New features in ibaAnalyzer v6.3.0

1 HD Server integration

In ibaAnalyzer 6.3.0 it is possible to query data from iba HD servers. An 'HD query dialog' is implemented that allows one to specify a HD server and HD store, connect to it, preview signals and select a time range along with a desired sample rate.

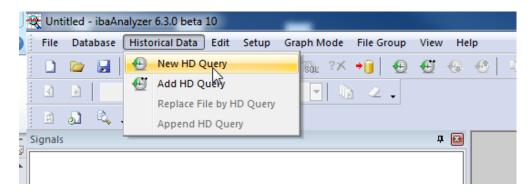
The result of the query is represented in ibaAnalyzer as a pseudo .dat file. This pseudo .dat file is similarly structured as an actual .dat file and basically any operation you can perform in ibaAnalyzer on regular .dat files (visualizing signals, performing calculations, reporting, extracting, ...) can be performed on the pseudo .dat files as well.

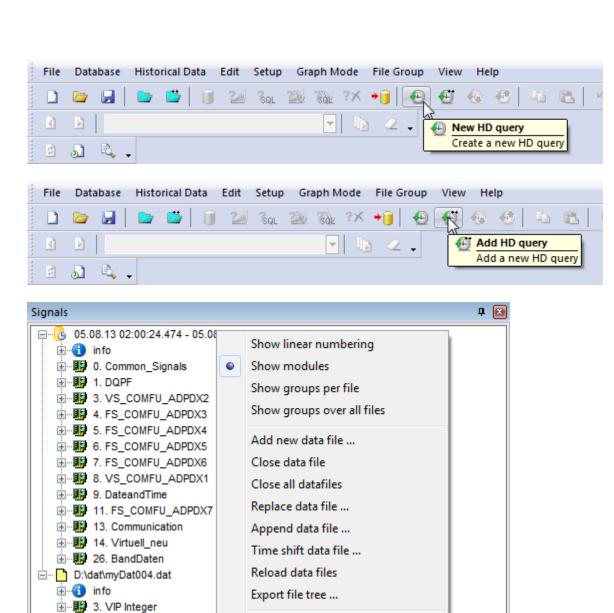
1.1 Menu and toolbar commands

A new group of commands is available in ibaAnalyzer that allows interaction with HD servers. In the ibaAnalyzer main menu there is a new submenu titled 'Historical data' and a new toolbar button group is added to the toolbar as well. The commands available are:

- <u>'New HD Query'</u>. This will open the 'HD query dialog' where one can specify the desired data store, time range and additional parameters. After setting all options and acknowledging the dialog a pseudo .dat file will be opened in the first slot in the signal tree
- 'Add HD Query'. This is similar as 'New HD query', but the resulting pseudo .dat file will be placed in the first available free file slot in the signal tree.
- <u>'Replace File by HD Query'</u>. Also opens the HD data query dialog but the resulting pseudo .dat file is placed in the file slot that is selected in the signal tree, this will be either a previously opened .dat file or a previously opened HD data query. The .dat file or pseudo .dat file already present will be closed by this operation.
- <u>'Append HD Query'</u>. Also opens the HD data query dialog but the resulting pseudo .dat file will be 'appended' to the .dat file or pseudo .dat file present in the file slot selected in the signal tree. This is entirely similar as how ordinary .dat files can be appended.

The latter three commands are also available in the context menu when one right clicks the signal tree. Note that these commands are similar to the commands for opening .dat files in the 'File' submenu ('Open Data File', 'Add New Data File', 'Replace Data File' and 'Append Data File' respectively). Pseudo .dat files can be closed from the 'File' submenu ('Close Selected File' or 'Close All data files') or from the signal tree context menu. Also from the file submenu or signal tree context menu, regular .dat files can be appended to pseudo .dat files or replace the pseudo .dat files.





Add new HD query...

Append HD query ...

Import file tree ...

Export ...

Replace we by HD query ...

⊕.... 5. Virtual

± ... 7. ibaCapture-CAM

1.2 The HD query dialog

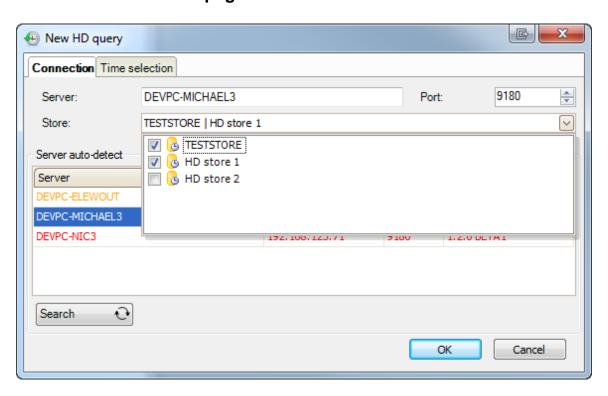
The *HD query dialog* currently has two tab pages:

- The first page contains all controls to specify the necessary parameters to connect to a HD server and select a particular data store on that server. This first tab page is titled 'Connection'.
- The second page contains the controls to preview signals and select an appropriate time range and sample period. This second tab page is titled '*Time selection*'.

Additional tab pages with more advanced options (e.g. event store querying) will be added in future implementations.

Any options you specify in the query dialog are persistent; after performing a successful query, the next time you visit the HD query dialog, the HD connection parameters, previewed signals, selected time range and preferred sample period will be already selected and the *'Time selection'* page will be automatically selected.

