# openSIMD

*Maike Waldmann & Roman Popat*

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# Contents

# Chapter 1

# Preface

The Scottish Index of Multiple Deprivation (SIMD) is the Scottish Government's official tool to find the most deprived areas in Scotland. SIMD is used by government, councils, charities and communities to make sure that the work they do is targeted to those areas that need it most.

SIMD is best known for how it ranks each small area in Scotland by how deprived it is. In addition to the rankings, all indicator datasets that go into SIMD are also published on a small area level. This wealth of granular data provides detailed information about the underlying issues in deprived areas.

**openSIMD** opens up SIMD further by making the code used to calculate SIMD available to anyone who wants to understand exactly how SIMD indicators are combined, or replicate the method for similar measures.

SIMD is updated every three years, and up until the latest edition (SIMD16), SIMDs have been calculated using the statistical package SAS rather than R. The results of both calculations differ slightly due to small differences in how each program runs a statistical procedure called factor analysis. SIMD16 as published on the SIMD website is the official version.

Future updates of SIMD will be calculated using R, and the **openSIMD** R code will produce SIMD ranks that are identical with the official SIMD ranks published by the Scottish Government.

The move from SAS to R through the **openSIMD** project was made possible by a collaboration between The Data Lab and The Scottish Government.

# Chapter 2

# Introduction

This is a step-by-step guide to the **openSIMD** R code, a code which creates the Scottish Index of Multiple Deprivation (SIMD), starting from the indicators.

SIMD is made up of over 30 indicators which are grouped into seven domains of deprivation. Each domain summarises one aspect of deprivation by combining some of the indicators and using the resulting domain scores to rank each area in Scotland. The seven domain rankings are then combined into an overall, multiple-deprivation SIMD ranking.

Before running the **openSIMD** R code, you will need the published SIMD indicators for four out of the seven domains. For the other three domains, you will need the published domain rankings. The reason for this is that for these three domains, the individual indicators were not published separately, and the published domain scores are rounded. The published domain rankings on the other hand are based on unrounded data and therefore more precise. Both datasets can be downloaded from the SIMD website.

After running the **openSIMD** R code, you will have created two csv documents which contain the domain rankings and the overall SIMD ranking for each small area (called data zone) in Scotland.

We tested this code with SIMD16 data, and you will need to adapt it for other versions of SIMD.

The rankings you get when using the **openSIMD** code with the published SIMD16 data slightly differ from the published, offical SIMD16 rankings, see my note in section 1. SIMD16 as published on the SIMD website is the official version.

Roman Popat from The Data Lab is now going to walk you through the R code. In section 3, he will explain the code used to calculate the individual domain scores. In section 4, he will go through the steps necessary for combining the domains into the overall SIMD, and finally, in section 5, he will introduce the functions used throughout the code for those calculation steps that came up repeatedly.

For any questions about the SIMD methodology have a look at the SIMD Technical Notes on the SIMD website, and feel free to contact the SIMD team at simd@gov.scot.

# Chapter 3

# Calculating Domains

In this section, I will explain the code used to calculate the individual domain scores.

## 3.1 Setting up

The first things to do are

- load a few packages
- source the script containing the utility functions, see section 5 for documentation on the functions used.
- read in the data

You will need to make sure that these file paths correspond to where your files are. If you have opened the `openSIMD_analysis.Rproj` then the directories of interest will be `scripts/utils` and `data`.

```
library(readxl)
library(dplyr)
source("../openSIMD_analysis/scripts/utils/helpers.R")
d <- read_excel("../openSIMD_analysis/data/SIMD2016_indicators.xlsx", sheet = 3, na = "*")
```

