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A.2.1 Managing humid and semi-humid ecosystems**

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(HKHdip) Version 4.0

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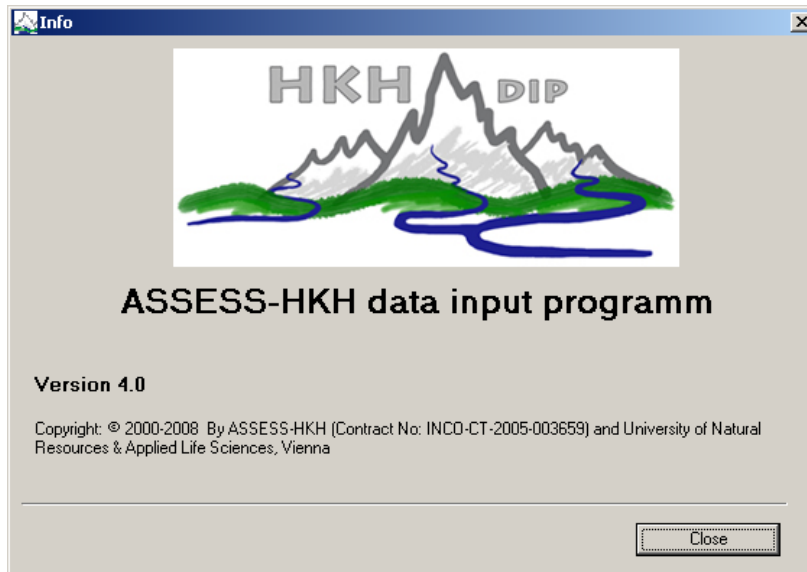
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PU	Public	✓
PP	Restricted to other programme participants (including the Commission Services)	
RE	Restricted to a group specified by the consortium (including the Commission Services)	
CO	Confidential, only for members of the consortium (including the Commission Services)	

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www.aqem.de



www.eu-star.at

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INSTALLATION AND FIRST RUN

- Installation of the HKHdip starts by running the setup.exe.
- The setup is installing the program to a folder of your choice and automatically creates two subfolders, one for the databases, one for pictures.
- Start the HKHdip.
- Login (see below).
- Select the menu **Extras** and subsequently the submenu **Options**.
- The program automatically sets the paths to the databases.
- Press **Connect** and a progress-bar shows that the program is connecting to its databases.
- Close the program and restart it again.

***Note:** You cannot change the country after the first start. To change the country the program must be installed again.*

LOGIN

For login enter 'assess' in the field 'User' and 'hkh' in the field 'Password'.
The login-password cannot be changed in the current program-version.

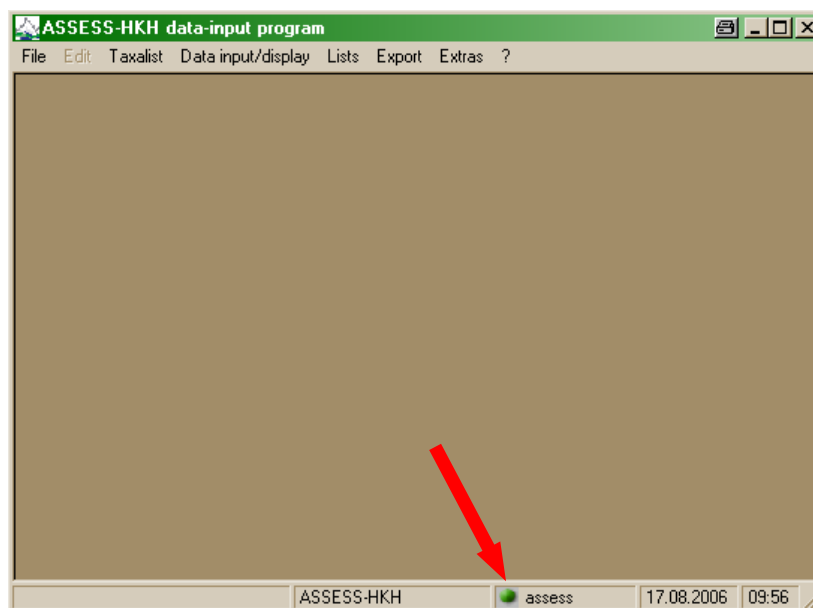
GENERAL COMMENTS / ERRORS

The status bar shows the current user name and a red/green light.

Red light in the status bar: no connection to the database was established during the start of the program for the following reasons:

- wrong or missing entries for the directories of the database; changes are possible in the **Extras/Options** menu
- incorrect login (user name and/or password)

Green light: connection with database was successful.



BACKUP OF YOUR DATA

It is recommended to make backups of your data on a regular base. The data you have entered into HKH*dip* are stored in the subfolder '*installation directory*\database'. There are 5 files with the extension '*.mdb' that you should backup (with the exception of 'ep_db.mdb', which **does not** contain any user entered data).

MAIN MENU

The main program menu bar contains the following menus:

- File
- Edit
- Taxalist
- Data input/display
- Lists
- Export
- Extras
- ?

File menu

- Printer optionsoptions for the standard printer
- Exitends the HKHdip

Edit menu

- Findsearches for family, genus, species or author in the opened taxalist

Taxalist menu

- Macro-invertebratesopens either the complete HKH taxalist (main taxalist) or the country specific taxalist (taxalist manager) of benthic macro-invertebrates. Opens also the synonym section of benthic macro-invertebrates (future version).

Data input/display menu

- Site & Sample Inputopens the general data structure that also serves for data input
- River Characteristicsopens the window for river characteristics data input (HKH site protocol)
- HKHscreeningopens the window for screening data input
- HKHbiosopens the window for bios data input
- HKHindexcalculates the HKH multimetric index und shows the result window

Lists menu

Sampling Instruments & Area...opens the window for defining and editing sampled areas and sampling instruments

Export menu

Export.....opens the window for exporting the data to Excel and Access

Extras menu

Optionsopens the window for setting program options

Backup.....opens the window for backup of your data

? menu

Use help.....opens a window for help information

Infoinformation about the program

DATA INPUT - ORGANISATION STRUCTURE

The 'Site & sample input' window to begin entering the organisation structure is opened by selecting **Data input/display** in the menu and subsequently selecting **Site & Sample Input** in the submenu.

The menu bar is equivalent to the main menu bar.

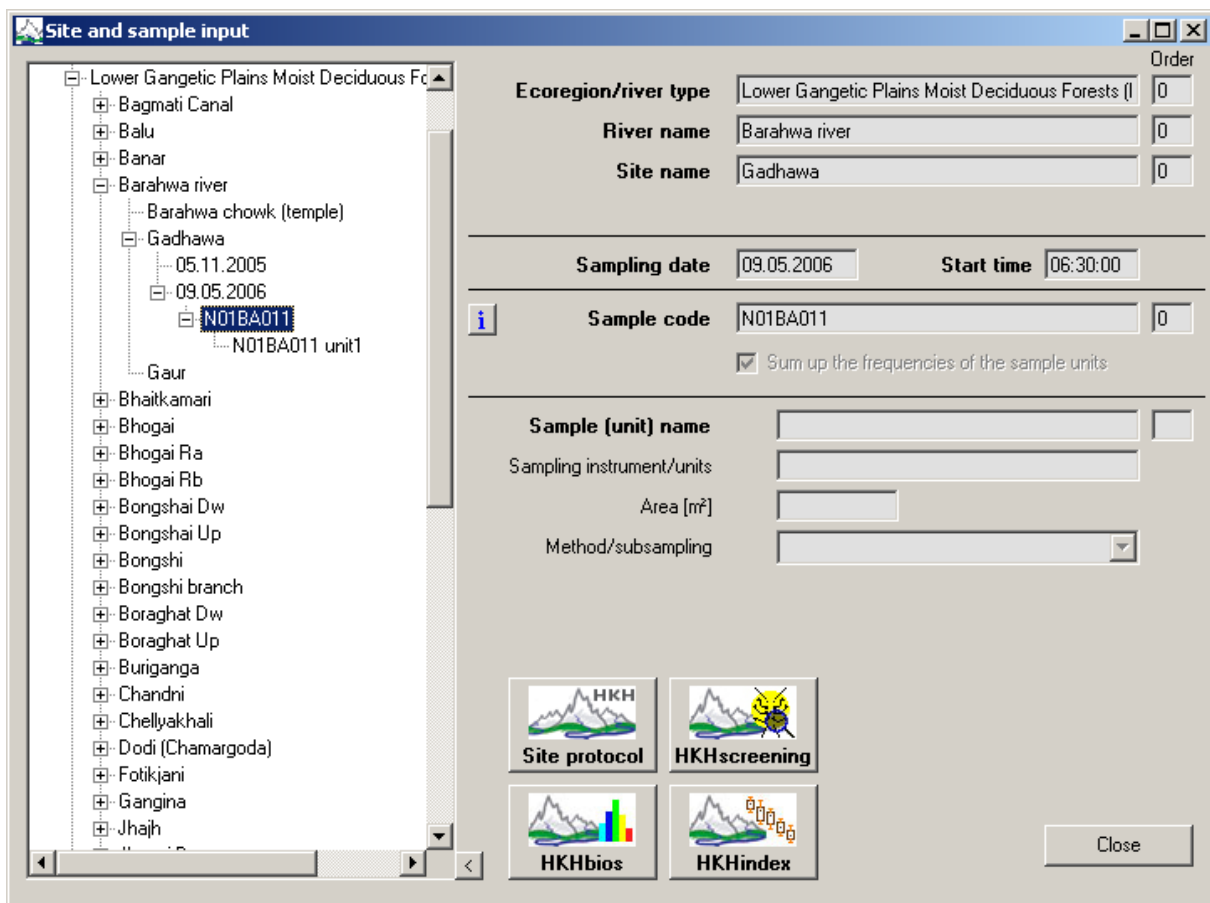
When opening the 'Site & sample input' window for the first time, the user is asked to choose a country from the selection list.

