

# Record matching

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```
library(janitor)
library(Hmisc)
library(readxl)
library(writexl)
library(reclin2)
library(lubridate)
library(RecordLinkage)
library(dgof) # for statistical testing
library(fdm2id) # for predict that works for kmeans
library(ppclust) # for cmeans
library(tidyverse)

commune_region_lookup <- read_excel("04_Data/Outputs/region_service_commune.xlsx") %>%
  clean_names() %>%
  select(-geometry)
#chile.adm3 <- st_read("04_Data/CHL_adm_humdata/chl_admbnda_adm3_bcn_20211008.shp") %>%
# mutate(commune_code = str_sub(ADM3_PCODE, start = 3, end = -1))

araucnorte_communes <- commune_region_lookup %>%
  filter(str_detect(health_service_name, "a Norte"))
araucsur_communes <- commune_region_lookup %>%
  filter(str_detect(health_service_name, "a Sur"))

chile_merged_raw <- read_csv("04_Data/Data_Chile_Merge.csv") %>% clean_names()

chile_merged <- chile_merged_raw %>%
  rename(sex_desc = sex,
         year = agno,
         school_code = rbd,
         school_check_code = dgv_rbd,
         school_name = nom_rbd,
         school_region_code = cod_reg_rbd,
         school_region_name_abr = nom_reg_rbd_a,
         school_province_code = cod_pro_rbd,
         school_commune_code = cod_com_rbd,
         school_commune_name = nom_com_rbd,
         school_dept_code = cod_deprov_rbd,
         school_dept_name = nom_deprov_rbd,
         school_dependency_code = cod_depe, # has categories 1-6, no1 and no2 here are no1 in grouped
         school_dependency_code_grouped = cod_depe2, # has categories 1-5
         school_rurality_code = rural_rbd,
         school_operation_status = estado_estab,
         teaching_code1 = cod_ense, # min = 10, max = 910, eg preschool, special education hearing impa
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teaching_code2 = cod_ense2, # subject matter coding, 1-8
teaching_code3 = cod_ense3, # age based coding, 1-7
grade_code1 = cod_grado, # grade of schooling, 1-10, 21-25, 31-34, nests in teaching_code1
grade_code2 = cod_grado2, # equivalent grade of schooling for adult special education, 1-8, 99
grade_letter = let_cur, # refers to the class within the grade, close to start of alphabet is
course_timing = cod_jor, # time of day, morning, afternoon, both, night, no info
course_type = cod_tip_cur, # 0 = simple course, 1-4 = combined course, 99 = no info
course_descr = cod_des_cur, # Description of course (TP secondary education only). 0: Does not
student_id = mrun,
sex = gen_alu, # 0 = no info, 1 = male, 2 = female
dob = fec_nac_alu_2, # The second one has DD
age_june30 = edad_alu, # age at 30th June 2021
special_needs_status = int_alu, # integrated student indicator, 0 = no, 1 = yes. Mostly no
special_needs_code = cod_int_alu, # ADHD, blindness, etc. 0 = none. 105 = autism, 203 = ADHD.
student_region_code = cod_reg_alu,
student_commune_code = cod_com_alu,
student_commune_name = nom_com_alu,
economic_sector_code = cod_sec,
economic_specialty_code = cod_espe,
economic_branch_code = cod_rama,
economic_profspec_code = cod_men,
teaching_code_new = ens) %>%
mutate(commune_code = ifelse(nchar(as.character(student_commune_code)) == 4,
                             paste0("0", as.character(student_commune_code)),
                             as.character(student_commune_code)))

```

```

clinical_large_raw <- read_excel("04_Data/dataset_ssas_2015_2021.xlsx") %>% clean_names
#describe(clinical_raw)

```

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clinical_large <- clinical_large_raw %>%
  select(c(-procedence, -ethnicity, -education_level, -disability, -foster_care)) %>%
  # Fix the date columns
  mutate(dob_eng = ifelse(str_detect(date_of_birth, "/"), 1,
                          ifelse(str_detect(date_of_birth, "-"), 0, NA)),
         apt_eng = ifelse(str_detect(date_appointment, "/"), 1, ifelse(str_detect(date_appointment, "-"),
         dob_day = ifelse(dob_eng == 1, as.integer(str_extract(date_of_birth, "^\\d+")),
                          ifelse(dob_eng == 0, as.integer(str_extract(date_of_birth, "^\\d+")), NA)),
         dob_month = ifelse(dob_eng == 1, as.integer(str_extract(date_of_birth, "(?<=/)\\d+(?=/)")),
                           ifelse(dob_eng == 0, str_extract(date_of_birth, "(?<=-)\\w+(?=-)", NA)),
         dob_year = ifelse(dob_eng == 1, as.integer(str_extract(date_of_birth, "\\d+$")),
                           ifelse(dob_eng == 0, as.integer(str_extract(date_of_birth, "\\d+$")) + 2000, NA)),
         dob_month_eng = as.integer(ifelse(dob_month == "ene", 1,
                                           ifelse(dob_month == "abr", 4,
                                           ifelse(dob_month == "ago", 8,
                                           ifelse(dob_month == "sept", 9,
                                           ifelse(dob_month == "dic", 12, dob_month))))),
         dob = make_date(year = dob_year, month = dob_month_eng, day = dob_day),
         apt_day = ifelse(apt_eng == 1, as.integer(str_extract(date_appointment, "^\\d+")),
                          ifelse(apt_eng == 0, as.integer(str_extract(date_appointment, "^\\d+")), NA)),
         apt_month = ifelse(apt_eng == 1, as.integer(str_extract(date_appointment, "(?<=/)\\d+(?=/)")),
                           ifelse(apt_eng == 0, str_extract(date_appointment, "(?<=-)\\w+(?=-)", NA)),
         apt_year = ifelse(apt_eng == 1, as.integer(str_extract(date_appointment, "\\d+$")),
                           ifelse(apt_eng == 0, as.integer(str_extract(date_appointment, "\\d+$")) + 2000, NA)),
         apt_month_eng = as.integer(ifelse(apt_month == "ene", 1,

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            ifelse(apt_month == "abr", 4,
            ifelse(apt_month == "ago", 8,
            ifelse(apt_month == "sept", 9,
            ifelse(apt_month == "dic", 12, apt_month))))),
    apt_date = make_date(year = apt_year, month = apt_month_eng, day = apt_day),
    age_june30 = trunc(time_length(interval(ymd(dob), ymd("2021-06-30")), unit = "year")),
    commune_name_upper = ifelse(comuna == "CHOL CHOL", "CHOLCHOL",
            ifelse(comuna == "CURACAUTIN", "CURACAUTÍN",
            ifelse(comuna == "PITRUFQUEN", "PITRUFQUÉN",
            ifelse(comuna == "PUCON", "PUCÓN",
            ifelse(comuna == "TOLTEN", "TOLTÉN",
            ifelse(comuna == "VILCUN", "VILCÚN", comuna))))),
    #commune_name_upper = comuna,
    ses_status = ifelse(socio_economic_level == "FONASA - A", 1,
            ifelse(socio_economic_level == "FONASA - B", 2,
            ifelse(socio_economic_level == "FONASA - C", 2,
            ifelse(socio_economic_level == "FONASA - D", 2,
            ifelse(socio_economic_level == "Private Health Insurance", 3,
            ifelse(socio_economic_level %in% c("COLMENA GOLDEN CROSS", "RIO BLANCO", "CARABINIEROS", "MACHALI", "TEMUCO", "DIEGO DE ALMAGRO"), 0))),
    autism = 1,
    intdisab = 0,
    aut_rank = 1
    ) %>%
left_join(commune_region_lookup, by = "commune_name_upper") %>%
select(id, gender, commune_code, commune_name, commune_name_upper, health_service_name, region_name,
aut_codes <- unique(clinical_large$codigo)

clinical_small_raw <- read_excel("04_Data/Dataset_Vill_2014_2021.xlsx", col_names = TRUE) %>% clean_names()

clinical_small <- clinical_small_raw %>%
  rename("dob" = "fecha_nacimiento",
        "apt_date" = "fecha_ejecutada",
        "type_appointment" = "appointment",
        "diagnosis" = "diagnostico_1") %>%
  mutate(gender = str_to_title(gender),
        autism = ifelse(cod_dg_1 %in% aut_codes |
                        cod_dg_2 %in% aut_codes |
                        cod_dg_3 %in% aut_codes, 1, 0),
        aut_rank = ifelse(cod_dg_1 %in% aut_codes, 1,
                        ifelse(cod_dg_2 %in% aut_codes, 2,
                        ifelse(cod_dg_3 %in% aut_codes, 3, NA))),
        age_june30 = trunc(time_length(interval(ymd(dob), ymd("2021-06-30")), unit = "year")),
        commune_name_upper = ifelse(comuna == "CHOL CHOL", "CHOLCHOL",
            ifelse(comuna == "CURACAUTIN", "CURACAUTÍN",
            ifelse(comuna == "PITRUFQUEN", "PITRUFQUÉN",
            ifelse(comuna == "PUCON", "PUCÓN",
            ifelse(comuna == "TOLTEN", "TOLTÉN",
            ifelse(comuna == "VILCUN", "VILCÚN",
            ifelse(comuna == "DIEGO DE ALMAGRO (#)", "DIEGO DE ALMAGRO",
            ifelse(comuna == "MACHALI", "MACHALÍ",
            ifelse(comuna == "TEMUCO (##)", "TEMUCO", comuna))))))))) ,
        ses_status = ifelse(socio_economic_level == "FONASA - A", 1,

```

```

        ifelse(socio_economic_level == "FONASA - B", 2,
        ifelse(socio_economic_level == "FONASA - C", 2,
        ifelse(socio_economic_level == "FONASA - D", 2,
        ifelse(socio_economic_level == "Private Health Insurance", 3,
        ifelse(socio_economic_level %in% c("COLMENA GOLDEN CROSS", "RIO BLANCO", "CARABINIEROS")
    ) %>%
left_join(commune_region_lookup, by = "commune_name_upper") %>%
#filter(autism == 1) %>%
select(id, gender, commune_code, commune_name, commune_name_upper, health_service_name, region_name,

## Warning in left_join(., commune_region_lookup, by = "commune_name_upper"): Each row in `x` is expected
## i Row 2030 of `x` matches multiple rows.
## i If multiple matches are expected, set `multiple = "all"` to silence this
##   warning.
# Throws a warning because there are 2 records for Tocopila which is in two regions. Will keep both bec

intdisab_codes <- unique(c(clinical_small_raw$cod_dg_1, clinical_small_raw$cod_dg_2, clinical_small_raw$cod_dg_3))
str_subset("F7") %>%
sort()

clinical_small <- clinical_small %>%
mutate(intdisab = ifelse(cod_dg_1 %in% intdisab_codes |
                        cod_dg_2 %in% intdisab_codes |
                        cod_dg_3 %in% intdisab_codes, 1, 0)) %>%
rename("codigo" = "cod_dg_1") %>%
select(c(-cod_dg_2, -cod_dg_3))

clinical <- rbind(clinical_large, clinical_small)

clinical_communes <- clinical %>% group_by(commune_code) %>% summarise() %>% arrange() %>%
mutate(commune_in_school_data = ifelse(commune_code %in% unique(chile_merged$commune_code), 1, 0)) #

```

Fixed the date columns because they were in English and Spanish. Redefined the age column to be age at 30th June 2021.

Get one row per person per commune to make matching more efficient. Take the earliest appointment for each person.

```

get.min.na <- function(x) ifelse( !all(is.na(x)), min(x, na.rm = TRUE), NA)
get.max.na <- function(x) ifelse( !all(is.na(x)), max(x, na.rm = TRUE), NA)

patients <- clinical %>%
  filter(commune_code %in% araucsur_communes$commune_code) %>%
  group_by(id, gender, dob, commune_name, region_name, ses_status) %>% # Maybe move SES back to here
  summarise(#ses_status = get.min.na(ses_status),
            autism = get.max.na(autism),
            #intdisab = get.max.na(intdisab),
            aut_rank = get.min.na(aut_rank)) %>%
  ungroup() %>%
  rename("student_commune_name" = "commune_name",
        "student_region_name" = "region_name",
        "sex_desc" = "gender") %>%
  rowid_to_column("row_id") %>%
  select(row_id,

```

```

      id,
      dob,
      sex_desc,
      student_commune_name,
      autism,
      ses_status,
      #intdisab,
      aut_rank) #, student_region_name) #, count)

## `summarise()` has grouped output by 'id', 'gender', 'dob', 'commune_name',
## 'region_name'. You can override using the `.groups` argument.

write_xlsx(patients, "04_Data/Outputs/patients.xlsx")

length(unique(patients$id))

## [1] 1688

patients_unique <- patients %>%
  group_by(id) %>%
  summarise(sex_desc = list(sex_desc),
            student_commune_name = list(student_commune_name),
            dob = list(dob),
            ses_status = list(ses_status))
write_csv(patients_unique, "04_Data/Outputs/patients_unique.csv") # can't write columns containing list.

```

NB: there are 1688 unique ID's in patients and it's 1747 rows long because some people are represented in 2 communes.

