_coefs: [95x1 double]
        num_coef_errors: [95x1 double]
        den_coefs: 1
        den_coef_errors: 0


parsed{5} =

        type: 'fir'
        nnum: 235
        nden: 1
        srate: 100
        dec_factor: 5
        seed_dec_offset: 0
        midpoint: -1
        num_coefs: [235x1 double]
        num_coef_errors: [235x1 double]
        den_coefs: 1
        den_coef_errors: 0

>> % Display one of the component vectors:
>> parsed{1}.poles

ans =

  -0.0355 + 0.0355i
  -0.0355 - 0.0355i

>>
```

parsepath

parsepath separates a pathname into its component parts. This is done entirely by text analysis of the input string, without any regard to whether the files, directories, or whatever they are actually exist. If the third output argument is specified, any suffix is separated from the basename of the file. Otherwise the file basename is left intact with any suffix.

```
>> [dir, base] = parsepath( '/home/kent/testfile.txt' )

dir =
```

```
/home/kent


base =

testfile.txt


>> [dir, base, suffix] = parsepath( '/home/kent/testfile.txt' )

dir =

/home/kent


base =

testfile


suffix =

txt

>>
```

pf2string

An entire parameter file (being essentially an ASCII file) or subsection thereof may be converted to a string.

```
>> pf=dbpf('dbfixids');
>> pf2string(pf)

ans =

css3.0  &Arr{
aliases &Arr{
magid   mbid msid mlid
orid    prefor
}
}
rt1.0   &Arr{
aliases &Arr{
```

```
magid   mbid msid mlid
orid    prefor
}
}

>>
```

pf2struct

The Matlab Antelope Toolbox allows an entire parameter file to be loaded into a Matlab struct. A Matlab struct has strong similarity to the data storage in a parameter file: namely a flexible set of key-value pairs. The 'recursive' option to **pf2struct** can be used to read a complex parameter file all at once into an easy-to-use Matlab-style object. This command can be extremely useful in making the entire contents of a parameter file available in one clean strike, rather than multiple independent **pfget** calls. With **pf2struct** in 'recursive' mode, one call converts every parameter in the parameter file into a like-named element of the returned structure. Parameter values that appear to be numeric will be converted to numbers via the Matlab **str2double** function [note that this is a change from earlier version of the Antelope Toolbox for Matlab]:

```
>> pf=dbpf('dbloc2');
>> pf2struct(pf)

ans =

    Define: [1x1 dbpf]
  Processes: [1x1 dbpf]
       Run: [1x1 dbpf]
     State: [1x1 dbpf]
      User: [1x1 dbpf]

>>
>> pf2struct(pf,'recursive')

ans =

    Define: [1x1 struct]
  Processes: [1x1 struct]
       Run: [1x1 struct]
     State: [1x1 struct]
      User: [1x1 struct]

>>
>> ans.Define

ans =
```

```
                Results_dir: 'results'
             Temporary_db: 'trial'
                  Work_dir: 'tmp'
              arrival_color: 'purple'
                arrival_info: 'arid sta time iphase deltim fm amp per auth'
            arrivals_height: 300
             arrivals_width: 800
              azimuth_font: '-Adobe-Helvetica-Bold-O-Normal--*-120-*'
              azimuth_info: 'azimuth delaz'
       bad_residual_color: 'orange'
                button_row: 49
 dbpick_channel_options: [1x1  struct]
    dbpick_options_order: 'Vertical Horizontal All Selected'
dbpick_revert_to_default: 'yes'
           fixedwidth_font: '-Adobe-Courier-Bold-R-Normal--*-120-*'
            ignored_color: 'gray60'
            max_event_delta: 5
max_event_time_difference: 25
                    maxcol: 25
                   maxrow: 50
            ok_residual_color: 'DodgerBlue'
                  origin_color: 'magenta'
                   origin_info: [1x69 char  ]
               origins_height: 150
                origins_width: 800
                  partial_color: 'cyan'
                     plain_font: '-Adobe-Helvetica-Bold-R-Normal--*-120-*'
                      site_info: 'staname {lat . "," . lon} gregion(lat,lon)'
              slowness_info: 'slow delslo'
               station_color: 'gray'
                    time_font: '-Adobe-Courier-Bold-R-Normal--*-120-*'
                  used_color: 'black'

>>
```

pffiles

The Antelope parameter-file mechanism allows the parameters to be extracted from any of the matching parameter files along an entire search path (specified in the PFPATH environment variable). The **pffiles** command shows which pathnames actually contributed to a given paramter-file-object's contents. The 'all' option shows all the files that were tested for existence and possible contribution.

```
>> pffiles('rtexec')
```

```
ans =

    '/opt/antelope/4.2u/data/pf/rtexec.pf'

>> pffiles('rtexec','all')

ans =

    '/opt/antelope/4.2u/data/maps/site/rtexec.pf'
    '/opt/antelope/4.2u/data/pf/rtexec.pf'
    '/opt/antelope/4.2u/data/pf/site/rtexec.pf'
    '/home/kent/data/pf/rtexec.pf'
    './rtexec.pf'

>>
```

pffree

This frees the resources used by a dbpf object when it is no longer needed.

```
>> pf = dbpf( 'dbloc2' );
>> pffree(pf)
>>
```

pfget

The **pfget** command retrieves the specified parameter from the dbpf object into an appropriate format. Parameter values that appear to be numeric will be converted to numbers via the Matlab **str2double** command [note that this is a change from earlier versions of the Antelope Toolbox for Matlab]:

```
>> pf = dbpf( 'rtexec' );
>> pfget( pf, 'Database' )

ans =

rtsys/rtsys

>> pfget( pf, 'Failure_threshold' )

ans =

     300
>>
```

pfget_arr

This retrieves an associative array from a parameter-file object.

```
>> pf = dbpf( 'rtexec');
>> pfget_arr(pf,'Limit')

ans =

       dbpf object: 1-by-1

>>
>> pfget_arr(pf,'Limit','recursive')

ans =

   coredumpsize: 'unlimited'
        cputime: 'unlimited'
       datasize: 'unlimited'
    descriptors: 'unlimited'
       filesize: 'unlimited'
      stacksize: 'unlimited'
    vmemoryuse: 'unlimited'

>>
```

pfget_boolean

This retrieves a boolean value from a parameter-file object, translating strings such as 'yes' or 'false' into numeric values.

