Supplement 3

Number of pain sites

Peter Kamerman

Last knitted: 26 May 2021

Contents

---

1 Import and check data

```
# Import
data <- read_rds('data-cleaned/data-pain-sites.rds')
demo <- read_rds('data-cleaned/data-demographics.rds')

# Check
```

```
## Pain sites
dim(data)
```

```
## [1] 596  21
```

```
names(data)
```

```
##  [1] "ID"                "Head"              "Throat"
##  [4] "Shoulder"          "Arms"              "Elbows"
##  [7] "Wrists.Hands"      "Chest"             "Upper_back"
## [10] "Lower_back"        "Abdomen"           "Cervical_spine"
## [13] "Thoracic_spine"    "Lumbosacral_spine" "Groin"
## [16] "Hips"              "Legs"              "Knees"
## [19] "Ankles.Feet"       "Buttocks"          "Site"
```

```
glimpse(data)
```

```
## Rows: 596
## Columns: 21
## $ ID                <chr> "RPB73", "RPB74", "RPB75", "RPB76", "RPB77", "RPB78"~
## $ Head              <chr> "No", "No", "No", "Yes", "Yes", "No", "No", "No", "Y~
## $ Throat            <chr> "No", "No", "No", "No", "No", "No", "No", "No", "Yes~
## $ Shoulder          <chr> "No", "No", "No", "No", "No", "No", "No", "No", "No"~
## $ Arms              <chr> "No", "No", "No", "No", "No", "No", "No", "No", "No"~
## $ Elbows            <chr> "No", "No", "No", "No", "No", "No", "No", "No", "No"~
## $ Wrists.Hands      <chr> "No", "No", "No", "No", "No", "No", "No", "No", "No"~
## $ Chest             <chr> "No", "No", "No", "Yes", "No", "No", "No", "No", "Ye~
## $ Upper_back        <chr> "No", "No", "No", "No", "No", "No", "No", "No", "No"~
## $ Lower_back        <chr> "No", "No", "No", "No", "No", "No", "No", "No", "No"~
## $ Abdomen           <chr> "No", "No", "Yes", "Yes", "No", "No", "Yes", "No", "~
## $ Cervical_spine    <chr> "No", "No", "No", "No", "No", "No", "No", "No", "No"~
## $ Thoracic_spine    <chr> "No", "No", "No", "No", "No", "No", "No", "No", "No"~
## $ Lumbosacral_spine <chr> "No", "No", "No", "No", "No", "No", "No", "No", "No"~
## $ Groin             <chr> "No", "No", "No", "No", "No", "No", "No", "No", "No"~
## $ Hips              <chr> "No", "No", "No", "No", "No", "No", "No", "Yes", "No~
## $ Legs              <chr> "No", "No", "No", "No", "No", "Yes", "No", "Yes", "N~
## $ Knees             <chr> "No", "No", "No", "No", "No", "Yes", "No", "Yes", "N~
## $ Ankles.Feet       <chr> "No", "No", "No", "No", "No", "Yes", "No", "Yes", "N~
## $ Buttocks          <chr> "No", "No", "No", "No", "No", "No", "No", "Yes", "No~
## $ Site              <chr> "RP", "RP", "RP", "RP", "RP", "RP", "RP", "RP", "RP"~
```

```
data %>%
    select(-ID, -Site) %>%
    mutate_if(is.character, factor) %>%
    skim()
```

Table 1: Data summary

Name	Piped data
Number of rows	596
Number of columns	19
Column type frequency:	
factor	19

Group variables	None

Variable type: factor

skim_variable	missing	complete	n_unique	top_counts
Head	0	596	2	No: 401, Yes: 195
Throat	0	596	2	No: 577, Yes: 19
Shoulder	0	596	2	No: 549, Yes: 47
Arms	0	596	2	No: 571, Yes: 25
Elbows	0	596	2	No: 574, Yes: 22
Wrists.Hands	0	596	2	No: 561, Yes: 35
Chest	0	596	2	No: 479, Yes: 117
Upper_back	0	596	1	No: 596
Lower_back	0	596	2	No: 554, Yes: 42
Abdomen	0	596	2	No: 437, Yes: 159
Cervical_spine	0	596	2	No: 566, Yes: 30
Thoracic_spine	0	596	2	No: 522, Yes: 74
Lumbosacral_spine	0	596	2	No: 504, Yes: 92
Groin	0	596	2	No: 542, Yes: 54
Hips	0	596	2	No: 556, Yes: 40
Legs	0	596	2	No: 497, Yes: 99
Knees	0	596	2	No: 512, Yes: 84
Ankles.Feet	0	596	2	No: 412, Yes: 184
Buttocks	0	596	2	No: 577, Yes: 19

```
## Demographics
dim(demo)
```

```
## [1] 596   8
```

```
names(demo)
```

```
## [1] "ID"                "Site"              "Sex"
## [4] "Age"               "Employment_status" "CD4_recent"
## [7] "ART_currently"     "Education"
```

```
glimpse(demo)
```

```
## Rows: 596
## Columns: 8
## $ ID                <chr> "RPB73", "RPB74", "RPB75", "RPB76", "RPB77", "RPB78"~
## $ Site              <chr> "RP", "RP", "RP", "RP", "RP", "RP", "RP", "RP", "RP"~
## $ Sex               <chr> "Female", "Female", "Female", "Female", "Female", "F~
## $ Age               <dbl> 36, 27, 39, 36, 31, 32, 28, 37, 31, 25, 31, 24, 35, ~
## $ Employment_status <chr> "Other", "Unemployed", "Other", "Unemployed", "Unemp~
## $ CD4_recent        <dbl> 391, 571, 591, 207, 126, 225, 543, 410, 74, 212, 579~
## $ ART_currently     <chr> "Yes", "Yes", "Yes", "Yes", "Yes", "Yes", "Yes", "Ye~
## $ Education         <chr> "Tertiary", "Secondary", "Secondary", "Primary", "Se~
```

```
demo %>%
    select(-ID, -Site) %>%
    mutate_if(is.character, factor) %>%
```

```
    skim()
```

Table 3: Data summary

Name	Piped data
Number of rows	596
Number of columns	6
Column type frequency:	
factor	4
numeric	2
Group variables	None

Variable type: factor

skim_variable	missing	complete	n_unique	top_counts
Sex	0	596	2	Fem: 481, Mal: 115
Employment_status	49	547	4	Une: 330, Ful: 131, Par: 52, Oth: 34
ART_currently	5	591	2	Yes: 460, No: 131
Education	37	559	3	Sec: 395, Pri: 99, Ter: 65

Variable type: numeric

skim_variable	missing	complete	mean	sd	p0	p25	p50	p75	p100
Age	8	588	37.28	9.06	19	31	36	42	76
CD4_recent	99	497	320.71	238.92	1	155	261	432	1232

2 Data analysis

2.1 Process data

```
# Remove upper_back (only one outcome -- no pain)
data <- data[, !(names(data) %in% c('Upper_back'))]

# Calculate number of sites per individual
pain_count <- data %>%
    # Format as long data
    pivot_longer(cols = -c(ID, Site),
                 names_to = 'pain_site',
                 values_to = 'pain_present') %>%
    group_by(ID) %>%
    summarise(Count = sum(pain_present == 'Yes', na.rm = TRUE))
```

```r
# Join datasets
analysis_set <- left_join(pain_count, demo)
```

2.2 Summary statistics

2.2.1 Total group

```r
analysis_set %>%
  select(Count) %>%
  skim()
```

Table 6: Data summary

Name	Piped data
Number of rows	596
Number of columns	1
Column type frequency:	
numeric	1
Group variables	None

Variable type: numeric

skim_variable	missing	complete	mean	sd	p0	p25	p50	p75	p100
Count	0	596	2.24	1.68	0	1	2	3	12

2.2.2 For each categorical variable

```r
analysis_set %>%
  select(Count, Sex) %>%
  group_by(Sex) %>%
  skim()
```

2.2.2.1 By sex

Table 8: Data summary

Name	Piped data
Number of rows	596
Number of columns	2
Column type frequency:	
numeric	1

Group variables	Sex

Variable type: numeric

skim_variable	Sex	missing	complete	mean	sd	p0	p25	p50	p75	p100
Count	Female	0	481	2.27	1.69	0	1	2	3	12
Count	Male	0	115	2.13	1.63	0	1	2	3	9

```
analysis_set %>%
  select(Count, ART_currently) %>%
  filter(complete.cases(.)) %>%
  group_by(ART_currently) %>%
  skim()
```

