Assignment 3

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#1:Load data

Load the following data: + applications from `app_data_sample.parquet` + edges from `edges_sample.csv`

```
# change to your own path!
data_path <- "Data/"
applications <- read_parquet(paste0(data_path,"app_data_sample.parquet"))
edges <- read_csv(paste0(data_path,"edges_sample.csv"))
```

```
## Rows: 32906 Columns: 4
## ── Column specification
────────────────────────────────────────────────────────
## Delimiter: ","
## chr  (1): application_number
## dbl  (2): ego_examiner_id, alter_examiner_id
## date (1): advice_date
##
## ℹ Use `spec()` to retrieve the full column specification for this data.
## ℹ Specify the column types or set `show_col_types = FALSE` to quiet this
message.
```

```
applications
```

```
## # A tibble: 2,018,477 × 16
##    applicat…¹ filing_d…² exami…³ exami…⁴ exami…⁵ exami…⁶ exami…⁷ uspc_…⁸
uspc_…⁹
##    <chr>      <date>     <chr>   <chr>   <chr>     <dbl>   <dbl> <chr>
<chr>
##  1 08284457   2000-01-26 HOWARD  JACQUE… V         96082    1764 508
273000
##  2 08413193   2000-10-11 YILDIR… BEKIR   L         87678    1764 208
179000
##  3 08531853   2000-05-17 HAMILT… CYNTHIA <NA>      63213    1752 430
271100
##  4 08637752   2001-07-20 MOSHER  MARY    <NA>      73788    1648 530
388300
##  5 08682726   2000-04-10 BARR    MICHAEL E         77294    1762 427
430100
##  6 08687412   2000-04-28 GRAY    LINDA   LAMEY     68606    1734 156
204000
##  7 08716371   2004-01-26 MCMILL… KARA    RENITA    89557    1627 424
401000
```

```
## 8 08765941   2000-06-23 FORD    VANESSA L         97543    1645 424
001210
## 9 08776818   2000-02-04 STRZEL… TERESA  E         98714    1637 435
006000
## 10 08809677  2002-02-20 KIM     SUN     U         65530    1723 210
645000
## # … with 2,018,467 more rows, 7 more variables: patent_number <chr>,
## #   patent_issue_date <date>, abandon_date <date>, disposal_type <chr>,
## #   appl_status_code <dbl>, appl_status_date <chr>, tc <dbl>, and
abbreviated
## #   variable names ¹application_number, ²filing_date, ³examiner_name_last,
## #   ⁴examiner_name_first, ⁵examiner_name_middle, ⁶examiner_id,
## #   ⁷examiner_art_unit, ⁸uspc_class, ⁹uspc_subclass

edges

## # A tibble: 32,906 × 4
##    application_number advice_date ego_examiner_id alter_examiner_id
##    <chr>              <date>                <dbl>             <dbl>
##  1 09402488           2008-11-17            84356             66266
##  2 09402488           2008-11-17            84356             63519
##  3 09402488           2008-11-17            84356             98531
##  4 09445135           2008-08-21            92953             71313
##  5 09445135           2008-08-21            92953             93865
##  6 09445135           2008-08-21            92953             91818
##  7 09479304           2008-12-15            61767             69277
##  8 09479304           2008-12-15            61767             92446
##  9 09479304           2008-12-15            61767             66805
## 10 09479304           2008-12-15            61767             70919
## # … with 32,896 more rows
```

Get gender for examiners

We'll get gender based on the first name of the examiner, which is recorded in the field `examiner_name_first`. We'll use library `gender` for that, relying on a modified version of their own example.

Note that there are over 2 million records in the applications table – that's because there are many records for each examiner, as many as the number of applications that examiner worked on during this time frame. Our first step therefore is to get all *unique* names in a separate list `examiner_names`. We will then guess gender for each one and will join this table back to the original dataset. So, let's get names without repetition:

```
library(gender)
#install_genderdata_package() # only run this line the first time you use the
package, to get data for it
# get a list of first names without repetitions
examiner_names <- applications %>%
  distinct(examiner_name_first)
examiner_names
```

```
## # A tibble: 2,595 × 1
##    examiner_name_first
##    <chr>
##  1 JACQUELINE
##  2 BEKIR
##  3 CYNTHIA
##  4 MARY
##  5 MICHAEL
##  6 LINDA
##  7 KARA
##  8 VANESSA
##  9 TERESA
## 10 SUN
## # … with 2,585 more rows
```

Now let's use function `gender()` as shown in the example for the package to attach a gender and probability to each name and put the results into the table `examiner_names_gender`

```
# get a table of names and gender
examiner_names_gender <- examiner_names %>%
  do(results = gender(.$examiner_name_first, method = "ssa")) %>%
  unnest(cols = c(results), keep_empty = TRUE) %>%
  select(
    examiner_name_first = name,
    gender,
    proportion_female
  )
examiner_names_gender
```

```
## # A tibble: 1,822 × 3
##    examiner_name_first gender proportion_female
##    <chr>               <chr>              <dbl>
##  1 AARON               male              0.0082
##  2 ABDEL               male              0
##  3 ABDOU               male              0
##  4 ABDUL               male              0
##  5 ABDULHAKIM          male              0
##  6 ABDULLAH            male              0
##  7 ABDULLAHI           male              0
##  8 ABIGAIL             female            0.998
##  9 ABIMBOLA            female            0.944
## 10 ABRAHAM             male              0.0031
## # … with 1,812 more rows
```

Finally, let's join that table back to our original applications data and discard the temporary tables we have just created to reduce clutter in our environment.

```
# remove extra colums from the gender table
examiner_names_gender <- examiner_names_gender %>%
  select(examiner_name_first, gender)
```

```
# joining gender back to the dataset
applications <- applications %>%
  left_join(examiner_names_gender, by = "examiner_name_first")
# cleaning up
rm(examiner_names)
rm(examiner_names_gender)
gc()
```

```
##             used  (Mb) gc trigger  (Mb) max used  (Mb)
## Ncells  4662327 249.0    8223900 439.3  5106618 272.8
## Vcells 49868964 380.5   93038134 709.9 80184719 611.8
```

Guess the examiner's race

We'll now use package `wru` to estimate likely race of an examiner. Just like with gender, we'll get a list of unique names first, only now we are using surnames.

```
library(wru)
examiner_surnames <- applications %>%
  select(surname = examiner_name_last) %>%
  distinct()
examiner_surnames
```

```
## # A tibble: 3,806 × 1
##    surname
##    <chr>
##  1 HOWARD
##  2 YILDIRIM
##  3 HAMILTON
##  4 MOSHER
##  5 BARR
##  6 GRAY
##  7 MCMILLIAN
##  8 FORD
##  9 STRZELECKA
## 10 KIM
## # … with 3,796 more rows
```

We'll follow the instructions for the package outlined here https://github.com/kosukeimai/wru.

```
examiner_race <- predict_race(voter.file = examiner_surnames, surname.only =
T) %>%
  as_tibble()
```

```
## Warning: Unknown or uninitialised column: `state`.

## Proceeding with last name predictions...

## ℹ All local files already up-to-date!

## 701 (18.4%) individuals' last names were not matched.
```

```
examiner_race

## # A tibble: 3,806 × 6
##    surname    pred.whi pred.bla pred.his pred.asi pred.oth
##    <chr>         <dbl>    <dbl>    <dbl>    <dbl>    <dbl>
##  1 HOWARD       0.597   0.295    0.0275   0.00690   0.0741
##  2 YILDIRIM     0.807   0.0273   0.0694   0.0165    0.0798
##  3 HAMILTON     0.656   0.239    0.0286   0.00750   0.0692
##  4 MOSHER       0.915   0.00425  0.0291   0.00917   0.0427
##  5 BARR         0.784   0.120    0.0268   0.00830   0.0615
##  6 GRAY         0.640   0.252    0.0281   0.00748   0.0724
##  7 MCMILLIAN    0.322   0.554    0.0212   0.00340   0.0995
##  8 FORD         0.576   0.320    0.0275   0.00621   0.0697
##  9 STRZELECKA   0.472   0.171    0.220    0.0825    0.0543
## 10 KIM          0.0169  0.00282  0.00546  0.943     0.0319
## # … with 3,796 more rows

write.csv(examiner_race, "examiner_race.csv", row.names=FALSE)
```

As you can see, we get probabilities across five broad US Census categories: white, black, Hispanic, Asian and other. (Some of you may correctly point out that Hispanic is not a race category in the US Census, but these are the limitations of this package.)