Are all the records in the small dataset in the big one? No

```

clinical %>% filter(id %in% clinical_small$id)

## # A tibble: 3,558 x 20
##   id          gender commune_c~1 commu~2 commu~3 healt~4 regio~5 socio~6 ses_s~7
##   <chr>      <chr> <chr>      <chr>  <chr>  <chr>  <chr>  <chr>  <dbl>
## 1 21282495-K Female 09109      Loncoc~ LONCOC~ Servic~ Región~ FONASA~ 2
## 2 21282495-K Female 09109      Loncoc~ LONCOC~ Servic~ Región~ FONASA~ 2
## 3 21294488-2 Male   09120      Villar~ VILLAR~ Servic~ Región~ Privat~ 3
## 4 21294488-2 Male   09120      Villar~ VILLAR~ Servic~ Región~ Privat~ 3
## 5 21294488-2 Male   09120      Villar~ VILLAR~ Servic~ Región~ Privat~ 3
## 6 21341924-2 Male   09115      Pucón   PUCÓN   Servic~ Región~ FONASA~ 2
## 7 21341924-2 Male   09115      Pucón   PUCÓN   Servic~ Región~ FONASA~ 2
## 8 21341924-2 Male   09115      Pucón   PUCÓN   Servic~ Región~ FONASA~ 2
## 9 21341924-2 Male   09115      Pucón   PUCÓN   Servic~ Región~ FONASA~ 2
## 10 21341924-2 Male   09115      Pucón   PUCÓN   Servic~ Región~ FONASA~ 2
## # ... with 3,548 more rows, 11 more variables: dob <date>, age_june30 <dbl>,
## # apt_date <date>, hospital <chr>, medical_specialty <chr>,
## # type_appointment <chr>, codigo <chr>, diagnosis <chr>, autism <dbl>,
## # intdisab <dbl>, aut_rank <dbl>, and abbreviated variable names
## # 1: commune_code, 2: commune_name, 3: commune_name_upper,
## # 4: health_service_name, 5: region_name, 6: socio_economic_level,
## # 7: ses_status

```

Assume this is because the big clinical dataset only has people with autism, not ADHD.

Only try to link clinical data to records in the schools data for the Southern health service in Araucanía

(ARAUC) because that's where the clinical data is from.

```

school <- chile_merged %>%
  # mutate(commune_code = ifelse(nchar(as.character(student_commune_code)) == 4,
  #                               paste0("0", as.character(student_commune_code)),
  #                               as.character(student_commune_code))) %>%
  select(-student_commune_name) %>%
  left_join(commune_region_lookup, by = "commune_code") %>%
  filter(commune_code %in% araucsur_communes$commune_code) %>%
  #filter(health_service_name == "Servicio de Salud Araucanía Sur") %>% # This should be filtered either
  filter(age_june30 >= 6 & age_june30 <= 18, sex != 0) %>% # Could try without this filter to pick up e
  # filter only the communes represented in the clinical data here?
  mutate(autism = ifelse(special_needs_code == 105, 1, 0),
         #intdisab = 0,
         aut_rank = 1,
         dob = ymd(dob),
         ses_status = ifelse(school_fee == "", NA,
                             ifelse(school_fee == "GRATUITO", 1,
                                     ifelse(school_fee == "$1.000 A $10.000", 2,
                                             ifelse(school_fee == "$10.001 A $25.000", 2,
                                                     ifelse(school_fee == "$25.001 A $50.000", 2,
                                                             ifelse(school_fee == "$50.001 A $100.000", 2,
                                                                     ifelse(school_fee == "MAS DE $100.000", 2,
                                                                             ifelse(school_fee == "SIN INFORMACION", NA, NA)))))))))) %>%
  filter(autism == 1) %>% # We only want to find additional autism cases in the clinical records, we do
  rename(student_commune_name = commune_name) %>%
  select(dob,
         sex_desc,
         student_commune_name,
         #commune_name,
         #health_service_name,
         autism,
         ses_status,
         #intdisab,
         aut_rank#,
         #student_region_name
  ) %>%
  rowid_to_column("id")
school[dim(school)[1]+1, ] <- c(dim(school)[1]+1, "2023-06-26", "Female", "Misc", 0, 3, 0)

# Do the commune names align well? Yes
table(sort(unique(patients$student_commune_name, sort(unique(school$student_commune_name)))))

```

```

##
##      Carahue      Cholchol      Cunco      Curarrehue      Freire
##          47          9          33          12          32
##      Galvarino      Gorbea      Lautaro      Loncoche      Melipeuco
##          22          21          106          89          5
## Nueva Imperial Padre Las Casas      Perquenco      Pitrufquén      Pucón
##          81          148          19          47          95
##      Saavedra      Temuco Teodoro Schmidt      Toltén      Vilcún
##          14          603          12          18          60
##      Villarrica
##          274

```

```
sort(unique(patients$student_commune_name))
```

```
## [1] "Carahue"      "Cholchol"      "Cunco"          "Curarrehue"
## [5] "Freire"       "Galvarino"     "Gorbea"         "Lautaro"
## [9] "Loncoche"     "Melipeuco"     "Nueva Imperial" "Padre Las Casas"
## [13] "Perquenco"    "Pitrufquén"    "Pucón"          "Saavedra"
## [17] "Temuco"       "Teodoro Schmidt" "Toltén"         "Vilcún"
## [21] "Villarrica"
```

```
sort(unique(school$student_commune_name))
```

```
## [1] "Carahue"      "Cholchol"      "Cunco"          "Curarrehue"
## [5] "Freire"       "Galvarino"     "Gorbea"         "Lautaro"
## [9] "Loncoche"     "Melipeuco"     "Misc"           "Nueva Imperial"
## [13] "Padre Las Casas" "Perquenco"     "Pitrufquén"     "Pucón"
## [17] "Saavedra"     "Temuco"        "Teodoro Schmidt" "Toltén"
## [21] "Vilcún"       "Villarrica"
```

Added a fake row at the end of school to have a ses=3 represented so that pairing works.

Perfect match in communes between patient and school dataset when both are filtered to only be communes in Arauc Sur health region.

## Try manual linkage

```
patients_grouped <- patients %>%
  group_by(sex_desc,
            dob,
            student_commune_name) %>%
  summarise(count = n(),
            ids = list(id))
```

## `summarise()` has grouped output by 'sex\_desc', 'dob'. You can override using  
## the `.groups` argument.

```
school_grouped <- school %>%
  group_by(sex_desc,
            dob,
            student_commune_name) %>%
  summarise(count = n(),
            #ids = list(rowid)
            ses = list(ses_status))
```

## `summarise()` has grouped output by 'sex\_desc', 'dob'. You can override using  
## the `.groups` argument.

```
sort(unique(patients$student_commune_name))
```

```
## [1] "Carahue"      "Cholchol"      "Cunco"          "Curarrehue"
## [5] "Freire"       "Galvarino"     "Gorbea"         "Lautaro"
## [9] "Loncoche"     "Melipeuco"     "Nueva Imperial" "Padre Las Casas"
## [13] "Perquenco"    "Pitrufquén"    "Pucón"          "Saavedra"
## [17] "Temuco"       "Teodoro Schmidt" "Toltén"         "Vilcún"
## [21] "Villarrica"
```

```
sort(unique(school$student_commune_name))
```



```
## [1] "Carahue"      "Cholchol"      "Cunco"          "Curarrehue"
## [5] "Freire"       "Galvarino"     "Gorbea"         "Lautaro"
## [9] "Loncoche"     "Melipeuco"     "Misc"           "Nueva Imperial"
## [13] "Padre Las Casas" "Perquenco"     "Pitrufulquén"  "Pucón"
## [17] "Saavedra"     "Temuco"        "Teodoro Schmidt" "Toltén"
## [21] "Vilcún"       "Villarrica"
```

```
merged <- merge(school, patients, by = c("sex_desc", "dob", "student_commune_name"), all = FALSE)
merged %>% filter(!is.na(id.x) & !is.na(id.y)) # 205 matches
```

	sex_desc	dob	student_commune_name	id.x	autism.x	ses_status.x
## 1	Female	2003-04-16	Loncoche	450	1	1
## 2	Female	2003-11-25	Temuco	437	1	2
## 3	Female	2005-12-07	Temuco	380	1	1
## 4	Female	2006-08-10	Lautaro	470	1	1
## 5	Female	2006-09-20	Freire	109	1	1
## 6	Female	2006-10-10	Padre Las Casas	263	1	1
## 7	Female	2008-05-20	Gorbea	187	1	1
## 8	Female	2008-06-21	Temuco	269	1	1
## 9	Female	2009-05-08	Temuco	57	1	1
## 10	Female	2009-06-22	Pucón	332	1	1
## 11	Female	2010-04-27	Temuco	426	1	1
## 12	Female	2011-04-20	Temuco	173	1	2
## 13	Female	2012-01-31	Villarrica	172	1	1
## 14	Female	2012-01-31	Villarrica	172	1	1
## 15	Female	2012-04-07	Pucón	425	1	1
## 16	Female	2012-05-28	Vilcún	214	1	1
## 17	Female	2012-06-18	Villarrica	41	1	1
## 18	Female	2012-09-13	Temuco	104	1	1
## 19	Female	2013-04-20	Galvarino	296	1	1
## 20	Female	2013-06-19	Temuco	267	1	1
## 21	Female	2013-08-30	Padre Las Casas	311	1	1
## 22	Female	2013-12-30	Villarrica	190	1	2
## 23	Female	2014-02-15	Temuco	105	1	1
## 24	Female	2014-10-09	Gorbea	419	1	1
## 25	Female	2014-10-16	Temuco	415	1	2
## 26	Female	2014-11-12	Temuco	351	1	1
## 27	Female	2014-12-11	Pucón	80	1	1
## 28	Female	2014-12-12	Temuco	464	1	1
## 29	Male	2003-01-27	Temuco	227	1	1
## 30	Male	2003-03-06	Temuco	465	1	1
## 31	Male	2003-06-14	Temuco	92	1	1
## 32	Male	2003-06-15	Temuco	165	1	1
## 33	Male	2003-06-29	Temuco	53	1	1
## 34	Male	2003-08-03	Temuco	313	1	1
## 35	Male	2003-10-21	Temuco	186	1	1
## 36	Male	2003-12-15	Temuco	389	1	1
## 37	Male	2004-03-05	Nueva Imperial	442	1	1
## 38	Male	2004-03-12	Temuco	133	1	1
## 39	Male	2004-07-07	Temuco	322	1	2
## 40	Male	2004-09-28	Loncoche	216	1	1
## 41	Male	2004-10-01	Freire	307	1	1
## 42	Male	2004-11-07	Temuco	362	1	1
## 43	Male	2004-12-25	Cunco	174	1	1
## 44	Male	2005-01-03	Temuco	39	1	2



## 45	Male	2005-01-09	Temuco	49	1	1
## 46	Male	2005-01-21	Temuco	202	1	1
## 47	Male	2005-05-24	Temuco	78	1	1
## 48	Male	2005-06-17	Temuco	123	1	1
## 49	Male	2005-06-17	Temuco	123	1	1
## 50	Male	2005-08-29	Temuco	70	1	1
## 51	Male	2005-09-06	Temuco	405	1	2
## 52	Male	2006-03-04	Temuco	147	1	1
## 53	Male	2006-03-22	Temuco	11	1	1
## 54	Male	2006-04-13	Padre Las Casas	301	1	1
## 55	Male	2006-09-09	Galvarino	434	1	1
## 56	Male	2006-09-19	Lautaro	219	1	1
## 57	Male	2006-10-06	Lautaro	448	1	1
## 58	Male	2006-10-10	Vilcún	478	1	1
## 59	Male	2006-10-27	Temuco	247	1	1
## 60	Male	2006-11-02	Padre Las Casas	176	1	2
## 61	Male	2006-11-06	Temuco	471	1	2
## 62	Male	2006-11-06	Temuco	471	1	2
## 63	Male	2007-01-08	Carahue	319	1	1
## 64	Male	2007-01-23	Villarrica	363	1	1
## 65	Male	2007-02-13	Temuco	235	1	1
## 66	Male	2007-03-22	Lautaro	265	1	1
## 67	Male	2007-04-09	Padre Las Casas	31	1	1
## 68	Male	2007-04-25	Lautaro	336	1	1
## 69	Male	2007-05-11	Temuco	355	1	1
## 70	Male	2007-06-16	Pitrufquén	358	1	1
## 71	Male	2007-08-20	Pitrufquén	237	1	1
## 72	Male	2007-11-06	Villarrica	295	1	1
## 73	Male	2007-12-28	Loncoche	130	1	1
## 74	Male	2008-01-28	Nueva Imperial	44	1	1
## 75	Male	2008-03-05	Pucón	420	1	1
## 76	Male	2008-03-14	Temuco	408	1	1
## 77	Male	2008-03-25	Temuco	289	1	1
## 78	Male	2008-03-25	Temuco	289	1	1
## 79	Male	2008-05-20	Padre Las Casas	100	1	1
## 80	Male	2008-06-18	Vilcún	55	1	1
## 81	Male	2008-08-24	Saavedra	158	1	1
## 82	Male	2008-10-10	Temuco	112	1	2
## 83	Male	2008-10-22	Villarrica	72	1	1
## 84	Male	2008-10-22	Villarrica	72	1	1
## 85	Male	2008-11-22	Nueva Imperial	467	1	1
## 86	Male	2008-12-06	Lautaro	22	1	1
## 87	Male	2008-12-21	Temuco	394	1	1
## 88	Male	2008-12-29	Temuco	93	1	1
## 89	Male	2009-01-07	Lautaro	361	1	1
## 90	Male	2009-01-12	Temuco	26	1	1
## 91	Male	2009-02-13	Pucón	3	1	1
## 92	Male	2009-02-26	Loncoche	168	1	1
## 93	Male	2009-04-23	Loncoche	314	1	1
## 94	Male	2009-04-23	Loncoche	314	1	1
## 95	Male	2009-08-05	Villarrica	60	1	1
## 96	Male	2009-08-05	Villarrica	60	1	1
## 97	Male	2009-08-14	Pucón	252	1	1
## 98	Male	2009-08-14	Pucón	252	1	1

