Cpts575 Hw3

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Part 1

```
library(dplyr)
#msleep = read.csv('https://scads.eecs.wsu.edu/wp-content/uploads/2017/10/msleep_ggplot2.csv')
msleep = read.csv('msleep_ggplot2.csv')
#heads = head(select(msleep, contains('sleep')))
msleep %>%
    select(contains('sleep'))%>%
    head()
```

```
##   sleep_total sleep_rem sleep_cycle
## 1        12.1        NA          NA
## 2        17.0       1.8          NA
## 3        14.4       2.4          NA
## 4        14.9       2.3   0.1333333
## 5         4.0       0.7   0.6666667
## 6        14.4       2.2   0.7666667
```

a.

```
#count_numbers = count(filter(msleep, bodywt<50, sleep_total>16))
msleep %>%
    filter(bodywt<50, sleep_total>16) %>%
    count()
```

```
## # A tibble: 1 x 1
##       n
##   <int>
## 1     7
```

b.

```
msleep %>%
    select(name, sleep_total, bodywt) %>%
    arrange(desc=msleep$sleep_total) %>%
    top_n(5)
```

```
## Selecting by bodywt
```

```
##                name sleep_total   bodywt
## 1           Giraffe         1.9  899.995
## 2      Pilot whale         2.7  800.000
## 3 African elephant         3.3 6654.000
## 4   Asian elephant         3.9 2547.000
## 5              Cow         4.0  600.000
```

c.

```
msleep = msleep %>%
    mutate(wt_ratio=brainwt/bodywt,
           rem_ratio=sleep_rem/sleep_total)
```

d.

```
order_sum = data.frame(
    msleep %>%
        group_by(order)%>%
        summarise(avg=mean(sleep_total),
                  max=max(sleep_total),
                  min=min(sleep_total))
    )
order_sum
```

```
##              order       avg  max  min
## 1      Afrosoricida 15.600000 15.6 15.6
## 2      Artiodactyla  4.516667  9.1  1.9
## 3         Carnivora 10.116667 15.8  3.5
## 4           Cetacea  4.500000  5.6  2.7
## 5        Chiroptera 19.800000 19.9 19.7
## 6         Cingulata 17.750000 18.1 17.4
## 7   Didelphimorphia 18.700000 19.4 18.0
## 8     Diprotodontia 12.400000 13.7 11.1
## 9    Erinaceomorpha 10.200000 10.3 10.1
## 10       Hyracoidea  5.666667  6.3  5.3
## 11       Lagomorpha  8.400000  8.4  8.4
## 12      Monotremata  8.600000  8.6  8.6
## 13   Perissodactyla  3.466667  4.4  2.9
## 14           Pilosa 14.400000 14.4 14.4
## 15         Primates 10.500000 17.0  8.0
## 16      Proboscidea  3.600000  3.9  3.3
## 17         Rodentia 12.468182 16.6  7.0
## 18       Scandentia  8.900000  8.9  8.9
## 19     Soricomorpha 11.100000 14.9  8.4
```

e.

```
#mutate(msleep, avg_ratio=order_sum[order_sum$order == order,]$avg)
head(msleep)
```

```
##                          name      genus  vore        order conservation
## 1                     Cheetah   Acinonyx carni    Carnivora           lc
## 2                  Owl monkey      Aotus  omni     Primates         <NA>
## 3             Mountain beaver Aplodontia herbi     Rodentia           nt
## 4 Greater short-tailed shrew    Blarina  omni Soricomorpha           lc
## 5                         Cow        Bos herbi Artiodactyla domesticated
## 6            Three-toed sloth   Bradypus herbi       Pilosa         <NA>
##   sleep_total sleep_rem sleep_cycle awake brainwt  bodywt   wt_ratio
## 1        12.1        NA          NA  11.9      NA  50.000         NA
## 2        17.0       1.8          NA   7.0 0.01550   0.480 0.03229167
## 3        14.4       2.4          NA   9.6      NA   1.350         NA
## 4        14.9       2.3   0.1333333   9.1 0.00029   0.019 0.01526316
## 5         4.0       0.7   0.6666667  20.0 0.42300 600.000 0.00070500
## 6        14.4       2.2   0.7666667   9.6      NA   3.850         NA
##   rem_ratio
## 1        NA
## 2 0.1058824
## 3 0.1666667
## 4 0.1543624
## 5 0.1750000
## 6 0.1527778
```

```
msleep_copy2 = data.frame(
    msleep %>%
        group_by(order) %>%
        mutate(brainwt)
                          )
```