The data here contains the published indicators, in this case from SIMD 2016.

```
str(d)
```

```
## Classes 'tbl_df', 'tbl' and 'data.frame':    6976 obs. of  36 variables:
##  $ Data_Zone                      : chr  "S01006506" "S01006507" "S01006508" "S01006509" ...
##  $ Intermediate_Zone              : chr  "Culter" "Culter" "Culter" "Culter" ...
##  $ Council_area                   : chr  "Aberdeen City" "Aberdeen City" "Aberdeen City" "Aberdeen Ci
##  $ Total_population               : num  904 830 694 573 676 ...
##  $ Working_age_population_revised: num  605 491 519 354 414 464 322 354 710 491 ...
##  $ Income_rate                    : num  0.07 0.07 0.05 0.05 0.1 0.03 0.02 0.03 0.01 0.01 ...
##  $ Income_count                   : num  60 60 30 30 70 25 10 20 15 10 ...
##  $ Employment_rate                : num  0.07 0.05 0.03 0.06 0.07 0.03 0.02 0.03 0.01 0.01 ...
##  $ Employment_count               : num  40 25 15 20 30 15 5 10 10 5 ...
##  $ CIF                            : num  60 40 45 65 75 50 35 55 25 35 ...
##  $ ALCOHOL                        : num  103.4 33 54.3 141.9 52.3 ...
##  $ DRUG                           : num  27.6 39.9 32.9 49.2 234.9 ...
##  $ SMR                            : num  67 86 43 88 149 68 77 137 86 61 ...
##  $ DEPRESS                        : num  0.123 0.148 0.127 0.154 0.197 ...
##  $ LBWT                           : num  0 0.0256 0.0556 0.037 0 ...
##  $ EMERG                          : num  80 97.7 70 87.9 105.1 ...
```

```
##  $ Attendance                    : num  0.863 0.825 0.877 0.942 0.805 ...
##  $ Attainment                    : num  5.93 5.57 5.8 5.62 5.33 ...
##  $ Noquals                       : num  52.8 95.9 38.6 80.1 77.2 ...
##  $ NEET                          : num  0.03 0.01 0 0.04 0.04 0.03 0.08 0.02 0.03 0.03 ...
##  $ HESA                          : num  0.1304 0.1014 0.1486 0.0816 0.0857 ...
##  $ drive_petrol                  : num  2.42 3.68 3.24 2.51 2.08 ...
##  $ drive_GP                      : num  2.92 4.02 3.6 2.47 2.17 ...
##  $ drive_PO                      : num  1.52 2.74 2.09 1.96 1.67 ...
##  $ drive_primary                 : num  2.03 3.13 2.66 1.44 1.51 ...
##  $ drive_retail                  : num  1.5 2.65 1.88 2.22 1.93 ...
##  $ drive_secondary               : num  10.8 11.5 11.5 10.8 10.6 ...
##  $ PT_GP                         : num  8.44 8.33 7.85 7.43 5.14 ...
##  $ PT_Post                       : num  5.99 7.26 5.83 8.31 6.63 ...
##  $ PT_retail                     : num  5.71 6.79 5.25 8.44 6.62 ...
##  $ crime_count                   : num  8.01 4 4 NA 12.01 ...
##  $ crime_rate                    : num  88.6 48.2 57.7 NA 177.7 ...
##  $ overcrowded_count             : num  87 85 31 42 50 27 27 15 10 29 ...
##  $ nocentralheat_count           : num  10 4 8 6 7 8 9 4 3 1 ...
##  $ overcrowded_rate              : num  0.1021 0.1017 0.0482 0.0724 0.0867 ...
##  $ nocentralheat_rate            : num  0.01174 0.00478 0.01244 0.01034 0.01213 ...
```

## 3.2 The recipe

For each domain the process has several steps, many of which are repeated across domains. To aid in applying this recipe I have defined some functions in `scripts/utils/helpers.R`, see section 5. The steps of the recipe and associated functions are as follows:

- Select the indicators (collumns) that are relevant to that domain, using the function `dplyr::select`.
- Calculate the 'normalised' ranks for each indicator, using the function `normalScores` defined herein.
- Replace missing values, using the function `replaceMissing` defined herein.
- Derive the factor analysis weights for each indicator, using the function `getFAWeights` defined herein.
- Combine the normalised ranks and weights to generate the indicator score, using the function `combineWeightsAndNorms` defined herein.
- Rank the indicator score, using the function `base::rank`.

There is some variation in this as you will see with some of the domains.

## 3.3 dplyr

Throughout this project, I make use of the tools in the `dplyr` package for data manipulation including the `%>%` notation for forwards piping. I won't introduce these tools but if they are unfamiliar, I recommend reading this article. See the section on chaining for an explanation of the `%>%` pipe.

