Co-financing model code documentation

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Contents

Setup

Loading packages.

```
library(tidyverse)
```

```
## -- Attaching packages ------------------------------------------------------------------------------
```

```
## v ggplot2 3.2.0     v purrr   0.3.2
## v tibble  2.1.3     v dplyr   0.8.3
## v tidyr   0.8.3     v stringr 1.4.0
## v readr   1.3.1     v forcats 0.4.0
```

```
## -- Conflicts ---------------------------------------------------------------------------------------
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

Some useful functions (for later)

Set some global values.

```
countries_model <- c("Ghana", "India", "Kenya",
                     "Nigeria", "Angola",   "Senegal")
```

Capitalise first letter function (to be used later).

```
firstup <- function(x) {
  substr(x, 1, 1) <- toupper(substr(x, 1, 1))
  x
}
```

Round up nicely for plotting (to be used later).

```
roundUp <- function(x, nice_val=c(1, 2, 3, 4, 5, 6, 7,  8, 9, 10)) {
    if(length(x) != 1) stop("'x' can only take vectors of length 1")
    10^floor(log10(x)) * nice_val[[which(x <= 10^floor(log10(x)) * nice_val)[[1]]]]
}
```

Donor-country (DC) model

Load the DC model function.

```
source("R/DCmodel.R")
```

Examples using the DC model

```
# Input one vaccine and use the threshold input
DCmodel(cost = 10000,
        benefit = 15,
        intervention = "vaccine 1",
        threshold = 500)
```

```
## # A tibble: 1 x 7
##   intervention  cost benefit   cer threshold domestic donor
##   <chr>        <dbl>   <dbl> <dbl>     <dbl>    <dbl> <dbl>
## 1 vaccine 1    10000      15   667       500     7500  2500
```

```
# Input one vaccine and use gdp_per_capita and
#   gdp_threshold_multiple
DCmodel(cost = 1000,
        benefit = 20,
        intervention = "vaccine 1",
        gdp_per_capita = 500,
        gdp_threshold_multiple = 1.5) %>%
  # Dropping gdp_threshold_multiple from output so see entire table
  #   in RMarkdown document
  select(-gdp_threshold_multiple)
```

```
## # A tibble: 1 x 8
##   intervention  cost benefit   cer gdp_per_capita threshold domestic donor
##   <chr>        <dbl>   <dbl> <dbl>          <dbl>     <dbl>    <dbl> <dbl>
## 1 vaccine 1     1000      20    50            500       750     1000     0
```

```
# Input several vaccines
DCmodel(cost = c(1.5, 4, 0.8, 10) * 1000000,
        benefit = c(2000, 2500, 1500, 1000),
        intervention = c("v1", "v2", "v3", "v4"),
        gdp_per_capita = 500,
        gdp_threshold_multiple = 1.5) %>%
  # Dropping gdp_threshold_multiple and gdp_per_caita from output so see entire
  #   table in RMarkdown document
  select(-gdp_threshold_multiple, -gdp_per_capita)
```

```
## # A tibble: 4 x 7
##   intervention     cost benefit   cer threshold domestic   donor
##   <chr>           <dbl>   <dbl> <dbl>     <dbl>    <dbl>   <dbl>
## 1 v1            1500000    2000   750       750  1500000       0
## 2 v2            4000000    2500  1600       750  1875000 2125000
## 3 v3             800000    1500   533       750   800000       0
## 4 v4           10000000    1000 10000       750   750000 9250000
```

```
# Input one vaccine and several thresholds
DCmodel(cost = 10000,
        benefit = 15,
        intervention = "vaccine 1",
        gdp_per_capita = rep(500, 4), # rep repeats 500 four times,
        gdp_threshold_multiple = c(0.5, 1, 3, 4.5)) %>%
  # Dropping gdp_threshold_multiple and gdp_per_caita from output so see entire
  #   table in RMarkdown document
  select(-gdp_threshold_multiple, -gdp_per_capita)
```

```
## # A tibble: 4 x 7
##   intervention  cost benefit   cer threshold domestic donor
##   <chr>        <dbl>   <dbl> <dbl>     <dbl>    <dbl> <dbl>
## 1 vaccine 1    10000      15   667       250     3750  6250
## 2 vaccine 1    10000      15   667       500     7500  2500
## 3 vaccine 1    10000      15   667      1500    10000     0
## 4 vaccine 1    10000      15   667      2250    10000     0
```

```
# Input several vaccines and several thresholds
DCmodel(cost = c(1.5, 4, 0.8, 10) * 1000000,
        benefit = c(8000, 5000, 1500, 10000),
        intervention = c("v1", "v2", "v3", "v4"),
        gdp_per_capita = rep(500, 3),
        gdp_threshold_multiple = c(0.5, 1, 3)) %>%
  # Dropping gdp_threshold_multiple and gdp_per_caita from output so see entire
  #   table in RMarkdown document
  select(-gdp_threshold_multiple, -gdp_per_capita)
```

