



Practical Sessions on RIVPACS III+

A series of step-by-step exercises to demonstrate some of the major options available in RIVPACS III+.

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CONTENTS

Installing RIVPACS III+

1. Interactive predictions
 - 1a) BMWP family level : manual data input
 - 1b) BMWP family level : data input from files
 - 1c) BMWP family level : O-E input from files, assign to quality bands
 - 1d) BMWP family level : manual O-E input, allow for sample bias
 - 1e) Abundance for all families and the abundance index
 - 1f) Multiple taxonomic levels (and/or seasons) on a single run
 - 1g) Setting up and using a customisation
2. Interactive sample comparisons
 - 2a) Compare : manual O-E input, differences in O/E and quality band
 - 2b) Compare : O-E input from files, allow for sample biases
3. Interactive classification
4. Setting up and using defaults files
5. Batch mode operation
 - 5a) Using the batch setup menu option
 - 5b) Running a simple batch mode prediction
 - 5c) Multiple predictions in batch mode
6. Bias file setup
7. Quality bands file setup

RIVPACS III+ : INTRODUCTORY NOTES

Loading the software

The RIVPACS software should be loaded in a directory of its own. This does not prevent input and output files being stored elsewhere if necessary (see later exercises).

To load the software, the PC should be switched on and set at the C: drive. To create the required directory for carrying RIVPACS III+, at the C:> prompt type
MD RIVPAC3P <<enter>>

The symbols << and >> are used throughout this document to signify a single key which must be pressed.

The PC should now be set to the new directory before loading the software. Therefore, at the C:> prompt type
CD RIVPAC3P

The RIVPACS software is provided on a single disk. To load it, insert the disk in drive A: and type
A:\INSTALLR <<enter>>

The software, which is compressed, will be expanded and loaded and the state of progress will be shown on the screen.

Getting going

Your PC should now be set at the C:\RIVPAC3P> prompt and the software loaded and ready for action.

To get going type
RIVPACS <<enter>>

The first screen is the title page and this is followed by two pages of background text. Each is exited by pressing <<enter>> or any other key.

The main menu panel offers the basic choice of type of run and the seven main options are described in this collection of exercises.

For each of the exercises that follow you need to select one of the main panel options. The exercises successively cover PREDICTION, COMPARE, CLASSIFICATION, DEFAULTS SETUP, AUTO/BATCH SETUP, SAMPLE BIAS SETUP and QUALITY BAND SETUP. HELP boxes with informative text are a menu option at many key stages. EXIT is used to leave RIVPACS and return to the C:\RIVPAC3P> prompt. At each exercise select the appropriate menu option.

General considerations

Throughout the following exercises the selected response to each on-screen prompt box or menu is determined by highlighting your chosen option, using the up/down, left/right arrows, and pressing <<enter>> or by typing the option number or initial letter of your selection.

Sometimes <<Esc>> can be used to terminate a run and return to the initial main menu. Many prompt boxes/menus offer the option to return to previous screens or return to the start (i.e. main menu panel)

Most prompt boxes allow only a single choice to be made but more than one taxonomic level or season can be selected for each run.

RIVPACS III+ : INTERACTIVE PREDICTIONS (1a)

Introductory note

Many keyboard operations are common to all RIVPACS III+ runs and are tedious to repeat throughout this primer. They are given in italics in this first example only and are assumed for subsequent exercises.

Pressing <<enter>> is not necessary if the initial letter of your chosen option or its menu number is used to select it.

BMWP family level - manual data input (Example 1a)

As a simple, introductory example, make the following choices:

Procedure	:	Prediction	<<enter>>
Country	:	Great Britain	<<enter>>
Taxonomic level(s)	:	BMWP families & BMWP indices (1)	<<enter>>
<i>The C: SELECTION COMPLETED bar is now highlighted Press <<C>> or <<enter>></i>			
Biological data on file?	:	NO	<<enter>>
File input of O-E values?	:	NO	<<enter>>
Screen input of O-E values?	:	NO	<<enter>>
Season (s)	:	Spring, summer & autumn combined (7)	<<enter>>
<i>The C: SELECTION COMPLETED bar is now highlighted Press <<C>> or <<enter>></i>			
Environmental variables	:	Option 1	<<enter>>
<i>Continue/Previous screen</i>	:	<i>Continue</i>	<<enter>>
Environmental data on file?	:	NO	<<enter>>
Proceed automatically?	:	NO	<<enter>>
[the environmental data to be manually entered]			
Predicted taxa on screen?	:	YES	<<enter>>
Outputs to disk file?	:	NO to each option	<<enter>> after each response
[in this run see taxa and scores on screen]			
Stop listing taxa?	:	Keep it as 0.1% for BMWP level	<<enter>>
<i>Continue/Previous screen</i>	:	<i>Continue</i>	<<enter>>

Now enter the following data (1 site only).