Our final step here is to pick the race category that has the highest probability for each last name and then join the table back to the main applications table. See this example for comparing values across columns: https://www.tidyverse.org/blog/2020/04/dplyr-1-0-0-rowwise/. And this one for `case_when()` function: https://dplyr.tidyverse.org/reference/case_when.html.

```
examiner_race <- examiner_race %>%
  mutate(max_race_p = pmax(pred.asi, pred.bla, pred.his, pred.oth, pred.whi))
%>%
  mutate(race = case_when(
    max_race_p == pred.asi ~ "Asian",
    max_race_p == pred.bla ~ "black",
    max_race_p == pred.his ~ "Hispanic",
    max_race_p == pred.oth ~ "other",
    max_race_p == pred.whi ~ "white",
    TRUE ~ NA_character_
  ))
examiner_race

## # A tibble: 3,806 × 8
##    surname    pred.whi pred.bla pred.his pred.asi pred.oth max_race_p race
##    <chr>         <dbl>    <dbl>    <dbl>    <dbl>    <dbl>      <dbl>
<chr>
##  1 HOWARD       0.597   0.295    0.0275   0.00690   0.0741      0.597
white
##  2 YILDIRIM     0.807   0.0273   0.0694   0.0165    0.0798      0.807
white
##  3 HAMILTON     0.656   0.239    0.0286   0.00750   0.0692      0.656
```

```
white
##   4 MOSHER       0.915   0.00425  0.0291   0.00917   0.0427      0.915
white
##   5 BARR         0.784   0.120    0.0268   0.00830   0.0615      0.784
white
##   6 GRAY         0.640   0.252    0.0281   0.00748   0.0724      0.640
white
##   7 MCMILLIAN    0.322   0.554    0.0212   0.00340   0.0995      0.554
black
##   8 FORD         0.576   0.320    0.0275   0.00621   0.0697      0.576
white
##   9 STRZELECKA   0.472   0.171    0.220    0.0825    0.0543      0.472
white
## 10 KIM          0.0169  0.00282  0.00546  0.943     0.0319      0.943
Asian
## # … with 3,796 more rows
```

Let's join the data back to the applications table.

```
# removing extra columns
examiner_race <- examiner_race %>%
  select(surname,race)
applications <- applications %>%
  left_join(examiner_race, by = c("examiner_name_last" = "surname"))
rm(examiner_race)
rm(examiner_surnames)
gc()
```

```
##             used  (Mb) gc trigger  (Mb) max used  (Mb)
## Ncells  4797280 256.3    8223900 439.3  8223900 439.3
## Vcells 54203029 413.6  111725760 852.4 92948874 709.2
```

#2. Focus on Art Unit:Descriptive Stats ## Work Unit Breakdown of people

We will compare genders and ethnicity across all work units within the US Patent office. First let's do some descriptive statistics on the overall population.

Lets keep only one observation per person for the data since once person could count twice for a work group

```
person_level_data <- applications %>%
  group_by(examiner_id) %>%
  summarise(
    art_unit = min(examiner_art_unit, na.rm = TRUE),
    gender = min(gender, na.rm = TRUE),
    race = min(race,na.rm=TRUE)) %>%
  mutate(
    tc = floor(art_unit/100)*100,
    work_group = as.factor(floor(art_unit/10)*10)
  ) %>%
  filter(!is.na(gender) & !is.na(race)) # dropping all records where we don't
```

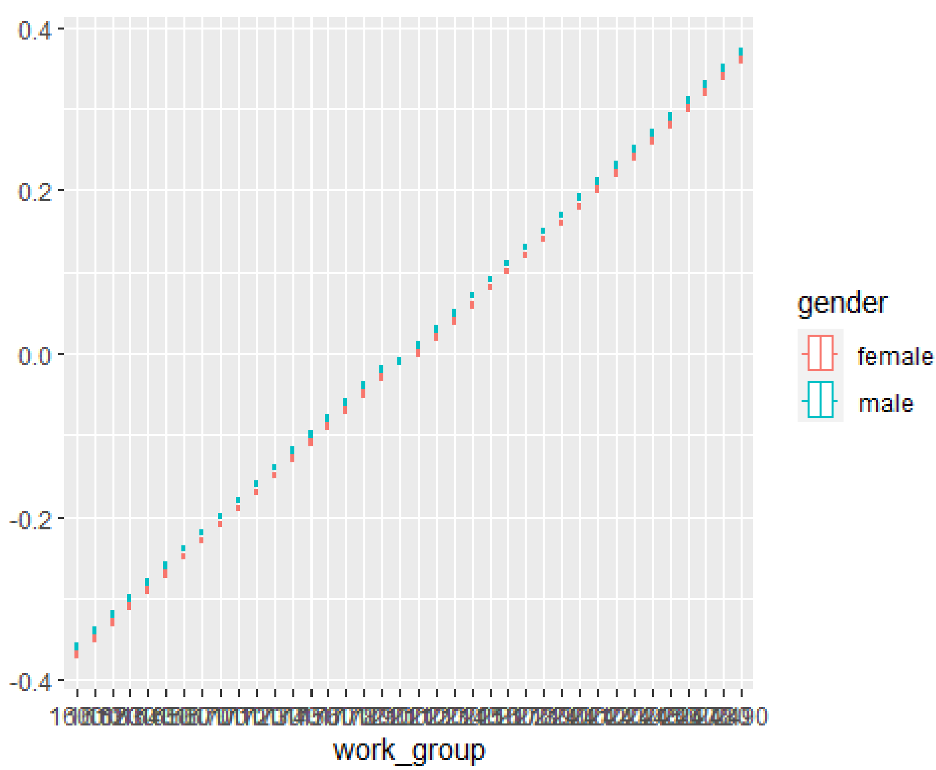
```r
know the gender
person_level_data

## # A tibble: 4,849 × 6
##    examiner_id art_unit gender race      tc work_group
##          <dbl>    <dbl> <chr>  <chr> <dbl> <fct>
##  1       59012     1716 male   white  1700 1710
##  2       59025     2465 male   Asian  2400 2460
##  3       59040     1724 female Asian  1700 1720
##  4       59052     2138 male   Asian  2100 2130
##  5       59055     2165 male   Asian  2100 2160
##  6       59056     2124 male   Asian  2100 2120
##  7       59081     2489 male   Asian  2400 2480
##  8       59086     2487 female white  2400 2480
##  9       59096     1612 male   white  1600 1610
## 10       59117     2439 male   white  2400 2430
## # … with 4,839 more rows

#grouping by work unit
work_unit_level_data <-person_level_data %>%
  group_by(work_group,race,gender) %>%
  summarize(
    n=n()
  )

## `summarise()` has grouped output by 'work_group', 'race'. You can override
## using the `.groups` argument.

work_unit_level_data

## # A tibble: 263 × 4
## # Groups:   work_group, race [146]
##    work_group race     gender     n
##    <fct>      <chr>    <chr>  <int>
##  1 1600       Asian    female     3
##  2 1600       black    female     1
##  3 1600       white    female    13
##  4 1600       white    male      18
##  5 1610       Asian    female    18
##  6 1610       Asian    male      15
##  7 1610       black    female     4
##  8 1610       black    male       2
##  9 1610       Hispanic female     2
## 10 1610       Hispanic male       3
## # … with 253 more rows

#we will also need to aggregated by total number of people in work_unit
work_unit_aggregated <- work_unit_level_data %>%
  group_by(work_group) %>%
  summarize(
    n=sum(n)
```

```
  ) %>%
  arrange (desc(n))
work_unit_aggregated
```