## 3.4 An example: Education

As an example of the process, here we will calculate the domain rank for the education domain. In this first chunk of code I will create the normalised ranks for the education domain as follows:

```
normalised_education <- d %>% # start with the raw data
  select(Attendance, Attainment, Noquals, NEET, HESA) %>% # select relevant collumns
  mutate(Attendance = normalScores(Attendance, forwards = FALSE)) %>% # replace each collumn with its n
```

```
  mutate(Attainment = normalScores(Attainment, forwards = FALSE)) %>%
  mutate(Noquals    = normalScores(Noquals, forwards = TRUE)) %>%
  mutate(NEET       = normalScores(NEET, forwards = TRUE)) %>%
  mutate(HESA       = normalScores(HESA, forwards = FALSE)) %>%
  mutate_all(funs(replaceMissing)) # replace missing values
```

```
## Warning in qnorm(rn, mean = 0, sd = 1, lower.tail = forwards): NaNs
## produced

## Warning in qnorm(rn, mean = 0, sd = 1, lower.tail = forwards): NaNs
## produced

## Warning in qnorm(rn, mean = 0, sd = 1, lower.tail = forwards): NaNs
## produced

## Warning in qnorm(rn, mean = 0, sd = 1, lower.tail = forwards): NaNs
## produced
```

**Note:** you may see a warning here because normalScores can generate missing values from missing values. This is fine, these will be replaced with 0, when you call `replaceMissing`.

The only decisions to make are (a) which collumns to select using `select` and (b) which orientation to rank (and then normalise) each indicator. The orientation is determined by the `forwards` argument to `normalScores` see normalScores for further information.

Now that we have the normalised scores we can peform the next steps. First we need to obtain factor analysis weights. Factor analysis is performed and the proportional loading on factor 1 is extracted to serve as the weighting of the indicators. This is achieved by the getFAWeights function as follows;

```
education_weights <- getFAWeights(normalised_education)
```

Now that we have the normalised indicator scores and weights derived from factor analysis, we can combine them with the utility function combineWeightsAndNorms. Each normalised indicator variable is multiplied by its proportional weight derived from factor analysis, as follows;

```
education_score <- combineWeightsAndNorms(education_weights, normalised_education)
```

Finally we rank these weighted scores to generate the domain rank.

```
education_rank <- rank(-education_score)
```

## 3.5 Variations

The remaining domains are calculated in a similar way with some variations, rather than explaining each one I will explain the possible variations.

The housing rank is the sum of the overcrowding rate and non-central heating rate ranked. For the crime, income and employment ranks we simply use the published ranks due to non-disclosure restrictions.

In the education example above, when applying the `normalScores` function, we needed to pay attention to the `forwards` argument to orient the variables (decide whether a high value was good or bad). In the other domains this is not the case and each indicator can take the default value `forwards = TRUE`. This means we can use the `dplyr::mutate_all()` function instead of mutating each variable indipendently. In addition, if domain indicators collumn names have something in common we can select them with `dplyr::select(contains("some_common_text"))`.

The access domain is unique in that it has 2 sud-domains (drive and public transport) which are processed in the normal way (normalise -> weight -> rank) before exponential transform (covered in the next section on calculating SIMD) and then summed in a 2:1 ratio before final ranking for the domain.

## 3.6 Re-assigning ranks

We have included some functionality to manually re-assign ranks to allow for certain exceptions. This is done via the reassignRank function.

# Chapter 4

# Calculating SIMD

For the final calculation of the SIMD score and ranks we follow a few simple steps, see the script `openSIMD_analysis/scripts/calculations/openSIMD.R`.

First we load the packages and data from the previous domain rank calculations.

```
library(dplyr)
source("../openSIMD_analysis/scripts/utils/helpers.R")
domains <- read.csv("../openSIMD_analysis/results/domain_ranks.csv")
```

Then we inverse rank the domain ranks (so that low values are most deprived) and exponentially transform, spreading out the most deprived areas for a finer distinction in this region.

```
invRank <- function(v) rank(-v)

exponential_domains <- domains %>%
  mutate_at(vars(-data_zone), funs(invRank)) %>%
  mutate_at(vars(-data_zone), funs(expoTransform))
```

We then combine the domain ranks via a weighting and rank the resulting combination.

```
with(exponential_domains, {
  simd_score <<-
    .28 * income +
    .28 * employment +
    .14 * health +
    .14 * education +
    .09 * access +
    .05 * crime +
    .02 * housing
})
```

Finally we invert the rank once more giving us the final SIMD rank.

```
simd_rank <- rank(-simd_score)
```

# Chapter 5

# Functions

Below is some documentation of the novel functions developed for this project and used repeatedly throughout the openSIMD proceedure.