Note: *You cannot change the country after the first start. To change the country the program must be installed again.*

The 'Site & sample input' window is divided into two sections

- the left window shows the organisation structure with sampling sites, for which data have already been entered
- the right window serves to show and edit data input (data input window)

Note: *The first line of the organisation structure automatically displays the selected country.*



General note: *Data input/edit is managed by the use of the right mouse-button and is to be done level by level. Select the favoured level in the left window, then press the right mouse-button and make your choice. To finish input/edit of the selected level please press 'Accept' to save the data or 'Cancel' to quit without saving.*

Entering new sites

- go to the country in the left window and click the right mouse button
- select **New river type/name** with the left mouse button
- a blinking cursor will now appear in the field 'Ecoregion/river type' in the right data input window: enter the appropriate river type here
- enter the river name in the proceeding field
- press the **Accept** button
- to enter a second river type/name: select first river type/name or the country in the left window with the right mouse button
- select **New river type/name**
- enter the second river type/name on the right side of the window
- press the **Accept** button
- all further river types/names should be entered in the same manner

Entering the site name

- click the appropriate **river name** with the right mouse button in the left window
- select **New site name** with the left mouse button
- a blinking cursor will now appear in the field 'site name' in the right data input window: enter the appropriate site name here
- press the **Accept** button
- to enter a second site name: select first site or river name with the right mouse button
- select **New site name**
- enter the second site name on the right side of the window
- press the **Accept** button
- all further site names should be entered in the same manner

Entering the sampling date

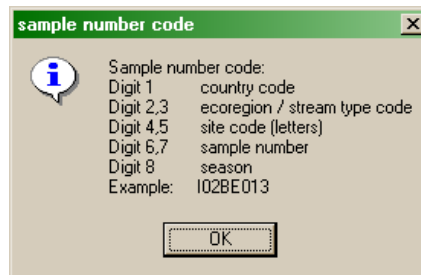
- click the appropriate **site name** with the right mouse button in the left window
- select **New date**
- a blinking cursor will now appear in the field 'date' in the right data input window: enter the appropriate sampling date and time (optional) here
- press the **Accept** button
- to enter a second sampling date: select first date (or the site name) with the right mouse button
- select **New date**
- enter the second sampling date on the right side of the window
- press the **Accept** button
- all further sampling dates should be entered in the same manner

Note: *The input of date and time format should correspond to the regional setting properties of your computer.*

Entering the sample code

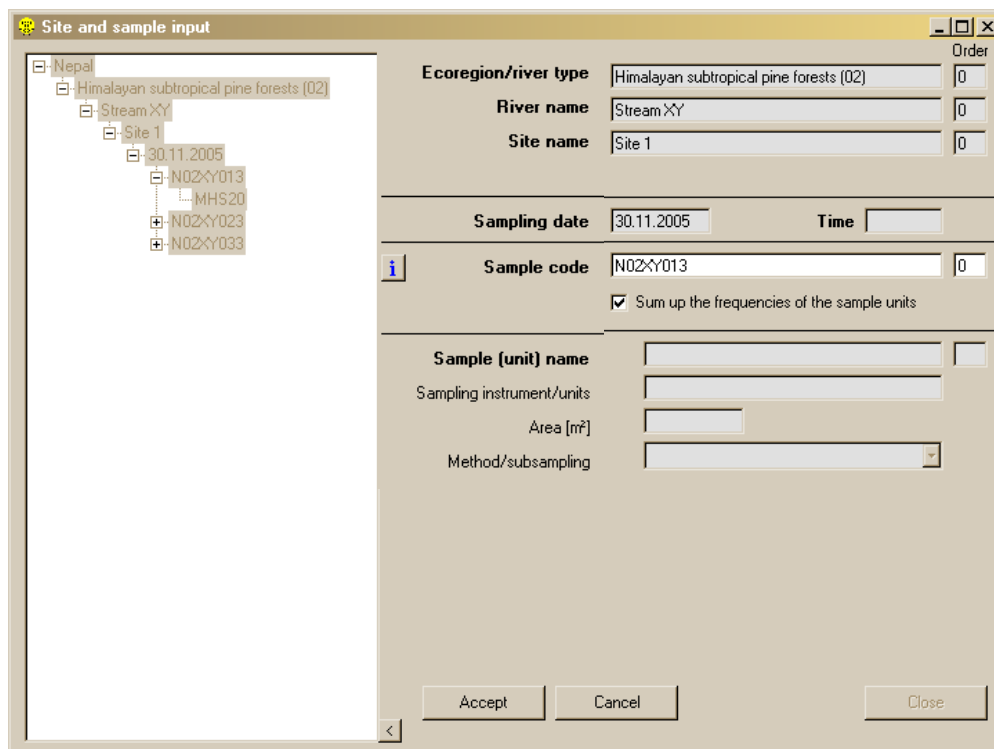
- click the appropriate **sampling date** with the right mouse button in the left window
- select **New sample code**
- a blinking cursor will now appear in the field 'sample code' in the right data input window:
enter the appropriate sample code here

***Note:** If you are not sure how the sample code should look like, press the **i** button left of the sample code field.*



- The 'sum up the frequencies of the sampling units' field will be ticked automatically. Change this status, if necessary.

***Note:** If you want to calculate the average of the frequencies of the sample units within this sample code, you have to remove the tick from the check box, otherwise the program will sum up the frequencies of all sample units!!*



- press the **Accept** button
- to enter a second sample code: select first sample code or the date with the right mouse button
- select **New sample code**
- enter the second sample code on the right side of the window
- press the **Accept** button
- all further sample code should be entered in the same manner

Entering the sample unit

- click the appropriate sample code with the right mouse button in the left window
- select **New sample unit** with the left mouse button
- the fields 'Sample (unit) name', 'Sampling instrument/units', 'Area [m²]' and 'Method/subsampling' in the right data input window will be automatically filled with default values
- a different name for 'Sampling (unit) name' can nevertheless be entered
- a 'Sampling instrument/units' (including sampling area) can also be chosen from the selection list
- a 'Method/subsampling' can also be chosen from the selection list
- press the **Accept** button

Note: *If you have sampled riffles and pools (or all sample units) separately you have to enter them as different "sampling units" (e.g. MHS unit 1 to 20). Please tick the check-box "sum up the frequencies" according to your choice (mark the 'sum up the frequencies of the sampling sites' field, if you want to have the frequencies of the sample units within the sample code summed up, otherwise the program will calculate the mean values !!).*

For the HKH Method the sampling area should be 1.25 m² for all 20 replicates. Please notice that the sum of your areas for a specific sample code must be 1.25 m²!!

Note: *The sampling area selection list can be modified in the menu 'lists'.*

Options within the 'Site & sample input' window

- The **order** of river types/river names/site names/sample codes and sample sites can be altered or fixed by changing the numbers in the small 'Order' fields on the right of the appropriate layer.
- To **delete** a river type/river name/site name/date/sample code or sample site click the appropriate layer with the right mouse button in the left window and subsequently choose 'Delete'.
- To **edit** a river type/river name/site name/date/sample code or sample site for changing your entries click the appropriate layer with the right mouse button in the left window and subsequently choose 'Edit'.

DATA INPUT - BIOLOGICAL DATA – BENTHIC INVERTEBRATES

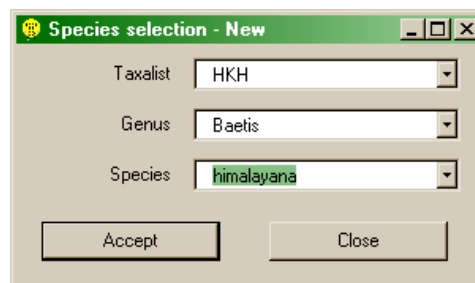
- choose a sample unit in the left part of the 'Site & sample input' window
- click the sampling unit with the right mouse button
- select **Edit** with the left mouse button or press the 'Taxa'-button at the lower end of the 'Data input' window



- a data input window according to your preceding choice (quant-no subsampling, quant-RIVPACS subsampling, quant-area subsampling, quant-volume subsampling; explanation of different windows see below) opens
- to enter a taxon click on the button **New**
- the window 'Species selection – New' opens
- select the 'Taxalist' from the selection list; the HKH list is loaded as the default setting, however each country taxalist may be selected alternatively
- select a 'Genus' and a 'Species' in the second and third field from the respective selection lists

Note: Once the genus is selected, only the possible species names according to the selected genus and taxalist appear in the species list.

By typing the first characters of the genus or species name, the process can be accelerated; the tabulator allows you to switch between the fields; using Alt and the cursor buttons, you can scroll up and down in the selection lists.



Note: If you cannot find a certain taxon neither in the taxalist of your country nor in the HKH taxalist, please open the synonym table (Menu Taxalist) and select the current name of the taxon. If the taxon is not listed there please inform Astrid Schmidt-Kloiber (astrid.schmidt-kloiber@boku.ac.at) AND Subodh Sharma (kuhimal@ku.edu.np).

- click the **Accept** button or press the enter key to finish this taxon input
- the taxon is loaded into the sampling site window
- the cursor is now automatically placed in the first available field
- enter the frequency of the taxon
- the input is finished by pressing the enter key
- the taxa input window 'Species selection – New' opens again automatically
- all further taxa entries are performed in the same manner
- after taxa input, click the **Close** button to finish data input

Options

- If the taxon was not securely determined, the 'cf' box can be marked.
- Juveniles can be identified by marking the 'juv' box.
- Adult individuals can be identified by marking the 'ad' box.