1.2.1 'Connection' tab page



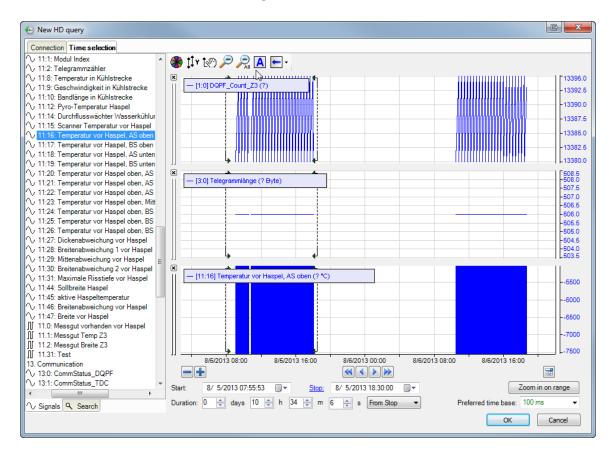
Here you specify the parameters to connect to the HD data store, the page has the following components:

- Server: Specify here the HD Server name or IP address.
- Port: Specify here the TCP/IP port.
- Store: Here you can select one or more time based stores on the HD server. There is a dropdown list where you can check the stores from if you have specified a valid *Server*. Each selected store will be returned as a separate pseudo .dat file in the signal tree. You can chose to select no stores in which case all stores will be opened as separate pseudo .dat files in the signal tree.

- When to the dialog is visited through 'Replace File by HD Query' or 'Append HD Query', a single store must be selected, an appropriate error message will be given when trying to acknowledge the dialog with multiple or no stores selected.
- <u>Server auto-detect</u>: This will list the detected HD servers on the network; you can select one to update the 'Server field'. Although all servers will be listed, only servers with Version 1.3.0 or later are supported. When trying to connect to a server that is earlier than 1.3.0 an appropriate error message will be given.

An actual connection to the HD server will happen when you switch from the 'Connect' to the 'Time selection' tab page. An appropriate error message will be given if the connection failed.

1.2.2 'Time selection' tab page



The 'Time selection' has the following controls:

- A signal tree: This shows the signals present in the HD stores, here one can select a number of signals that will be shown in the preview trend graph by dragging them to the preview or double clicking the signals. A search tab is also present to search on the name or in the comments of a signal.
- An HD trend graph view: Here a preview of the signals is shown.

 A toolbar is present containing the usual buttons also present in the ibaPDA client, except that the button to pause or resume the live mode is absent because the preview is permanently in paused mode.

The view contains the usual time navigation controls also present in the ibaPDA client:

- A time axis that can be scrolled to zoom in or out and panned to move the time range further or back.
- o A minus and plus button to zoom out or in by a fixed configurable amount.
- Step buttons to navigate further or back by fixed configurable amounts.
- A date time picker.
- A Start and Stop marker. Two green markers are depicted on top of the graphs in the preview. With these markers a time range can be selected by dragging them.
 - The mouse cursor changes if one moves the mouse over the markers:

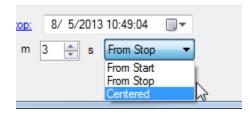
 o

 is shown when one is over the Start marker.
 - o is shown when one is over the Stop marker.

You can press and hold the shift key while dragging the markers to keep the length of the selected time range constant.



- A date-time picker is present to select the <u>Start</u> of the selected time range. When dragging the Start marker the value displayed in the date-time picker will change accordingly. Likewise editing the time in the date-time picker will reposition the Start marker on the X-axis.
- A second date-time picker is present to select the end of the selected time range. It is labelled <u>Stop</u> and is linked to the Stop marker in the same way that the Start date-time picker is linked to the Start marker. The label in front is blue and underlined, which means it is a link-label and hence clickable. When clicking on the label, the Stop marker and date-time picker are positioned on the current date and time, also all signals should be updated with any new data available in the HD server. While clicking on the label, you can press and hold the shift key to keep the length of the selected time range constant.
- A button to zoom in on the selected <u>range</u> is present. The Start and Stop marker are 'anchored' to the X-axis, which means that they stay on the same time stamp if you zoom in our out. By clicking the button, you adapt the zoom range so that the Start marker is at 1/4th of the zoom range and the Stop marker at 3/4ths. This does not change the selected time range.
- Following a label with the text <u>duration</u>, four numeric fields are present to display the length of the selected time range in days, hours, minutes and seconds. These fields are updated when you move the markers. They are editable and will move the markers. Which one of the markers will move depends on the next control (see next item in this list).
 - You can press and hold the Control key while editing the duration fields, this causes the other fields besides the one you are editing to be set to zero.
- Next to the duration fields is a drop down list where you can select the *reference* to determine how to move the markers when adapting the duration fields. It has the following options
 - o <u>From Start:</u> The Start marker will remain stationary while the Stop marker moves to accommodate for the selected duration.
 - o <u>From Stop</u>: The Stop marker will remain stationary while the Start marker moves to accommodate for the selected duration. This option is the default.
 - <u>Centered</u>: Both markers will move; the center of the selected range will stay stationary.



There is a dropdown list labelled "<u>Preferred time base</u>" where one can select the sample period that the loaded signals would preferably have. The HD server will try to match the preferred time base as well as possible, see the next paragraph (paragraph 1.2.3) on how the HD server will try to match the preferred time base.

Note that the dates and times depicted on the X-axis of the preview and in the date-time pickers are all local system time.

1.2.3 Signal sample periods and "preferred time base"

One can select the preferred time base in the HD query dialog. However the actual sample period that the signals will have depends on the levels still stored on the HD server. If no finer level is available than the selected preferred time base (e.g. because the signal was originally sampled at a coarser sample rate or the finer levels have been removed by the HD server clean up), the finest sampled level still available will be returned.

If both a coarser and a finer level are available, the coarser level will be selected if the following inequality is true:

$$\frac{sample \ period \ of \ coarser \ level}{preferred \ time \ base} < \frac{preferred \ time base}{sample \ period \ of \ finer \ level}$$

Otherwise the finer level will be selected.

The dropdown list in the HD query dialog has a list of predefined time bases to choose from. They are in natural units (seconds, minutes, hours, days) or powers of 10 times the natural time units.