2.2.2.2 By HAART

Table 10: Data summary

Name	Piped data
Number of rows	591
Number of columns	2
Column type frequency:	
numeric	1
Group variables	ART_currently

Variable type: numeric

skim_variable	ART_currently	missing	complete	mean	sd	p0	p25	p50	p75	p100
Count	No	0	131	2.18	1.64	0	1	2	3	12
Count	Yes	0	460	2.27	1.70	0	1	2	3	9

```
analysis_set %>%
  select(Count, Education) %>%
  filter(complete.cases(.)) %>%
  group_by(Education) %>%
  skim()
```

2.2.2.3 By education

Table 12: Data summary

Name	Piped data
Number of rows	559
Number of columns	2
Column type frequency:	
numeric	1
Group variables	Education

Variable type: numeric

skim_variable	Education	missing	complete	mean	sd	p0	p25	p50	p75	p100
Count	Primary	0	99	2.38	1.64	0	1	2	3	8
Count	Secondary	0	395	2.24	1.73	0	1	2	3	12
Count	Tertiary	0	65	2.06	1.52	0	1	2	3	6

```
analysis_set %>%
  select(Count, Employment_status) %>%
  filter(complete.cases(.)) %>%
  group_by(Employment_status) %>%
  skim()
```

2.2.2.4 By employment status

Table 14: Data summary

Name	Piped data
Number of rows	547
Number of columns	2
Column type frequency:	
numeric	1
Group variables	Employment_status

Variable type: numeric

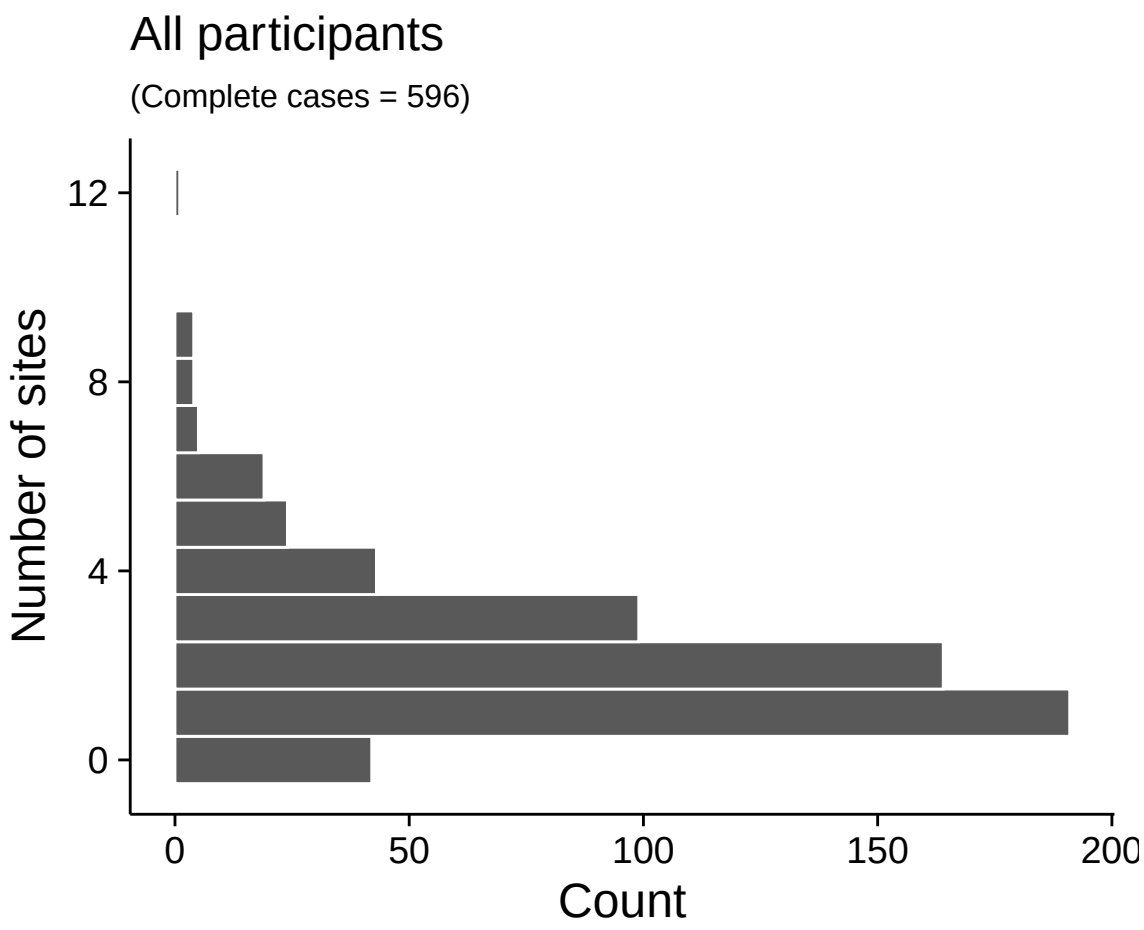
skim_variable	Employment_status	missing	complete	mean	sd	p0	p25	p50	p75	p100
Count	Full-time work	0	131	2.21	1.46	0	1	2	3	6
Count	Other	0	34	2.18	1.64	0	1	2	4	5
Count	Part-time work	0	52	2.50	1.89	0	1	2	3	9

skim_variable	Employment_status	missing	complete	mean	sd	p0	p25	p50	p75	p100
Count	Unemployed	0	330	2.21	1.75	0	1	2	3	12

2.3 Exploratory plots

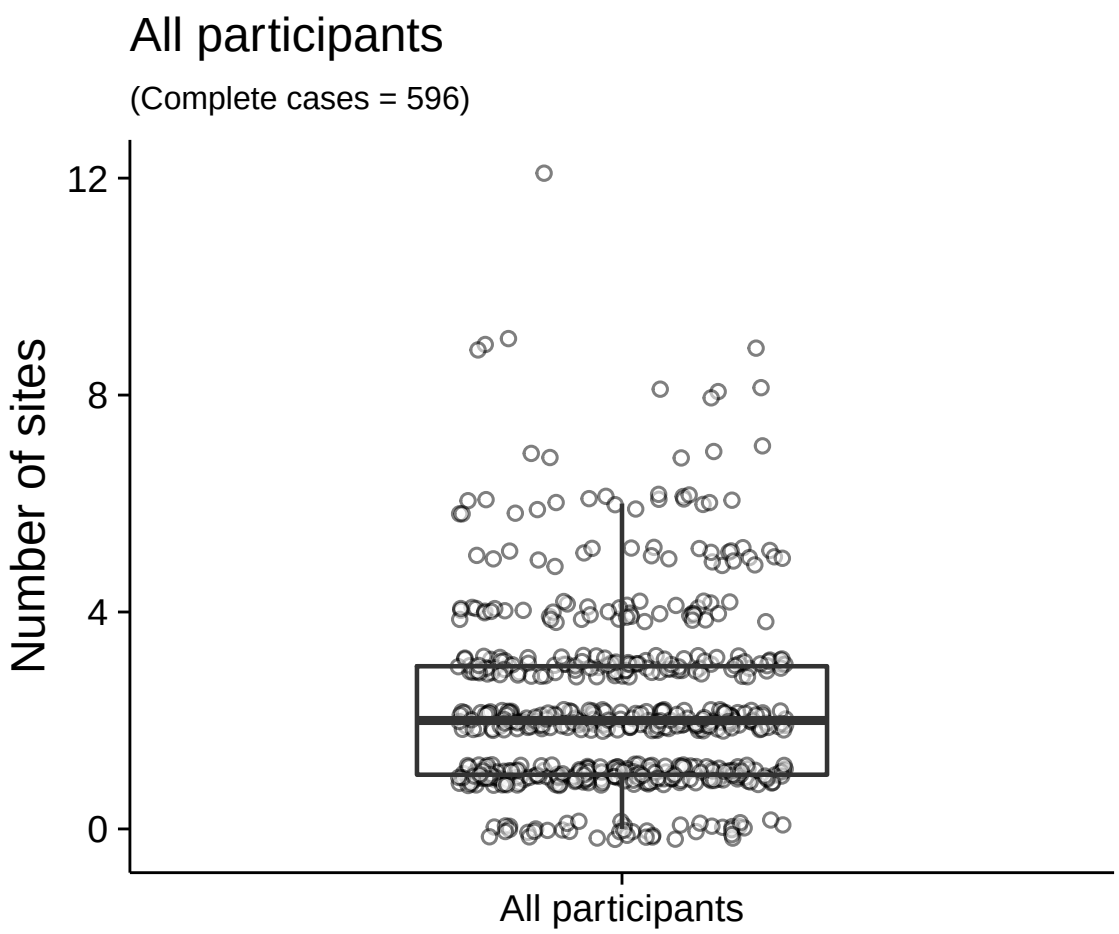
2.3.1 Overall count frequency

```
all <- analysis_set %>%
    select(Count) %>%
    filter(complete.cases(.)) %>%
    ggplot(data = .) +
    aes(Count) +
    geom_histogram(binwidth = 1,
                   colour = '#FFFFFF') +
    labs(title = 'All participants',
         subtitle = str_glue('(Complete cases = {nrow(analysis_set[!is.na(
                             analysis_set$Count), ])})'),
         x = 'Number of sites',
         y = 'Count') +
    coord_flip() +
    theme_minimal(base_size = 18) +
    theme(plot.title = element_text(size = 18),
          plot.subtitle = element_text(size = 12),
          panel.grid = element_blank(),
          axis.text = element_text(colour = '#000000'),
          axis.line = element_line(size = 0.5),
          axis.ticks = element_line(size = 0.5)); all
```




```
all <- analysis_set %>%
    select(Count) %>%
    filter(complete.cases(.)) %>%
    ggplot(data = .) +
    aes(y = Count,
        x = 'All participants') +
    geom_point(size = 2,
               shape = 21,
               position = position_jitter(height = 0.2, width = 0.2),
               fill = '#FFFFFF',
               colour = '#000000',
               stroke = 0.8,
               alpha = 0.5) +
    geom_boxplot(outlier.colour = '#FFFFFF',
                 outlier.size = 0,
                 width = 0.5,
                 size = 0.8,
                 alpha = 0) +
    labs(title = 'All participants',
         subtitle = str_glue('(Complete cases = {nrow(analysis_set[!is.na(
                             analysis_set$Count), ])})'),
         y = 'Number of sites') +
    theme_minimal(base_size = 18) +
    theme(plot.title = element_text(size = 18),
          plot.subtitle = element_text(size = 12),
```

```
        plot.caption = element_text(size = 12),
        panel.grid = element_blank(),
        axis.title.x = element_blank(),
        axis.text = element_text(colour = '#000000'),
        axis.line = element_line(size = 0.5),
        axis.ticks = element_line(size = 0.5)); all
```

