Ch3. 논비건, 비건 특징 분석-1

4 조

2022 5 13

앞서 논비건과 비건의 나이, 성별 등의 특징을 확인했습니다. 이번에는 **논비건과 비건의 식습관, 자주 먹는 식품** 등에 대해 비교 분석을 진행하였습니다.

- 먼저 고기와 같은 식품군과 비건 식품군을 얼마나 자주 섭취하는지 빈도수를 확인해보았습니다.

라이브러리 로드

```
library(readxl)
library(dplyr)
library(tidyverse)
library(reshape)
library(ggplot2)
```

원본 데이터 파일 불러오기 및 필요 행 추출 - non_vegan

```
vegan_raw <- read_excel("C:/Rstudy/mini_team1/data/vegan_Raw_data_c.xls")

vegan_raw1 <- vegan_raw %>%
  filter(!(eat_beef == "Never" & eat_chicken == "Never" &eat_dairy =="Never"&
             eat_eggs =="Never" & eat_fish_seafood =="Never"& eat_pork =="Nev
er"))
```

원본데이터 파일 불러오기 및 필요 컬럼 추출 - vegan

```
vegan_raw2 <- read_excel("C:/Rstudy/mini_team1/data/only_vegan.xlsx")

non_eat_food <- vegan_raw2 %>% select(eat_non_dairy, eat_seitan, eat_tempeh,
eat_tofu, eat_vegetarian_meats)
```

고기 등의 식품 – 비건은 고기를 섭취하지 않기 때문에 논비건만 분석

필요 컬럼 추출- non-vegan

```
eat_food1 <- vegan_raw1 %>%
  select(eat_beef ,eat_chicken, eat_dairy, eat_eggs, eat_fish_seafood, eat_po
rk)
```

추출한 데이터의 결측치 확인- non-vegan

```
table(is.na(eat_food1))

##
## FALSE
## 10590

table(is.na(eat_food1$eat_beef))
table(is.na(eat_food1$eat_chicken))
table(is.na(eat_food1$eat_dairy))
table(is.na(eat_food1$eat_eggs))
table(is.na(eat_food1$eat_fish_seafood))
table(is.na(eat_food1$eat_pork))

head(table(eat_food1))
```

결측치 대체 및 변수 생성 저장- non-vegan

```
beef2 <-ifelse(is.na(eat_food1$eat_beef), "skip", eat_food1$eat_beef)
beef3 <- table(beef2)


chicken2 <-ifelse(is.na(eat_food1$eat_chicken), "skip", eat_food1$eat_chicke
n)
chicken3 <- table(chicken2)


dairy2 <-ifelse(is.na(eat_food1$eat_dairy), "skip", eat_food1$eat_dairy)
dairy3 <- table(dairy2)


eggs2 <-ifelse(is.na(eat_food1$eat_eggs), "skip", eat_food1$eat_eggs)
eggs3 <- table(eggs2)


fish_seafood2 <-ifelse(is.na(eat_food1$eat_fish_seafood), "skip", eat_food1$e
at_fish_seafood)
```

```
fish_seafood3 <- table(fish_seafood2)


pork2 <-ifelse(is.na(eat_food1$eat_pork), "skip", eat_food1$eat_pork)
pork3 <- table(pork2)
```

결측치 대체한 각 변수를 하나의 데이터프레임으로 가공- non-vegan

```
s_eat_food1 <-cbind(beef3, chicken3, dairy3, eggs3, fish_seafood3, pork3)

str(s_eat_food1)
s_eat_food1 <- data.frame(s_eat_food1)
```

인덱스로 들어간 항목을 꺼내서 answer 컬럼 데이터로 넣어주기- non-vegan

```
s_eat_food_g1 <- dplyr::add_rownames(s_eat_food1, var="answer")

head(s_eat_food_g1)
```

skip 제거- non-vegan

```
s_eat_food_g1 <- s_eat_food_g1 %>% filter(answer != "skip")
```

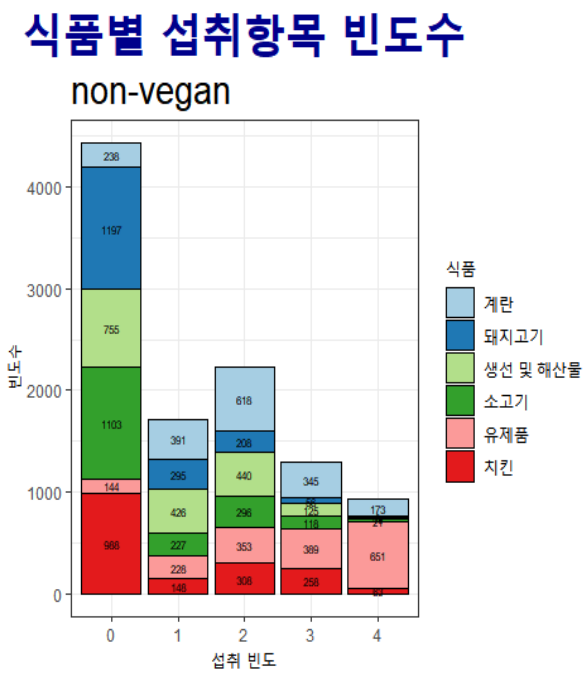
컬럼명 및 데이터명 변경- non-vegan

```
s_eat_food_g1 <- dplyr::rename(s_eat_food_g1, "소고기" = "beef3",
                                    "치킨" = "chicken3", "유제품" = "dairy3", "
계란" = "eggs3",
                                    "생선 및 해산물" = "fish_seafood3", "돼지고
기" = "pork3")


s_eat_food_g1$answer <- ifelse(s_eat_food_g1$answer =="Never", 0,
                          ifelse(s_eat_food_g1$answer =="About 1 day per month
", 1,
                                 ifelse(s_eat_food_g1$answer =="About 1 day per
 week", 2 ,
                                        ifelse(s_eat_food_g1$answer =="About ev
ery other day", 3,
                                               ifelse(s_eat_food_g1$answer =="A
```

```
lmost every day", 4, s_eat_food_g1$answer
                                                    )))))
```

그래프 시각화- non-vegan

```
s_eat_food_g1%>%
  pivot_longer(-answer) %>%
  ggplot(aes(x = answer, y = value, fill = name)) +
  geom_col(position = position_stack(), colour = "black") +
  geom_text(aes(label = value), size = 2, position = position_stack(0.5)) +
  scale_fill_brewer(name = '식품', palette = 'Paired') +
  theme_bw() + xlab("섭취 빈도") + ylab("빈도수") +
  ggtitle("식품별 섭취항목 빈도수", subtitle = "non-vegan") +
  theme(plot.title = element_text(face = "bold", hjust = 0.5, size = 30, colo
r = "darkblue"),
        plot.subtitle = element_text(size = 20))
```



위 그래프를 확인해보면 논 비건 사람들이 가장 많이 섭취하지 않은 식품은
돼지고기(1197 명)이며, 거의 매일 섭취하는 식품은 유제품(651 명)으로 확인할 수 있습니다.

예상외로 논 비건 사람들은 돼지고기나 소고기 섭취를 많이 하지 않는것을 확인할 수 있습니다.

그래프에서 x 축

0: 없음

1: 한달에 한번

2: 일주일에 한번

3: 격일마다

4: 거의 매일

비건 식품

필요 컬럼 추출 및 결측치 확인- non-vegan

```
non_eat_food1 <- vegan_raw1 %>%
  select(eat_non_dairy, eat_seitan, eat_tempeh, eat_tofu, eat_vegetarian_meat
s)
table(is.na(non_eat_food1))
```

결측치 대체 및 변수 생성 저장- non-vegan

```
table(is.na(non_eat_food1$eat_non_dairy))
non_dairy2 <-ifelse(is.na(non_eat_food1$eat_non_dairy), "skip", non_eat_food1
$eat_non_dairy)
non_dairy3 <- table(non_dairy2)


table(is.na(non_eat_food1$eat_seitan))
seitan2 <-ifelse(is.na(non_eat_food1$eat_seitan), "skip", non_eat_food1$eat_s
eitan)
seitan3 <- table(seitan2)


table(is.na(non_eat_food1$eat_tempeh))
tempeh2 <- ifelse(is.na(non_eat_food1$eat_tempeh), "skip", non_eat_food1$eat_
tempeh)
tempeh3 <- table(tempeh2)


table(is.na(non_eat_food1$eat_tofu))
tofu2 <- ifelse(is.na(non_eat_food1$eat_tofu), "skip", non_eat_food1$eat_tof
u)
tofu3 <- table(tofu2)


table(is.na(non_eat_food1$eat_vegetarian_meats))
```

```
vegetaian_meats2 <- ifelse(is.na(non_eat_food1$eat_vegetarian_meats), "skip",
 non_eat_food1$eat_vegetarian_meats)
vegetaian_meats3 <- table(vegetaian_meats2)
```

결측치 대체 및 변수 생성 저장- vegan

```
table(is.na(non_eat_food))

non_dairy1 <-ifelse(is.na(non_eat_food$eat_non_dairy), "skip", non_eat_food$e
at_non_dairy)
non_dairy <- table(non_dairy1)

table(is.na(non_eat_food$eat_non_dairy))

table(is.na(non_eat_food$eat_seitan))


seitan1 <-ifelse(is.na(non_eat_food$eat_seitan), "skip", non_eat_food$eat_sei
tan)
seitan <- table(seitan1)

table(is.na(non_eat_food$eat_tempeh))

tempeh1 <- ifelse(is.na(non_eat_food$eat_tempeh), "skip", non_eat_food$eat_te
mpeh)
tempeh <- table(tempeh1)


table(is.na(non_eat_food$eat_tofu))

tofu1 <- ifelse(is.na(non_eat_food$eat_tofu), "skip", non_eat_food$eat_tofu)
tofu <- table(tofu1)

table(is.na(non_eat_food$eat_vegetarian_meats))

vegetaian_meats1 <- ifelse(is.na(non_eat_food$eat_vegetarian_meats), "skip",
non_eat_food$eat_vegetarian_meats)
vegetaian_meats <- table(vegetaian_meats1)
```

결측치 대체한 각 변수를 하나의 데이터프레임으로 가공- non-vegan

```
s_non_eat_food1 <-cbind(non_dairy3, seitan3, tempeh3, tofu3, vegetaian_meats
3)
```

```
str(s_non_eat_food1)
s_non_eat_food_g1 <- data.frame(s_non_eat_food1)
```

결측치 대체한 각 변수를 하나의 데이터프레임으로 가공- vegan

```
s_non_eat_food <-cbind(non_dairy, seitan, tempeh, tofu, vegetaian_meats)

str(s_non_eat_food)
s_non_eat_food_g <- data.frame(s_non_eat_food)
```

인덱스로 들어간 항목을 꺼내서 answer 컬럼 데이터로 넣어주기- non-vegan

```
s_non_eat_food_g1 <- dplyr::add_rownames(s_non_eat_food_g1, var="answer")
head(s_non_eat_food_g1)
```

인덱스로 들어간 항목을 꺼내서 answer 컬럼 데이터로 넣어주기- vegan

```
s_non_eat_food_g <- dplyr::add_rownames(s_non_eat_food_g, var="answer")
head(s_non_eat_food_g)
```

skip 제거 및 컬럼명 변경- non-vegan

```
s_non_eat_food_g1 <- s_non_eat_food_g1 %>% filter(answer != "skip")

s_non_eat_food_g1 <- dplyr::rename(s_non_eat_food_g1, "유제품이 아닌" = "non_dairy3",
                                   "세이탄" = "seitan3", "템페" = "tempeh3", "두부" = "tofu3",
                                   "대체육" = "vegetaian_meats3")

s_non_eat_food_g1$answer <- ifelse(s_non_eat_food_g1$answer =="Never", 0,
                                   ifelse(s_non_eat_food_g1$answer =="About 1 day per month", 1,
                                          ifelse(s_non_eat_food_g1$answer =="About 1 day per week", 2 ,
                                                 ifelse(s_non_eat_food_g1$answer =="About every other day", 3,
                                                        ifelse(s_non_eat_food_g1$answer =="Almost every day", 4, s_non_eat_food_g1$answer
                                                        )))))
```

skip 제거 및 컬럼명 변경- vegan

```
s_non_eat_food_g <- s_non_eat_food_g %>% filter(answer != "skip")

s_non_eat_food_g <- dplyr::rename(s_non_eat_food_g, "유제품이 아닌" = "non_dai
ry", "세이탄" = "seitan", "템페" = "tempeh", "두부" = "tofu", "대체육" = "veget
aian_meats")

s_non_eat_food_g$answer <- ifelse(s_non_eat_food_g$answer =="Never", 0,
                                  ifelse(s_non_eat_food_g$answer =="About 1 day
per month", 1,
                                         ifelse(s_non_eat_food_g$answer =="About
 1 day per week", 2 ,
                                                ifelse(s_non_eat_food_g$answer =
="About every other day", 3,
                                                       ifelse(s_non_eat_food_g$a
nswer =="Almost every day", 4,s_non_eat_food_g$answer
                                                       )))))
```

