data_analysis

2023-05-11

Import data

```
pmd <- read.csv("../../data/pmd-en.csv")
head(pmd, 3)
```

```
##         DBUID DBPOP    DAUID DAPOP  CSDUID    CSDNAME CSDTYPE  CSDPOP CMAUID
## 1 10010165001   160 10010165   506 1001519 St. John's      CY 108,860      1
## 2 10010165002    25 10010165   506 1001519 St. John's      CY 108,860      1
## 3 10010165006   268 10010165   506 1001519 St. John's      CY 108,860      1
##   CMAPUID    CMANAME CMATYPE  CMAPOP PRUID
## 1   10001 St. John's       B 205,955    10
## 2   10001 St. John's       B 205,955    10
## 3   10001 St. John's       B 205,955    10
##                                             PRNAME   PRPOP      lon     lat
## 1 Newfoundland and Labrador / Terre-Neuve-et-Labrador 519,716 -52.7765 47.5300
## 2 Newfoundland and Labrador / Terre-Neuve-et-Labrador 519,716 -52.7793 47.5290
## 3 Newfoundland and Labrador / Terre-Neuve-et-Labrador 519,716 -52.7768 47.5265
##   in_db_emp prox_idx_emp in_db_pharma prox_idx_pharma in_db_childcare
## 1         1       0.0202            0          0.0121               0
## 2         1       0.0193            0           0.014               0
## 3         1       0.0199            1          0.0205               1
##   prox_idx_childcare in_db_health prox_idx_health in_db_grocery
## 1             0.0402            0          0.0069             0
## 2             0.0257            0          0.0028             0
## 3             0.0395            1           0.007             0
##   prox_idx_grocery in_db_educpri prox_idx_educpri in_db_educsec
## 1               ..             0           0.0384             0
## 2               ..             0           0.0562             0
## 3               ..             0           0.0734             0
##   prox_idx_educsec in_db_lib prox_idx_lib in_db_parks prox_idx_parks
## 1           0.0495         0       0.0486           0         0.0141
## 2           0.0375         0           ..           0             ..
## 3           0.0436         0       0.0545           0             ..
##   in_db_transit prox_idx_transit transit_na amenity_dense suppressed
## 1             1           0.0058          0             0          0
## 2             0           0.0046          0             0          0
## 3             1           0.0101          0             0          0
```

DATA Summary

```r
# no. of rows and columns
dim(pmd)
```

```
## [1] 489676     41
```

489676 rows and 41 columns

```r
# dataset summary
str(pmd)
```

```
## 'data.frame':    489676 obs. of  41 variables:
##  $ DBUID             : num  1e+10 1e+10 1e+10 1e+10 1e+10 ...
##  $ DBPOP             : chr  "160" "25" "268" "53" ...
##  $ DAUID             : int  10010165 10010165 10010165 10010165 10010166 10010166 10010166 10010167 1
##  $ DAPOP             : chr  "506" "506" "506" "506" ...
##  $ CSDUID            : int  1001519 1001519 1001519 1001519 1001519 1001519 1001519 1001519 1001519 1
##  $ CSDNAME           : chr  "St. John's" "St. John's" "St. John's" "St. John's" ...
##  $ CSDTYPE           : chr  "CY" "CY" "CY" "CY" ...
##  $ CSDPOP            : chr  "108,860" "108,860" "108,860" "108,860" ...
##  $ CMAUID            : int  1 1 1 1 1 1 1 1 1 1 ...
##  $ CMAPUID           : int  10001 10001 10001 10001 10001 10001 10001 10001 10001 10001 ...
##  $ CMANAME           : chr  "St. John's" "St. John's" "St. John's" "St. John's" ...
##  $ CMATYPE           : chr  "B" "B" "B" "B" ...
##  $ CMAPOP            : chr  "205,955" "205,955" "205,955" "205,955" ...
##  $ PRUID             : int  10 10 10 10 10 10 10 10 10 10 ...
##  $ PRNAME            : chr  "Newfoundland and Labrador / Terre-Neuve-et-Labrador" "Newfoundland and L
##  $ PRPOP             : chr  "519,716" "519,716" "519,716" "519,716" ...
##  $ lon               : num  -52.8 -52.8 -52.8 -52.8 -52.8 ...
##  $ lat               : num  47.5 47.5 47.5 47.5 47.5 ...
##  $ in_db_emp         : chr  "1" "1" "1" "1" ...
##  $ prox_idx_emp      : chr  "0.0202" "0.0193" "0.0199" "0.0204" ...
##  $ in_db_pharma      : chr  "0" "0" "1" "0" ...
##  $ prox_idx_pharma   : chr  "0.0121" "0.014" "0.0205" "0.0238" ...
##  $ in_db_childcare   : chr  "0" "0" "1" "0" ...
##  $ prox_idx_childcare: chr  "0.0402" "0.0257" "0.0395" "0.0425" ...
##  $ in_db_health      : chr  "0" "0" "1" "0" ...
##  $ prox_idx_health   : chr  "0.0069" "0.0028" "0.007" "0.0074" ...
##  $ in_db_grocery     : chr  "0" "0" "0" "0" ...
##  $ prox_idx_grocery  : chr  ".." ".." ".." ".." ...
##  $ in_db_educpri     : chr  "0" "0" "0" "0" ...
##  $ prox_idx_educpri  : chr  "0.0384" "0.0562" "0.0734" "0.0733" ...
##  $ in_db_educsec     : chr  "0" "0" "0" "0" ...
##  $ prox_idx_educsec  : chr  "0.0495" "0.0375" "0.0436" "0.0548" ...
##  $ in_db_lib         : chr  "0" "0" "0" "0" ...
##  $ prox_idx_lib      : chr  "0.0486" ".." "0.0545" "0.0796" ...
##  $ in_db_parks       : chr  "0" "0" "0" "0" ...
##  $ prox_idx_parks    : chr  "0.0141" ".." ".." "0.013" ...
##  $ in_db_transit     : chr  "1" "0" "1" "0" ...
##  $ prox_idx_transit  : chr  "0.0058" "0.0046" "0.0101" "0.0098" ...
##  $ transit_na        : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ amenity_dense     : chr  "0" "0" "0" "0" ...
##  $ suppressed        : int  0 0 0 0 0 0 0 0 0 0 ...
```

```
unique(pmd$PRNAME)
```

```
##  [1] "Newfoundland and Labrador / Terre-Neuve-et-Labrador"
##  [2] "Prince Edward Island / Île-du-Prince-Édouard"
##  [3] "Nova Scotia / Nouvelle-Écosse"
##  [4] "New Brunswick / Nouveau-Brunswick"
##  [5] "Quebec / Québec"
##  [6] "Ontario"
##  [7] "Manitoba"
##  [8] "Saskatchewan"
##  [9] "Alberta"
## [10] "British Columbia / Colombie-Britannique"
## [11] "Yukon"
## [12] "Northwest Territories / Territoires du Nord-Ouest"
## [13] "Nunavut"
```

```
pmd$PRNAME <- gsub("Newfoundland and Labrador / Terre-Neuve-et-Labrador", "Newfoundland and Labrador", p
pmd$PRNAME <- gsub("Prince Edward Island / Île-du-Prince-Édouard", "Prince Edward Island", pmd$PRNAME)
pmd$PRNAME <- gsub("Nova Scotia / Nouvelle-Écosse", "Nova Scotia", pmd$PRNAME)
pmd$PRNAME <- gsub("New Brunswick / Nouveau-Brunswick", "New Brunswick", pmd$PRNAME)
pmd$PRNAME <- gsub("Quebec / Québec", "Quebec", pmd$PRNAME)
pmd$PRNAME <- gsub("British Columbia / Colombie-Britannique", "British Columbia", pmd$PRNAME)
pmd$PRNAME <- gsub("Northwest Territories / Territoires du Nord-Ouest", "Northwest Territories", pmd$PR
```

```
# percentage of missing values in each column in dataset
p <- function(x) {sum(is.na(x))/length(x)*100}
sort(apply(pmd, 2, p), decreasing = TRUE) # marmin = 2 means function will be applied in each column
```

```
##             CMAUID            CMAPUID              DBUID              DBPOP
##           43.48059           43.48059            0.00000            0.00000
##              DAUID              DAPOP             CSDUID            CSDNAME
##            0.00000            0.00000            0.00000            0.00000
##            CSDTYPE             CSDPOP            CMANAME            CMATYPE
##            0.00000            0.00000            0.00000            0.00000
##             CMAPOP              PRUID             PRNAME              PRPOP
##            0.00000            0.00000            0.00000            0.00000
##                lon                lat         in_db_emp       prox_idx_emp
##            0.00000            0.00000            0.00000            0.00000
##       in_db_pharma    prox_idx_pharma    in_db_childcare prox_idx_childcare
##            0.00000            0.00000            0.00000            0.00000
##       in_db_health    prox_idx_health      in_db_grocery   prox_idx_grocery
##            0.00000            0.00000            0.00000            0.00000
##      in_db_educpri   prox_idx_educpri      in_db_educsec   prox_idx_educsec
##            0.00000            0.00000            0.00000            0.00000
##          in_db_lib       prox_idx_lib        in_db_parks     prox_idx_parks
##            0.00000            0.00000            0.00000            0.00000
##      in_db_transit   prox_idx_transit         transit_na      amenity_dense
##            0.00000            0.00000            0.00000            0.00000
##         suppressed
##            0.00000
```