## 5.1 normalScores

The `normalScores` function is the first in the work flow. This calculates the normal scores for each indicator. The normal score is defined as follows:

$$y_i = \phi^{-1}\frac{r_i}{n+1}$$

where: $\phi^{-1}$ is the inverse cumulative normal (probit) function, $r_i$ is the rank of the i'th observation and $n$ is the number of non-missing observations for the ranking variable. This is the inverse cumulative normal probability density of proportional ranks. The resulting variable should appear normally distributed regardless of the input data. We translated this approach using the SAS documentation as a guide resulting in the following R function.

```
normalScores <- function(
  v,                    # a numeric vector as the input variable
  ties = "average",     # passed to ties.method argument in rank()
  forwards = TRUE       # smallest numerical value on left? default is TRUE
) {

  r <- rank(v, ties.method = ties)
  n <- length(na.omit(v))

  rn <- r / (n + 1)

  y <- qnorm(rn, mean = 0, sd = 1, lower.tail = forwards)

  return(y)

}
```

The function takes a numeric vector as its input `v`. It first ranks this input `r` and then calculates the proportional rank `rn`. The final step is to apply the cumulative normal probability using the `qnorm` function. The return value is a numeric vector of the same length as the input `v`.

## 5.2 replaceMissing

A simple utility function to replace missing values, once normalised indicator scores have been calculated. A convenience wrapper around `replace`. The function find missing values (as well as `Inf` and `-Inf`) in a vector and replaces them with `0`. The use case is for example when a data zone is empty, has a missing value for an indicator but we want it to sit in the centre of the distribution and so we assign a value of 0.

```
replaceMissing <- function(v) replace(v, is.na(v) | v == Inf | v == -Inf, 0)
```

Pass a numeric vector `v` and return a vector of equal length with missing values filled.

## 5.3 getFAWeights

This function performs a factor analysis using the `psych::fa` function. It then extracts the weights on the first resulting factor, converts then to poportions (of the sum of weights) and then returns them as individual elements of a list. This is designed to be equivalent to the SAS procedure in previous SIMD calculations, however the results are only comparable to two decimal places, likely due to differences in the implementation of factor analysis in the two packages (see section on tests).

```
getFAWeights <- function(dat, ...) {

  fact <- psych::fa(dat, nfactors = 1, fm = "ml", rotate = "none", ...)

  f1_scores <- as.data.frame(fact$weights) %>% select(ML1)

  f1_weights <- f1_scores / sum(f1_scores)

  # This is just to make each weight an individual element of a list
  # For compatibility with purrr::map2() in the next step, combineWeightsAndNorms()
  return(lapply(seq_along(f1_weights$ML1), function(i) f1_weights$ML1[i]))

  }
```

The function takes a data frame `dat` as its main argument, it is assumed that this data frame contains all of the variables for factor analysis and in the required order. The return value is a list with individual elements corresponding to the proportional weight of variables in the same order as the input data. A list is returned here for compatibility with the next function `combineWeightsAndNorms` however this can be easily converted to a vector with `unlist`.

## 5.4 combineWeightsAndNorms

This function takes the normalised indicator scores and the weights derived from factor analysis, multiplies them out and then takes the sum of these weighted indicator scores to get the final score for that domain.

```
combineWeightsAndNorms <- function(weights, norms) {

  combined <- purrr::map2(weights, norms, ~ .x * .y)

  combined %>% data.frame %>% rowSums

}
```

The function takes a list of weights (generated by `getFAWeights` and a data.frame of normalised scores, it returns a numeric vector containing the combined domain score.

## 5.5 expoTransform

This function recapitulates the exponential transformation used in SIMD to transform the weighted domain ranks before combining domains.

```
expoTransform <- function(ranks) {

  prop_ranks <- ranks / max(ranks)

  expo <- -23 * log(1 - prop_ranks * (1 - exp( -100 / 23)))

  return(expo)
}
```

The function takes an numeric vector (of the ranks) and returns a numeric vector of equal length containing the transformed values.