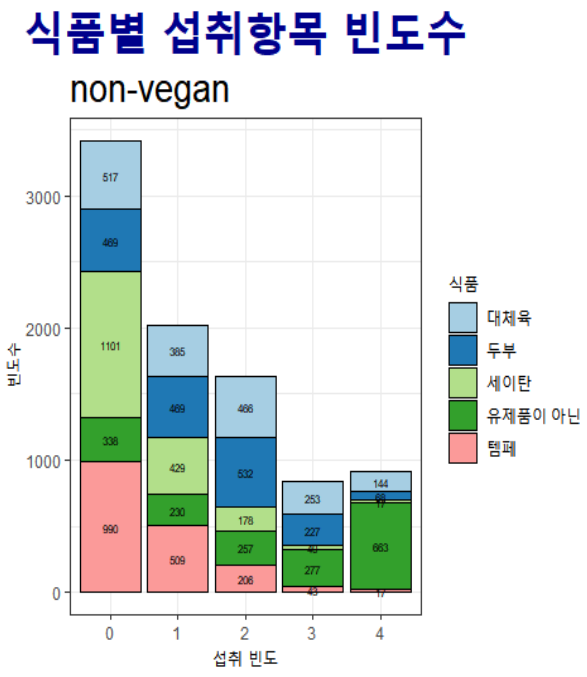
그래프 시각화- non-vegan

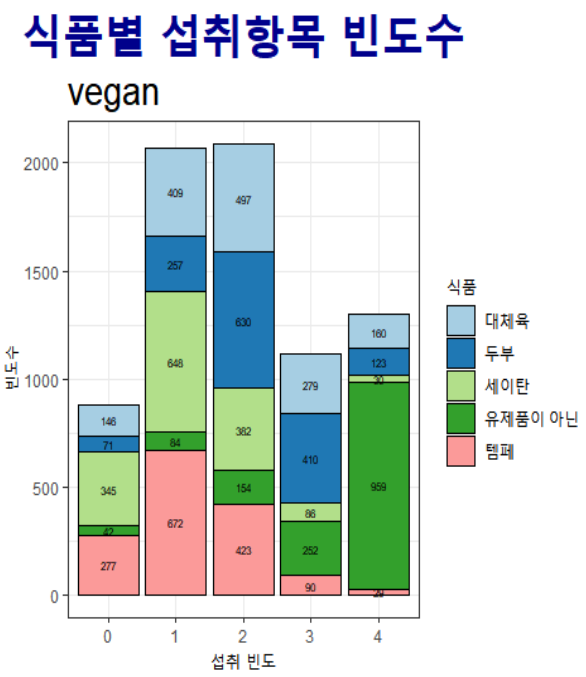
```
s_non_eat_food_g1 %>%
  pivot_longer(-answer) %>%
  ggplot(aes(x = answer, y = value, fill = name)) +
  geom_col(position = position_stack(), colour = "black") +
  geom_text(aes(label = value),size = 2, position = position_stack(0.5)) +
  scale_fill_brewer(name = '식품', palette = 'Paired') +
  theme_bw() + xlab("섭취 빈도") + ylab("빈도수") +
  ggtitle("식품별 섭취항목 빈도수", subtitle = "non-vegan") +
  theme(plot.title = element_text(face = "bold", hjust = 0.5, size = 30, colo
r = "darkblue"),
        plot.subtitle = element_text(size = 20))
```

그래프 시각화- vegan

```
s_non_eat_food_g %>%
  pivot_longer(-answer) %>%
  ggplot(aes(x = answer, y = value, fill = name)) +
  geom_col(position = position_stack(), colour = "black") +
  geom_text(aes(label = value), size = 2, position = position_stack(0.5))+
  scale_fill_brewer(name = '식품', palette = 'Paired') +
  theme_bw() + xlab("섭취 빈도") + ylab("빈도수") +
  ggtitle("식품별 섭취항목 빈도수", subtitle = "vegan") +
```

```
  theme(plot.title = element_text(face = "bold", hjust = 0.5, size = 30, colo
r = "darkblue"),
        plot.subtitle = element_text(size = 20))
```





위 그래프는 각 식품(비건 식품) 항목마다 섭취한 빈도수를 나타낸 것으로 논 비건 사람들과 비건 사람들이 가장 많이 섭취하지 않은 식품은 세이탄(1101 명, 63 명)이며, 거의 매일 섭취하는 식품은 유제품 아닌(663 명, 959 명) 식품으로 보여집니다.

참고사항: 유제품이 아닌 식품은 주로 두유 등이 있습니다.

그래프에서 x 축

0: 없음

1: 한달에 한번

2: 일주일에 한번

3: 격일마다

4: 거의 매일

다음은 논비건과 비건의 동물성 식품을 **어떤 식품으로 대체하여 섭취**하는지에 대해 분석해보았습니다.

Install. packages:

```
library(readxl)
library(dplyr)
library(ggplot2)
library(tidyverse)
```

Raw Data- Non-Vegan

```
vegan_raw <- read_excel("C:/Rstudy/teamR/rvd.xls")

vegan_raw1 <- vegan_raw %>% filter(!(eat_beef == "Never" & eat_chicken == "Ne
ver" &eat_dairy =="Never"&
                                     eat_eggs =="Never" & eat_fish_seafood
=="Never"& eat_pork =="Never"))
```

Vegan

```
vegan_raw <- read_excel("C:/Rstudy/0506/newProj/rvd.xls") #vegan
```

Filter Non-Vegan from Columns- Non-Vegan

Unique values from column

```
unique(alf[c("sub_beans_lentils")])
```

```
## # A tibble: 6 x 1
##   sub_beans_lentils
##   <chr>
## 1 To a large extent
## 2 To a moderate extent
## 3 To some extent
## 4 <NA>
## 5 To little extent
## 6 Not at all
```

```
unique(alf[c("sub_extra_vegetables")])
```

```
## # A tibble: 6 x 1
##   sub_extra_vegetables
##   <chr>
## 1 To a large extent
## 2 To a moderate extent
## 3 To some extent
## 4 <NA>
## 5 To little extent
## 6 Not at all
```

Filter Vegan from Columns- Vegan

```
vegan_raw1 <- vegan_raw %>% filter(eat_beef == "Never" & eat_chicken == "Neve
r" &eat_dairy =="Never"&
                                     eat_eggs =="Never" & eat_fish_seafood
=="Never"& eat_pork =="Never")

View(vegan_raw1)
```

Sort Unique value from column without NA- Non-Vegan

```
sort(unique(alf$sub_beans_lentils), decreasing=TRUE)
```

```
## [1] "To some extent"       "To little extent"     "To a moderate extent"
## [4] "To a large extent"    "Not at all"
```

Select Columns- Vegan

```
alf<- vegan_raw1 %>% select(sub_beans_lentils,  sub_extra_vegetables,
                            sub_grains, sub_nuts,   sub_seitan, sub_tempeh, s
ub_tofu,   sub_vegetarian_meats)
View(alf)

head(
  select(alf, sub_beans_lentils,    sub_extra_vegetables,
         sub_grains,    sub_nuts,   sub_seitan, sub_tempeh, sub_tofu,   sub_v
egetarian_meats)
)
```

Data.frame- Non-Vegan

```
df_alf <- data.frame(alf)
df_alf
View(df_alf)
```

Check NA from table- Non-Vegan

```
#
t_alf <- table(is.na(alf))
t_alf

##
## FALSE  TRUE
##  8704  5416
```

Rename NA to “skip” - Non-Vegan

```
alf_beans <-ifelse(is.na(alf$sub_beans_lentils), "skip", alf$sub_beans_lentil
s)
alf_beans
beans <- table(alf_beans)
beans



alf_vegetables <-ifelse(is.na(alf$sub_extra_vegetables), "skip", alf$sub_extr
a_vegetables)
alf_vegetables
vegetables <- table(alf_vegetables)
vegetables



alf_grains <-ifelse(is.na(alf$sub_grains), "skip", alf$sub_grains)
alf_grains
grains <- table(alf_grains)
grains

alf_nuts <-ifelse(is.na(alf$sub_nuts), "skip", alf$sub_nuts)
alf_nuts
nuts <- table(alf_nuts)
nuts

alf_seitan <-ifelse(is.na(alf$sub_seitan), "skip", alf$sub_seitan)
alf_seitan
seitan <- table(alf_seitan)
seitan

alf_tempeh <-ifelse(is.na(alf$sub_tempeh), "skip", alf$sub_tempeh)
alf_tempeh
tempeh <- table(alf_tempeh)
tempeh

alf_tofu <-ifelse(is.na(alf$sub_tofu), "skip", alf$sub_tofu)
alf_tofu
```

```
tofu <- table(alf_tofu)
tofu

alf_meats <-ifelse(is.na(alf$sub_vegetarian_meats), "skip", alf$sub_vegetaria
n_meats)
alf_meats
meats<-table(alf_meats)
meats
```

Rename NA to “skip” - Vegan

```
alf_beans <-ifelse(is.na(alf$sub_beans_lentils), "skip", alf$sub_beans_lentil
s)
alf_beans
beans <- table(alf_beans)
beans

alf_vegetables <-ifelse(is.na(alf$sub_extra_vegetables), "skip", alf$sub_extr
a_vegetables)
alf_vegetables
vegetables <- table(alf_vegetables)
vegetables

alf_grains <-ifelse(is.na(alf$sub_grains), "skip", alf$sub_grains)
alf_grains
grains <- table(alf_grains)
grains

alf_nuts <-ifelse(is.na(alf$sub_nuts), "skip", alf$sub_nuts)
alf_nuts
nuts <- table(alf_nuts)
nuts

alf_seitan <-ifelse(is.na(alf$sub_seitan), "skip", alf$sub_seitan)
alf_seitan
seitan <- table(alf_seitan)
seitan

alf_tempeh <-ifelse(is.na(alf$sub_tempeh), "skip", alf$sub_tempeh)
alf_tempeh
tempeh <- table(alf_tempeh)
tempeh

alf_tofu <-ifelse(is.na(alf$sub_tofu), "skip", alf$sub_tofu)
alf_tofu
tofu <- table(alf_tofu)
tofu

alf_meats <-ifelse(is.na(alf$sub_vegetarian_meats), "skip", alf$sub_vegetaria
```

```
n_meats)
alf_meats
meats<-table(alf_meats)
meats
```

Group columns- Non-Vegan

```
alf_group <- cbind (beans,  vegetables, grains, nuts,   seitan, tempeh, tofu,
   meats)
str(alf_group)
```

```
##  int [1:6, 1:8] 57 677 459 256 113 203 15 677 573 277 ...
##  - attr(*, "dimnames")=List of 2
##   ..$ : chr [1:6] "Not at all" "skip" "To a large extent" "To a moderate e
xtent" ...
##   ..$ : chr [1:8] "beans" "vegetables" "grains" "nuts" ...
```