Site reference	:	Frome at East Stoke	<<enter>>
Grid reference	:	SY 866 867	<<enter>>
Altitude (m)	:	13	<<enter>>
Distance from source (km)	:	43	<<enter>>
Water width (m)	:	18	<<enter>>
Water depth (cm)	:	64	<<enter>>
Discharge category	:	6	<<enter>>
Boulders (% cover)	:	13	<<enter>>
Gravel (% cover)	:	61	<<enter>>
Sand (% cover)	:	22	<<enter>>
Silt (% cover)	:	4	<<enter>>
Alkalinity (mg l ⁻¹ CaCO ₃)	:	172	<<enter>>
Slope (m km ⁻¹)	:	10	<<enter>>
Are environmental data correct?	:	Y (YES)	<<enter>>
Enter data for another site?	:	N (NO)	<<enter>>
Environmental data are then displayed	:		<<enter>>
Probabilities of group membership are given	:		<<enter>>
Predicted BMWP families are listed	:		<<enter>>
BMWP index values are presented	:		<<enter>>

*Press <<enter>> to scroll through the list
Press <<enter>> to return to the main panel*

RIVPACS III+ : INTERACTIVE PREDICTIONS (1b)

BMWP family level - data input from files (Example 1b)

Initially, we offer a straightforward example to familiarise you with the use of input/output files and confidence limits for O/E values.

This can be followed by examples of your own using different responses at each asterisk (*).

The responses for this exercise are as follows:

	Procedure	:	Prediction
*	Country	:	Great Britain
	Taxonomic level(s)	:	BMWP family & BMWP indices (1)
	Biological data on file?	:	YES
*	Season(s)	:	Spring, summer & autumn combined (7)
	Biological file name	:	TSTFAMGB.ASC
*	Environmental variables	:	Option 1
	Environmental data on file?	:	YES
*	Type of file	:	ASCII
	Environmental filename	:	TSTENVGB.ASC
	Allow for sample bias?	:	NO
	Assign to quality bands	:	NO
	Proceed automatically?	:	YES
	Output to disk file?	:	YES
	Output listing filename	:	WKBMWPIB.LST
*	Include predicted taxa?	:	YES
*	Do not create additional output files on this run		
*	Stop listing taxa?	:	0.1%

The three Great Britain test file sites are flagged as the prediction proceeds, before the main panel reappears.

Examine your output file WKBMWPIB.LST as follows:

Exit from main panel

At the prompt C:\RIVPAC3P> type

EDIT WKBMWPIB.LST <<enter>>

To close the DOS editor press the following three keys in sequence

<<Alt>> <<F>> <<X>>

Then re-enter RIVPACS from the C:\RIVPAC3P> prompt, type

RIVPACS <<enter>>

Now do another run and make your own choice at each asterisk. When making your own choices, refer to the list of example input files in Appendix 3 of the RIVPACS III+ manual to be sure of entering the correct file names.

RIVPACS III+ : INTERACTIVE PREDICTIONS (1c)

BMWP family level - file input O-E values, assign samples to quality bands (Example 1c)

This example introduces the option to use previously calculated observed(O) and expected(E) BMWP index values for the samples as an input file and the facility to assign samples probabilistically to quality bands. The O-E file to be used as input in RIVPACS III+ could have been derived as an output file from a run of RIVPACS III which used the biological and environmental data files for the samples.

Use the procedure detailed under example (1b) to view the contents of O-E input file TSTOET2.DAT to be used in this example.

Procedure	:	Prediction
Country	:	Great Britain
Taxonomic level(s)	:	BMWP family & BMWP indices (1)
Biological data on file?	:	NO
Input O-E values from file?	:	YES
O-E input data filename	:	TSTOET2.DAT
Allow for sample bias?	:	No
Assign to quality bands	:	YES use default GQA limits (2)
Proceed automatically?	:	NO
Output to disk file?	:	YES
Output listing filename	:	WKBMWP1C.LST
Output O-E type 1 file?	:	NO

The confidence limits for the O/E ratios for a sample and the subsequent estimated probabilities of belonging to each quality band are presented, for convenience, on one output screen. As the band given to a sample based on the GQA banding system is the lower of its bands based on each of O/E for number of taxa and ASPT, no information is given for O/E based on BMWP score.

