

Exploratory Data Analysis

1 Personal Information

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Github link: <https://github.com/adenoooy2/MSc-Thesis.git>

2 Data Context

This exploratory data analysis is conducted using R and RStudio. There are two main sets of data to be considered, linked to the two main sections of the project.

The first set of data represents the baseline or standard of care output produced by the existing patient pathway model. For the baseline there are 20 data output files (in csv format). Multiple files had been generated to account for model stochasticity, with the results of each simulation being based on a different set of random probabilities. The data files have a consistent structure and represent the population of individuals who move through the TB diagnostic patient pathway. In this, each column represents either a patient disease status or a point in the patient pathway that the individual may or may not have reached.

The second data set consists of TB burden estimates for Kenya produced by the World Health Organization (WHO) as well as the accompanying data dictionary. The estimates cover a range of data variables and their estimated values between the years 2000 and 2022. Several key variables include estimates on TB incidence (new cases), notifications (diagnoses) and deaths. Estimates are also provided for different groups of individuals (for example HIV positive patients) and for different types of TB.

3 Data Description: Baseline TB model

3.1 Load baseline data

```
# Set path to baseline data
baseline_path = "/Users/adenoooy/Library/CloudStorage/OneDrive-Personal/UVA/Thesis/MSc-Thesis/data/statistics"

# Determine how many files
files = list.files(baseline_path)
num_files = length(files)
print(paste("Number of baseline files: ", num_files, sep = ""))

## [1] "Number of baseline files: 20"
```

3.2 Explore variables and format of one baseline file

Each baseline data file represents a population of individuals (one per row) and various columns representing the different states or points in the patient pathway reached by each individual.

3.2.1 File Structure

```
b_data = read_excel(paste(baseline_path, files[1], sep = ""))
```

```
print(paste("Each data file consists of ", dim(b_data)[1],  
  " rows and ", dim(b_data)[2], " columns", sep = ""))
```

```
## [1] "Each data file consists of 10000 rows and 35 columns"
```

```
# List of column names  
colnames(b_data)
```

```
## [1] "hiv" "rnum"  
## [3] "tb_status" "tb_present"  
## [5] "rif_status" "num_visits"  
## [7] "patient_time" "tb_seek_care"  
## [9] "do_triage" "tb_screened"  
## [11] "sens_screen" "spec_screen"  
## [13] "screen_result" "do_confirmatory"  
## [15] "tb_triaged" "sens_triage"  
## [17] "spec_triage" "tb_triage_result"  
## [19] "tb_confirmatory_offered" "patient_referred_for_sample"  
## [21] "patient_reached_sample_site" "conf_test"  
## [23] "spec_conf" "sens_conf"  
## [25] "rif_sens" "rif_spec"  
## [27] "conf_sample_provided" "conf_initial_sample_provided"  
## [29] "conf_sample_status" "conf_sample_tested"  
## [31] "conf_sample_referred" "conf_sample_result"  
## [33] "patient_conf_result_received" "conf_res_same_encounter"  
## [35] "emp_notification"
```

```
print(b_data[1:3, ])
```

```
## # A tibble: 3 x 35  
##   hiv rnum tb_sta~1 tb_pr~2 rif_s~3 num_v~4 patie~5 tb_se~6 do_tr~7  
##   <dbl> <dbl> <chr>      <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>  
## 1 1 0.705 eptb 1 0 2 5 1 1  
## 2 1 0.394 eptb 1 0 3 8 1 1  
## 3 1 0.968 eptb 1 0 3 8 1 1  
## # ... with 26 more variables: tb_screened <dbl>, sens_screen <dbl>,  
## # spec_screen <dbl>, screen_result <lgl>, do_confirmatory <dbl>,  
## # tb_triaged <dbl>, sens_triage <dbl>, spec_triage <dbl>,  
## # tb_triage_result <lgl>, tb_confirmatory_offered <dbl>,  
## # patient_referred_for_sample <dbl>,  
## # patient_reached_sample_site <dbl>, conf_test <chr>,  
## # spec_conf <dbl>, sens_conf <dbl>, rif_sens <dbl>, ...
```

```
# Type of each column
sapply(b_data, class)
```

```
##                hiv                rnum
##          "numeric"          "numeric"
##          tb_status          tb_present
##          "character"          "numeric"
##          rif_status          num_visits
##          "numeric"          "numeric"
##          patient_time          tb_seek_care
##          "numeric"          "numeric"
##          do_triage          tb_screened
##          "numeric"          "numeric"
##          sens_screen          spec_screen
##          "numeric"          "numeric"
##          screen_result          do_confirmatory
##          "logical"          "numeric"
##          tb_triaged          sens_triage
##          "numeric"          "numeric"
##          spec_triage          tb_triage_result
##          "numeric"          "logical"
##          tb_confirmatory_offered patient_referred_for_sample
##          "numeric"          "numeric"
##          patient_reached_sample_site          conf_test
##          "numeric"          "character"
##          spec_conf          sens_conf
##          "numeric"          "numeric"
##          rif_sens          rif_spec
##          "numeric"          "numeric"
##          conf_sample_provided conf_initial_sample_provided
##          "numeric"          "numeric"
##          conf_sample_status          conf_sample_tested
##          "numeric"          "numeric"
##          conf_sample_referred          conf_sample_result
##          "numeric"          "numeric"
##          patient_conf_result_received          conf_res_same_encounter
##          "numeric"          "numeric"
##          emp_notification
##          "numeric"
```