Group columns- Vegan

```
alf_group <- cbind (beans,  vegetables, grains, nuts,   seitan, tempeh, tofu,
   meats)
str(alf_group)
```

```
##  int [1:6, 1:8] 61 216 502 334 132 246 24 216 609 339 ...
##  - attr(*, "dimnames")=List of 2
##   ..$ : chr [1:6] "Not at all" "skip" "To a large extent" "To a moderate e
xtent" ...
##   ..$ : chr [1:8] "beans" "vegetables" "grains" "nuts" ...
```

```
alf_group_df <- data.frame(alf_group)
alf_group_df
```

```
##                       beans vegetables grains nuts seitan tempeh tofu meats
## Not at all               61         24     30  103    507    467  127   145
## skip                    216        216    216  216    216    216  216   216
## To a large extent       502        609    471  179     73     71  302   389
## To a moderate extent    334        339    392  298    129    135  342   312
## To little extent        132         91     91  305    356    372  209   189
## To some extent          246        212    291  390    210    230  295   240
```

Add_index row_name- Vegan

```
alf_group_df1 <- dplyr::add_rownames(alf_group_df, var="answers")
head(alf_group_df1)
```

```
## # A tibble: 6 x 9
##   answers              beans vegetables grains  nuts seitan tempeh  tofu m
eats
```

```
##   <chr>                <int>      <int>  <int> <int>  <int>  <int> <int> <
int>
## 1 Not at all              61         24     30   103    507    467   127
 145
## 2 skip                   216        216    216   216    216    216   216
 216
## 3 To a large extent      502        609    471   179     73     71   302
 389
## 4 To a moderate extent   334        339    392   298    129    135   342
 312
## 5 To little extent       132         91     91   305    356    372   209
 189
## 6 To some extent         246        212    291   390    210    230   295
 240
```

Data.frame- Non-Vegan

```
alf_group_df <- data.frame(alf_group)
alf_group_df
```

```
##                      beans vegetables grains nuts seitan tempeh tofu meats
## Not at all              57         15     34  115    673    614  241   201
## skip                   677        677    677  677    677    677  677   677
## To a large extent      459        573    362  186     38     35  203   296
## To a moderate extent   256        277    345  228     52     63  229   235
## To little extent       113         59    121  243    208    240  210   169
## To some extent         203        164    226  316    117    136  205   187
```

Add_index row_name- Non-Vegan

```
alf_group_df1 <- dplyr::add_rownames(alf_group_df, var="answers")
head(alf_group_df1)
```

```
## # A tibble: 6 x 9
##   answers              beans vegetables grains  nuts seitan tempeh  tofu m
eats
##   <chr>                <int>      <int>  <int> <int>  <int>  <int> <int> <
int>
## 1 Not at all              57         15     34   115    673    614   241
 201
## 2 skip                   677        677    677   677    677    677   677
 677
## 3 To a large extent      459        573    362   186     38     35   203
 296
## 4 To a moderate extent   256        277    345   228     52     63   229
 235
## 5 To little extent       113         59    121   243    208    240   210
```

```
 169
## 6 To some extent         203        164    226   316    117    136   205
 187
```

Drop NA from column Answers- Non-Vegan

```
alf_group_df <- alf_group_df1 %>% filter(answers != "skip")
alf_group_df
```

```
## # A tibble: 5 x 9
##   answers              beans vegetables grains  nuts seitan tempeh  tofu m
eats
##   <chr>                <int>      <int>  <int> <int>  <int>  <int> <int> <
int>
## 1 Not at all              57         15     34   115    673    614   241
 201
## 2 To a large extent      459        573    362   186     38     35   203
 296
## 3 To a moderate extent   256        277    345   228     52     63   229
 235
## 4 To little extent       113         59    121   243    208    240   210
 169
## 5 To some extent         203        164    226   316    117    136   205
 187
```

Rename Column values- Non-Vegan

```
alf_group_df$answers <- ifelse(alf_group_df$answers =="Not at all", "0",
                               ifelse(alf_group_df$answers =="To a large exte
nt", "4",
                                      ifelse(alf_group_df$answers =="To a mod
erate extent", "3" ,
                                             ifelse(alf_group_df$answers =="T
o little extent", "2",
                                                    ifelse(alf_group_df$answe
rs =="To some extent", "1", alf_group_df$answers)))))

alf_group_df
```

```
## # A tibble: 5 x 9
##   answers beans vegetables grains  nuts seitan tempeh  tofu meats
##   <chr>   <int>      <int>  <int> <int>  <int>  <int> <int> <int>
## 1 0          57         15     34   115    673    614   241   201
## 2 4         459        573    362   186     38     35   203   296
## 3 3         256        277    345   228     52     63   229   235
## 4 2         113         59    121   243    208    240   210   169
## 5 1         203        164    226   316    117    136   205   187
```

Drop NA from column Answers- Vegan

```
alf_group_df <- alf_group_df1 %>% filter(answers != "skip")
alf_group_df
```

```
## # A tibble: 5 x 9
##   answers              beans vegetables grains  nuts seitan tempeh  tofu m
eats
##   <chr>                <int>      <int>  <int> <int>  <int>  <int> <int> <
int>
## 1 Not at all              61         24     30   103    507    467   127
 145
## 2 To a large extent      502        609    471   179     73     71   302
 389
## 3 To a moderate extent   334        339    392   298    129    135   342
 312
## 4 To little extent       132         91     91   305    356    372   209
 189
## 5 To some extent         246        212    291   390    210    230   295
 240
```

```
alf_group_df$answers <- ifelse(alf_group_df$answers =="Not at all", "0",
                               ifelse(alf_group_df$answers =="To a large
extent", "4",
                                      ifelse(alf_group_df$answers =="To a
 moderate extent", "3" ,
                                             ifelse(alf_group_df$answers
=="To little extent", "2",
                                                    ifelse(alf_group_df$a
nswers =="To some extent", "1", alf_group_df$answers)))))

alf_group_df
```

```
## # A tibble: 5 x 9
##   answers beans vegetables grains  nuts seitan tempeh  tofu meats
##   <chr>   <int>      <int>  <int> <int>  <int>  <int> <int> <int>
## 1 0          61         24     30   103    507    467   127   145
## 2 4         502        609    471   179     73     71   302   389
## 3 3         334        339    392   298    129    135   342   312
## 4 2         132         91     91   305    356    372   209   189
## 5 1         246        212    291   390    210    230   295   240
```

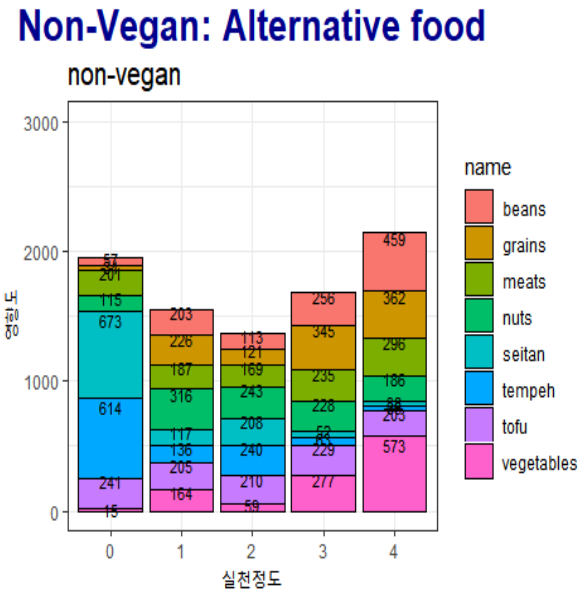
Graphic- Non-Vegan

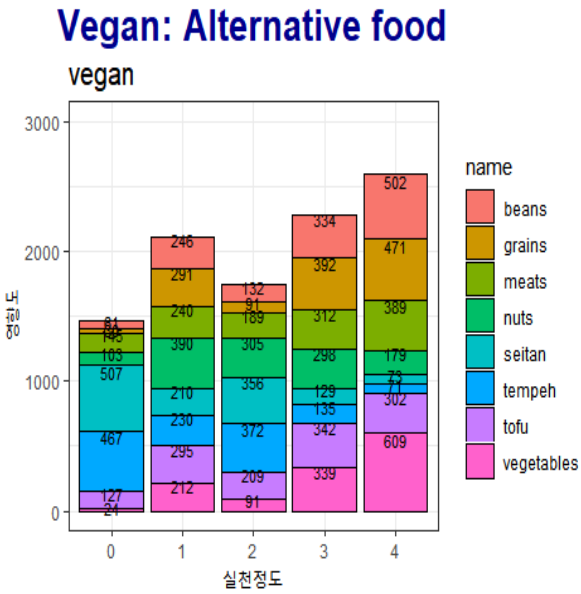
```
library(reshape)
library(tidyverse)
library(plotly)
```

```
alf_group_df_p <- alf_group_df %>% pivot_longer(-answers)

non_veg_alt<-ggplot(alf_group_df_p, aes(x = answers, y=value, fill = name)) +

  geom_col(position = position_stack(), colour = "black") +
  geom_text(aes(label=value), size=3, position = position_stack(0.9)) +
  scale_y_continuous(limits = c(0, 3000)) +
  theme_bw() + xlab("실천정도") + ylab("영향도") +
  ggtitle("Non-Vegan: Alternative food", subtitle = "non-vegan") +
  theme(plot.title = element_text(face = "bold", hjust = 0.5, size = 20, colo
r = "darkblue"),
        plot.subtitle = element_text(size = 15))

non_veg_alt
```

Graphic- Vegan

```
library(reshape)
library(tidyverse)
library(plotly)


alf_group_df_p <- alf_group_df %>% pivot_longer(-answers)

veg_alt<-ggplot(alf_group_df_p, aes(x = answers, y=value, fill = name)) +
  geom_col(position = position_stack(), colour = "black") +
  geom_text(aes(label=value), size=3, position = position_stack(0.9)) +
  scale_y_continuous(limits = c(0, 3000)) +
  theme_bw() + xlab("실천정도") + ylab("영향도") +
  ggtitle("Vegan: Alternative food", subtitle = "vegan") +
  theme(plot.title = element_text(face = "bold", hjust = 0.5, size = 20, colo
r = "darkblue"),
        plot.subtitle = element_text(size = 15))

veg_alt
```





논 비건 사람들과 비건 사람들은 대체 식품 중 vegetable 을 가장 많이 섭취한 것을 확인할 수 있습니다. 반대로 대체식품 중 세티안을 전혀 실천해 보지 않았음을 확인할 수 있습니다.

위 그래프를 통해 대체적으로 비건 사람들이 논 비건 사람들보다 동물성 제품을 대체하는 식품을 더 많이 선택한 것을 확인할 수 있습니다.

그래프 y 축

Beans: Beans & lentils.

Vegetables: Plant, cabbage, potato, carrot Grains: Grains, rice, pasta, cereal, bread.

Nuts: Almonds, pistachios, walnuts, hazelnuts.

Seitan: High-protein vegetarian food.

Tempeh: Fry fermented soybeans.

Tofu: Product from soybeans.

Meats: Vegetarian meats, veggie burgers, nuggets.

다음은 논비건과 비건의 **식습관 변화**에 대해 알아보았습니다. 바뀐 식습관은 현재의 식습관이 아니며 **바뀌는 과정을 확인**해보고자 시각화 하였습니다.

