

representing a site in central Siberia. I use the Global Soil Particle Size Properties as an example here only because one of its authors, Robin Webb, so brutally out-skied me last year while we were conducting observations of late-spring snow conditions and discussing the GED in Colorado!

RANDOM ACCESS COMPUTER KEYS (RACKs)

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To make visual identifications of objects we resort to comparison with identified specimens, illustrations, descriptions and keys. In biology these keys commonly require choice between sequences of often subtle taxonomic characters. In contrast, random access keys permit selection of taxa using the more obvious characters of the unknown specimen. Random access keys take three forms: determinative tables for identifying minerals and wood, the edge-perforated card key illustrated in Faegri and Iversen (1964, p. 200) for identifying pollen grains, and the Random Access Computer Key (RACK).

A RACK is basically a two-dimensional array of characters versus taxa. You work the key by entering the most obvious characters in any order; taxa having these characters are immediately listed on the monitor. Our BASIC program was modified from Ogden and Mitchell (1990) to which Maher added an editor to ease making changes.

The type of RACK we describe is handy, easy to use and modify, inexpensive to operate, and it makes an excellent teaching device. Although the European and North American Pollen Databases are organized and available by random access, they are not easy to learn, and they require a user have Paradox®.

Our first RACK was designed to handle North American Pollen grains and spores, and we call it NAPKEY.-BAS. It is a text-based key, and this was done to keep it simple and cheap. We are not competing with The South Pacific Pollen Atlas Project (Hope *et al.* 1992) or Cushing's (1991) Macintosh HyperStack® key SARI; both make use of screen graphics and are much more complex to set up and maintain. NAPKEY comes up with a screen that provides information and a few rules. The user then sees a screen like Fig. 1. There are 105 pollen/spore characters or character values grouped into nine menu categories. The main categories are shown in yellow capital letters. You can type a number or the letters N, R, or Q. If the number is between 1 and 105, the corresponding character item changes color, and the number of taxa with that character appears at the screen's upper left. You can see the names of these taxa by pressing the letter N. Normally one has several characters set simultaneously to reduce the number of possible taxa. If setting a character results in 0 taxa with that combination of characters, typing the number again *prefixed with a minus sign* turns the character off. If you want to reset everything and start again, touch the letter R. Touch Q to quit.

While it is not overly helpful to a student to see a list of taxon names, a lot of names indicates more grain characteristics are going to be needed to narrow down the possibilities. Whereas the microscope is best for deciding which taxon matches the unknown grain, RACKS should be used with a paper manual. NAPKEY uses McAndrews *et al.* (1973); when the taxa names appear, the user is given helpful comments as well as reference to figures showing the grain.

GRAIN	POLAR/EQUATOR	SIZE (µm)	APERATURES	NAPKEY
1 nonad	21 >2.00	42 <10	63 0	85 p.elliptical
2 dyad	22 2.00-1.33	43 10-15	64 1	86 p.rectangular
3 tetrad	23 1.33-1.14	44 15-20	65 2	87 p.constricted
4 polysad	24 1.14-0.90	45 20-25	66 3	88
5 fenestrate	25 0.90-0.75	46 25-30	67 4	89
6 bilateral	26 0.75-0.58	47 30-40	68 5	90
7 broken	27 0.58	48 40-50	69 6	91
8	28 heteropolar	49 50-75	70 7-12	92
9 >44 u sac	29 rhomboidal	50 75-100	71 >12	93 peltate
10 >44 u sac	30 rectangular	51 100-150	72 colpua	94 foveolate
11 0.5 sphere	31 pear	52 150-200	73 pore	95 foveolate
12 >0.5 sphere	32 angle aperture	53 200	74 poroid	96 gemmate
13 dist. var.	33 intang. aper.	54 <15	75 compound	97 wabrate
14 dist. slit	34 circular	55 15-20	76 with membrane	98 verrucate
15 cap irreg.	35 polar area <8.6	56 20-25	77 p.eq.along.	99 rugulate
16	36 polar area >8.6	57 25-30	78 p.with arci	100 striate
17 alete	37 no polarity	58 30-35	79 p.protruding	101 echinate
18 nonolete	38 triangular	59 35-40	80 p.chambered	102 ret. homo
19 trilete	39 lobata	60 40-50	81 margin/annulus	103 ret. het.
20 perline	40	61 >50	82 operculum	104
Character?	41	62	84	105

Figure 1. NAPKey Work Screen.

