Module 5: advanced data manipulation

BIOSTAT 213: Introduction to Computing in the R Software Environment

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Brief Exercise

Date objects

rbind() and cbind()

Importing other data files

Merging data

Reshaping data

Data structures

Wide to long "manually"

Wide to long using reshape()

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Brief Exercise

You may work in groups of 2–3. Save your code in a script file.

1. Re-import `nhanes.csv` into R, using `read.csv()`.
2. List the 10th, 20th, 30th, ..., through 100th values of body mass index (`bmxbmi`). Are we indexing a 1-dimensional object or a 2-dimensional object? Are we indexing using a numeric, logical, or character object?
3. List the second measurement of diastolic blood pressures (`bpxdi2`) of individuals with a first measurement (`bpxdi1`) equal to 0. Are we indexing a 1-dimensional object or a 2-dimensional object? Are we indexing using a numeric, logical, or character object?

More on the next slide...

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4. List the 201st through 210th rows of ID (`seqn`), age (`ridageyr`), and age group (`agegroup`). Are we indexing a 1-dimensional object or a 2-dimensional object? For the rows, are we indexing using a numeric, logical, or character object? For the columns, are we indexing using a numeric, logical, or character object?
5. Using indexing, create a subset of the data, including only individuals with 4 hours of sleep (`sleep`) per night on average. Check the number of rows. Using `subset()`, create a subset of the data, including only individuals with 4 hours of sleep (`sleep`) per night on average. Check the number of rows.

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Indexing, continued

```
> pp[seq(10,nrow(pp),10),c('start','end')]
        start        end
10  4/04/1841  4/03/1845
20  4/03/1881 19/09/1881
30   2/8/1923  4/03/1929
40 20/01/1981 20/01/1989
```


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Date objects

```
> pp$end-pp$start
Warning in Ops.factor(pp$end, pp$start): '-' not meaningful
for factors
 [1] NA NA NA NA NA NA NA NA NA NA NA NA NA NA NA NA NA NA NA
[19] NA NA NA NA NA NA NA NA NA NA NA NA NA NA NA NA NA NA NA
[37] NA NA NA NA NA NA NA NA
```


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Date objects

- the subtraction failed because R is not currently recognizing `start` and `end` as dates:

```
> class(pp$start)
[1] "factor"
> class(pp$end)
[1] "factor"
```


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Date objects

- one method for converting to dates is `as.Date()`

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Date objects

```
> head(pp$start)
[1] 30/04/1789 4/03/1797  4/03/1801  4/03/1809  4/03/1817
[6] 4/03/1825
44 Levels: 12/4/1945 14/9/1901 15/04/1865 ... 9/8/1974
> pp$start<-as.Date(pp$start,format='%d/%m/%Y')
```

- the `format` should replicate the way the date is stored
- for this variable, that means including `/` in between values
- `%d`: day of the month
- `%m`: month, as a number
- `%Y`: year, stored with 4 digits (if the year is stored with 2 digits, use %y)

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Date objects

```
> head(pp$start)
[1] "1789-04-30" "1797-03-04" "1801-03-04" "1809-03-04"
[5] "1817-03-04" "1825-03-04"
```


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Date objects

```
> class(pp$start)
[1] "Date"
> is.vector(pp$start)
[1] FALSE
```

- `start` is now a Date object, a type of date object
- Date objects look like vectors but are not vectors

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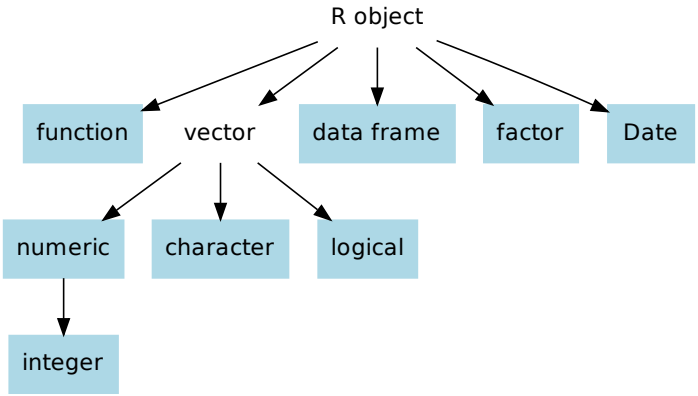
Date objects