Depending on the selected time range, the smaller time bases might be inappropriate as loading signals over the selected time range and time base would require too much memory. Hence a colour scheme is applied in the drop down list:

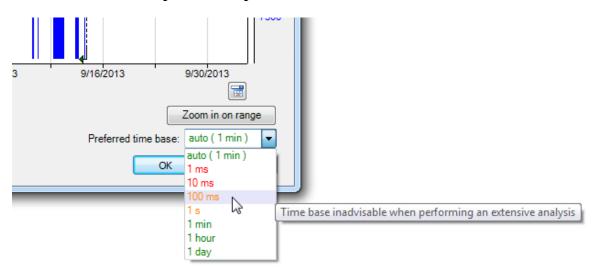
- Red: This means loading signals with the currently selected time range and the candidate time base would require more memory than ibaAnalyzer can safely allocate. When selecting such time base without altering your selected time range, an error message will be given when trying to acknowledge the dialog with the 'OK' button. After dismissing the error message, one will be returned to the *time selection* page where one then has the option to select a different time range or time base.
- Orange: This means ibaAnalyzer can safely allocate memory when loading signals with the currently selected time range and the candidate time base provided one does only a limited analysis; i.e. only a couple of signals or expressions can be shown. When selecting such time base without altering your selected time range, a warning message will be given when trying to acknowledge the dialog with the 'OK' button; however one will be able to proceed anyway.

- Green: This means ibaAnalyzer does not anticipate problems when loading signals even when an extensive analysis is performed.

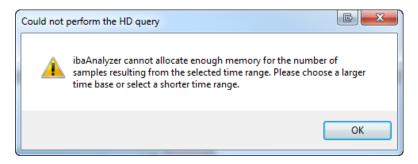
Each item in the dropdown list has a tooltip describing the meaning of the colours.

Additionally the dropdown list has the option 'Auto' at the top of the list. Selecting this option means that the smallest time base should be chosen that is still green when performing the query. The actually selected time base is mentioned in the Auto item between brackets.

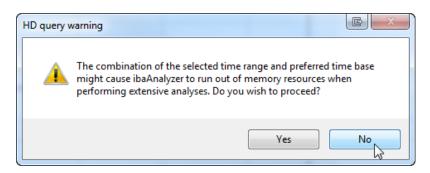
Colour scheme + Auto option + tooltip



Error message when selecting a red time base

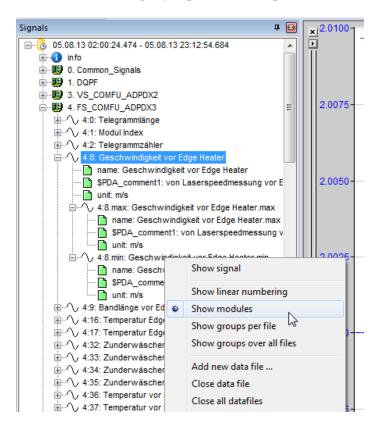


Warning message when selecting an orange time base

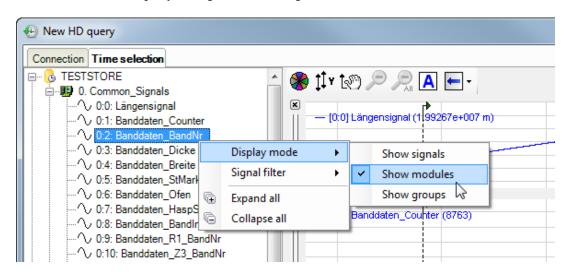


1.3 Pseudo .dat files

The result of an HD query is presented as a pseudo .dat file in the ibaAnalyzer signal tree.



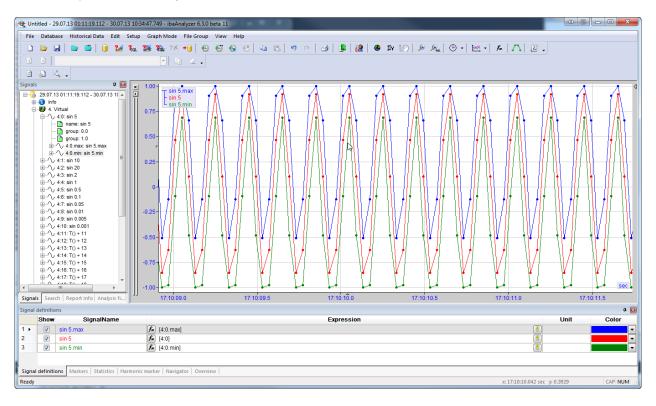
Like ordinary .dat files, one can show the signals flat (*Show linear numbering*), grouped in modules or grouped in groups (if any are defined) by selecting this in the context menu. Note that changing the option in the context menu of the ibaAnalyzer signal tree will cause the signals in the signal tree of the HD query dialog (time selection page) to be grouped the same the next time you visit the HD query dialog. Likewise changing the "*Display mode*" of the signal tree in the HD query dialog (also through a context menu) will cause ibaAnalyzer to group signals in the same manner after the HD query dialog is acknowledged with the 'OK' button.



From the signal tree, one can double click or drag and drop signals to the recorder view to depict the signals, just like one can with ordinary .dat files.

One can also perform calculations by creating expressions or logicals. In expressions, HD signals are referenced identically as signals in a .dat file. Hence if one has both a file data store and HD data store in ibaPDA, any analysis on the .dat files can be applied on the HD queries as well.