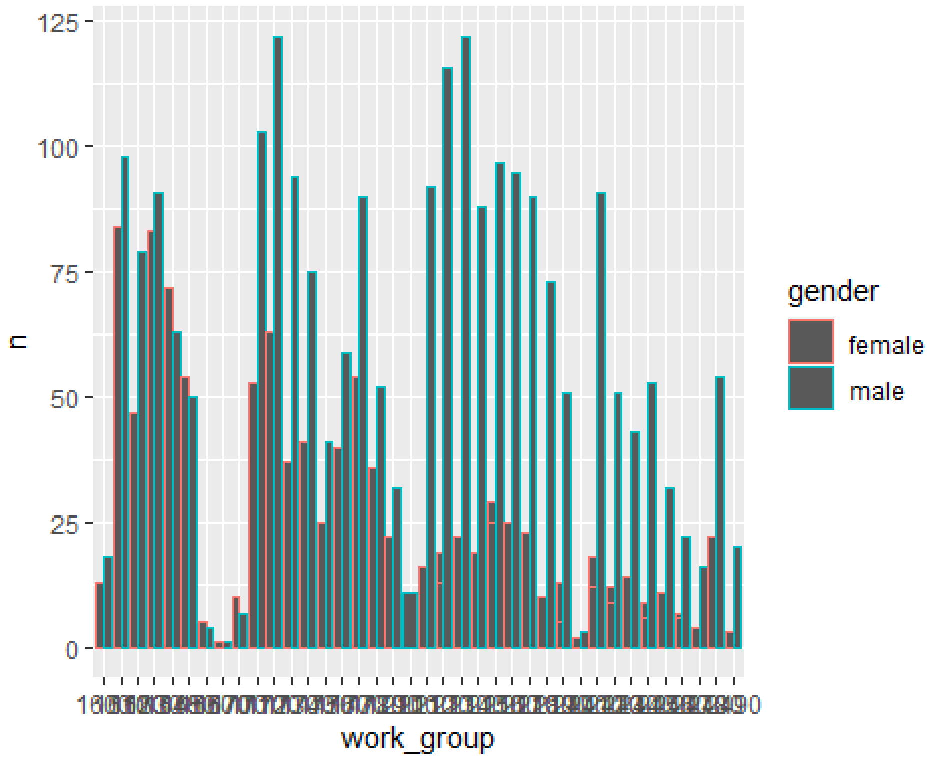
```
## # A tibble: 38 × 2
##    work_group     n
##    <fct>      <int>
##  1 2130         237
##  2 1610         226
##  3 2150         226
##  4 1720         225
##  5 2120         210
##  6 1710         208
##  7 1630         207
##  8 2410         203
##  9 2160         197
## 10 1770         189
## # … with 28 more rows
```

Let's plot the race, and gender as a function of workgroup. First looking at counts then distributions

```
library(ggplot2)
ggplot(work_unit_level_data) +
  geom_boxplot(aes(x = work_group, color = gender))
```

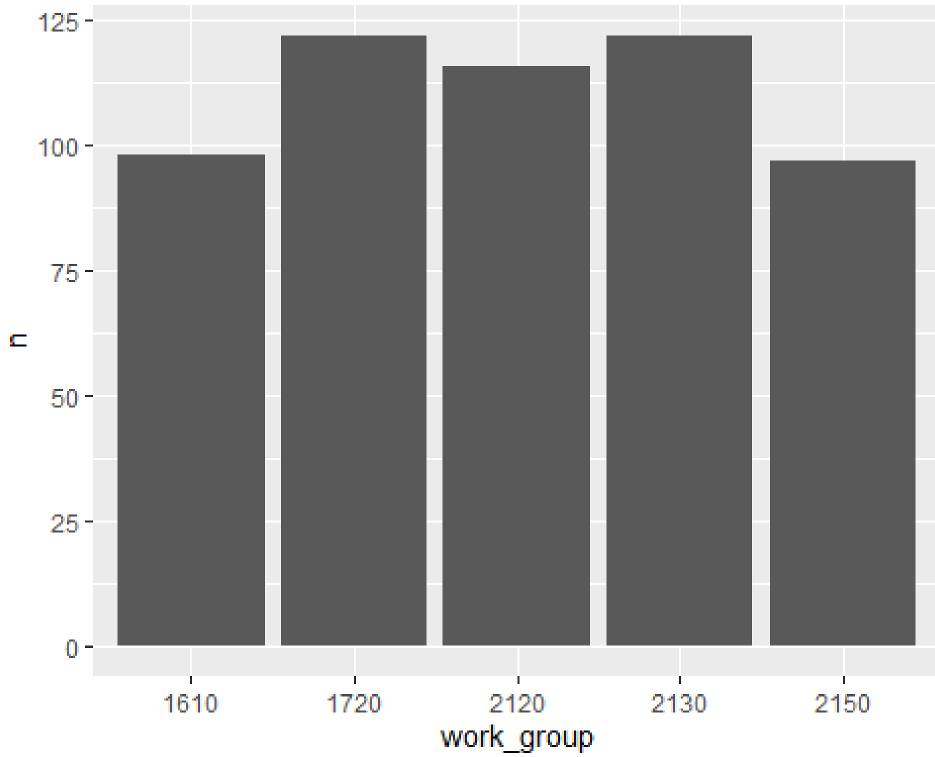


```
ggplot(work_unit_level_data,aes(x = work_group, color = gender, y=n)) +
  geom_bar(stat="identity", position=position_dodge())
```

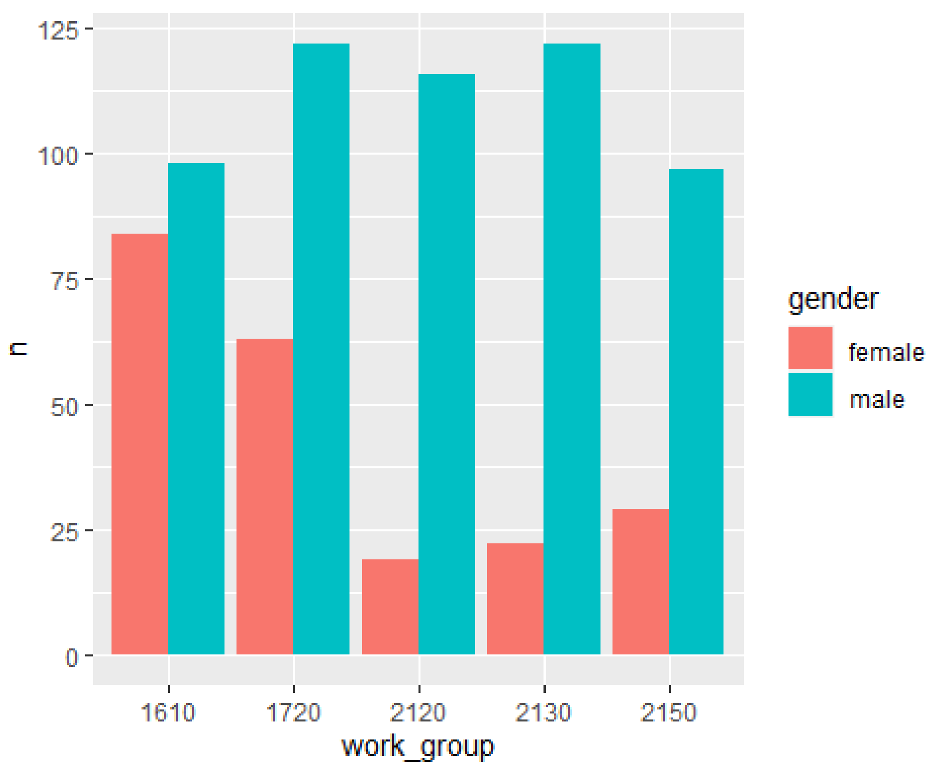


Let's plot for the top 5 work groups to make it easier to read. First we will look at the number (counts) then we will look at the distributions using box plots.

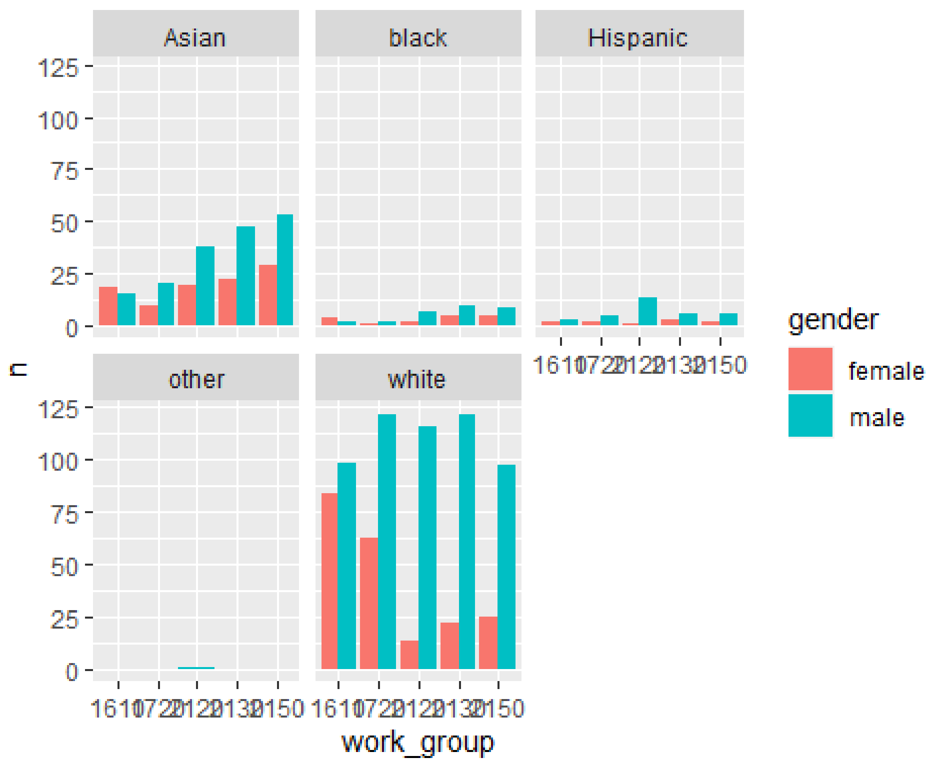
```
work_unit_level_data_top5 <- work_unit_level_data %>%
  filter(work_group %in% head(work_unit_aggregated$work_group,5))

ggplot(work_unit_level_data_top5,aes(x = work_group, y=n)) +
  geom_bar(stat="identity", position=position_dodge())
```




```
ggplot(work_unit_level_data_top5,aes(x = work_group, fill = gender, y=n)) +
  geom_bar(stat="identity", position=position_dodge())
```