Notably there are many columns in the dataframe listed as numeric, but only have values 0-1

3.2.2 Missing Data

The code below highlights only a few columns with missing data. These columns all relate to the result of a TB test (screen_result, tb_triage_result, conf_sample_result, patient_conf_result_received). In the design of the baseline model, these missing values are not as a result of data being incorrectly recorded or collected, but rather represent a status themselves - that is, no result was available at that point in the patient pathway

```
# count the missing values by column wise
print("Count of missing values by column wise")
```

```
## [1] "Count of missing values by column wise"
```

```
sapply(b_data, function(x) sum(is.na(x)))
```

```
##          hiv          rnum
##          0          0
##      tb_status      tb_present
##          0          0
##      rif_status      num_visits
##          0          0
##      patient_time      tb_seek_care
##          0          0
##          do_triage      tb_screened
##          0          0
##      sens_screen      spec_screen
##          0          0
##      screen_result      do_confirmatory
##      10000          0
##      tb_triaged      sens_triage
##          0          0
##      spec_triage      tb_triage_result
##          0      10000
##      tb_confirmatory_offered      patient_referred_for_sample
##          0          0
##      patient_reached_sample_site      conf_test
##          0          0
##          spec_conf      sens_conf
##          0          0
##          rif_sens      rif_spec
##          0          0
##      conf_sample_provided      conf_initial_sample_provided
##          0          0
##      conf_sample_status      conf_sample_tested
##          0          0
##      conf_sample_referred      conf_sample_result
##          0      2330
##      patient_conf_result_received      conf_res_same_encounter
##          2945          0
##      emp_notification
##          0
```

3.2.3 HIV and TB summary

```
# Group by hiv and TB status and count
hiv_tb_counts = b_data %>%
  group_by(tb_status, hiv) %>%
  count()
hiv_tb_counts$hiv_status = "hiv_pos"
hiv_tb_counts$hiv_status[hiv_tb_counts$hiv == 0] = "hiv_neg"
hiv_tb_counts$hiv = NULL
hiv_tb_counts = hiv_tb_counts %>%
```

```
spread(hiv_status, n)

print(hiv_tb_counts)
```

```
## # A tibble: 3 x 3
## # Groups:   tb_status [3]
##   tb_status   hiv_neg hiv_pos
##   <chr>       <int>   <int>
## 1 eptb         77      24
## 2 ptb        741     213
## 3 tb_negative 8376     569
```

```
# Summarise counts
print(paste("Total HIV positive: ", sum(hiv_tb_counts$hiv_pos),
  sep = ""))
```

```
## [1] "Total HIV positive: 806"
```

```
print(paste("Total HIV Negative: ", sum(hiv_tb_counts$hiv_neg),
  sep = ""))
```

```
## [1] "Total HIV Negative: 9194"
```

```
print(paste("Total EPTB: ", hiv_tb_counts$hiv_neg[hiv_tb_counts$tb_status ==
  "eptb"] + hiv_tb_counts$hiv_pos[hiv_tb_counts$tb_status ==
  "eptb"], sep = ""))
```

```
## [1] "Total EPTB: 101"
```

```
print(paste("Total PTB: ", hiv_tb_counts$hiv_neg[hiv_tb_counts$tb_status ==
  "ptb"] + hiv_tb_counts$hiv_pos[hiv_tb_counts$tb_status ==
  "ptb"], sep = ""))
```

```
## [1] "Total PTB: 954"
```

```
print(paste("Total TB positive: ", hiv_tb_counts$hiv_neg[hiv_tb_counts$tb_status ==
  "eptb"] + hiv_tb_counts$hiv_pos[hiv_tb_counts$tb_status ==
  "eptb"] + hiv_tb_counts$hiv_neg[hiv_tb_counts$tb_status ==
  "ptb"] + hiv_tb_counts$hiv_pos[hiv_tb_counts$tb_status ==
  "ptb"], sep = ""))
```

```
## [1] "Total TB positive: 1055"
```

```
print(paste("Total TB Negative: ", hiv_tb_counts$hiv_neg[hiv_tb_counts$tb_status ==
  "tb_negative"] + hiv_tb_counts$hiv_pos[hiv_tb_counts$tb_status ==
  "tb_negative"], sep = ""))
```

```
## [1] "Total TB Negative: 8945"
```