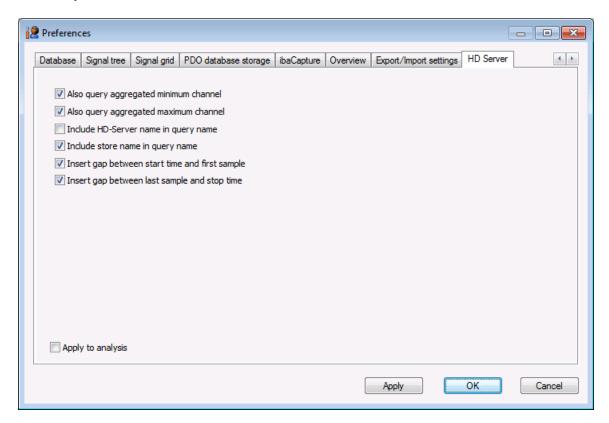
Depending on your preferences (See paragraph 0) each signal in the signal tree will have up to two sub signals available tagged 'max' and 'min'. This is entirely identical to signals queried from a database if one has selected to store the maximum and minimum aggregates; the main signal corresponds with the average aggregated signal, while the sub channels tagged 'max' and 'min' correspond with respectively the maximum and minimum aggregated signal. When the finest level on the HD server is queried (i.e. with the same sample period as the signals were acquisitioned) the three signals are the same and ibaAnalyzer is optimized to not use more memory than for one signal.



A note on the memory usage of ibaAnalyzer; only signals that are referenced in the analysis (i.e. they are used in an expression or the signal itself was visualized) are stored in memory and the signal is stored in memory entirely. Zooming in or out or panning does not cause data to be loaded from the HD server (contrary to PDA).

1.4 HD preference options

Some options can be set that affect what signals are present in the .pseudo .dat file and how they are loaded and visualized. For preferences to be applied to new analyses, these options are available currently in the last tab page of the preferences dialog. The tab page is titled 'HD server'. An identical page is present in the settings of the current analysis; changing settings there causes any current HD data to be reloaded.

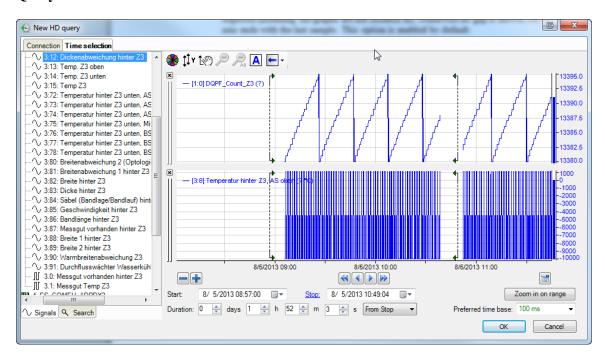


The options are:

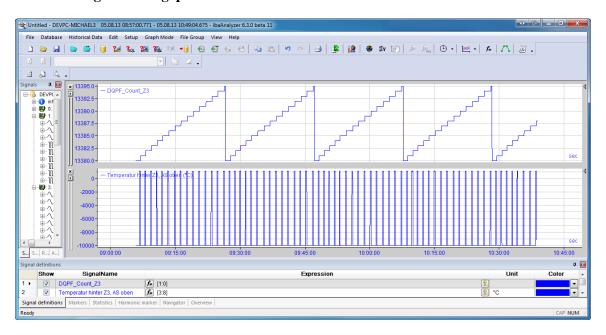
- Also query aggregated minimum channel: Disabling this option will make the 'min' sub channel unavailable. When loading signals, the normal (average) signal, minimum signal and maximum signal are loaded all at once unless one or more of the sub channels is disabled. Hence disabling this option can save some memory. This option is by default enabled.
- <u>Also query aggregated maximum channel</u>: Similarly one can disable the 'max' sub channel. This option is by default enabled.
- Include HD-Server name in query name: In the name of the pseudo .dat file, by default the HD server name, the store name and the start and stop time of the queried range is mentioned. One can shorten the name by disabling this option in which case the server name is removed from the pseudo .dat file name. This option is disabled by default.
- <u>Include store name in query name:</u> One can shorten the pseudo .dat file name even further by disabling this option which will cause the store name to be omitted. This option is enabled by default.
- <u>Insert gap between start time and first sample:</u> If one queries over a time range where there is no data on the HD server in the initial part of the time range, enabling this option will cause a 'gap' to be shown between the start-time and the first sample when signals

- are depicted (assuming the graphs are not zoomed in). Otherwise no gap is shown, i.e. the X-axis starts with the first sample. This option is enabled by default.
- Insert gap between last sample and stop: If one queries over a time range where there is no data on the HD server in the final part of the time range, enabling this option will cause a 'gap' to be shown between the last sample and stop-time when signals are depicted (assuming the graphs are not zoomed in). Otherwise no gap is shown, i.e. the X-axis ends with the last sample. This option is enabled by default.

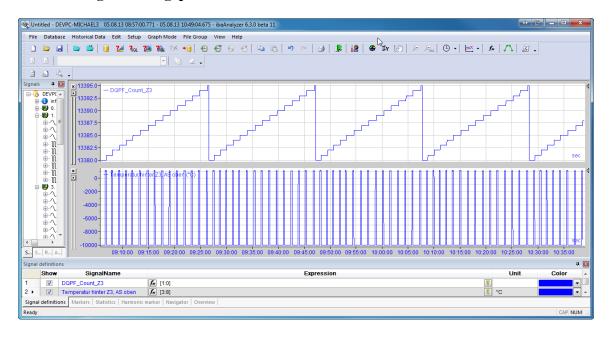
Query:



Visualized signals with gaps enabled:



Visualized signals with gaps disabled:



1.5 Drill down

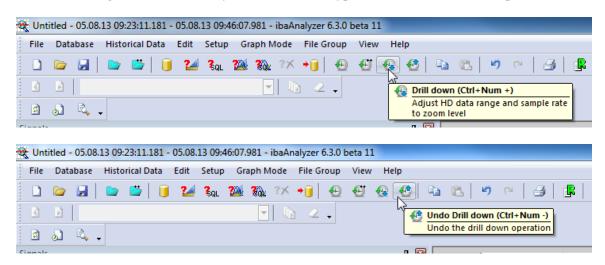
Contrary to the ibaPDA client, zooming in or out on the signals does not cause the signals to be automatically reloaded from the HD server on a finer or coarser level.