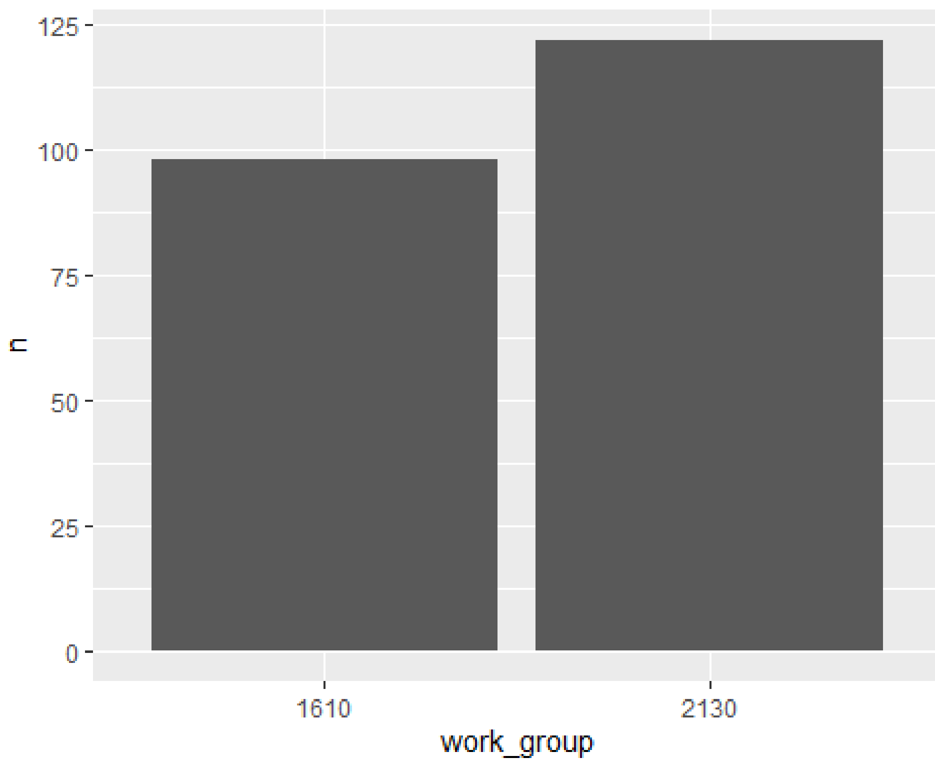
```r
ggplot(work_unit_level_data_top5,aes(x = work_group, fill = gender, y=n)) +
  geom_bar(stat="identity", position=position_dodge())+
  facet_wrap(~race)
```



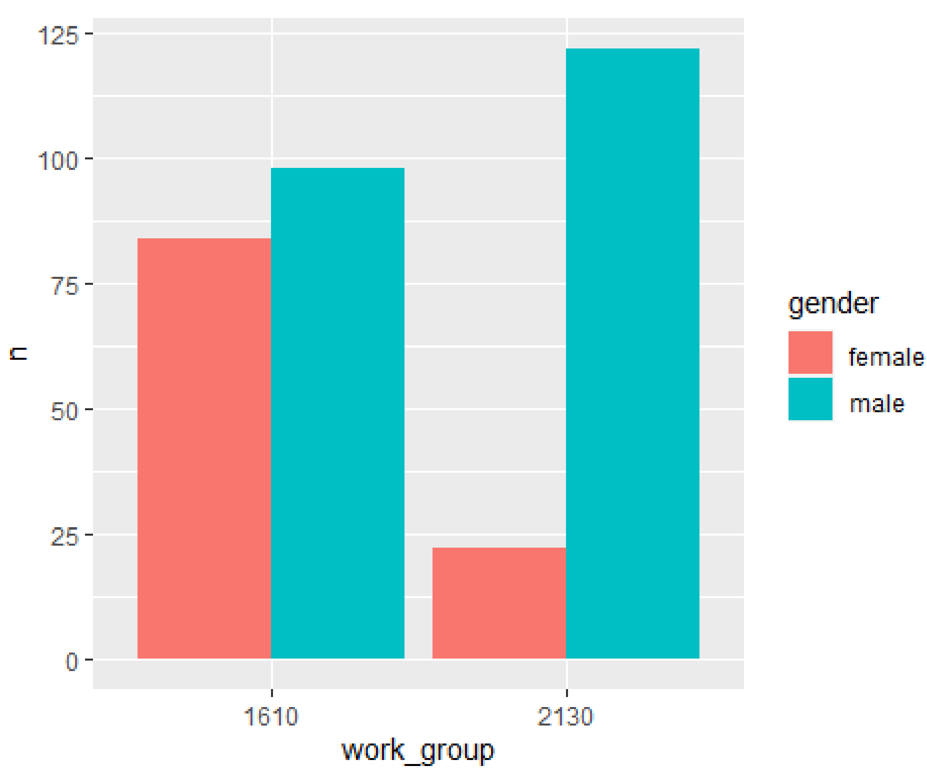

```r
#
# ggplot(work_unit_level_data_top5) +
#   geom_boxplot(aes(x = (work_group),y=n, color = gender))
#
# ggplot(work_unit_level_data_top5) +
#   geom_boxplot(aes(x = (work_group),y=n, color = gender))+
#   facet_wrap(~race)
remove(work_unit_level_data_top5)
```

Even the top 5 is alot of data. For the remaining analysis we will focus on the top 2 work_units: 2130 and 1610. Since we are only using 2 art units the ditribution is not as relenvant to plot at the moment.

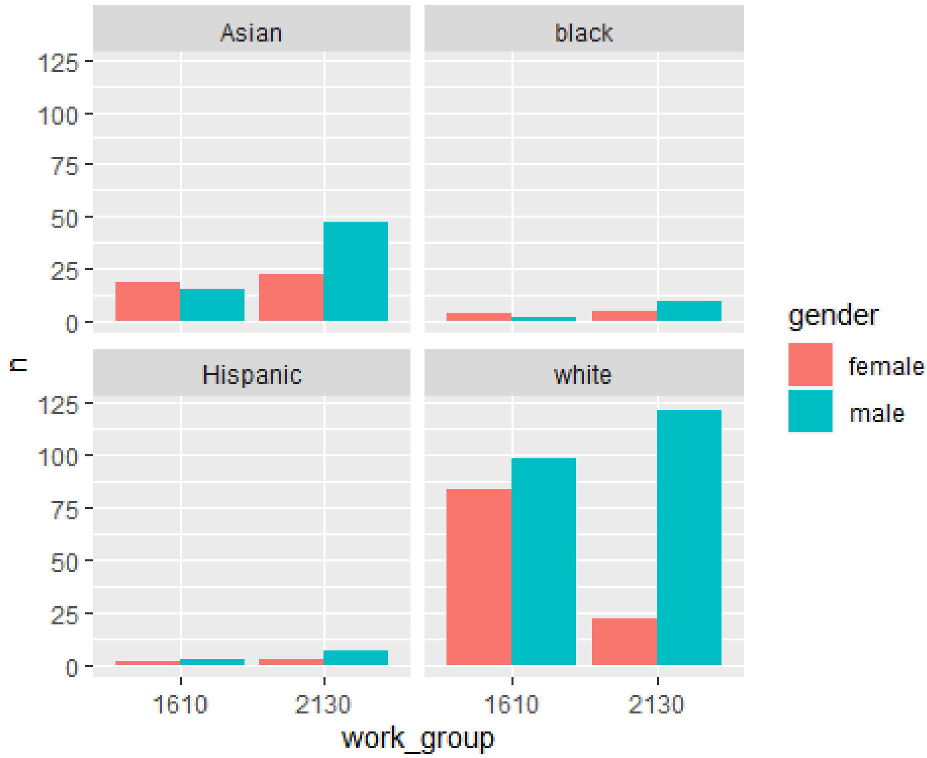
```r
work_unit_level_data_top2 <- work_unit_level_data %>%
  filter(work_group %in% head(work_unit_aggregated$work_group,2))

ggplot(work_unit_level_data_top2,aes(x = work_group, y=n)) +
  geom_bar(stat="identity", position=position_dodge())
```




```
ggplot(work_unit_level_data_top2,aes(x = work_group, fill = gender, y=n)) +
  geom_bar(stat="identity", position=position_dodge())
```



```
ggplot(work_unit_level_data_top2,aes(x = work_group, fill = gender, y=n)) +
  geom_bar(stat="identity", position=position_dodge())+
  facet_wrap(~race)
```




```
# ggplot(work_unit_level_data_top2) +
#   geom_boxplot(aes(x = (work_group),y=n, color = gender))

subset_app_data <- person_level_data %>%
  #here we make sure on ly the top 2 work groups are picked
  filter(work_group %in% head(work_unit_aggregated$work_group,2)) %>%
  mutate(race = race, gender =gender) %>%
  select(gender, race, work_group)
```