In head of dataset we saw there were missing values in `prox_idx_lib` but the above output suggest there is no missing values. Because Statistics Canada use some specific notation for missing values. The following

standard symbols are used in Statistics Canada publications:
..− > not available for a specific reference period
$F-$ > to unreliable to be published

```
# percentage of missing values in each column
p <- function(x) {sum(x == ".." | x == "F")/length(x)*100}
sort(apply(pmd, 2, p), decreasing = TRUE)
```

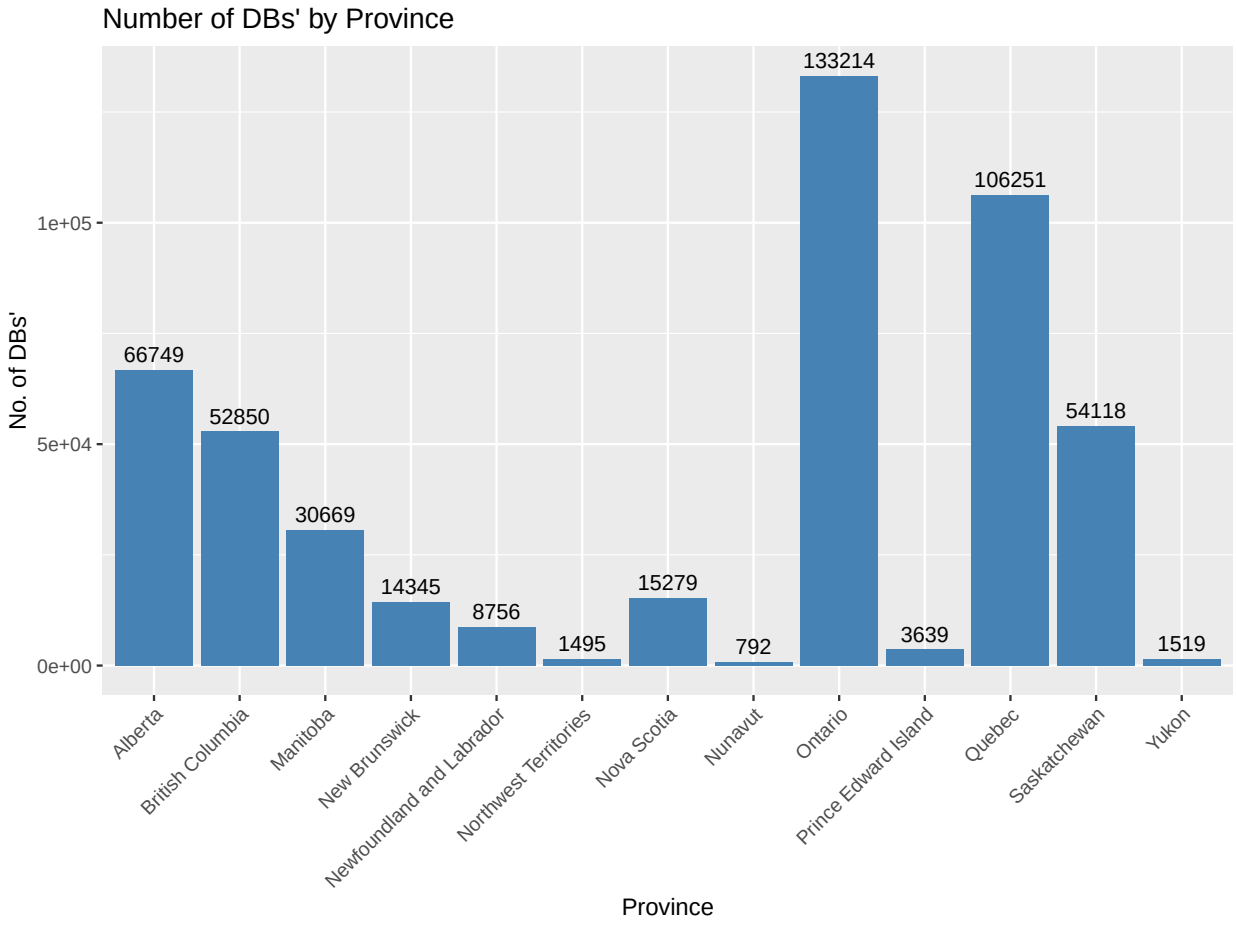
```
##       prox_idx_lib   prox_idx_grocery   prox_idx_educsec    prox_idx_pharma
##          76.993972          71.192584          71.161952          63.543037
##   prox_idx_transit   prox_idx_educpri     prox_idx_parks prox_idx_childcare
##          62.974497          53.977936          52.199413          50.178485
##    prox_idx_health       prox_idx_emp          in_db_emp       in_db_pharma
##          38.640040          13.493412           1.096031           1.096031
##    in_db_childcare       in_db_health      in_db_grocery      in_db_educpri
##           1.096031           1.096031           1.096031           1.096031
##      in_db_educsec          in_db_lib        in_db_parks      in_db_transit
##           1.096031           1.096031           1.096031           1.096031
##      amenity_dense              DBUID              DBPOP              DAUID
##           1.096031           0.000000           0.000000           0.000000
##              DAPOP              CSDUID             CSDNAME            CSDTYPE
##           0.000000           0.000000           0.000000           0.000000
##             CSDPOP             CMANAME            CMATYPE             CMAPOP
##           0.000000           0.000000           0.000000           0.000000
##              PRUID              PRNAME              PRPOP                lon
##           0.000000           0.000000           0.000000           0.000000
##                 lat         transit_na         suppressed
##           0.000000           0.000000           0.000000
```

```
pmd[pmd == ".." | pmd == "F"] <- NA
```