McAndrews, J.H. and Z. Yu. 1994. Random access computer keys (RACKs). INQUA Commission for the Study of the Holocene, Working Group on Data Handling Newsletter 11:10-12.

HARDWOOD RANDOM ACCESS KEY		
= GENERAL		
2 Heartwood distinct	24 Simple	= PARENCHYMA
3 Heartwood odor distinct	25 Scalariform	46 Rare or absent
4 Ring-porous	26 More than 10 bars	47 Marginal
5 Semi-ring-porous	= VESSEL PITS	48 Paratracheal-scurty
6 Diffuse-porous	28 Opposite	49 Paratracheal-vascular
7	29 Alternata	50 Paratracheal-alliform
8	30 Scalariform	51 Paratracheal-confluent
= GEOGRAPHIC ORIGIN	31 Less than 5 u	52 Apotracheal-diffuse
18 Eastern	32 Less than 12 u	53 Apotracheal-dif.in ag.
11 Western	33 More than 12 u	54 Banded
12 Other	34 Linear	= RAYS
13	35 Vestured	56 Uniseriate
= VESSEL PORE ARRANGEMENT	36	57 Up to 4 seriate
15 Earlywood pores in 1 row	37 Tracheids vascular	58 Widest 5 to 10 seriate
16 Mostly military	38 Tracheids vascular	59 Widest >10 seriate
17 Multiple	= FIBERS	60 Aggregate
18 Chain	40 Libriform	61 Homocellular
19 Wavy bands	41 Fiber tracheids	62 Heterocellular
20 Mixed	42 Septate	63 Storied
21	43 Spirals	64 Ray-vessel pitting I
22 Vessel with spirals	44	65 Ray-vessel pitting II
Character?		66 Ray-vessel pitting III
	M: Names	R: Reset
	H: Help	Q: Quit

ROCK COLOR	TEXTURE/CRYSTALS OR FRACMENTS	ROCK CATEGORY	MINERAL CATEGORY
1 Light	28 Interlocking	35 Smooth	55 < 2.5
2 Dark	21 Packed	36 Uneven	56 2.5-6
3 Intermediate	22 Porphyritic	37 Snow Facies	57 > 6
4 Black	23 X-tals V. Fine	38 Equant	58 Metallic
5 Red/Purple	24 Glassy	39 Prismatic	59 Non Met.
6 Brown/Tan		40 Bladed	60 U. Low
7 Yellow		41 Tabular	61 > 4
8 Green		42 Pyramidal	62 Crystalline
= MINERAL COLOR		43 Blocky	63 Earth/Mass
9 White/Clear		44 Columnar	64 Crust/Thin
10 Gray		45 Micaceous	65 Radiating
11 Black		46 Headless	66 Branching
12 Yellow/Orange		47 Striations	67 Banded
13 Red/Pink		48 None Visible	68 Rounded
14 Brown		49 At least 1	69 Only 1
15 Green		50 Only 2	70 3 or more
16 Blue/Purple		51 Only 1	71 Right Angle
17 Silver		52 3 or more	72 Not Right
= SPLITS		53 Right Angle	
18 Regular Layers		54 Not Right	
19 Irreg. Layers			
Character?		M: Names	R: Reset
		H: Help	Q: Quit

TYPE	ENGINE POSITION	WING PLAN	AIR KEY
1 Commercial	28 In Body	37 Swept	54 Ice
2 General Av.	21 Over Wing	38 Not Swept	55 Mid
3 Ag Plane	22 Under Wing	39 Delta	56 Low
4 Military	23 At Tail	40 Parallel Slab	57 With Dihedral
5 Propeller		41 Conat. Taper	58 Two
6 Tractor		42 Center-Taper	59 Three
7 Pusher		43 Curved Tip	60 Normal
8 Piston		44 Blunt Tip	61 Boom
9 Jet		45 Winglets	
= ENGINE		46 None	
10 Radial		47 One to Four	
11 In Line		48 > Four	
12 Vee			
13 Hor. Opposed			
14 Gas Turbine			
= ENGINE MFR			
15 None			
16 One			
17 Two			
18 Three			
19 > Four			
Character?			