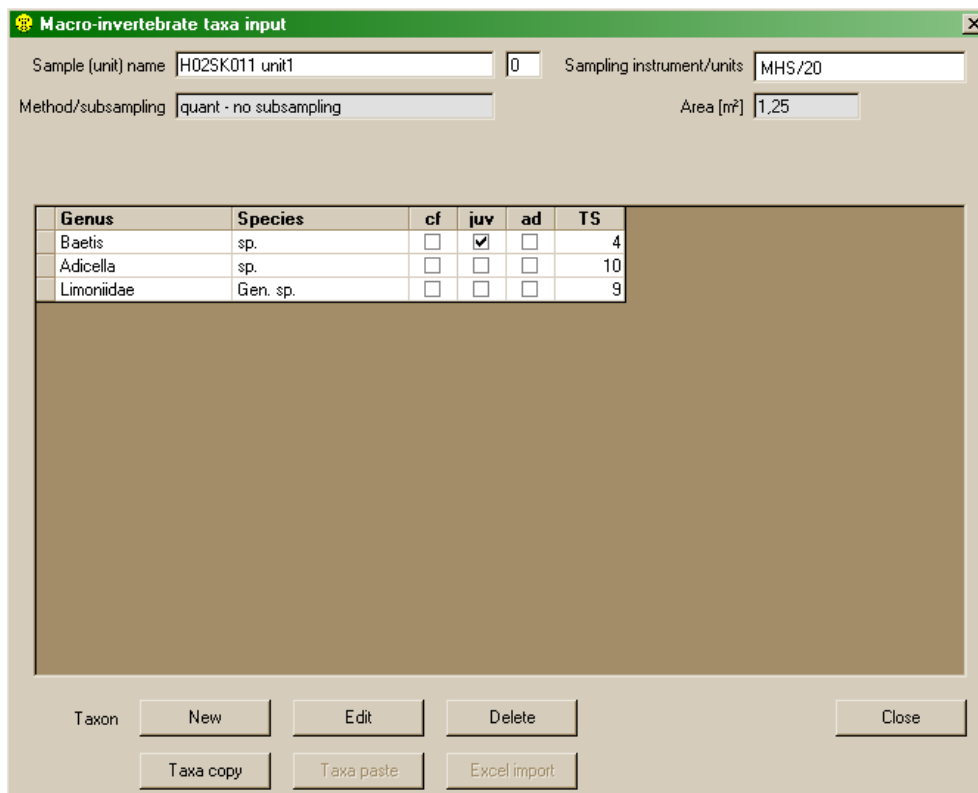
Note: *If you want mark one of these options in addition to an already entered taxon you have to enter the one with the addition first (e.g. if you want to enter Baetis himalayana and Baetis himalayana juv. you have to start with Baetis himalayana juv.).*

- If you wish to change a species, place the cursor in the respective field and press the **Edit** button.
- To delete a species from the list, place the cursor in the row to be deleted and press the **Delete** button.

Window Macro-invertebrate taxa input - 'quant - no subsampling'

The following column is available:

- TS = total sample: frequency of the taxon within the total sample



Sample (unit) name: H02SK011 unit1 0 Sampling instrument/units: MHS/20
 Method/subsampling: quant - no subsampling Area [m²]: 1,25

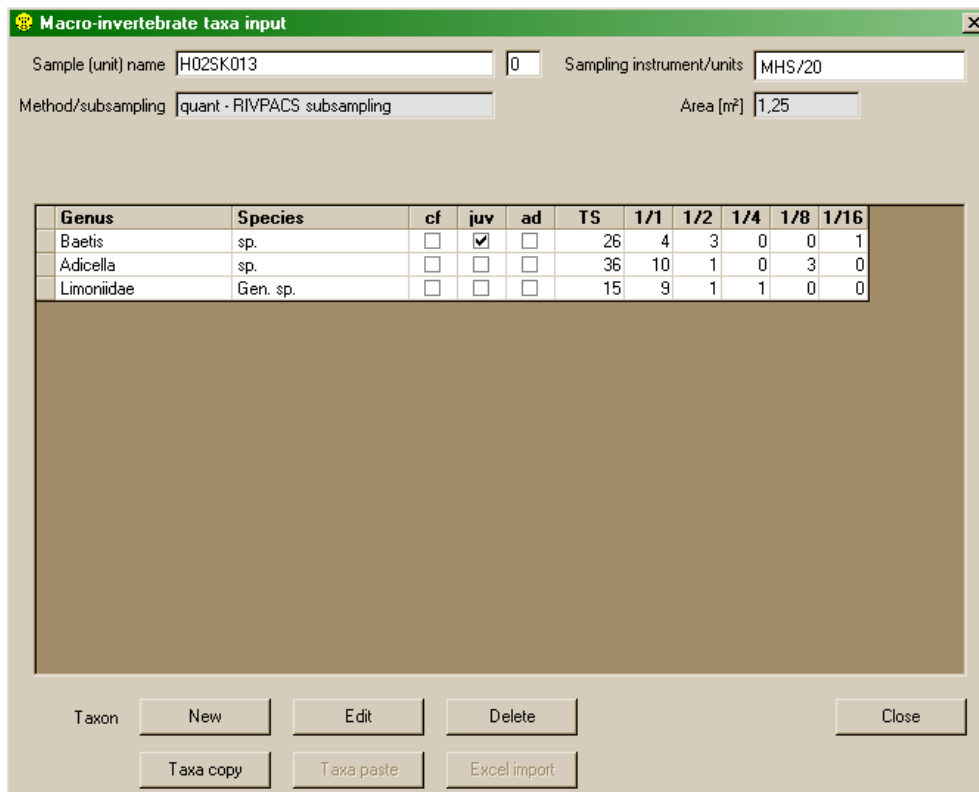
Genus	Species	cf	juv	ad	TS
Baetis	sp.	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	4
Adicella	sp.	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	10
Limoniidae	Gen. sp.	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9

Taxon: [New] [Edit] [Delete] [Close]
 [Taxa copy] [Taxa paste] [Excel import]

Window Macro-invertebrate taxa input - 'quant - RIVPACS subsampling'

The following columns are available:

- TS = total sample: frequency of the taxon within the total sample (this is calculated automatically according to entries of the fraction-columns)
- 1/1: input column for the 1/1 vial
- 1/2: input column for the 1/2 vial
- 1/4: input column for the 1/4 vial
- 1/8: input column for the 1/8 vial
- 1/16: input column for the 1/16 vial



Genus	Species	cf	juv	ad	TS	1/1	1/2	1/4	1/8	1/16
Baetis	sp.	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	26	4	3	0	0	1
Adicella	sp.	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	36	10	1	0	3	0
Limoniidae	Gen. sp.	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	15	9	1	1	0	0

Window Macro-invertebrate taxa input - 'quant - area subsampling'

The following columns are available:

- TS = total sample: frequency of the taxon within the total sample (this is calculated automatically according to the number of processed cells and the 1/1-column)
- CS = cells sample: frequency within the processed cells
- 1/1 = 1/1-fraction: input column for pre-picked or post-picked taxa

Macro-invertebrate taxa input

Sample (unit) name: H03HC011 | 0 | Sampling instrument/units: MHS/20

Method/subsampling: quant - area subsampling | Area [m²]: 1.25

No. Cells: 5

Genus	Species	cf	juv	ad	TS	CS	1/1
Oligoneuriella	kashmirensis	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	30	5	0
Agabus	freudei	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	30	5	0
Yola	consanguinea	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	7	1	1
Psephenidae	Gen. sp.	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	48	8	0
Ablabesmyia (Karelia)	sp.	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	7	1	1

Taxon:

Note: The number of processed cells is defined in the 'Site & sample input' window, but can be changed here. The total sample is then calculated accordingly.

Window Macro-invertebrate taxa input - 'quant - volume subsampling'

First of all the sampling fractions have to be specified:

- enter the percentage of the aliquot used for determination of the coarse fraction in the field 'CF' (if subsampling was performed); default value is 100 %
- enter the percentages of the aliquots used for determination of the fine fractions in the fields 'FF1' to 'FF4' (if subsampling was performed)

The following columns are available:

- TS = total sample: frequency of the taxon within the total sample (this is calculated by summing up the specific fractions multiplied with the specific percentage values)
- CF = coarse fraction: frequency within the coarse fraction
- FFx = fine fraction: frequency within the fine fraction(s)

Macro-invertebrate taxa input

Sample (unit) name: H03HC013 0 Sampling instrument/units: MHS/20

Method/subsampling: quant - volume subsampling Area [m²]: 1,25

Sampling fractions: CF FF1 FF2 FF3 FF4

100 % 20 % 0 % 0 % 0 %

Genus	Species	cf	juv	ad	TS	CF	FF1	FF2	FF3	FF4
Yola	consanguinea	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	5	5	0	0	0	0
Psephenidae	Gen. sp.	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	26	1	5	0	0	0
Adicella	dhurvasena	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	56	1	11	0	0	0

Taxon

Note: The percentages of the sampling fractions can be changed at any time. The total sample is then calculated accordingly.

Taxa copy/Taxa paste buttons

In HKHdip 4.0 you can copy taxa from one sample unit to another. Only the taxa names without frequencies will be copied.

- click the appropriate sampling unit with the right mouse button in the left window
- select **Edit** with the left mouse button
- the data input window opens
- mark a taxon with the mouse
- add other taxa by keeping the shift-button pressed
- press the **Taxa copy** button
- edit another sample unit
- press the **Taxa paste** button
- add the frequencies of the new taxa

Note: To avoid double entries of the same taxon, it is only possible to copy taxa into an empty sample unit.

Macro-invertebrate data import (Excel import button)

Existing macro-invertebrate data files (MS Excel) can be imported into HKHdip 4.0 via an import-interface. Before the data-import can be started, it is necessary to create the whole sample structure (i.e. it is necessary to enter a river type, a river name, a site name, a sampling date, a sample code, a sample unit name).