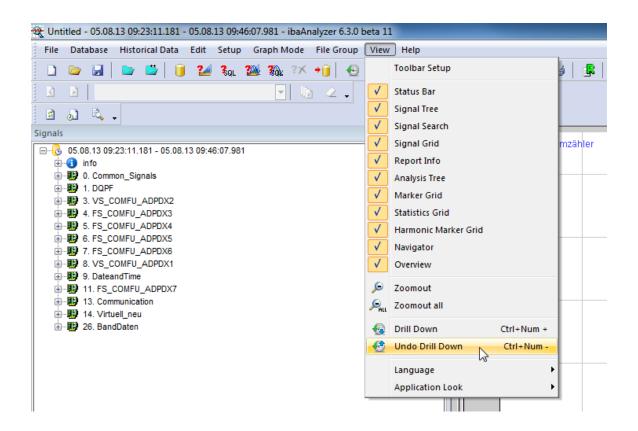
However, when zoomed in, one can perform a 'drill down' operation, which causes the selected time range and preferred time base to be adapted to the current zoom level and the HD data to be reloaded.

A stack of 'drill down' operations is maintained, each subsequent drill down operation can be 'undone' to restore the time range and preferred time base to the previous level.

One performs a 'drill down' operation or one undoes one by clicking the button from the toolbar or selecting the operation from the View submenu. Also keyboard shortcuts are defined:

- Pressing Ctrl and the '+' key on the numeric keypad performs a 'drill down' operation.
- Pressing Ctrl and the '-' key of the numeric keypad undoes a 'drill down' operation.





The 'drill down' operation is only executed for the pseudo .dat files where one or more of the channels in the currently selected graph are dependent on; i.e. the currently selected graph must contain either a signal of the pseudo .dat file or it must contain an expression that has a sub expression that is dependent on the pseudo .dat file. Likewise 'drill down' operations can only be undone for the pseudo .dat files that have a dependent channel in the currently selected graph.

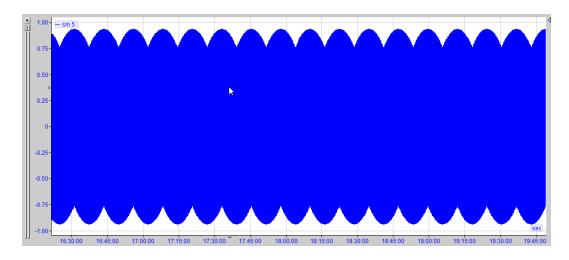
When performing a 'drill down' operation, the pseudo .dat file is replaced by the result of an HD query with the following parameters:

- The same HD server and store
- A time range equalling the current X-axis zoom range.
- A preferred time base calculated from the following formula

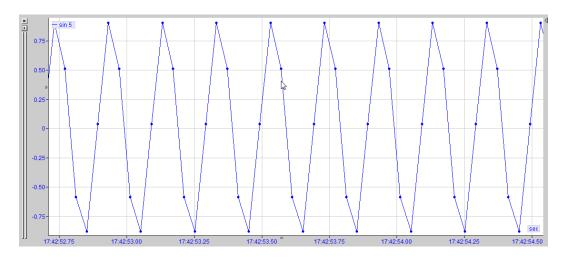
 $new\ preferred\ time\ base = \frac{zoomed\ time\ range\ length}{old\ queried\ time\ range\ length} \times old\ preferred\ time\ base$

This way the amount of data loaded stays roughly the same.

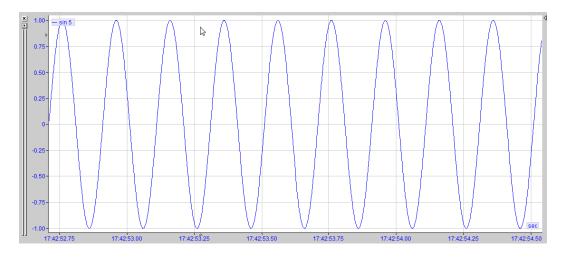
Unzoomed



Zoomed

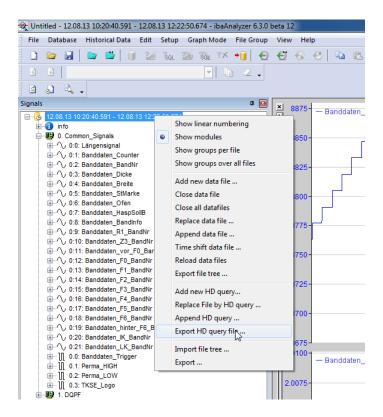


Drilled down

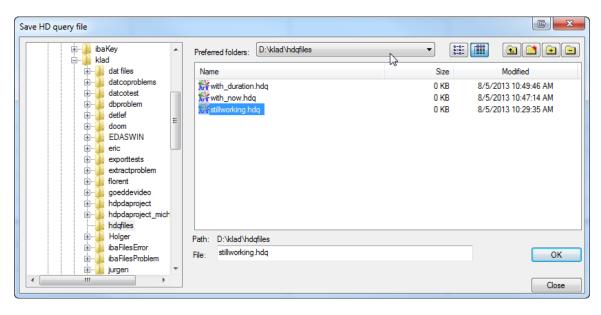


1.6 HD query files

The parameters to open a HD query can be saved to a small text file. One does this by right clicking on an opened pseudo .dat file and selecting the option "Export HD query file ..." from the context menu.



This opens a file save dialog where the location and name of the file can be specified. The file save dialog is similar to the dialog ibaAnalyzer presents when exporting or extracting text or .dat files, hence the location where you last saved will be remembered and you will have access to your preferred ibaAnalyzer folders.