Figure 2. HDKey, MINKey and AIRKey

We have just completed a RACK for Hardwood (HWKEY.BAS) based on a table in Panshin and de Zeew (1970). Maher made a Rock and Mineral Key (MINKEY.BAS) based on Bowser *et al.* (1968), as well as one for identifying airplanes (AIRKEY.BAS) which refers to page illustrations in Montgomery and Foster (1984). The main screens of these RACKs are shown in Fig. 2. RACKs for tropical pollen, seeds and minnows are in progress.

Because we are sure you are going to want to make a RACK for your own use, we have produced Generic RACK forms. They require no screen mapping to complete, and you can just fill in the blanks. The working screen comes in versions of two, three, four or five columns, together with editors for each type. Fewer columns are simpler and require fewer abbreviations. The group label on the generic RACKs is just another character with a CAPITALIZED name, and thus it is edited as a character.

A RACK is most useful when a user can add or delete taxa or change the characters associated with taxon. Lou Maher will discuss his EDITRACK program in the next article. These programs can run using QBASIC that come with DOS 5. You can get them by ftp from the INQUA File Boutique. They occur in the self-extracting file RACKS.EXE in directory: /pub/inqua on geology.wisc.edu (ftp 144.92.137.14).

References.

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Ogden, E.C. and R.S. Mitchel. 1990. Identifications of plants with fleshy fruits. New York State Museum Bulletin No. 467.

EDITKEY: FOR WHEN YOU CHANGE YOUR MIND

Louis J. Maher

When Jock McAndrews first let me see NAPKEY.BAS, I immediately wanted to add the information from my "edge-notched" card key that has lain on my desk for 30 years. Notched cards were so much fun when they were new; you ran a rod through the hole representing a character of the unknown grain, and all those grains with that character hole cut out fell on the desk. If you had put the grain's picture on the card, there would often be a good match. You could add a new card, cut a new slot, or repair a wrong cut, and the key went right back to work. Problems arose when there were more than about 50 cards; notched ones tended to stick in the deck, and they were hard to shuffle back into order. With NAPKEY you could alphabetize the cards and check their pictures against the RACK's suggestions.

The algorithm Ogden and Mitchel (1990) use in their key to fleshy fruits is written in BASIC with numbered lines. It is quite efficient, very fast, and all the data are stored right in the program so there are no external files to get lost. Three variable groups are involved; all are "character strings" that BASIC reads from lines prefixed with the word DATA. One group includes the words used in the screen menu, the second group is composed of lines with the taxon names, figure references and comments, and the third group is nothing but long lines of 0's and 1's. Each of these "gibberish" lines correspond to one of the key characters, and each position from left to right along the line represents one of the taxa. If the taxon has the character there is a "1"; if it does not there is a "0". The program reads each of these lines as a single string variable and sorts things out using BASIC's excellent string-handling features.

One *could* edit the original BASIC lines, of course, but it is tedious and time-consuming, and there is a high probability something will be messed up and the program will not run at all.

My plan for making a program to edit NAPKEY involved the removal of all the line numbers and grouping the parts into a structure with which it is easier to deal. I wanted to divide the program into two pieces: first the part with the algorithm and a second part with all the variables. The part with the variables would be a subroutine to which control is passed when the program starts. If the two parts were separated with a line that could be recognized, the editing program would simply read the BASIC program as lines of text and save them immediately as a file with a name like "ZZZPART1.TXT". That text file will always end with a line like "<<< Do not move this line >>>" because the editing program looks for consecutive ">>>" characters to separate the two parts.