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Date objects

```
> head(pp$end)
[1] 4/03/1797 4/03/1801 4/03/1809 4/03/1817 4/03/1825
[6] 4/03/1829
44 Levels: 12/4/1945 14/9/1901 15/04/1865 ... 9/8/1974
> pp$end<-as.Date(pp$end,format='%d/%m/%Y')
> head(pp$end)
[1] "1797-03-04" "1801-03-04" "1809-03-04" "1817-03-04"
[5] "1825-03-04" "1829-03-04"
> class(pp$end)
[1] "Date"
```


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Date objects

```
> pp$duration<-pp$end-pp$start
> min(pp$duration)
Time difference of 31 days
> max(pp$duration)
Time difference of 4422 days
```


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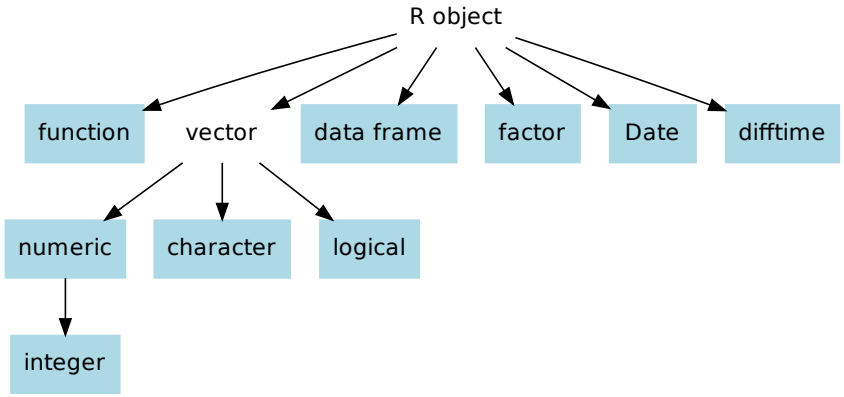
difftime objects

```
> head(pp$duration)
Time differences in days
[1] 2865 1460 2922 2922 2922 1461
> class(pp$duration)
[1] "difftime"
> is.vector(pp$duration)
[1] FALSE
```

- `duration` is a difftime object
- difftime objects look like vectors but are not vectors

difftime objects



difftime objects

- to convert a Date object to a numeric object (if for example, you find the unit labels distracting) use `as.numeric()`:

```
> head(pp$duration)
Time differences in days
[1] 2865 1460 2922 2922 2922 1461
> pp$duration<-as.numeric(pp$duration)
> head(pp$duration)
[1] 2865 1460 2922 2922 2922 1461
```

Date objects

```
> head(pp$dob)
[1] February 22, 1732 October 30, 1735  April 13, 1743
[4] March 16, 1751    April 28, 1758    July 11, 1767
43 Levels: April 13, 1743 April 23, 1791 ... September 15, 1857
> pp$dob<-as.Date(pp$dob,format='%B %d, %Y')
```

- %B for month, as non-abbreviated names (if the month names are abbreviated, use %b)
- the spaces and comma replicate the format seen in head()

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Date objects

- it's a good idea to check your work:

```
> head(pp$dob)
[1] "1732-02-22" "1735-10-30" "1743-04-13" "1751-03-16"
[5] "1758-04-28" "1767-07-11"
> class(pp$dob)
[1] "Date"
```


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idu5.csv

```
> idu5<-read.csv('idu5.csv')
```

- a stripped-down data set of individuals from San Francisco's 5th implementation of CDC's National HIV Behavioral Surveillance for injection drug users (IDU)

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Date objects

```
> head(idu5$idate)
[1] 21394 21394 21394 21394 21394 21394
> class(idu5$idate)
[1] "integer"
> idu5$idate<-as.Date(idu5$idate,origin='1960-01-01')
```