The query files have extension .hdq (Historical Data Query). and this extension is registered with windows during ibaAnalyzer install. The query files have the following icon:



The query files can be opened in ibaAnalyzer just like they were .dat files:

- Double clicking them in explorer will immediately start ibaAnalyzer and perform the HD query.
- One can drag and drop the query files into ibaAnalyzer like they were .dat files. Dropping them on the signal tree allows one to immediately append the resulting pseudo .dat file to an already opened (pseudo or regular) .dat file.
- Recently opened query files are present in the recent file list along with recently opened .dat files.
- They can be opened from the ibaAnalyzer file open dialog, along with fully functioning preview of the signals.
- They can be opened from the command line, simply specify the file name after the executable. This can be freely mixed with other query files, .dat or text files or other ibaAnalyzer commands.

A query file can be edited in a text editor or it can be generated by a script or program.

The contents of a query file might look like this:

```
[HDQ file]
portnumber=9180
server=DEVPC-MICHAEL3
starttime=05.08.2013 09:04:34.544000
stoptime=05.08.2013 10:27:15.793000
store=FSQDR_TKSE
timebase=0.01
type=time
```

The first line is a mandatory header line having the text "HDQ file" between square brackets ("[...]"). This is followed by a number of parameters. Each parameter is a key-value pair as in a windows .ini file, i.e. the name of the parameter followed by its value separated by an '=' sign. The parameters do not need to be in any order and the key name is not case sensitive.

The following parameters exist:

- <u>type</u>: the type of the HD query. Currently only 'time' is supported but more types will be supported in the future (length-based, events). This parameter is mandatory.
- <u>server</u>: the name or IP address of the HD Server to connect to. This parameter is mandatory.
- <u>portnumber</u>: the port number ibaAnalyzer will use to communicate with the HD server over the TCP/IP protocol. This parameter is mandatory.
- store: the name of the store to query from the HD Server. This parameter is mandatory.

- starttime: the start time of the desired time range in local system time. The value needs to be formatted as an ibaAnalyzer timestamp: a date separated from a time by a space. The date must be formatted as 'dd.MM.yyyy', i.e. two digits for the day, two digits for the month and four digits for the year, each separated by a dot ('.'). The time must be formatted as 'HH:mm:ss.fff", i.e. the hours must be two digits in 24h format, the minutes and the integral part of the seconds are also two digits each. Hours, minutes and seconds are separated by a column sign (':'). The seconds part may have a decimal part of any digits, as decimal symbol a dot ('.') must be used.
- <u>stoptime</u>: the stop time of the desired time range in local system time. The value needs to be formatted as an ibaAnalyzer timestamp similar as the start time parameter. Rather than specifying a time stamp you can also specify the text "now". These means that the current time will be taken as stop time.

This parameter is mandatory if no 'duration' parameter is present (See below)

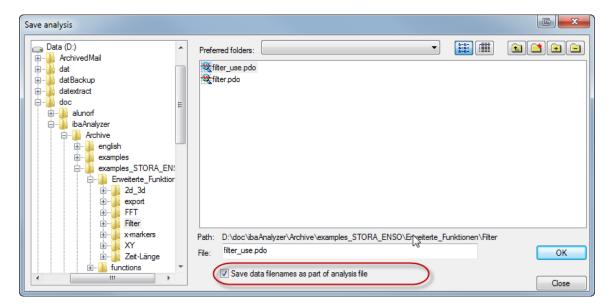
- timebase: the preferred sample period in seconds. Use a dot (".") as decimal symbol.

Besides the above standard parameters, two additional parameters can be specified:

- <u>temporary</u>: include this parameter with value equaling '1' (i.e. include the line "temporary=1"), to make the query file 'temporary'. This means that ibaAnalyzer will delete the file as soon as it has finished the HD query.
- <u>duration</u>: length of the desired time range in seconds. Use a dot (".") as decimal symbol if required. If this parameter is present, ibaAnalyzer will behave differently depending on the presence of the 'starttime' and 'stoptime' parameters:
 - o If only the 'starttime' parameter is present, a range starting at 'starttime' and lasting 'duration' seconds will be queried.
 - o If only the 'stoptime' parameter is present, a range ending at 'stoptime' and starting 'duration' seconds earlier will be queried.
 - o If both 'starttime' and 'stoptime' are present, a range centered on the middle of 'starttime' and 'stoptime' will be queried. The length of the range will be 'duration' seconds.
 - o If neither 'startime' or 'stoptime' is present, the query file will be considered invalid and an error message will be given by ibaAnalyzer when attempting to open the file.

1.7 Saving HD Queries in an analysis

When saving your analysis through 'Save Analysis as' you have the option to 'Save data filenames as part of analysis file'



For ordinary .dat files, checking this option causes the .dat file location to be saved in the analysis so that on opening the analysis, the .dat file is loaded if found.

For pseudo .dat files resulting from an HD query, checking this option causes the necessary parameters to be stored in the analysis, so the HD query is performed again when opening the analysis.

Note that if the HD query was performed by opening an HD query file, the actual query parameters will be stored in the analysis and not the location of the .hdq file.

1.8 Exporting / Extracting HD Queries

HD Query results can be exported and extracted similarly as ordinary . dat files.

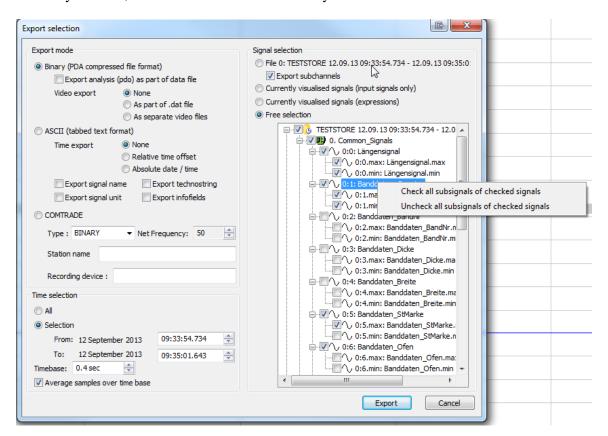
1.8.1 Export dialog

The time base parameter (in the Time selection group, bottom left) will be initially set to the smallest time base of all loaded channels. If no channels are loaded yet, the desired time base given at the time of the query in the HD dialog is chosen.