Then EDITNAP watches for lines with "MENU =", "TAXA =", and "CHAR =", and it reads the numbers after the "=" sign. The present version of NAPKEY has the lines:

MENU = 115

TAXA = 144

CHAR = 105

MENU will contain all the phrases that appear on the menu screen. CHAR refers to the number of characteristics in the key, and the difference between MENU and CHAR (here 10) will be the lines used for group titles. Phrases for the titles will be put on the screen last with a different color.

The editing program then looks for lines beginning with "DATA", reads each in as a single string variable, strips off the parts it does not want and interprets the rest as the variables it needs. Once the values are in, their editing can begin.

My initial plan had to be altered when I began to deal with the characters and group titles for the screen. The screen labels are strings placed by their starting line (1 to 25) and starting column (1 to 80). One would have to read these locations and try to map out the screen. For example in Fig. 1 of Jock and Zicheng's article, "25 0.88-0.75" starts at line 7, column 16; but to what does that refer? It could be size or range of some other factor; it happens to be the ratio of polar axis to equatorial axis. When a user edits a taxon's characters,

it does no good to offer to toggle the presence or absence of "25 0.88-0.75" unless he/she knows what it is. It would probably be possible for the computer to figure out the titles for each character in NAPKEY, but I imagine someone could make a key's screen that would foil any procedure I might produce. So I have put the screen variables *before* the "cut line." This means there can not be a single EDIT-KEY program; rather for NAPKEY there must be EDITNAP, for MINKEY, there must be EDITMIN, etc. To make EDITNAP, the user must read NAPKEY into a text editor and find the part dealing with the screen labels:

```
....
DATA 3, 16, *21 >2.00*
DATA 4, 16, *22 2.00-1.33*
DATA 5, 16, *23 1.33-1.14*
DATA 6, 16, *24 1.14-0.88*
DATA 7, 16, *25 0.88-0.75*
DATA 8, 16, *26 0.75-0.50*
DATA 9, 16, *27 <0.50*
DATA 10, 16, *28 heteropolar*
DATA 11, 16, *29 rhomboidal*
```

The fragment above would be expanded into something like:

```
....
DATA * EQUATOR SHAPE - 21   perprolate *
DATA * EQUATOR SHAPE - 22   prolate *
DATA * EQUATOR SHAPE - 23   subprolate *
DATA * EQUATOR SHAPE - 24   spheroidal *
DATA * EQUATOR SHAPE - 25   suboblate *
DATA * EQUATOR SHAPE - 26   oblate *
DATA * EQUATOR SHAPE - 27   peroblate *
DATA * EQUATOR SHAPE - 28   heteropolar *
DATA * EQUATOR SHAPE - 29   rhomboidal *
```

which would be pasted near the end of EDITNAP.BAS after the lines:

```
.....other needed items----
REM Data for Screen follows; As new characters
REM are added to NAPKEY.BAS, add their names to
REM the following list as well.
```

Actually this is not too bad. It gives the user the chance to see how the program works and to make the phrases clearer. The Generic RACKs Jock and Zicheng made save time setting up a new key's screen, but one must still see that the categories in, say, EDIT_X conform to those in X_KEY.

It is important to remember that EDITNAP expects to find that NAPKEY.BAS is an ASCII text file. If you use a wordprocessor, be sure to save changes as simple ASCII text.

When EDITNAP runs it sets aside some space for new taxa you may add, shows you the directory and asks which file to edit. When it is loaded you will see a screen listing the first taxon in the key. A line below begins with the phrase **Letter and/or <Enter>**, followed by a flashing cursor. You can step through the taxa by pressing the <Enter> key (or back up by

pressing <Ctrl+Enter>). If you type a letter or letters, the program jumps to the first taxon starting with that combination. If you want to add a new taxon to the key, type the taxon name, capitalized the way you wish, and press "&" rather than <Enter>. The program will place this taxon in alphabetical order and let you indicate its characteristics. Instructions are always at the bottom of the screen. The <F1> key deletes the taxon whose name is shown. The <F4> key allows you to edit the taxon's name line--*never the spelling* (see below). The <F5> key shows you the taxon's physical characteristics and allows you to step through them quickly with the up/down arrow keys. When you find one you wish to change, press <Enter> and the characteristic will toggle between "Present" and "0." Pressing <F10> drops you back to select another taxon. When you are finished, the <F10> will save the results by reconstructing a new addition of NAPKEY.BAS, saving the original version as NAPKEY.BAK. You can delete that later when you are satisfied with the new version.