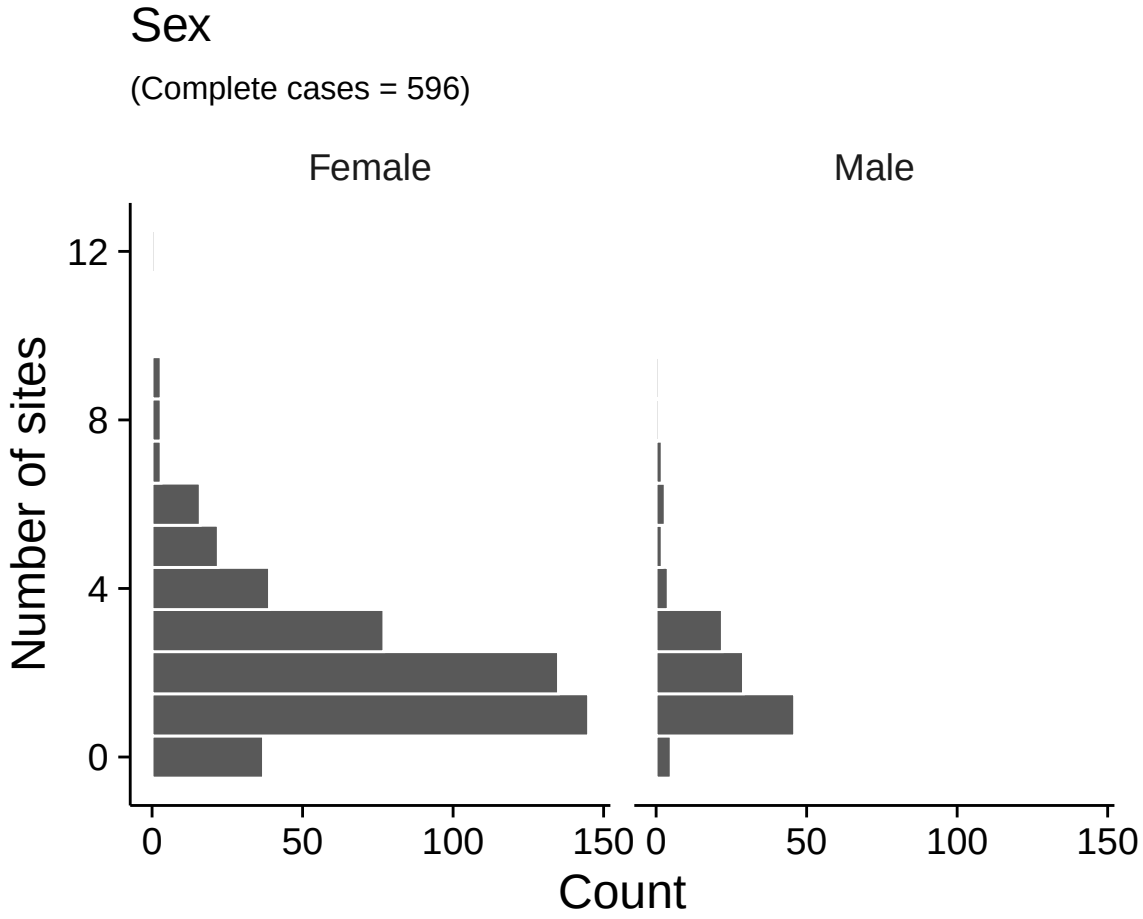


2.3.2 For each categorical variable

```
analysis_set %>%
    select(Count, Sex) %>%
    filter(complete.cases(.)) %>%
    ggplot(data = .) +
    aes(Count) +
    geom_histogram(binwidth = 1,
                   colour = '#FFFFFF') +
    labs(title = 'Sex',
         subtitle = str_glue('(Complete cases = {nrow(analysis_set[!is.na(
                             analysis_set$Sex), ])})'),
         x = 'Number of sites',
         y = 'Count') +
    facet_wrap(~Sex) +
```

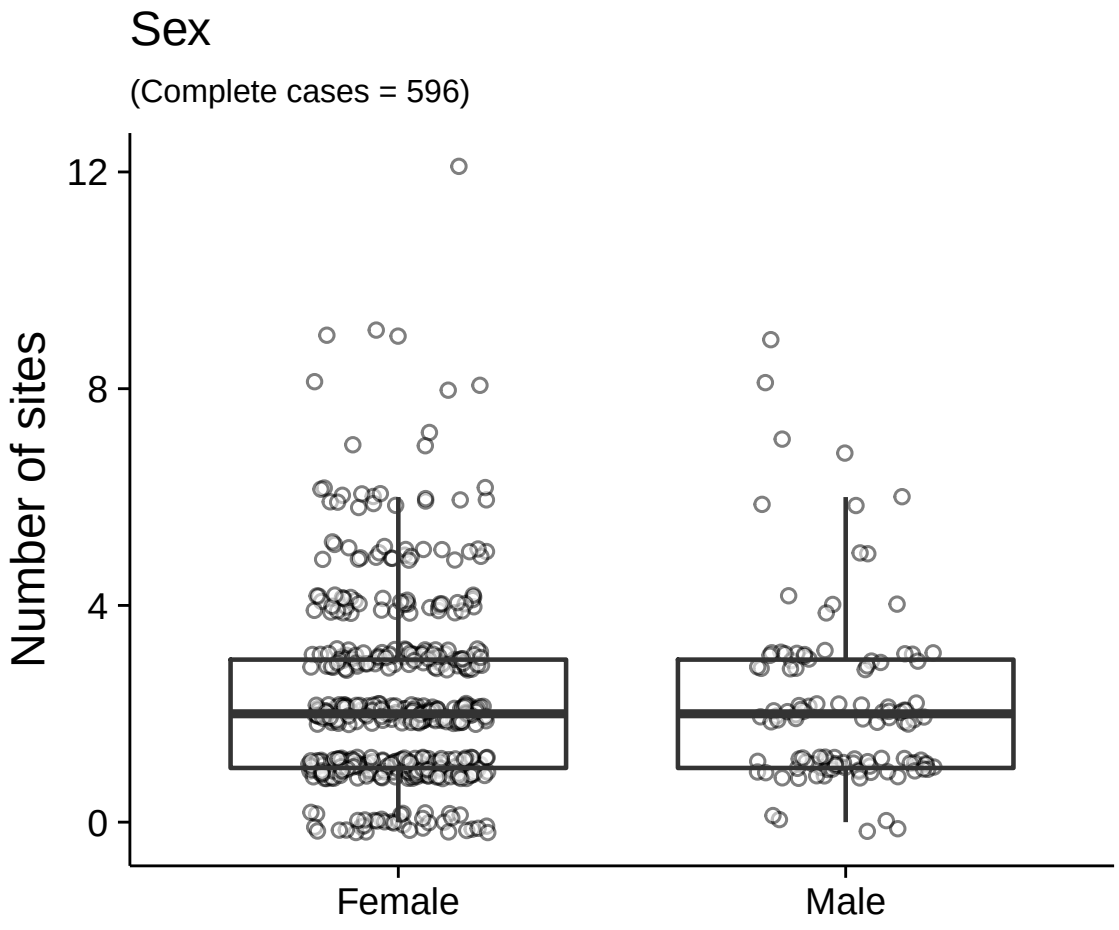
```
    coord_flip() +
    theme_minimal(base_size = 18) +
    theme(plot.title = element_text(size = 18),
          plot.subtitle = element_text(size = 12),
          panel.grid = element_blank(),
          axis.text = element_text(colour = '#000000'),
          axis.line = element_line(size = 0.5),
          axis.ticks = element_line(size = 0.5))
```