라이브러리 로드

```
library(readxl)
library(dplyr)
```

```
library(tidyverse)
library(ggplot2)
```

원본 데이터 파일 불러오기 및 필요 행 추출 - non_vegan

```
vegan_raw <- read_excel("C:/Rstudy/mini_team1/data/vegan_Raw_data_c.xls")

vegan_raw1 <- vegan_raw %>% filter(!(eat_beef == "Never" & eat_chicken == "Ne
ver" &eat_dairy =="Never"&
                                       eat_eggs =="Never" & eat_fish_seafood
=="Never"& eat_pork =="Never"))
```

원본 데이터 파일 불러오기 및 필요 행 추출 - vegan

```
vegan_raw <- read_excel("C:/Rstudy/mini_team1/data/only_vegan.xlsx")
```

원본 데이터 파일 불러오기 및 필요 행 추출 - non-vegan

```
change_routine3 <- vegan_raw1 %>% select(routine)

change_routine4 <- vegan_raw1 %>% select(routine2)
```

원본 데이터 파일 불러오기 및 필요 행 추출 - vegan

```
change_routine1 <- vegan_raw %>% select(routine)

change_routine2 <- vegan_raw %>% select(routine2)
```

결측치 확인 및 대체 - non-vegan

```
table(is.na(change_routine3$routine))
table(is.na(change_routine4$routine2))

change_routine3$routine <- ifelse(is.na(change_routine3$routine), "skip", cha
nge_routine3$routine)
change_routine4$routine2 <- ifelse(is.na(change_routine4$routine2), "skip", c
hange_routine4$routine2)
```

결측치 확인 및 대체 - vegan

```
table(is.na(change_routine1$routine))
table(is.na(change_routine2$routine2))
```

```
change_routine1$routine <- ifelse(is.na(change_routine1$routine), "skip", cha
nge_routine1$routine)
change_routine2$routine2 <- ifelse(is.na(change_routine2$routine2), "skip", c
hange_routine2$routine2)
```

그룹화 및 요약 - non-vegan

```
change_routine_g3 <- change_routine3 %>% filter(routine != "skip") %>% group_
by(routine) %>% summarise(n3=n())

change_routine_g4 <- change_routine4 %>% filter(routine2 != "skip") %>% group
_by(routine2) %>% summarise(n4=n())
```

그룹화 및 요약 - vegan

```
change_routine_g1 <- change_routine1 %>% group_by(routine) %>% summarise(n=n
())

change_routine_g2 <- change_routine2 %>% group_by(routine2) %>% summarise(n2=
n())
```

컬럼명 통일 및 rbind - non-vegan

```
change_routine_g4 <- dplyr::rename(change_routine_g4, routine = routine2)
change_routine_g4 <- dplyr::rename(change_routine_g4, n3 = n4)

change_routine_g0 <- rbind(change_routine_g3, change_routine_g4)
table(change_routine_g4)
```

컬럼명 통일 및 rbind - vegan

```
change_routine_g2 <- dplyr::rename(change_routine_g2, routine = routine2)
change_routine_g2 <- dplyr::rename(change_routine_g2, n = n2)

change_routine_g <- rbind(change_routine_g1, change_routine_g2)
table(change_routine_g2)
```

그래프 그룹화를 위한 열 추가 - non-vegan

```
change_routine_g0$group<-c("routine1","routine1","routine1","routine1","routi
ne1","routine1",
```

```
                              "routine2","routine2","routine2","routine2","routi
ne2", "routine2")
```

그래프 그룹화를 위한 열 추가 - vegan

```
change_routine_g$group<-c("routine1","routine1","routine1","routine1","routin
e1","routine1","routine1",
                          "routine2","routine2","routine2","routine2","routin
e2","routine2","routine2")
```

skip 제거 - non-vegan

```
change_routine_g0 <- change_routine_g0 %>% filter(routine != "skip")
```

skip 제거 - vegan

```
change_routine_g <- change_routine_g %>% filter(routine != "skip")
```

항목명 변경- non-vegan

```
change_routine_g0$routine <- ifelse(change_routine_g0$routine =="Did not eat
red meat, chicken or fish", "X meat,chicken or fish",
                                                          ifelse(change_ro
utine_g0$routine =="Did not eat red meat, but ate everything else", "X meat",
                                                                 ifelse(ch
ange_routine_g0$routine =="Did not eat red meat or chicken, but ate fish, egg
s and dairy", "X meat or chicken" , ifelse(change_routine_g0$routine =="Did n
ot eat any animal products", "X" , ifelse(change_routine_g0$routine =="Ate al
l types of animal products but was now eating less of them", "eating less" ,i
felse(change_routine_g0$routine =="Ate all types of animal products", "all ty
pes" ,
                                                                          c
hange_routine_g0$routine

 ))))))
```

항목명 변경- vegan

```
change_routine_g$routine <- ifelse(change_routine_g$routine =="Did not eat re
d meat, chicken or fish", "X meat,chicken or fish",
                                                          ifelse(change_ro
utine_g$routine =="Did not eat red meat, but ate everything else", "X meat",
```

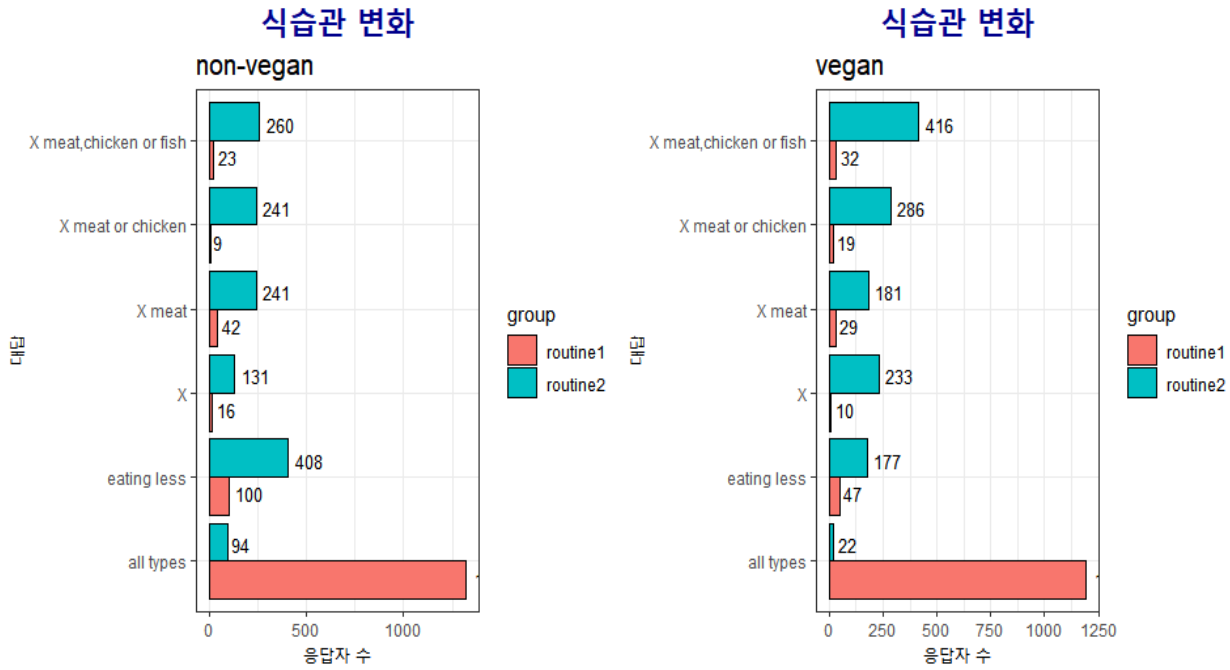
```
                                                                    ifelse(ch
ange_routine_g$routine =="Did not eat red meat or chicken, but ate fish, eggs
 and dairy", "X meat or chicken" , ifelse(change_routine_g$routine =="Did not
 eat any animal products", "X" , ifelse(change_routine_g$routine =="Ate all t
ypes of animal products but was now eating less of them", "eating less" ,ifel
se(change_routine_g$routine =="Ate all types of animal products", "all types"
 ,
                                                                        c
hange_routine_g$routine

 ))))))
```

그래프 시각화 - non-vegan

```
ggplot(change_routine_g0, aes(routine, n3, group = group, fill = group)) +
  geom_bar(stat = "identity", position = "dodge", colour = "black") +
  xlab('대답') + ylab('응답자 수') +
  coord_flip() +
  geom_text(aes(label=n3), position = position_dodge(width=0.8), hjust=-.25,
size=3.5) +
      theme_bw() +
  ggtitle("식습관 변화", subtitle = "non-vegan") +
  theme(plot.title = element_text(face = "bold", hjust = 0.5, size = 20, colo
r = "darkblue"),
        plot.subtitle = element_text(size = 15))
```

그래프 시각화 - vegan

```
ggplot(change_routine_g, aes(routine, n, group = group, fill = group)) +
  geom_bar(stat = "identity", position = "dodge", colour = "black") +
  xlab('대답') + ylab('응답자 수') +
  coord_flip() +
  geom_text(aes(label=n), position = position_dodge(width=0.8), hjust=-.25,
size=3.5) +
  theme_bw() +
  ggtitle("식습관 변화", subtitle = "vegan") +
  theme(plot.title = element_text(face = "bold", hjust = 0.5, size = 20,
color = "darkblue")
```



그래프 y 축

X meat, chicken or fish: 고기와 치킨 또는 생선(해산물) 섭취하지 않음

X meat or chicken: 고기 또는 치킨을 섭취하지 않음

X meat: 고기 섭취하지 않음

X: 동물성 제품 섭취하지 않음

eatingless: 동물성 제품 섭취 줄임

all types: 모든 동물성 제품 섭취함

논 비건 사람들은 대체적으로 모든 종류의 식품을 섭취하였지만, 동물성 제품 섭취를 줄이는 식습관 변화를 볼 수 있습니다.

비건 사람들은 대체적으로 모든 종류의 식품을 섭취하였지만, 고기와 치킨 또는 생선(해산물) 섭취를 하지 않는 식습관 변화를 볼 수 있습니다.

다음은 **동물 제품 소비**를 줄인 적이 있다면 **줄이게 된 이유**에 대해 분석해 보았습니다.

라이브러리 로드

```
library(readxl)
library(dplyr)
library(tidyverse)
library(ggplot2)
```

원본 데이터 파일 불러오기 및 필요 행 추출 - non_vegan

```
vegan_raw <- read_excel("C:/Rstudy/mini_team1/data/vegan_Raw_data_c.xls")

vegan_raw1 <- vegan_raw %>% filter(!(eat_beef == "Never" & eat_chicken == "Ne
ver" &eat_dairy =="Never"&
                                       eat_eggs =="Never" & eat_fish_seafood
=="Never"& eat_pork =="Never"))
```

원본데이터 파일 불러오기 및 필요 컬럼 추출 - vegan

```
vegan_raw2 <- read_excel("C:/Rstudy/mini_team1/data/only_vegan.xlsx")
inspire_reducing_consumption <- vegan_raw2%>% select(inspire_ani,inspire_env,
 inspire_ff, inspire_ht, inspire_hr,
                                                      inspire_nt, inspire_rg,
inspire_sb, inspire_wh)
```

필요 컬럼 추출- non-vegan

```
non_inspire_reducing_consumption <- vegan_raw1 %>% select(inspire_ani,inspire
_env, inspire_ff, inspire_ht, inspire_hr,inspire_nt, inspire_rg, inspire_sb,
inspire_wh)
```

추출한 데이터의 결측치 확인- non-vegan

```
table(is.na(non_inspire_reducing_consumption))
```

추출한 데이터의 결측치 확인- vegan

```
table(is.na(inspire_reducing_consumption))
```

결측치 대체 및 변수 생성 저장- non-vegan

```
table(is.na(non_inspire_reducing_consumption$inspire_ani))
non_inspire_ani1 <- ifelse(is.na(non_inspire_reducing_consumption$inspire_an
i), "skip", non_inspire_reducing_consumption$inspire_ani)
non_inspire_ani <- table(non_inspire_ani1)
```

```
table(is.na(non_inspire_reducing_consumption$inspire_env))
non_inspire_env1 <- ifelse(is.na(non_inspire_reducing_consumption$inspire_en
v), "skip", non_inspire_reducing_consumption$inspire_env)
non_inspire_env <- table(non_inspire_env1)


table(is.na(non_inspire_reducing_consumption$inspire_ff))
non_inspire_ff1 <- ifelse(is.na(non_inspire_reducing_consumption$inspire_ff),
 "skip", non_inspire_reducing_consumption$inspire_ff)
non_inspire_ff <- table(non_inspire_ff1)


table(is.na(non_inspire_reducing_consumption$inspire_ht))
non_inspire_ht1 <- ifelse(is.na(non_inspire_reducing_consumption$inspire_ht),
 "skip", non_inspire_reducing_consumption$inspire_ht)
non_inspire_ht <- table(non_inspire_ht1)


table(is.na(non_inspire_reducing_consumption$inspire_hr))
non_inspire_hr1 <- ifelse(is.na(non_inspire_reducing_consumption$inspire_hr),
 "skip", non_inspire_reducing_consumption$inspire_hr)
non_inspire_hr <- table(non_inspire_hr1)


table(is.na(non_inspire_reducing_consumption$inspire_nt))
non_inspire_nt1 <- ifelse(is.na(non_inspire_reducing_consumption$inspire_nt),
 "skip", non_inspire_reducing_consumption$inspire_nt)
non_inspire_nt <- table(non_inspire_nt1)


table(is.na(non_inspire_reducing_consumption$inspire_rg))
non_inspire_rg1 <- ifelse(is.na(non_inspire_reducing_consumption$inspire_rg),
 "skip", non_inspire_reducing_consumption$inspire_rg)
non_inspire_rg <- table(non_inspire_rg1)


table(is.na(non_inspire_reducing_consumption$inspire_sb))
non_inspire_sb1 <- ifelse(is.na(non_inspire_reducing_consumption$inspire_sb),
 "skip", non_inspire_reducing_consumption$inspire_sb)
non_inspire_sb <- table(non_inspire_sb1)


table(is.na(non_inspire_reducing_consumption$inspire_wh))
non_inspire_wh1 <- ifelse(is.na(non_inspire_reducing_consumption$inspire_wh),
```

```
 "skip", non_inspire_reducing_consumption$inspire_wh)
non_inspire_wh <- table(non_inspire_wh1)
```