Gender

let’s investigate gender, first accros borht work groups then within the workgroup

```
subset_app_data %>%
  count(gender) %>%
  mutate(pct = n/sum(n))

## # A tibble: 2 × 3
##   gender     n   pct
##   <chr>  <int> <dbl>
## 1 female   160 0.346
## 2 male     303 0.654
```

```
subset_app_data %>%
  group_by(work_group) %>%
  count(gender) %>%
  mutate(pct = n/sum(n))

## # A tibble: 4 × 4
## # Groups:   work_group [2]
##   work_group gender     n   pct
##   <fct>      <chr>  <int> <dbl>
## 1 1610       female   108 0.478
## 2 1610       male     118 0.522
## 3 2130       female    52 0.219
## 4 2130       male     185 0.781
```

Race

let's investigate race with the same process as above, first accros borht work groups then within the workgroup

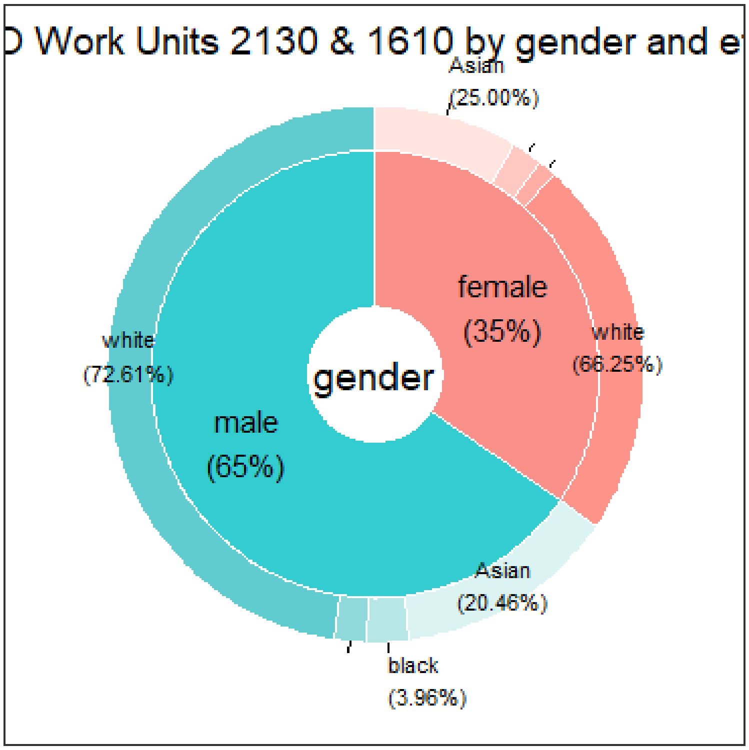
```
subset_app_data %>%
  group_by(work_group) %>%
  count(race) %>%
  mutate(pct = n/sum(n))

## # A tibble: 8 × 4
## # Groups:   work_group [2]
##   work_group race         n    pct
##   <fct>      <chr>    <int>  <dbl>
## 1 1610       Asian       33 0.146
## 2 1610       black        6 0.0265
## 3 1610       Hispanic     5 0.0221
## 4 1610       white      182 0.805
## 5 2130       Asian       69 0.291
## 6 2130       black       15 0.0633
## 7 2130       Hispanic     9 0.0380
## 8 2130       white      144 0.608
```

Puttin it together

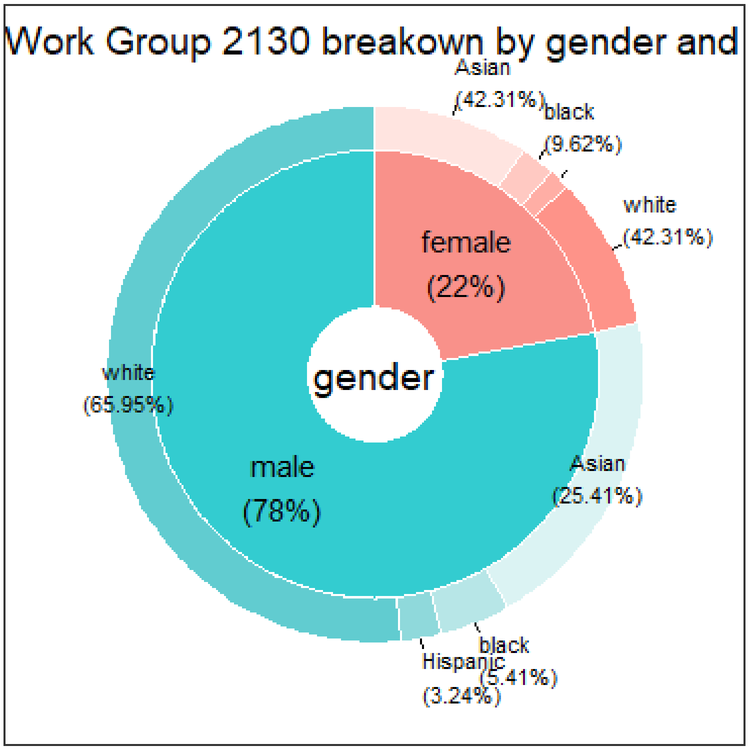
Let's investgate both at the same time

```
library(webr)
PieDonut(subset_app_data, aes(gender,race), title = "USPTO Work Units 2130 &
1610 by gender and ethnicity")

## Warning: The `<scale>` argument of `guides()` cannot be `FALSE`. Use
"none" instead as
## of ggplot2 3.3.4.
## ℹ The deprecated feature was likely used in the webr package.
##   Please report the issue at
```

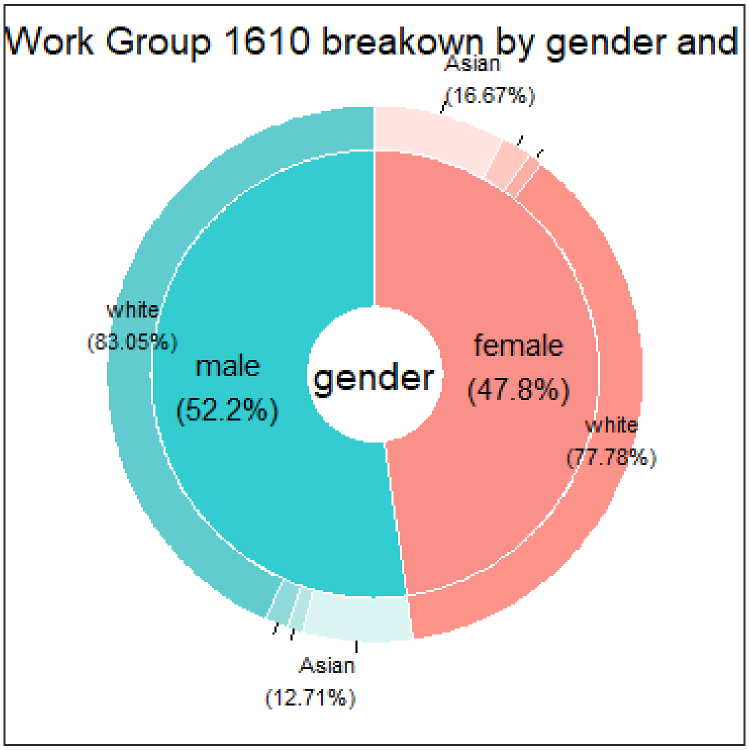
```
<]8;;https://github.com/cardiomoon/webr/issueshttps://github.com/cardiomoon/w
ebr/issues]8;;>.
```




```
subset_app_data1 <- subset_app_data %>% filter(work_group==2130)
subset_app_data2 <- subset_app_data %>% filter(work_group==1610)

PieDonut(subset_app_data1, aes(gender,race), title = "USPTO Work Group 2130
breakown by gender and ethnicity", explodeDonut=TRUE)

## Warning in geom_arc_bar(aes_string(x0 = "x", y0 = "y", r0 =
as.character(r1), :
## Ignoring unknown aesthetics: explode
```




```
PieDonut(subset_app_data2, aes(gender,race), title = "USPTO Work Group 1610
breakown by gender and ethnicity", explodeDonut=TRUE)

## Warning in geom_arc_bar(aes_string(x0 = "x", y0 = "y", r0 =
as.character(r1), :
## Ignoring unknown aesthetics: explode
```




```
remove(subset_app_data1, subset_app_data2)
```