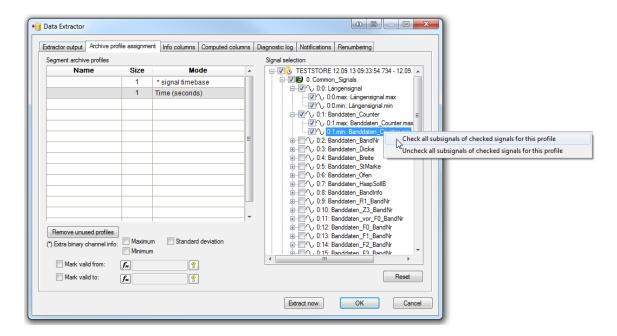
In the groupbox "Signal selection" under the first radio button option "File ..." an additional option labeled 'Export sub channels' is available. When selecting the first radio button option Sub channels will be exported if and only if this checkbox is checked.

When choosing either of the "Currently visualized signals..." options, the subchannels will only be extracted if the subchannels are visualized as well. If a subchannel is visualized but its parent channel is not, the parent channel will be exported anyway.

When choosing "Free selection", you have to select or deselect the subchannels in the signal tree yourself. However, the options to check or uncheck the subsignals of currently checked signals are available from a context menu when right-clicking on the signal tree. By default, for each channel you select, the subchannels are automatically selected.



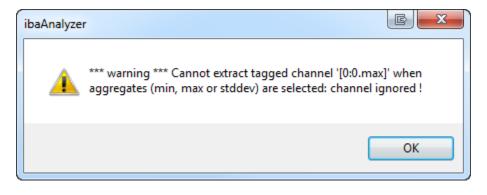
1.8.2 Extract dialog



When extracting to .dat file, subchannels behave similar as they behave in "Free selection" in the export dialog, a similar context menu is available when right-clicking on the signal tree.

When extracting to database, the subchannels are not available as currently the database tables do not provide a way to store subchannels other than the subchannels obtained from selecting aggregates.

Selecting aggregates (below the archive profiles tables) and subchannels are incompatible, if you have selected subchannels and aggregates simultaneously for a given profile, a warning message will be given during the extract and the subchannel will be skipped.

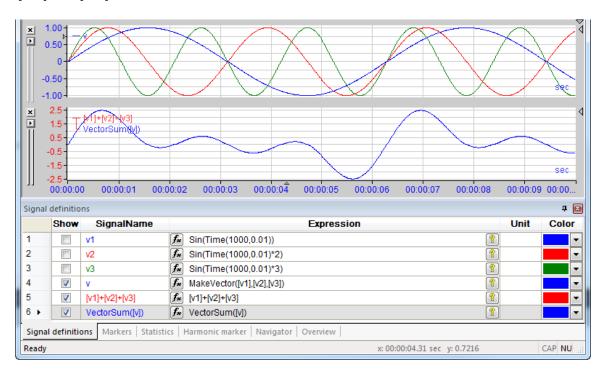


2 New functions

Note, these functions were implemented in version 6.1.1 of ibaAnalyzer but haven't been documented in a "New features" document until now.

2.1 VectorSum function

This function is similar to the VectorAvg function, but rather than taking the averages, it simply sums the elements of the vector in cross-profile direction. For example if a vector 'v' consists out of three signals 'v1', 'v2' and 'v3', then VectorSum([v]) will return the signal [v1] + [v2] + [v3].



The function takes only one parameter, namely the vector to sum the elements from.

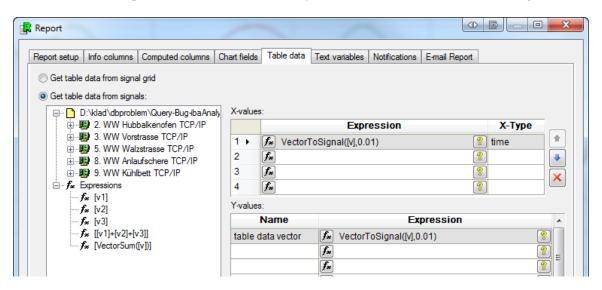
2.2 VectorToSignal function

This function creates a (1 dimensional) signal from the elements of a vector. Each sample of the resulting signal corresponds with an element in the vector. The elements in the vector are expected to be constant signals, if they are signals that vary over time, they will be averaged first before being used as samples in the resulting signal.

The function takes two parameters:

- <u>Vector</u>: The vector to take the samples from.
- XBase: The sample rate of the returned signal.

This function was implemented to be used in the "Table data" tab of the report generator in the case that the data required to feed the tables is only available as a vector rather than a signal.