After this is done

- click the appropriate sampling site with the right mouse button in the left window
- select **Edit** with the left mouse button or press the 'Taxa'-button at the lower end of the 'Data input' window
- a data input window according to your preceding choices opens

***Note:** The number of processed cells (area subsampling) and the percentages of fractions have to be specified **before** you start the import.*

- to import an Excel file click the button **Excel import** at the lower end of the form

The 'macro-invertebrate taxa input – taxa import'-window opens.

- click on the button '...' and select an Excel file from your hard disk
- press the **Load** button to load the file
- select an Excel sheet within the loaded file
- define the columns in which the taxa names are stored in your Excel file
- define the rows that should be imported
- define the columns in which the number of individuals are stored

***Note:** The selection lists and names of the columns change according to the method defined when creating the sample unit.*

- choose if you only want to import rows with values greater than 0
- press the **Read in** button

The imported file can be seen in the lower window. The first one or two columns contain the original entries of your Excel-file, the next two columns contain the values that will be imported by HKHdip.

Macro-invertebrate taxa input - taxa import

Select Excel file: D:_Uni\HKH\dip\import_test1.xls

Select Excel sheet: Tabelle1

Taxa column(s): A B

From row: 2 to 7

TS: C

Taxalist: HKH

Excel file	ASSESS-HKH data-input program					
Taxa	Genus	Species	cf.	juv.	TS	
2 Baetis	sp. juv.	Baetis	sp.	<input type="checkbox"/>	<input checked="" type="checkbox"/>	4
3 Baetis	sp. 2					6
4 Baetis	sp. 1					5
5 Limoniidae	Gen. sp.	Limoniidae	Gen. sp.	<input type="checkbox"/>	<input type="checkbox"/>	9
6 Adicella	sp.	Adicella	sp.	<input type="checkbox"/>	<input type="checkbox"/>	10
7 Nemoura	schmidi	Nemoura	schmidi	<input type="checkbox"/>	<input type="checkbox"/>	1

Buttons: Load, Read in, Taxalist export, Import, Close

Options: All rows, Rows with TS > 0 only, Do not import taxa with TS = 0

The following colour codes are possible:

- green: the taxon was identified by the HKHdip taxa-database and read in correctly
- yellow: the taxon was identified by the HKHdip taxa-database and basically read in correctly; the status of the taxon (e.g. juv., cf.) was automatically adapted by HKHdip, a check is therefore reasonable
- white: the taxon was not identified by the HKHdip taxa-database (e.g. because of a spelling mistake) and could not be read in; if another taxon should be entered instead, click into the field in column 3 and choose a taxon from the selection list

If all changes and specifications are done click on the **Import** button and the file will be read in into your sample unit form.

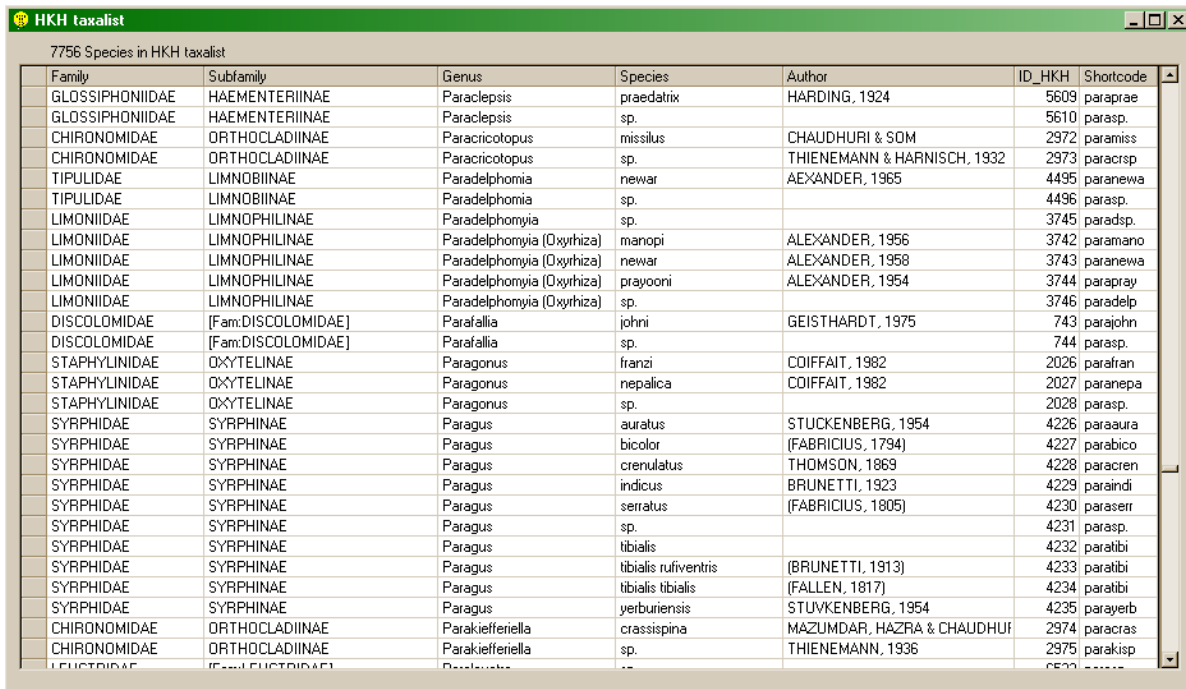
Note: The numbers on the left side of the import-window correspond to the row-numbers of your original Excel-file.

If you press the button **Taxalist export** a documentation of the import is exported to Excel.

It is only possible to import an Excel-file into an empty sample unit form.

TAXALISTS

The taxalists for macro-invertebrates are opened by choosing **Taxalist** in the menu and subsequently opening **Macro-invertebrates** in the submenu. The options 'HKH taxalist' and 'Taxalist manager' as well as 'Synonyms' (future version) can be chosen. The taxalists serve as compendium. The columns can be ordered alphabetically by pressing on the column's heading. The synonym sections serve to consult the current name of a taxon.



Family	Subfamily	Genus	Species	Author	ID_HKH	Shortcode
GLOSSIPHONIIDAE	HAEMENTERIINAE	Paraclepsis	praedatrix	HARDING, 1924	5609	paraprae
GLOSSIPHONIIDAE	HAEMENTERIINAE	Paraclepsis	sp.		5610	parasp.
CHIRONOMIDAE	ORTHOCLADIINAE	Paracricotopus	missilus	CHAUDHURI & SOM	2972	paramiss
CHIRONOMIDAE	ORTHOCLADIINAE	Paracricotopus	sp.	THIENEMANN & HARNISCH, 1932	2973	paracrsp
TIPULIDAE	LIMNOBIINAE	Paradelphomia	newar	ALEXANDER, 1965	4495	paranewa
TIPULIDAE	LIMNOBIINAE	Paradelphomia	sp.		4496	parasp.
LIMONIIDAE	LIMNOPHILINAE	Paradelphomyia	sp.		3745	paradsp.
LIMONIIDAE	LIMNOPHILINAE	Paradelphomyia (Oxyrhiza)	manopi	ALEXANDER, 1956	3742	paramano
LIMONIIDAE	LIMNOPHILINAE	Paradelphomyia (Oxyrhiza)	newar	ALEXANDER, 1958	3743	paranewa
LIMONIIDAE	LIMNOPHILINAE	Paradelphomyia (Oxyrhiza)	prayooni	ALEXANDER, 1954	3744	parapray
LIMONIIDAE	LIMNOPHILINAE	Paradelphomyia (Oxyrhiza)	sp.		3746	paradelp
DISCOLOMIDAE	[Fam:DISCOLOMIDAE]	Parafallia	johni	GEISTHARDT, 1975	743	parajohn
DISCOLOMIDAE	[Fam:DISCOLOMIDAE]	Parafallia	sp.		744	parasp.
STAPHYLINIDAE	OXYTELINAE	Paragonus	franzi	COIFFAIT, 1982	2026	parafran
STAPHYLINIDAE	OXYTELINAE	Paragonus	nepalica	COIFFAIT, 1982	2027	paranepa
STAPHYLINIDAE	OXYTELINAE	Paragonus	sp.		2028	parasp.
SYRPHIDAE	SYRPHINAE	Paragus	auratus	STUCKENBERG, 1954	4226	paraaura
SYRPHIDAE	SYRPHINAE	Paragus	bicolor	(FABRICIUS, 1794)	4227	parabico
SYRPHIDAE	SYRPHINAE	Paragus	crenulatus	THOMSON, 1869	4228	paracren
SYRPHIDAE	SYRPHINAE	Paragus	indicus	BRUNETTI, 1923	4229	paraindi
SYRPHIDAE	SYRPHINAE	Paragus	serratus	(FABRICIUS, 1805)	4230	paraserr
SYRPHIDAE	SYRPHINAE	Paragus	sp.		4231	parasp.
SYRPHIDAE	SYRPHINAE	Paragus	tibialis		4232	paratibi
SYRPHIDAE	SYRPHINAE	Paragus	tibialis rufiventris	(BRUNETTI, 1913)	4233	paratibi
SYRPHIDAE	SYRPHINAE	Paragus	tibialis tibialis	(FALLEN, 1817)	4234	paratibi
SYRPHIDAE	SYRPHINAE	Paragus	yerbuiensis	STUCKENBERG, 1954	4235	parayerb
CHIRONOMIDAE	ORTHOCLADIINAE	Parakiefferiella	crassispina	MAZUMDAR, HAZRA & CHAUDHURI	2974	paracras
CHIRONOMIDAE	ORTHOCLADIINAE	Parakiefferiella	sp.	THIENEMANN, 1936	2975	parakisp

Note: If taxa are missing or if you note spelling/taxonomic mistakes please contact Astrid Schmidt-Kloiber (astrid.schmidt-kloiber@boku.ac.at) AND Subodh Sharma (kuhimal@ku.edu.np).