Part 2

```
library(tidyr)
head(who)
```

```
## # A tibble: 6 x 60
##   country iso2  iso3   year new_sp_m014 new_sp_m1524 new_sp_m2534
##   <chr>   <chr> <chr> <int>       <int>        <int>        <int>
## 1 Afghan~ AF    AFG    1980          NA           NA           NA
## 2 Afghan~ AF    AFG    1981          NA           NA           NA
## 3 Afghan~ AF    AFG    1982          NA           NA           NA
## 4 Afghan~ AF    AFG    1983          NA           NA           NA
## 5 Afghan~ AF    AFG    1984          NA           NA           NA
## 6 Afghan~ AF    AFG    1985          NA           NA           NA
## # ... with 53 more variables: new_sp_m3544 <int>, new_sp_m4554 <int>,
## #   new_sp_m5564 <int>, new_sp_m65 <int>, new_sp_f014 <int>,
## #   new_sp_f1524 <int>, new_sp_f2534 <int>, new_sp_f3544 <int>,
## #   new_sp_f4554 <int>, new_sp_f5564 <int>, new_sp_f65 <int>,
## #   new_sn_m014 <int>, new_sn_m1524 <int>, new_sn_m2534 <int>,
## #   new_sn_m3544 <int>, new_sn_m4554 <int>, new_sn_m5564 <int>,
## #   new_sn_m65 <int>, new_sn_f014 <int>, new_sn_f1524 <int>,
## #   new_sn_f2534 <int>, new_sn_f3544 <int>, new_sn_f4554 <int>,
## #   new_sn_f5564 <int>, new_sn_f65 <int>, new_ep_m014 <int>,
## #   new_ep_m1524 <int>, new_ep_m2534 <int>, new_ep_m3544 <int>,
## #   new_ep_m4554 <int>, new_ep_m5564 <int>, new_ep_m65 <int>,
## #   new_ep_f014 <int>, new_ep_f1524 <int>, new_ep_f2534 <int>,
## #   new_ep_f3544 <int>, new_ep_f4554 <int>, new_ep_f5564 <int>,
## #   new_ep_f65 <int>, newrel_m014 <int>, newrel_m1524 <int>,
## #   newrel_m2534 <int>, newrel_m3544 <int>, newrel_m4554 <int>,
## #   newrel_m5564 <int>, newrel_m65 <int>, newrel_f014 <int>,
## #   newrel_f1524 <int>, newrel_f2534 <int>, newrel_f3544 <int>,
## #   newrel_f4554 <int>, newrel_f5564 <int>, newrel_f65 <int>
```

```
mywho = who %>%
    gather(key, value, new_sp_m014:newrel_f65, na.rm = TRUE) %>%
    mutate(key = stringr::str_replace(key, "newrel", "new_rel")) %>%
    separate(key, c("new", "var", "sexage")) %>%
    select(-new, -iso2, -iso3) %>%
    separate(sexage, c("sex", "age"), sep = 1)
head(mywho)
```

```
## # A tibble: 6 x 6
##   country      year var   sex   age   value
##   <chr>       <int> <chr> <chr> <chr> <int>
## 1 Afghanistan  1997 sp    m     014       0
## 2 Afghanistan  1998 sp    m     014      30
## 3 Afghanistan  1999 sp    m     014       8
## 4 Afghanistan  2000 sp    m     014      52
## 5 Afghanistan  2001 sp    m     014     129
## 6 Afghanistan  2002 sp    m     014      90
```

a.

This line tries to replace all the strings name "newrel" to "new_rel". So it tidy the key name of the data. If I skip this line, we will have one more key called "newrel" and it's data cannot be select when we use the key "new_rel".

b.

```
unremoved = who %>%
    gather(new_sp_m014:newrel_f65, key="key", value="cases")
Delete_Number = nrow(unremoved) - nrow(mywho)
Delete_Number
```

```
## [1] 329394
```

c.

1. Explicit missing value means the data is 'NA', 'NAN' or some other Null value.
2. Implicit missing value means the data is just doesn't apear on the table. From the data we can find that the data after tidy is begin from 1997, but it was begin from 1980. The data between 1980 and 1997 is missing.