Use the procedure detailed under example (1b) to view the contents of output file WKBMWP1C.LST

RIVPACS III+ : INTERACTIVE PREDICTIONS (1d)

BMWP family level - screen input of O-E values, allow for bias, assign to quality bands (Example 1d)

This example introduces the ability to allow for the effect of sample bias on an assessment of O/E values and on the assignment of samples to quality bands. It demonstrates the ability to input the O and E values, the seasons involved and the sample biases from the screen.

```
Procedure           : Prediction
Country            : Great Britain
Taxonomic level(s) : BMWP family & BMWP indices (1)
Biological data on file? : NO
Input O-E values from file? : NO
Screen input of O-E values? : YES
* Store in O-E data filename : WKOET1D.DAT
* Sample code                : Tumbledown
* Observed BMWP score        : 139
* Observed number of taxa    : 25
    Observed ASPT calculated automatically as 139/25 = 5.56
* Expected BMWP score        : 190.1
* Expected number of taxa    : 30.2
* Expected ASPT              : 6.29
* Seasons involved  Spring  : N
*                       Summer : Y
*                       Autumn : Y
* Specify sample biases?    : Y
* Bias for      Summer    : 1.9
*               Autumn    : 2.4
* Enter another sample?     : N
* Assign to quality bands   : YES use default GQA limits (2)
* Proceed automatically?   : NO
* Output to disk file?     : YES
* Output listing filename   : WKBMWP1D.LST
* Output O-E type 1 file?  : YES
* O-E output filename      : WKBMWP1D.OE1
```

The confidence limits for the O/E ratios for a sample and the estimated probabilities of belonging to each quality band are presented, for convenience, on one output screen with the results uncorrected for bias on the left-hand side and results corrected for bias on the right-hand side.

Use the procedure detailed under example (1b) to examine the contents of output file WKBMWP1D.LST.

Examine O-E type 1 output file WKBMWP1C.OE1 (one long line for each of the two samples) and check the meaning of the output statistics by referring to section 6.11 of the RIVPACS III+ User Manual. (Such files could be read into EXCEL for further analysis.)

Now do other runs and make your own choice at each asterisk.

RIVPACS III+ INTERACTIVE PREDICTIONS (1e)

Abundance for all families and the abundance index (Example 1e)

This example involves making predictions of mean expected abundances (weighted arithmetic means of log categories) and of the experimental abundance index Q14.

The required responses for this exercise are:

Procedure	:	Prediction
Country	:	Great Britain
Taxonomic level(s)	:	Abundance for all families and abundance index (2)
Biological data on file?	:	YES
Season(s)	:	Spring (1)
Biological filename	:	TSTSPRGB.ASC
Environmental variables	:	Option 1
Environmental data on file?	:	YES
Type of file?	:	ASCII
Environmental filename	:	TSTENVGB.ASC
* Proceed automatically?	:	YES
Output to disk file?	:	YES
Output filename	:	WKSPABUN.LST
Include predicted taxa?	:	YES

Do not create additional output files on this run

Stop listing taxa? : Retain 0.0 log abundance.

As in the previous example (b), the three test sites are flagged as the prediction proceeds, before the main panel reappears.

Use the procedure detailed under example (b) to view contents of WKSPABUN.LST

* Alternatively the full prediction may be viewed at leisure on screen if you answer NO at this point and then request that predicted taxa are to be listed on screen. You still retain the option of creating output files if required.

RIVPACS III+ : INTERACTIVE PREDICTIONS (1f)

Multiple taxonomic levels (and/or seasons) on a single run (Example 1f)

In theory it is possible to request predictions at 5 taxonomic levels (1-5) and for 7 seasons/seasonal combinations (1-7). However, when using BMWP families and indices (taxonomic level 1) with error assessment, no other taxonomic level should be selected. Also, we recommend that you exclude taxonomic level 5 (Existing customisation) until you have become familiar with this option (see next section on setting up a customisation).

Merely excluding taxonomic levels 1 and 5 could still generate 17 predictions for each site if you request all of taxonomic levels 2-4 and seasons 1-7 (NB taxonomic level 2, abundance for all families only operates on seasons 1-3 (i.e. single seasons) at present).

Hence, we suggest that you are selective in your initial choice. Bear in mind that there are 3 sites in the environmental data example files and that if you request output files they will be substantial if you ask for the inclusion of predicted taxa.