2.3.2.1 Count by sex




```
sex <- analysis_set %>%
    select(Count, Sex) %>%
    filter(complete.cases(.)) %>%
    ggplot(data = .) +
    aes(y = Count,
        x = Sex) +
    geom_point(size = 2,
               shape = 21,
               position = position_jitter(height = 0.2, width = 0.2),
               fill = '#FFFFFF',
               colour = '#000000',
               stroke = 0.8,
               alpha = 0.5) +
    geom_boxplot(outlier.colour = '#FFFFFF',
```

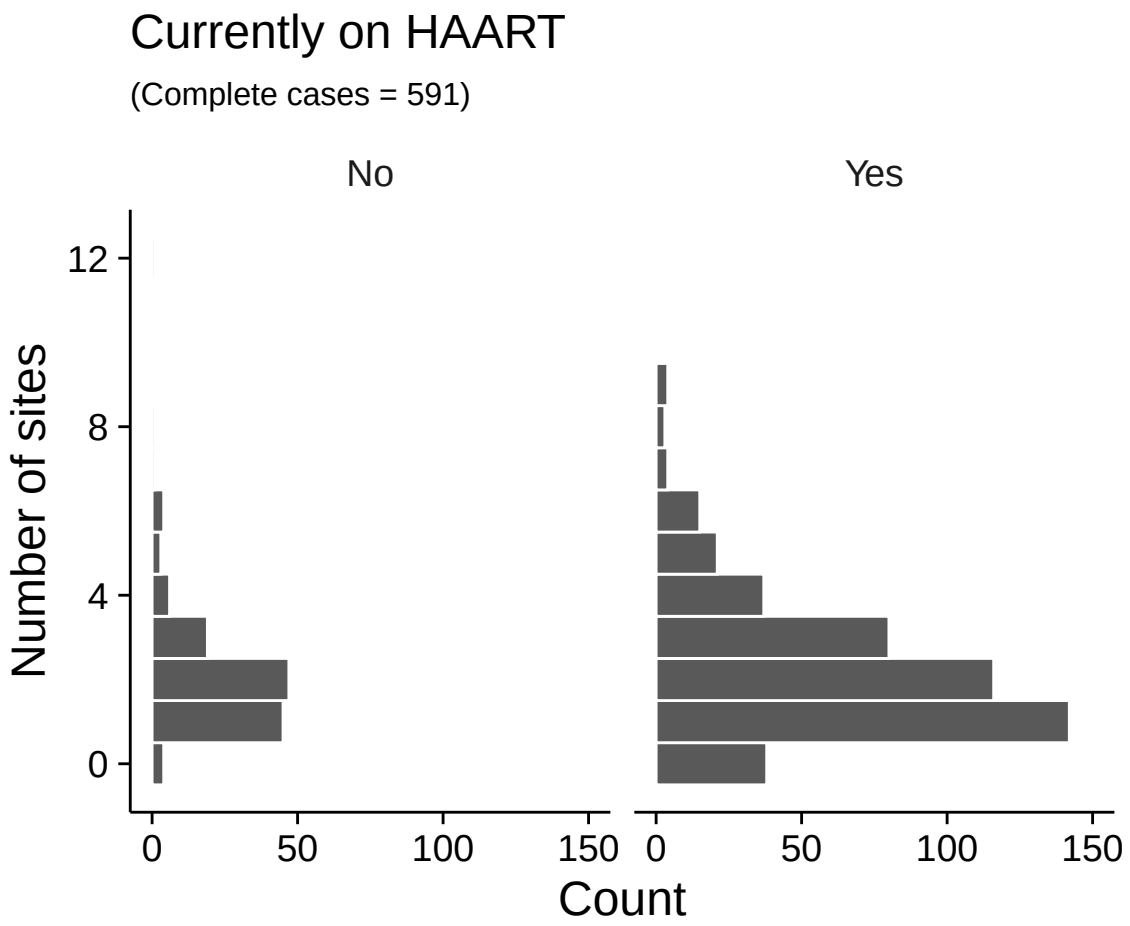
```
                outlier.size = 0,
                size = 0.8,
                alpha = 0) +
    scale_x_discrete(labels = c('Female', 'Male')) +
    labs(title = 'Sex',
         subtitle = str_glue('(Complete cases = {nrow(analysis_set[!is.na(
                             analysis_set$Sex), ])})'),
         y = 'Number of sites') +
    theme_minimal(base_size = 18) +
    theme(plot.title = element_text(size = 18),
          plot.subtitle = element_text(size = 12),
          plot.caption = element_text(size = 12),
          panel.grid = element_blank(),
          axis.title.x = element_blank(),
          axis.text = element_text(colour = '#000000'),
          axis.line = element_line(size = 0.5),
          axis.ticks = element_line(size = 0.5)); sex
```




```
analysis_set %>%
    select(Count, ART_currently) %>%
    filter(complete.cases(.)) %>%
    ggplot(data = .) +
    aes(Count) +
```