d.

```
mywho2 = mywho %>%
    select(country, year, var, sex, age, value)
```

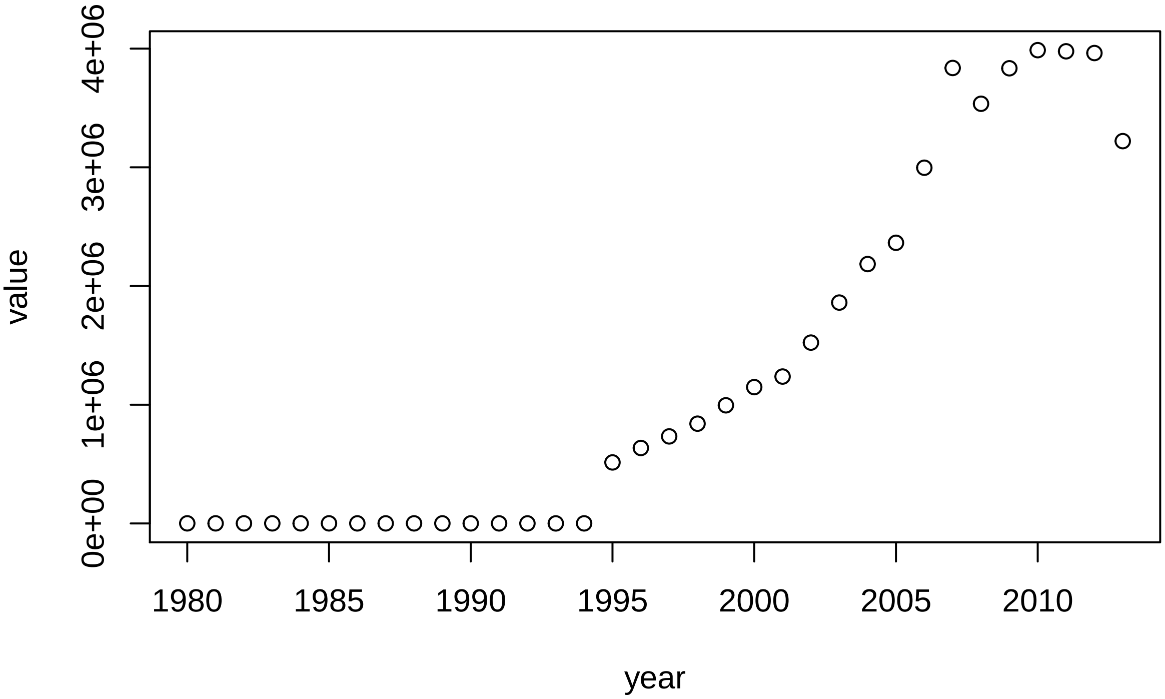
I think the 'age' should change it's type to 'int', since ages are all int numbers.

e.

In my opinion, gather is the operation that would help people focus on the characteristics of one or some typical object. For example, when we have the data of a lot of cars, when we want to compare the details of two cars, then we can gather two cars. Also, spread do the similar things as gather, but it would catch the different objects' one or some typical characteristics, then compare the characteristics of different object to know the difference between different unities.

f.

```
mywho3 <- mywho %>%
    group_by(year) %>%
    summarise(value=sum(value))
plot(mywho3)
```



```
c(mywho3['year'])
```

```
## $year
##  [1] 1980 1981 1982 1983 1984 1985 1986 1987 1988 1989 1990 1991 1992 1993
## [15] 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003 2004 2005 2006 2007
## [29] 2008 2009 2010 2011 2012 2013
```

From this scatter I can know the amount of cases is increasing from 1995, but is decrese in the 2013. I want to know whether the cases decrease with the development of the modern medicine.

g.

```
siteDemo <- data.frame(Site = c("facebook", "myspace", "snapchat", "twitter"),
                       U30.F = c(32, 1, 6, 17),
                       U30.M = c(31, 5, 4, 23),
                       O30.F = c(60, 3, 3, 12),
                       O30.M = c(58, 6, 2, 17))
siteDemo_new <- siteDemo %>%
    gather('U30.F', 'U30.M', 'O30.F', 'O30.M', key="AGG", value = "Count")
siteDemo_new
```

```
##        Site   AGG Count
## 1  facebook U30.F    32
## 2   myspace U30.F     1
## 3  snapchat U30.F     6
## 4   twitter U30.F    17
## 5  facebook U30.M    31
## 6   myspace U30.M     5
## 7  snapchat U30.M     4
## 8   twitter U30.M    23
## 9  facebook O30.F    60
## 10  myspace O30.F     3
## 11 snapchat O30.F     3
## 12  twitter O30.F    12
## 13 facebook O30.M    58
## 14  myspace O30.M     6
## 15 snapchat O30.M     2
## 16  twitter O30.M    17
```

```
siteDemo_new <- siteDemo_new %>%
    separate('AGG', into = c("AgeGroup", "Gender"))
siteDemo_new
```

```
##        Site AgeGroup Gender Count
## 1  facebook      U30      F    32
## 2   myspace      U30      F     1
## 3  snapchat      U30      F     6
## 4   twitter      U30      F    17
## 5  facebook      U30      M    31
## 6   myspace      U30      M     5
## 7  snapchat      U30      M     4
## 8   twitter      U30      M    23
## 9  facebook      O30      F    60
## 10  myspace      O30      F     3
## 11 snapchat      O30      F     3
## 12  twitter      O30      F    12
## 13 facebook      O30      M    58
## 14  myspace      O30      M     6
## 15 snapchat      O30      M     2
## 16  twitter      O30      M    17
```