```
>> pf=dbpf('dbloc2')

pf =

       dbpf object: 1-by-1

>>
>> subpf=pfget(pf,'State')

subpf =

       dbpf object: 1-by-1

>>
```

```
>> pfget_boolean(subpf,'auto_save')

ans =

   -1

>>
>> pfget_boolean(subpf,'auto_associate')

ans =

    0

>>
```

pfget_num

This command retrieves a numeric value from a parameter file (the numeric conversion is based on the Matlab **str2double** command):

```
>> pf = dbpf( 'rtexec');
>> pfget_num( pf, 'Time_to_die' )

ans =

   20

>>
```

pfget_string

This command retrieves a string value from a parameter file.

```
>> pf = dbpf( 'rtexec');
>> pfget_string( pf, 'Database' )

ans =

rtsys/rtsys

>>
```

pfget_tbl

This command retrieves a table of values from a parameter file.

```
>> pf = dbpf( 'rtexec');
>> pfget_tbl( pf, 'Buttons' )

ans =

   'top     xterm -geom 80x25 -e top'
   'clients xterm -geom 132x25 -e orbstat -c localhost 5'
   'sources xterm -geom 132x60 -e orbstat -s localhost 5'
   'rtd     orbmonrtd localhost'
   'dbevents dbevents archive/nw'
   'qtmon      qtmon localhost localhost localhost'

>>
```

pfkeys

This command extracts the key names for the key-value pairs in a parameter file.

```
>> pf = dbpf( 'rtexec');
>> pfkeys(pf)

ans =

   'ANTELOPE'
   'Buttons'
   'Crontab'
   'Database'
   'Env'
   'Limit'
   'Minimum_period_between_starts'
   'Network_database'
   'Parameter_files'
   'Processes'
   'ROOT'
   'Run'
   'Shutdown_order'
   'Shutdown_tasks'
   'Start_period'
   'Startup_tasks'
   'Time_to_die'
   'Use_UTC'
   'disks'
   'orbname'
```

```
    'orbtasks'

>>
```

pfname

This command returns the parameter-file name from which a parameter-file object was created.

```
>> pf = dbpf( 'rtexec');
>> pfname(pf)

ans =

rtexec

>>
```

pfput_boolean

This function puts a value into a parameter file as a boolean.

```
>> pf = dbpf;
>> pfput_boolean( pf, 'myboolean', 'True' )

>> pf2string( pf )

ans =

myboolean       True

>>
```

pfput

The **pfput** command is a very general routine to put strings, numbers, cellarrays (as tables), or structures (as associative arrays) into a parameter-file object.

```
>> pf = dbpf;
>>
>> pfput( pf, 'mydouble', 3.14 )
>> pfput( pf, 'myint', 24 )
>> pfput( pf, 'mystring', 'test string' )
>>
>> z.a = 21;
```

```
>> z.b = 'hello';
>> z.c = '45.6';
>> pfput( pf, 'myarray', z )
>>
>> pfput( pf, 'mytable', {'hello' 'yes' 'no' 'goodbye'} )
>>
>>
>> pf2string( pf )

ans =

myarray &Arr{
a       21
b       hello
c       45.6
}
mydouble        3.14
myint   24
mystring        test string
mytable &Tbl{
hello
yes
no
goodbye
}

>>
```

pfresolve

This is an alternative interface to the parameter-file objects with a naming convention that reflects any nesting in the parameter-file components (tables and hashes). For further detail see the Datascope man pages.

```
>> pf = dbpf( 'rtexec');
>> pfresolve(pf,'Limit{filesize}')

ans =

unlimited

>>
```

pftype

Only top-level parameter-file objects are of file type. Subsidiary key-value structures (arrays) inside a parameter file will have dbpf objects of type PFARR.

```
>> pf = dbpf( 'rtexec');
>> pftype(pf)

ans =

PFFILE

>>
```

pfupdate

This command allows your program to stay current with a parameter file if outside forces are changing it while your program is running.

```
>> % Create a parameter file and put one value in it
>> unix( 'echo myint 13 > /tmp/myfile.pf' );

>> % Open the parameter file and extract the parameter:
>> pf = dbpf( '/tmp/myfile.pf' );
>> pfget_num( pf, 'myint' )

ans =

   13

>> % Now change the parameter file from outside the Matlab context:
>> unix( 'echo myint 25 >! /tmp/myfile.pf' );

>> % a retrieval of the parameter returns the previously cached value:
>> pfget_num( pf, 'myint' )

ans =

   13

>> % Updating the parameter-file object refreshes the cached values:
>> [pf, modified] = pfupdate( pf )

pf =

      dbpf object: 1-by-1
```

```
modified =

     1

>> % Now the retrieved parameter reflects the changed file:
>> pfget_num( pf, 'myint' )

ans =

    25

>>
```

pfwrite

A dbpf object, possibly modified, may be written out to the specified filename.

```
>> pf = dbpf( 'rtexec');
>> pfwrite(pf,'/tmp/rtexec_copy.pf')
>>
```

str2epoch

This utility is a very powerful and flexible parsing utility to turn a human-readable time string into an epoch time.

```
>> format long
>> str2epoch('now')

ans =

     9.237016155097741e+08

>> str2epoch('3/17/99 15:24:16.5')

ans =

     9.216842565000000e+08

>>
>> str2epoch('January 27, 1973 4:00 pm')

ans =

    96998400
```

>>

strdate

This utility takes a Unix epoch time and returns a stock day format.

>> **strdate(96998400)**

ans =

1/27/1973

>>

strtdelta

This utility turns the input number of seconds into a reasonably-formatted value for a time interval.

>> **strtdelta(7200)**

ans =

2:00 hours

>> **strtdelta(3*86400+15*3600)**

ans =

3 days 15.0 hours

>> **strtdelta(912343243)**

ans =

28 years 339 days

>>

strtime

This function takes a Unix epoch time and returns a stock-format time and day string.

>> **strtime(96998400)**

ans =

1/27/1973 16:00:00.000

>>

strydtime

This function is the same as the strtime function but includes as well the day number of the year.

>> **strydtime(96998400)**

ans =

1/27/1973 (027) 16:00:00.000

>>

tr_endtime

This is a safe macro to reliably construct an endtime from a starting time, sample rate, and number of samples. All other useful permutations of this routine exist as well (below).

>> **time, endtime, nsamp, samprate**

time =

7.061397152000000e+08

endtime =

7.061398415000000e+08

nsamp =

2527

samprate =

20