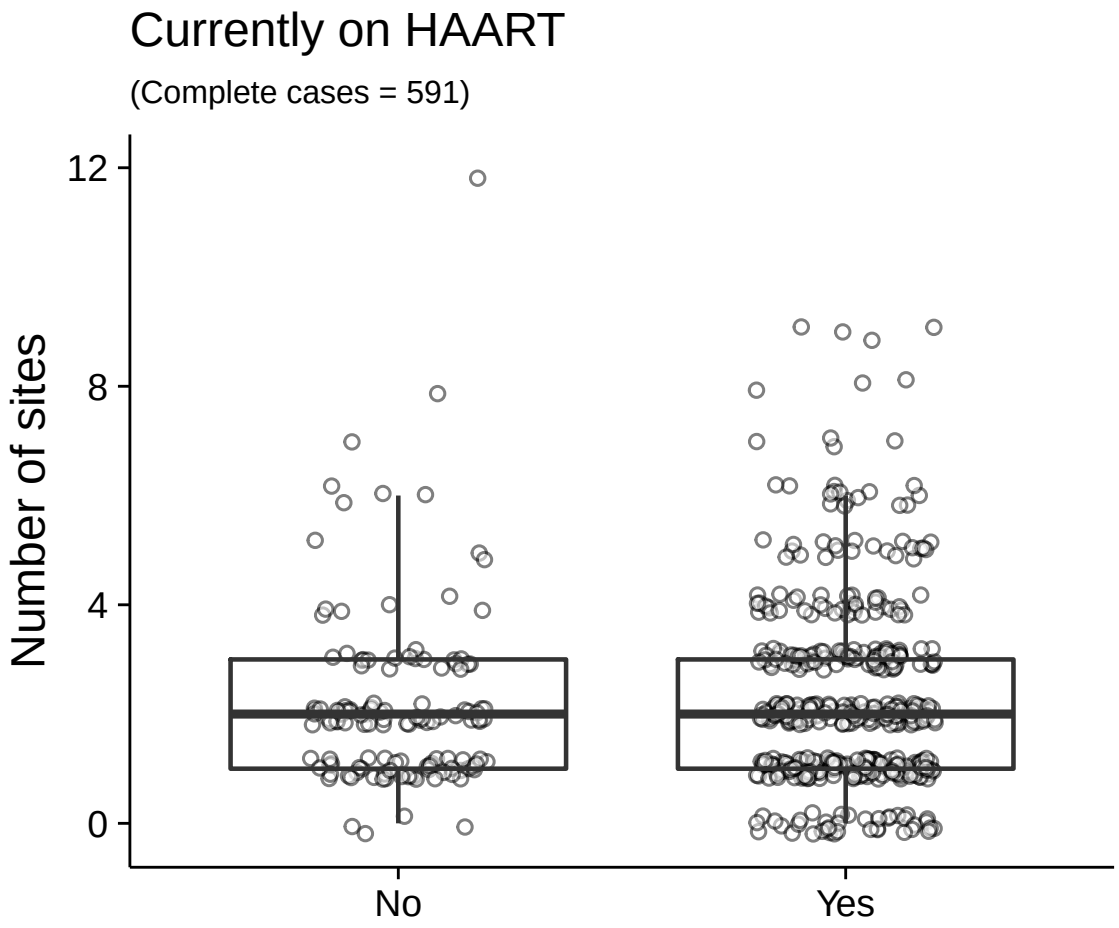
```
    geom_histogram(binwidth = 1,
                   colour = '#FFFFFF') +
    scale_y_continuous(limits = c(0, 150),
                       breaks = c(0, 50, 100, 150)) +
    labs(title = 'Currently on HAART',
         subtitle = str_glue('(Complete cases = {nrow(analysis_set[!is.na(
                             analysis_set$ART_currently), ])})'),
         x = 'Number of sites',
         y = 'Count') +
    facet_wrap(~ART_currently) +
    coord_flip() +
    theme_minimal(base_size = 18) +
    theme(plot.title = element_text(size = 18),
          plot.subtitle = element_text(size = 12),
          panel.grid = element_blank(),
          axis.text = element_text(colour = '#000000'),
          axis.line = element_line(size = 0.5),
          axis.ticks = element_line(size = 0.5))
```

2.3.2.2 Count by HAART



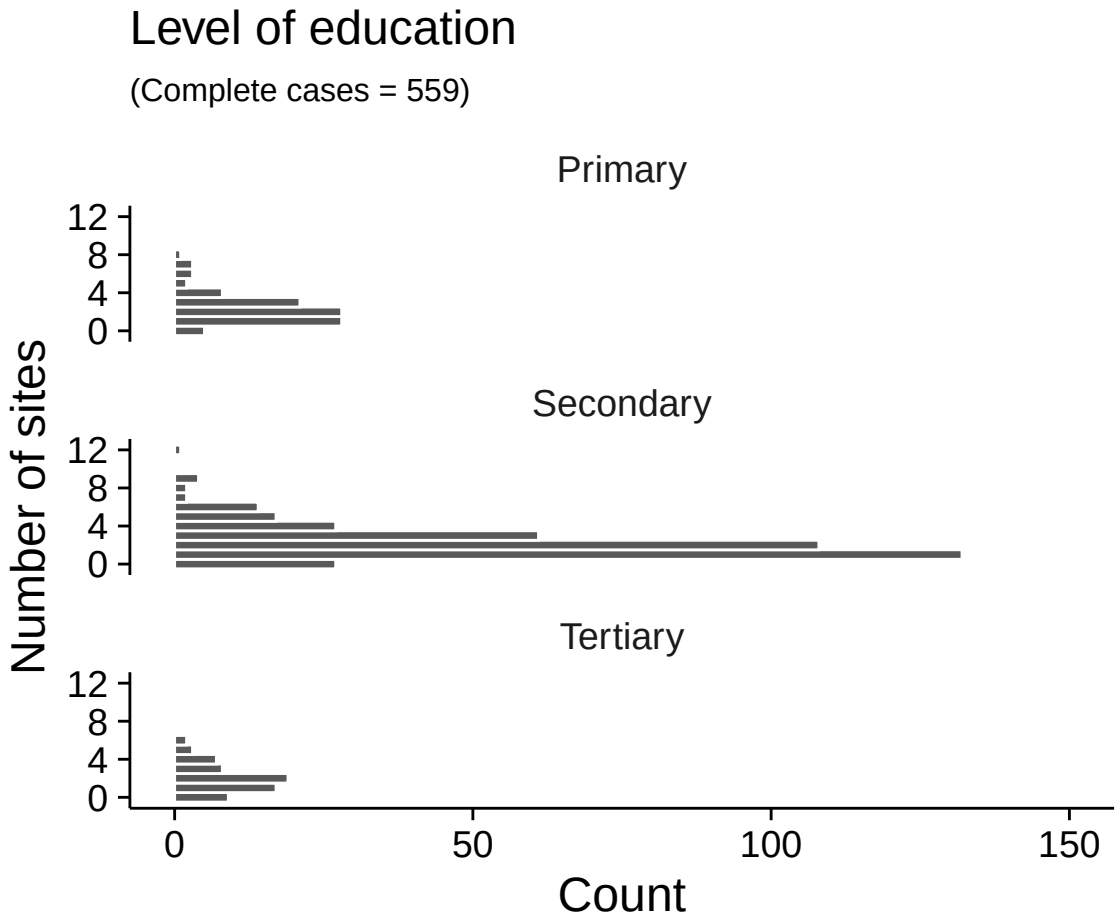

```
haart <- analysis_set %>%
    select(Count, ART_currently) %>%
    filter(complete.cases(.)) %>%
    ggplot(data = .) +
```

```
    aes(y = Count,
        x = ART_currently) +
    geom_point(size = 2,
               shape = 21,
               position = position_jitter(height = 0.2, width = 0.2),
               fill = '#FFFFFF',
               colour = '#000000',
               stroke = 0.8,
               alpha = 0.5) +
    geom_boxplot(outlier.colour = '#FFFFFF',
                 outlier.size = 0,
                 size = 0.8,
                 alpha = 0) +
    scale_x_discrete(labels = c('No', 'Yes')) +
    labs(title = 'Currently on HAART',
         subtitle = str_glue('(Complete cases = {nrow(analysis_set[!is.na(
                             analysis_set$ART_currently), ])})'),
         y = 'Number of sites') +
    theme_minimal(base_size = 18) +
    theme(plot.title = element_text(size = 18),
          plot.subtitle = element_text(size = 12),
          plot.caption = element_text(size = 12),
          panel.grid = element_blank(),
          axis.title.x = element_blank(),
          axis.text = element_text(colour = '#000000'),
          axis.line = element_line(size = 0.5),
          axis.ticks = element_line(size = 0.5)); haart
```