3.2.4 TB patient pathway summary

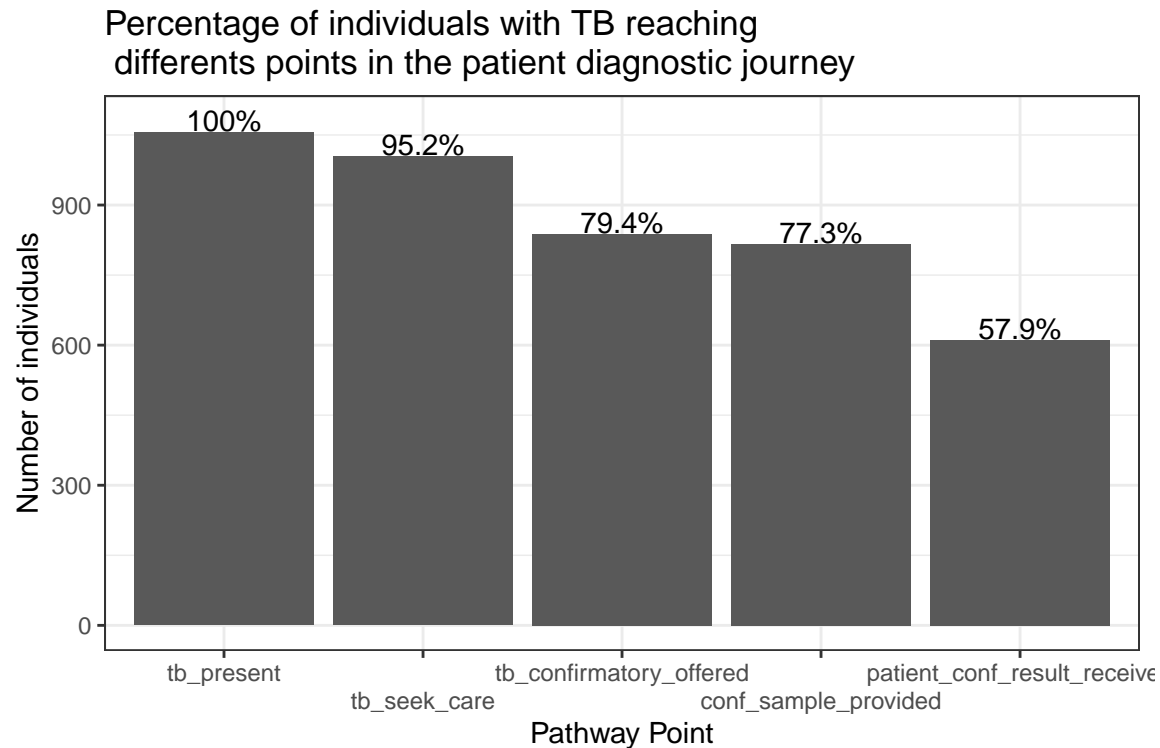
Given the format of the model, it is useful to summarise the number of individuals reaching key points in the patient pathway. An initial analysis is conducted only for those people with TB. Based on descriptions of the model, key variables representing some of these points are: `tb_present`, `tb_seek_care`, `tb_confirmatory_offered`, `conf_sample_provided`, `patient_conf_result_received`. Summarising these variables will provide an indication of how many individuals with TB reach each point in the pathway and are diagnosed correctly.

```
# Filter to only those with TB
b_data_tb_path = b_data %>%
  filter(tb_present == 1) %>%
  select(tb_present, tb_seek_care, tb_confirmatory_offered,
         conf_sample_provided, , patient_conf_result_received)

# Count pathway points
tb_path_counts = data.frame(colSums(b_data_tb_path, na.rm = TRUE))
colnames(tb_path_counts)[1] = "count"
tb_path_counts$variable = rownames(tb_path_counts)

# Calculate percentages
tb_path_counts$perc = round(tb_path_counts$count/max(tb_path_counts$count) *
  100, 1)

# Plot TB cascade
ggplot(tb_path_counts, aes(x = reorder(variable, -count),
  y = count)) + geom_bar(stat = "identity") + theme_bw() +
  xlab("Pathway Point") + ylab("Number of individuals") +
  labs(title = "Percentage of individuals with TB reaching \n different points in the patient diagnosis pathway") +
  geom_text(aes(x = reorder(variable, -count), y = count +
    25, label = paste(perc, "%", sep = ""))) + scale_x_discrete(guide = guide_axis(n.dodge = 2))
```



4 Data Description: WHO Tuberculosis Data

This dataset represent the WHO TB estimates for Kenya.