결측치 대체 및 변수 생성 저장- vegan

```
inspire_ani1 <- ifelse(is.na(inspire_reducing_consumption$inspire_ani), "skip
", inspire_reducing_consumption$inspire_ani)
inspire_ani <- table(inspire_ani1)


table(is.na(inspire_reducing_consumption$inspire_env))
inspire_env1 <- ifelse(is.na(inspire_reducing_consumption$inspire_env), "skip
", inspire_reducing_consumption$inspire_env)
inspire_env <- table(inspire_env1)


table(is.na(inspire_reducing_consumption$inspire_ff))
inspire_ff1 <- ifelse(is.na(inspire_reducing_consumption$inspire_ff), "skip",
 inspire_reducing_consumption$inspire_ff)
inspire_ff <- table(inspire_ff1)


table(is.na(inspire_reducing_consumption$inspire_ht))
inspire_ht1 <- ifelse(is.na(inspire_reducing_consumption$inspire_ht), "skip",
 inspire_reducing_consumption$inspire_ht)
inspire_ht <- table(inspire_ht1)


table(is.na(inspire_reducing_consumption$inspire_hr))
inspire_hr1 <- ifelse(is.na(inspire_reducing_consumption$inspire_hr), "skip",
 inspire_reducing_consumption$inspire_hr)
inspire_hr <- table(inspire_hr1)


table(is.na(inspire_reducing_consumption$inspire_nt))
inspire_nt1 <- ifelse(is.na(inspire_reducing_consumption$inspire_nt), "skip",
 inspire_reducing_consumption$inspire_nt)
inspire_nt <- table(inspire_nt1)


table(is.na(inspire_reducing_consumption$inspire_rg))
inspire_rg1 <- ifelse(is.na(inspire_reducing_consumption$inspire_rg), "skip",
 inspire_reducing_consumption$inspire_rg)
inspire_rg <- table(inspire_rg1)

table(is.na(inspire_reducing_consumption$inspire_sb))
inspire_sb1 <- ifelse(is.na(inspire_reducing_consumption$inspire_sb), "skip",
 inspire_reducing_consumption$inspire_sb)
```

```
inspire_sb <- table(inspire_sb1)



table(is.na(inspire_reducing_consumption$inspire_wh))
inspire_wh1 <- ifelse(is.na(inspire_reducing_consumption$inspire_wh), "skip",
 inspire_reducing_consumption$inspire_wh)
inspire_wh <- table(inspire_wh1)
```

결측치 대체한 각 변수를 하나의 데이터프레임으로 가공- non-vegan

```
non_inspire <-cbind(non_inspire_ani, non_inspire_env, non_inspire_ff, non_ins
pire_hr, non_inspire_ht, non_inspire_nt, non_inspire_rg, non_inspire_sb, non_
inspire_wh)

non_inspire<- data.frame(non_inspire)
```

결측치 대체한 각 변수를 하나의 데이터프레임으로 가공- vegan

```
inspire <-cbind(inspire_ani, inspire_env, inspire_ff, inspire_hr, inspire_ht,
 inspire_nt, inspire_rg, inspire_sb, inspire_wh)

inspire<- data.frame(inspire)
```

인덱스로 들어간 항목을 꺼내서 answer 컬럼 데이터로 넣어주기- non-vegan

```
non_inspire_g <- dplyr::add_rownames(non_inspire, var="answer")

## Warning: `add_rownames()` was deprecated in dplyr 1.0.0.
## Please use `tibble::rownames_to_column()` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
generated.
```

인덱스로 들어간 항목을 꺼내서 answer 컬럼 데이터로 넣어주기- vegan

```
inspire_g <- dplyr::add_rownames(inspire, var="answer")
```

컬럼명 및 데이터명 변경- non-vegan

```
non_inspire_g <- dplyr::rename(non_inspire_g, "Animal welfare" = non_inspire_
ani,
                      "Environment" = non_inspire_env,
                      "Family Friend" = non_inspire_ff,
                      "Health" = non_inspire_ht,
                      "Human rights" = non_inspire_hr,
                      "Nutrition" = non_inspire_nt,
                      "Religion" = non_inspire_rg,
                      "Someone" = non_inspire_sb,
                      "World Hunger" = non_inspire_wh)

non_inspire_g$answer <- ifelse(non_inspire_g$answer =="Not at all", 0,
                               ifelse(non_inspire_g$answer =="To little ex
```

```
tent", 1,
                                          ifelse(non_inspire_g$answer =="To so
me extent", 2 ,
                                                 ifelse(non_inspire_g$answer =
="To a moderate extent", 3,
                                                        ifelse(non_inspire_g$a
nswer =="To a large extent", 4,non_inspire_g$answer
                                                        )))))
```

컬럼명 및 데이터명 변경- vegan

```
inspire_g <- dplyr::rename(inspire_g, "Animal welfare" = inspire_ani,
                     "Environment" = inspire_env,
                     "Family Friend" = inspire_ff,
                     "Health" = inspire_ht,
                     "Human rights" = inspire_hr,
                     "Nutrition" = inspire_nt,
                     "Religion" = inspire_rg,
                     "Someone" = inspire_sb,
                     "World Hunger" = inspire_wh)

inspire_g$answer <- ifelse(inspire_g$answer =="Not at all", 0,
                           ifelse(inspire_g$answer =="To little extent
", 1,
                                  ifelse(inspire_g$answer =="To some e
xtent", 2 ,
                                         ifelse(inspire_g$answer =="To
 a moderate extent", 3,
                                                ifelse(inspire_g$answe
r =="To a large extent", 4,inspire_g$answer)))))
```

skip 제거- non-vegan

```
non_inspire_g <- non_inspire_g %>% filter(answer != "skip")
```

skip 제거- vegan

```
inspire_g <- inspire_g %>% filter(answer != "skip")
```

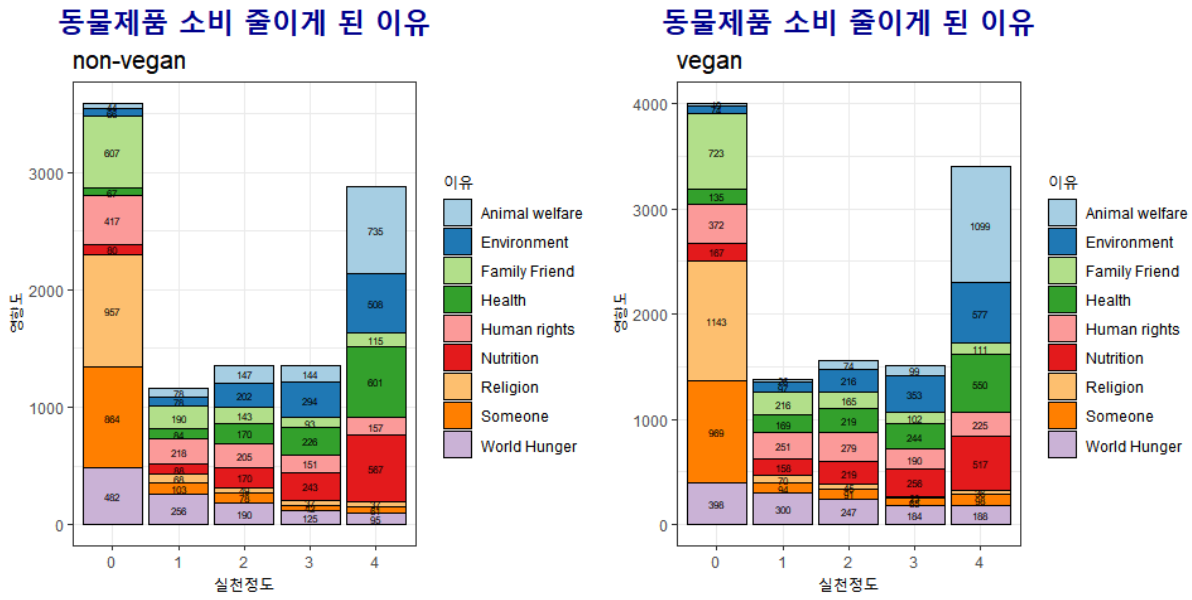
그래프 시각화- non-vegan

```
non_inspire_g %>%
  pivot_longer(-answer) %>%
  ggplot(aes(x = answer, y = value, fill = name)) +
  geom_col(position = position_stack(), colour = "black") +
  geom_text(aes(label = value), size = 2, position = position_stack(0.5))+
  scale_fill_brewer(name = '이유', palette = 'Paired') +
  theme_bw() + xlab("실천정도") + ylab("영향도") +
  ggtitle("동물제품 소비 줄이게 된 이유", subtitle = "non-vegan") +
  theme(plot.title = element_text(face = "bold", hjust = 0.5, size = 20, colo
```

```
r = "darkblue"),
        plot.subtitle = element_text(size = 15))
```

그래프 시각화- vegan

```
inspire_g %>%
  pivot_longer(-answer) %>%
  ggplot(aes(x = reorder(answer,-value), y = value, fill = name)) +
geom_col(position = position_stack(), colour = "black") +
  geom_text(aes(label = value), size = 2, position = position_stack(0.5))+
  scale_fill_brewer(name = '이유', palette = 'Paired') +
  theme_bw() + xlab("실천정도") + ylab("영향도") +
  ggtitle("동물제품 소비 줄이게 된 이유", subtitle = "vegan") +
  theme(plot.title = element_text(face = "bold", hjust = 0.5, size = 20, colo
r = "darkblue"),
        plot.subtitle = element_text(size = 15))
```



x 축

0: 전혀 실천해보지 않음

1: 실천 거의 없음

2: 실천 조금 있음

3: 실천 보통

4: 실천 매우 많음

y 축

Animal welfare: 동물복지를 위해

Environment: 환경을 위해

Family Friend: 가족이나 친구들에 의해

Health: 건강을 위해
Human rights: 인권을 위해
Nutrition: 영양을 위해
Religion: 종교적인 이유로
Someone: 누군가에 의해
World Hunger: 기아를 위해

논 비건 사람들은 동물 제품 소비 감소 실천을 많이 해본 이유 중 동물복지(735)와 영양(567), 건강(508)이 많은 것으로 확인할 수 있습니다.

종교는 동물제품을 소비를 줄이는 실천에 영향이 거의 없음(957)을 확인할 수 있습니다.

비건 사람들은 동물 제품 소비 감소 실천을 많이 해본 이유 중 동물복지(1099)와 환경(577), 건강(550)이 많은 것으로 확인할 수 있습니다.

또한 종교는 동물제품을 소비를 줄이는 실천에 영향이 거의 없음(1143)을 확인할 수 있습니다.

다음은 동물성 제품 소비를 줄인 가장 큰 이유에 대해 알아보았습니다.