## 5.6 reassignRank

A function to make manual reassignments of ranks to individual data zones, can be used when there are strange exceptions such as empty data zones.

```
reassignRank <- function(data, domain, data_zone, end = "max", offset = 0) {

  if(end == "max") {
    data[data$data_zone == data_zone, domain] <-
      max(data[, domain], na.rm = TRUE) - (offset + 0.1)
  }else
    if(end == "min") {
      data[data$data_zone == data_zone, domain] <-
        min(data[, domain], na.rm = TRUE) + (offset + 0.1)
    }

  data[, domain] <- rank(data[, domain])

  return(data)
}
```

The function needs a data.frame of ranks containing a collumn named 'data_zone'. The function will take that data.frame change the rank of the indicator in question (with an optional offset) and then re-rank. The function returns the corrected data.frame.

# Chapter 6

# Tests

In this section we will present a series of tests examining the accuracy of our translation of the SIMD process in SAS to R.

## 6.1 Normalisation

The first step is calculating the normalised scores. To recap, this is the inverse (right tail) of the cumulative normal (probit) function of the proportional indicator rank (see normalScores function). First we read in some data, raw data and normalised scores calculated in SIMD, pertaining to the number of individuals with no qualifications.

```
noquals <- read_excel("../openSIMD_analysis/data/NOQUALSDATA.xls")
str(noquals)
```

```
## Classes 'tbl_df', 'tbl' and 'data.frame':    6976 obs. of  3 variables:
##  $ DZ      : chr  "S01006506" "S01006507" "S01006508" "S01006509" ...
##  $ Noquals : num  52.8 95.9 38.6 80.1 77.2 ...
##  $ nnoquals: num  -0.7981 0.0512 -1.2185 -0.2042 -0.2607 ...
```

Now we can perform the normalisation in R with the function defined in the previous section.

```
noquals$r_nnoquals <- normalScores(noquals$Noquals)
```

Now we can compare the two, asking to which degree of precision we have reproduced the result obtained in SAS. In the following code chunk we compare numeric vectors obtained in SAS and R, rounded to the `n` decimal places. We print some output, a collumn to remind us which decimal place and a logical flag, the result of the comparison using `identical`.

```
checkEquivalence <- function(x, y, sig_figs) {
  same <- lapply(sig_figs, function(n) identical(signif(x, n), signif(y, n))) %>% unlist
  data.frame(significant_figures = sig_figs, is_identical = same)
}

checkEquivalence(noquals$nnoquals, noquals$r_nnoquals, 1:16)
```

```
##    significant_figures is_identical
## 1                    1         TRUE
## 2                    2         TRUE
## 3                    3         TRUE
## 4                    4         TRUE
```

```
## 5                        5          TRUE
## 6                        6          TRUE
## 7                        7          TRUE
## 8                        8          TRUE
## 9                        9          TRUE
## 10                      10          TRUE
## 11                      11          TRUE
## 12                      12          TRUE
## 13                      13         FALSE
## 14                      14         FALSE
## 15                      15         FALSE
## 16                      16         FALSE
```

As you can see the normalisation score in this particular example is identical to 11 decimal places and then the two diverge. The authors put this down to small differences in implementation of core functionality across the two platforms.

## 6.2 Factor analysis weights

Next we will examine the correspondence between SAS and R in the factor analysis step. To recap, in this step of the proceedure, we perform factor analysis on all of the indicators within a domain. Then we extract the weights on the first factor and convert them to proportions of the summed weights. This then constitutes the weights with which we combine the normalised indicator scores.

To test the equivelence of this proceedure we first load some data, the published indicators from SIMD 2016. We then also load the weights derived from SAS.

```
indicators <- read_excel("../openSIMD_analysis/data/SIMD2016_indicators.xlsx", sheet = 3, na = "*")
sas_weights <- read_excel("../openSIMD_analysis/data/WEIGHTS.xlsx")
```

Now we need to calculate the weights in R, lets do this for the health domain.

```
r_weights <- indicators %>%
  select(CIF, SMR, LBWT, DRUG, ALCOHOL, DEPRESS, EMERG) %>%
  mutate_all(funs(normalScores)) %>%
  mutate_all(funs(replaceMissing)) %>%
  getFAWeights %>%
  unlist
```

```
## Warning in qnorm(rn, mean = 0, sd = 1, lower.tail = forwards): NaNs
## produced

## Warning in qnorm(rn, mean = 0, sd = 1, lower.tail = forwards): NaNs
## produced
```

```
sas_weights <- sas_weights %>% select(wt_cif:wt_emerg) %>% unlist
names(sas_weights) <- NULL
```

