

Psychology 350: Special Topics

An introduction to R for psychological research data manipulation

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Outline

Core R commands

- Input

- Combining objects

psych and *psychTools*

- Simple input

- Data manipulation using `vJoin`

Recoding and scrubbing

- Changing coding values for variable using `recode`
`scrub`



Basic data manipulation

1. Data input

- find files

```
file.choose(new = FALSE)
```

- input from files

```
read.table(file, header = FALSE, sep = "", quote = "\"'",  
           dec = ".", numerals = c("allow.loss", "warn.loss", "no.loss"),  
           row.names, col.names, as.is = !stringsAsFactors, tryLogical = TRUE,  
           na.strings = "NA", colClasses = NA, nrows = -1,  
           skip = 0, check.names = TRUE, fill = !blank.lines.skip,  
           strip.white = FALSE, blank.lines.skip = TRUE,  
           comment.char = "#",  
           allowEscapes = FALSE, flush = FALSE,  
           stringsAsFactors = FALSE,  
           fileEncoding = "", encoding = "unknown", text, skipNul = FALSE)
```

```
read.csv(file, header = TRUE, sep = ",", quote = "\"",  
         dec = ".", fill = TRUE, comment.char = "", ...)
```

```
read.csv2(file, header = TRUE, sep = ";", quote = "\"",  
          dec = ",", fill = TRUE, comment.char = "", ...)
```

```
read.delim(file, header = TRUE, sep = "\t", quote = "\"",  
           dec = ".", fill = TRUE, comment.char = "", ...)
```

```
read.delim2(file, header = TRUE, sep = "\t", quote = "\"",  
            dec = ",", fill = TRUE, comment.char = "", ...)
```



cbind rbind **Combining two data frames/matrices**

R code

```
x <- matrix(1:30, ncol=5)
y <- matrix(1:40, ncol=8)
xy <- rbind(x,y) #does not work
xy <- cbind(x,y) #nor does this
xy <- rbind(x,y[,1:5]) #this works
XY <- cbind(x[1:5,],y)
```

```
x <- matrix(1:30, ncol=5)
> y <- matrix(1:40, ncol=8)
> xy <- rbind(x,y) #does not work
Error in rbind(x, y) :
  number of columns of matrices must match (see arg 2)
> xy <- cbind(x,y) #nor does this
Error in cbind(x, y) : number of rows of matrices must match (see arg 2)
> xy <- rbind(x,y[,1:5]) #this works
> XY <- cbind(x[1:5,],y)
> xy
```

```
      [,1] [,2] [,3] [,4] [,5]
[1,]    1    7   13   19   25
[2,]    2    8   14   20   26
[3,]    3    9   15   21   27
```

```
...
[10,]    4    9   14   19   24
[11,]    5   10   15   20   25
```

```
> XY
```

```
      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13]
[1,]    1    7   13   19   25    1    6   11   16   21   26   31   36
[2,]    2    8   14   20   26    2    7   12   17   22   27   32   37
[3,]    3    9   15   21   27    3    8   13   18   23   28   33   38
[4,]    4   10   16   22   28    4    9   14   19   24   29   34   39
```



Merge

Combines two files according to a common id field. “Merge two data frames by common columns or row names, or do other versions of database join operations.”

R code

```
merge(x, y, by = intersect(names(x), names(y)),
      by.x = by, by.y = by, all = FALSE, all.x = all, all.y = all,
      sort = TRUE, suffixes = c(".x", ".y"), no.dups = TRUE,
      incomparables = NULL, ...)
```

```
x <- data.frame(k1 = c(NA, NA, 3, 4, 5), k2 = c(1, NA, NA, 4, 5), data = 1)
y <- data.frame(k1 = c(NA, 2, NA, 4, 5), k2 = c(NA, NA, 3, 4, 5), data = 1:5)
merge(x, y, by = c("k1", "k2")) # NA's match
merge(x, y, by = "k1") # NA's match, so 6 rows
merge(x, y, by = "k2", incomparables = NA) # 2 rows
```

```
merge(x, y, by = c("k1", "k2")) # NA's match
  k1 k2 data.x data.y
1  4  4      4      4
2  5  5      5      5
3 NA NA      2      1
> merge(x, y, by = "k1") # NA's match, so 6 rows
  k1 k2.x data.x k2.y data.y
1  4  4      4      4      4
2  5  5      5      5      5
3 NA  1      1     NA      1
4 NA  1      1      3      3
```