```
## # A tibble: 12 x 7
##    intervention     cost benefit   cer threshold domestic    donor
##    <chr>           <dbl>   <dbl> <dbl>     <dbl>    <dbl>    <dbl>
##  1 v1            1500000    8000   188       250  1500000        0
##  2 v2            4000000    5000   800       250  1250000  2750000
##  3 v3             800000    1500   533       250   375000   425000
##  4 v4           10000000   10000  1000       250  2500000  7500000
##  5 v1            1500000    8000   188       500  1500000        0
##  6 v2            4000000    5000   800       500  2500000  1500000
##  7 v3             800000    1500   533       500   750000    50000
##  8 v4           10000000   10000  1000       500  5000000  5000000
##  9 v1            1500000    8000   188      1500  1500000        0
## 10 v2            4000000    5000   800      1500  4000000        0
## 11 v3             800000    1500   533      1500   800000        0
## 12 v4           10000000   10000  1000      1500 10000000        0
```

Data

Load data

```
gdp_data <- read_csv("data/data_gdp_per_capita.csv")
```

```
## Parsed with column specification:
## cols(
##   Country = col_character(),
##   `2001` = col_double(),
##   `2002` = col_double(),
##   `2003` = col_double(),
##   `2004` = col_number(),
##   `2005` = col_number(),
##   `2006` = col_number(),
##   `2007` = col_number(),
##   `2008` = col_number(),
##   `2009` = col_number(),
##   `2010` = col_number(),
##   `2011` = col_number(),
##   `2012` = col_number(),
##   `2013` = col_number(),
##   `2014` = col_number(),
##   `2015` = col_number(),
##   `2016` = col_number(),
##   `2017` = col_number(),
##   `2018` = col_number()
## )
```

```
cea_data <- read_csv("data/data_cea.csv")
```

```
## Warning: Missing column names filled in: 'X15' [15], 'X16' [16],
## 'X17' [17], 'X18' [18], 'X19' [19], 'X20' [20], 'X21' [21], 'X22' [22],
## 'X23' [23], 'X24' [24]
```

```
## Parsed with column specification:
## cols(
##   .default = col_logical(),
##   Country = col_character(),
##   Vaccine = col_character(),
##   `Indicator (e.g. deaths averted)` = col_character(),
##   `Total cost for the period` = col_number(),
##   `Costs per year` = col_number(),
##   `Total benefit for the period` = col_number(),
##   `Benefits per year` = col_number(),
##   `Cost-effectiveness` = col_number(),
##   `Start year` = col_double(),
##   `End year` = col_double(),
##   `Year of dollar rate used` = col_double(),
##   Perspective = col_character(),
##   Assumptions = col_character(),
##   `Author(s)` = col_character()
## )

## See spec(...) for full column specifications.
```

```
fund_data <- read_csv("data/data_vaccine_funding.csv")
```

```
## Warning: Missing column names filled in: 'X9' [9], 'X10' [10], 'X11' [11],
## 'X12' [12], 'X13' [13], 'X14' [14], 'X15' [15]

## Parsed with column specification:
## cols(
##   Country = col_character(),
##   Vaccine = col_character(),
##   Year = col_double(),
##   Total = col_double(),
##   `Domestic contribution ($)` = col_double(),
##   `Gavi contribution ($)` = col_double(),
##   `Domestic (%)` = col_double(),
##   `Gavi (%)` = col_double(),
##   X9 = col_logical(),
##   X10 = col_logical(),
##   X11 = col_logical(),
##   X12 = col_logical(),
##   X13 = col_logical(),
##   X14 = col_logical(),
##   X15 = col_logical()
## )
```

```
gdp_deflator <- read_csv("data/gdp_deflator.csv")
```

```
## Parsed with column specification:
## cols(
##   .default = col_double(),
##   `Country Name` = col_character(),
##   `Country Code` = col_character(),
##   `Indicator Name` = col_character(),
##   `Indicator Code` = col_character(),
##   `2019` = col_logical()
## )
## See spec(...) for full column specifications.
```

```
ex_rate <- read_csv("data/ex_rate.csv")
```

```
## Parsed with column specification:
## cols(
##   .default = col_double(),
##   `Country Name` = col_character(),
##   `Country Code` = col_character(),
##   `Indicator Name` = col_character(),
##   `Indicator Code` = col_character(),
##   `2019` = col_logical()
## )
## See spec(...) for full column specifications.
```

```
population_data <- read_csv("data/population_data.csv")
```

```
## Parsed with column specification:
## cols(
##   `Country Name` = col_character(),
##   `2012` = col_double(),
##   `2013` = col_double(),
##   `2014` = col_double(),
##   `2015` = col_double(),
##   `2016` = col_double(),
##   `2017` = col_double(),
##   `2018` = col_double()
## )
```

Clean data

Population data

```
# Change to long format data
population_data <-
  population_data %>%
  rename(country = `Country Name`) %>%
  gather(key = year, value = population, `2012`:`2018`) %>%
  mutate(year = as.numeric(year)) %>%
  filter(country %in% countries_model)
```

Gross domestic product deflator and exchange rate

Clean and combine Gross domestic product (GDP) deflator and exchange rate data.