#3: Advice Network ##Nodes & Edges First we need to subset the data and remove the examiners who are not in the work groups we are looking at

```
#copy data in case
edges_full <- edges
edges <- edges_full

subset_exam_id <- person_level_data %>%
  filter(work_group %in% head(work_unit_aggregated$work_group,2)) %>%
  select(examiner_id,work_group) %>%
  drop_na()

#crete the edges
edges <- edges %>%
  filter(ego_examiner_id %in% subset_exam_id$examiner_id)%>%
  drop_na() %>%
  mutate(from=ego_examiner_id,to=alter_examiner_id) %>%
  select(from, to)

#create the nodes
#many issues with nodes will try pulling from edges list
# nodes_all <- unique(select(edges_full, ego_examiner_id)) %>%
#   mutate(id=ego_examiner_id, verticies =ego_examiner_id) %>%
#   select(id,verticies) %>%
#   drop_na
```

```
nodes_all <-
as.data.frame(do.call(rbind,append(as.list(edges$from),as.list(edges$to))))

nodes_all <- nodes_all %>%
  mutate(id=V1) %>%
  select(id) %>%
  distinct(id) %>%
  drop_na()
nodes <- nodes_all
# nodes <- nodes_all %>%
#   mutate(label=as.character(ego_examiner_id)) %>%
#   filter(id %in% edges$from | id %in% edges$to ) %>%
#   drop_na() %>%
#   select(id,label)

library(visNetwork)
visNetwork(nodes, edges)%>%
  visLegend() %>%
  visEdges(arrows ="to")%>%
  visEdges(arrows ="from")
```

Based on this data we will only have about 121 employees in the work groups we are interested in

3.1 Degree Centrality

The count of the number of links each node has to other nodes. For instance, seat A(labelled as 3 above) has a degree centrality of 3 since it is connected to 3 other nodes: 2, B & C (B labelled as 4 and C labelled as 5 above)

We can validate this with the igraph package wich has a built in functionality for centrality degree

```
library(igraph)

##
## Attaching package: 'igraph'

## The following objects are masked from 'package:lubridate':
##
##     %--%, union

## The following objects are masked from 'package:dplyr':
##
##     as_data_frame, groups, union

## The following objects are masked from 'package:purrr':
##
##     compose, simplify

## The following object is masked from 'package:tidyr':
##
##     crossing

## The following object is masked from 'package:tibble':
##
##     as_data_frame

## The following objects are masked from 'package:stats':
##
##     decompose, spectrum

## The following object is masked from 'package:base':
##
##     union

library(tidygraph)

##
## Attaching package: 'tidygraph'

## The following object is masked from 'package:igraph':
##
##     groups

## The following object is masked from 'package:stats':
##
##     filter

library(tidyverse)

g <- igraph::graph_from_data_frame(edges, vertices = nodes) %>%
as_tbl_graph(directed=TRUE)
```

```
#not sure why this isnt working
#g = tbl_graph(nodes = nodes, edges = edges, directed = FALSE)
g <- g %>%
  activate(nodes) %>%
  mutate(degree = centrality_degree()) %>%
  activate(edges)

tg_nodes <-
  g %>%
  activate(nodes) %>%
  data.frame() %>%
  arrange(desc(degree)) %>%
  rename(Centrality_Degree=degree) %>%
  mutate(name=as.integer(name))

nodes_all <- nodes_all %>%
  left_join(tg_nodes,by=c("id"="name"))

remove(g,tg_nodes)
```

There is agreement between our calculations and the calculations for the package therefore we can use them!

3.2 Closeness centrality

```
A measure that calculates the ability to spread information efficiently via
the edges the node is connected to. It is calculated as the inverse of the
average shortest path between nodes.
```

For instance, for node A (labelled 3), the closeness is 1/((1+2+1+1+2+2+2+2+3))=0.0625. The higher the number, the closer the node is to the center based on distance. See appendix For details

```
g <- igraph::graph_from_data_frame(edges, vertices = nodes) %>%
as_tbl_graph(directed=TRUE)

g <- g %>%
  activate(nodes) %>%
  mutate(degree = centrality_closeness()) %>%
  activate(edges)

tg_nodes <-
  g %>%
  activate(nodes) %>%
  data.frame() %>%
  arrange(desc(degree)) %>%
  rename(Centrality_Closeness=degree) %>%
  mutate(name=as.integer(name))

nodes_all <- nodes_all %>%
```

```
  left_join(tg_nodes,by=c("id"="name"))
remove(g,tg_nodes)
```

3.3 Betweenness centrality

A measure that detects a node's influence over the flow of information within a graph. This is the sum of the shortest paths between two points i and j divided by the number of shortest paths that pass-through node v.

```
g <- igraph::graph_from_data_frame(edges, vertices = nodes) %>%
as_tbl_graph(directed=TRUE)

g <- g %>%
  activate(nodes) %>%
  mutate(degree = centrality_betweenness()) %>%
  activate(edges)

tg_nodes <-
  g %>%
  activate(nodes) %>%
  data.frame() %>%
  arrange(desc(degree)) %>%
  rename(Centrality_Betweenness=degree) %>%
  mutate(name=as.integer(name))

nodes_all <- nodes_all %>%
  left_join(tg_nodes,by=c("id"="name"))
remove(g,tg_nodes)
```

Visualize all together

LEt's put all the data together now!

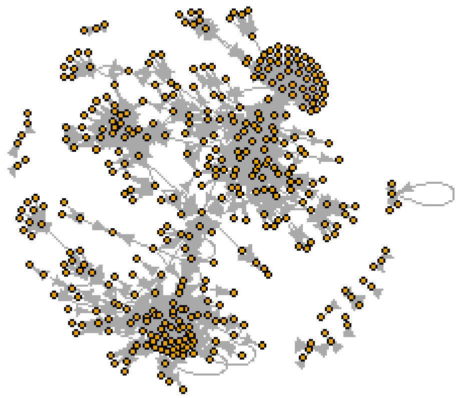
```
nodes <- nodes_all %>%
  left_join(subset_exam_id,by=c("id"="examiner_id")) %>%
  mutate(label = paste("Examiner:",id,"\n",
                      "Centrality Degre:",format(Centrality_Degree, digits =
2),"\n",
                      "Closenness:",format(Centrality_Closeness, digits =
2),"\n",
                      "Betweenness:",format(Centrality_Betweenness, digits =
2),"\n",
                      sep = " "),
         group=work_group) %>%
  mutate(font.size = 12) %>%
  drop_na()

visNetwork(nodes, edges)%>%
  visLegend() %>%
```

```
  visEdges(arrows ="to")%>%
  visEdges(arrows ="from")
```

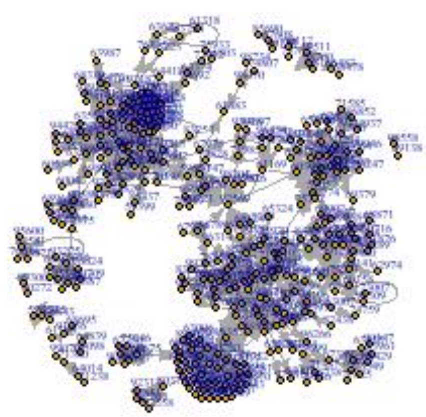
Igraph version

labels must be removed for igraph or else it does not work well.

```
net <- igraph::graph_from_data_frame(edges, vertices = nodes_all) %>%
as_tbl_graph(directed=TRUE)
plot(net, edge.arrow.size=.4,vertex.label=NA,vertex.size=4)
```