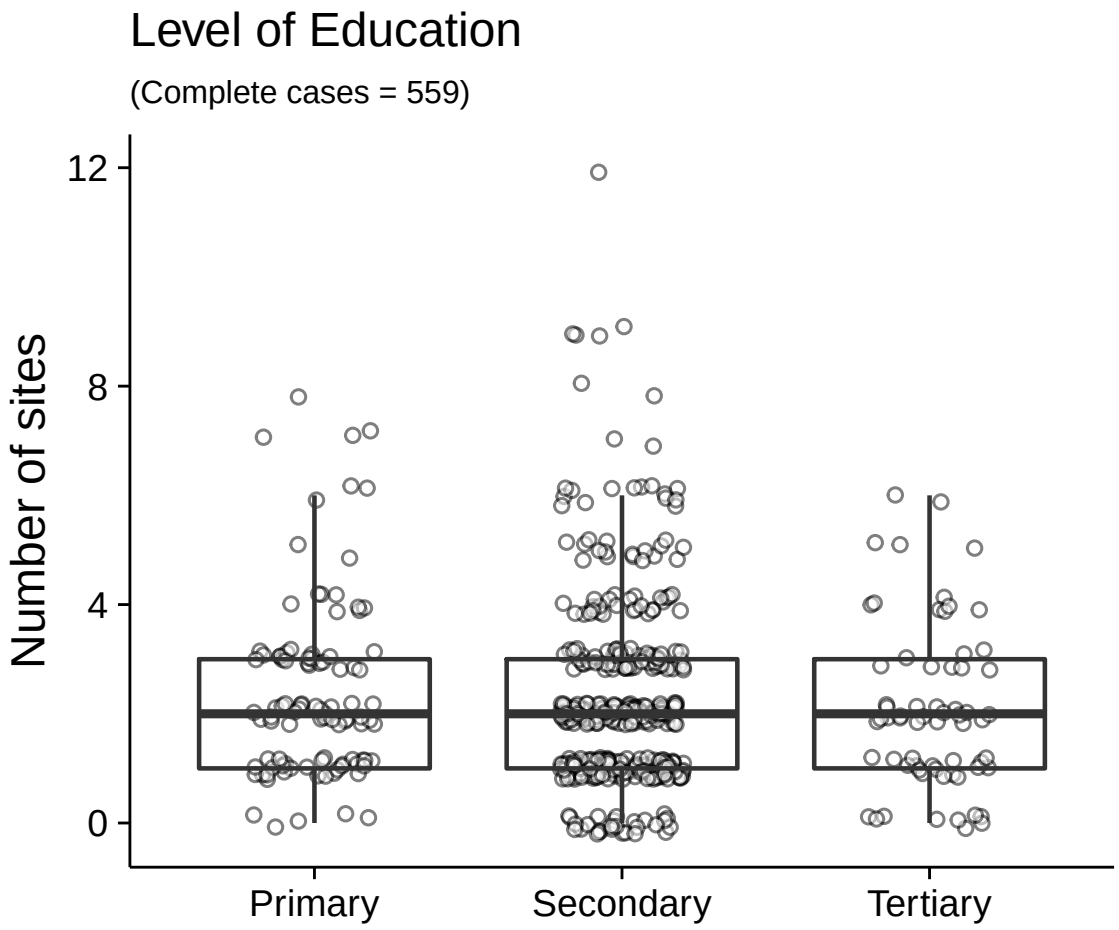

```
analysis_set %>%
    select(Count, Education) %>%
    filter(complete.cases(.)) %>%
    ggplot(data = .) +
    aes(Count) +
    geom_histogram(binwidth = 1,
                   colour = '#FFFFFF') +
    scale_y_continuous(limits = c(0, 150),
                       breaks = c(0, 50, 100, 150)) +
    labs(title = 'Level of education',
         subtitle = str_glue('(Complete cases = {nrow(analysis_set[!is.na(
                             analysis_set$Education), ])})'),
         x = 'Number of sites',
         y = 'Count') +
    facet_wrap(~Education, ncol = 1) +
    coord_flip() +
    theme_minimal(base_size = 18) +
    theme(plot.title = element_text(size = 18),
          plot.subtitle = element_text(size = 12),
          panel.grid = element_blank(),
          axis.text = element_text(colour = '#000000'),
          axis.line = element_line(size = 0.5),
          axis.ticks = element_line(size = 0.5))
```

2.3.2.3 Count education




```
edu <- analysis_set %>%
    select(Count, Education) %>%
    filter(complete.cases(.)) %>%
    ggplot(data = .) +
    aes(y = Count,
        x = Education) +
    geom_point(size = 2,
               shape = 21,
               position = position_jitter(height = 0.2, width = 0.2),
               fill = '#FFFFFF',
               colour = '#000000',
               stroke = 0.8,
               alpha = 0.5) +
    geom_boxplot(outlier.colour = '#FFFFFF',
                 outlier.size = 0,
                 size = 0.8,
                 alpha = 0) +
    scale_x_discrete(labels = c('Primary', 'Secondary',
                                'Tertiary')) +
    labs(title = 'Level of Education',
         subtitle = str_glue('(Complete cases = {nrow(analysis_set[!is.na(
                             analysis_set$Education), ])})'),
```

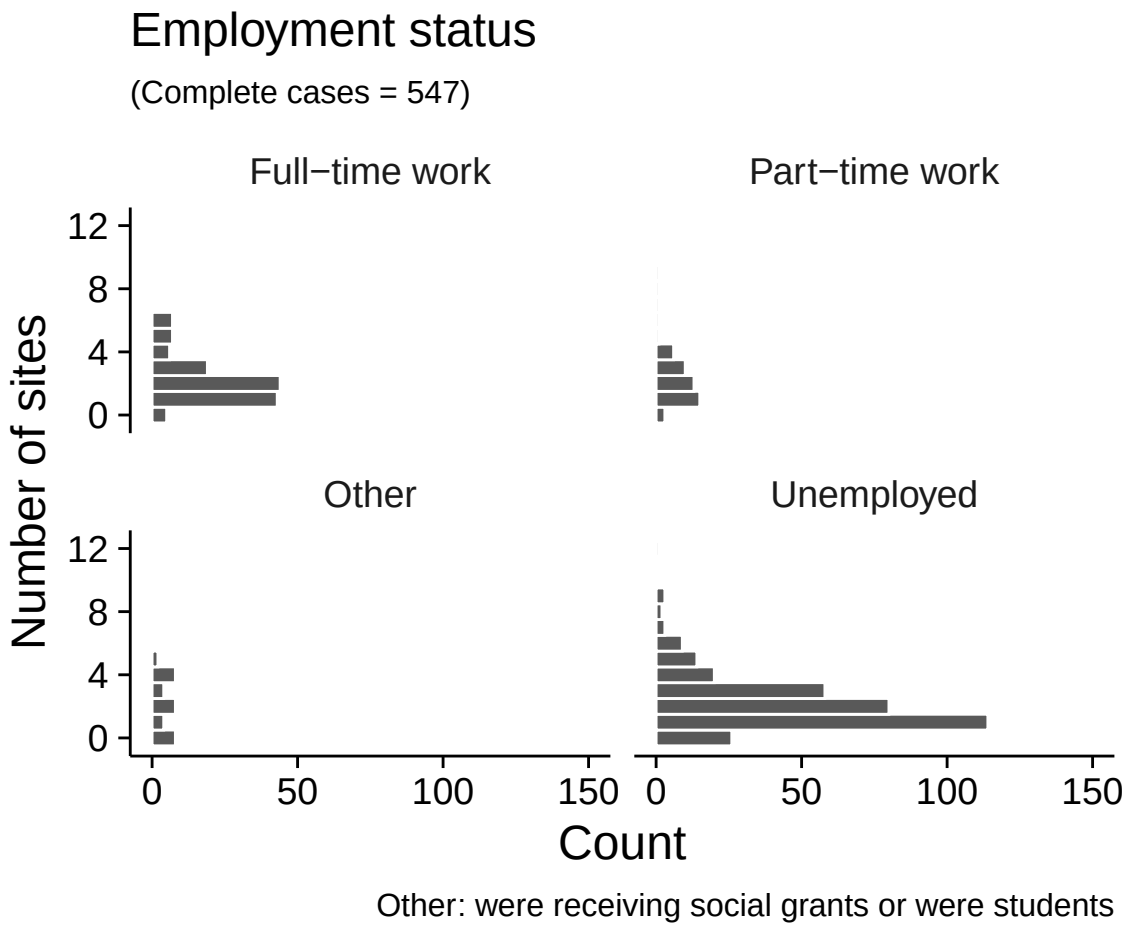
```
        y = 'Number of sites') +
    theme_minimal(base_size = 18) +
    theme(plot.title = element_text(size = 18),
          plot.subtitle = element_text(size = 12),
          plot.caption = element_text(size = 12),
          panel.grid = element_blank(),
          axis.title.x = element_blank(),
          axis.text = element_text(colour = '#000000'),
          axis.line = element_line(size = 0.5),
          axis.ticks = element_line(size = 0.5)); edu
```




```
analysis_set %>%
    select(Count, Employment_status) %>%
    filter(complete.cases(.)) %>%
    mutate(Employment_status = factor(Employment_status,
                                      levels = c('Full-time work',
                                                 'Part-time work',
                                                 'Other',
                                                 'Unemployed'),
                                      ordered = TRUE)) %>%
    ggplot(data = .) +
    aes(Count) +
```

```
    geom_histogram(binwidth = 1,
                   colour = '#FFFFFF') +
    scale_y_continuous(limits = c(0, 150),
                       breaks = c(0, 50, 100, 150)) +
    labs(title = 'Employment status',
         subtitle = str_glue('(Complete cases = {nrow(analysis_set[!is.na(
                             analysis_set$Employment_status), ])})'),
         caption = 'Other: were receiving social grants or were students',
         x = 'Number of sites',
         y = 'Count') +
    facet_wrap(~Employment_status, ncol = 2) +
    coord_flip() +
    theme_minimal(base_size = 18) +
    theme(plot.title = element_text(size = 18),
          plot.subtitle = element_text(size = 12),
          plot.caption = element_text(size = 12),
          panel.grid = element_blank(),
          axis.text = element_text(colour = '#000000'),
          axis.line = element_line(size = 0.5),
          axis.ticks = element_line(size = 0.5))
```