Data display

R code

```
head(attitude)    #defaults to 6 rows
```

```
tail(attitude,n=8) #specify the number to show
```

```
> head(attitude)    #defaults to 6 rows
  rating complaints privileges learning raises critical advance
1     43          51         30      39      61        92       45
2     63          64         51      54      63        73       47
3     71          70         68      69      76        86       48
4     61          63         45      47      54        84       35
5     81          78         56      66      71        83       47
6     43          55         49      44      54        49       34
```

```
> tail(attitude,n=8) #specify the number to show
  rating complaints privileges learning raises critical advance
23     53          66         52      50      63        80       37
24     40          37         42      58      50        57       49
25     63          54         42      48      66        75       33
26     66          77         66      63      88        76       72
27     78          75         58      74      80        78       49
28     48          57         44      45      51        83       38
29     85          85         71      71      77        74       55
30     82          82         39      59      64        78       39
```



psych and psychTools

1. Developed for specific applications to psychology research
2. Attempts to make R easier to use but still using core-R
3. Many of the functions take advantage of core-R functions



Basic data manipulation

1. Input from a file

Will search for file and then read it depending upon suffix

```
read.file(file=NULL,header=TRUE,use.value.labels=FALSE,to.data.frame=TRUE,sep="," ,
quote="\\"",widths=NULL,f=NULL,filetype=NULL,...)
#for .txt, .text, TXT, .csv, .sav, .xpt, XPT, R, r, Rds, .rds, or .rda,
# .Rda, .RData, .Rdata, .dat and .DAT files

#includes the following given appropriate suffix
read.https(filename,header=TRUE)
read.file.csv(file=NULL,header=TRUE,f=NULL,...)
```

2. Input from clipboard

```
read.clipboard(header = TRUE, ...) #assumes headers and tab or space delimited
read.clipboard.csv(header=TRUE,sep=',',...) #assumes headers and comma delimited
read.clipboard.tab(header=TRUE,sep='\\t',...) #assumes headers and tab delimited
#read in a matrix given the lower off diagonal
read.clipboard.lower(diag=TRUE,names=FALSE,...)
read.clipboard.upper(diag=TRUE,names=FALSE,...)
#read in data using a fixed format width (see read.fwf for instructions)
read.clipboard.fwf(header=FALSE,widths=rep(1,10),...)
```

3. For output:

creates file if not specified and then writes according to suffix.

```
write.file(x,file=NULL,row.names=FALSE,f=NULL,...)
write.file.csv(x,file=NULL,row.names=FALSE,f=NULL,...)
```



Combine two matrices/data frames

- Core-R functions
 1. `rbind` adds rows if the columns match
 2. `cbind` combines columns if number of rows is the same
 3. `merge` combines rows and columns matching on a variable
- *psych* and *psychTools*
 1. `vJoin` combines rows and columns matching on row names

Combining two matrices or data frames using vJoin

R code

```
x <- matrix(1:30, ncol=5)
y <- matrix(1:40, ncol=8)
xy <- vJoin(x,y)
headTail(xy, top=2, bottom=2)
XY <- vJoin(x,y, cnames=FALSE)
headTail(XY)
```

```
> x <- matrix(1:30, ncol=5)
> y <- matrix(1:40, ncol=8)
> xy <- vJoin(x,y)
> headTail(xy, top=2, bottom=2)
```

	x1	x2	x3	x4	x5	y1	y2	y3	y4	y5	y6	y7	y8
Sx1	1	7	13	19	25	<NA>	<NA>	<NA>	<NA>	<NA>	<NA>	<NA>	<NA>
Sx2	2	8	14	20	26	<NA>	<NA>	<NA>	<NA>	<NA>	<NA>	<NA>	<NA>
...	...	...	...	...	...	...	...	...	...	...	...	...	...
Sy4	<NA>	<NA>	<NA>	<NA>	<NA>	4	9	14	19	24	29	34	39
Sy5	<NA>	<NA>	<NA>	<NA>	<NA>	5	10	15	20	25	30	35	40

	x1	x2	x3	x4	x5	y1	y2	y3	y4	y5	y6	y7	y8
Sx1	1	7	13	19	25	NA	NA	NA	NA	NA	NA	NA	NA
Sx2	2	8	14	20	26	NA	NA	NA	NA	NA	NA	NA	NA
Sx3	3	9	15	21	27	NA	NA	NA	NA	NA	NA	NA	NA
Sx4	4	10	16	22	28	NA	NA	NA	NA	NA	NA	NA	NA
Sx5	5	11	17	23	29	NA	NA	NA	NA	NA	NA	NA	NA
Sx6	6	12	18	24	30	NA	NA	NA	NA	NA	NA	NA	NA
Sy1	NA	NA	NA	NA	NA	1	6	11	16	21	26	31	36
Sy2	NA	NA	NA	NA	NA	2	7	12	17	22	27	32	37
Sy3	NA	NA	NA	NA	NA	3	8	13	18	23	28	33	38
Sy4	NA	NA	NA	NA	NA	4	9	14	19	24	29	34	39
Sy5	NA	NA	NA	NA	NA	5	10	15	20	25	30	35	40