Count the dissemination block per province.

```
# Count the number dbs' that fall under each province
db_counts <- pmd %>% count(prov = pmd$PRNAME)

# Create bar chart
ggplot(db_counts, aes(x=prov, y=n)) +
  geom_bar(stat="identity", fill="steelblue") +
  geom_text(aes(label=n), vjust=-0.5, color="black", size=3.5) +
  labs(title = "Number of DBs' by Province",
       x = "Province",
       y = "No. of DBs'") +
  theme(axis.text.x = element_text(angle = 45, hjust = 1))
```




```
# summary of the dataset
# sapply(pmd, function(x) if(is.numeric(x)) summary(x))
sapply(Filter(is.numeric, pmd), summary)
```

```
## $DBPOP
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##    0.00    5.00   29.00   71.83   81.00 7607.00     315
##
## $DAPOP
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##     0.0   431.0   523.0   727.8   675.0 22077.0     315
##
## $CSDPOP
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##       0    2559   13678  235937  134413 2731571     315
##
## $CMAPOP
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##   10741  103811  747545 1670003 2463431 5928040  212914
##
## $PRPOP
##     Min.  1st Qu.   Median     Mean  3rd Qu.     Max.
##    35874  1278365  4648055  6748994 13448494 13448494
```

```
##
## $lon
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## -140.91 -110.03  -80.53  -90.30  -73.78  -52.66
##
## $lat
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   41.75   45.29   47.35   48.00   50.49   82.50
##
## $prox_idx_emp
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##    0.00    0.00    0.01    0.03    0.03    1.00   66074
##
## $prox_idx_pharma
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##    0.00    0.01    0.03    0.04    0.05    1.00  311155
##
## $prox_idx_childcare
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##    0.00    0.02    0.05    0.08    0.10    1.00  245712
##
## $prox_idx_health
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##    0.00    0.00    0.00    0.01    0.01    1.00  189211
##
## $prox_idx_grocery
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##     0.0     0.0     0.0     0.1     0.1     1.0  348613
##
## $prox_idx_educpri
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##    0.00    0.05    0.09    0.12    0.15    1.00  264317
##
## $prox_idx_educsec
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##     0.0     0.0     0.1     0.1     0.1     1.0  348463
##
## $prox_idx_lib
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##     0.0     0.1     0.1     0.1     0.1     1.0  377021
##
## $prox_idx_parks
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##    0.00    0.02    0.05    0.07    0.09    1.00  255608
##
## $prox_idx_transit
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##    0.00    0.00    0.01    0.02    0.02    1.00  308371
```

```r
# Subset columns that start with "prox_idx"
prox_cols <- colnames(pmd)[grepl("^prox_idx", colnames(pmd))]

# Check if there are any dbs where all proximity measures are missing
all_prox_na <- pmd[rowSums(is.na(pmd[,prox_cols])) == length(prox_cols), ]
```

```
nrow(all_prox_na)
```

```
## [1] 64764
```

```
head(all_prox_na[prox_cols], 3)
```

```
##     prox_idx_emp prox_idx_pharma prox_idx_childcare prox_idx_health
## 300           NA              NA                 NA              NA
## 768           NA              NA                 NA              NA
## 779           NA              NA                 NA              NA
##     prox_idx_grocery prox_idx_educpri prox_idx_educsec prox_idx_lib
## 300               NA               NA               NA           NA
## 768               NA               NA               NA           NA
## 779               NA               NA               NA           NA
##     prox_idx_parks prox_idx_transit
## 300             NA               NA
## 768             NA               NA
## 779             NA               NA
```

So, there are 64764 dissemination blocks where none of the proximity measures are available. Let's check the population of those dissemination blocks.

```
unique(all_prox_na$DBPOP)[1:5]
```

```
## [1]  0 33 78 30 19
```

```
sort(unique(all_prox_na$DBPOP), decreasing = TRUE)[1:5]
```

```
## [1] 1858 1522 1501 1404 1265
```

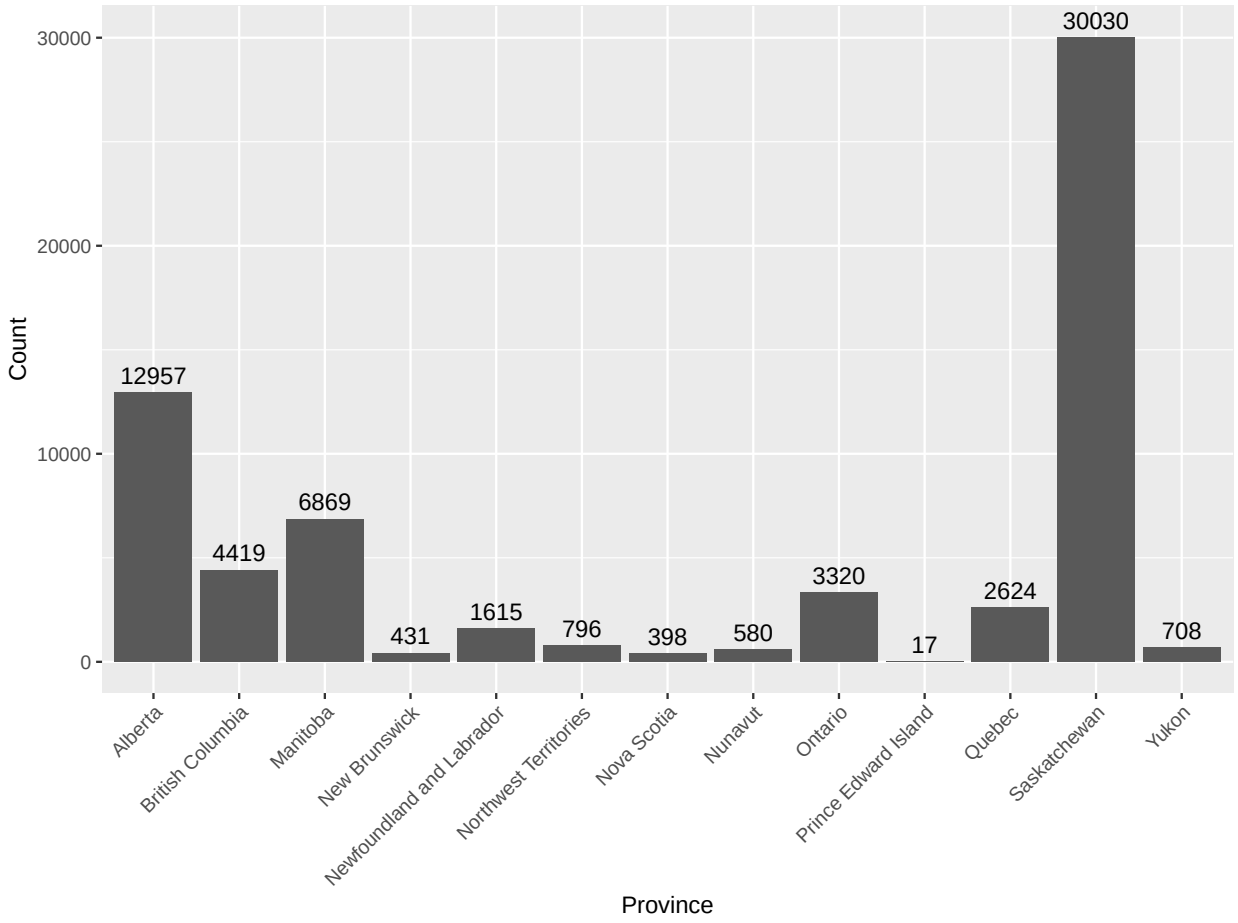
When the DBPOP is 0, it is understandable that there are no proximity measures because they might not have been calculated. However, even for DB populations with large values, there are missing values for proximity measures, which is not expected.

```
unique(all_prox_na$PRNAME)[1:5]
```

```
## [1] "Newfoundland and Labrador" "Prince Edward Island"
## [3] "Nova Scotia"               "New Brunswick"
## [5] "Quebec"
```