2.3.2.4 Count by employment status




```
employment <- analysis_set %>%
```

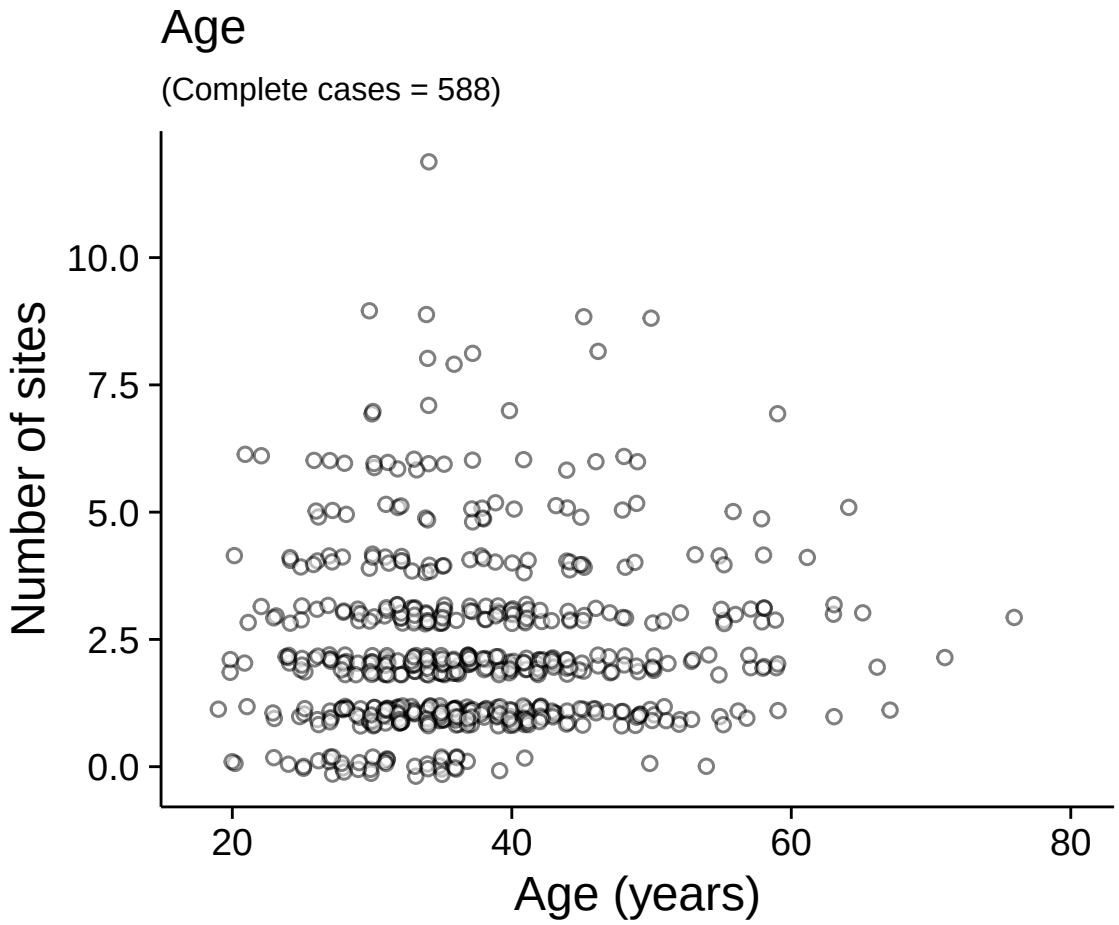
```
    select(Count, Employment_status) %>%
    filter(complete.cases(.)) %>%
    mutate(Employment_status = factor(Employment_status,
                                      levels = c('Full-time work',
                                                 'Part-time work',
                                                 'Other',
                                                 'Unemployed'),
                                      ordered = TRUE)) %>%
    ggplot(data = .) +
    aes(y = Count,
        x = Employment_status) +
    geom_point(size = 2,
               shape = 21,
               position = position_jitter(height = 0.2, width = 0.2),
               fill = '#FFFFFF',
               colour = '#000000',
               stroke = 0.8,
               alpha = 0.5) +
    geom_boxplot(outlier.colour = '#FFFFFF',
                 outlier.size = 0,
                 size = 0.8,
                 alpha = 0) +
    scale_x_discrete(labels = c('Full-time\nwork', 'Part-time\nwork',
                                'Other', 'Unemployed')) +
    labs(title = 'Employment status',
         subtitle = str_glue('(Complete cases = {nrow(analysis_set[!is.na(
                             analysis_set$Employment_status), ])})'),
         caption = 'Other: were receiving social grants or were students',
         y = 'Number of sites') +
    theme_minimal(base_size = 18) +
    theme(plot.title = element_text(size = 18),
          plot.subtitle = element_text(size = 12),
          plot.caption = element_text(size = 12),
          panel.grid = element_blank(),
          axis.title.x = element_blank(),
          axis.text = element_text(colour = '#000000'),
          axis.line = element_line(size = 0.5),
          axis.ticks = element_line(size = 0.5)); employment
```

2.3.3 Continuous variables

```
age <- analysis_set %>%
    select(Count, Age) %>%
    filter(complete.cases(.)) %>%
    ggplot(data = .) +
    aes(y = Count,
        x = Age) +
    geom_point(size = 2,
               shape = 21,
               position = position_jitter(height = 0.2, width = 0.2),
               fill = '#FFFFFF',
               colour = '#000000',
               stroke = 0.8,
               alpha = 0.5) +
    labs(title = 'Age',
         subtitle = str_glue('(Complete cases = {nrow(analysis_set[!is.na(
                             analysis_set$Age), ])})'),
         x = 'Age (years)',
         y = 'Number of sites') +
    scale_x_continuous(limits = c(18, 80),
                       breaks = seq(20, 80, by = 20)) +
```

```
    theme_minimal(base_size = 18) +
    theme(plot.title = element_text(size = 18),
          plot.subtitle = element_text(size = 12),
          plot.caption = element_text(size = 12),
          panel.grid = element_blank(),
          axis.text = element_text(colour = '#000000'),
          axis.line = element_line(size = 0.5),
          axis.ticks = element_line(size = 0.5)); age
```