- to convert SAS-like dates, use the `origin` argument
- specify the `origin` using a `year-month-day` format

Date objects

- checking work:

```
> head(idu5$idate)
[1] "2018-07-29" "2018-07-29" "2018-07-29" "2018-07-29"
[5] "2018-07-29" "2018-07-29"
> class(idu5$idate)
[1] "Date"
> summary(idu5$idate)
        Min.      1st Qu.       Median         Mean
"2018-07-29" "2018-09-02" "2018-10-07" "2018-10-07"
     3rd Qu.         Max.
"2018-11-08" "2018-12-20"
```


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Visualization of the data

```
> ggplot(aes(x=idate,y=age),data=idu5)+geom_point()+
+   geom_smooth(method='loess')+
+   xlab('Date')+ylab('Age')
```


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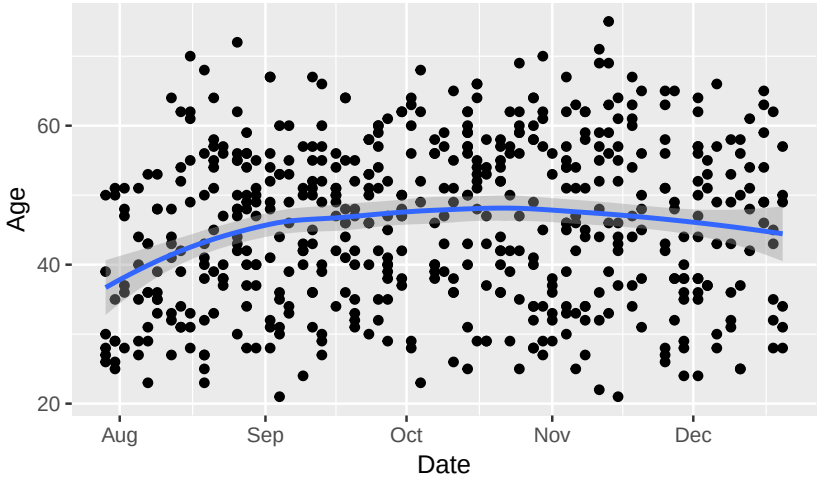
Visualization of the data



Date objects

- Date objects (capital D) do not store time
- other date objects in R, however, do
- to convert to date objects that store time as well, try `strptime()`

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rbind()

```
> ii.123<-ii[1:3,c('bmxht','bmxwt','bmxbmi')]
> ii.45<-ii[4:5,c('bmxht','bmxwt','bmxbmi')]
> rbind(ii.123,ii.45)
  bmxht bmxwt bmxbmi
1 171.3  78.3   26.7
2 176.8  89.5   28.6
3 175.3  88.9   28.9
4 162.4  52.0   19.7
5 158.7 105.0   41.7
```

- `rbind()` stands for row bind and, as the name implies, combines ("binds") data vertically

rbind()

```
> very.high<-ii[!is.na(ii$ldlcat)&(ii$ldlcat=='Very high'),
+               c('bmxht','bmxwt','bmxbmi')]
> high<-ii[!is.na(ii$ldlcat)&(ii$ldlcat=='High'),
+               c('bmxht','bmxwt','bmxbmi')]
> dim(very.high)
[1] 38  3
> dim(high)
[1] 182   3
> high.or.very.high<-rbind(high,very.high)
> dim(high.or.very.high)
[1] 220   3
```


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rbind()

- it is possible to `rbind()` more than 2 objects:

```
> ii.1<-ii[1,]
> ii.2<-ii[2,]
> ii.3<-ii[3,]
> ii.123<-rbind(ii.1,ii.2,ii.3)
> nrow(ii.123)
[1] 3
```


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rbind()

- the number of columns must match
- the column names must also match, if column names exist

rbind()