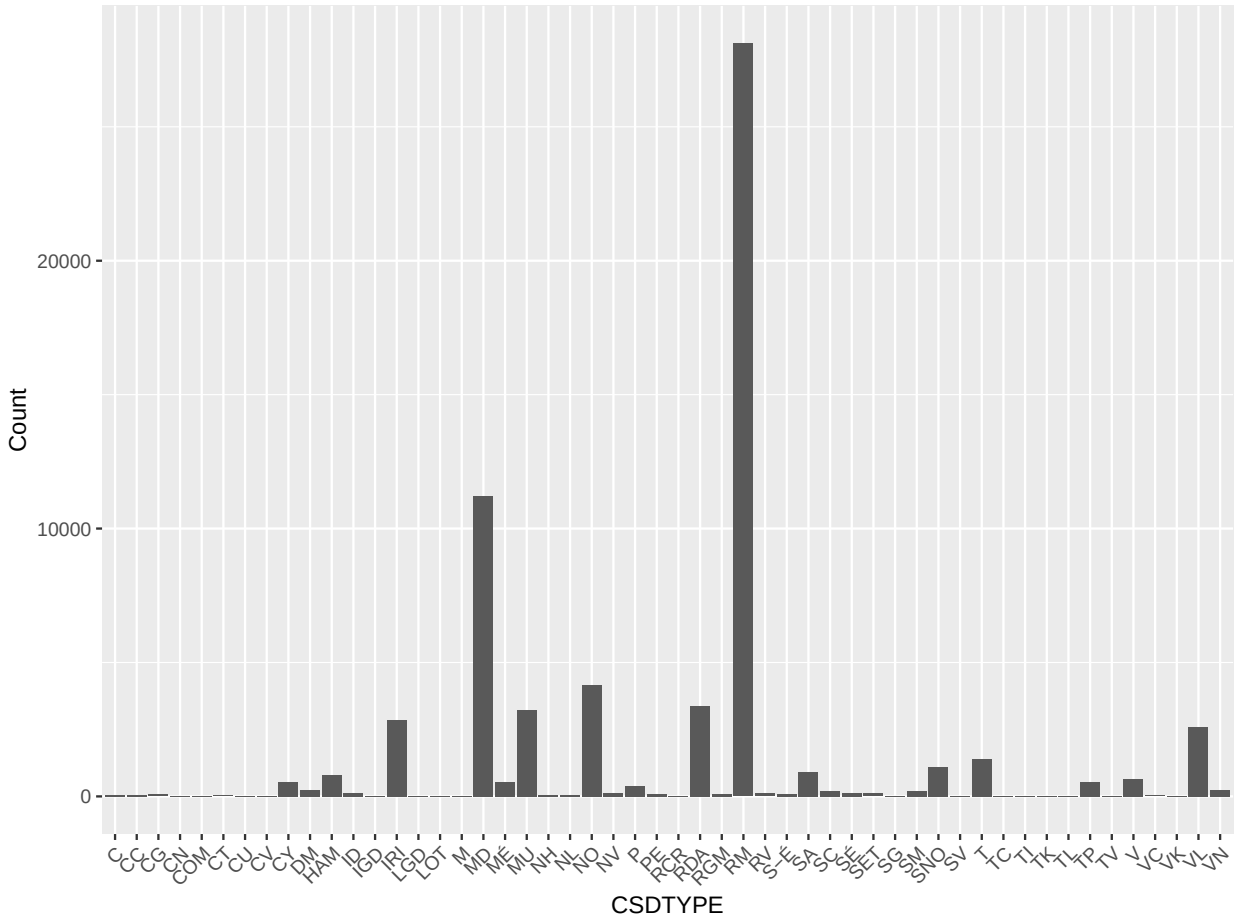
```
# Count the occurrences of each CSDTYPE value
pr_counts <- data.frame(table(all_prox_na$PRNAME))

# Create a bar plot
ggplot(data = pr_counts,
       aes(x = Var1, y = Freq)) +
  geom_bar(stat = "identity") +
  geom_text(aes(label = Freq), vjust = -0.5) +
  xlab("Province") +
  ylab("Count") +
  theme(axis.text.x = element_text(angle = 45, hjust = 1))
```




```r
# Count the occurrences of each CSDTYPE value
csdtype_counts <- data.frame(table(all_prox_na$CSDTYPE))

# Create a bar plot
ggplot(data = csdtype_counts,
       aes(x = Var1, y = Freq)) +
  geom_bar(stat = "identity") +
  # geom_text(aes(label = Freq), vjust = -0.5) +
  xlab("CSDTYPE") +
  ylab("Count") +
  theme(axis.text.x = element_text(angle = 45, hjust = 1))
```



We can see that These DBs are from different province and different csd. If we can plot them on map then it may make sense! Majority portions of db where all proximity measures are null from Regional municipality and Municipal district.

```
# Check if there are any dbs where all proximity measures are 0
all_prox_0 <- pmd[rowSums(pmd[, prox_cols] == 0, na.rm = TRUE) == length(prox_cols), ]
nrow(all_prox_0)
```

```
## [1] 0
```

There are no dissemination blocks for which all the proximity measures of amenities are 0. So, dissemination blocks with no populations still has the proximity measures of amenities may be those dissemination blocks are close from other populated dissemination blocks, or the dissemination blocks contain parks, office buildings, industrial area etc.

Outliers

Outliers can have a significant impact on the clustering results by pulling the centroids towards themselves, creating biased clusters, and reducing the effectiveness of the clustering algorithm.

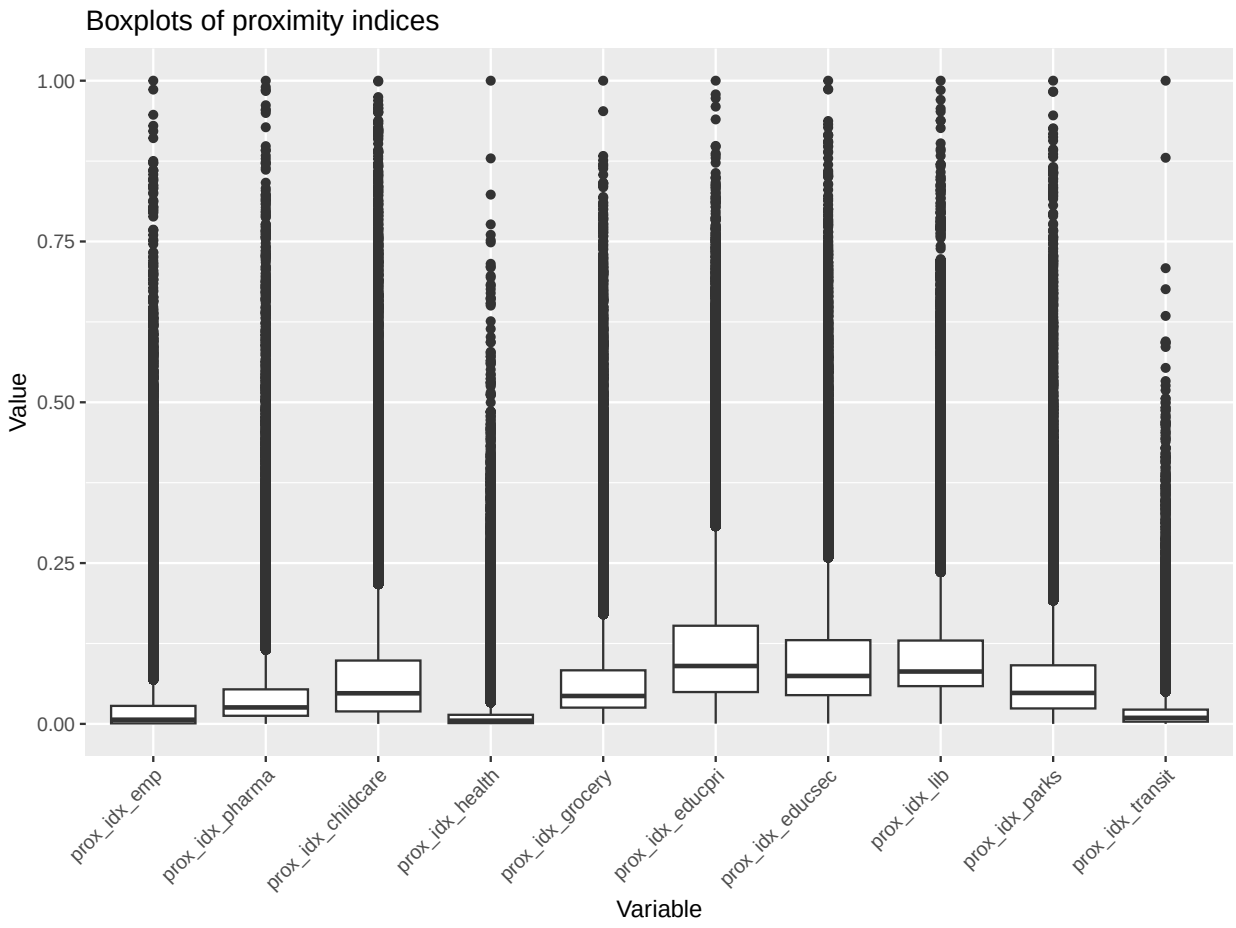
```
# boxplot(pmd$prox_idx_educsec,
#   ylab = "prox_idx_emp"
# )
```

```
# Create a melted data frame for the boxplot
df <- reshape2::melt(pmd[, prox_cols])
```

```
## No id variables; using all as measure variables
```

```
# Create the boxplot
ggplot(df, aes(x = variable, y = value)) +
  geom_boxplot() +
  xlab("Variable") +
  ylab("Value") +
  ggtitle("Boxplots of proximity indices") +
  theme(axis.text.x = element_text(angle = 45, hjust = 1))
```

```
## Warning: Removed 2714545 rows containing non-finite values (`stat_boxplot()`).
```



The proximity measures are already normalized but we can still see outliers in these. So, we should use clustering algorithms that can handle outliers.