## 99	Male	2009-08-29	Temuco	159	1	2
## 100	Male	2009-10-01	Temuco	328	1	1
## 101	Male	2009-10-26	Temuco	341	1	1
## 102	Male	2010-01-02	Freire	272	1	1
## 103	Male	2010-01-25	Padre Las Casas	73	1	2
## 104	Male	2010-02-21	Loncoche	180	1	1
## 105	Male	2010-02-26	Teodoro Schmidt	213	1	1
## 106	Male	2010-03-07	Lautaro	242	1	1
## 107	Male	2010-03-16	Gorbea	246	1	1
## 108	Male	2010-05-20	Villarrica	396	1	1
## 109	Male	2010-06-07	Temuco	476	1	1
## 110	Male	2010-06-08	Nueva Imperial	292	1	1
## 111	Male	2010-07-21	Cholchol	194	1	1
## 112	Male	2010-07-28	Freire	382	1	1
## 113	Male	2010-08-29	Villarrica	365	1	1
## 114	Male	2010-09-13	Padre Las Casas	312	1	1
## 115	Male	2010-10-12	Temuco	201	1	1
## 116	Male	2010-12-09	Pucón	346	1	1
## 117	Male	2010-12-09	Temuco	107	1	1
## 118	Male	2011-01-13	Villarrica	18	1	2
## 119	Male	2011-01-24	Temuco	87	1	1
## 120	Male	2011-02-11	Cunco	368	1	1
## 121	Male	2011-02-22	Temuco	139	1	1
## 122	Male	2011-03-03	Lautaro	228	1	1
## 123	Male	2011-04-13	Villarrica	275	1	1
## 124	Male	2011-04-13	Villarrica	275	1	1
## 125	Male	2011-06-13	Temuco	203	1	1
## 126	Male	2011-07-02	Lautaro	475	1	1
## 127	Male	2011-08-02	Carahue	113	1	1
## 128	Male	2011-09-06	Teodoro Schmidt	229	1	1
## 129	Male	2011-09-08	Temuco	277	1	1
## 130	Male	2011-10-27	Teodoro Schmidt	283	1	1
## 131	Male	2011-11-10	Freire	300	1	1
## 132	Male	2011-11-12	Padre Las Casas	278	1	1
## 133	Male	2012-01-11	Pucón	290	1	1
## 134	Male	2012-01-11	Pucón	290	1	1
## 135	Male	2012-03-06	Villarrica	243	1	1
## 136	Male	2012-03-12	Temuco	261	1	1
## 137	Male	2012-04-16	Temuco	472	1	1
## 138	Male	2012-05-29	Temuco	8	1	1
## 139	Male	2012-06-01	Padre Las Casas	66	1	1
## 140	Male	2012-06-02	Temuco	141	1	1
## 141	Male	2012-06-25	Galvarino	183	1	1
## 142	Male	2012-07-08	Temuco	315	1	1
## 143	Male	2012-07-16	Galvarino	152	1	1
## 144	Male	2012-07-29	Vilcún	16	1	1
## 145	Male	2012-09-07	Temuco	293	1	1
## 146	Male	2012-09-21	Cunco	264	1	1
## 147	Male	2012-10-13	Villarrica	45	1	1
## 148	Male	2012-10-13	Villarrica	45	1	1
## 149	Male	2012-10-18	Villarrica	392	1	1
## 150	Male	2012-11-03	Lautaro	443	1	1
## 151	Male	2012-11-05	Temuco	447	1	1
## 152	Male	2012-12-10	Pitrufquén	304	1	<NA>

## 153	Male	2012-12-25	Padre Las Casas	29	1	1
## 154	Male	2013-01-26	Gorbea	385	1	1
## 155	Male	2013-01-30	Pitrufquén	97	1	1
## 156	Male	2013-02-12	Temuco	366	1	1
## 157	Male	2013-02-25	Gorbea	294	1	1
## 158	Male	2013-02-27	Nueva Imperial	24	1	1
## 159	Male	2013-03-24	Villarrica	386	1	1
## 160	Male	2013-04-23	Toltén	350	1	1
## 161	Male	2013-05-20	Temuco	280	1	1
## 162	Male	2013-05-23	Lautaro	189	1	1
## 163	Male	2013-05-30	Villarrica	469	1	1
## 164	Male	2013-07-07	Vilcún	338	1	1
## 165	Male	2013-10-16	Vilcún	111	1	1
## 166	Male	2013-10-23	Pitrufquén	324	1	1
## 167	Male	2013-11-05	Villarrica	211	1	1
## 168	Male	2013-11-05	Villarrica	211	1	1
## 169	Male	2013-11-14	Temuco	71	1	1
## 170	Male	2014-02-19	Temuco	326	1	1
## 171	Male	2014-02-19	Temuco	326	1	1
## 172	Male	2014-02-19	Temuco	451	1	1
## 173	Male	2014-02-19	Temuco	451	1	1
## 174	Male	2014-04-17	Temuco	335	1	1
## 175	Male	2014-04-21	Temuco	129	1	1
## 176	Male	2014-05-06	Villarrica	271	1	1
## 177	Male	2014-05-17	Cunco	125	1	1
## 178	Male	2014-05-20	Temuco	287	1	1
## 179	Male	2014-05-24	Loncoche	407	1	1
## 180	Male	2014-06-02	Temuco	162	1	1
## 181	Male	2014-06-16	Temuco	77	1	1
## 182	Male	2014-07-07	Temuco	116	1	1
## 183	Male	2014-08-30	Galvarino	6	1	1
## 184	Male	2014-09-06	Temuco	145	1	1
## 185	Male	2014-09-06	Temuco	145	1	1
## 186	Male	2014-09-12	Loncoche	310	1	1
## 187	Male	2014-09-12	Loncoche	310	1	1
## 188	Male	2014-10-07	Temuco	98	1	1
## 189	Male	2014-10-07	Temuco	98	1	1
## 190	Male	2014-10-07	Temuco	118	1	1
## 191	Male	2014-10-07	Temuco	118	1	1
## 192	Male	2014-10-28	Temuco	15	1	1
## 193	Male	2014-11-02	Temuco	399	1	1
## 194	Male	2014-11-16	Lautaro	91	1	1
## 195	Male	2014-11-19	Pucón	357	1	1
## 196	Male	2014-12-29	Padre Las Casas	456	1	2
## 197	Male	2015-01-03	Villarrica	353	1	1
## 198	Male	2015-01-19	Vilcún	157	1	1
## 199	Male	2015-01-25	Padre Las Casas	270	1	1
## 200	Male	2015-02-02	Teodoro Schmidt	466	1	1
## 201	Male	2015-03-06	Nueva Imperial	458	1	1
## 202	Male	2015-03-10	Galvarino	181	1	1
## 203	Male	2015-03-11	Temuco	387	1	1
## 204	Male	2015-03-13	Temuco	256	1	1
## 205	Male	2015-05-02	Temuco	376	1	1
##	aut_rank.x row_id		id.y autism.y ses_status.y aut_rank.y			

## 1	1	21	21282495-K	1	2	1
## 2	1	81	21449127-3	1	2	1
## 3	1	295	21994583-3	1	1	1
## 4	1	360	22183641-3	1	2	1
## 5	1	371	22213761-6	1	2	1
## 6	1	377	22234827-7	1	2	1
## 7	1	568	22724176-4	1	1	1
## 8	1	580	22752332-8	1	1	1
## 9	1	692	23021556-1	1	2	1
## 10	1	702	23054104-3	1	2	1
## 11	1	818	23310188-5	1	2	1
## 12	1	966	23624343-5	1	2	1
## 13	1	1063	23860402-8	1	1	1
## 14	1	1064	23860402-8	1	2	1
## 15	1	1081	23917587-2	1	2	1
## 16	1	1109	23959967-2	1	3	1
## 17	1	1120	23987283-2	1	1	1
## 18	1	1162	24064290-5	1	2	1
## 19	1	1253	24249709-0	1	1	1
## 20	1	1276	24307066-K	1	2	1
## 21	1	1303	24396036-3	1	2	1
## 22	1	1336	24495784-6	1	2	1
## 23	1	1353	24539730-5	1	1	1
## 24	1	1447	24763669-2	1	2	1
## 25	1	1451	24771215-1	1	2	1
## 26	1	1458	24797188-2	1	1	1
## 27	1	1470	24825751-2	1	2	1
## 28	1	1467	24824555-7	1	2	1
## 29	1	46	21338851-7	1	2	1
## 30	1	14	21251752-6	1	1	1
## 31	1	37	21319146-2	1	1	1
## 32	1	38	21319994-3	1	2	1
## 33	1	43	21332821-2	1	1	1
## 34	1	49	21354095-5	1	2	1
## 35	1	76	21417599-1	1	1	1
## 36	1	87	21464033-3	1	2	1
## 37	1	102	21520695-5	1	2	1
## 38	1	108	21543736-1	1	2	1
## 39	1	138	21619878-6	1	2	1
## 40	1	162	21670184-4	1	2	1
## 41	1	165	21679874-0	1	2	1
## 42	1	174	21700914-6	1	1	1
## 43	1	192	21737462-6	1	2	1
## 44	1	196	21748664-5	1	2	1
## 45	1	198	21750199-7	1	2	1
## 46	1	202	21759050-7	1	1	1
## 47	1	242	21859877-3	1	2	1
## 48	1	245	21867880-7	1	2	1
## 49	1	244	21862073-6	1	2	1
## 50	1	262	21921022-1	1	1	1
## 51	1	264	21925304-4	1	2	1
## 52	1	316	22065375-7	1	1	1
## 53	1	320	22079654-K	1	2	1
## 54	1	328	22095157-K	1	2	1

## 55	1	365	22204715-3	1	1	1
## 56	1	370	22211545-0	1	2	1
## 57	1	376	22226291-7	1	2	1
## 58	1	378	22237373-5	1	1	1
## 59	1	384	22245810-2	1	1	1
## 60	1	385	22249166-5	1	2	1
## 61	1	388	22253752-5	1	2	1
## 62	1	389	22253904-8	1	2	1
## 63	1	412	22300065-7	1	2	1
## 64	1	416	22312842-4	1	2	1
## 65	1	427	22327040-9	1	2	1
## 66	1	436	22356979-K	1	2	1
## 67	1	443	22370213-9	1	2	1
## 68	1	450	22386477-5	1	2	1
## 69	1	453	22395859-1	1	2	1
## 70	1	458	22426890-4	1	2	1
## 71	1	483	22491627-2	1	2	1
## 72	1	499	22549846-6	1	2	1
## 73	1	518	22592217-9	1	1	1
## 74	1	529	22637968-1	1	2	1
## 75	1	536	22663017-1	1	2	1
## 76	1	544	22670294-6	1	1	1
## 77	1	547	22678488-8	1	1	1
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## 79	1	567	22723986-7	1	1	1
## 80	1	582	22755037-6	1	2	1
## 81	1	602	22805100-4	1	1	1
## 82	1	621	22838644-8	1	2	1
## 83	1	631	22852889-7	1	1	1
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## 85	1	638	22881315-K	1	1	1
## 86	1	642	22891576-9	1	2	1
## 87	1	647	22901266-5	1	2	1
## 88	1	652	22907807-0	1	2	1
## 89	1	654	22915922-4	1	2	1
## 90	1	655	22920380-0	1	2	1
## 91	1	666	22945155-3	1	2	1
## 92	1	672	22958693-9	1	1	1
## 93	1	689	23006189-0	1	2	1
## 94	1	688	23006189-0	1	1	1
## 95	1	715	23093195-K	1	3	1
## 96	1	714	23093195-K	1	2	1
## 97	1	717	23099554-0	1	3	1
## 98	1	716	23099554-0	1	2	1
## 99	1	721	23111138-7	1	2	1
## 100	1	732	23136875-2	1	2	1
## 101	1	748	23157810-2	1	2	1
## 102	1	779	23216852-8	1	1	1
## 103	1	788	23233498-3	1	2	1
## 104	1	796	23258114-K	1	1	1
## 105	1	803	23266559-9	1	1	1
## 106	1	801	23263729-3	1	1	1
## 107	1	806	23273376-4	1	2	1
## 108	1	827	23330047-0	1	2	1

## 109	1	833	23343300-4	1	2	1
## 110	1	834	23346792-8	1	1	1
## 111	1	849	23378083-9	1	2	1
## 112	1	852	23386130-8	1	1	1
## 113	1	865	23410879-4	1	2	1
## 114	1	868	23423713-6	1	2	1
## 115	1	877	23448369-2	1	2	1
## 116	1	907	23506849-4	1	1	1
## 117	1	902	23501831-4	1	2	1
## 118	1	921	23534842-K	1	2	1
## 119	1	926	23543378-8	1	1	1
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## 121	1	939	23567468-8	1	2	1
## 122	1	943	23574393-0	1	1	1
## 123	1	967	23625011-3	1	1	1
## 124	1	968	23625011-3	1	2	1
## 125	1	983	23667140-2	1	2	1
## 126	1	987	23683414-K	1	2	1
## 127	1	996	23713649-7	1	1	1
## 128	1	1005	23737580-7	1	2	1
## 129	1	1007	23740506-4	1	2	1
## 130	1	1030	23785220-6	1	1	1
## 131	1	1035	23794254-K	1	1	1
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## 133	1	1055	23843993-0	1	1	1
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## 135	1	1075	23896217-K	1	2	1
## 136	1	1076	23900150-5	1	3	1
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## 139	1	1113	23968562-5	1	2	1
## 140	1	1114	23969130-7	1	2	1
## 141	1	1123	23994954-1	1	1	1
## 142	1	1130	24005478-7	1	1	1
## 143	1	1135	24014350-K	1	2	1
## 144	1	1142	24026293-2	1	2	1
## 145	1	1156	24058690-8	1	1	1
## 146	1	1169	24073081-2	1	2	1
## 147	1	1178	24092534-6	1	2	1
## 148	1	1179	24092534-6	1	3	1
## 149	1	1180	24093718-2	1	2	1
## 150	1	1196	24121753-1	1	1	1
## 151	1	1184	24107434-K	1	2	1
## 152	1	1202	24139241-4	1	2	1
## 153	1	1209	24152537-6	1	1	1
## 154	1	1220	24182326-1	1	2	1
## 155	1	1219	24180190-K	1	2	1
## 156	1	1223	24190413-K	1	2	1
## 157	1	1230	24204418-5	1	2	1
## 158	1	1235	24210618-0	1	1	1
## 159	1	1240	24230863-8	1	1	1
## 160	1	1254	24251559-5	1	1	1
## 161	1	1264	24281126-7	1	1	1
## 162	1	1266	24286764-5	1	1	1