LISTS MENU

The menu for changing the sampling area is opened by choosing **Lists** in the menu and subsequently opening **Sampling instruments & area** in the submenu.

Entering a new sampling area

- press **Add new**
- enter a new area in m² in the field 'Area'
- enter a sampling instrument in the field 'Sampling instrument'
- choose a value from the selection list, if you want to define the sampling instrument & area as default for a certain method (optional)
- enter a description in the field 'Description' (optional)
- press **Close**

DATA INPUT – RIVER CHARACTERISTICS

At the lower end of the 'Data input' window a button to open the HKH site protocol is available.



The 'River Characteristics' window is opened by clicking the **Site Protocol** button in the 'Site & sample input' window or by selecting **Data input/display** in the menu and subsequently selecting **River characteristics/HKH Site protocol** in the submenu.

The input of river characteristics data is based on the site protocol.

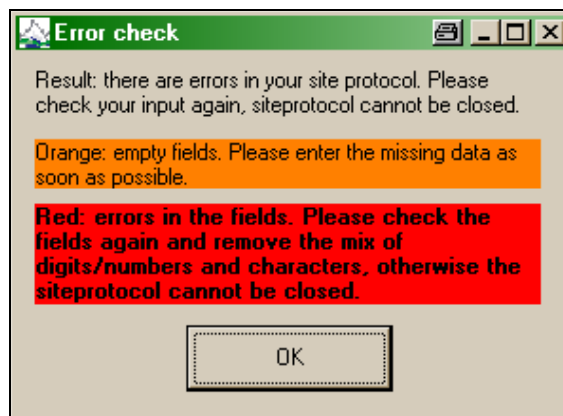
General information

- In addition to the possibilities of the site protocol, the option 'not available' ('n.a.') was added, for parameters, which were not or could not be collected.
- Values in tables can be edited after being double clicked.
- The tabulator key selects the input fields in numerical order.
- In tables, the correctness of input is checked (5 %- or 10 %-steps, sum = 100 %). A correct sum is marked green, an incorrect one is marked red.
- The **decimal separator** has to correspond to the regional setting properties of your computer.
- Fields that require **digits or numbers** are marked in yellow, fields that allow **any character** are marked in blue.
- **Fields that are to be filled obligatory are labelled in *italic and underlined*.**

***Note:** The program automatically saves all entered values when it is closed with the 'x'-button in the upper right corner of the window.*

Error check

Data can be checked for correctness by pressing the button **Error check**. Incorrect fields will be **labelled in red**, empty fields will be **labelled in orange**.



***Note:** The site protocol cannot be closed unless all red fields are corrected.*

The following parameters are checked:

- whether the fields are empty or not
- whether fields contain letters instead of digits
- whether data correspond with selection list entries
- whether values were selected in optional fields
- whether the sum of tables corresponds to 100 %

Note: The program **cannot** check whether or not the values entered are reasonable or not. When you open the site protocol display, all values are noted as missing in the database and more than 150 errors occur, if the input window is closed without data entry. Please perform the error check **before** closing the site protocol and correct any possible errors, otherwise data can be lost if an error occurs during saving data to the database.

Comments on some individual parameters

- Parameter 10 and 11: longitude and latitude are to be entered in decimal values. Enter the coordinates as simple decimal coordinates, 2 digits before and 7 digits after decimal (e.g. longitude: 13.2064925; latitude: 52.2152457), Date WGS 84. Use negative values for coordinates west of Greenwich. This makes data entry as simple as possible and enables to export coordinates as decimal numbers to GIS. Other systems, such as UTM, may need to re-format the data for analysis.
- The 'MHS table' automatically writes values into the table 'sampling replicates'. The values are only transmitted when the values in the 'habitat' tables equal the sum of 100 % or 20 replicates respectively. Otherwise all entries in table 'sampling replicates' are deleted.
- Table 'sampling replicates' is restricted in parts; microhabitats can only be altered in the 'habitat' tables.
- Parameter 95: the picture in 'sketch/map' is not saved, only the path to the corresponding file is saved (minimises the database in size); only *.jpg files can be inserted (size limitation: 1200 x 1000 pixel).
 - path: \installation path\pics
 - filename: sample_no_map.jpg (recommended filename)
 - sample_no_pic.jpg (recommended filename)

DATA INPUT AND CALCULATION – HKHscreening

Important note

In HKHdip Version 4.0 a revised HKHscreening protocol is implemented. The scientific fundamentals of the revised **HKHscreening** protocol are laid down in Deliverable 10 – 'ASSESS-HKH Methodology Manual describing fundamentals & application of three approaches to evaluate the river quality based on benthic invertebrates: HKH screening, HKH score bioassessment & HKH multimetric bioassessment'.

If you open previously entered HKHscreening samples, the results will be automatically adapted to the new version of the HKHscreening protocol.

***Note:** If you want to view your old data in the previous version of HKHscreening, please use an older version of HKHdip (HKHdip 3.2).*

Data input and calculation

The 'HKHscreening' window is opened by clicking the **HKHscreening** button in the 'Site & sample input' window or by selecting **Data input/display** in the menu and subsequently selecting **HKHscreening** in the submenu.



At the top of the HKHscreening-window the ecoregion, the river name, the site and sample name, the sampling date and time of the chosen sample are shown.

***Note:** These entries can only be altered in the 'Site & sample input' window (see page 9).*

The input of HKHscreening data is based on the Screening Protocol for assessing the river quality of streams in the ASSESS-HKH region that was completed during sampling in the field.

Entering the ecological features

Data input takes place in the column that is marked in orange colour:

- select one parameter and choose the appropriate answer from the selection list, which opens when you click into the orange column
- the scores for the different river quality classes will fill automatically when you leave the active cell or press the 'Enter'-key
- all the number entries will be summed up **automatically** and the **river quality class** with the highest number will be **highlighted** in **dark orange**

***Note:** Only fill those parameters where the criterion exists without any doubt!!!!*

Entering taxa recorded in the field

In the lower end of the window two headlines for the input of macro-invertebrate taxa are available. If you tick the checkbox left of the headline, then a taxalist will open, comprising the taxa of the particular region.

- Taxa (all ecoregions except Gangetic Plains): use this list if you want to fill the HKHscreening taxa for ecoregions **other than the Gangetic Plains**
- Taxa (ecoregion Gangetic Plains only!): use this list if you want to fill the HKHscreening taxa for the ecoregion **Gangetic Plains**

Note: The sixth river quality class (black colour) that was added to the HKHscreening field protocol for rivers (sections) with no higher life cannot be entered into HKHscreening. In case you have ticked parameters of the sixth river quality class in your decision support table in the field (e.g. species richness, chironomids with red colour or air-breathing animals) choose the according parameter in the selection list of the fifth river quality class.

The screenshot shows a software window titled "sample input" with the following fields:

- Ecoregion: Eastern Himalayan Broadleaf Forests (IMD401)
- River name: Cheri Chhu
- Site name: Cheri Lhakhang
- Sampling date: 23.11.2005
- Sampling time: 09:45:00
- Sample name: H03TC013

Below these fields is a "Decision support table" with the following structure:

Decision support table	Exists without doubt	River quality class				
		I	II	III	IV	V
Sensory features (if not in accordance with natural river type)						
Non natural turbidity, suspended solids						
Non natural colour						
Foam						
Odour (water)						
Waste dumping						
Ferro-sulphide reduction (water velocity < 0,25 m/s)	no	1				
Mud reduced but with aerobic surface						
Mud reduced but with anaerobic surface						
Lower surface of stones (% cover black dots)						
Upper & lower surfaces of stones						
Ferro-sulphide reduction (water velocity 0,25-0,75 m/s)	no	1	1			
Mud reduced but with aerobic surface						
Mud reduced but with anaerobic surface						
Lower surface of stones (% cover black dots)						
Upper & lower surfaces of stones						
Ferro-sulphide reduction (water velocity > 0,75 m/s)						
Lower surface of stones (% cover black dots)						
Upper & lower surfaces of stones						
Bacteria, fungi, periphyton						
Sewage fungi & bacteria (visible to the naked eyes)						
Sulphur bacteria (visible to the naked eyes)						
Stones with algal vegetation (periphyton) in thin layers	yes	2	2			
% of thick, significant layers of algae	< 25 %	2				2
Filamentous green algae	none to few	2				

sample input

Ecoregion: Eastern Himalayan Broadleaf Forests (IM0401) River name: Cheri Chhu
 Site name: Cheri Lhakhang Sampling date: 23.11.2005 Sampling time: 09:45:00
 Sample name: H03TC013

Decision support table	Exists without doubt	River quality class				
		I	II	III	IV	V
Benthic macro-invertebrates						
Species richness	high	2	2			
Dominance of very sensitive organisms (9 to 10)						
Dominance of sensitive organisms (6 to 8)	yes	1	3	1		
Dominance of medium tolerant organisms (4 to 6)						
Dominance of tolerant organisms (3 to 4)						
Dominance of extremely tolerant organisms (1 to 2)						
<input checked="" type="checkbox"/> Taxa (all ecoregions except Gangetic Plains)						
Rhithrogena spp.						
Perlidae	yes	2	1			
Plecoptera	yes	2	1			
Euphaeidae						
Stenopsyche spp.	yes	2	1	1		
Rhyacophilidae	yes	3	2	1		
Caenis spp.						
Heptageniidae	yes	2	2	1		
Psephenidae	yes	2	3	1		
Glossosomatidae						
Sphaeriidae						
Simuliidae	yes	1	2	2		
Psychomyiidae	yes	1	3	2		
Tabanidae						
Potamidae						
Libellulidae/Corduliidae						
Hydropsychidae (medium to many)						
Planorbidae						
Lymnaeidae						
Physa spp.						
Leeches (more than naturally occurring)						
Chironomids with red colour	none					3
Bezzia-group						
Psychodidae (white)						
Air-breathing animals, e.g. rat-tail maggots	yes					3
Oligochaeta/Tubificidae (mud-worms)	none					2
<input type="checkbox"/> Taxa (ecoregion Gangetic Plains only!)						
Result - Sum of columns		26	23	9	0	10

Clipboard Delete Save Close

Options

- If you want to **copy** the HKHscreening data of this sample into another Windows software (e.g. MS Word or MS Excel), press the 'Clipboard'-button, open the other software and choose 'insert' from the right-mouse-button-menu; the sample data, the HKHscreening data and the HKHscreening result will be copied.
- If you want to **delete** an already entered **entry**, choose the empty entry in the orange column.
- If you want to **delete** the complete HKHscreening data of this sample, press the 'Delete'-button.