- however, the columns do not need to be in the same order:

```
> ii.1<-ii[1,c('bmxwt','bmxht')]
> ii.2<-ii[2,c('bmxht','bmxwt')]
> rbind(ii.1,ii.2)
  bmxwt bmxht
1  78.3 171.3
2  89.5 176.8
```


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cbind()

```
> ii.bmx<-ii[1:3,c('bmxht','bmxwt')]
> ii.dmd<-ii[1:3,c('dmdborn4','dmdcitzn')]
> cbind(ii.bmx,ii.dmd)
  bmxht bmxwt dmdborn4 dmdcitzn
1 171.3  78.3        1        1
2 176.8  89.5        1        1
3 175.3  88.9        1        1
```

- `cbind()` stands for column bind and, as the name implies, combines ("binds") data horizontally

cbind()

- the number of rows must match
- the row names do not need to match, if row names exist

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cbind()

- it is possible to misalign rows:

```
> ii.bmx<-ii[1:3,c('bmxht','bmxwt')]
> ii.dmd<-ii[101:103,c('dmdborn4','dmdcitzn')]
> cbind(ii.bmx,ii.dmd)
  bmxht bmxwt dmdborn4 dmdcitzn
1 171.3  78.3        1        1
2 176.8  89.5        1        1
3 175.3  88.9        1        1
```


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kevin_love.txt

- kevin_love.txt contains data on Kevin Love's NBA career
- it is a tab-delimited text file

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Importing tab-delimited text files

- to import tab-delimited text files, use `read.delim()`:

```
> ll<-read.delim('kevin_love.txt')
> ll[1:3,1:10]
   season age  tm  lg pos  g gs   mp  fg  fga
1 2008-09  20 MIN NBA   C 81 37 25.3 3.9  8.5
2 2009-10  21 MIN NBA  PF 60 22 28.6 4.9 10.8
3 2010-11  22 MIN NBA  PF 73 73 35.8 6.6 14.1
```


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Importing text files

- `read.delim()` and `read.csv()` are special cases of `read.table()`
- some useful arguments:
  - `header`: `TRUE` if the first row of the data contains the variable names
  - `sep`: the value used to separate cells (eg, `'\t'` for tab-delimited data)
  - `na.strings`: the character used to indicate missing values (eg, `''` for empty cells)

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Importing other data files

- useful packages for reading other data files:
  - foreign for reading Stata, SPSS, or SAS XPORT files
  - readstata13 for reading Stata 13+ files
  - sas7bdat for reading SAS sas7bdat files
  - readxl for reading Excel files

DR1TOT_H.XPT

- DR1TOT_H.XPT contains data from the dietary interview component of NHANES, also known as What We Eat in America (WWEIA)
- documentation is available here

Importing SAS XPORT files

- just once ever:

```
> install.packages('foreign')
```

- just once per session:

```
> library(foreign)
```


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Importing SAS XPORT files

```
> dietary<-read.xport('DR1TOT_H.XPT')
```


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Importing SAS XPORT files

- checking work:

```
> dietary[1:5,1:7]
   SEQN    WTDRD1    WTDR2D DR1DRSTZ DR1EXMER DRABF DRDINT
1 73557  16888.33  12930.89        1       49     2      2
2 73558  17932.14  12684.15        1       59     2      2
3 73559  59641.81  39394.24        1       49     2      2
4 73560 142203.07 125966.37        1       54     2      2
5 73561  59052.36  39004.89        1       63     2      2
```


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Importing SAS XPORT files

- I like making variable names lower case:

```
> names(dietary)<-tolower(names(dietary))
```


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Merging data

- prior to merging, it's useful to check for duplicated IDs:

```
> table(duplicated(ii$seqn))

FALSE
 5769
> table(duplicated(dietary$seqn))

FALSE
 9813
```


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Merging data

- to merge data frames, use `merge()`:

```
> ii.new<-merge(ii,dietary,by='seqn',all.x=TRUE,all.y=FALSE)
```

- `by` specifies the identifying variable (usually some ID number)
- if the variable names differ, use `by.x` and `by.y` for the first the first and second data, respectively
- `all.x` and `all.y` indicate whether to keep all rows in the first and second data, respectively