## 163	1	1269	24291235-7	1	2	1
## 164	1	1284	24324822-1	1	1	1
## 165	1	1312	24417134-6	1	2	1
## 166	1	1316	24426016-0	1	2	1
## 167	1	1319	24447255-9	1	1	1
## 168	1	1320	24447255-9	1	2	1
## 169	1	1541	24989671-3	1	2	1
## 170	1	1355	24540729-7	1	2	1
## 171	1	1354	24540592-8	1	2	1
## 172	1	1355	24540729-7	1	2	1
## 173	1	1354	24540592-8	1	2	1
## 174	1	1376	24598516-9	1	1	1
## 175	1	1378	24599994-1	1	3	1
## 176	1	1383	24612954-1	1	2	1
## 177	1	1390	24627145-3	1	2	1
## 178	1	1392	24628839-9	1	1	1
## 179	1	1393	24629598-0	1	1	1
## 180	1	1397	24636672-1	1	2	1
## 181	1	1404	24653340-7	1	2	1
## 182	1	1424	24703686-5	1	1	1
## 183	1	1433	24729625-5	1	1	1
## 184	1	1437	24737432-9	1	1	1
## 185	1	1442	24743808-4	1	2	1
## 186	1	1440	24743750-9	1	1	1
## 187	1	1441	24743802-5	1	1	1
## 188	1	1446	24761476-1	1	2	1
## 189	1	1449	24766324-K	1	2	1
## 190	1	1446	24761476-1	1	2	1
## 191	1	1449	24766324-K	1	2	1
## 192	1	1453	24786561-6	1	1	1
## 193	1	1452	24786417-2	1	2	1
## 194	1	1460	24801153-K	1	2	1
## 195	1	1461	24806938-4	1	2	1
## 196	1	1482	24842142-8	1	3	1
## 197	1	1485	24851058-7	1	1	1
## 198	1	1491	24867787-2	1	3	1
## 199	1	1496	24878818-6	1	1	1
## 200	1	1500	24887657-3	1	1	1
## 201	1	1514	24923775-2	1	1	1
## 202	1	1513	24922934-2	1	2	1
## 203	1	1515	24926007-K	1	2	1
## 204	1	1517	24927693-6	1	1	1
## 205	1	1534	24972952-3	1	2	1

```
length(unique(merged$id.x))
```

```
## [1] 187
```

```
length(unique(merged$id.y))
```

```
## [1] 191
```

187 unique school records can be perfectly matched to clinical records, representing 191 patients.



## Probabilistic record linkage

<https://rpubs.com/ahmademad/RecordLinkage> <https://www.bristol.ac.uk/media-library/sites/cmm/migrated/documents/problinkage.pdf> <https://cran.r-project.org/web/packages/diyar/vignettes/links.html>

Mismatch on ses is slightly higher weighted than match on everything. Unclear why and doesn't occur for epiWeights() below.

```
# Try supplying error information. Works better when sex_desc and dob are both in blocking as otherwise
# Still quick for whole school dataset
a2 <- compare.linkage(school,
  #select(school, -ses_status),
  select(patients, -row_id),
  #select(patients, -ses_status),
  blockfld = c("sex_desc", "dob"), # Block on sex and dob because we really want the
  #blockfld = FALSE,
  phonetic = FALSE,
  strcmp = c(2), # Do string comparison on DOB
  exclude = c(1) # Exclude the id column in both datasets
)
a2_pairs <- a2$pairs # Issue with ses matching here
b2 <- epiWeights(a2, e = c(0.01, # Default for DOB
  0.01, # Default for sex
  0.01, # Default for commune because we want a good match
  0.01, # Keep small so autism in clinical (not intellectual disability) is pr
  0.4, # Have more error for ses_status because it is loosely defined
  #0.3, # Allow more mismatch intellectual disability status so that autism ma
  0.01 # Allow some mismatch on whether autism is the primary diagnosis so we
))
summary(b2)
```

```
##
## Linkage Data Set
##
## 488 records in data set 1
## 1747 records in data set 2
## 312 record pairs
##
## 0 matches
## 0 non-matches
## 312 pairs with unknown status
##
##
## Weight distribution:
##
## [0.55,0.6] [0.6,0.65] [0.65,0.7] [0.7,0.75] [0.75,0.8] [0.8,0.85] [0.85,0.9]
##          6          66          35          0          0          120          85
```

```
allPairs2 <- getPairs(b2)
head(allPairs2, n = 20)
```

	id	id	dob	sex_desc	student_commune_name	autism	ses_status
## 1	437	437	2003-11-25	Female	Temuco	1	2
## 2	81	21449127-3	2003-11-25	Female	Temuco	1	2
## 3							
## 4	380	380	2005-12-07	Female	Temuco	1	1

```
## 5 295 21994583-3 2005-12-07 Female Temuco 1 1
## 6
## 7 187 187 2008-05-20 Female Gorbea 1 1
## 8 568 22724176-4 2008-05-20 Female Gorbea 1 1
## 9
## 10 269 269 2008-06-21 Female Temuco 1 1
## 11 580 22752332-8 2008-06-21 Female Temuco 1 1
## 12
## 13 173 173 2011-04-20 Female Temuco 1 2
## 14 966 23624343-5 2011-04-20 Female Temuco 1 2
## 15
## 16 172 172 2012-01-31 Female Villarrica 1 1
## 17 1063 23860402-8 2012-01-31 Female Villarrica 1 1
## 18
## 19 41 41 2012-06-18 Female Villarrica 1 1
## 20 1120 23987283-2 2012-06-18 Female Villarrica 1 1
## aut_rank Weight
## 1 1
## 2 1 0.8882294
## 3
## 4 1
## 5 1 0.8882294
## 6
## 7 1
## 8 1 0.8882294
## 9
## 10 1
## 11 1 0.8882294
## 12
## 13 1
## 14 1 0.8882294
## 15
## 16 1
## 17 1 0.8882294
## 18
## 19 1
## 20 1 0.8882294
```

```
classifyPairs2 <- emClassify(b2, threshold.upper = 1, threshold.lower = 0.8)
a2_pairs$weight <- classifyPairs2$Wdata
a2_pairs$pred <- classifyPairs2$prediction

a2_pairs_clean <- a2_pairs %>%
  rename(".x" = id1, ".y" = id2) %>%
  select(-is_match)

finalPairs2 <- getPairs(b2, max.weight = 1, min.weight = 0, single.rows = TRUE) # Take them all when bl

#kmeansRes2 <- classifyUnsup(a2, method = "kmeans")
#a2_pairs$pred <- kmeansRes2$prediction
# Works but prioritises ses over commune and doesn't use epiWeights found above so not that useful.
```

finalPairs2 is the same size as finalPairs and probably contains the same matches but was much quicker to run because of the blocking. Assume in kmeansRes2, N = not a match, L = likely a match.

```

# reclin has a 1-1 matching fuction so regenerate the pairs using reclin so they're a pairs
# type object and can be passed to select_n_to_m

pairs <- pair_blocking(school, patients, on = c("sex_desc", "dob")) %>%
  mutate(student_commune_name = (school$student_commune_name[.x] == patients$student_commune_name[.y]) &
    #ses = get_num_diff(school$ses_status[.x], patients$ses_status[.y])$val
    ) %>%
  left_join(a2_pairs_clean, by = c(".x", ".y")) %>%
  select(c(-student_commune_name.x)) %>%
  rename("student_commune_name" = "student_commune_name.y")

matches <- select_n_to_m(pairs, threshold = 0.5, score = "weight", n = 1, m = 1, var = "match") %>%
  filter(match == TRUE) %>%
  rename("id" = ".x",
    "row_id" = ".y") %>%
  mutate(id = as.character(id))

# Now add the matched clinical records to the school records
school_matched <- school %>%
  filter(student_commune_name != "Misc") %>%
  left_join(matches, by = "id") %>%
  rename(id.school = id,
    dob.school = dob.x,
    sex_desc.school = sex_desc.x,
    student_commune_name.school = student_commune_name.x,
    ses_status.school = ses_status.x,
    dob.matched = dob.y,
    sex_desc.matched = sex_desc.y,
    student_commune_name.matched = student_commune_name.y,
    ses_status.matched = ses_status.y) %>%
  select(c(-pred, -match)) %>%
  left_join(patients, by = "row_id") %>%
  rename(id.patient = row_id,
    patient_id = id,
    dob.patient = dob,
    sex_desc.patient = sex_desc,
    student_commune_name.patient = student_commune_name,
    ses_status.patient = ses_status) %>%
  select(id.school, id.patient, patient_id,
    dob.school, dob.patient, dob.matched,
    sex_desc.school, sex_desc.patient, sex_desc.matched,
    student_commune_name.school, student_commune_name.patient, student_commune_name.matched,
    ses_status.school, ses_status.patient, ses_status.matched,
    weight) %>%
  arrange(desc(weight))

write_csv(school_matched, "04_Data/Outputs/school_matched.csv")

#school_matched_yes <- school_matched %>% filter(!is.na(weight))
#school_matched_no <- school_matched %>% filter(is.na(weight))

# commune_nums <- data.frame(student_commune_name.school = sort(unique(school_matched$student_commune_name.school)),
#                             commune_num = c(1:length(unique(school_matched$student_commune_name.school))))

```

```

school_matched_small <- school_matched %>%
  mutate(matched = ifelse(is.na(patient_id), 0, 1),
         sex.school = ifelse(sex_desc.school == "Male", 1, ifelse(sex_desc.school == "Female", 2, NA)))
merge(commune_region_lookup, by.x = "student_commune_name.school", by.y = "commune_name") %>% # doesn't work
select(id.school, dob.school, sex_desc.school, sex.school, student_commune_name.school, commune_code)

# Now add the matched clinical records to the school records
patients_matched <- patients %>%
  left_join(matches, by = "row_id") %>%
  rename(id.patient = row_id,
         patient_id = id.x,
         dob.patient = dob.x,
         sex_desc.patient = sex_desc.x,
         student_commune_name.patient = student_commune_name.x,
         id = id.y,
         ses_status.patient = ses_status.x,
         dob.matched = dob.y,
         sex_desc.matched = sex_desc.y,
         student_commune_name.matched = student_commune_name.y,
         ses_status.matched = ses_status.y) %>%
  select(c(-pred, -match)) %>%
  left_join(school, by = "id") %>%
  rename(id.school = id,
         dob.school = dob,
         sex_desc.school = sex_desc,
         student_commune_name.school = student_commune_name,
         ses_status.school = ses_status) %>%
  select(id.school, id.patient, patient_id,
         dob.school, dob.patient, dob.matched,
         sex_desc.school, sex_desc.patient, sex_desc.matched,
         student_commune_name.school, student_commune_name.patient, student_commune_name.matched,
         ses_status.school, ses_status.patient, ses_status.matched,
         weight) %>%
  arrange(desc(weight))

write_csv(patients_matched, "04_Data/Outputs/patients_matched.csv")

patients_matched_small <- patients_matched %>%
  mutate(matched = ifelse(is.na(id.school), 0, 1),
         sex.patient = ifelse(sex_desc.patient == "Male", 1, ifelse(sex_desc.patient == "Female", 2, NA)))
merge(commune_region_lookup, by.x = "student_commune_name.patient", by.y = "commune_name") %>%
select(id.patient, dob.patient, sex_desc.patient, sex.patient, student_commune_name.patient, commune_code)

```

## Consider whether the matched and unmatched school records are different

We hope they are not different

```

#library(coin)

#pt.sex <- oneway_test(sex.school ~ as.factor(matched), data = school_matched_small, distribution = app
#confint(pt.sex)