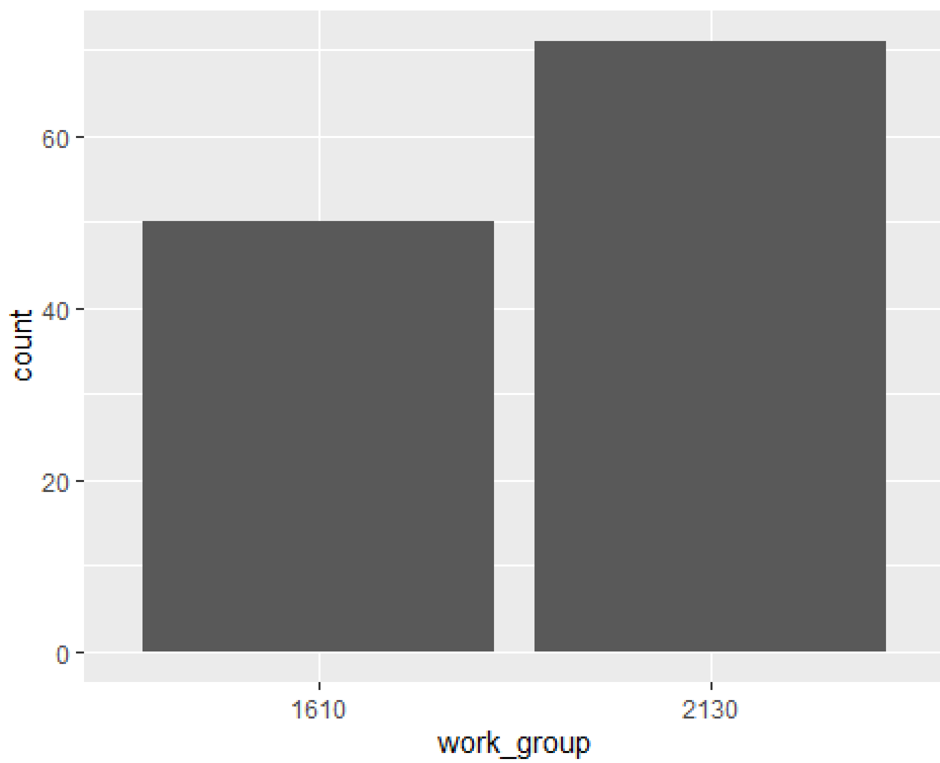


```
plot(net,
edge.arrow.size=.4,vertex.label.cex=.4,vertex.label.dist=1,vertex.size=4)
```

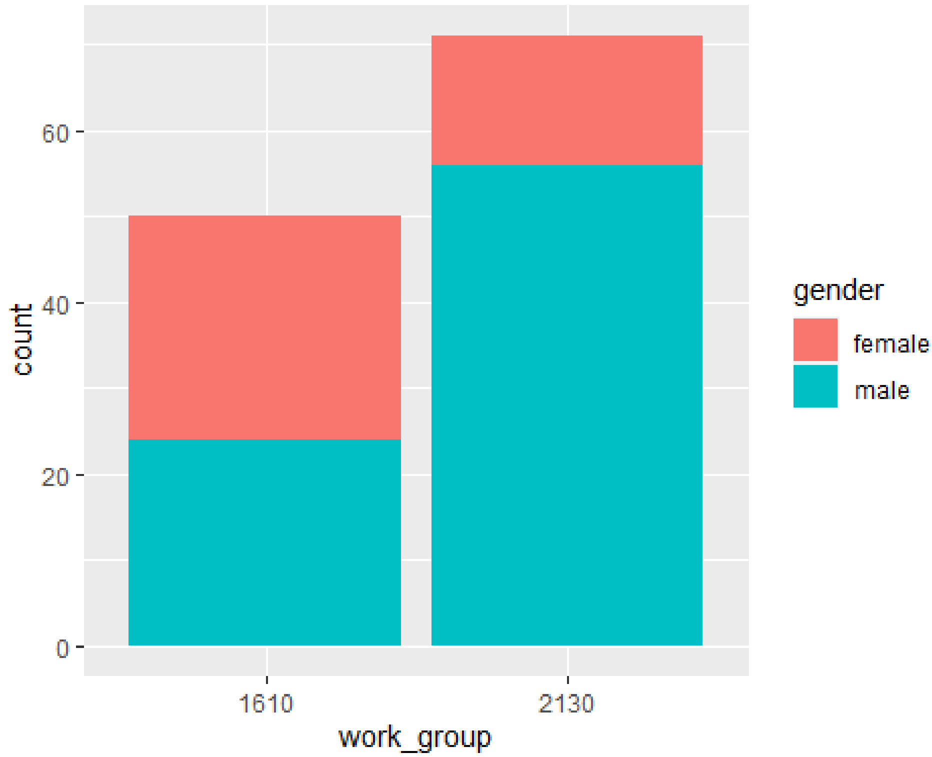


Now to look at measures of centrality accross ethnicities and genders

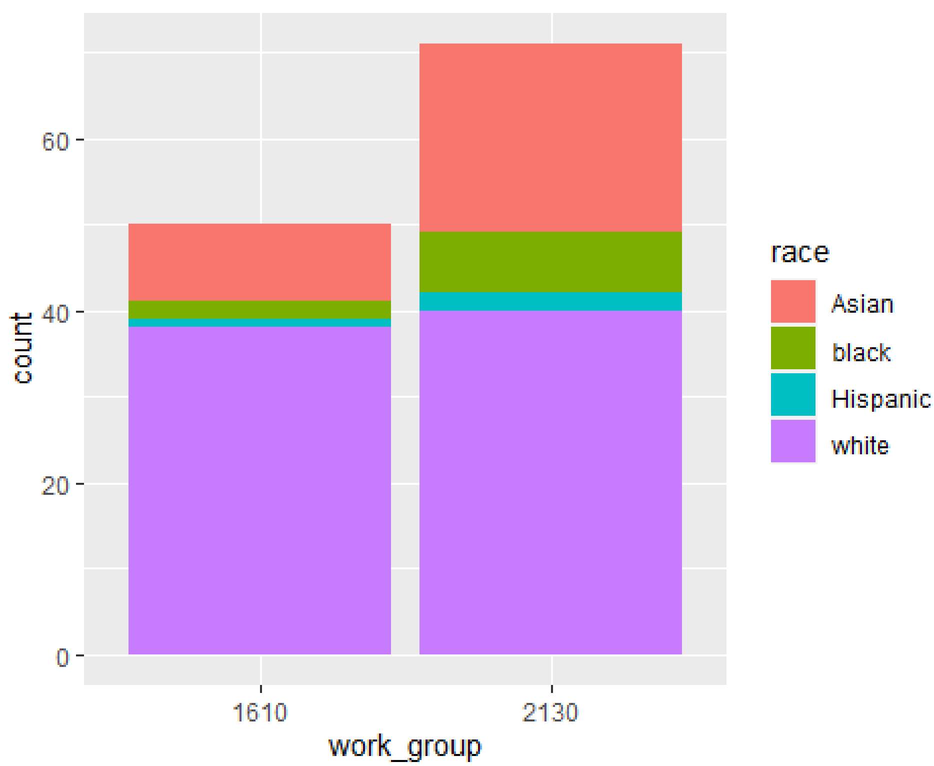
```
#join race and gender data to nodes
library(gt)
nodes <- nodes %>%

left_join(person_level_data,by=c("id"="examiner_id","work_group"="work_group"
))

ggplot(nodes) +
  geom_bar(aes(x = work_group))
```




```
ggplot(nodes) +
  geom_bar(aes(x = work_group ,fill=gender))
```




```
ggplot(nodes) +
  geom_bar(aes(x = work_group ,fill=race))
```



```
nodes %>%
  group_by(work_group) %>%
  count(work_group) %>%
  mutate(pct_within_work_group = round(n/sum(n)*100,0)) %>% gt()
```

n	pct_within_work_group
1610	
50	100
2130	
71	100

```
nodes %>%
  group_by(work_group) %>%
  count(gender) %>%
  mutate(pct_within_work_group = round(n/sum(n)*100,0)) %>% gt()
```

gender	n	pct_within_work_group
1610		
female	26	52
male	24	48
2130		
female	15	21
male	56	79

```
nodes %>%
  group_by(work_group) %>%
  count(race) %>%
  mutate(pct_within_work_group = round(n/sum(n)*100,0)) %>% gt()
```

race	n	pct_within_work_group
1610		
Asian	9	18
black	2	4
Hispanic	1	2
white	38	76
2130		
Asian	22	31
black	7	10
Hispanic	2	3
white	40	56

```
nodes %>%
  group_by(work_group) %>%
  summarize(
    Sum_of_Centrality_Degree=sum(Centrality_Degree),
    Sum_of_Centrality_Closeness=sum(Centrality_Closeness),
```

```
    Sum_of_Centrality_Betweenness=sum(Centrality_Betweenness),
    Count=n()
  ) %>% gt()
```