For example DBSCAN clustering is robust against outliers when we choose minimum number of points (minPts) - (a threshold) large enough.
Ordering points to identify the clustering structure (OPTICS) is an algorithm for finding density-based clusters in spatial data which is also robust against outliers.
https://en.wikipedia.org/wiki/OPTICS_algorithm#cite_note-1 But we can't use general k-means: the squared error approach is sensitive to outliers. But there are variants such as k-medians for handling outliers.
(https://www.researchgate.net/publication/220490566_A_review_of_robust_clustering_methods)

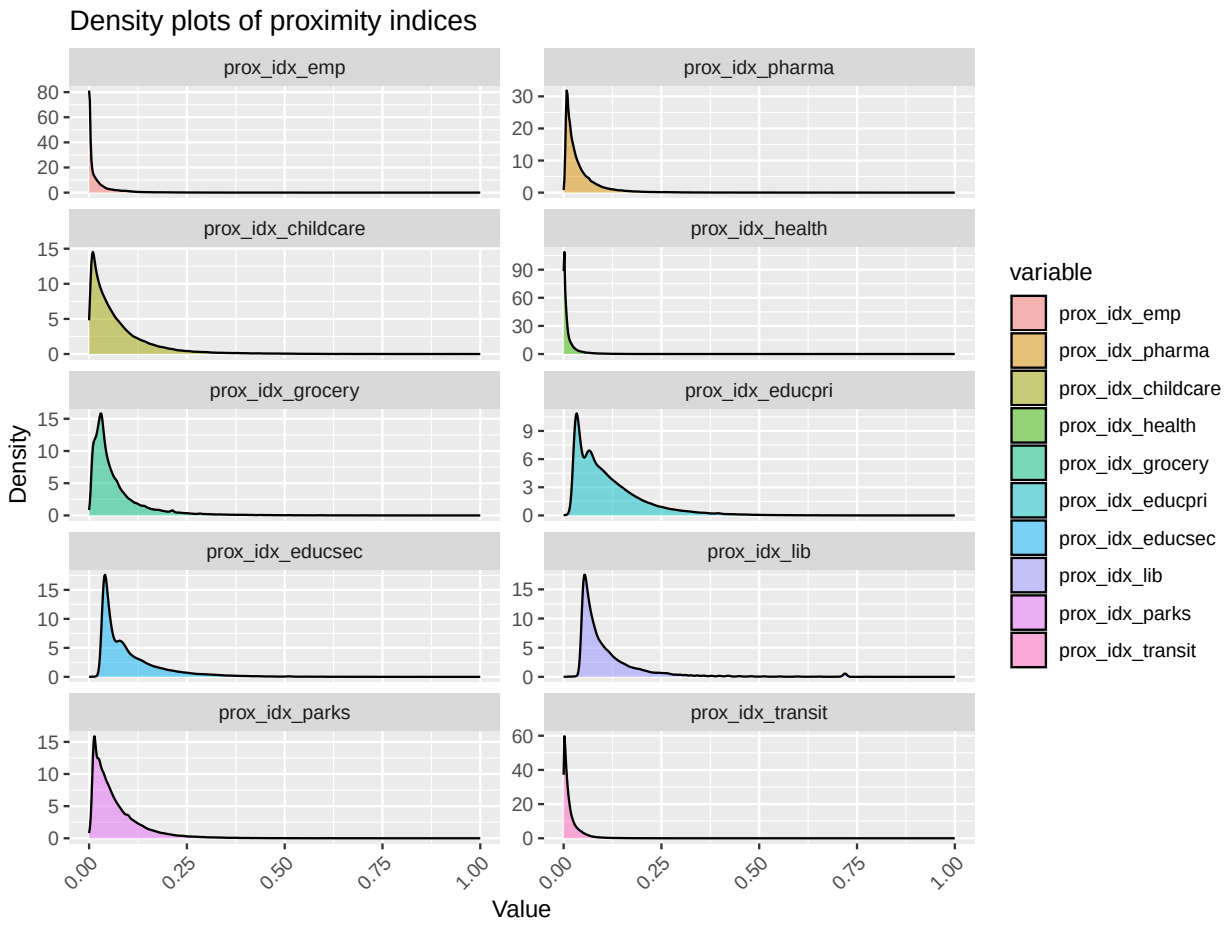
Another approach is to apply a transformation to the data that can reduce the impact of outliers. For example, we could apply a log transformation or a power transformation to the data. These transformations can help to reduce the influence of extreme values and make the data more symmetric.

Distributions

```
# plot(density(pmd$prox_idx_health, na.rm = TRUE))
```

```
# Create the density plot
ggplot(df, aes(x = value, fill = variable)) +
  geom_density(alpha = 0.5) +
  xlab("Value") +
  ylab("Density") +
  ggtitle("Density plots of proximity indices") +
  theme(axis.text.x = element_text(angle = 45, hjust = 1)) +
  facet_wrap(~variable, scales = 'free_y', nrow = 5)
```

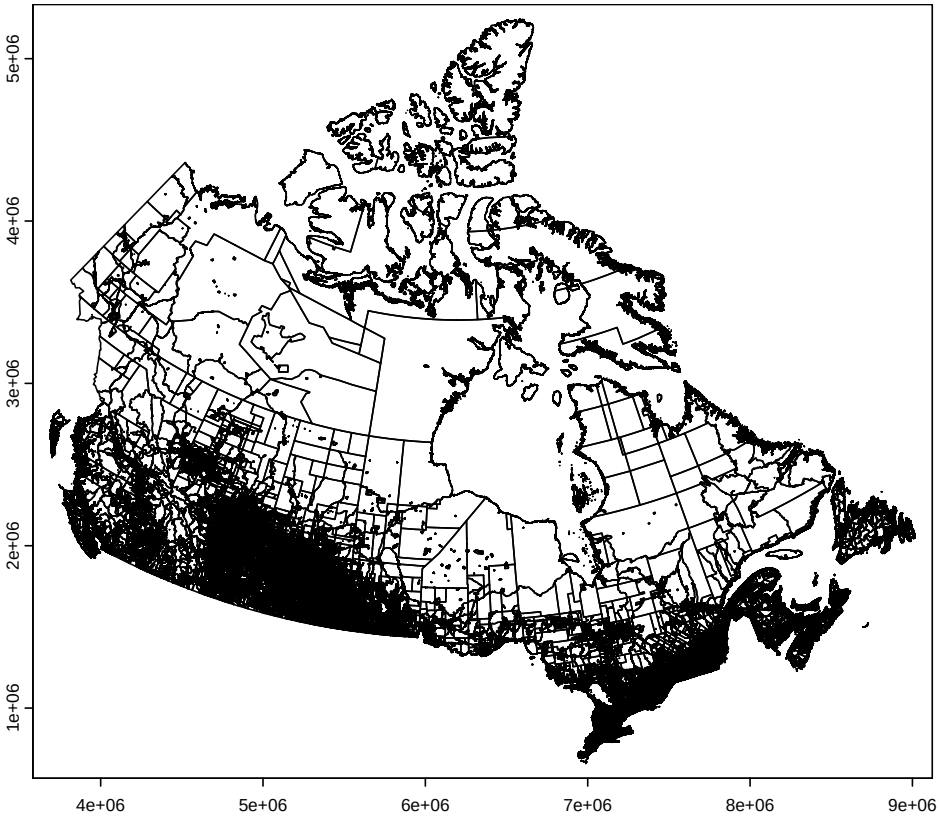
```
## Warning: Removed 2714545 rows containing non-finite values (`stat_density()`).
```



Density of Categorical and binary Variables

```
ggplot(pmd, aes(x=as.factor(amenity_dense) )) +
  geom_bar(width=0.7, fill="steelblue") +
  geom_text(stat="count", aes(label=..count..), vjust=-0.5) +
  labs(x = "Amenity Dense")
```

```
## Warning: The dot-dot notation (‘..count..‘) was deprecated in ggplot2 3.4.0.
## i Please use ‘after_stat(count)‘ instead.
```



A dissemination block is an amenity dense neighbourhood, a high amenity density neighbourhood, a non-amenity dense neighbourhood.