**Note** you should see a warning here when `normalScores` propagates a few missing values.

Now we have the weights derived from sas and R, we can use the same method as above to examine their equivalence.

```
checkEquivalence(sas_weights, r_weights, 1:5)
```

```
##   significant_figures is_identical
## 1                   1         TRUE
```

```
## 2                    2         TRUE
## 3                    3        FALSE
## 4                    4        FALSE
## 5                    5        FALSE
```

As you can see the factor analysis weights are equivalent between the two platforms but only to 2 significant figures. This the hardest step in the process to replicate and again, the authors conclude that this is due to the specific implementation of the factor analysis algorithm in the two platforms.

## 6.3 Domain ranks

The next step is to measure the correspondence in domain ranks across the board. First we need a few more packages and we will load in the SAS results and R results.

```
library(tidyr)
library(ggplot2)
library(purrr)
sas_results <- read_excel("../openSIMD_analysis/data/updated SIMD and domain ranks.xlsx", sheet = 1)
r_results <- read.csv("../openSIMD_analysis/results/domain_ranks.csv")
```

Now we need to do a little bit of wrangling, we need to select some collumns and then rename them. Then we need to join the two datasets together for plotting.

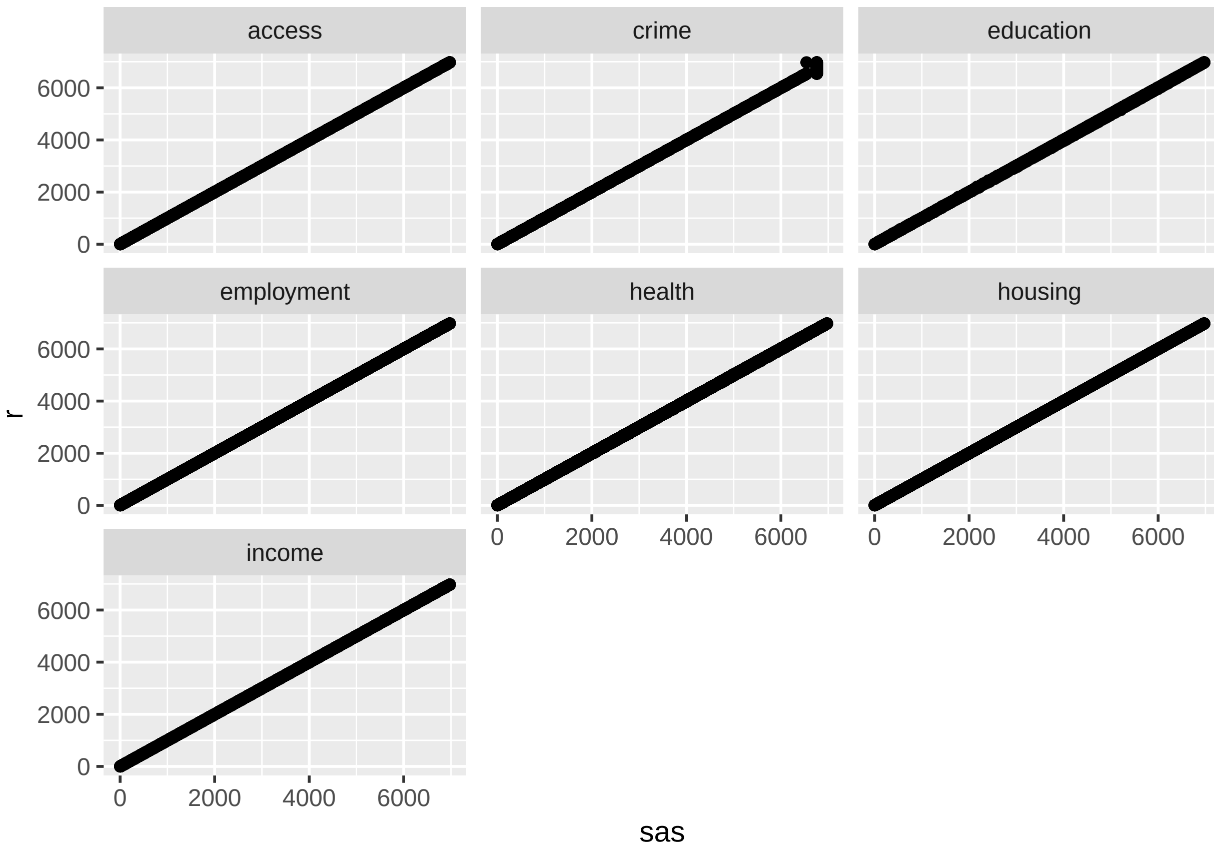
```
sas_domains <- sas_results %>%
  select(-IZ, -LA, -pop, -wapop, -SIMD)
names(sas_domains) <- c("data_zone", "income", "employment", "health",
                        "education", "access", "crime", "housing")

sas_domains$source <- "sas"
r_results$source <- "r"

sas_domains <- gather(sas_domains, domain, rank, -data_zone, -source)
r_results <- gather(r_results, domain, rank, -data_zone, -source)
results <- rbind(sas_domains, r_results) %>% spread(source, rank)
```