4.1 Load and merge WHO TB burden data and data dictionary

```
# Path to directory
basePath = "/Users/adenooy/Library/CloudStorage/OneDrive-Personal/UVA/Thesis/MSc-Thesis/"

# Load data dictionary
datadict = read.csv(paste(basePath, "data/dynamic/TB_data_dictionary_2024-01-30.csv",
    sep = ""))
colnames(datadict)
```

```
## [1] "variable_name" "dataset"          "code_list"        "definition"
```

```
print(datadict[1:3, ])
```

```
##      variable_name dataset code_list
## 1 budget_cpp_dstb  Budget
## 2 budget_cpp_mdr   Budget
## 3 budget_cpp_tpt   Budget
##
## 1 Average cost of drugs budgeted per patient for drug-susceptible TB treatment, excluding buffer sto
```

```
## 2           Average cost of drugs budgeted per patient for MDR-TB treatment, excluding buffer sto
## 3           Average cost of drugs budgeted per patient for TB preventive treatment, excluding buffer sto
```

```
# Load TB data
```

```
tb_estimates = read_excel(paste(basePath, "data/dynamic/kenya_tb_burden.xlsx",
                                sep = ""))
colnames(tb_estimates)
```

```
## [1] "country"           "iso2"
## [3] "iso3"              "iso_numeric"
## [5] "g_whoregion"       "year"
## [7] "e_pop_num"         "e_inc_100k"
## [9] "e_inc_100k_lo"     "e_inc_100k_hi"
## [11] "e_inc_num"         "e_inc_num_lo"
## [13] "e_inc_num_hi"      "e_tbhiv_prct"
## [15] "e_tbhiv_prct_lo"   "e_tbhiv_prct_hi"
## [17] "e_inc_tbhiv_100k"   "e_inc_tbhiv_100k_lo"
## [19] "e_inc_tbhiv_100k_hi" "e_inc_tbhiv_num"
## [21] "e_inc_tbhiv_num_lo" "e_inc_tbhiv_num_hi"
## [23] "e_mort_exc_tbhiv_100k" "e_mort_exc_tbhiv_100k_lo"
## [25] "e_mort_exc_tbhiv_100k_hi" "e_mort_exc_tbhiv_num"
## [27] "e_mort_exc_tbhiv_num_lo" "e_mort_exc_tbhiv_num_hi"
## [29] "e_mort_tbhiv_100k"   "e_mort_tbhiv_100k_lo"
## [31] "e_mort_tbhiv_100k_hi" "e_mort_tbhiv_num"
## [33] "e_mort_tbhiv_num_lo" "e_mort_tbhiv_num_hi"
## [35] "e_mort_100k"        "e_mort_100k_lo"
## [37] "e_mort_100k_hi"     "e_mort_num"
## [39] "e_mort_num_lo"      "e_mort_num_hi"
## [41] "cfr"                "cfr_lo"
## [43] "cfr_hi"             "cfr_pct"
## [45] "cfr_pct_lo"         "cfr_pct_hi"
## [47] "c_newinc_100k"      "c_cdr"
## [49] "c_cdr_lo"           "c_cdr_hi"
```

```
print(tb_estimates[1:3, ])
```

```
## # A tibble: 3 x 50
##   country iso2 iso3 iso_num~1 g_who~2 year e_pop~3 e_inc~4 e_inc~5
##   <chr>   <chr> <chr>   <dbl> <chr>   <dbl>   <dbl>   <dbl>   <dbl>
## 1 Kenya KE    KEN      404 AFR     2000  3.09e7   451     182
## 2 Kenya KE    KEN      404 AFR     2001  3.18e7   499     178
## 3 Kenya KE    KEN      404 AFR     2002  3.28e7   534     174
## # ... with 41 more variables: e_inc_100k_hi <dbl>, e_inc_num <dbl>,
## #   e_inc_num_lo <dbl>, e_inc_num_hi <dbl>, e_tbhiv_prct <dbl>,
## #   e_tbhiv_prct_lo <dbl>, e_tbhiv_prct_hi <dbl>,
## #   e_inc_tbhiv_100k <dbl>, e_inc_tbhiv_100k_lo <dbl>,
## #   e_inc_tbhiv_100k_hi <dbl>, e_inc_tbhiv_num <dbl>,
## #   e_inc_tbhiv_num_lo <dbl>, e_inc_tbhiv_num_hi <dbl>,
## #   e_mort_exc_tbhiv_100k <dbl>, e_mort_exc_tbhiv_100k_lo <dbl>, ...
```

```
# Merge tb data with data dictionary
```

```
tbData = tb_estimates %>%
```



```
gather("variable_name", "value", 7:50) %>%
left_join(datadict)
```

```
## Joining, by = "variable_name"
```

```
# remove unnecessary regional columns, blank code_list
# column
tbData = subset(tbData, select = -c(iso2, iso3, iso_numeric,
  g_whoregion, code_list))
print(tbData[1:5, ])
```

```
## # A tibble: 5 x 6
##   country year variable_name value dataset definition
##   <chr>   <dbl> <chr>         <dbl> <chr>   <chr>
## 1 Kenya 2000 e_pop_num    30851606 Estimates Estimated total popu~
## 2 Kenya 2001 e_pop_num    31800343 Estimates Estimated total popu~
## 3 Kenya 2002 e_pop_num    32779823 Estimates Estimated total popu~
## 4 Kenya 2003 e_pop_num    33767122 Estimates Estimated total popu~
## 5 Kenya 2004 e_pop_num    34791836 Estimates Estimated total popu~
```

4.1.1 Structure of combined dataset and data dictionary

```
print(paste("The dataframe consists of ", dim(tbData)[1],
  " rows and ", dim(tbData)[2], " columns", sep = ""))
```

```
## [1] "The dataframe consists of 1012 rows and 6 columns"
```

```
# List of column names
colnames(tbData)
```

```
## [1] "country"      "year"          "variable_name" "value"
## [5] "dataset"      "definition"
```

```
print(tbData[1:3, ])
```

```
## # A tibble: 3 x 6
##   country year variable_name value dataset definition
##   <chr>   <dbl> <chr>         <dbl> <chr>   <chr>
## 1 Kenya 2000 e_pop_num    30851606 Estimates Estimated total popu~
## 2 Kenya 2001 e_pop_num    31800343 Estimates Estimated total popu~
## 3 Kenya 2002 e_pop_num    32779823 Estimates Estimated total popu~
```

```
# Type of each column
sapply(tbData, class)
```

```
##      country      year variable_name      value      dataset
## "character" "numeric" "character"    "numeric" "character"
## definition
## "character"
```