As one example, try the following:

Procedure	:	Prediction
Country	:	Great Britain
Taxonomic level(s)	:	Choose 3 & 4
Biological data on file?	:	NO - on this initial run. [On a later run, reply YES, but bear in mind the need to input the appropriate example files when requested]
Season(s)	:	Choose 1 & 7
Environmental variables	:	Option 1
Environmental data on file?	:	YES
Type of file	:	ASCII
Environmental filename	:	TSTENVGB.ASC
Proceed automatically?	:	YES
Output to disk file?	:	YES
Output biological filename	:	WKSPMULT.LST
Include predicted taxa?	:	YES
Do not create additional output files	:	
Stop listing taxa?	:	Retain as 0.1 for all families Change to 50.0 for species

Follow the previous instructions for example (b) to examine the output file.

For each of the 3 example sites, the output sequence is,

Site name/code		
Environmental data		
Probabilities of group membership		
Predicted families	Spring	To 0.1%
	Spring, summer and autumn combined	To 0.1%
Predicted species	Spring	To 50.0%
	Spring, summer and autumn combined	To 50.0%

RIVPACS III+ : INTERACTIVE PREDICTIONS (1g)

Setting up and using a customisation.

At the outset, go through the sequence of operations to familiarise yourself with the procedure. Do not attempt to set up a useful customisation. This can be done later.

In the simple (and unlikely!) example below, we want a prediction in which all members of the Tricladida (flatworms) are identified at generic level. The remaining invertebrates are predicted at major taxonomic group only.

Procedure	:	Prediction	
Country	:	Great Britain	
Taxonomic level(s)	:	Chose new customisation (6)	
Name?	:	CUSTOM1	
Description?	:	Triclads to genus	
Country	:	Great Britain (G)	
Current taxon	:	Tricladida.	Select? N
		Planariidae.	Select? N
		<i>Planaria</i> sp.	Select? Y
		<i>Polycelis</i> sp.	Select? Y
		<i>Phagocata</i> sp.	Select? Y
		<i>Crenobia</i> sp.	Select? Y
		<i>Dugesia</i> sp.	Select? Y
		Dendrocoelidae	Select? N
		<i>Bdellocephala</i> sp.	Select? Y
		<i>Dendrocoelum</i> sp.	Select? Y
Current taxon	:	Gastropoda	Select? Y

Answer Y to all subsequent questions.

At the end, the screen indicates that this customisation generates 31 taxa. The necessary files are then created before the taxonomic level panel reappears. The customisation is thus saved to file and can be accessed in subsequent runs as follows:

Taxonomic level(s)	:	Existing customisation (5)
--------------------	---	----------------------------

On the next screen choose the UP or DOWN options in the upper menu box as often as necessary to scroll to the required customisation (CUSTOM1) in the lower menu box. After highlighting the required customisation, choose SELECT. Choose SELECT again on the subsequent screen to re-enforce your choice. [This screen also offers the option of deleting unwanted customisations. Use it on a subsequent occasion to delete CUSTOM1]

Biological data on file?	:	NO
Season(s)	:	Spring (1)
Environmental variables	:	Option 1
Environmental data on file?	:	YES
Type of file?	:	ASCII
Environmental filename	:	TSTENVGB.ASC
Proceed automatically?	:	YES
Output to disk file?	:	YES
Output biological filename	:	WKSPCUST.BIO
Include predicted taxa?	:	YES
Do not create additional output files	:	
Stop listing taxa?	:	Retain 0.1%

Follow previous instructions in example (b) to examine output file.

RIVPACS III+ : INTERACTIVE COMPARE (2a)

Compare two samples - screen input of O-E values, assess differences in O/E values and likelihood of differences in quality bands (Example 2a)

This example introduces main menu procedure Compare. This is used to compare two samples (or multiple pairs of samples) by assessing the statistical significance of the differences in their O/E values and by assessing the likelihood of a difference in quality bands.

The two samples can be the same site at different times, or two different sites; the season(s) involved can be the same or different. The only information needed for each sample is:

- (i) the previously calculated observed(O) and expected(E) values of BMWP score, number of taxa and ASPT for the two samples.
- (ii) the seasons involved
- (iii) the sample biases applicable to each season involved (optional)
- (iv) whether the expected values of both samples were based on the same values of the environmental variables.

In this example, the information is input from the screen; in later examples it is read from files.