Note: If you press the 'Delete'-button only HKHscreening data will be deleted. Other data from the same sample will be maintained.

- If you want to **save** the HKHscreening data of this sample, press the 'Save'-button.
- If you want to **close** the 'HKHscreening' window, press the 'Close'-button.

Comments on some individual parameters

- parameter '% of thick, significant layers of algae': if you have ticked 'few' in your decision support table in the field, please choose '<25 %' in the selection list
- parameter 'Filamentous green algae': if you have ticked 'filaments, tufts' in your decision support table in the field, please choose either 'filaments' or 'tufts' in the selection list according to your observations in the field
- parameter 'Species richness': if you have ticked 'medium/high' in your decision support table in the field, please choose either 'medium' or 'high' in the selection list according to your observations in the field; if you have ticked 'none' in the sixth river quality class column in your decision support table in the field, please choose 'none' in the selection list of the fifth river quality class column
- parameter 'Tubificidae (mud-worms)': if you have ticked 'few/medium' in your decision support table in the field, please choose either 'few' or 'medium' in the selection list according to your observations in the field; if you have ticked 'medium/many' in your decision support table in the field, please choose either 'medium' or 'many' in the selection list according to your observations in the field; if you have ticked 'none' in the sixth river quality class column in your decision support table in the field, please choose 'none' in the selection list of the fifth river quality class column
- parameter 'Chironomids with red colour': if you have ticked 'none' in the sixth river quality class column in your decision support table in the field, please choose 'none' in the selection list of the fifth river quality class column

Note: *If you are not sure regarding the different ecological features please also consult your photos of the respective sites!*

DATA INPUT AND CALCULATION – HKHbios

Scientific fundamentals of **HKHbios** are laid down in Deliverable 10 – 'ASSESS-HKH Methodology Manual describing fundamentals & application of three approaches to evaluate the river quality based on benthic invertebrates: HKH screening, HKH score bioassessment & HKH multimetric bioassessment'.

The 'HKHbios' window is opened by clicking the **HKHbios** button in the 'Site & sample input' window or by selecting **Data input/display** in the menu and subsequently selecting **HKHbios** in the submenu.



At the top of the HKHbios-window the ecoregion, the river name, the site and sample name, the sampling date and time of the chosen sample are shown.

***Note:** These entries can only be altered in the 'Site & sample input' window (see page 9).*

According to the selected ecoregion the list of displayed taxa changes.

Entering the HKHbios taxa

Before the HKHbios taxa can be entered, one of the following options has to be chosen according to how the abundance of taxa was recorded in the field:

- Abundance class: taxa were recorded in abundance classes; values from 1 to 5 with intermediate levels can be selected from the appropriate selection list
- Abundance: taxa were recorded per sample area; two areas can be chosen: 1,25 m² for 20 Multi-Habitat-Samples or 0,625 m² for 10 Multi-Habitat-Samples

Regarding the display of the taxa different orders can be chosen:

- taxonomic unit: systematic order
- alphabetically: alphabetical order

sample input

Ecoregion: Eastern Himalayan Broadleaf Forests (IM0401) River name: Cheri Chhu
 Site name: Cheri Lhakhang Sampling date: 23.11.2005 Sampling time: 09:45:00
 Sample name: H03TC013 Abundance class: Abundance 1,25 (MHS/20)

Order by: Taxonomic unit Show selected taxa only

Taxon	Abundance	Score	Weight
Acentrella	3	8	1
Baetiella	1	8	1
Baetis	10	0	1
Cincticostella	11	8	1
Drunella	4	9	1
Ecdyonurus s.l.	4	8	1
LEUCTRIDAE	4	10	1
Amphinemura	8	9	5
PELTOPERLIDAE	1	10	5
PERLIDAE	3	8	1
PERLODIDAE	18	9	1
Psephenoidinae	1	8	1
SCIRTIDAE	12	8	1
Micrasema	3	10	5
HYDROPSYCHIDAE	23	7	1
LEPIDOSTOMATIDAE	1	8	5
PHILOPOTAMIDAE	1	7	1
PSYCHOMYIIDAE	194	7	1
RHYACOPHILIDAE	60	8	1
Stenopsyche	1	8	1
ATHERICIDAE	2	9	1
DEUTEROPHLEBIIDAE	4	8	1
EMPIDIDAE	2	8	1
LIMONIIDAE	3	8	1
cf. Dicranota	1	8	1
Number of taxa	24		
HKH-biotic score	8,68		
HKH-biotic class	reference		

Data input takes place in the column that is marked in orange colour (named either 'Abundance class' or 'Abundance'):

- select one taxon and choose the relevant abundance class from the selection list, which opens when you click into the orange column, or enter the number of individuals
- the scores and weights for the different taxa will fill automatically when you leave the active cell or press the 'Enter'-key
- all entries will be treated automatically and as a result the number of taxa, the **HKH-biotic score** and the **HKH-biotic class** (river quality class) will be displayed at the end of the table

Note: If you tick the checkbox 'Show selected taxa only' only those taxa that you have chosen and which occur in your sample will be displayed.

Options

- If you want to **copy** the HKHbios data of this sample into another Windows software (e.g. MS Word or MS Excel), press the 'Clipboard'-button, open the other software and choose 'insert' from the right-mouse-button-menu; the sample data, the HKHbios taxa and the HKHbios result will be copied.

***Note:** If you have ticked the checkbox 'Show selected taxa only' only those taxa that occur in your sample will be copied to the clipboard.*

- If you want to **delete** the HKHbios data of this sample, press the 'Delete sample'-button.

***Note:** If you press the 'Delete sample'-button only HKHbios data will be deleted. Other data from the same sample will be maintained.*

- If you want to **save** the HKHbios data of this sample, press the 'Save sample'-button.
- If you want to **close** the 'HKHbios' window, press the 'Close'-button.

DATA CALCULATION – HKHindex

Scientific fundamentals of **HKHindex** are laid down in Deliverable 10 – 'ASSESS-HKH Methodology Manual describing fundamentals & application of three approaches to evaluate the river quality based on benthic invertebrates: HKH screening, HKH score bioassessment & HKH multimetric bioassessment'.

Taxa data for calculating the HKHindex can be entered as explained in the chapter 'Data input - biological data – Benthic invertebrates' (see page 13).

The calculation of **HKHindex** can be started by choosing a sample code in the 'Site & sample input' window and by subsequently clicking the **HKHindex** button or by selecting **Data input/display** in the menu and subsequently selecting **HKHindex** in the submenu.



All required metrics as well as the HKHindex for the particular sample site are calculated. After completion of the HKHindex window opens automatically.

Note: *If you have already calculated the HKHindex of the particular sample, you will be asked whether you want to load the previously calculated data or whether you want to calculate the HKHindex again.*

Note: *Depending on your hardware requisite HKHindex calculation can last for some time. Please do not press any other key during the calculation process.*

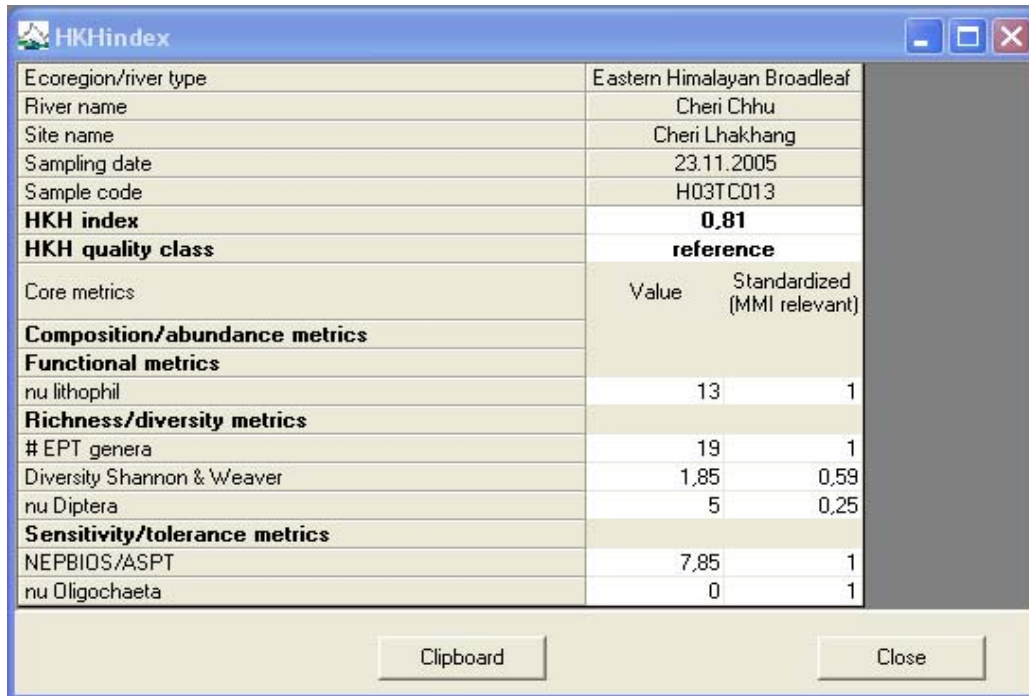
Note: *If you want to stop the HKHindex calculation during the calculation process, please press the 'ESC' button.*

If an error occurs during the calculation process, please check your input data. If the error remains please contact ROBERT VOGL (irv@irv-software.at) and OTTO MOOG (otto.moog@boku.ac.at) including the text of the error message.