##Missing Data

From the code below it is seen that there are no missing data elements in the WHO TB data and every indicator has a value for the year 2000 to 2022.

```
# count the missing values by column wise
print("Count of missing values by column wise")
```

```
## [1] "Count of missing values by column wise"
```

```
sapply(tb_estimates, function(x) sum(is.na(x)))
```

```
##          country          iso2
##           0           0
##         iso3         iso_numeric
##           0           0
##       g_whoregion          year
##           0           0
##       e_pop_num       e_inc_100k
##           0           0
##   e_inc_100k_lo   e_inc_100k_hi
##           0           0
##       e_inc_num       e_inc_num_lo
##           0           0
##   e_inc_num_hi       e_tbhiv_prct
##           0           0
##   e_tbhiv_prct_lo   e_tbhiv_prct_hi
##           0           0
##   e_inc_tbhiv_100k   e_inc_tbhiv_100k_lo
##           0           0
##   e_inc_tbhiv_100k_hi   e_inc_tbhiv_num
##           0           0
##   e_inc_tbhiv_num_lo   e_inc_tbhiv_num_hi
##           0           0
##   e_mort_exc_tbhiv_100k e_mort_exc_tbhiv_100k_lo
##           0           0
##   e_mort_exc_tbhiv_100k_hi   e_mort_exc_tbhiv_num
##           0           0
##   e_mort_exc_tbhiv_num_lo   e_mort_exc_tbhiv_num_hi
##           0           0
##   e_mort_tbhiv_100k   e_mort_tbhiv_100k_lo
##           0           0
##   e_mort_tbhiv_100k_hi   e_mort_tbhiv_num
##           0           0
##   e_mort_tbhiv_num_lo   e_mort_tbhiv_num_hi
##           0           0
##       e_mort_100k       e_mort_100k_lo
##           0           0
##   e_mort_100k_hi       e_mort_num
##           0           0
##   e_mort_num_lo       e_mort_num_hi
##           0           0
##           cfr           cfr_lo
```

```
##          0          0
##          cfr_hi          cfr_pct
##          0          0
##          cfr_pct_lo          cfr_pct_hi
##          0          0
##          c_newinc_100k          c_cdr
##          0          0
##          c_cdr_lo          c_cdr_hi
##          0          0
```

4.1.2 Exploring WHO variables

Within the dataset there are multiple indicators listed under the column `variable_name`, each representing a certain measurement or quantity related to TB. Not all of these will be relevant to the model calibration but it is important to see what is available to determine those which are the most useful.

Notably, indicator values are presented yearly over an approximate two decade period between 2000-2022

```
# List individual indicators
tbData_vars = tbData$variable_name %>%
  unique()
print(tbData_vars)
```

```
## [1] "e_pop_num"          "e_inc_100k"
## [3] "e_inc_100k_lo"      "e_inc_100k_hi"
## [5] "e_inc_num"          "e_inc_num_lo"
## [7] "e_inc_num_hi"       "e_tbhiv_prct"
## [9] "e_tbhiv_prct_lo"    "e_tbhiv_prct_hi"
## [11] "e_inc_tbhiv_100k"    "e_inc_tbhiv_100k_lo"
## [13] "e_inc_tbhiv_100k_hi" "e_inc_tbhiv_num"
## [15] "e_inc_tbhiv_num_lo"  "e_inc_tbhiv_num_hi"
## [17] "e_mort_exc_tbhiv_100k" "e_mort_exc_tbhiv_100k_lo"
## [19] "e_mort_exc_tbhiv_100k_hi" "e_mort_exc_tbhiv_num"
## [21] "e_mort_exc_tbhiv_num_lo" "e_mort_exc_tbhiv_num_hi"
## [23] "e_mort_tbhiv_100k"    "e_mort_tbhiv_100k_lo"
## [25] "e_mort_tbhiv_100k_hi" "e_mort_tbhiv_num"
## [27] "e_mort_tbhiv_num_lo"  "e_mort_tbhiv_num_hi"
## [29] "e_mort_100k"          "e_mort_100k_lo"
## [31] "e_mort_100k_hi"       "e_mort_num"
## [33] "e_mort_num_lo"        "e_mort_num_hi"
## [35] "cfr"                  "cfr_lo"
## [37] "cfr_hi"               "cfr_pct"
## [39] "cfr_pct_lo"           "cfr_pct_hi"
## [41] "c_newinc_100k"        "c_cdr"
## [43] "c_cdr_lo"             "c_cdr_hi"
```

```
print(paste("Within the dataset there are ", length(tbData_vars),
  " indicators. Most indicators are grouped into categories of three with a mean, lower and upper bound",
  sep = ""))
```

```
## [1] "Within the dataset there are 44 indicators. Most indicators are grouped into categories of three"
```

```

# Time period
tbData_time = tbData$year %>%
  unique()
print(list(tbData_time))

## [[1]]
## [1] 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012
## [14] 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022

```

4.2 Exploring new incident infections (all infections and HIV)

Incident infections are the number of estimated people being infected with and acquiring active TB each year. The number of new infections is an estimate and is different from the number of reported cases or diagnoses - which is reliant on the identification, testing and treating of people with TB. This data represents a key element in the transmission model and it is important in understanding the past dynamics of TB in Kenya and provides an idea on the current trend.