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Merging data

- thinking about sets or a Venn diagram:
  - `all=TRUE` means *X OR Y*
  - `all=FALSE` means *X AND Y*
  - `all.x=TRUE, all.y=FALSE` means *X*
  - `all.x=FALSE, all.y=TRUE` means *Y*

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Merging data

- checking work:

```
> nrow(ii)
[1] 5769
> nrow(dietary)
[1] 9813
> nrow(ii.new)
[1] 5769
```


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- checking work:

```
> tail(names(ii))
[1] "vra"     "aspirin" "sleep"   "is"      "hs"
[6] "ldlcat"
> tail(names(ii.new))
[1] "drd370sq" "drd370t"  "drd370tq" "drd370u"  "drd370uq"
[6] "drd370v"
```


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Merging data

- replacing the original data:

```
> ii<-ii.new
```

- I could have done this at the very beginning, avoiding `ii.new` altogether, but it can be helpful to wait until after checking the new data

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Wide data

- wide data refer to data structures in which each row is an individual (or unit of analysis)
- if there are repeated measures, the measurements appear as multiple columns
- for example, in the NHANES data, there are 4 variables for diastolic blood pressure: `bpxdi1`, `bpxdi2`, `bpxdi3`, and `bpxdi4`

Wide data

- diastolic blood pressure in NHANES:

```
> ii[1:4,c('seqn','bpxdi1','bpxdi2','bpxdi3','bpxdi4')]
   seqn bpxdi1 bpxdi2 bpxdi3 bpxdi4
1 73557     72     76     74     NA
2 73558     62     80     42     NA
3 73559     90     76     80     NA
4 73561     86     88     86     NA
```


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Long data

- long data refer to data structures in which each individual (or unit of analysis) may appear in more than one row
- I prefer thinking of "long data" as "tall data" since long doesn't, in my view, unambiguously refer to height

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Long data

- the UNPS data:

```
> uu[uu$pid=='10830027090305',c('pid','wave')]
                  pid wave
1753 10830027090305 2009
3355 10830027090305 2010
4778 10830027090305 2011
```


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Long data

- example of long data, from a hypothetical longitudinal study of 2 individuals, with 3 visits per individual:

	individual	visit	systolic	daistolic
1	1	1	92	64
2	1	2	102	62
3	1	3	108	66
4	2	1	144	62
5	2	2	132	72
6	2	3	116	74

- each row represents a person-visit

Long data

- example of long data, from a hypothetical cross-sectional study of 2 individuals, with information collected on up to 5 sexual partners per individual:

	individual	partner	partner.age	condomless
1	1	1	25	1
2	1	2	32	0
3	1	3	27	0
4	1	4	29	1
5	2	1	42	0
6	2	2	46	0

- each row represents a sexual partnership

Wide or long?

- what we consider wide or long can depend on what we consider the unit of analysis to be (and this can change within project!)
- for example, with the Kevin Love data:
  - if we say that the unit of analysis is an individual's NBA season, the data are in wide format, because each row represents an individual's NBA season
  - if we say that the unit of analysis is the individual, the data are in long format, because each individual can appear in multiple rows

Wide to long “manually”

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Reshaping wide to long "manually"

- suppose we want to create long data, for the first 2 measurements of diastolic blood pressure
- we could do this "manually" as follows:

```
> dia1<-data.frame(seqn=ii$seqn,order=1,diastolic=ii$bpxdi1)
> dia2<-data.frame(seqn=ii$seqn,order=2,diastolic=ii$bpxdi2)
> mm<-rbind(dia1,dia2)
```


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Reshaping wide to long "manually"

- checking work:

```
> head(mm[order(mm$seqn),])
      seqn order diastolic
1    73557     1        72
5770 73557     2        76
2    73558     1        62
5771 73558     2        80
3    73559     1        90
5772 73559     2        76
```

Reshaping wide to long "manually"

- checking work:

```
> nrow(ii)*2
[1] 11538
> nrow(mm)
[1] 11538
> length(unique(mm$seqn))
[1] 5769
> nrow(ii)
[1] 5769
```


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- we have 4 measurements of diastolic blood pressure though
- we could create a long data frame of all 4 measurements manually, but this would be slightly tedious
- with other data sets, and more complex requirements, this would be even more tedious
- even with the NHANES data, for example, what if we also wanted to include systolic blood pressure?