라이브러리 로드

```
library(readxl)
library(dplyr)
library(tidyverse)
library(ggplot2)
```

원본 데이터 파일 불러오기 및 필요 행 추출 - non-vegan

```
vegan_raw <- read_excel("C:/Rstudy/mini_team1/data/vegan_Raw_data_c.xls")

vegan_raw1 <- vegan_raw %>%
  filter(!(eat_beef == "Never" & eat_chicken == "Never" &eat_dairy =="Never"&
             eat_eggs =="Never" & eat_fish_seafood =="Never"& eat_pork =="Nev
er"))
```

원본데이터 파일 불러오기 및 필요 컬럼 추출 - vegan

```
library(readxl)
vegan_raw2 <- read_excel("C:/Rstudy/mini_team1/data/only_vegan.xlsx")
```

동물성 제품 줄이는 가장 큰 이유

필요 컬럼 추출 - non-vegan

```
non_reducing_products_one <- vegan_raw1$reducing_ap
```

필요 컬럼 추출 - vegan

```
reducing_products_one <- vegan_raw2$reducing_ap
```

결측치 대체한 각 변수를 하나의 데이터프레임으로 가공 - non vegan

```
non_reducing_products_one_s <- ifelse(is.na(non_reducing_products_one), "skip
", non_reducing_products_one)
non_reducing_products_one1 <- data.frame(non_reducing_products_one_s)
```

결측치 대체한 각 변수를 하나의 데이터프레임으로 가공 - vegan

```
reducing_products_one_s <- ifelse(is.na(reducing_products_one), "skip", reduc
ing_products_one)
reducing_products_one1 <- data.frame(reducing_products_one_s)
```

skip 제거 및 그룹화 요약- non-vegan

```
non_reducing_products_one2 <-non_reducing_products_one1 %>% filter(non_reduci
ng_products_one_s != "skip") %>%  group_by(non_reducing_products_one_s) %>%
  summarise(n=n())
```

skip 제거 및 그룹화 요약- vegan

```
reducing_products_one2 <-reducing_products_one1 %>% filter(reducing_products_
one_s != "skip")%>% group_by(reducing_products_one_s) %>%
  summarise(n=n())
```

항목명 변경- non-vegan

```
non_reducing_products_one2$non_reducing_products_one_s <- ifelse(non_reducing
_products_one2$non_reducing_products_one_s =="Animal welfare concerns", "Anim
al welfare",
                                                                 ifelse(non_reduc
ing_products_one2$non_reducing_products_one_s =="Environmental concerns", "En
vironment",
                                                                        ifelse(no
n_reducing_products_one2$non_reducing_products_one_s =="Family or friend doin
g it", "Family Friend" ,
                                                                               if
else(non_reducing_products_one2$non_reducing_products_one_s =="Someone made t
he transition with me", "Someone", non_reducing_products_one2$non_reducing_pr
oducts_one_s

 ))))
```

항목명 변경- vegan

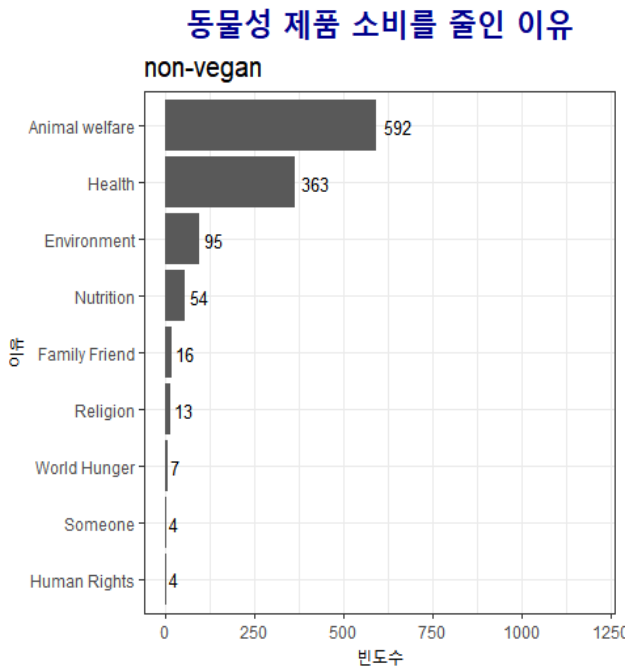
```
reducing_products_one2$reducing_products_one_s <- ifelse(reducing_products_on
e2$reducing_products_one_s =="Animal welfare concerns", "Animal welfare",
                                                         ifelse(reducing_
products_one2$reducing_products_one_s =="Environmental concerns", "Environmen
t",
                                                                ifelse(re
ducing_products_one2$reducing_products_one_s =="Family or friend doing it", "
Family Friend" ,
                                                                       if
else(reducing_products_one2$reducing_products_one_s =="Someone made the trans
ition with me", "Someone", reducing_products_one2$reducing_products_one_s

 ))))
```

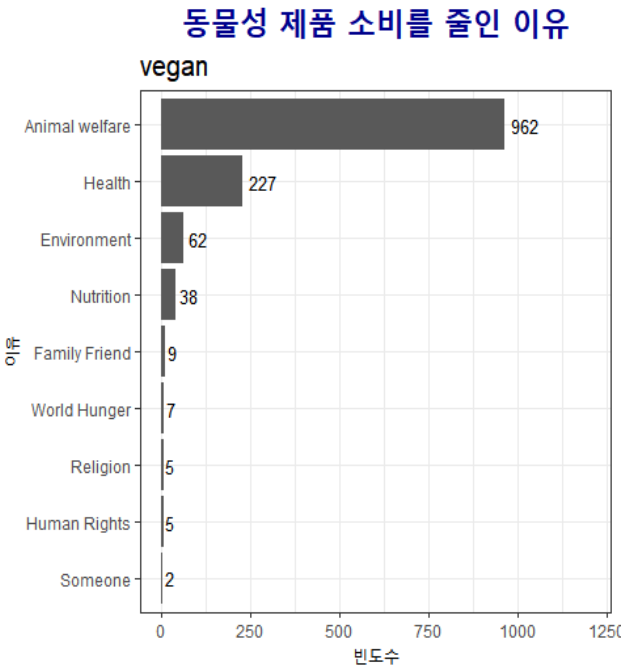
그래프 시각화 - non-vegan

```
ggplot(non_reducing_products_one2, aes(x=reorder(non_reducing_products_one_s,
 n), y= n)) +
  geom_col() + coord_flip() +
  scale_y_continuous(limits = c(0, 1200)) +
  geom_text(aes(label=n), hjust=-.25, size=3.5) +
  theme_bw() + xlab("이유") + ylab("빈도수") +
    ggtitle("동물성 제품 소비를 줄인 이유", subtitle = "non-vegan") +
  theme(plot.title = element_text(face = "bold", hjust = 0.5, size = 20, colo
r = "darkblue"),
        plot.subtitle = element_text(size = 15))
```

그래프 시각화 - vegan

```
ggplot(reducing_products_one2, aes(x=reorder(reducing_products_one_s, n), y=
n)) +
  geom_col() + coord_flip() +
  scale_y_continuous(limits = c(0, 1200)) +
  geom_text(aes(label=n), hjust=-.25, size=3.5) +
  theme_bw() + xlab("이유") + ylab("빈도수") +
    ggtitle("동물성 제품 소비를 줄인 이유", subtitle = "vegan") +
  theme(plot.title = element_text(face = "bold", hjust = 0.5, size = 20, colo
r = "darkblue"),
        plot.subtitle = element_text(size = 15))
```





동물 복지 선택자들의 이유

결측치 확인 - non-vegan

```
non_reducing_aw <- vegan_raw1$aw_reason
table(is.na(non_reducing_aw))
```

결측치 확인 - vegan

```
reducing_aw <- vegan_raw2$aw_reason
table(is.na(reducing_aw))
```

결측치 대체 및 데이터프레임으로 가공 - non-vegan

```
non_reducing_aw_s <- ifelse(is.na(non_reducing_aw), "skip", non_reducing_aw)
non_reducing_aw_s <- data.frame(non_reducing_aw_s)



#### 12 cbind 로 합치기 여기서 one1 은 11 번에서 선택한 항목임 ####
non_reducing_pro_aw_inf <- cbind(non_reducing_products_one1, non_reducing_aw_
s)
```

결측치 대체 및 데이터프레임으로 가공 - vegan

```
reducing_aw_s <- ifelse(is.na(reducing_aw), "skip", reducing_aw)
reducing_aw_s <- data.frame(reducing_aw_s)
```

skip 제거 및 동물 복지 선택 안한사람들 제외 - non-vegan

```
non_reducing_pro_aw_inf_f <- non_reducing_pro_aw_inf %>% filter(non_reducing_
aw_s != "skip" &
                                                                non_reducin
g_aw_s != "Not applicable" &
                                                              non_reducing_produc
ts_one_s =="Animal welfare concerns")
```

skip 제거 및 동물 복지 선택 안한사람들 제외 - vegan

```
reducing_pro_aw_inf <- cbind(reducing_products_one1, reducing_aw_s)

reducing_pro_aw_inf_f <- reducing_pro_aw_inf %>% filter(reducing_aw_s != "ski
p" &
                                                          reducing_aw_s != "N
ot applicable" &
                                                          reducing_products_o
ne_s =="Animal welfare concerns")
```

그룹화 및 요약 - non-vegan

```
non_reducing_pro_aw_inf_f <- non_reducing_pro_aw_inf_f %>% group_by(non_reduc
ing_aw_s) %>%
  summarise(n5=n())
```

그룹화 및 요약 - vegan

```
reducing_pro_aw_inf_f <- reducing_pro_aw_inf_f %>% group_by(reducing_aw_s) %
>%
  summarise(n=n())
```

항목명 변경- non-vegan

```
non_reducing_pro_aw_inf_f$non_reducing_aw_s <- ifelse(non_reducing_pro_aw_inf
_f$non_reducing_aw_s =="I learned about how farm animals have intelligence an
d emotions", "animal-friendly",
```

```
                                                                    ifelse(non_reduc
ing_pro_aw_inf_f$non_reducing_aw_s =="I do not like the fact that farm animal
s are killed", "don't like kill",
                                                                        ifelse(no
n_reducing_pro_aw_inf_f$non_reducing_aw_s =="I do not like the fact that farm
 animals are raised in very cruel conditions", "hate bad environment" ,
                                                                               n
on_reducing_pro_aw_inf_f$non_reducing_aw_s

 )))
```

항목명 변경- vegan

```
reducing_pro_aw_inf_f$reducing_aw_s <- ifelse(reducing_pro_aw_inf_f$reducing_
aw_s =="I learned about how farm animals have intelligence and emotions", "an
imal-friendly",
                                                                    ifelse(reducing_
pro_aw_inf_f$reducing_aw_s =="I do not like the fact that farm animals are ki
lled", "don't like kill",
                                                                        ifelse(re
ducing_pro_aw_inf_f$reducing_aw_s =="I do not like the fact that farm animals
 are raised in very cruel conditions", "hate bad environment" ,
                                                                               r
educing_pro_aw_inf_f$reducing_aw_s

 )))
```