HKHindex results

The 'HKHindex' window shows the results of the HKHindex calculation. The following results are displayed:

- sample information: ecoregion, river name, site name, sampling date and time, sample code
- HKHindex results: value of the **HKHindex** and the corresponding **HKH quality class** (river quality class)
- single calculation results of the underlying core metrics: raw and standardised values



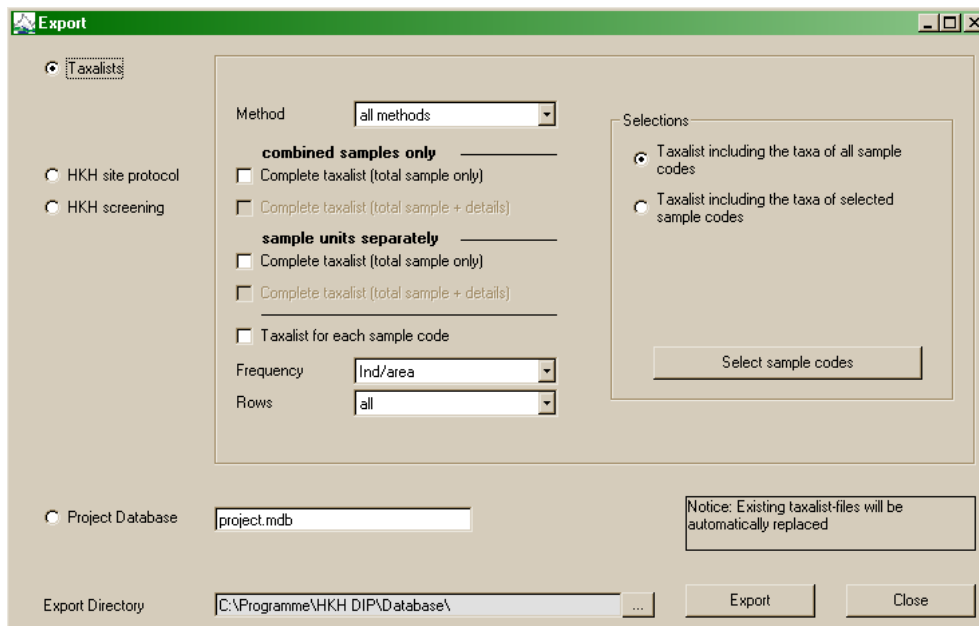
Ecoregion/river type	Eastern Himalayan Broadleaf	
River name	Cheri Chhu	
Site name	Cheri Lhakhang	
Sampling date	23.11.2005	
Sample code	H03TC013	
HKH index	0,81	
HKH quality class	reference	
Core metrics	Value	Standardized (MMI relevant)
Composition/abundance metrics		
Functional metrics		
nu lithophil	13	1
Richness/diversity metrics		
# EPT genera	19	1
Diversity Shannon & Weaver	1,85	0,59
nu Diptera	5	0,25
Sensitivity/tolerance metrics		
NEPBIOS/ASPT	7,85	1
nu Oligochaeta	0	1

Options

- If you want to **copy** the HKHindex data of this sample into another Windows software (e.g. MS Word or MS Excel), press the 'Clipboard'-button, open the other software and choose 'insert' from the right-mouse-button-menu; the sample information, the HKHindex results and the underlying metrics will be copied.
- If you want to **save** the HKHindex calculation data of this sample, press the 'Save sample'-button.
- If you want to **close** the 'HKHindex' window, press the 'Close'-button.

EXPORT

The 'Export' window is opened by selecting **Export** in the menu.



EXPORT – TAXALISTS

The following selections/options are available:

Method

- all methods: all different methods available in the database
- quant – no subsampling
- quant – RIVPACS subsampling
- quant – area subsampling
- quant – volume subsampling

Taxalists

- Combined samples only: export of only combined samples (if you have entered more than one sample unit); sample units are not listed in separate columns
- Sample units separately: export of all investigated sample units in separate columns
- Complete taxalist (total sample only): export of a taxalist containing all selected sample codes in one Excel-sheet;
frequencies: sum of all different fractions per sample unit; total number of taxa is given at the end of the list
- Complete taxalist (total sample + details): export of a taxalist containing all selected sample codes in one Excel-sheet;
frequencies: all different fractions in separate columns; total number of taxa is given at the end of the list
- Taxalist for each sample code: export of taxalists for the selected sample codes, each sample code in a separate Excel-sheet;

frequencies: all fractions (details), all sample units in separate columns; total number of taxa is given at the end of the list

Note: *Not all options are possible for all methods.*

Frequency

- Ind/area: individuals per sampled area
- Ind/m²: individuals per m²
- p/a: presence/absence data

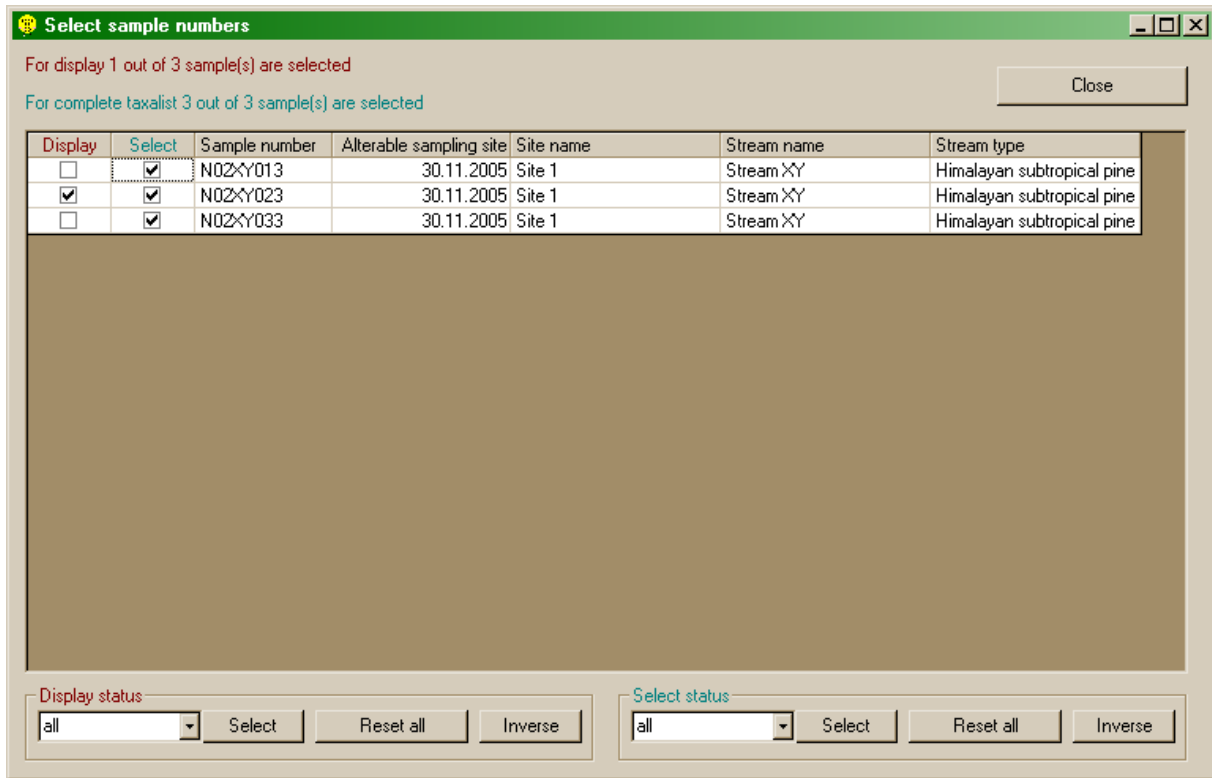
Rows

- all: all rows are exported including higher taxonomic units
- Families only: only families are exported; frequencies of the taxa are summed up to family level
- Species only: only species are exported without higher taxonomic units

Selections

- Taxalist including the taxa of all sample codes: export of a taxalist containing all taxa occurring in all ever entered sample codes (in the entire database).
- Taxalist including the taxa of selected sample codes: exports a taxalist containing only those taxa occurring in the samples with the selected sample codes; the taxalist consists of all taxa occurring in those sample codes marked in the column 'Select'; sample codes which are to be displayed (abundances or p/a-data) are to be marked in the column 'Display'.

Note: *The first option displays all entered taxa irrespective of the fact whether the taxa occur in the selected sample site or not (so you may get some empty rows). The second option may be useful if you want to display for example only the taxa occurring in a certain river type.*



Note: It is possible to select all sample codes belonging to one river type/river name/method together. This is to be done at the lower end of the window by selecting the appropriate level (River type, River name, Main or Replicate, Method, Substratum (only algae)) in the selection list. Place the cursor in a favoured sample codes. Then press **Select** and all sample codes belonging to the selected type of the appropriate level will be marked automatically.