Finally we can plot it and see the correlations between R and SAS domain ranks.

```
ggplot(results, aes(x = sas, y = r)) +
  geom_point() +
  facet_wrap(~ domain)
```




We can also ask what the correlation coefficient is for each comparison, and what the median difference in rank is between R and SAS domain ranks.

```
results %>%
  group_by(domain) %>%
  nest %>%
  mutate(rho = map_dbl(data, ~ cor.test(.$sas, .$r, method = "spearman", exact = FALSE)$estimate)) %>%
  mutate(median_diff = map_dbl(data, ~ median(.$r - .$sas))) %>%
  select(domain, rho, median_diff)
```

```
## # A tibble: 7 × 3
##       domain       rho median_diff
##        <chr>     <dbl>       <dbl>
## 1     access 0.9999999           0
## 2      crime 0.9998754           0
## 3  education 0.9999923           1
## 4 employment 1.0000000           0
## 5     health 0.9999911           0
## 6    housing 1.0000000           0
## 7     income 1.0000000           0
```

The results tell us that the results are highly correlated but not exactly equal. Again this is most probably due to the numerical discrepancies in the factor analysis step.

## 6.4 SIMD ranks

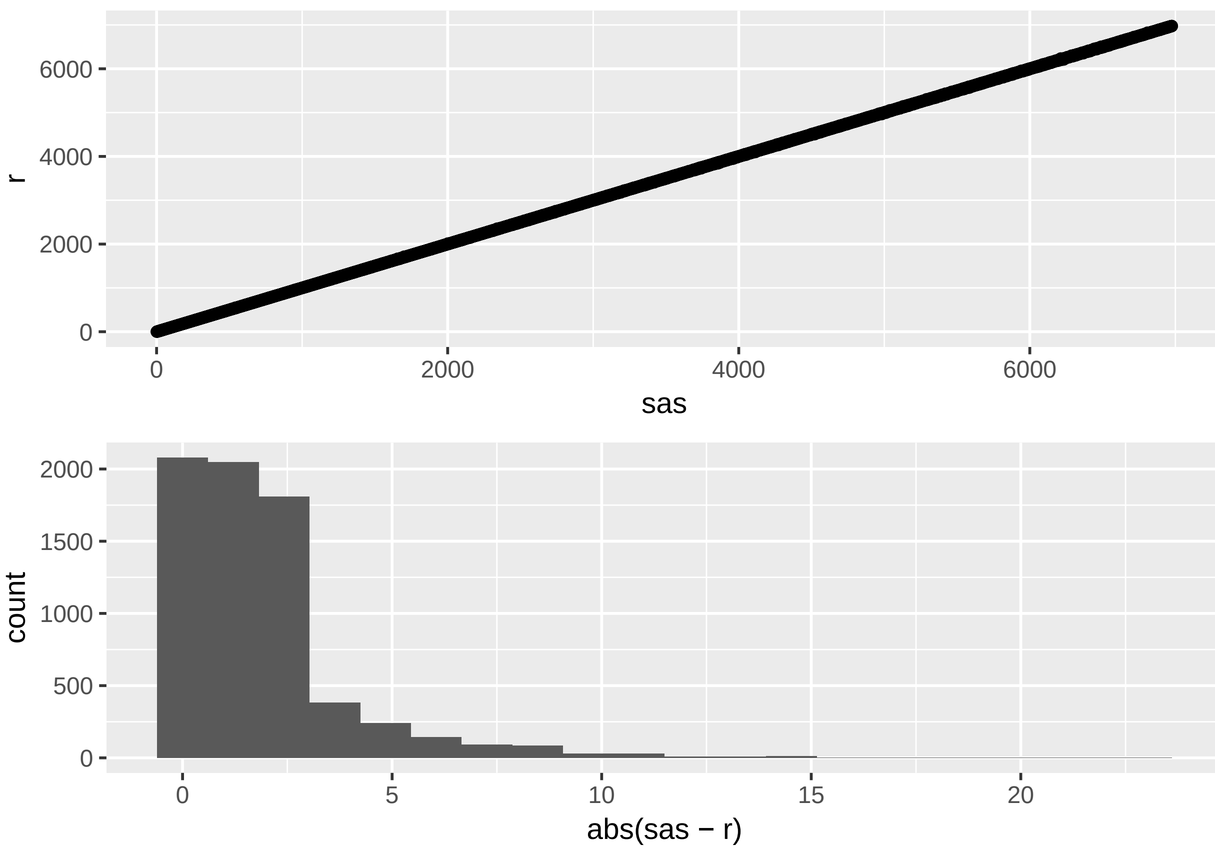
The final step is to compare the final SIMD rankings between the two platforms. Again we need to read in the data and join it up.

```
sas_simd <- sas_results %>% select(DZ, SIMD)
r_simd <- read.csv("../openSIMD_analysis/results/openSIMD_ranks.csv")
names(sas_simd) <- c("data_zone", "sas")
names(r_simd) <- c("data_zone", "r")
simd_results <- left_join(sas_simd, r_simd)
```

```
## Warning in left_join_impl(x, y, by$x, by$y, suffix$x, suffix$y): joining
## factor and character vector, coercing into character vector
```