Do NOT edit the spelling of an existing taxon's name.

Record a list of the taxon's characteristics, if they are already entered, and use <F1> to delete the incorrectly spelled taxon. Then add the correctly-spelled taxon name with "&", remembering to use <F5> to annotate its characteristics. *It is important to let the program do the alphabetizing.* If you edited a taxon name from *Ambrosia* to *Xanthium*, for example, and then added *Pinus* (by typing *Pinus&*) you would find it placed just before *Xanthium* somewhere among the taxa beginning with "A". You will be alright if you let the program do the alphabetizing of the taxon names you add appended with &.

If you think a student would benefit from constructing his/her own NAP key just from the specimens seen in class, you might want to keep the key structure without its data. You can do that by copying NAPKEY.BAS to NEWKEY.BAS. Search for the line "CHAR = 144" and change the number to 1. Because the screen categories remain the same, you can edit NEWKEY with EDITNAP. When you edit NEWKEY.BAS the first taxon, *Abies*, will be on the screen. Immediately type *Dummy&* to add a dummy taxon. Then delete *Abies* and exit. Your student can start off with a key containing only a single dummy taxon that holds a place until he/she enters the class taxa while learning pollen at the same time.

Jock and Zicheng's Generic RACK templates may save time in making new keys, but you may like the challenge of designing your own screen. Get a piece of graph paper and mark out a rectangle 25 spaces high by 80 spaces wide. Use a pencil to place your group titles and characteristics--remembering to stay out of lines 1 and 25; the program uses those. Leave at least 2 spaces at the right too because the characters move right one space when they are selected. If they are moved into column 80, *bad* things will happen.

Is there a limit to the number of taxa you can use in the key? Yes, and it has to do with how QBASIC and QUICKBASIC store strings. AIRKEY.BAS lists 306 different airplanes. It will not run under QBASIC, which reports it is "out of string space." You can run it with QUICKBASIC because it can put the strings in a far off space by themselves. You cannot compile AIRKEY with QUICKBASIC because its compiler cannot reference "far strings." AIRKEY will compile with Microsoft's Professional BASIC, but that introduces other problems and defeats the charm of these Keys. Figure you can get a couple of hundred taxa into a key without too much difficulty. If you really need more, make a key for pollen and another for spores. Or move up to the complex databases. You will probably get more speed and power, but you will not feel the wind in your face.

Reference.

Ogden, E.C. and R.S. Mitchel. 1990. Identifications of plants with fleshy fruits. New York State Museum Bulletin No. 467.

AN INTERNET GUIDE TO QUATERNARY LIBRARY RESOURCES

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The following is the first of what may be several evaluations of library resources available to the average network computer user. For those unfamiliar with

network use, I recommend "The Whole Internet User's Guide & Catalog" (Krol, 1992).

As a starting point, I have somewhat arbitrarily chosen libraries at what are thought of as "good" universities, and evaluated them for Quaternary subjects which I consider common (you will note the biological and glacial bias I have--your interests may differ). Each topic was rated from 0 (worst) to 5 (best), and the topics were added to produce a cumulative total out of a possible 80 points. Thus, each library can be rated according to either specific personal taste (individual subjects), or comprehensively (all topics). All rating results are shown on Fig. 1.

All libraries were accessed by modem or Ethernet connection with our Sun Unix operating system, using either telnet or tn3270 to directly address the host machine. Remember when using Unix that the operating system, unlike others, is case sensitive. If something does not work as it should, first make sure that upper and lower case are used correctly.