HIV is an important factor to consider, given that Kenya has relatively high HIV/TB coinfection and because HIV impacts the likelihood of contracting TB, becoming infectious or of becoming severely ill.

```

# select relevant variables related to incidence
inc_data = tbData %>%
  filter(variable_name %in% c("e_inc_num", "e_inc_num_lo",
    "e_inc_num_hi")) %>%
  mutate(var = "e_inc_num")
hiv_inc = tbData %>%
  filter(variable_name %in% c("e_inc_tbhiv_num", "e_inc_tbhiv_num_lo",
    "e_inc_tbhiv_num_hi")) %>%
  mutate(var = "e_inc_tbhiv_num")
hiv_perc_inc = tbData %>%
  filter(variable_name %in% c("e_tbhiv_prct", "e_tbhiv_prct_lo",
    "e_tbhiv_prct_hi")) %>%
  mutate(var = "e_tbhiv_prct")

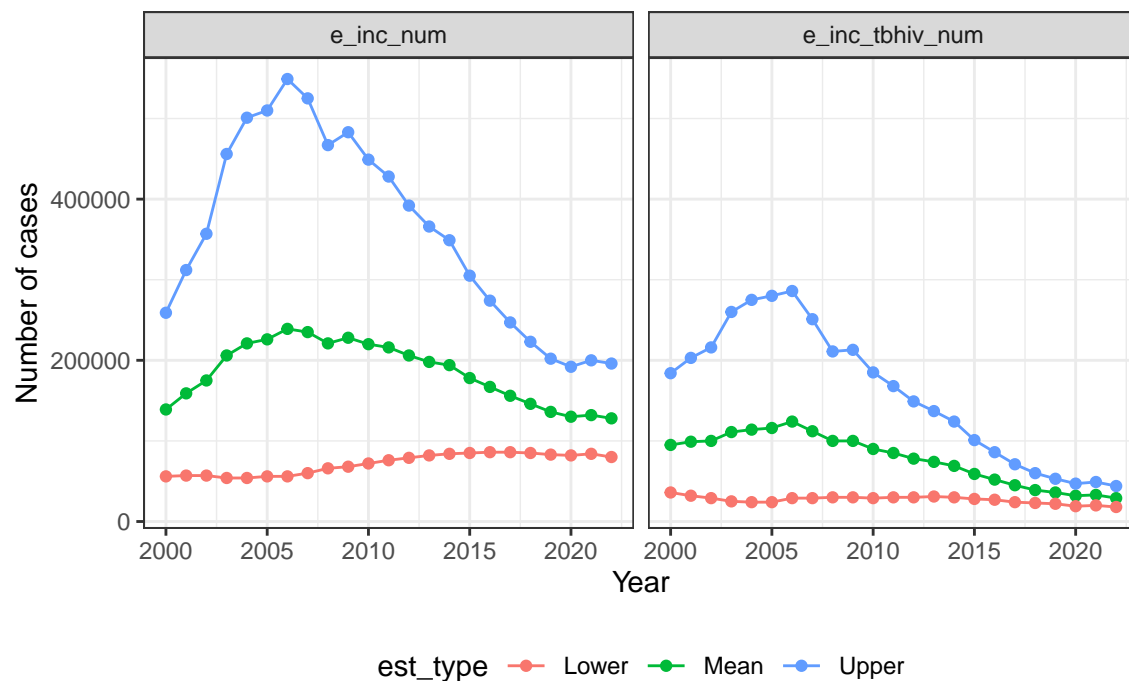
# label upper, lower and mean estimates
all_inc = rbind(inc_data, hiv_inc)
all_inc$est_type = "Mean"
all_inc$est_type[grepl("_lo", all_inc$variable_name, fixed = TRUE) ==
  TRUE] = "Lower"
all_inc$est_type[grepl("_hi", all_inc$variable_name, fixed = TRUE) ==
  TRUE] = "Upper"

hiv_perc_inc$est_type = "Mean"
hiv_perc_inc$est_type[grepl("_lo", hiv_perc_inc$variable_name,
  fixed = TRUE) == TRUE] = "Lower"
hiv_perc_inc$est_type[grepl("_hi", hiv_perc_inc$variable_name,
  fixed = TRUE) == TRUE] = "Upper"

# Incident cases (all and HIV)
ggplot(all_inc, aes(x = year, y = value, group = variable_name,
  color = est_type)) + geom_point() + geom_line() + theme_bw() +
  xlab("Year") + ylab("Number of cases") + labs(title = "Estimated number of new cases per year") +
  theme(legend.position = "bottom") + facet_wrap(. ~ var)

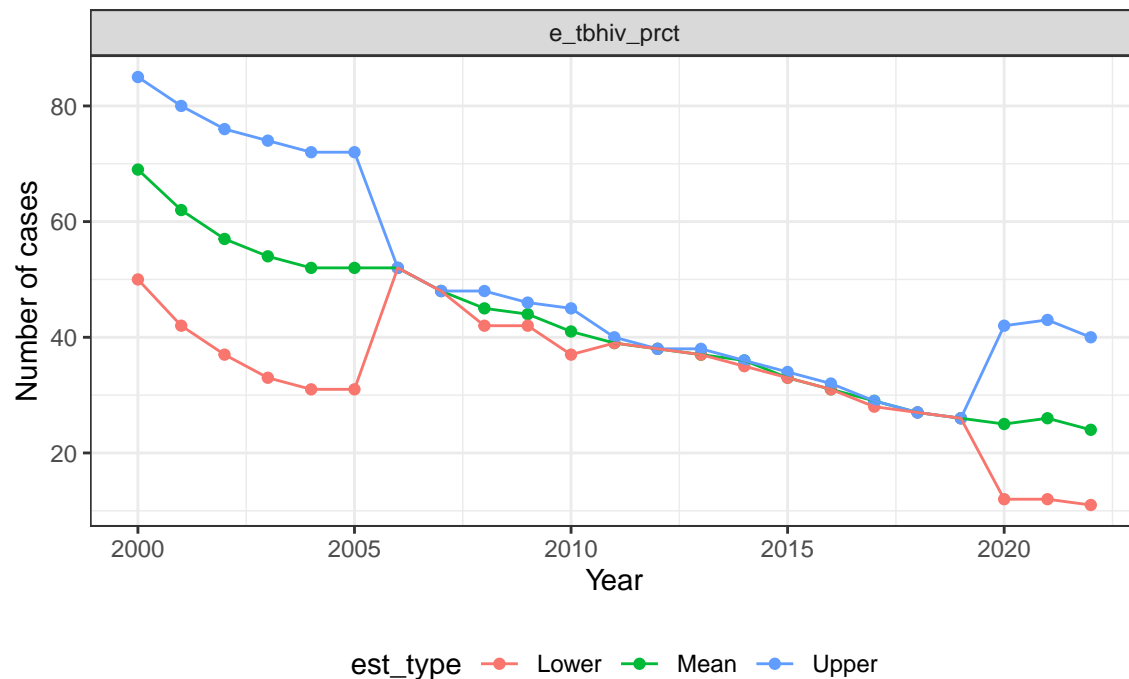
```