Spat

```
library(terra)
db_shp <- vect("../../data/boundary/ldb_000b21a_e.shp")
db_shp
```

```
##  class       : SpatVector
##  geometry    : polygons
##  dimensions  : 498547, 6  (geometries, attributes)
##  extent      : 3689321, 9015751, 659305, 5242009  (xmin, xmax, ymin, ymax)
##  source      : ldb_000b21a_e.shp
##  coord. ref. : NAD83 / Statistics Canada Lambert (EPSG:3347)
##  names       :       DBUID            DGUID  DBRPLAMX  DBRPLAMY LANDAREA PRUID
##  type        :       <chr>            <chr>     <num>     <num>    <num> <chr>
##  values      : 10010165001 2021S0513100101~ 8.978e+06 2.147e+06   0.0599    10
##                10010165002 2021S0513100101~ 8.978e+06 2.146e+06   0.0084    10
##                10010165006 2021S0513100101~ 8.978e+06 2.146e+06   0.3063    10
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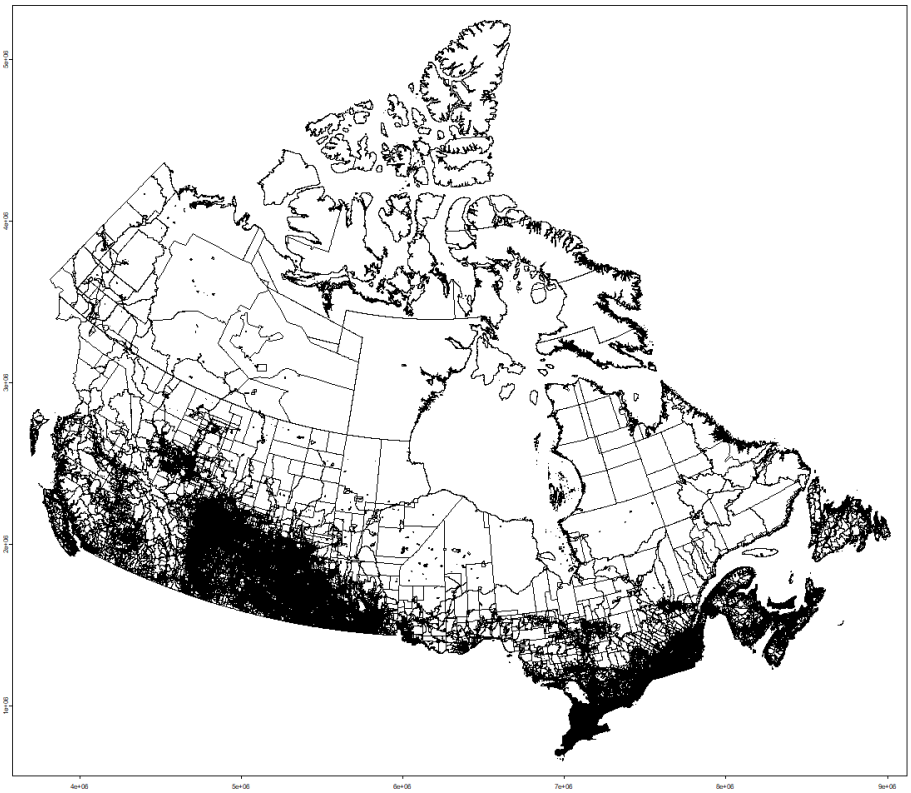