Or, can assume variable are in same order

R code

```
x <- matrix(1:30, ncol=5)
y <- matrix(1:40, ncol=8)
XY <- vJoin(x,y, cnames=FALSE)
XY
```

XY

	x1	x2	x3	x4	x5	x6	x7	x8
Sx1	1	7	13	19	25	NA	NA	NA
Sx2	2	8	14	20	26	NA	NA	NA
Sx3	3	9	15	21	27	NA	NA	NA
Sx4	4	10	16	22	28	NA	NA	NA
Sx5	5	11	17	23	29	NA	NA	NA
Sx6	6	12	18	24	30	NA	NA	NA
Sy1	1	6	11	16	21	26	31	36
Sy2	2	7	12	17	22	27	32	37
Sy3	3	8	13	18	23	28	33	38
Sy4	4	9	14	19	24	29	34	39
Sy5	5	10	15	20	25	30	35	40

vJoin will also combine data.frames and matrices

R code

```
vJoin(bfi[1:5, 1:6], x)
```

```
vJoin(bfi[1:5, 1:6], x)
```

	A1	A2	A3	A4	A5	C1	y1	y2	y3	y4	y5
61617	2	4	3	4	4	2	NA	NA	NA	NA	NA
61618	2	4	5	2	5	5	NA	NA	NA	NA	NA
61620	5	4	5	4	4	4	NA	NA	NA	NA	NA
61621	4	4	6	5	5	4	NA	NA	NA	NA	NA
61622	2	3	3	4	5	4	NA	NA	NA	NA	NA
Sy1	NA	NA	NA	NA	NA	NA	1	7	13	19	25
Sy2	NA	NA	NA	NA	NA	NA	2	8	14	20	26
Sy3	NA	NA	NA	NA	NA	NA	3	9	15	21	27
Sy4	NA	NA	NA	NA	NA	NA	4	10	16	22	28
Sy5	NA	NA	NA	NA	NA	NA	5	11	17	23	29
Sy6	NA	NA	NA	NA	NA	NA	6	12	18	24	30

vJoin uses several core R functions

vJoin just strings together a number of standard R functions

1. NCOL and NROW (ncol and nrow)
2. colnames, rownames
3. paste and paste0
4. unique
5. length
6. data.frame



How does vJoin work?

Examine the code

```
#Created 05/04/23 to combine two data frames by rows and columns
#slight modification 05/06/23 to create column names if missing
vJoin <- function(x,y, rnames=TRUE,cnames=TRUE) {
  n.x <- NCOL(x)
  n.y <- NCOL(y)
  n.obsx <- NROW(x)
  n.obsy <- NROW(y)
  if(is.null(colnames(x))) colnames(x) <- paste0("x",1:n.x)
  if(is.null(colnames(y))) if(cnames) {colnames(y) <- paste0("y",1:n.y)}
  else {colnames(y) <- paste0("x",1:n.y)}
  if(is.null(rownames(x))) rownames(x) <- paste0("Sx",1:n.obsx)
  if(is.null(rownames(y))) rownames(y) <- paste0("Sy",1:n.obsy)

  xy <- unique(c(colnames(x),colnames(y)))
  n.xy.col <- length(xy)
  if(!rnames) { new.names <- n.obsx + 1:n.obsy
  rownames(y) <- new.names}
  xy.rows <- unique(c(rownames(x),rownames(y)))
  n.xy.rows <- length(xy.rows)

  #now, put them together -- matching on row and column names
  new <- data.frame(matrix(NA, ncol=n.xy.col,nrow = n.xy.rows))
  colnames(new) <- xy
  rownames(new) <- xy.rows
  new[rownames(x),colnames(x)] <- x[rownames(x),colnames(x)]
  new[rownames(y),colnames(y)] <- y[rownames(y),colnames(y)]
  return(new)
}
```