Estimated number of new cases per year



```
# Percentage of new cases HIV positive
ggplot(hiv_perc_inc, aes(x = year, y = value, group = variable_name,
  color = est_type)) + geom_point() + geom_line() + theme_bw() +
  xlab("Year") + ylab("Number of cases") + labs(title = "Estimated number of new cases per year") +
  theme(legend.position = "bottom") + facet_wrap(. ~ var)
```

Estimated number of new cases per year



4.3 Exploring mean estimates of key factors - population, incidence, case detection, mortality (for whole population)

Key definitions from WHO indicator metadata registry and estimate methodology appendix

- Case Detection rate (%) : Proportion of estimated new and relapse TB (incident) cases diagnosed in a year

-Number of deaths: Product of incidence and case fatality rate

-Case fatality rate: risk of death among people with active (incident) TB, adapted to account for low coverage/reporting

```
# Collect key factors relevant to understanding the
# dynamics of TB transmission
key_fact = tbData %>%
  filter(variable_name %in% c("e_pop_num", "e_inc_num",
    "e_inc_rr_num", "e_mort_num", "c_cdr", "cfr", "cfr_pct")) %>%
  select(variable_name, year, value) %>%
  spread(variable_name, value)

# Conduct additional calculations for rates or use
# rates to estimate numbers
key_fact$calc_cfr_inc = 100 * (key_fact$e_mort_num/key_fact$e_inc_num)
key_fact$calc_case_detect = key_fact$c_cdr/100 * key_fact$e_inc_num
key_fact$calc_cfr_case = 100 * (key_fact$e_mort_num/key_fact$calc_case_detect)
key_fact$deaths_cal = key_fact$cfr * key_fact$e_inc_num

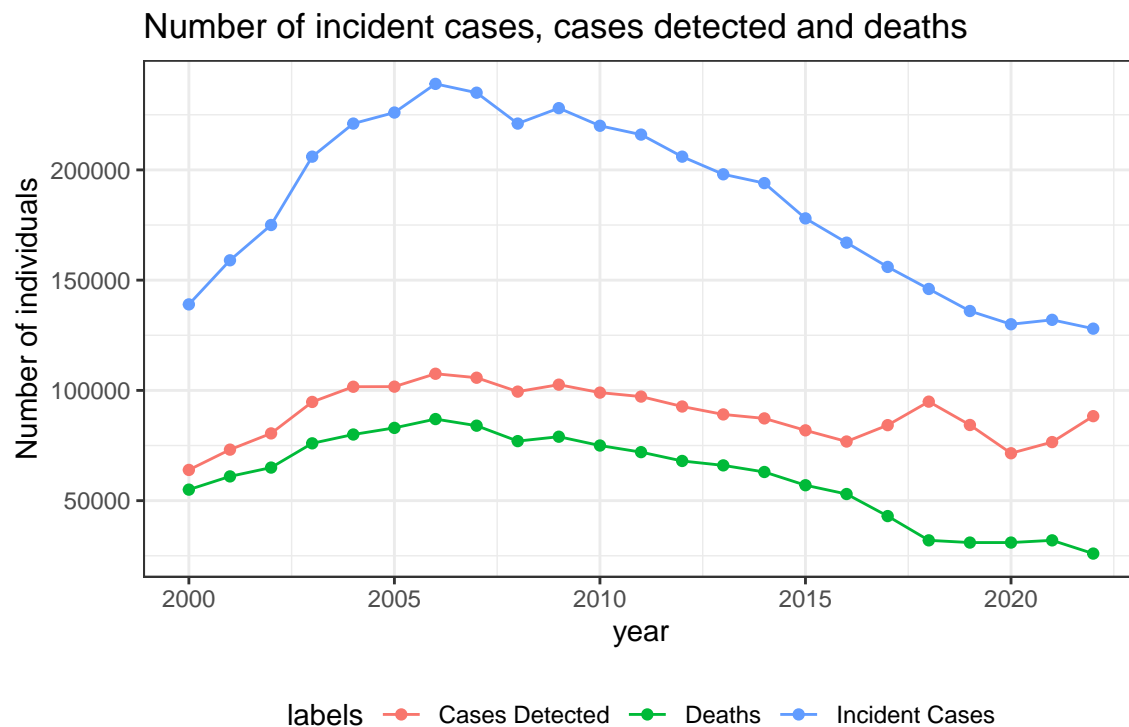
# Add user friendly labels
```

```
variable = c("e_pop_num", "e_inc_num", "e_inc_rr_num", "e_mort_num",
             "c_cdr", "cfr", "cfr_pct", "calc_case_detect")
labels = c("Population", "Incident Cases", "Incident RR Cases",
           "Deaths", "Case Detection Rate", "Case fatality Rate",
           "Case Fatality Rate (%)", "Cases Detected")
labs = data.frame(cbind(variable, labels))
```

```
# Plot key factors with absolute numbers (other than
# population)
key_fact_num = key_fact %>%
  select(year, e_inc_num, calc_case_detect, e_mort_num) %>%
  gather("variable", "value", 2:4) %>%
  left_join(labs)
```

```
## Joining, by = "variable"
```