```
>>
>> tr_endtime(time,samprate,nsamp)

ans =

    7.061398415000000e+08

>>
```

tr_nsamp

```
>> tr_nsamp(time,samprate,endtime)

ans =

      2527

>>
```

tr_samp2time

```
>> tr_samp2time(time,samprate,1000)

ans =

    7.061397651500001e+08

>>
```

tr_samprate

```
>> tr_samprate(time,nsamp,endtime)

ans =

  20.00000000755087

>>
```

tr_time2samp

```
>> tr_time2samp(time,samprate,7.061397651500001e+08)
```

```
ans =

      1000

>>
```

tr2struct

tr2struct is most useful for creating a standalone structure of waveform data and its vital statistics. This structure can be saved for export to a Matlab user who wants waveform data but does not have the Antelope toolbox. This utility is implemented as a *.m* function rather than a mex file, thus users may modify it easily to change its behavior. The input is a trace object containing the waveform data to package for export.

```
>> db = dbopen( demodb_path,'r' );
>> db=dblookup_table( db,'wfdisc' );
>> dbsite=dblookup_table( db,'site' );
>> db=dbjoin( db, dbsite );

>> % For now just use the time window of the first row to decide what to get:
>> db.record=0;
>> [time,endtime]=dbgetv( db,'time','endtime' );

>> tr = trload_css( db, time, endtime );

>> s = tr2struct( tr );

>> % Save the structure to a file to send elsewhere:
>> save '/tmp/dbexample_data.mat' s

>> trdestroy( tr );   % Don't forget to clean up
```

trapply_calib

This function applies the calibration constant to waveform data contained in the trace object.

```
>> db = dbopen(demodb_path,'r');
>> db=dblookup_table(db,'wfdisc');
>> db.record=0;
>> [time,endtime,nsamp,samprate]=dbgetv(db,'time','endtime','nsamp','samprate');
>> tr = trload_css(db,time,endtime);
>> trapply_calib(tr)
>> % do something interesting with the data, most likely starting with trextract_data
>> trdestroy( tr );   % Don't forget to clean up
```

trdestroy

This routine frees all resources associated with a trace-object. This is a critical command for users handling waveform data loaded from a database, especially if they are doing so in large quantities. The trace-library commands in the Antelope Toolbox for Matlab are actually links to the underlying C routines in the Antelope *tr* library. When one of the trace-library data-access methods (such as **trload_css** or **trload_cssgrp**) is called to load data from a database into a trace-object, an actual copy is made from the database (i.e. the disk files) into RAM memory allocated by the Antelope trace-library. This memory is not under the control of the Matlab interpreter--it can be neither freed nor accessed directly by default Matlab commands. Normally the user will at some point call a command like **trextract_data** to make a third, useful copy of the trace data (the first copy is on disk and the second in memory controlled by the trace library), pulling the data into the Matlab workspace. This third copy is fully under the control of Matlab and the user can treat it just like any other Matlab variable. However, the 'middle' copy of the waveform data, the one in the RAM memory allocated by the trace library, must be freed 'by hand' after the user is done with it. This step is accomplished with the **trdestroy** command [Note: it is also possible to use the **trfree** command to free this data, however in general the **trdestroy** command is preferred. **trfree** surgically frees parts of the memory allocated in the trace object, whereas **trdestroy** cleanly and completely destroys the whole thing. The latter is preferable because of its robustness and simplicity; it is much less prone to programming mistakes and oversights].

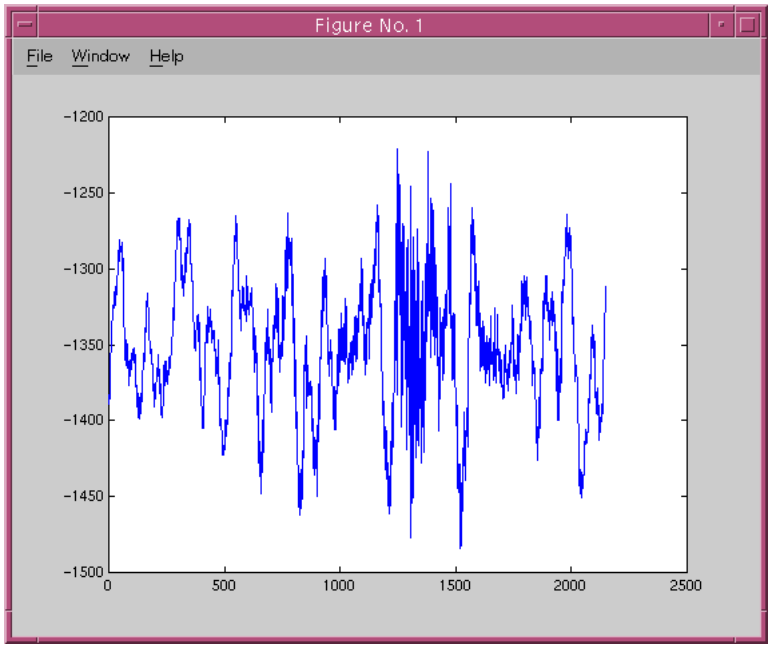
```
>> db = dbopen(demodb_path,'r');
>> db=dblookup_table(db,'wfdisc');
>> db.record=0;
>> [time,endtime,nsamp,samprate]=dbgetv(db,'time','endtime','nsamp','samprate');
>> tr = trload_css(db,time,endtime);
>> % do something interesting with the data, most likely starting with trextract_data
>> trdestroy( tr )   % Don't forget to clean up
>>
```

trextract_data

A trace-object is just a database pointer, pointing to an open database in the Trace4.0 schema. The "trace" table of this database has a field called "data", which contains the address of some waveform data in memory. The **trextract_data** command gets this address and loads the data contained into a Matlab vector. A further description of the general model may be found under the section for the **trload_css** command. The **trextract_data** command is a critical part of waveform-data access in the Antelope Toolbox for Matlab: it is the access method for getting a Matlab matrix of waveform data out of a trace object and into a Matlab variable.