```

```

#ks.ses <- ks.test(data1$ses_status.school, data2$ses_status.school, alternative = "two.sided", simulate.p.value = TRUE)
#ks.ses

# SES
#data1 <- school_matched_yes %>% select(ses_status.school)
#data2 <- school_matched_no %>% select(ses_status.school)
#hist(data1$ses_status.school, breaks = 10)
#hist(data2$ses_status.school, breaks = 10)
#data1 %>% group_by(ses_status.school) %>% summarise(count = n()) %>% mutate(freq = count/sum(count))
#data2 %>% group_by(ses_status.school) %>% summarise(count = n()) %>% mutate(freq = count/sum(count))

school_yes <- school_matched_small %>% filter(matched == 1) #>% select(sex.school)
school_no <- school_matched_small %>% filter(matched == 0)

# Kolmogorov tests for our matched results
ks.school.sex <- ks.test(na.omit(school_yes$sex.school),
                        na.omit(school_no$sex.school),
                        alternative = "two.sided", simulate.p.value = TRUE)
ks.school.sex

##
## Two-sample Kolmogorov-Smirnov test
##
## data: na.omit(school_yes$sex.school) and na.omit(school_no$sex.school)
## D = 0.011834, p-value = 1
## alternative hypothesis: two-sided
ks.school.ses_status <- ks.test(as.numeric(na.omit(school_yes$ses_status.school)),
                                as.numeric(na.omit(school_no$ses_status.school)),
                                alternative = "two.sided", simulate.p.value = TRUE)
ks.school.ses_status

##
## Two-sample Kolmogorov-Smirnov test
##
## data: as.numeric(na.omit(school_yes$ses_status.school)) and as.numeric(na.omit(school_no$ses_status.school))
## D = 0.087291, p-value = 0.3193
## alternative hypothesis: two-sided
ks.school.commune_code <- ks.test(as.numeric(na.omit(school_yes$commune_code)),
                                  as.numeric(na.omit(school_no$commune_code)),
                                  alternative = "two.sided", simulate.p.value = TRUE)
ks.school.commune_code

##
## Two-sample Kolmogorov-Smirnov test
##
## data: as.numeric(na.omit(school_yes$commune_code)) and as.numeric(na.omit(school_no$commune_code))
## D = 0.20101, p-value = 0.0001077
## alternative hypothesis: two-sided

# Try manual Kolmogorov for SES
# bins <- unique(na.omit(school_matched_small$ses_status.school))
# ecdf.ses_status.yes <- ecdf(school_yes$ses_status.school)
# ecdf.ses_status.yes(school_yes$ses_status.school)
# ecdf.ses_status.no <- ecdf(school_no$ses_status.school)

```

```

# plot(ecdf.ses_status.yes) ; plot(ecdf.ses_status.no)

# Kolmogorov tests with permutation distributions
set.seed(123)
nPerm <- 200 # change to 2000
ks_perm.school.pvals <- data.frame(sex = numeric(nPerm),
                                   commune_code = numeric(nPerm),
                                   ses_status = numeric(nPerm))

school_matched_small_perm <- school_matched_small

for (i in 1:nPerm) {
  #print(i)
  school_matched_small_perm$matched <- school_matched_small$matched[sample(nrow(school_matched_small))]
  school_perm_yes <- school_matched_small_perm %>% filter(matched == 1)
  school_perm_no <- school_matched_small_perm %>% filter(matched == 0)

  ks_perm.school.sex <- ks.test(na.omit(school_perm_yes$sex.school),
                               na.omit(school_perm_no$sex.school),
                               alternative = "two.sided")
  ks_perm.school.commune_code <- ks.test(as.numeric(na.omit(school_perm_yes$commune_code)),
                                         as.numeric(na.omit(school_perm_no$commune_code)),
                                         alternative = "two.sided")
  ks_perm.school.ses_status <- ks.test(as.numeric(na.omit(school_perm_yes$ses_status.school)),
                                       as.numeric(na.omit(school_perm_no$ses_status.school)),
                                       alternative = "two.sided")

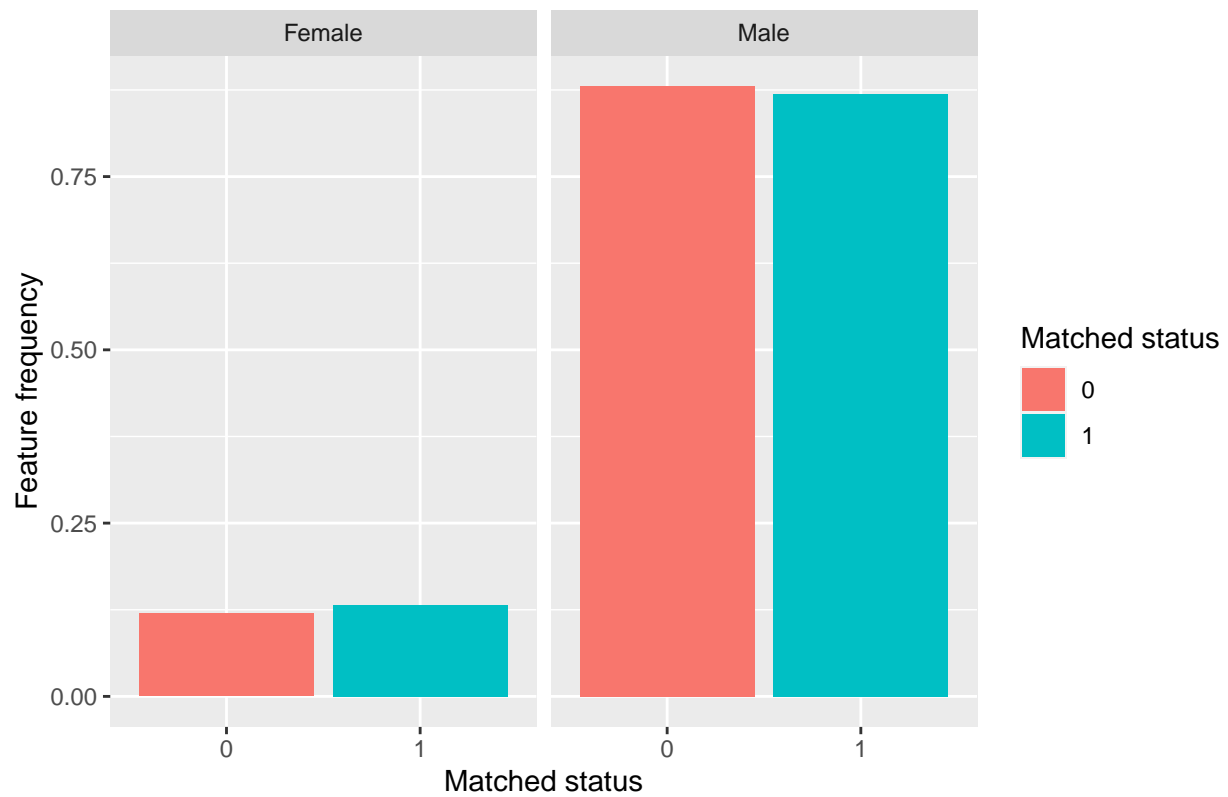
  ks_perm.school.pvals$sex[i] <- ks_perm.school.sex$p.value
  ks_perm.school.pvals$commune_code[i] <- ks_perm.school.commune_code$p.value
  ks_perm.school.pvals$ses_status[i] <- ks_perm.school.ses_status$p.value
}

# Results for sex
school_match_yes.sex <- school_yes %>% group_by(sex.school) %>% summarise(count = n()) %>% mutate(freq = count)
school_match_no.sex <- school_no %>% group_by(sex.school) %>% summarise(count = n()) %>% mutate(freq = count)
school_match.sex <- rbind(school_match_yes.sex, school_match_no.sex) %>%
  mutate(sex_desc = ifelse(sex.school == 1, "Male", ifelse(sex.school == 2, "Female", NA))) %>%
  arrange(sex_desc, matched)

ggplot(school_match.sex) +
  geom_col(aes(x = as.factor(matched), y = freq, fill = as.factor(matched))) +
  facet_wrap(~sex_desc) +
  labs(title = "Matching of school record to clinical record by feature (sex)",
       x = "Matched status",
       y = "Feature frequency",
       fill = "Matched status")

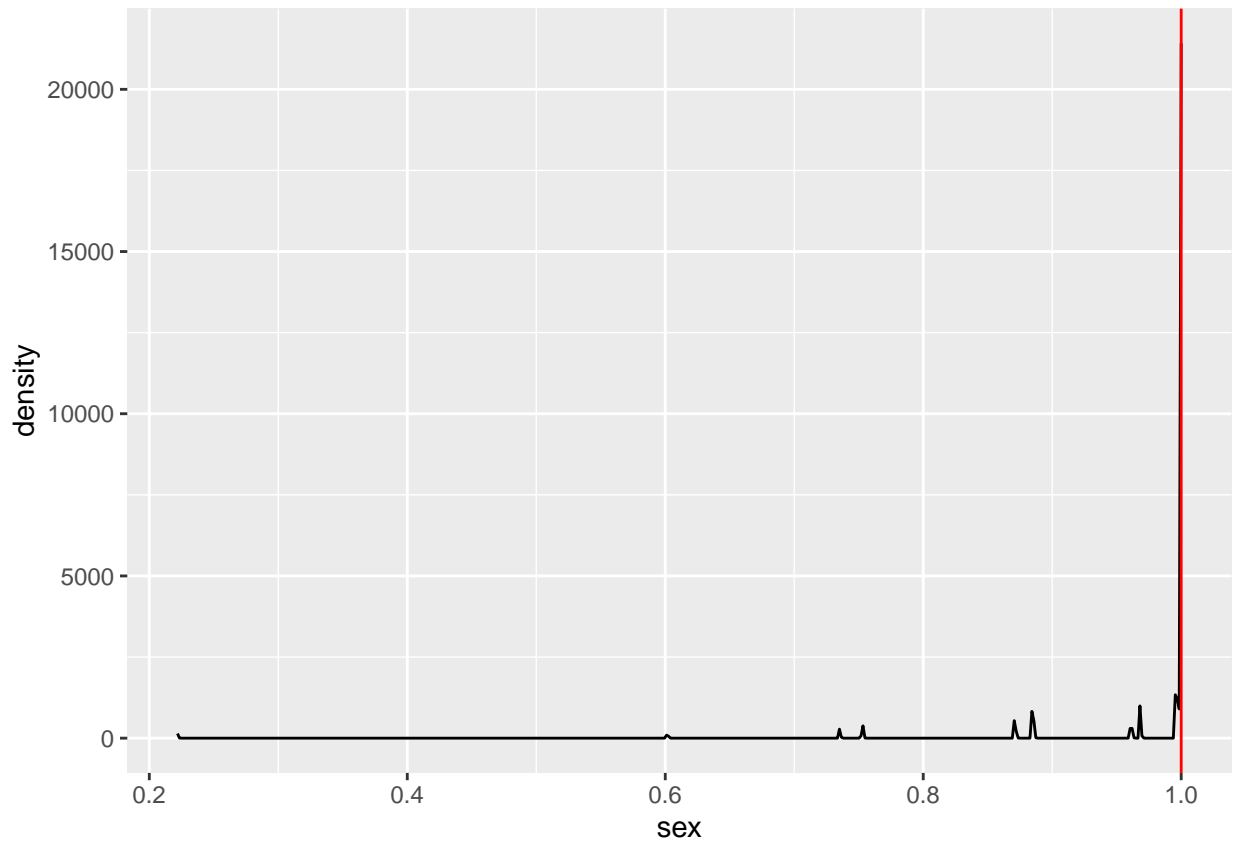
```

Matching of school record to clinical record by feature (sex)



```
ggplot(ks_perm.school.pvals, aes(x = sex, y = after_stat(density))) +  
  geom_density() +  
  geom_vline(xintercept = ks.school.sex$p.value, color = "red")
```