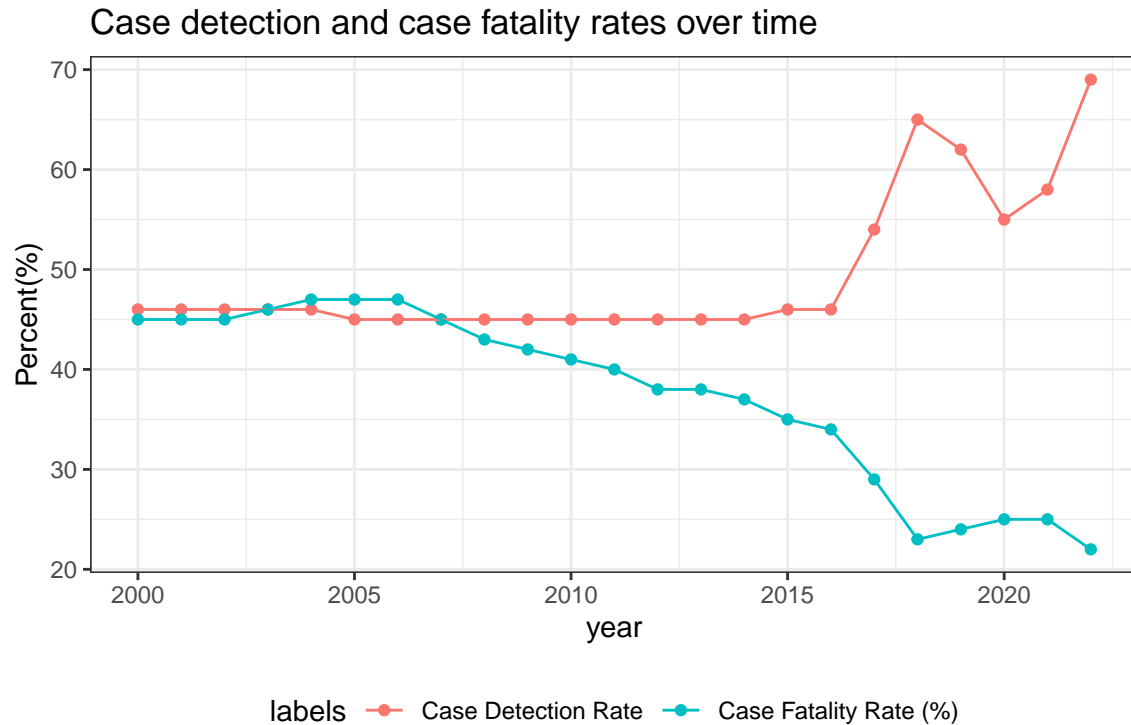
```
ggplot(key_fact_num, aes(x = year, y = value, group = variable,
                        colour = labels)) + geom_point() + geom_line() + theme_bw() +
  labs(title = "Number of incident cases, cases detected and deaths") +
  ylab("Number of individuals") + theme(legend.position = "bottom")
```



```
# Plot key factors which are rates
key_fact_rate = key_fact %>%
  select(year, c_cdr, cfr_pct) %>%
  gather("variable", "value", 2:3) %>%
  left_join(labs)
```

```
## Joining, by = "variable"
```

```
ggplot(key_fact_rate, aes(x = year, y = value, group = variable,
  colour = labels)) + geom_point() + geom_line() + theme_bw() +
  labs(title = "Case detection and case fatality rates over time") +
  ylab("Percent(%)") + theme(legend.position = "bottom")
```



4.4 Set up calibration data for transmission model

The transmission model will be calibrated against data from this set. In this case incidence data over time will be the key comparator, however, later it will be useful to compare other variables - like cases detected.

```
# Collect incidence data in correct format - key
# variables and wide format
cal_data = all_inc %>%
  select(year, var, est_type, value) %>%
  spread(est_type, value) %>%
  filter(var == "e_inc_num")

# Save data
write.csv(cal_data, "/Users/adenooy/Library/CloudStorage/OneDrive-Personal/UVA/Thesis/MSc-Thesis/data/dy")
```