```
>> db = dbopen(demodb_path,'r');
>> db=dblookup_table(db,'wfdisc');
>> db.record=0;
>> [time,endtime,nsamp,samprate]=dbgetv(db,'time','endtime','nsamp','samprate');
```

```
>> tr = trload_css(db,time,endtime);
>> tr.record=0;
>> data=trextract_data(tr);
>> whos data
  Name       Size         Bytes  Class

  data    2150x1          17200  double array

Grand total is 2150 elements using 17200 bytes

>> plot(data)
```



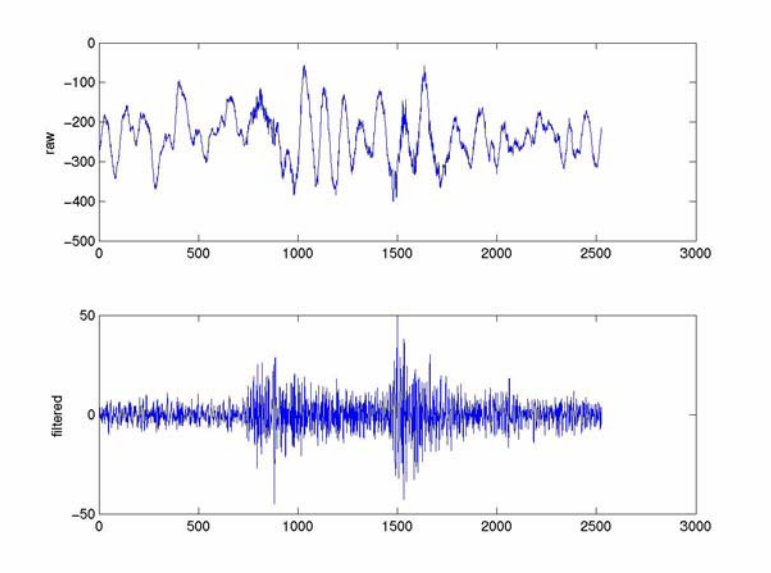

```
>> trdestroy( tr );   % Don't forget to clean up
>>
```

trfilter

trfilter performs time-domain filtering on all of the traces in the input trace-object. The filter is specified in a *filter_string* argument, as described by the Unix man-page *trfilter*(3). For example, to apply a Butterworth Band-pass filter from 1 to 5 Hz with eight poles, the *filter_string* would be "BW 1 4 5 4". For full details on *filter_string* options, please see the referenced man page. The data arrays are filtered in place so that original sample values are replaced with the new filtered values (note, of course, that this affects only the data in memory, not the data on disk).

```
>> db = dbopen( demodb_path,'r' );
>> db=dblookup_table( db,'wfdisc' );
>> db.record=0;
```

```
>> format long
>> [time,endtime,nsamp,samprate]=dbgetv( db,'time','endtime','nsamp','samprate' );
>> db = dblist2subset( db, 0 );
>> tr = trload_css( db,time,endtime );

>> tr.record = 0;
>> subplot( 2, 1, 1 );
>> plot( trextract_data( tr ) );
>> ylabel( 'raw' );

>> trfilter( tr, 'BW 1 4 5 4' );
>> subplot( 2, 1, 2 );
>> plot( trextract_data( tr ) );
>> ylabel( 'filtered' );
```




```
>> trdestroy( tr );
```

trfree

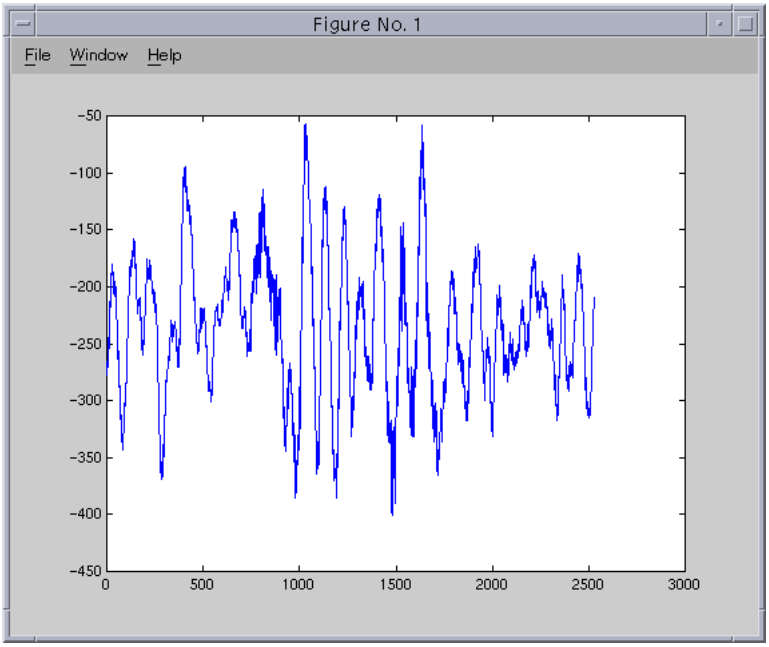
The **trfree** command is a way to free resources for part of a trace-object structure. Please strongly consider using **trdestroy** instead of **trfree**. The **trfree** command is intended for the experienced programmer who is thoroughly familiar with the underlying Antelope C-callable trace-library and its concepts. The **trfree** command will free the memory resources associated with exactly the part (and only the part) of the trace-object to which a given input pointer points. Because of this, while highly involved data operations may be constructed with **trfree**, the general user will be much more likely to avoid pitfalls with the robust, straightforward, and clean **trdestroy** command.

```
>> db = dbopen(demodb_path,'r');
>> db=dblookup_table(db,'wfdisc');
>> db.record=0;
>> [time,endtime,nsamp,samprate]=dbgetv(db,'time','endtime','nsamp','samprate');
>> tr = trload_css(db,time,endtime);
>> % do something interesting with the data, most likely starting with trextract_data

>> trfree( tr )
>>
```

trgetwf

This command is one of several methods to extract waveform data from a database. It is older and simpler than many of the other tr routines. Instead of returning a trace-object, it returns simply a Matlab vector of waveform data from the single database row specified by the input pointer. It has the disadvantage that the output is not conducive to splicing, there is no provision to limit the returned segment to a given time window, and it cannot handle waveform segments that span multiple wfdisc rows. The advantage is in the relative simplicity. Unlike the other trace-library access routines such as **trload_css** and **trload_cssgrp**, there is no need to call **trdestroy** after calling this routine.