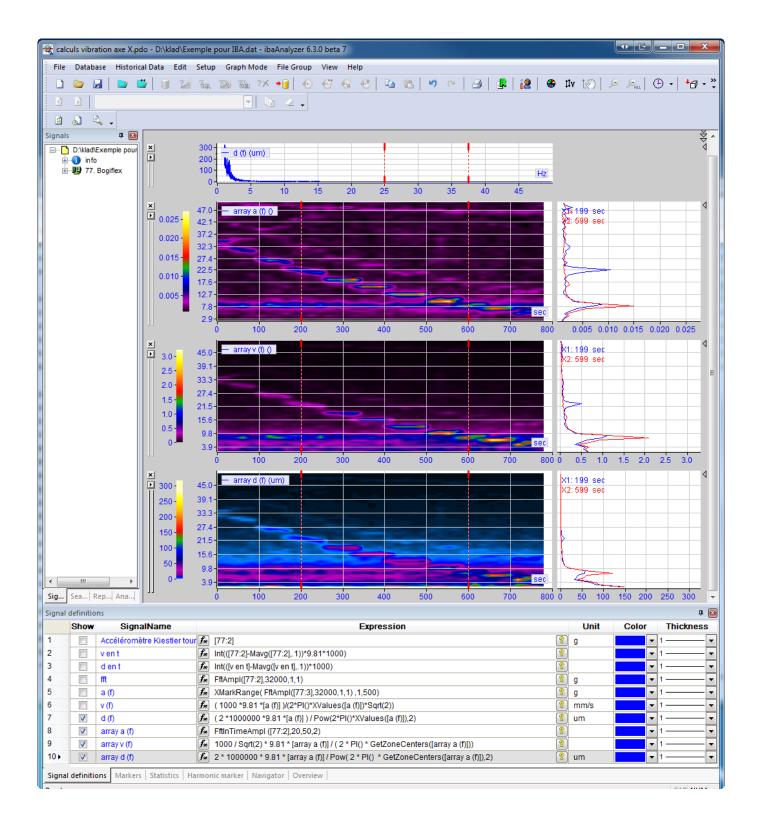


2.3 GetZoneCenters

Since ibaAnalyzer 6.1.0, 'zones' with a particular width can be associated with the elements of a multidimensional signal or vector. This allows for cross profile plots where the signals are non-equidistantly spaced, most commonly used when the measurement locations along the cross profile are non-equidistantly spaced either. There was already a function GetZoneWidths available that would return the widths of the zones associated with a multidimensional signal or vector, now there is also a function available that returns the centers of the zones, taking into account any offset that might have been specified in the *logicals* dialog.

The function takes only one parameter, namely the vector from which to take the associated zone centers from.

This function is particularly useful when applied to the result of an *FftInTime* function. The *FftInTime* function returns FFT results with 'zones' corresponding to frequency bins. Hence the *GetZoneCenters* function can retrieve the frequency vector of such results. This allows for differentiation or integration in the frequency domain by respectively multiplying or dividing the *FftInTime* result with the *GetZoneCenters* result.



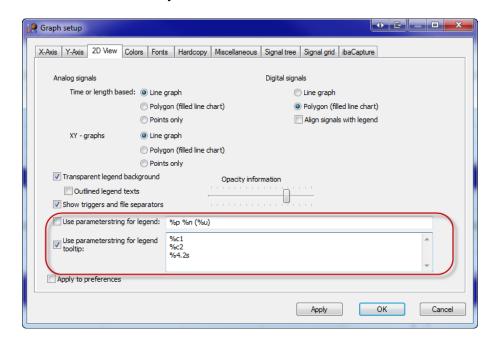
3 Miscellaneous new features

3.1 Parameterizable legend tooltips

The tooltip shown when hovering over a legend is *parameterizable* similar as the legend text itself. In previous versions of ibaAnalyzer, only comments (parameters 'c1' and 'c2') where shown as a tooltip and if no *parameterstring* is enabled, the behavior is still the same.

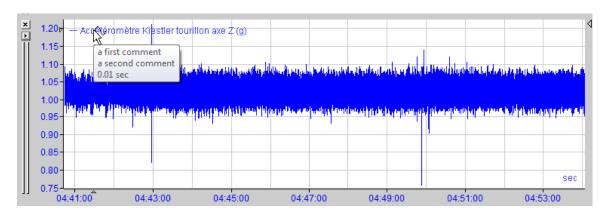
The format string can be specified in 'Graph Setup'→'2D view'

Preferences for new analysis can be set in 'Preferences'→'2D view'



A new parameter "%s" is available that corresponds with the signal sample period (both for the tooltip and the original legend text).

Note that the tooltip can consist of multiple lines; hence the format string for the tooltip can consist of multiple lines as well.



3.1.1 Numeric formatting of parameters

For parameters that translate to numeric values ('%x1', '%x2', '%dx', '%y1', '%y2', '%dy' and '%s') one can specify a width and precision between the percent sign and the parameter name. The two values are separated by a dot.

This is similar as width formatting by the 'printf' statement in C programming languages:

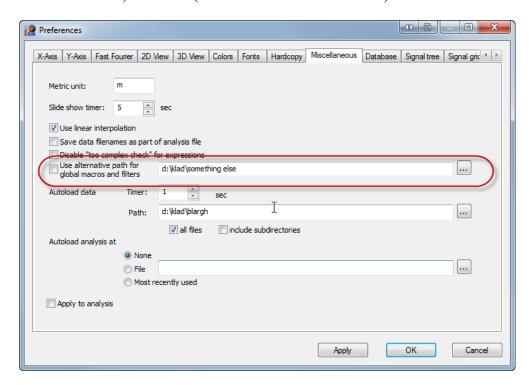
- The 'width' parameter is the minimum number of characters to be shown. If the value to be printed is shorter than this number, the result is padded with blank spaces. The value is not truncated even if the result is larger.
- The '.precision' is the number of decimal digits behind the decimal separator.

E.g. "%4.2s" means that the sample period will be shown, at least 4 characters will be visible and 2 digits will be behind the decimal point.

If the width and .precision parameters are omitted, the numerical value will be formatted depending on your ibaAnalyzer settings and the zoom level of the graph. This is the same formatting as in the marker grid or axis labeling.

3.2 Alternative path for macros and filters

An alternative path can be specified for the location ibaAnalyzer loads it macros (files with the extention '.mcr') and filters (files with the extension '.fil') from.



The path can be specified in 'Setup' → 'Miscellaneous' Preferences for new analyses can be set in 'Preferences' → 'Miscellaneous'

3.3 Resizable controls

The grids in the *macro design* dialog and the *logicals* dialog are now resizable, allowing for more or less space to edit the expressions.