Procedure	:	Compare	
Input O-E values from file?	:	NO	
* Store in O-E data filename	:	WKOET2A.DAT	
* Sample code	:	Tumbledown	Pickmeup Place
* Observed BMWP score	:	139	83
* Observed number of taxa	:	25	17
<i>Observed ASPT calculated automatically as:</i>		$139/25 = 5.56$	$83/17 = 4.88$
* Expected BMWP score	:	190.1	175.6
* Expected number of taxa	:	30.2	27.1
* Expected ASPT	:	6.29	6.48
* Seasons involved Spring	:	N	N
* Summer	:	Y	Y
* Autumn	:	Y	N
* Specify sample biases?	:	Y	
* Bias for Summer	:	1.9	2.5
* Autumn	:	2.4	
* Enter another sample?	:	N	
* Same values for variables	:	N	
Assign to quality bands	:	YES use default GQA limits (2)	
* Proceed automatically?	:	NO	
Output to disk file?	:	YES	
Output listing filename	:	WKCOMP2A.LST	
* Tables of change in band	:	Taxa, ASPT and Overall table	
Output O-E type 1 file?	:	No	
Output O-E type 2 file?	:	No	

The assessment of the O/E values and probabilistic banding for each of the two individual samples is given first; this part of the output to the screen and/or listing file and O-E type 1 file is exactly the same as for procedure Prediction for the individual samples. Next is a statistical assessment for differences in O/E values between the two samples and finally an assessment of the likelihood of differences in quality band when based on O/E for number of taxa, ASPT or the overall GQA band.

Use the procedure detailed under example (1b) to view the contents of O-E input file WKOET2A.DAT made from the screen input and the output listing file WKCOMP2A.LST.

RIVPACS III+ : INTERACTIVE COMPARE (2b)

Compare two samples - file input of O-E values, assess differences in O/E values and likelihood of differences in quality bands both ignoring and corrected for sample biases (Example 2b)

This example demonstrates the potential effect of allowing for sample biases in the comparison of two samples. The observed(O) and expected(E) values for the samples are also read from an O-E input file; this input file could have been derived as an output file, from a previous run of RIVPACS III+ or RIVPACS III, based on the biological and environmental data files for the samples.

Use the procedure detailed under example (1b) to view the contents of O-E input file TSTOET2.DAT to be used in this example.

Procedure	:	Compare
Input O-E values from file?	:	YES
Single or pair of files	:	1
O-E input data filename	:	TSTOET2.DAT
* Same values for variables	:	No
* Allow for sample bias?	:	YES
Obtain biases from?	:	bias file (1)
Bias filename	:	TSTBIAS.DAT
Assign to quality bands	:	YES use default GQA limits (2)
* Proceed automatically?	:	NO
Output to disk file?	:	YES
Output listing filename	:	WKCOMP2B.LST
* Tables of change in band	:	Overall table only
Output O-E type 1 file?	:	Yes
* O-E type 1 output filename	:	WKCOMP2B.OE1
Output O-E type 2 file?	:	Yes
* O-E type 1 output filename	:	WKCOMP2B.OE2

When correction for sample bias is requested all assessments are first given uncorrected for bias and then corrected for bias.

The assessment of the O/E values and probabilistic banding for each of the two individual samples is given first; this part of the output to the screen and/or listing file and O-E type 1 file is exactly the same as for procedure Prediction for the individual samples. Next is a statistical assessment for differences in O/E values between the two samples. The assessment of the likelihood of differences in quality band is given in a sequence of output screens based on (in order) O/E for number of taxa, ASPT or the overall GQA band, uncorrected for bias, then corrected for bias.

Use the procedure detailed under example (1b) to view the contents of output listing file WKBMWP2B.LST

Examine O-E type 1 output file WKBMWP2B.OE1 (one long line for each of the two samples) and O-E type 2 output file WKCOMP2B.OE2 (one long line for sample comparison statistics ignoring bias and a second corrected for bias). Check the meaning of the output statistics in both files by referring to sections 6.11 and 6.12 of the RIVPACS III+ User Manual. (Such files could be read into EXCEL for further analysis).

RIVPACS III+ : INTERACTIVE BIOLOGICAL CLASSIFICATION (3)

Species level classification

The classification procedures are simple to operate and depend upon the biological data being held on file. Only one practical example is given here.

A new site may only be classified using species level data (three seasons combined) or BMWP family data (three seasons combined).

Bear in mind that when the reference sites were used to develop the 35 group Great Britain and seven group Northern Ireland classifications, information on both species composition and family abundances was utilised. Use of this same procedure for classification of new sites would have been very cumbersome and is unlikely to have been used in practice. The simplified options of species or BMWP family classification have, thus, been retained from RIVPACS II.

We recommend that classification results are used, with caution, to allocate sites to a restricted area of the classification. It is unwise to place great importance to the individual classification group with which the site has most in common.

As an example, use the following procedure:

Procedure	:	Biological classification
Country	:	Great Britain
Taxonomic level	:	Species
Type of file?	:	ASCII
Biological filename	:	TSTSPRGB.ASC
Output to disk file?	:	NO
Proceed automatically?	:	NO

Then view the results on screen.