Although telnet instructions and logon procedures are given here, by far the easiest way to do this is to use your hytelnets facility, usually through the Unix operating system. The hytelnets system I used was developed by Peter Scott, and provides essentially the same service as telnet, but is more sophisticated and easier as it does not require remembering details of the host system. Hytelnets itself is transparent, and allows communication with both the remote (host) and local system if desired. Peter provides frequent updates to the hytelnets system, giving network postings of new or changed library systems, network access facilities and public information services.

This may be subscribed to by e-mailing listserv@kentvm.kent.edu and sending the following message:
SUBSCRIBE HYTEL-L First Name Last Name

To unsubscribe, send the following to the same address:
UNSUBSCRIBE HYTEL-L

To try hytelnets on your local system, get into the Unix operating system, and type "hytelnets" [return]. This should start hytelnets. If at any time you wish to exit the hytelnets system, type [Ctrl]] or [Ctrl] C and this should release you to the telnet portion of your Unix operating system. To get out of telnet, type "quit", and this should return you to the Unix operating system you started from.

INQUA-COMMISSION FOR THE STUDY OF THE HOLOCENE

Working Group on Data-Handling Methods

Newsletter 11, January 1994

NOTE FROM THE COORDINATOR

In the Newsletter this time Joel Guiot provides some thoughtful recommendations for those using biological proxy data. Keith Bennett announces psimpoll version 2.23 that now runs on *any* machine for which an ANSI C compiler is available. He has put DOS and Mac versions in the INQUA Boutique. Even if you are happy with your present system for drafting pollen diagrams, you owe it to yourself to look at the feature-filled 70-page psimpoll manual to get a inkling of the thorough work he has done. Glen MacDonald continues his frolic through the CDRom world, and he offers advice about the CDRom drive that you *should* have ordered. Jock McAndrews and Zicheng Yu introduce their fascinating world of RACKs (Random Access Computer Keys) and I discuss how to edit them. Alan Walanus provides a humorous philosophy on using computers as pollen counters. Dana Naldrett tells how to do library searches on the Internet, describing and ranking the assets of 20 colleges in Canada and the U.S. John Birks supplies another of his useful book columns. David Green keeps us up to date with the World Wide Web. I asked Paula Reimer to provide some common questions she gets about CALIB3, the ¹⁴C calibration program from the University of Washington. I discuss the Global Positioning System and tell how you can always find where your research sites are even in trackless wastes. And a number of other topics are wedged in where they fit.

My sabbatical year continues. My thanks go to colleagues in Europe, Canada, Australia, and New Zealand who made me feel welcome while teaching me about computers and geology. I will be visiting John Birks in Bergen during April and Raymonde Bonnefille in Marseille during May.

I ask the readers of the Newsletter to send me information on any of the data-handling techniques that you have used which could be helpful to others. Please check your regular and e-mail addresses for accuracy. Send any corrections/suggestions to:

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THE QUANTITATIVE PALEOENVIRONMENTAL RECONSTRUCTIONS USING BIOLOGICAL PROXY DATA: RECOMMENDATIONS

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Fauna and flora now respond and have responded in the past to a more or less complex combination of environmental changes. A good knowledge of their modern ecology coupled to adequate mathematical methods permits a quantitative approach for reconstructing these changes from biological proxy data. Such reconstruction methods are often called "transfer functions", but this name must be used only figuratively because they are no longer based on the calibration of a function. These transfer functions may convert two types of proxies into environmental information: either assemblages (i.e. the relative abundance of a great number of species or more simply their presence/absence), or parameters related to the growth of selected individuals of a given species (e.g. tree-ring width, density, isotopic content ...). That type of approach needs a reference dataset containing the same type of proxies as in the fossil data associated with the environmental variables assumed to be the most explicative. I would like to review briefly--as much for the data provider as for the data user (e.g. climate modeller)--problems met in quantification, and to suggest possible solutions.

Problems

1. Such a quantitative approach implies that their response has not significantly changed in the past, which limits the time span of such approach. Moreover the use of proxy data requires the existence of modern analogues for these proxies. In some extreme climates, or during rapid transition, there may be no modern analogues.