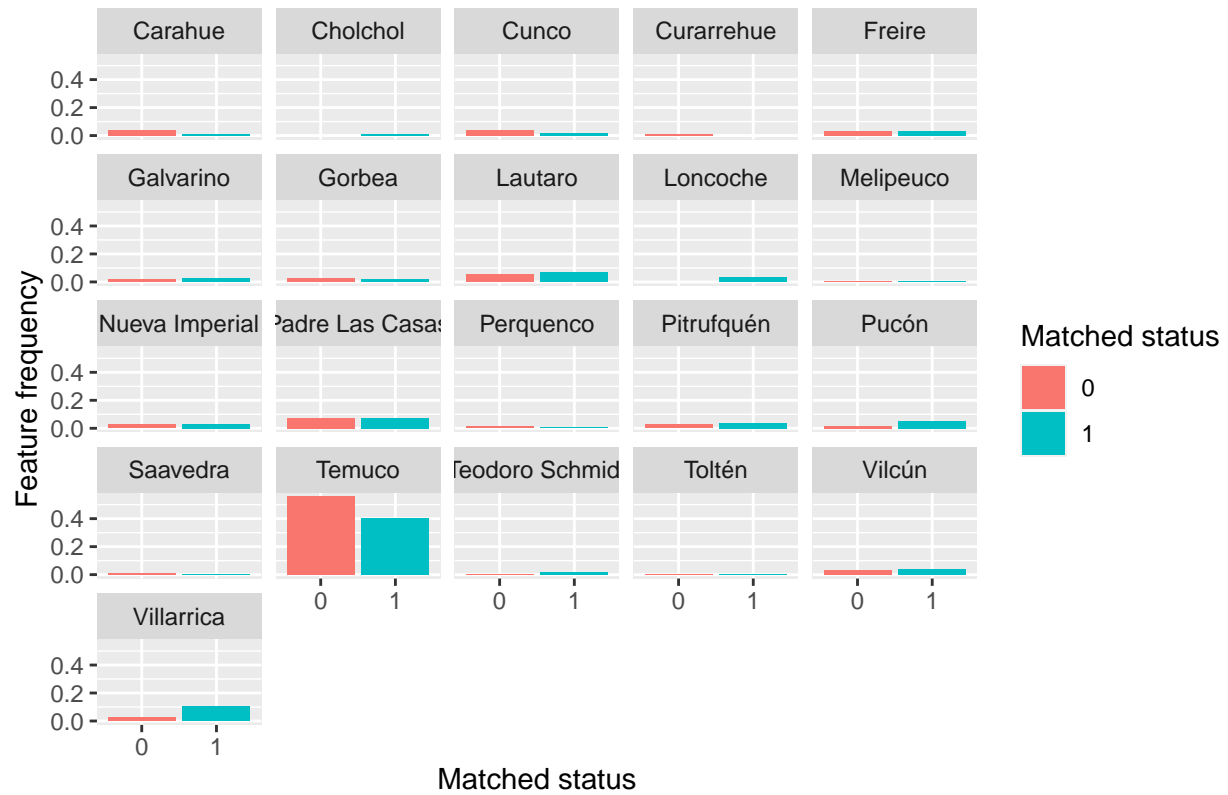


```
# Results for commune
school_match_yes.student_commune_name <- school_yes %>% group_by(student_commune_name.school) %>%
  summarise(count = n()) %>% mutate(freq = count/sum(count)) %>%
  # Would need to merge to a list of commune names and numbers if want to display all communes for all schools
#merge(commune_, by = "commune_num", all = TRUE) %>%
  mutate(matched = 1)
school_match_no.student_commune_name <- school_no %>% group_by(student_commune_name.school) %>%
  summarise(count = n()) %>% mutate(freq = count/sum(count)) %>%
  #merge(commune_nums, by = "commune_num", all = TRUE) %>%
  mutate(matched = 0)

school_match.student_commune_name <- rbind(school_match_yes.student_commune_name, school_match_no.student_commune_name)
arrange(student_commune_name.school, matched)

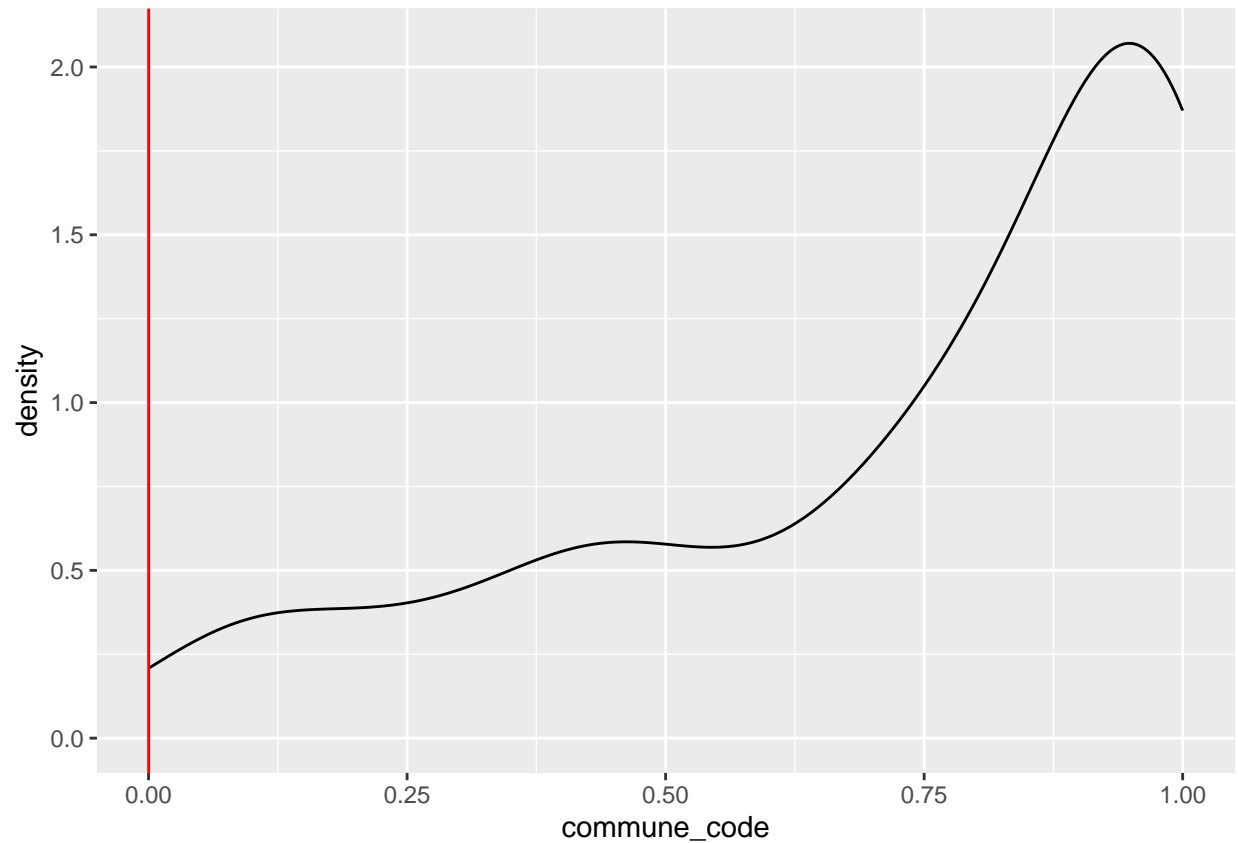
ggplot(school_match.student_commune_name) +
  geom_col(aes(x = as.factor(matched), y = freq, fill = as.factor(matched))) +
  facet_wrap(~student_commune_name.school, scales = "fixed") +
  #facet_wrap(~student_commune_name.school, scales = "free") +
  labs(title = "Matching of school record to clinical record by feature (commune)",
       x = "Matched status",
       y = "Feature frequency",
       fill = "Matched status")
```

## Matching of school record to clinical record by feature (commune)



*# most of the difference in matched commune frequency is for Temuco which is the biggest commune.*

```
ggplot(ks_perm.school.pvals, aes(x = commune_code, y = after_stat(density))) +
  geom_density() +
  geom_vline(xintercept = ks.school.commune_code$p.value, color = "red")
```

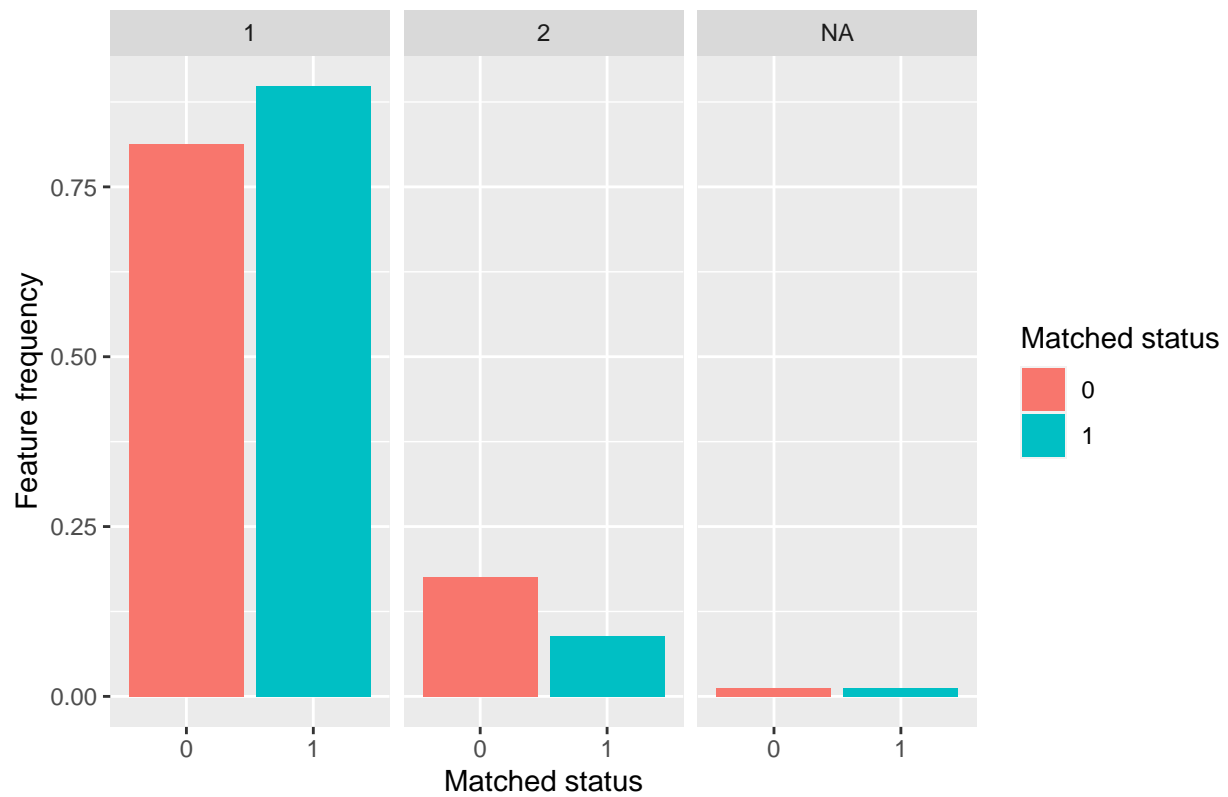


*# Results for ses status*

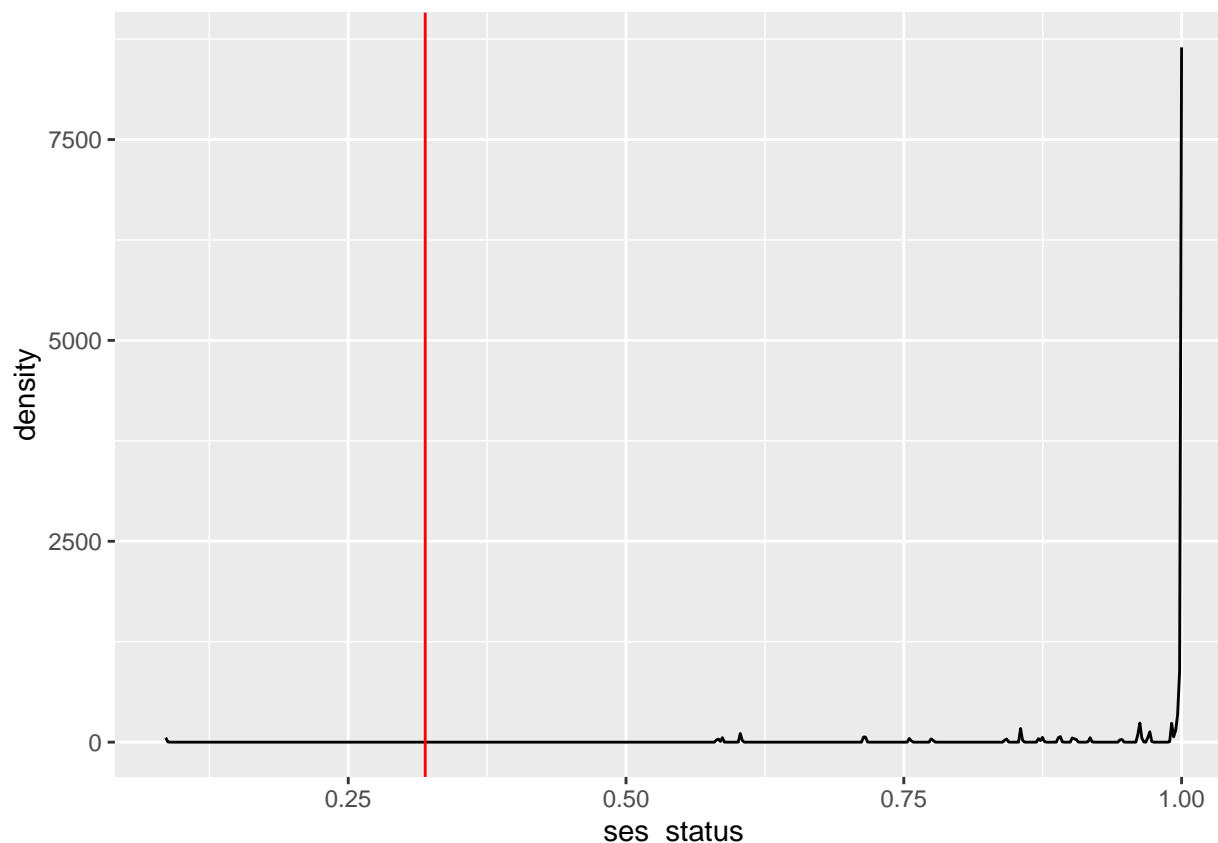
```
school_match_yes.ses_status <- school_yes %>% group_by(ses_status.school) %>% summarise(count = n()) %>%
school_match_no.ses_status <- school_no %>% group_by(ses_status.school) %>% summarise(count = n()) %>%
school_match.ses_status <- rbind(school_match_yes.ses_status, school_match_no.ses_status) %>%
  arrange(ses_status.school, matched)
```

```
ggplot(school_match.ses_status) +
  geom_col(aes(x = as.factor(matched), y = freq, fill = as.factor(matched))) +
  facet_wrap(~ses_status.school) +
  labs(title = "Matching of school record to clinical record by feature (SES status)",
       x = "Matched status",
       y = "Feature frequency",
       fill = "Matched status")
```

Matching of school record to clinical record by feature (SES status)



```
ggplot(ks_perm.school.pvals, aes(x = ses_status, y = after_stat(density))) +
  geom_density() +
  geom_vline(xintercept = ks.school.ses_status$p.value, color = "red")
```



Bit easier to match SES status of 1 (probably more common)

Our matched/non-matched are not different by sex (p-value in Kolmog is same as most of distribution of permuted pvals) but are different by commune and ses status. Cohen's D test isn't suitable to compare the matched and un-matched because the data don't have standard deviations.