Sometime need to reorganize/recode variables

1. Consider education: High school, Some college, College, graduate work, graduate degree.

2. With numerical values of 1, 2, 3, 4, 5 (in bfi)

```
bfi$education[50:60]
```

```
[1] 3 3 4 4 3 4 5 3 5 2 5
```

```
temp$education[50:60]
```

```
[1] "College" "College"
```

```
"graduate_work"
```

```
"graduate_work"
```

```
"College"
```

```
[6] "graduate_work" "graduate_degree" "College"
```

```
"graduate_degree" "Some_coll"
```

```
[11] "graduate_degree"
```

3. So far, so good. But now describe them

```
describe(bfi[26:28])
```

	vars	n	mean	sd	median	trimmed	mad	min	max	range	skew	kurtosis	se
gender	1	2800	1.67	0.47	2	1.71	0.00	1	2	1	-0.73	-1.47	0.01
education	2	2577	3.19	1.11	3	3.22	1.48	1	5	4	-0.05	-0.32	0.02
age	3	2800	28.78	11.13	26	27.43	10.38	3	86	83	1.02	0.56	0.21

```
> describe(temp[26:28])
```

	vars	n	mean	sd	median	trimmed	mad	min	max	range	skew	kurtosis	se
gender	1	2800	1.67	0.47	2	1.71	0.00	1	2	1	-0.73	-1.47	0.01
education*	2	2577	2.18	1.40	2	1.98	1.48	1	5	4	0.84	-0.66	0.03
age	3	2800	28.78	11.13	26	27.43	10.38	3	86	83	1.02	0.56	0.21



What happened?

1. The character values are sorted in terms of alphabetical order

```
table(bfi[27])
education
  1    2    3    4    5
224 292 1249 394 418
> table(temp[27])
education
      College graduate_degree graduate_work High_school Some_college
      1249             418             394             224             292
```

2. We need to recode the character strings into the appropriate numeric values.
3. Hence the recode function.



Change to numeric, and recode

R code

```
temp2 <- char2numeric(temp, flag=FALSE)
new.education <- c(3,5,4,1,2)
temp3 <- recode(temp2, isvalue=1:6, newvalue=new.education)
describe(temp3[26:28])
```

```
temp2 <- char2numeric(temp, flag=FALSE)
> new.education <- c(3,5,4,1,2)
> temp3 <- recode(temp2, isvalue=1:6, newvalue=new.education)
> describe(temp3[26:28])
```

	vars	n	mean	sd	median	trimmed	mad	min	max	range	skew	kurtosis	se
gender	1	2800	1.67	0.47	2	1.71	0.00	1	2	1	-0.73	-1.47	0.01
education	2	2577	3.19	1.11	3	3.22	1.48	1	5	4	-0.05	-0.32	0.02
age	3	2800	28.78	11.13	26	27.43	10.38	3	86	83	1.02	0.56	0.21

```
describe(bfi[26:28])
```

	vars	n	mean	sd	median	trimmed	mad	min	max	range	skew	kurtosis	se
gender	1	2800	1.67	0.47	2	1.71	0.00	1	2	1	-0.73	-1.47	0.01
education	2	2577	3.19	1.11	3	3.22	1.48	1	5	4	-0.05	-0.32	0.02
age	3	2800	28.78	11.13	26	27.43	10.38	3	86	83	1.02	0.56	0.21



Convert numbers to character strings

R code

```
n.names <- cs(one,two, three, four, five, six)
temp <-recode(bfi, where =1:6, isvalue=1:6, newvalue = n.names)
headTail(temp,from=1, to=8)
headTail(bfi,from=1, to=8)
```

```
n.names <- cs(one,two, three, four, five, six)
> temp <-recode(bfi, where =1:6, isvalue=1:6, newvalue = n.names)
> headTail(temp,from=1, to=8)
```

	A1	A2	A3	A4	A5	C1	C2	C3
61617	two	four	three	four	four	two	3	3
61618	two	four	five	two	five	five	4	4
61620	five	four	five	four	four	four	5	4
61621	four	four	six	five	five	four	4	3
...	<NA>	<NA>	<NA>	<NA>	<NA>	<NA>	...	...
67552	two	four	four	three	five	two	3	4
67556	two	three	five	two	five	five	5	5
67559	five	two	two	four	four	five	5	5
67560	two	three	one	four	two	five	5	3

```
> headTail(bfi,from=1, to=8)
```

	A1	A2	A3	A4	A5	C1	C2	C3
61617	2	4	3	4	4	2	3	3
61618	2	4	5	2	5	5	4	4
61620	5	4	5	4	4	4	5	4
61621	4	4	6	5	5	4	4	3
...	...	...	...	...	...	...	...	...
67552	2	4	4	3	5	2	3	4
67556	2	3	5	2	5	5	5	5
67559	5	2	2	4	4	5	5	5
67560	2	3	1	4	2	5	5	3