```
>> db = dbopen(demodb_path,'r');
>> db=dblookup_table(db,'wfdisc');
>> db.record=0;
>> [data,nsamp,t0,t1]=trgetwf(db);
>> whos data
  Name       Size         Bytes  Class

  data    2527x1          20216  double array

Grand total is 2527 elements using 20216 bytes

>> plot(data)
```



trinsert_data

This is the converse of the **trextract_data** command, described above.

```
>> tr=trnew;
>> tr=dblookup_table(tr,'trace');
>>
>> % Construct a fake waveform:
>> data=sin([0:999]);
>> nsamp=1000;
>> sta='SINE';
>> chan='BHZ';
>> time=str2epoch('now');
>> samprate=20;
>> endtime=tr_endtime(time,samprate,nsamp);
>>
>> % Put the waveform into the trace-object:
>> tr.record=dbaddnull(tr);
>> dbputv(tr,'time',time,'samprate',samprate,'endtime',endtime,'sta',sta,'chan',chan);
>> trinsert_data(tr,data)
>> % do something interesting with the data
>> trdestroy( tr );   % Don't forget to clean up
```

trload_css

The **trload_css** command loads the specified time range of data from a database pointer into a trace object. Note that the record number of the input database pointer is ignored by this routine: all data that appears in the input table matching the specified time range is loaded. To prevent more data being loaded than one desires, one should precede the **trload_css** call with appropriate calls to **dbsubset** to make sure only the desired data are read from the database. A trace object is just another Datascope database pointer, although it is in a different database schema (*Trace4.0*) than most on-disk waveform databases (usually *css3.0* or *rt1.0*). Because the trace-object is really just another database pointer, many of the standard database routines will work on it, such as **dbgetv**, **dbsort**, **dbsubset** etc. By convention, database pointers that point to trace objects have often been given variable names like *tr* instead of *db*. This convention is of course very informal, since the name of a variable is completely arbitrary and can be chosen to suit the whims of the programmer. However, the common usage does help programmers write code that is easier to understand and maintain. There are a couple main differences between a database pointer that points to a trace object and a database pointer that points to a set of waveforms on disk. One of these differences is the table names. In *css3.0* and *rt1.0* database schemas, waveforms on disk are described by a database table called *wfdisc*. In the *Trace4.0* database schema, waveforms are described by a database table called *trace*. The goal of the *Trace4.0* schema is to provide a way to describe waveforms in physical memory (RAM, Random Access Memory) instead of waveforms on disk. Thus the second main difference is that whereas a *wfdisc* table has fields *dir* and *dfile* to point to a block of waveform data on disk, the *trace* table has a field called *data* that points to a block of waveform data in random-access memory. The **trload_css** command is designed to take a database pointer that points to a wfdisc table of waveforms on disk, and load both the raw data and the metadata (descriptive info such as station and channel names, times, number of samples etc) into random-access memory and into a descriptive *trace* table. Thus, the *data* field of the *trace* table holds the address of a block of data in memory. Since the waveform data is loaded by **trload_css** into memory controlled by the Antelope trace-library rather than Matlab itself, **trload_css** is only the first of two steps to get data from a waveform database on disk into matrices of useful time series data in Matlab. Specifically, the time-series loaded into the *data* address by **trload_css** must be extracted into the Matlab workspace. That step is accomplished with the command **trextract_data**, described separately. As a final note, the matrix returned by **trextract_data** is fully in the Matlab workspace and obeys its memory handling rules completely--it can be copied, cleared etc. like any other Matlab variable. However, a critical point is that the memory allocated by **trload_css** is actually under the control of the Antelope trace library, not under the control of Matlab. *Thus when one is finished with a trace object, one should call* ***trdestroy*** *on the trace-object to free this underlying memory.*

```
>> db = dbopen(demodb_path,'r');
>> db=dblookup_table(db,'wfdisc');
>> db.record=0;
>> format long
>> [time,endtime,nsamp,samprate]=dbgetv(db,'time','endtime','nsamp','samprate')

time =
```

```
    7.061397152000000e+08

endtime =

    7.061398415000000e+08

nsamp =

       2527

samprate =

   20

>> tr = trload_css(db,time,endtime)

tr =

    database: 1
      table: 5
      field: -501
     record: -501

>>
>> % do something interesting with the data, most likely starting with trextract_data
>> trdestroy( tr );   % Don't forget to clean up
```

trload_cssgrp

This command is similar to **trload_css** described above. The user should be forewarned that this routine is an exposure of a C library (libtr) routine which was designed more for the core programmer than the general user. Thus, there are some characteristics that must be known and accounted for. Most importantly, it is critical that the input database view is sorted by 'sta', then 'chan', then 'time'. This may be done with the **dbsort** command in the example below. Also, the **trload_cssgrp** loads a copy of all returned data into memory allocated inside the trace-library itself. In order to free this memory, the user is required to call the **trdestroy** command on the trace-object pointer. This is true regardless of whether or not the data have been extracted into the Matlab workspace by the **trextract_data** command (those data loaded into the Matlab workspace, of course, follow the standard patterns of memory-handling for Matlab data--they can be copied or cleared as necessary by Matlab commands without further concern). While the **trdestroy** command may be omitted for small programs and small data requests, it is good program-

ming practice to include it consistently. Otherwise attempts to run any developed code on large data sets may create a situation that swamps the machine (uses up all available memory and swap space).

```
>> db = dbopen( demodb_path,'r' );
>> db=dblookup_table( db,'wfdisc' );
>> db= dbsort( db, 'sta', 'chan', 'time' );     % REQUIRED
>> [time,endtime,nsamp,samprate]=dbgetv( db,'time','endtime','nsamp','samprate' );
>> tr = trload_cssgrp( db,time(1),endtime(1) )

tr =

    database: 8
       table: 5
       field: -501
      record: -501

>> tr.record=0;
>> data=trextract_data( tr );
>> plot(data)
>> trdestroy( tr );   % Don't forget to clean up
```

trnew

The **trnew** command creates a new, empty trace-object database.