??Add commune maps here with size of sample for school and clinical?? Also size of other features.

```
patients_yes <- patients_matched_small %>% filter(matched == 1) #>% select(sex.school)
patients_no <- patients_matched_small %>% filter(matched == 0)
```

```
# Kolmogorov tests for our matched results
```

```
ks.patients.sex <- ks.test(na.omit(patients_yes$sex.patient),
                           na.omit(patients_no$sex.patient),
                           alternative = "two.sided", simulate.p.value = TRUE)
```

```
ks.patients.sex
```

```
##
```

```
## Two-sample Kolmogorov-Smirnov test
```

```
##
```

```
## data: na.omit(patients_yes$sex.patient) and na.omit(patients_no$sex.patient)
```

```
## D = 0.10094, p-value = 0.03123
```

```
## alternative hypothesis: two-sided
```

```
ks.patients.ses_status <- ks.test(as.numeric(na.omit(patients_yes$ses_status.patient)),
                                   as.numeric(na.omit(patients_no$ses_status.patient)),
                                   alternative = "two.sided", simulate.p.value = TRUE)
```

```
ks.patients.ses_status
```

```

##
## Two-sample Kolmogorov-Smirnov test
##
## data: as.numeric(na.omit(patients_yes$ses_status.patient)) and as.numeric(na.omit(patients_no$ses_status.patient))
## D = 0.05398, p-value = 0.5916
## alternative hypothesis: two-sided

ks.patients.commune_code<- ks.test(as.numeric(na.omit(patients_yes$commune_code)),
                                   as.numeric(na.omit(patients_no$commune_code)),
                                   alternative = "two.sided", simulate.p.value = TRUE)

ks.patients.commune_code

##
## Two-sample Kolmogorov-Smirnov test
##
## data: as.numeric(na.omit(patients_yes$commune_code)) and as.numeric(na.omit(patients_no$commune_code))
## D = 0.093189, p-value = 0.05772
## alternative hypothesis: two-sided

# Kolmogorov tests with permutation distributions
set.seed(123)
nPerm <- 200 # change to 2000
ks_perm.patients.pvals <- data.frame(sex = numeric(nPerm),
                                     commune_code = numeric(nPerm),
                                     ses_status = numeric(nPerm))

patients_matched_small_perm <- patients_matched_small

for (i in 1:nPerm) {
  #print(i)
  patients_matched_small_perm$matched <- patients_matched_small$matched[sample(nrow(patients_matched_small), nPerm)]
  patients_perm_yes <- patients_matched_small_perm %>% filter(matched == 1)
  patients_perm_no <- patients_matched_small_perm %>% filter(matched == 0)

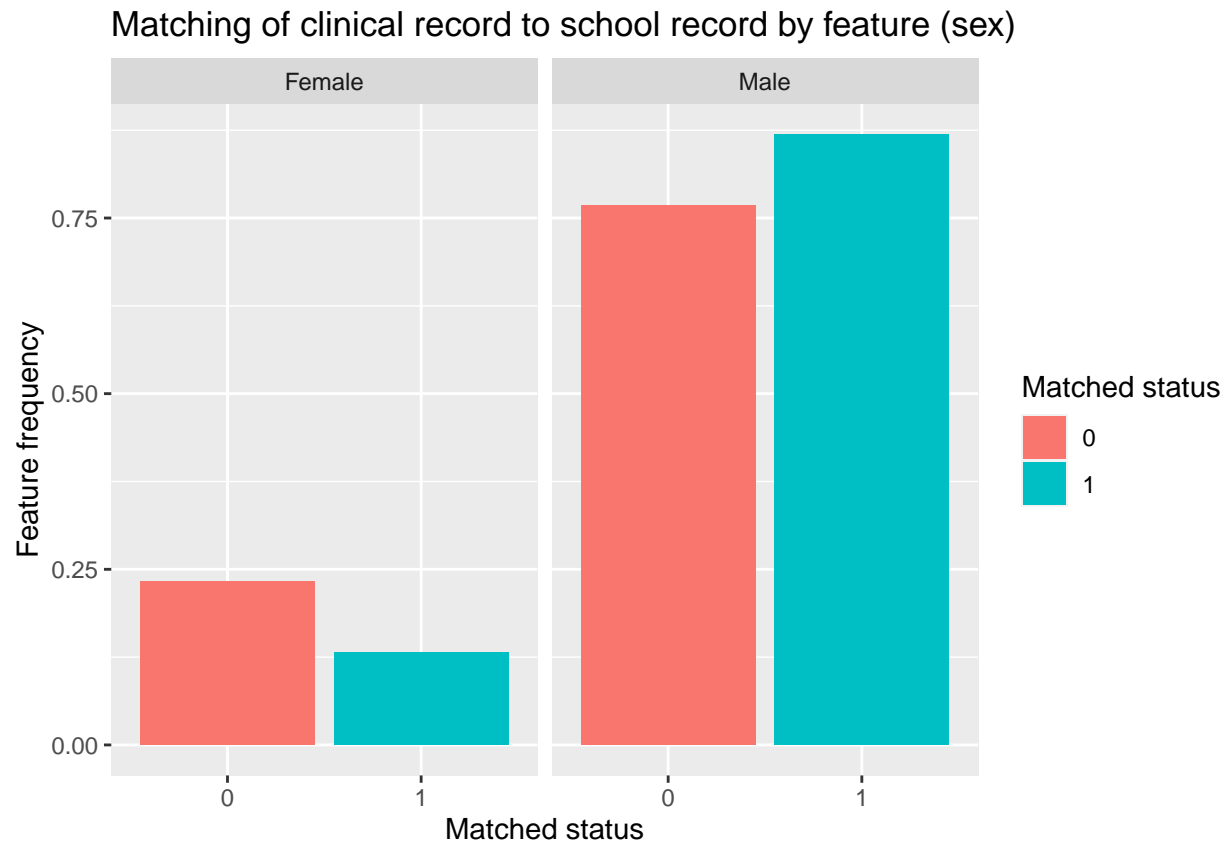
  ks_perm.patients.sex <- ks.test(na.omit(patients_perm_yes$sex.patient),
                                 na.omit(patients_perm_no$sex.patient),
                                 alternative = "two.sided")
  ks_perm.patients.commune_code <- ks.test(as.numeric(na.omit(patients_perm_yes$commune_code)),
                                           as.numeric(na.omit(patients_perm_no$commune_code)),
                                           alternative = "two.sided")
  ks_perm.patients.ses_status <- ks.test(as.numeric(na.omit(patients_perm_yes$ses_status.patient)),
                                         as.numeric(na.omit(patients_perm_no$ses_status.patient)),
                                         alternative = "two.sided")

  ks_perm.patients.pvals$sex[i] <- ks_perm.patients.sex$p.value
  ks_perm.patients.pvals$commune_code[i] <- ks_perm.patients.commune_code$p.value
  ks_perm.patients.pvals$ses_status[i] <- ks_perm.patients.ses_status$p.value
}

# Results for sex
patients_match_yes.sex <- patients_yes %>% group_by(sex.patient) %>% summarise(count = n()) %>% mutate(fr = count/n())
patients_match_no.sex <- patients_no %>% group_by(sex.patient) %>% summarise(count = n()) %>% mutate(fr = count/n())
patients_match.sex <- rbind(patients_match_yes.sex, patients_match_no.sex) %>%
  mutate(sex_desc = ifelse(sex.patient == 1, "Male", ifelse(sex.patient == 2, "Female", NA))) %>%
  arrange(sex_desc, matched)

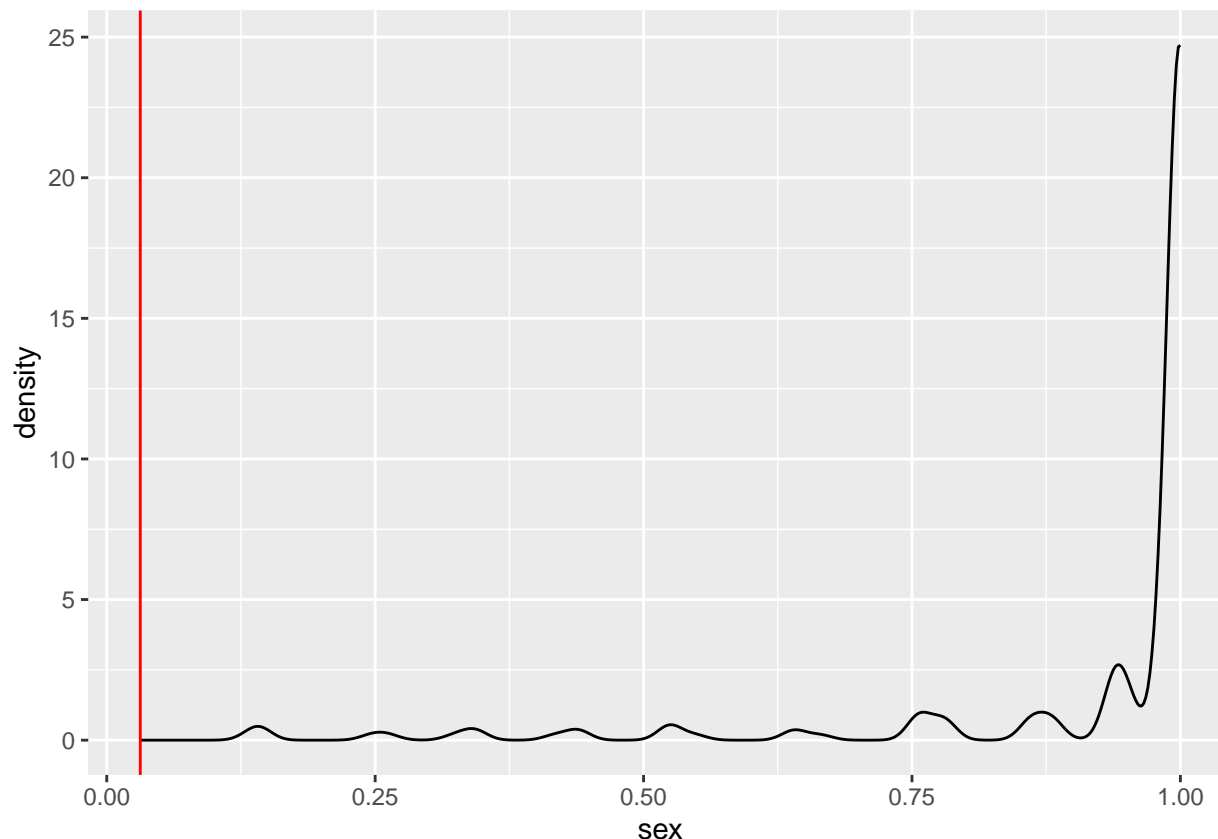
```

```
ggplot(patients_match.sex) +
  geom_col(aes(x = as.factor(matched), y = freq, fill = as.factor(matched))) +
  facet_wrap(~sex_desc) +
  labs(title = "Matching of clinical record to school record by feature (sex)",
       x = "Matched status",
       y = "Feature frequency",
       fill = "Matched status")
```



```
ggplot(ks_perm.patients.pvals, aes(x = sex, y = after_stat(density))) +
  geom_density() +
  geom_vline(xintercept = ks.patients.sex$p.value, color = "red")
```