work_group	Sum_of_Centrality_Degree	Sum_of_Centrality_Closeness	Sum_of_Centrality_Betweenness	Count
1610	579	21.77945	124	50
2130	566	24.99051	164	71

```
nodes %>%
  group_by(gender) %>%
  summarize(
    Sum_of_Centrality_Degree=sum(Centrality_Degree),
    Sum_of_Centrality_Closeness=sum(Centrality_Closeness),
    Sum_of_Centrality_Betweenness=sum(Centrality_Betweenness),
    Count=n()
  ) %>% gt()
```

gender	Sum_of_Centrality_Degree	Sum_of_Centrality_Closeness	Sum_of_Centrality_Betweenness	Count
female	442	15.66323	102.1905	41
male	703	31.10673	185.8095	80

```
nodes %>%
  group_by(race) %>%
  summarize(
    Sum_of_Centrality_Degree=sum(Centrality_Degree),
    Sum_of_Centrality_Closeness=sum(Centrality_Closeness),
    Sum_of_Centrality_Betweenness=sum(Centrality_Betweenness),
    Count=n()
  ) %>% gt()
```

race	Sum_of_Centrality_Degree	Sum_of_Centrality_Closeness	Sum_of_Centrality_Betweenness	Count
Asian	360	12.330561	72.66667	31
black	47	4.922756	1.00000	9
Hispanic	55	1.375000	51.14286	3
white	683	28.141638	163.19048	78

```
nodes %>%
  group_by(work_group,race) %>%
  summarize(
    Sum_of_Centrality_Degree=sum(Centrality_Degree),
    Sum_of_Centrality_Closeness=sum(Centrality_Closeness),
    Sum_of_Centrality_Betweenness=sum(Centrality_Betweenness),
    Count=n()
  ) %>% gt()

## `summarise()` has grouped output by 'work_group'. You can override using
the
## `.groups` argument.
```

race	Sum_of_Centrality_Degree	Sum_of_Centrality_Closeness	Sum_of_Centrality_Betweenness	Count
1610				
Asian	111	5.27777778	6.666667	9
black	3	1.50000000	0.000000	2
Hispanic	51	0.04166667	46.142857	1
white	414	14.96000602	71.190476	38
2130				
Asian	249	7.05278347	66.000000	22
black	44	3.42275641	1.000000	7
Hispanic	4	1.33333333	5.000000	2
white	269	13.18163211	92.000000	40

```
nodes %>%
  group_by(race,gender) %>%
  summarize(
    Sum_of_Centrality_Degree=sum(Centrality_Degree),
    Sum_of_Centrality_Closeness=sum(Centrality_Closeness),
    Sum_of_Centrality_Betweenness=sum(Centrality_Betweenness),
    Count=n()
  ) %>% gt()

## `summarise()` has grouped output by 'race'. You can override using the
## `.groups` argument.
```

gender	Sum_of_Centrality_Degree	Sum_of_Centrality_Closeness	Sum_of_Centrality_Betweenness	Count
Asian				
female	230	4.815007	60.00000	13
male	130	7.515554	12.66667	18
black				
female	36	2.339423	1.00000	5
male	11	2.583333	0.00000	4
Hispanic				
male	55	1.375000	51.14286	3
white				
female	176	8.508796	41.19048	23
male	507	19.632842	122.00000	55

```
nodes %>%
  group_by(work_group,race,gender) %>%
  summarize(
    Sum_of_Centrality_Degree=sum(Centrality_Degree),
    Sum_of_Centrality_Closeness=sum(Centrality_Closeness),
    Sum_of_Centrality_Betweenness=sum(Centrality_Betweenness),
    Count=n()
  ) %>% gt()
```

```
## `summarise()` has grouped output by 'work_group', 'race'. You can override
## using the `.groups` argument.
```

gender	Sum_of_Centrality_Degree	Sum_of_Centrality_Closeness	Sum_of_Centrality_Betweenness	Count
1610 - Asian				
female	96	3.77777778	0.000000	6
male	15	1.50000000	6.666667	3
1610 - black				
female	1	1.00000000	0.000000	1
male	2	0.50000000	0.000000	1
1610 - Hispanic				
male	51	0.04166667	46.142857	1
1610 - white				
female	163	7.32546296	41.190476	19
male	251	7.63454306	30.000000	19
2130 - Asian				
female	134	1.03722944	60.000000	7
male	115	6.01555404	6.000000	15
2130 - black				
female	35	1.33942308	1.000000	4
male	9	2.08333333	0.000000	3
2130 - Hispanic				
male	4	1.33333333	5.000000	2
2130 - white				
female	13	1.18333333	0.000000	4
male	256	11.99829878	92.000000	36

```
node_matrix_all <- edges %>%
  left_join(nodes, by=c("from"="id")) %>%
  select(from,to,race,gender) %>%
  rename(from_gender=gender, from_race=race) %>%
  left_join(nodes, by=c("to"="id")) %>%
  select(from,to,race,gender,from_gender,from_race) %>%
  rename(to_gender=gender, to_race=race) %>%
  drop_na()

node_matrix <- node_matrix_all %>%
  group_by(to_race,from_race) %>%
  summarize(
    count=n()
  )

## `summarise()` has grouped output by 'to_race'. You can override using the
## `.groups` argument.
```

```
pivot_wider(node_matrix, names_from = to_race, values_from = count )

## # A tibble: 4 × 5
##   from_race Asian black Hispanic white
##   <chr>     <int> <int>    <int> <int>
## 1 Asian         1    NA        1    22
## 2 Hispanic      1    NA       NA     1
## 3 white         6     2        3    70
## 4 black        NA    NA        5    10

node_matrix <- node_matrix_all %>%
  group_by(to_gender,from_gender) %>%
  summarize(
    count=n()
  )

## `summarise()` has grouped output by 'to_gender'. You can override using
the
## `.groups` argument.

pivot_wider(node_matrix, names_from = to_gender, values_from = count )

## # A tibble: 2 × 3
##   from_gender female  male
##   <chr>        <int> <int>
## 1 female          19    21
## 2 male            16    66

node_matrix <- node_matrix_all %>%
  group_by(from_race,to_gender,from_gender,to_race) %>%
  summarize(
    count=n()
  )

## `summarise()` has grouped output by 'from_race', 'to_gender',
'from_gender'.
## You can override using the `.groups` argument.

pivot_wider(node_matrix, names_from = c(to_race,to_gender), values_from =
count )

## # A tibble: 7 × 8
## # Groups:   from_race, from_gender [7]
##   from_race from_gender white_female Asian_fem…¹ white…² Hispa…³ Asian…⁴
black…⁵
##   <chr>     <chr>              <int>       <int>   <int>   <int>   <int>
<int>
## 1 Asian     female                 5          NA       4      NA      NA
NA
## 2 Asian     male                  NA           1      13       1      NA
NA
## 3 black     female                NA          NA       9       5      NA
```

```
NA
## 4 black     male                      NA          NA       1       NA       NA
NA
## 5 Hispanic  male                       1          NA      NA       NA        1
NA
## 6 white     female                    12          NA       2        1       NA
2
## 7 white     male                       9           5      47        2        1
NA
## # … with abbreviated variable names ¹Asian_female, ²white_male, ³
Hispanic_male,
## #   ⁴Asian_male, ⁵black_female
```

appendix

testing to make sure examiners in edges data

```
test<-merge(edges,person_level_data,by.x="to",by.y="examiner_id")
test %>%
  group_by(work_group) %>%
  count(work_group) %>%
  arrange(desc(n))
```

```
## # A tibble: 27 × 2
## # Groups:   work_group [27]
##    work_group     n
##    <fct>      <int>
##  1 2130         223
##  2 1610         214
##  3 2110          66
##  4 2180          27
##  5 2400          26
##  6 1710          16
##  7 2120          14
##  8 1630          13
##  9 2150          12
## 10 1600          11
## # … with 17 more rows
```

Nodes and edges mismatch solving

```
test <- edges %>%
  filter(from %in% nodes$id)

test <- edges %>%
  filter(from %in% nodes$id | to %in% nodes$id)

test <- nodes %>%
  filter(id %in% edges$to)
```

```
edges[(!edges$from %in% nodes_all$id) ,]

## # A tibble: 0 × 2
## # … with 2 variables: from <dbl>, to <dbl>

edges[(!edges$to %in% nodes_all$id) ,]

## # A tibble: 0 × 2
## # … with 2 variables: from <dbl>, to <dbl>
```