```
>> tr=trnew

tr =

    database: 0
       table: -501
       field: -501
      record: -501

>> dbquery(tr,'dbDATABASE_NAME')

ans =

/tmp/trdb0ewpxx

>> dbquery(tr,'dbSCHEMA_NAME')

ans =
```

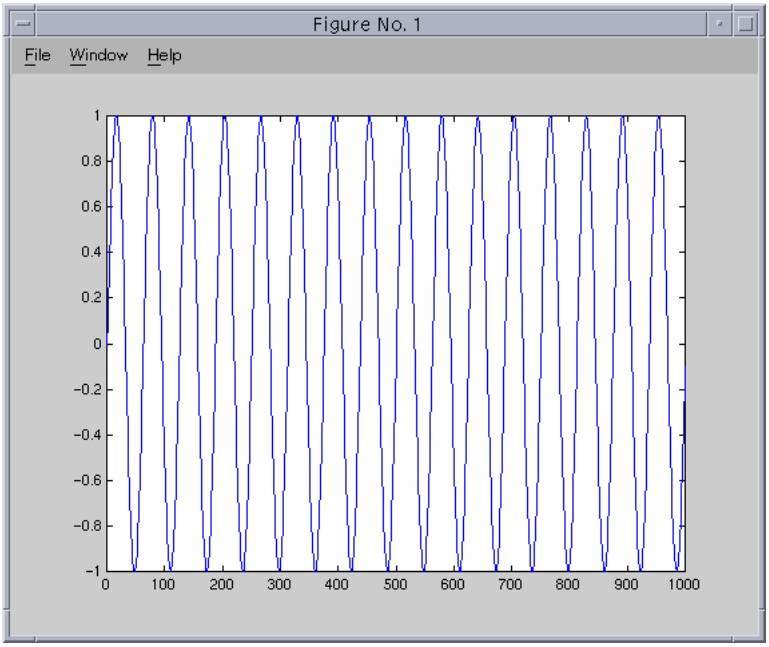
Trace4.0

>>
>> **trdestroy(tr)** % Don't forget to clean up

trputwf

This is a deprecated interface for putting waveform data into a database. Please switch to **trsave_wf**.

```
>> db=dbopen('/tmp/newdb','r+');
>> db = dblookup_table( db, 'wfdisc' );
>>
>> % Construct a fake waveform:
>> data = (0:999);
>> data = data * 32 * pi / 1000;
>> data = sin( data );
>>
>> % Construct some variables describing the waveform:
>> nsamp = 1000;
>> samprate = 20;
>> foff = 0;
>> datatype='t4';
>> dir='/tmp';
>> dfile='demo_sinewave';
>> sta='SINE';
>> chan='BHZ';
>> time = str2epoch('5/12/97 13:57:18.143');
>> endtime = tr_endtime( time, samprate, nsamp );
>>
>> % Enter the description of the waveform data into the wfdisc table:
>> db.record = dbaddv(db,'sta',sta,'chan',chan, 'nsamp', nsamp, ...
'samprate', samprate, 'time', time, 'endtime',endtime, ...
'foff',foff, 'datatype',datatype, 'dir',dir,'dfile', dfile);
>>
>> % Now put the actual data samples into the file, in the specified format:
>> trputwf( db, data );
>> % As a test, get the data back out:
>> [newdata, nsamp, t0, t1] = trgetwf( db, time-1, endtime+1 );
>>
>> plot( newdata );
>>
```

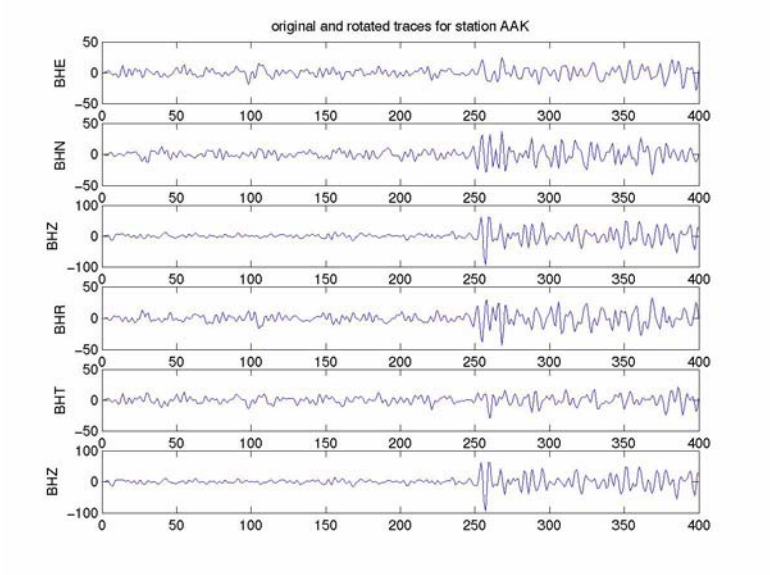


trrotate

trrotate rotates three-component traces of waveform data by the specified angles *phi* and *theta*, translating the input 'E', 'N', and 'Z' components (X1, X2, X3) into the three-component, right-handed coordinate system specified by *newchans*. *phi* is the azimuthal rotation around the X3 axis in degrees (positive clockwise looking towards negative X3). *theta* is the rotation in the X1-X3 plane about the X2 axis (positive clockwise looking towards negative X2). *newchans* is a three-element cell-array of strings, such as {'BHR','BHT','BHZ'}, specifying the channel-names of the rotated E,N, and Z components. The **trrotate** command is a direct link to the underlying C-library *trrotate*(3) command, including the return codes of that routine. There are a number of important caveats in using this routine. Therefore, if problems are encountered, one should consult the Unix man page for trrotate(3). Among these concerns is the necessity to call **trapply_calib** before calling **trrotate** on real data. Also see the routine **trrotate_to_standard**.

```
>> db = dbopen( demodb_path,'r' );
>> db = dblookup_table( db,'origin' );
>> db = dbsubset( db, 'orid == 645' ); % Pick an orid known to have waveforms

>> dbt = dblookup_table( db,'site' );
>> db = dbjoin( db, dbt );

>> db = dbsubset( db, 'sta == "AAK"' ); % Pick a station known to have an arrival

>> db.record = 0;
>> time = dbeval( db, 'parrival() - 10' );
```

```
>> endtime = dbeval( db, 'parrival() + 10' );
>> phi = dbeval( db, 'azimuth( site.lat, site.lon, origin.lat, origin.lon )' )

phi =

    2.386163334024687e+02


>> db = dblookup_table( db,'wfdisc' );
>> db = dbsubset( db, 'sta == "AAK"' );

>> tr = trload_css( db,time,endtime );
>> trapply_calib( tr ); % Probably necessary!!