Wide to long using `reshape()`

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```
> kk<-c('seqn','ridageyr','bpxdi1','bpxdi2','bpxdi3','bpxdi4')
> mm<-reshape(data=ii[,kk],
+             varying=kk[3:6],
+             sep='',direction='long',
+             idvar='seqn',timevar='order')
```

- data: the data to reshape (could use ii, but using a subset here for simplicity of presentation)
- varying: the variable names of the repeated measurements
- sep: if varying use a naming convention of some stub name plus some number, sep is the character separating the stub and the number
- direction: the direction of reshaping

Reshaping wide to long using reshape()

```
> kk<-c('seqn','ridageyr','bpxdi1','bpxdi2','bpxdi3','bpxdi4')
> mm<-reshape(data=ii[,kk],
+             varying=kk[3:6],
+             sep='',direction='long',
+             idvar='seqn',timevar='order')
```

- `idvar` (*optional*): an ID variable, possibly using a variable name in the original data (if you don't include this, R will create a new variable called `id`)
- `timevar` (*optional*): the name for the new variable that will distinguish rows (the default name is `time`)

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- checking work:

```
> head(mm[order(mm$seqn),])
         seqn ridageyr order bpxdi
73557.1 73557       69     1    72
73557.2 73557       69     2    76
73557.3 73557       69     3    74
73557.4 73557       69     4    NA
73558.1 73558       54     1    62
73558.2 73558       54     2    80
```

- notice that `reshape()` automatically adds row names

Reshaping wide to long using `reshape()`

- checking work:

```
> nrow(ii)*4
[1] 23076
> nrow(mm)
[1] 23076
> length(unique(mm$seqn))
[1] 5769
> length(unique(ii$seqn))
[1] 5769
```


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- what if we had omitted `idvar` and `timevar`?

```
> kk<-c('seqn','ridageyr','bpxdi1','bpxdi2','bpxdi3','bpxdi4')
> mm<-reshape(data=ii[,kk],
+             varying=kk[3:6],
+             sep='',direction='long',
+             idvar='seqn',timevar='order')
> mm.simpler<-reshape(data=ii[,kk],
+                     varying=kk[3:6],
+                     sep='',direction='long')
```

Reshaping wide to long using `reshape()`

```
> mm[mm$seqn==73557,]
         seqn ridageyr order bpxdi
73557.1 73557       69     1    72
73557.2 73557       69     2    76
73557.3 73557       69     3    74
73557.4 73557       69     4    NA
> mm.simpler[mm.simpler$seqn==73557,]
     seqn ridageyr time bpxdi id
1.1 73557       69    1    72  1
1.2 73557       69    2    76  1
1.3 73557       69    3    74  1
1.4 73557       69    4    NA  1
```


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- including systolic blood pressure as well:

```
> kk<-c(kk,'bpxsy1','bpxsy2','bpxsy3','bpxsy4')
> mm<-reshape(data=ii[,kk],
+             varying=kk[3:10],
+             sep='',direction='long',
+             idvar='seqn',timevar='order')
```

Reshaping wide to long using `reshape()`

- checking work:

```
> head(mm[order(mm$seqn),])
         seqn ridageyr order bpxdi bpxsy
73557.1 73557       69     1    72   122
73557.2 73557       69     2    76   114
73557.3 73557       69     3    74   102
73557.4 73557       69     4    NA    NA
73558.1 73558       54     1    62   156
73558.2 73558       54     2    80   160
```


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- checking work:

```
> nrow(ii)*4
[1] 23076
> nrow(mm)
[1] 23076
> length(unique(mm$seqn))
[1] 5769
> length(unique(ii$seqn))
[1] 5769
```


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- reshaping the Kevin Love data:

```
> mm<-reshape(ll[c('season','age','fgp','ftp')],
+             varying=c('fgp','ftp'),
+             v.names='value',timevar='stat',
+             direction='long',
+             idvar='season',
+             times=c('Field goals','Free throws'))
```

- we don't have repeating variable names, so instead of `sep` we use:
  - `v.names` to specify the name for the new "value" variable
  - `timevar` to specify the name for the new "label" variable

Reshaping wide to long using `reshape()`

```
> mm<-reshape(ll[c('season','age','fgp','ftp')],
+             varying=c('fgp','ftp'),
+             v.names='value',timevar='stat',
+             direction='long',
+             idvar='season',
+             times=c('Field goals','Free throws'))
```

- `times` (*optional*): specifies the values for the "label" variable (the default would be sequential numbering)

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- checking work:

```
> head(mm[order(mm$season),])
                     season age        stat value
2008-09.Field goals 2008-09  20 Field goals 0.459
2008-09.Free throws 2008-09  20 Free throws 0.789
2009-10.Field goals 2009-10  21 Field goals 0.450
2009-10.Free throws 2009-10  21 Free throws 0.815
2010-11.Field goals 2010-11  22 Field goals 0.470
2010-11.Free throws 2010-11  22 Free throws 0.850
```

Reshaping wide to long using `reshape()`

- checking work:

```
> nrow(ll)*2
[1] 22
> nrow(mm)
[1] 22
> length(unique(mm$season))
[1] 11
> length(unique(ll$season))
[1] 11
```


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Reshaping wide to long using `reshape()`

- what if we had omitted `times`?

```
> mm.simpler<-reshape(ll[c('season','age','fgp','ftp')],
+             varying=c('fgp','ftp'),
+             v.names='value',timevar='stat',
+             direction='long',
+             idvar='season')
```


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```
> head(mm.simpler[order(mm.simpler$season),])
           season age stat value
2008-09.1 2008-09  20    1 0.459
2008-09.2 2008-09  20    2 0.789
2009-10.1 2009-10  21    1 0.450
2009-10.2 2009-10  21    2 0.815
2010-11.1 2010-11  22    1 0.470
2010-11.2 2010-11  22    2 0.850
```

Visualization of the long data

```
> mm$season<-as.numeric(substr(mm$season,0,4))
> mm$stat<-factor(mm$stat,c('Free throws','Field goals'))
> ggplot(aes(x=season,y=value,col=stat),data=mm)+
+   geom_point()+geom_line()+
+   xlab('')+ylab('')+labs(col='Statistic')+
+   scale_y_continuous(labels=scales::percent)+
+   scale_x_continuous(breaks=seq(2008,2018,2))
```


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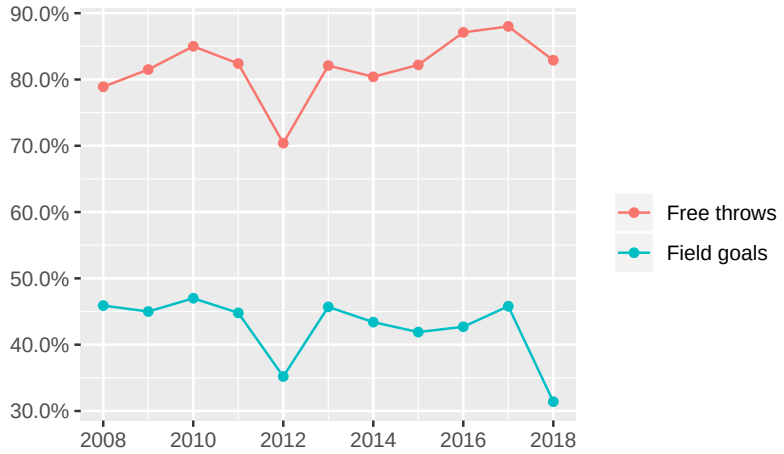
Visualization of the long data



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