Unfortunately, converting back produces something wrong

R code

```
new.temp <- char2numeric(temp)
headTail(new.temp, from=1, to=8)
```

```
new.temp <- char2numeric(temp)
> headTail(new.temp, from=1, to=8)
      A1. A2. A3. A4. A5. C1.  C2  C3
61617   6   2   5   2   2   6   3   3
61618   6   2   1   6   1   1   4   4
61620   1   2   1   2   2   2   5   4
61621   2   2   4   1   1   2   4   3
...     ...
67552   6   2   2   5   1   6   3   4
67556   6   5   1   6   1   1   5   5
67559   1   6   6   2   2   1   5   5
67560   6   5   3   2   6   1   5   3
```

We need to recode the data

R code

```
new.map <- c(3,6,5,2,1,4)
correct.temp <- recode(new.temp,1:6, isvalue=new.map,newvalue=1:6)
headTail(correct.temp, from=1, to=8)
#or compare the two files
sum(correct.temp-bfi,na.rm=TRUE)
```

```
new.map <- c(3,6,5,2,1,4)
> correct.temp <- recode(new.temp,1:6, isvalue=new.map,newvalue=1:6)
> headTail(correct.temp, from=1, to=8)
      A1. A2. A3. A4. A5. C1.  C2  C3
61617   2   4   3   4   4   2   3   3
61618   2   4   5   2   5   5   4   4
61620   5   4   5   4   4   4   5   4
61621   4   4   6   5   5   4   4   3
...     ...
67552   2   4   4   3   5   2   3   4
67556   2   3   5   2   5   5   5   5
67559   5   2   2   4   4   5   5   5
67560   2   3   1   4   2   5   5   3
> #or compare the two files
> sum(correct.temp-bfi,na.rm=TRUE)
[1] 0
```



`recode` combines conventional R functions

1. `missing`
2. `unique` (`unique` returns a vector, data frame or array like `x` but with duplicate elements/rows removed.)
3. `unlist`
4. `any` (Given a set of logical vectors, is at least one of the values true?)
5. `max`, `min`
6. `for(var in seq) expr`



How does recode work.

Examine the code

```
#added 5/6/23
#code is truly ugly
"recode" <- function(x,where,isvalue,newvalue) {
  if (missing(where)) where <- 1:NCOL(x)
  all.values <- unique(unlist(x[,where]))
  if(!any(all.values %in% isvalue)) {stop ("data has more values than specified in isvalue")}
}

maxv <- max(isvalue)
minv <- min(isvalue)
tempv <- isvalue + maxv + minv
x[,where] <- x[,where] + maxv + minv #make these larger to allow swaps in place
for (k in 1:length(where)) {where1 <- where[k] #begin the where loop
  for(j in 1:NROW(x)) { #replace across all cases
    for (i in (1: length(isvalue)) ) {#search one column for each possible value
      if(!is.na(x[j,where1])) {
        if((x[j,where1] == tempv[i])) x[j,where1] <- newvalue[i]}
      } #end of values loop
    } #end of subjects loop
  } #end of where loop
  return(x)
}
```

scrub

A tedious part of data analysis is addressing the problem of miscoded data that need to be converted to NA or some other value. For a given data.frame or matrix, scrub will set all values of columns from=from to to=to that are less than a set (vector) of min values or more than a vector of max values to NA. Can also be used to do basic recoding of data for all values=isvalue to newvalue. Will also recode continuous variables into fewer categories. Will convert Nan, -Inf and Inf to NA

R code

```
x <- scrub(attitude,isvalue=55) #make all occurrences of 55 NA
x1 <- scrub(attitude, where=c(4,5,6), isvalue =c(30,40,50),
  newvalue = c(930,940,950)) #will do this for the 4th, 5th, and 6th
x2 <- scrub(attitude, where=c(4,4,4), isvalue =c(30,40,50),
  newvalue = c(930,940,950)) #will just do it for the 4th column
new <- scrub(attitude,1:3,cuts= c(10,40,50,60,100)) #change many values
y <- scrub(attitude,where=2:4,min=c(20,30,40),max= c(120,110,100),isvalue=55)
y1 <- scrub(attitude,where="learning",isvalue=55,newvalue=999) #change a column by name
y2 <- scrub(attitude,where="learning",min=45,newvalue=999) #change a column by name
y3 <- scrub(attitude,where="learning",isvalue=c(45,48),
  newvalue=999) #change a column by name look for multiple values
```