>> trfilter( tr, 'BW 1 4 5 4' ); % See online example for a bug workaround

>> trrotate( tr, -1 * phi, 0, { 'BHR', 'BHT', 'BHZ' } );

>> nrecs = dbnrecs( tr );
>> for i=1:nrecs,
subplot(nrecs,1,i)
tr.record=i-1;
data=trextract_data(tr);
plot(data)
ylabel(dbgetv(tr,'chan'));
>> end
>> subplot(nrecs,1,1)
>> title( 'original and rotated traces for station AAK' );
```



>> **trdestroy(tr);**

trrotate_to_standard

trrotate_to_standard takes all traces pointed to by a trace-object and rotates them to a standard coordinate system, i.e. standard geographical coordinates comonly used in seismology where the first coordinate (X1) is positive to the East, the second (X2) is positive North, and the third (X3) is positive upward. *newchans* is a three-element cell-array of strings, such as {'BHE','BHN','BHZ'}, specifying the channel-names of the newly rotated components. The **trrotate_to_standard** command is a direct link to the underlying C-library rotate_to_standard(3) command, including the return codes of that routine. There are a number of important caveats in using this routine. Therefore, if problems are encountered, one should consult the Unix man page for rotate_to_standard(3). Among these concerns is the necessity to call **trapply_calib** before calling **trrotate_to_standard** on real data. Also see the command **trrotate**.

>> **db = dbopen(demodb_path,'r');**
>> **db=dblookup_table(db,'wfdisc');**
>> **db.record=0;**
>> **format long**
>> **[time,endtime,nsamp,samprate]=dbgetv(db,'time','endtime','nsamp','samprate');**
>> **tr = trload_css(db,time,endtime);**

>> **trapply_calib(tr);**

>> **nrecs_before_rotate = dbnrecs(tr);**

>> % Rotate all data to standard coordinates. This command actually
>> % does nothing in this case since the sample database is already
>> % aligned with E,N,Z...
>> **trrotate_to_standard(tr, {'BHE','BHN','BHZ'});**

>> **nrecs_after_rotate = dbnrecs(tr);**

>> % Since we probably only care about the newly rotated components,
>> % subset to ignore the rest:
>> **tr = dblist2subset(tr, nrecs_before_rotate:nrecs_after_rotate-1);**
>> % Do something interesting with the data....
>> **trdestroy(tr);** % Don't forget to clean up

trsave_wf

This command is the generic interface to put waveform database from a trace object into a database. For details see the Datascope man page on **trsave_wf**.

```
>> tr=trnew;
>> tr=dblookup_table(tr,'trace');
>>
>> % Construct a fake waveform:
>> amp = 10000;
>> data = amp * sin([0:999]);
>> nsamp=1000;
>> sta='SINE';
>> chan='BHZ';
>> time=str2epoch('now');
>> samprate=20;
>> endtime=tr_endtime(time,samprate,nsamp);
>>
>> % Put the waveform into the trace-object:
>> tr.record=dbaddv( tr, 'net', 'AK', 'sta', 'SINE', 'chan', 'BHZ', 'nsamp', ...
>> 'samprate', samprate, 'time', time, 'endtime', endtime );
>> trinsert_data(tr,data)
>>
>> % Save the trace data in a new database, with the underlying file in miniseed format:
>> db=dbopen('/tmp/newdb','r+');
>> db=dblookup_table(db,'wfdisc');
>> trsave_wf(tr,db,'sd','')
>> trdestroy( tr )   % Don't forget to clean up
```

trsplice

This routine attempts to splice together as many data segments as possible that are contained in the input trace object. The second argument to **trsplice** is a tolerance value: neighboring traces must be within this many samples (0.5 samples in the example below) to be considered contiguous and therefore spliceable.

```
>>  db = dbopen(demodb_path,'r');
>> db=dblookup_table(db,'wfdisc');
>> db=dbsubset(db,'sta == "CHM" && chan == "BHZ"');
>> db.record=0;
>> [time,endtime,samprate,nsamp]=dbgetv(db,'time','endtime','samprate','nsamp')

time =

   7.0614e+08


endtime =

   7.0614e+08
```

```
samprate =

   20


nsamp =

      2527

>>
>> tr=trload_css(db,time,time+10);
>> tr=trload_css(db,time+10,time+20,tr);
>> dbquery(tr,'dbRECORD_COUNT')

ans =

    2

>>
>> strtime(dbgetv(tr,'time'))

ans =

    ' 5/17/1992  21:55:15.200'
    ' 5/17/1992  21:55:25.200'

>> strtime(dbgetv(tr,'endtime'))

ans =

    ' 5/17/1992  21:55:25.150'
    ' 5/17/1992  21:55:35.150'

>>
>> trsplice(tr,0.5)
>> dbquery(tr,'dbRECORD_COUNT')

ans =

    1

>> strtime(dbgetv(tr,'time'))

ans =
```

```
 5/17/1992  21:55:15.200

>> strtime(dbgetv(tr,'endtime'))

ans =

 5/17/1992  21:55:35.150

>>
>> % do something interesting with the spliced data, most likely starting with trextract_data
>> trdestroy( tr )   % Don't forget to clean up
```

trwfname

The **trwfname** command helps generate file and pathnames for external files.When given a database row filled with information on an external file, and with *dir* and *dfile* fields that need to be filled in, **trwfname** will construct appropriate *dir* and *dfile* values, add them to the database row, create the external directories for the path if necessary, and return the resulting path. If no pattern is specified, **trwfname** uses a default pattern of information taken from the *sta*, *chan*, and *time* fields of the input row. Optionally, one can specify a different pattern for the filename and path, using the '%' escape codes from **epoch2str** and '%{field}' tokens to refer to fields in the database row. For more detail, see the Unix man page on *trwfname*(3).