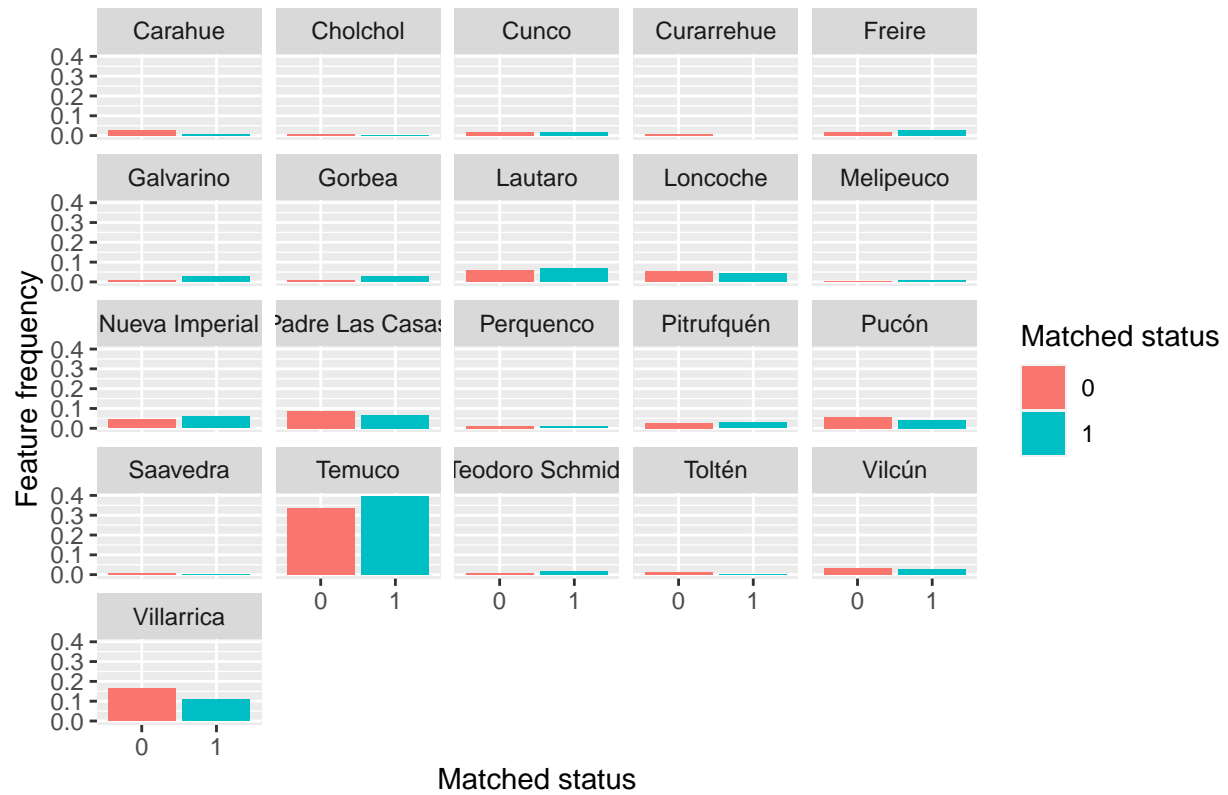


```
# Results for commune
patients_match_yes.student_commune_name <- patients_yes %>% group_by(student_commune_name.patient) %>%
  summarise(count = n()) %>% mutate(freq = count/sum(count)) %>%
  # Would need to merge to a list of commune names and numbers if want to display all communes for all
#merge(commune_, by = "commune_num", all = TRUE) %>%
  mutate(matched = 1)
patients_match_no.student_commune_name <- patients_no %>% group_by(student_commune_name.patient) %>%
  summarise(count = n()) %>% mutate(freq = count/sum(count)) %>%
  #merge(commune_nums, by = "commune_num", all = TRUE) %>%
  mutate(matched = 0)

patients_match.student_commune_name <- rbind(patients_match_yes.student_commune_name, patients_match_no)
  arrange(student_commune_name.patient, matched)

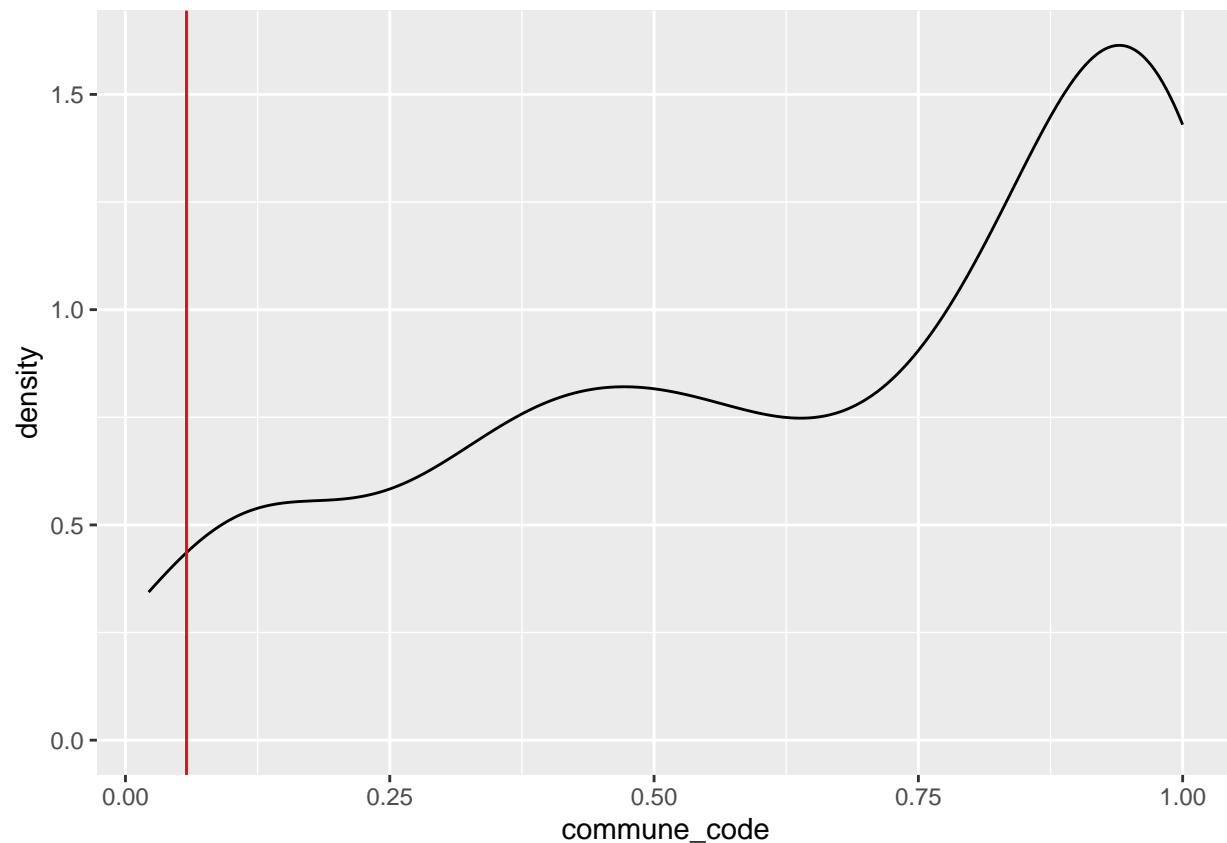
ggplot(patients_match.student_commune_name) +
  geom_col(aes(x = as.factor(matched), y = freq, fill = as.factor(matched))) +
  facet_wrap(~student_commune_name.patient, scales = "fixed") +
  #facet_wrap(~student_commune_name.school, scales = "free") +
  labs(title = "Matching of clinical record to school record by feature (commune)",
       x = "Matched status",
       y = "Feature frequency",
       fill = "Matched status")
```

## Matching of clinical record to school record by feature (commune)



*# most of the difference in matched commune frequency is for Temuco which is the biggest commune.*

```
ggplot(ks_perm.patients.pvals, aes(x = commune_code, y = after_stat(density))) +
  geom_density() +
  geom_vline(xintercept = ks.patients.commune_code$p.value, color = "red")
```

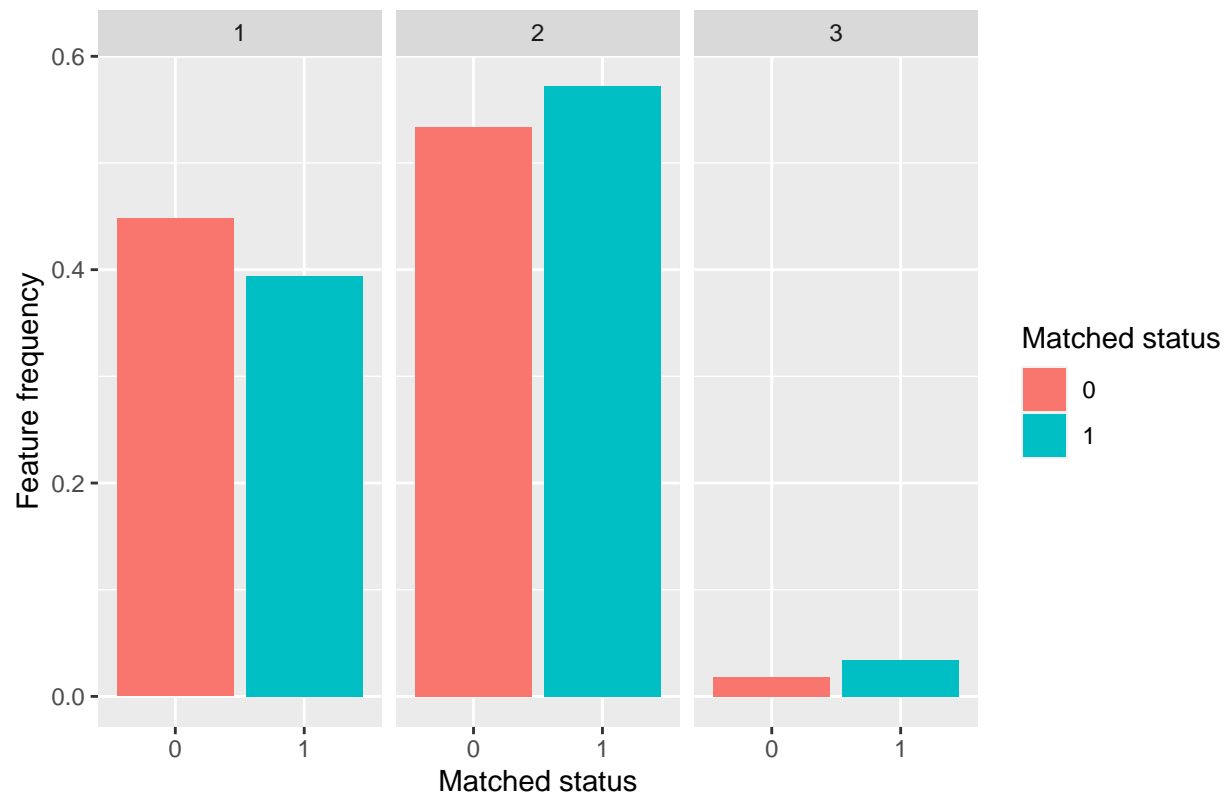


*# Results for ses status*

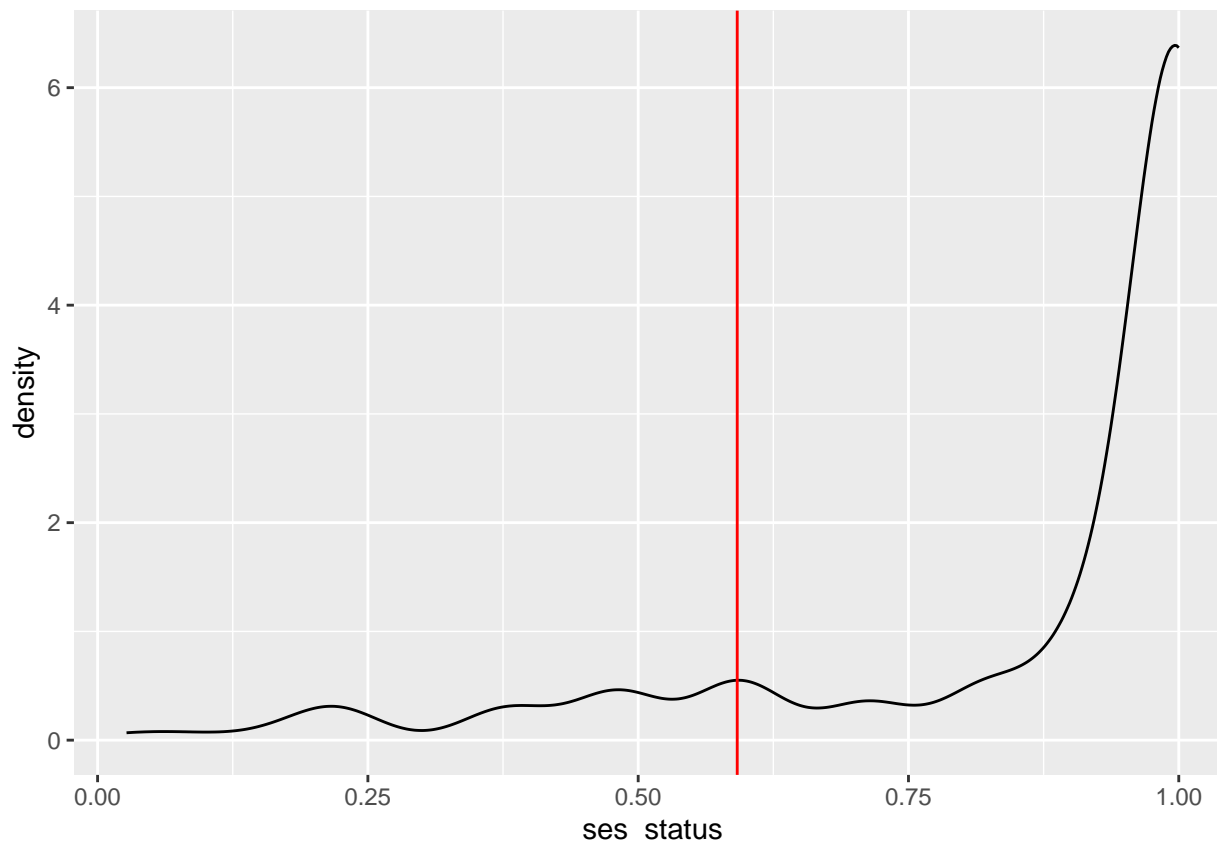
```
patients_match_yes.ses_status <- patients_yes %>% group_by(ses_status.patient) %>% summarise(count = n())
patients_match_no.ses_status <- patients_no %>% group_by(ses_status.patient) %>% summarise(count = n())
patients_match.ses_status <- rbind(patients_match_yes.ses_status, patients_match_no.ses_status) %>%
  arrange(ses_status.patient, matched)
```

```
ggplot(patients_match.ses_status) +
  geom_col(aes(x = as.factor(matched), y = freq, fill = as.factor(matched))) +
  facet_wrap(~ses_status.patient) +
  labs(title = "Matching of clinical record to school record by feature (SES status)",
       x = "Matched status",
       y = "Feature frequency",
       fill = "Matched status")
```

Matching of clinical record to school record by feature (SES status)



```
ggplot(ks_perm.patients.pvals, aes(x = ses_status, y = after_stat(density))) +
  geom_density() +
  geom_vline(xintercept = ks.patients.ses_status$p.value, color = "red")
```



Then quantify clinical records for ARAUC Sur that haven't been matched.

Need to bring in the missing communes so that ks test is better.

**Dumping ground, don't use below here.**

## Record linkage using machine learning

Try linkage using ML, as done by Jan van der Laan here [https://cran.r-project.org/web/packages/reclin2/vignettes/record\\_linkage\\_using\\_machine\\_learning.html](https://cran.r-project.org/web/packages/reclin2/vignettes/record_linkage_using_machine_learning.html)

In reclin2 package, use `?identical()` to see available matching algorithms.

The Jaro-Winkler distance is a string metric for measuring the edit distance between two sequences. It is a variant of the Jaro distance metric proposed by William E. Winkler in 1990 <sup>1</sup>. The Jaro-Winkler distance uses a prefix scale which gives more favorable ratings to strings that match from the beginning for a set prefix length. The higher the Jaro-Winkler distance for two strings is, the less similar the strings are. The score is normalized such that 0 means an exact match and 1 means there is no similarity <sup>1</sup>.

Need to explore different comparator algorithms. Currently it's exact match. Would be good to do communes that are neighbours and ages off by 1.

## Try bayesian linkage?

Follow Thomas Stringham <https://arxiv.org/pdf/2003.04238.pdf> who followed Sadinle <https://arxiv.org/abs/1601.06630> Not doing this as limited value when not matching strings.