Then we can examine the correlation in SIMD rankings between R and SAS, and the distribution of differences in SIMD rank.

```
p1 <- ggplot(simd_results, aes(x = sas, y = r)) +
  geom_point()
p2 <- ggplot(simd_results, aes(x = abs(sas - r))) +
  geom_histogram(bins = 20)
gridExtra::grid.arrange(p1, p2)
```




While there is a tight correlation in final SIMD rankings there are some differences. Mostly these differences lie between 0 and 10 with a few as high as 20.

# Chapter 7

# Appendix

This book was compiled in the following R session:

```r
sessionInfo()
```

```
## R version 3.4.0 (2017-04-21)
## Platform: x86_64-apple-darwin15.6.0 (64-bit)
## Running under: macOS Sierra 10.12.3
##
## Matrix products: default
## BLAS: /Library/Frameworks/R.framework/Versions/3.4/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/3.4/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_GB.UTF-8/en_GB.UTF-8/en_GB.UTF-8/C/en_GB.UTF-8/en_GB.UTF-8
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
## [1] purrr_0.2.2   ggplot2_2.2.1 tidyr_0.6.1   dplyr_0.5.0   readxl_1.0.0
##
## loaded via a namespace (and not attached):
##  [1] Rcpp_0.12.10     knitr_1.15.1     magrittr_1.5     munsell_0.4.3
##  [5] mnormt_1.5-5     colorspace_1.3-2 lattice_0.20-35  R6_2.2.0
##  [9] plyr_1.8.4       stringr_1.2.0    tools_3.4.0      parallel_3.4.0
## [13] grid_3.4.0       gtable_0.2.0     nlme_3.1-131     psych_1.7.3.21
## [17] DBI_0.6-1        htmltools_0.3.6  yaml_2.1.14      lazyeval_0.2.0
## [21] rprojroot_1.2    digest_0.6.12    assertthat_0.2.0 tibble_1.3.0
## [25] bookdown_0.3     gridExtra_2.2.1  evaluate_0.10    rmarkdown_1.5
## [29] labeling_0.3     stringi_1.1.5    compiler_3.4.0   cellranger_1.1.0
## [33] scales_0.4.1     backports_1.0.5  foreign_0.8-67
```