```
>> output_dbname = ['/tmp/newdb_' getenv('USER')];
>> unix( ['/bin/rm -f ' output_dbname '*'] );
>> db = dbopen( output_dbname,'r+' );
>> db = dblookup_table( db, 'wfdisc' );

>> nsamp = 1000;
>> amp = 10000;
>> samprate = 20;
>> time = str2epoch( '9/30/02 11:15 AM' );
>> endtime = tr_endtime( time, samprate, nsamp );

>> db.record = dbaddv( db, ...
        'sta', 'FAKE', 'chan', 'BHZ', 'nsamp',  nsamp, ...
        'samprate', samprate, 'time', time, 'endtime', endtime );

>> path = trwfname( db )

path =

/tmp/2002/273/FAKE.BHZ.2002:273:11:15:00
```

>> **% Alternatively:**
>> **path = trwfname(db, 'Mydir/station_%{sta}/%A_%B_%o_%Y.data')**

path =

/tmp/Mydir/station_FAKE/Monday_September_30th_2002.data

>>

yearday

This command takes a Unix epoch time and returns year*1000 + day-of-year.

>> **yearday(96998400)**

ans =

1973027

>>

zepoch2str

The zepoch2str command is similar to epoch2str, however one may specify the time-zone in which one wants the result expressed. An empty string for the time-zone will default to the setting of the TZ environment variable on the host, which should be the local time-zone on a properly configured system.

>> **myepoch = str2epoch('10/13/02 12:00 am')**

myepoch =

1.0345e+09

>> **zepoch2str(myepoch, '%m/%d/%Y %H:%M:%S %Z', 'US/Alaska')**

ans =

10/12/2002 16:00:00 AKDT

>> **zepoch2str(myepoch, '%m/%d/%Y %H:%M:%S %Z', 'US/Pacific')**

ans =

10/12/2002 17:00:00 PDT

```
>> zepoch2str( myepoch, '%m/%d/%Y %H:%M:%S %Z', 'GMT-2')

ans =

10/13/2002 02:00:00 GMT

>> zepoch2str( myepoch, '%m/%d/%Y %H:%M:%S %Z', '')

ans =

10/12/2002 16:00:00 AKDT

>>
```

Differences between the Matlab Antelope Toolbox and other Antelope language interfaces

The Matlab Antelope toolbox differs in several aspects from the Antelope language interfaces in C, Tcl, Fortran, and Perl. First, the natural mode of operation in Matlab is to work on entire arrays at once. Therefore, where possible, Antelope database commands have been expanded to read in entire matrices of results when appropriate (e.g. **dbgetv**), or to act on entire matrices at once (e.g. **epoch2str**). Similarly, where naming conventions permit, parameter-files may be loaded wholesale into Matlab structures with **pf2struct**, and database tables may be loaded into structures with **db2struct**.

Special options to Antelope commands are usually specified with string input arguments, such as 'backwards' for **dbfind**. In many cases the order of placement of these options is important--see the help pages on each command for details.

The most general interface to Antelope, the C language interface, allows temporary views to be given user-specified names. This feature is not supported in the current release of the Matlab toolbox.

Caveats

This toolbox was developed on Sun-solaris 2.6, Matlab version 5.3. It has not been tested with other platforms and versions. The current version is tested against Sun Solaris 2.8, Linux with the 2.4 kernel, and Matlab 6.5.

Several aspects of this current beta release must be treated with caution. First, the database-pointer DBPTR and trace-pointer TRPTR objects refer to databases and memory open by the underlying Antelope libraries. Freeing these objects with the Matlab clear command does not appropriately close the underlying databases, nor free the corresponding memory. These objects must be removed from the Matlab workspace with the DBCLOSE and TRDESTROY commands provided. Note that the DBPTR and TRPTR structures are not objects in the Matlab sense--the word is being used loosely here, paralleling the Datascope documentation (for the trace objects). Conceptually they are very similar to objects, though the user can see and manipulate the private variables directly (useful, for example, to loop over the DBPTR.record field), and also there is no Matlab class tag. These items have been kept as Matlab structures rather than Objects to preserve similarity between the Matlab Antelope toolbox and other programming interfaces for Antelope.

The parameter-file objects actually are Matlab objects. Again, though, they must be cleared carefully. The clear function is overloaded for the DBPF class of Objects, however at least in Matlab 5.2 the command/function duality is broken by the CLEAR command, and apparently the generic CLEAR command is not smart enough to call the overloaded methods for DBPF objects. One must specifically call the CLEAR function (i.e. use parentheses around the argument), or the equivalent PFFREE function, on the DBPF object. Also, the pf routines may at times return derivative DBPF objects, representing complex entries in the parent parameter-file (DBPF object). These first of all are not allowed to be cleared by the PFFREE command. Second, they lose meaning but unfortunately stay resident when the parent DBPF object (the one returned when the whole parameter file was read in) is cleared. Acting on them after destroying the originating DBPF may produce unpredictable results.

There are a lot more trace-library commands available, many of which have not yet been implemented.

The response-file objects are also actually Matlab objects. Just as with the DBPF objects, these need to be explicitly cleared with the overloaded clear functions, CLEAR(DBRESPONSE) or equivalently FREE_RESPONSE.

While the doc command works for Antelope Toolbox commands, the Matlab helpdesk search engine does not yet recognize them. In order to search for Antelope Toolbox commands, use the matlab **lookfor** command or the search window in the Matlab **helpwin** help window.

Unlike the other Antelope language interfaces, the Matlab **dbeval** is able to return entire columns of values if the input database pointer refers to more than one row. As a standard feature, dbeval can return values that are aggregate expressions over the whole table such as max(). If more than one row is passed to such an aggregate expression in Matlab, the aggregate expression will be recalculated for each row, which redundancy can cause huge performance drops for a large database. Therefore, unless otherwise necessary, the user should avoid passing multiple rows to **dbeval** when using aggregate expressions. See the Unix dbex_eval(3) man pages for the list of aggregate functions in the Antelope expressions calculator.

The Matlab interface to the orb routines is fairly new, and though tested, the Matlab toolbox routines have not been extensively used in implementation. There is the possibility of some change if initial experience shows any inconveniences.

Author

The Antelope Software system, including the Datascope relational-database management system, is a product of Boulder Real-Time Technologies, Inc., http://brtt.com/

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