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4e+06
3e+06
2e+06
1e+06
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5e+06
6e+06
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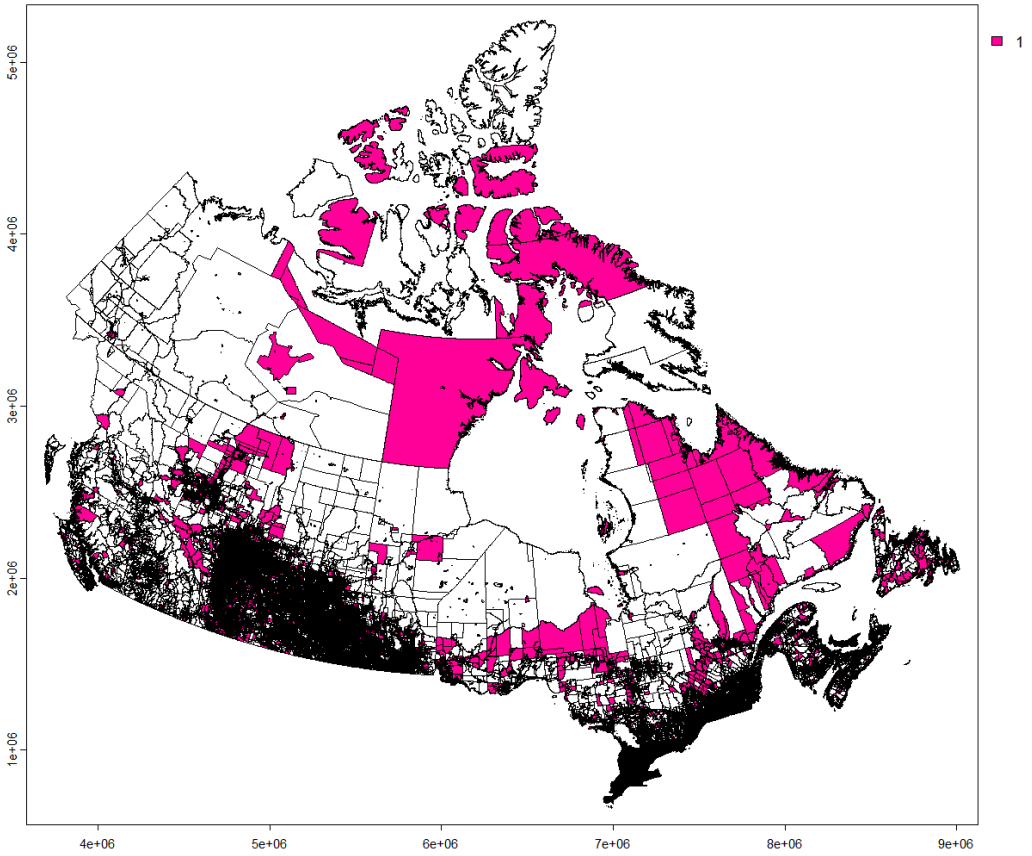
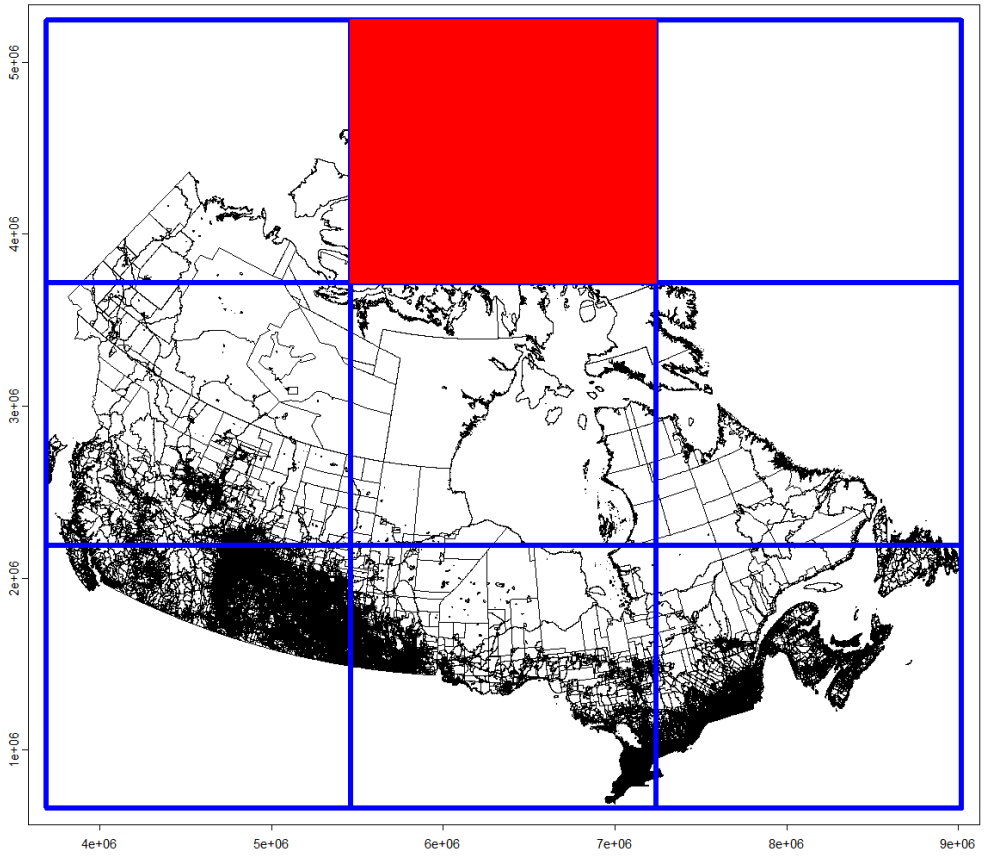
9e+06



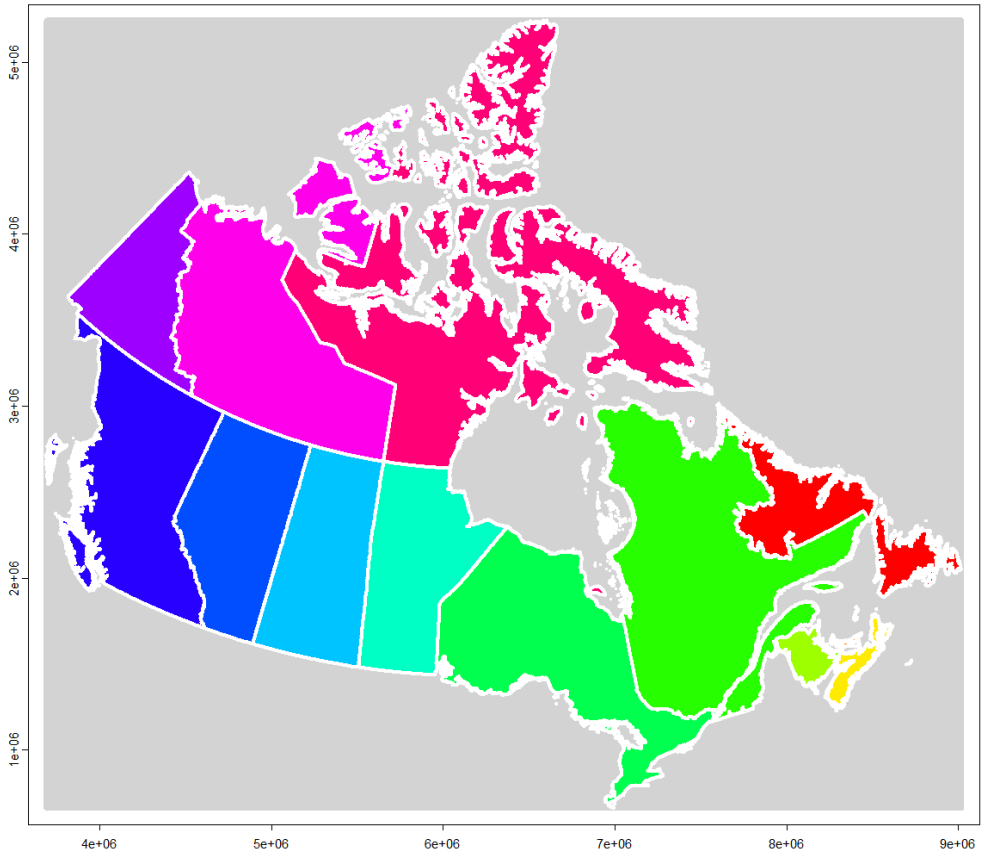
So where all proximity measures are missing are not randomly distributed. We have seen before that these areas have population. But our main target is to cluster the proximity measures. As all the proximity measures are missing here we can delete these rows from our database then do the clustering and also we can do clustering by keeping them aswell and see the difference.

Cut into 9 zones.