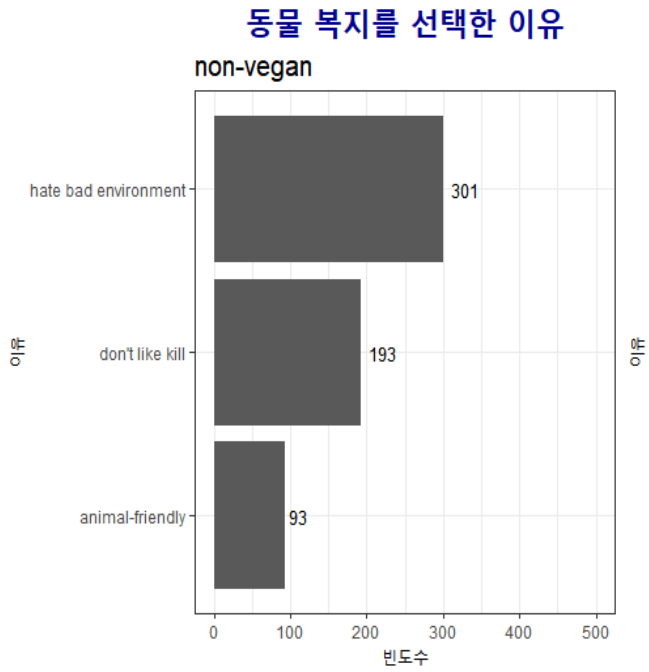
그래프 시각화 - non-vegan

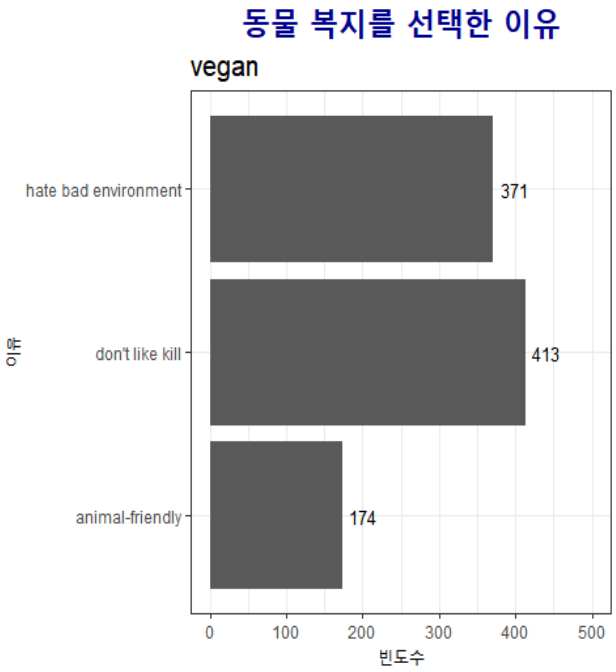
```
library(ggplot2)
ggplot(non_reducing_pro_aw_inf_f, aes(x = reorder(non_reducing_aw_s,n5), y =n
5)) +
  geom_col() + coord_flip() +
  scale_y_continuous(limits = c(0, 500)) +
  geom_text(aes(label=n5), hjust=-.25, size=3.5) +
  theme_bw() + xlab("이유") + ylab("빈도수") +
    ggtitle("동물 복지를 선택한 이유", subtitle = "non-vegan") +
  theme(plot.title = element_text(face = "bold", hjust = 0.5, size = 20, colo
r = "darkblue"),
        plot.subtitle = element_text(size = 15))
```

그래프 시각화 - vegan

```
library(ggplot2)
ggplot(reducing_pro_aw_inf_f, aes(x = reducing_aw_s, y =n)) +
  geom_col() + coord_flip() +
  scale_y_continuous(limits = c(0, 500)) +
  geom_text(aes(label=n), hjust=-.25, size=3.5) +
  theme_bw() + xlab("이유") + ylab("빈도수") +
```

```
    ggtitle("동물 복지를 선택한 이유", subtitle = "vegan") +
  theme(plot.title = element_text(face = "bold", hjust = 0.5, size = 20, colo
r = "darkblue"),
        plot.subtitle = element_text(size = 15))
```





건강 영양 선택자들의 이유

필요 컬럼 추출- non-vegan

```
non_reducing_ht <- vegan_raw1 %>%
  select(hn_animal_disease, hn_energy, hn_weight, hn_certain_diseases, hn_oth
er)
```

필요 컬럼 추출- vegan

```
reducing_ht <- vegan_raw2 %>%
  select(hn_animal_disease, hn_energy, hn_weight, hn_certain_diseases, hn_oth
er)
```

데이터 합치기- non-vegan

```
non_reducing_pro_ht <- cbind(non_reducing_products_one1, non_reducing_ht)
```

데이터 합치기- vegan

```
reducing_pro_ht <- cbind(reducing_products_one1, reducing_ht)
```

건강 영양 선택자들만 추출- non-vegan

```
non_reducing_pro_ht_f <- non_reducing_pro_ht %>% filter(non_reducing_products
_one_s =="Health" |
                                                       non_reducing_produc
ts_one_s =="Nutrition")
```

건강 영양 선택자들만 추출- vegan

```
reducing_pro_ht_f <- reducing_pro_ht %>% filter(reducing_products_one_s =="He
alth" |
                                                  reducing_products_one_s ="
Nutrition")
```

결측치 대체 및 변수 생성 저장- non-vegan

13 각 컬럼들 빈도수, 4 개의 컬럼 중 2 개 선택이므로 결측치 제거하면 안됨 -> ex) 1 번 고르고 3 번 고르면 2,4 번은 결측치임

각 컬럼의 항목들은 같은 데이터임 -> ex) animal_disease 컬럼의 입력 항목들은 동물 죽는게 싫다임

```
non_animal_disease1 <- table(non_reducing_pro_ht_f$hn_animal_disease)
non_energy1 <- table(non_reducing_pro_ht_f$hn_energy)
non_weight1 <- table(non_reducing_pro_ht_f$hn_certain_diseases)
non_other1 <- table(non_reducing_pro_ht_f$hn_other)
```

결측치 대체 및 변수 생성 저장- vegan

```
animal_disease1 <- table(reducing_pro_ht_f$hn_animal_disease)
energy1 <- table(reducing_pro_ht_f$hn_energy)
weight1 <- table(reducing_pro_ht_f$hn_certain_diseases)
other1 <- table(reducing_pro_ht_f$hn_other)
```

데이터프레임으로 가공- non-vegan

```
non_reducing_pro_ht_f1 <- as.data.frame(c(non_animal_disease1, non_energy1, n
on_weight1, non_other1))
```

데이터프레임으로 가공- vegan

```
reducing_pro_ht_f1 <- as.data.frame(c(animal_disease1, energy1, weight1, othe
r1))
```

인덱스로 들어간 항목을 꺼내서 answer 컬럼 데이터로 넣어주기- non-vegan

```
non_reducing_pro_ht_f1 <- dplyr::add_rownames(non_reducing_pro_ht_f1, var="an
swer")

## Warning: `add_rownames()` was deprecated in dplyr 1.0.0.
## Please use `tibble::rownames_to_column()` instead.
```

```
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
generated.
```

인덱스로 들어간 항목을 꺼내서 answer 컬럼 데이터로 넣어주기- vegan

```
reducing_pro_ht_f1 <- dplyr::add_rownames(reducing_pro_ht_f1, var="answer")
```

컬럼명 및 데이터명 변경- non-vegan

```
non_reducing_pro_ht_f1 <- dplyr::rename(non_reducing_pro_ht_f1, n = "c(non_an
imal_disease1, non_energy1, non_weight1, non_other1)")
```

컬럼명 및 데이터명 변경- vegan

```
reducing_pro_ht_f1 <- dplyr::rename(reducing_pro_ht_f1, n = "c(animal_disease
1, energy1, weight1, other1)")
```

항목명 변경- non-vegan

```
non_reducing_pro_ht_f1$answer <- ifelse(non_reducing_pro_ht_f1$answer =="Othe
r (Please Specify)", "Other",
                                                                    ifelse(non_reduc
ing_pro_ht_f1$answer =="I wanted more energy/well-being", "energy well-being
",
                                                                           ifelse(no
n_reducing_pro_ht_f1$answer =="I’m concerned about antibiotics/hormones/disea
ses in animal products", "concern diseases from animal" , ifelse(non_reducing
_pro_ht_f1$answer =="I wanted to reduce my risk of developing certain disease
s", "reduce diseases" ,
                                                                                  n
on_reducing_pro_ht_f1$answer

 ))))
```

항목명 변경- vegan

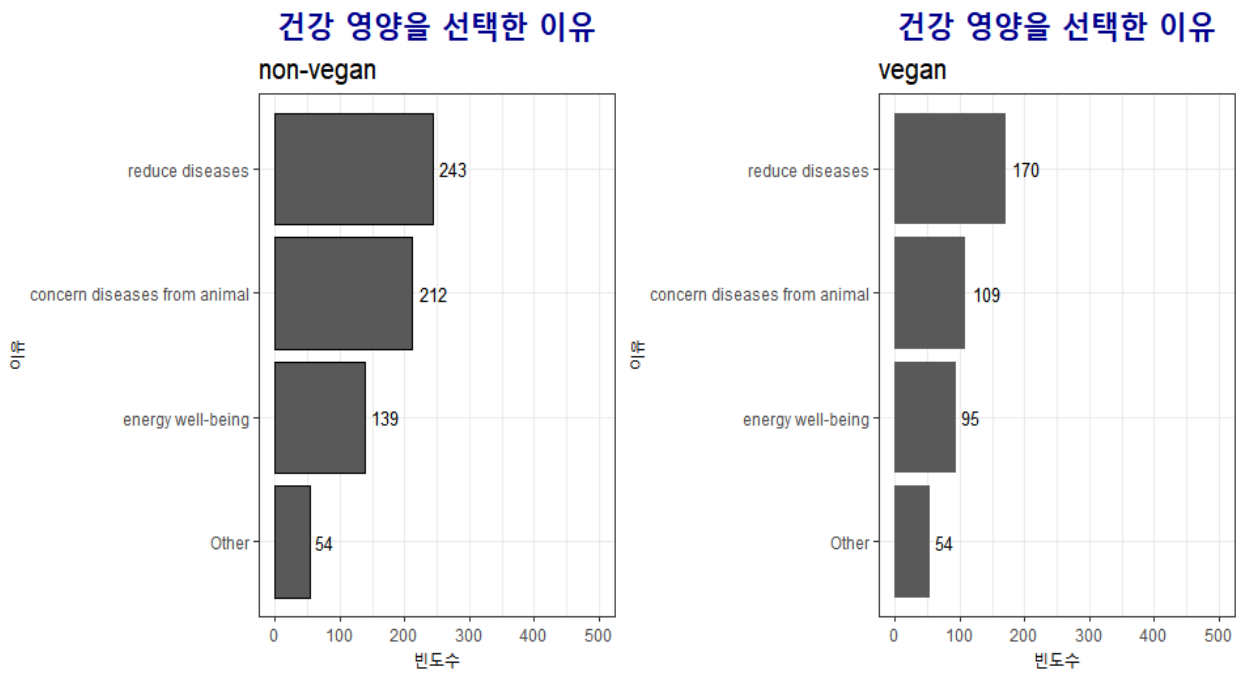
```
reducing_pro_ht_f1$answer <- ifelse(reducing_pro_ht_f1$answer =="Other (Pleas
e Specify)", "Other",
                                                                    ifelse(reducing_
pro_ht_f1$answer =="I wanted more energy/well-being", "energy well-being",
                                                                           ifelse(re
ducing_pro_ht_f1$answer =="I’m concerned about antibiotics/hormones/diseases
in animal products", "concern diseases from animal" , ifelse(reducing_pro_ht_
f1$answer =="I wanted to reduce my risk of developing certain diseases", "red
uce diseases" ,
                                                                                  r
educing_pro_ht_f1$answer

 ))))
```

그래프 시각화- non-vegan

```
library(ggplot2)
ggplot(non_reducing_pro_ht_f1, aes(x = reorder(answer, n), y=n)) + geom_col(colour = "black") + coord_flip() +
  scale_y_continuous(limits = c(0, 500)) +
  geom_text(aes(label=n), hjust=-.25, size=3.5) +
    theme_bw() + xlab("이유") + ylab("빈도수") +
  ggtitle("건강 영양을 선택한 이유", subtitle = "non-vegan") +
  theme(plot.title = element_text(face = "bold", hjust = 0.5, size = 20, color = "darkblue"),
        plot.subtitle = element_text(size = 15))
```

그래프 시각화- vegan

```
library(ggplot2)
ggplot(reducing_pro_ht_f1, aes(x = reorder(answer, n), y=n)) + geom_col() + coord_flip() +
  scale_y_continuous(limits = c(0, 500)) +
  geom_text(aes(label=n), hjust=-.25, size=3.5) +
    theme_bw() + xlab("이유") + ylab("빈도수") +
  ggtitle("건강 영양을 선택한 이유", subtitle = "vegan") +
  theme(plot.title = element_text(face = "bold", hjust = 0.5, size = 20, color = "darkblue"),
        plot.subtitle = element_text(size = 15))
```



y 축
Animal welfare: 동물복지를 위해
Environment: 환경을 위해
Family Friend: 가족이나 친구들에 의해
Health: 건강을 위해
Human rights: 인권을 위해
Nutrition: 영양을 위해
Religion: 종교적인 이유로
Someone: 누군가에 의해
World Hunger: 기아를 위해

논비건 사람들과 비건 사람들 모두 동물 복지를 위해 동물성 제품을 줄인 것을 확인할 수 있습니다.

다음은 논비건과 비건의 동물성 제품 소비를 예상한 것을 분석하였습니다.