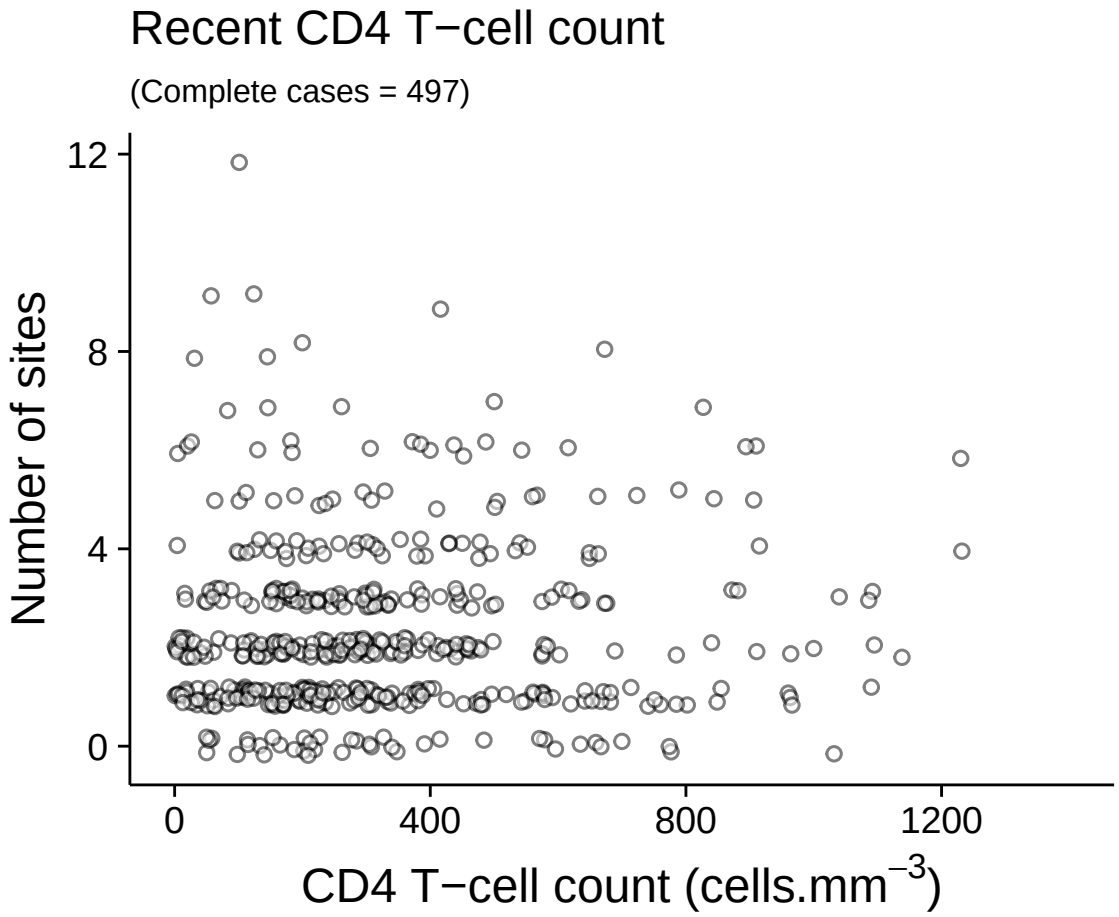
2.3.3.1 Age




```
cd4 <- analysis_set %>%
    select(Count, CD4_recent) %>%
    filter(complete.cases(.)) %>%
    ggplot(data = .) +
    aes(y = Count,
        x = CD4_recent) +
    geom_point(size = 2,
               shape = 21,
               position = position_jitter(height = 0.2, width = 0.2),
               fill = '#FFFFFF',
               colour = '#000000',
```

```
              stroke = 0.8,
              alpha = 0.5) +
  labs(title = 'Recent CD4 T-cell count',
       subtitle = str_glue('(Complete cases = {nrow(analysis_set[!is.na(
                           analysis_set$CD4_recent), ])})'),
       x = expression('CD4 T-cell count (cells.mm'^-3*')'),
       y = 'Number of sites') +
  scale_x_continuous(limits = c(0, 1400),
                     breaks = seq(0, 1400, by = 400)) +
  scale_y_continuous(breaks = seq(0, 12, 4)) +
  theme_minimal(base_size = 18) +
  theme(plot.title = element_text(size = 18),
        plot.subtitle = element_text(size = 12),
        plot.caption = element_text(size = 12),
        panel.grid = element_blank(),
        axis.text = element_text(colour = '#000000'),
        axis.line = element_line(size = 0.5),
        axis.ticks = element_line(size = 0.5)); cd4
```

2.3.3.2 Current CD4 T-cell count



2.4 Regression analysis

2.4.1 Process data

```
analysis_set <- analysis_set %>%
    # Re-factor Employment_status
    mutate(Employment_status = case_when(
        Employment_status == 'Unemployed' ~ ' 1_unemployed',
        Employment_status == 'Part-time work' ~ ' 3_employed PT',
        Employment_status == 'Full-time work' ~ ' 2_employed FT',
        Employment_status == 'Other' ~ ' 4_other'
    )) %>%
    filter(complete.cases(.))
```

2.4.2 Negative binomial regression for count data

```
# Full model
mod.nb <- glm.nb(Count ~ Sex +
                   Age +
                   CD4_recent +
                   Employment_status +
                   Education +
                   ART_currently,
                 data = analysis_set)

# Summary of coefficients
cbind(Estimate = coef(mod.nb)[-1],
      confint(mod.nb)[-1, ],
      summary(mod.nb)$coefficients[-1, 3:4]) %>%
    kable(caption = 'Coefficients and 95% CI',
          digits = 3,
          col.names = c('Estimate', 'Lower 95%CI', 'Upper 95%CI',
                        'z-value', 'P-value'))
```

Table 16: Coefficients and 95% CI

	Estimate	Lower 95%CI	Upper 95%CI	z-value	P-value
SexMale	-0.104	-0.302	0.089	-1.046	0.296
Age	0.010	0.001	0.018	2.159	0.031
CD4_recent	0.000	0.000	0.000	0.733	0.463
Employment_status 2_employed FT	-0.004	-0.182	0.172	-0.044	0.965
Employment_status 3_employed PT	0.195	-0.043	0.427	1.627	0.104
Employment_status 4_other	0.012	-0.270	0.284	0.088	0.930
EducationSecondary	-0.055	-0.245	0.139	-0.558	0.577
EducationTertiary	-0.183	-0.460	0.091	-1.302	0.193
ART_currentlyYes	0.041	-0.142	0.228	0.435	0.663

```
# Summary of exponentiated coefficients (incidence rate ratios)
cbind(Estimate = exp(coef(mod.nb))[-1],
      exp(confint(mod.nb))[-1, ],
      summary(mod.nb)$coefficients[-1, 3:4]) %>%
```

```
    kable(caption = 'Exponentiate coefficients and 95% CI (incidence rate ratios)',
          digits = 3,
          col.names = c('Estimate', 'Lower 95%CI', 'Upper 95%CI',
                        'z-value', 'P-value'))
```

Table 17: Exponentiate coefficients and 95% CI (incidence rate ratios)

	Estimate	Lower 95%CI	Upper 95%CI	z-value	P-value
SexMale	0.901	0.740	1.093	-1.046	0.296
Age	1.010	1.001	1.018	2.159	0.031
CD4_recent	1.000	1.000	1.000	0.733	0.463
Employment_status 2_employed FT	0.996	0.833	1.187	-0.044	0.965
Employment_status 3_employed PT	1.215	0.958	1.532	1.627	0.104
Employment_status 4_other	1.013	0.763	1.328	0.088	0.930
EducationSecondary	0.947	0.783	1.149	-0.558	0.577
EducationTertiary	0.833	0.631	1.095	-1.302	0.193
ART_currentlyYes	1.042	0.868	1.256	0.435	0.663

2.5 Publication plot

```
# Fix figures for patchwork plot
all2 <- all

sex2 <- sex +
  theme(axis.title.y = element_blank())

haart2 <- haart

employment2 <- employment

edu2 <- edu +
  theme(axis.title.y = element_blank())

age2 <- age +
  theme(axis.title.y = element_blank())

cd42 <- cd4

pubs <- all2 + sex2 + haart2 + edu2 + employment2 + age2 + cd42 +
  plot_layout(ncol = 2)

ggsave(filename = 'figures/figure_2.png',
       width = 10,
       height = 18)
```

3 Session information

```
sessionInfo()
```

```
## R version 4.0.4 (2021-02-15)
## Platform: x86_64-apple-darwin17.0 (64-bit)
## Running under: macOS Catalina 10.15.7
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/4.0/Resources/lib/libRblas.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.0/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
##  [1] patchwork_1.1.1 knitr_1.31      skimr_2.1.3     forcats_0.5.1
##  [5] stringr_1.4.0   dplyr_1.0.5     purrr_0.3.4     readr_1.4.0
##  [9] tidyr_1.1.3     tibble_3.1.0    ggplot2_3.3.3   tidyverse_1.3.0
## [13] MASS_7.3-53.1
##
## loaded via a namespace (and not attached):
##  [1] tidyselect_1.1.0  xfun_0.22         repr_1.1.3        haven_2.3.1
##  [5] colorspace_2.0-0  vctrs_0.3.6       generics_0.1.0    htmltools_0.5.1.1
##  [9] base64enc_0.1-3   yaml_2.2.1        utf8_1.2.1        rlang_0.4.10
## [13] pillar_1.5.1      glue_1.4.2        withr_2.4.1       DBI_1.1.1
## [17] dbplyr_2.1.0      modelr_0.1.8      readxl_1.3.1      lifecycle_1.0.0
## [21] munsell_0.5.0     gtable_0.3.0      cellranger_1.1.0  rvest_1.0.0
## [25] evaluate_0.14     labeling_0.4.2    fansi_0.4.2       highr_0.8
## [29] broom_0.7.5       Rcpp_1.0.6        scales_1.1.1      backports_1.2.1
## [33] jsonlite_1.7.2    farver_2.1.0      fs_1.5.0          hms_1.0.0
## [37] digest_0.6.27     stringi_1.5.3     grid_4.0.4        cli_2.3.1
## [41] tools_4.0.4       magrittr_2.0.1    crayon_1.4.1      pkgconfig_2.0.3
## [45] ellipsis_0.3.1    xml2_1.3.2        reprex_1.0.0      lubridate_1.7.10
## [49] assertthat_0.2.1  rmarkdown_2.7     httr_1.4.2        rstudioapi_0.13
## [53] R6_2.5.0          compiler_4.0.4
```