Names of the exported taxalists

The taxalists are exported to the specified export directory.

name of the taxalist	name of Excel file	name of Excel sheet
Complete TL - combined sample - TS	CompleteTaxalist.xls	Taxalist_[Frequency]_#[Sheetnumber]
Complete TL - combined sample - TS + Details	CompleteTaxalist_Details.xls	Taxalist_[Frequency]_#[Sheetnumber]
Complete TL - sample units - TS	CompleteTaxalist_SU.xls	Taxalist_[Frequency]_#[Sheetnumber]
Complete TL - sample units - TS + Details	CompleteTaxalist_SU_Details.xls	Taxalist_[Frequency]_#[Sheetnumber]
TL for each sample code	SampleTaxalist.xls	[Samplenumber]_[Frequency]_#[Sheetnumber]

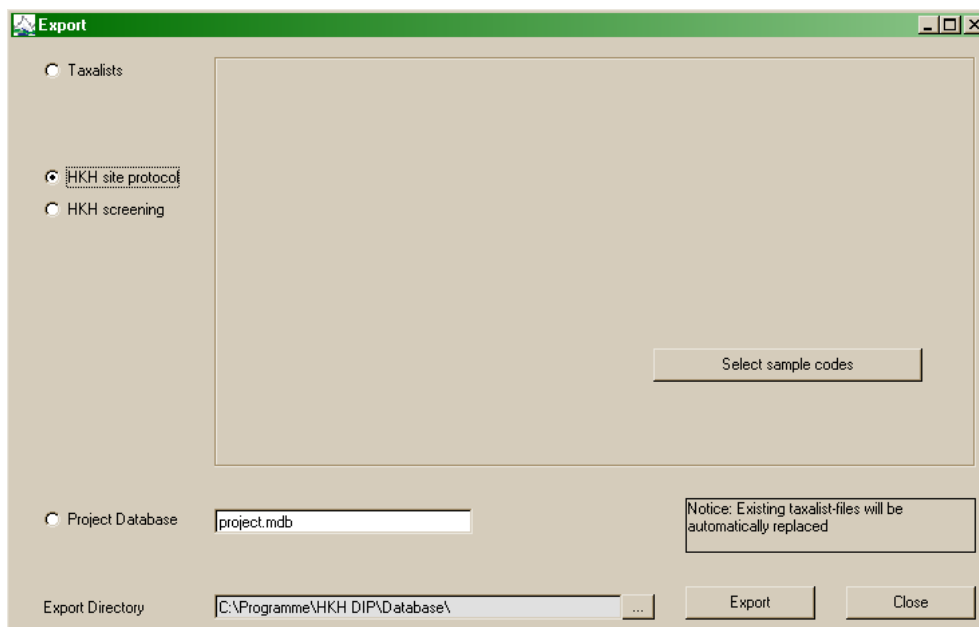
- The entries within the []-brackets are replaced by the current data during taxalist-compilation.
- [Frequency]: Ind_m², Ind_Ar, Ind_pa according to the selection in the export window
- [Sheetnumber] – continuous number starting with 1
- [Samplenummer] – Sample code

Note: The export will automatically replace existing taxalist-files with the same name.

Please close your Excel first before doing any export!!!

EXPORT – RIVER CHARACTERISTICS

Exports the HKH site protocol to MS Excel. Choose the sampling sites that should be exported by pressing 'Select sample codes'.



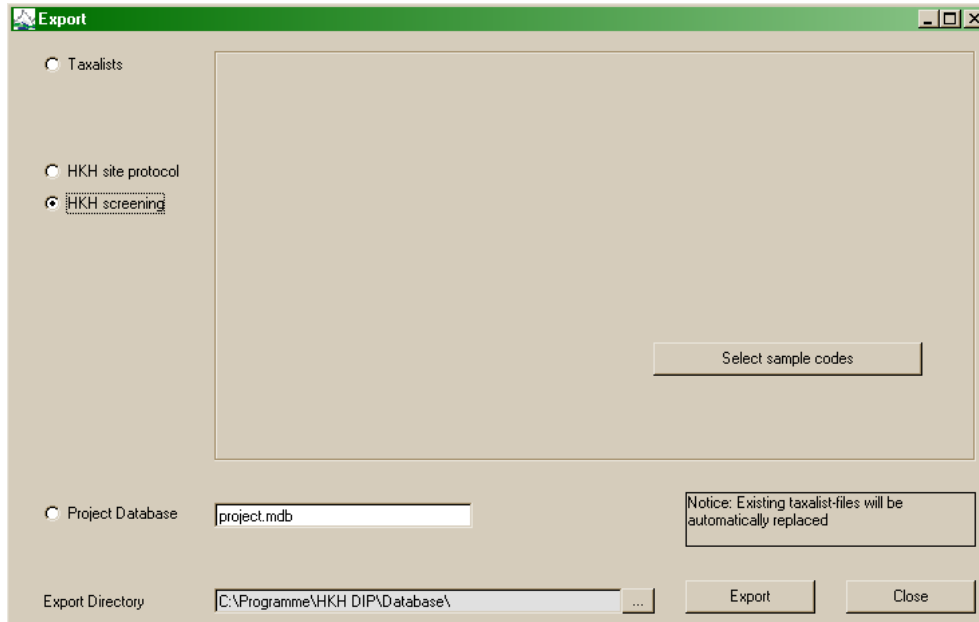
- Columns: sample codes
- Rows: parameters of the site protocol
- Tables 'MHS table' and 'sample replicates' will be exported in separate Excel-sheets.

Note: All missing values are exported as -2.

Note: Please close your Excel first before doing any export!!!

EXPORT – HKHscreening

Exports the HKHscreening protocol to MS Excel. Choose the sampling sites that should be exported by pressing 'Select sample codes'.



Note: Please close your Excel first before doing any export!!!

EXPORT – HKHbios

To export HKHbios data to another Windows software, press the 'Clipboard'-button in the 'HKHbios'-window, open the other software and choose 'insert' from the right-mouse-button-menu. The sample data, the HKHbios taxa and the HKHbios result will be copied into the other software.

Note: If you have ticked the checkbox 'Show selected taxa only' only those taxa that occur in your sample will be copied to the clipboard.

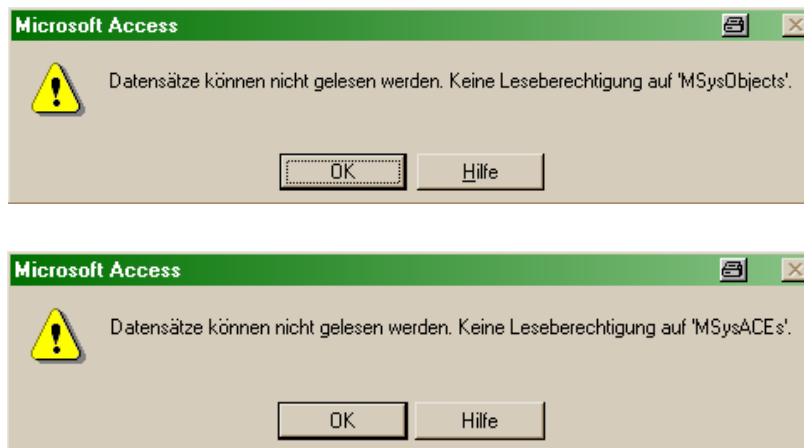
EXPORT – HKHindex

To export HKHindex data to another Windows software, press the 'Clipboard'-button in the 'HKHindex'-window, open the other software and choose 'insert' from the right-mouse-button-menu. The sample information, the HKHindex results and the underlying core metrics will be copied into the other software.

DATABASE EXPORT TO ACCESS

HKHdip taxa data can be exported to MS Access by choosing the export option 'Project database'.

Note: When opening the MS Access database two error messages may occur. Just confirm them with "OK".



The Access-database includes the following tables:

- Project: contains all information regarding the investigated sites
- Projecttaxa_MZB_NoSubsampling: contains the occurrence of macro-invertebrate taxa per sample codes for all samples that were not subsampled
- Projecttaxa_MZB_RIVPACS: contains the occurrence of macro-invertebrate taxa per sample codes for all RIVPACS subsampled samples
- Projecttaxa_MZB_Area: contains the occurrence of macro-invertebrate taxa per sample code for all area subsampled samples
- Projecttaxa_MZB_Volume: contains the occurrence of macro-invertebrate taxa per sample code for all volume subsampled samples
- Taxa: contains all information on the occurring macro-invertebrate taxa

The following table contains those column headings of the 'project.mdb' that are not self-explaining or that do not correspond to the fields of the different input windows.

Table	heading	Description
Project	ID_UUS	internal identity number of the sampling site
	ID_VUS	internal identity number of the sampling date
	ID_TR	internal identity number of the sample code
	ID_PS	internal identity number of the sampling site
	Fraction*	percentage of the different sample fractions (if applied)

HELP-HOTLINES

- For technical problems please contact ROBERT VOGL (irv@irv-software.at).
- For problems with the 'River characteristics' (input and export) please contact JÖRG STRACKBEIN (joerg.strackbein@uni-essen.de).
- For problems with 'Taxa input'/export and for mistakes in and additions to the taxalist please contact ASTRID SCHMIDT-KLOIBER (astrid.schmidt-kloiber@boku.ac.at).
- For problems with HKHscreening please contact ANNE HARTMANN (anne.hartmann@boku.ac.at) and OTTO MOOG (otto.moog@boku.ac.at).
- For problems with HKHbios please contact THOMAS OFENBÖCK (thomas.ofenboeck@boku.ac.at) and Otto Moog (otto.moog@boku.ac.at).
- For problems with HKHindex please contact THOMAS OFENBÖCK (thomas.ofenboeck@boku.ac.at) and Thomas Korte (thomas.korte@uni-due.de).
- For other problems regarding site protocol content and general questions please contact OTTO MOOG (otto.moog@boku.ac.at).