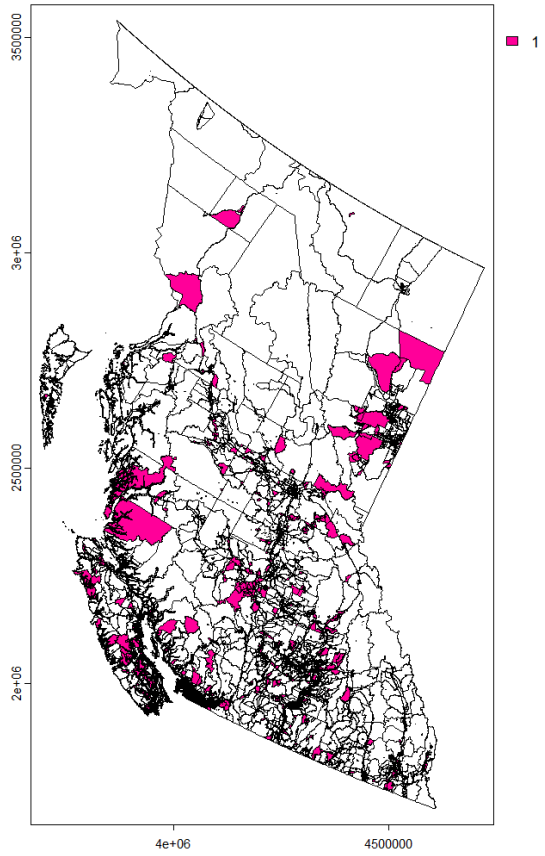


Left Lower portions of Canada

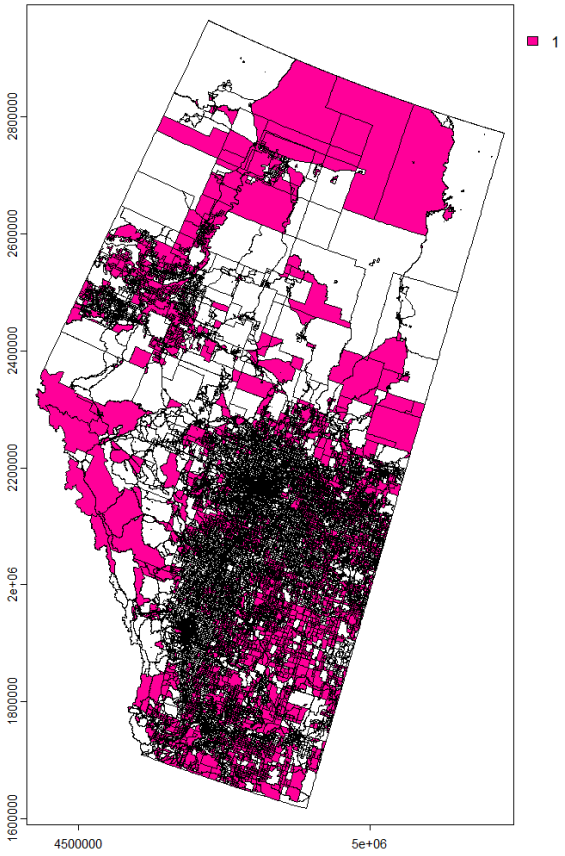
Provinces



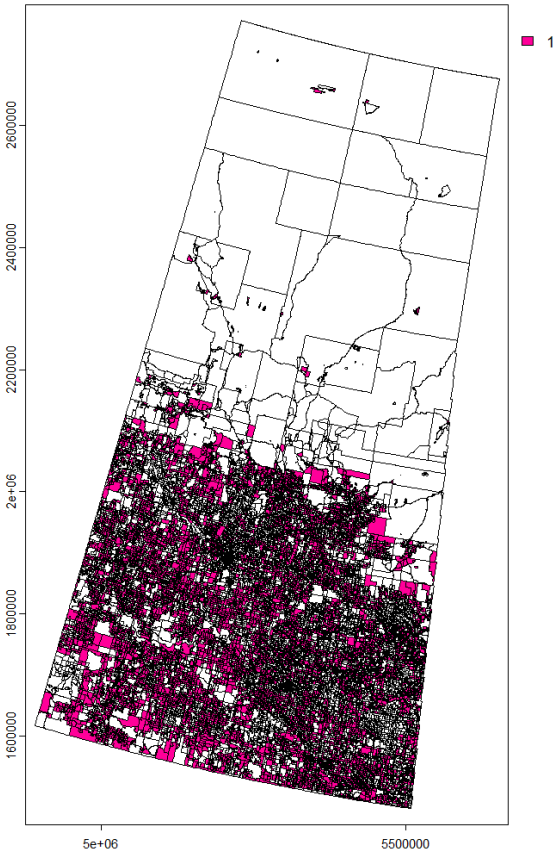
Closer look to all null proximity measures of BC.



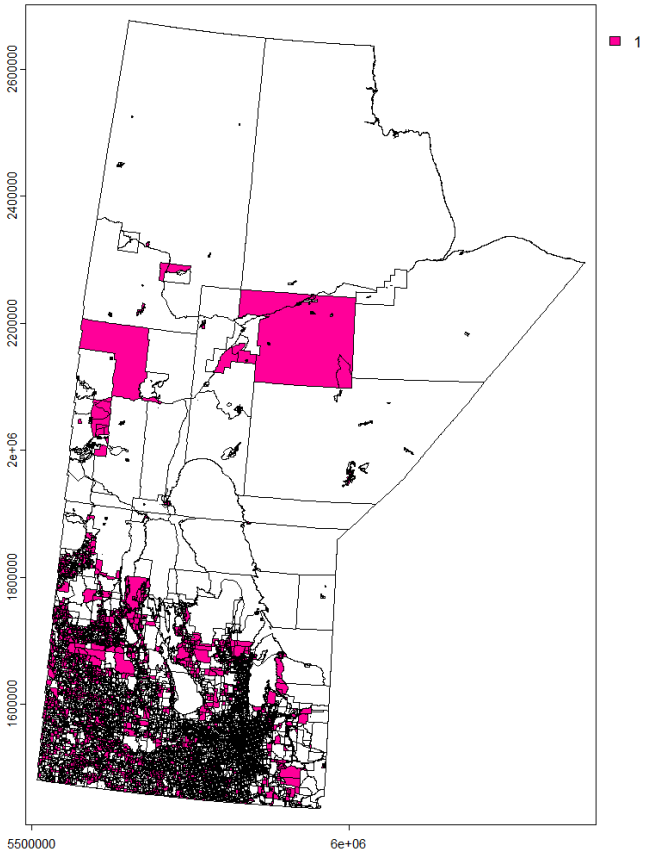
Closer look to all null proximity measures of Alberta.



Closer look to all null proximity measures of Saskatchewan

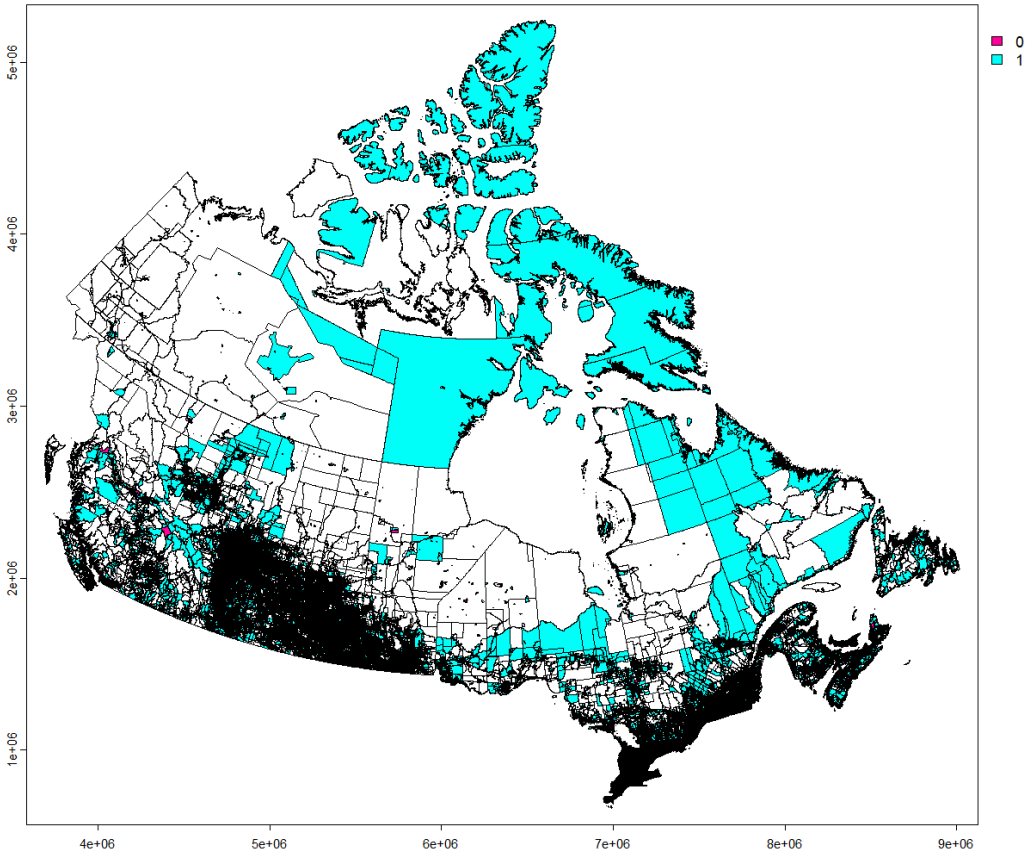


Closer look to all null proximity measures of Manitoba

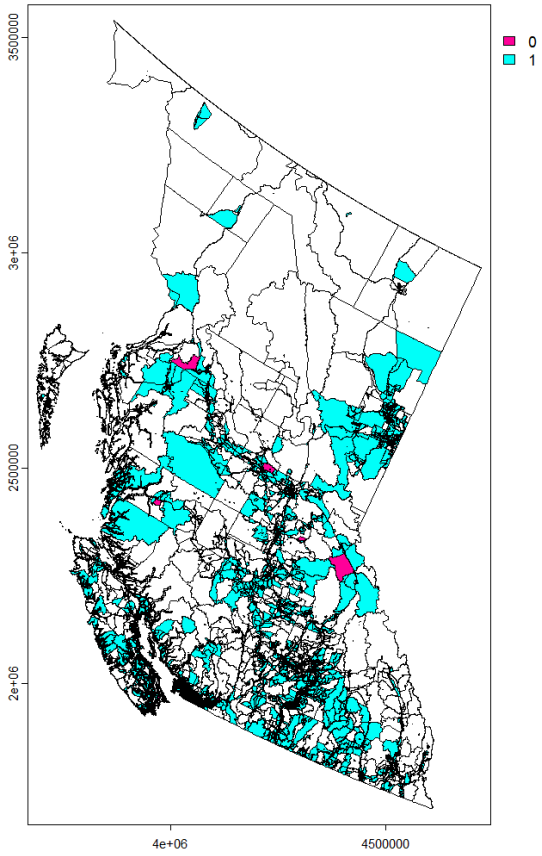


Now let's look at the proximity measures na values aminity wise.

Let's look where grocery proximity measures are missing all over Canada.



Closer look to null grocery proximity measures of BC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1
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4e+06
4500000