논비건 사람들의 동물성 제품 소비 예상 Non-Vegan

Install. packages:

```
library(readxl)
library(dplyr)
library(ggplot2)
```

Raw Data

```
#31. "Consumption of animal products"

vegan_raw <- read_excel("C:/Rstudy/0506/newProj/rvd.xls")
```

Filter Non-Vegan from Columns

```
vegan_raw1 <- vegan_raw %>% filter(!(eat_beef == "Never" & eat_chicken == "Ne
ver" &eat_dairy =="Never"&
                                     eat_eggs =="Never" & eat_fish_seafood
=="Never"& eat_pork =="Never"))
```

Select Column from data

```
consumption <- vegan_raw1 %>% select(consumption)
consumption
```

```
## # A tibble: 1,765 x 1
##    consumption
##    <chr>
##  1 I will eat fewer animal products
##  2 I will eat fewer animal products
##  3 It will stay the same
##  4 It will stay the same
##  5 I will eat fewer animal products
##  6 I will eat fewer animal products
##  7 It will stay the same
##  8 I will eat fewer animal products
##  9 I will eat fewer animal products
## 10 <NA>
## # ... with 1,755 more rows
```

Check NA from Column

```
#how to count the number of non NA values in R
sum(!is.na(vegan_raw1$consumption))
```

```
## [1] 1519
```

```
#False and True
t_df_c <- table(is.na(vegan_raw1$consumption))
t_df_c
```

```
##
## FALSE  TRUE
##  1519   246
```

Rename Column values

```
consump<- ifelse(vegan_raw1$consumption =="It will stay the same", "eat same
",
          ifelse(vegan_raw1$consumption =="I will eat fewer animal products",
 "eat fewer",
          ifelse(vegan_raw1$consumption =="I will eat more animal products",
"eat more",
                                                          vegan_raw1$consu
mption)))
consump
```

```
##    [1] "eat fewer" "eat fewer" "eat same"  "eat same"  "eat fewer" "eat fe
wer"
##    [7] "eat same"  "eat fewer" "eat fewer" NA          "eat fewer" "eat fe
wer"
##   [13] "eat fewer" "eat same"  "eat fewer" NA          NA          "eat sa
me"
```

Rename NA to “skip”

```
consump <- ifelse(is.na(vegan_raw1$consumption), "skip", consump)
consump
```

```
##    [1] "eat fewer" "eat fewer" "eat same"  "eat same"  "eat fewer" "eat fe
wer"
"
## [1555] "skip"      "skip"      "skip"      "eat same"  "skip"      "eat fe
wer"
## [1717] "skip"      "eat same"  "eat same"  "eat same"  "eat fewer" "eat sa
me"
```

Data Frame

```
df_c <- data.frame(consump)
df_c
```

```
##        consump
## 1    eat fewer
## 2    eat fewer
## 3     eat same
## 4     eat same
View(df_c)
```

Column Unique values

```
unique(df_c[c("consump")])
```

```
##      consump
## 1  eat fewer
## 3   eat same
## 10      skip
## 28  eat more
```

Add_index row_name

```
df_c <- dplyr::add_rownames(df_c, var="Answers")
head(df_c)
```

```
## # A tibble: 6 x 2
##   Answers consump
##   <chr>   <chr>
## 1 1       eat fewer
## 2 2       eat fewer
## 3 3       eat same
## 4 4       eat same
## 5 5       eat fewer
## 6 6       eat fewer
```

Drop NA=”skip” from column Answers

```
df_c <- df_c %>% filter(consump != "skip")
View(df_c)
```

Column Unique values

```
#Finding the unique values in column "consump"
unique(df_c[c("consump")])
```

```
## # A tibble: 3 x 1
##   consump
##   <chr>
## 1 eat fewer
## 2 eat same
## 3 eat more
```

```
#Get Maximum value of the column by column position
df_c %>% summarise_if(is.character, max)
```

```
## # A tibble: 1 x 2
##   Answers consump
##   <chr>   <chr>
## 1 998     eat same
```

Summarise

```
df_c1 <- df_c %>% group_by(consump) %>% summarise(n=n())
df_c1
```

```
## # A tibble: 3 x 2
##   consump       n
##   <chr>     <int>
## 1 eat fewer   808
```

```
## 2 eat more     10
## 3 eat same    701
```

Install. packages:

```
library(reshape)
library(tidyverse)
library(plotly)

cons_p <- df_c1  %>% pivot_longer(-consump)

cons_graph<-ggplot(cons_p, aes(x = consump,y=value, fill =consump)) +
  geom_col(position = position_stack(), colour = "black") +
  geom_text(aes(label=value), size=3, position = position_stack(0.9)) +
  scale_y_continuous(limits = c(0, 1500)) +
  theme_bw() + xlab("예상") + ylab("응답수") +
  ggtitle("Consumption of the animal products", subtitle = "non-vegan") +
  theme(plot.title = element_text(face = "bold", hjust = 0.5, size = 20, colo
r = "darkblue"),
        plot.subtitle = element_text(size = 15))

cons_graph
```

비건 사람들의 동물성 제품 소비 예상 Vegan

Install. packages:

```
library(readxl)
library(dplyr)
library(ggplot2)
```

Raw Data

```
# ”Consumption of animal products"

vegan_raw <- read_excel("C:/Rstudy/0506/newProj/rvd.xls")
```

Select Column from data

```
consumption <- vegan_raw %>% select(consumption)
consumption
```

```
## # A tibble: 3,258 x 1
##    consumption
##    <chr>
##  1 I will eat fewer animal products
##  2 It will stay the same
##  3 It will stay the same
##  4 It will stay the same

## # ... with 3,248 more rows
```

Check NA from Column

```
#how to count the number of non NA values in R
sum(!is.na(vegan_raw1$consumption))

## [1] 1519

#False and True
t_df_c <- table(is.na(vegan_raw$consumption))
t_df_c

##
## FALSE  TRUE
##  2856   402
```

Rename Column values

```
consump<- ifelse(vegan_raw$consumption =="It will stay the same", "eat same",

          ifelse(vegan_raw$consumption =="I will eat fewer animal products",
"eat fewer",
          ifelse(vegan_raw$consumption =="I will eat more animal products", "
eat more",
                                                                vegan_raw$consum
ption)))
consump

##    [1] "eat fewer" "eat same"  "eat same"  "eat same"  "eat same"  "eat sa
me"
##    [7] "eat same"  "eat same"  "eat same"  NA          "eat same"  "eat sa
me"
##   [13] "eat same"  "eat fewer" "eat same"  "eat same"  "eat same"  "eat sa
me"
##   [19] "eat fewer" "eat same"  "eat same"  "eat fewer" "eat same"  "eat sa
```

```
me"
```

Rename NA to “skip”

```
consump <- ifelse(is.na(vegan_raw$consumption), "skip", consump)
consump
```

```
##    [1] "eat fewer" "eat same"  "eat same"  "eat same"  "eat same"  "eat sa
me"
##    [7] "eat same"  "eat same"  "eat same"  "skip"      "eat same"  "eat sa
me"
##   [13] "eat same"  "eat fewer" "eat same"  "eat same"  "eat same"  "eat sa
me"
##   [19] "eat fewer" "eat same"  "eat same"  "eat fewer" "eat same"  "eat sa
me" "
## [1381] "eat same"  "eat same"  "eat fewer" "eat same"  "eat same"  "eat sa
me"
```

Data Frame

```
df_c <- data.frame(consump)
df_c
```

```
##        consump
## 1    eat fewer
## 2     eat same
## 3     eat same
## 4     eat same
```

```
View(df_c)
```

Column Unique values

```
unique(df_c[c("consump")])
```

```
##      consump
## 1  eat fewer
## 2   eat same
## 10      skip
## 33  eat more
```

Add_index row_name

```
df_c <- dplyr::add_rownames(df_c, var="Answers")
head(df_c)
```

```
## # A tibble: 6 x 2
##   Answers consump
##   <chr>   <chr>
## 1 1       eat fewer
## 2 2       eat same
## 3 3       eat same
## 4 4       eat same
## 5 5       eat same
## 6 6       eat same
```

Drop NA=”skip” from column consump

```
df_c <- df_c %>% filter(consump != "skip")
View(df_c)
```

```
## # A tibble: 3 x 1
##   consump
##   <chr>
## 1 eat fewer
## 2 eat same
## 3 eat more
```

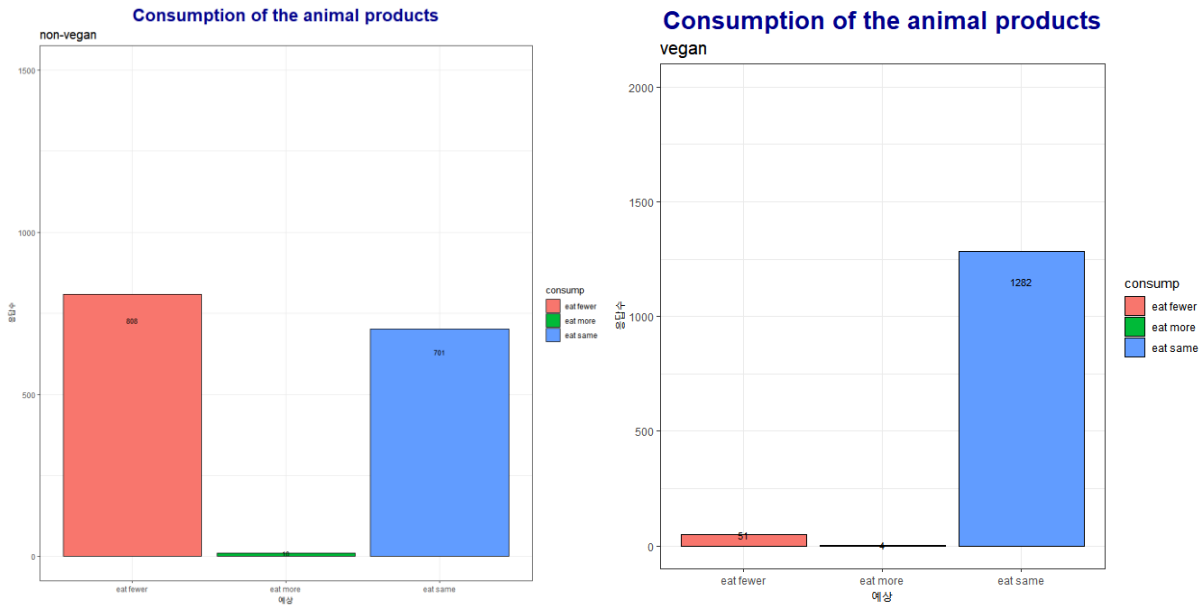
Summarise

```
df_c1 <- df_c %>% group_by(consump) %>% summarise(n=n())
df_c1
```

```
## # A tibble: 3 x 2
##   consump       n
##   <chr>     <int>
## 1 eat fewer   859
## 2 eat more     14
## 3 eat same   1983
```

Install. packages:

```
library(reshape)
library(tidyverse)
library(plotly)


cons_p <- df_c1  %>% pivot_longer(-consump)

cons_graph<-ggplot(cons_p, aes(x = consump,y=value, fill =consump)) +
  geom_col(position = position_stack(), colour = "black") +
  geom_text(aes(label=value), size=3, position = position_stack(0.9)) +
  scale_y_continuous(limits = c(0, 1500)) +
  theme_bw() + xlab("예상") + ylab("응답수") +
  ggtitle("Consumption of the animal products", subtitle = "vegan") +
  theme(plot.title = element_text(face = "bold", hjust = 0.5, size = 20, colo
r = "darkblue"),
        plot.subtitle = element_text(size = 15))

cons_graph
```



x 축

eat fewer: 동물성 제품 섭취를 줄일 것임

eat more: 동물성 제품 섭취를 늘릴 것임

eat same: 동물성 제품 섭취를 기존과 같이 유지할 것임

논 비건 사람들은 동물성 제품 섭취를 적게할(808) 예정이 가장 높게 나왔으며 유지할 예정이 그 다음으로 높게 나왔음을 확인할 수 있습니다.

비건 사람들은 동물성 제품 섭취를 기존과 같이 유지할(1282) 예정이 가장 높게 나왔음을 확인할 수 있습니다.