```
# Clean and remove unnecessary columns
gdp_deflator <- gdp_deflator %>% rename(country = `Country Name`) %>%
  select(country, `2000`:`2018`) %>%
  filter(country %in% countries_model) %>%
  gather(key = year, value = deflator, `2000`:`2018`)

# Add 2018 year to get multiplier of def_2018/def_year
gdp_deflator <- left_join(gdp_deflator,
          gdp_deflator %>% filter(year == 2018) %>% select(-year) %>%
            rename(deflator2018 = deflator),
          by = "country") %>%
  mutate(def_multiplier = deflator2018/deflator) %>%
  select(country, year, def_multiplier)

# Clean exchange rate tibble
ex_rate <- ex_rate %>% rename(country = `Country Name`) %>%
  select(country, `2000`:`2018`) %>%
  filter(country %in% countries_model) %>%
  gather(key = year, value = ex, `2000`:`2018`)

# Add exchange rate multiplier to get ex_2018/ex_year
#   multiplying by both multipliers will give
#   to local_currency = reported$$ * ex
#   to 2018_local-currency = local_currency * def_2018/def
#   to 2018_$ = 2018_local_currency / ex_2018
#   i.e. (reported$$ * ex * def_2018/def) / ex_2018 =
#   reported$$ * def_2018/def * ex/ex_2018
ex_rate <- left_join(ex_rate,
          ex_rate %>% filter(year == 2018) %>% select(-year) %>%
            rename(ex2018 = ex),
          by = "country") %>%
  mutate(ex_multiplier = ex/ex2018) %>%
  select(country, year, ex_multiplier)

# Create currency exchange deflating and exchanging
currency_conv <- left_join(gdp_deflator, ex_rate, by = c("country", "year")) %>%
  mutate(currency_mult = def_multiplier * ex_multiplier) %>%
  mutate(dollar_year = as.numeric(year)) %>%
  select(country, dollar_year, currency_mult)
```

Cost-effectiveness data and GDP per capita

Clean the cost-effectiveness analysis (CEA) data.

```
cea_data <- cea_data %>%
  # Rename to more data-friendly
  rename(country = Country, vaccine = Vaccine,
         indicator = `Indicator (e.g. deaths averted)`,
         cost_for_horizon = `Total cost for the period`,
         cost = `Costs per year`,
         benefit_for_horizon = `Total benefit for the period`,
         benefit = `Benefits per year`, cea = `Cost-effectiveness`,
         s_year = `Start year`, e_year = `End year`,
         dollar_year = `Year of dollar rate used`,
         perspective = Perspective, assumptions = Assumptions,
         authors = `Author(s)`) %>%
  select(country:authors) %>%
  # Consistent naming of indicators
  mutate(indicator = firstup(indicator)) %>%
  mutate(indicator = gsub("DALY ", "DALYs ", indicator)) %>%
  mutate(indicator = gsub("Death ", "Deaths ", indicator)) %>%
  mutate(indicator = gsub("Case ", "Cases ", indicator)) %>%
  mutate(indicator = gsub("YLL", "YLLs averted", indicator)) %>%
  # Some of the vaccine names differ between fund_data and cea_data
  mutate(vaccine = ifelse(grepl("DTP-Hep", vaccine, ignore.case = TRUE),
                          "DTP-hep B",
                          vaccine)) %>%
  mutate(vaccine = ifelse(grepl("Yellow Fever", vaccine),
                          "Yellow Fever",
                          vaccine)) %>%
  mutate(vaccine = ifelse(grepl("Measles", vaccine),
                          "Measles",
                          vaccine)) %>%
  mutate(vaccine = ifelse(grepl("Pneumococcal", vaccine),
                          "PCV",
                          vaccine)) %>%
  mutate(vaccine = ifelse(grepl("Rota", vaccine),
                          "Rotavirus",
                          vaccine)) %>%
  mutate(vaccine = ifelse(grepl("BCG", vaccine),
                          "BCG",
                          vaccine)) %>%
  # Select only countries in the analysis
  filter(country %in% countries_model)
```

Perform some checks on CEA data.

```
# Check diff between calculated and CEA reported in papers
#   Small differences are likely due to rounding errors
cea_data %>% select(cost, benefit, cea) %>%
  mutate(cea2 = round(cost/benefit,2)) %>%
  mutate(diff = cea - cea2) %>%
  arrange(desc(abs(diff))) %>%
  filter(abs(diff) > 1e-09)
```

```
## # A tibble: 19 x 5
##         cost benefit    cea   cea2     diff
##        <dbl>   <dbl>  <dbl>  <dbl>    <dbl>
##  1   3689149     303 12196. 12175. 20.1
##  2   1409658     303  4660.  4652.  7.69
##  3   6409006     634 10102. 10109. -6.37
##  4  11783120     888 13274. 13269.  4.48
##  5  18747118    1303 14392. 14388.  4.01
##  6   3721375     634  5866.  5870. -3.7
##  7   1505569     311  4844.  4841.  3.11
##  8   7390364     888  8325.  8322.  2.81
##  9   1083447     311  3486.  3484.  2.24
## 10    379910     311  1222.  1222.  0.780
## 11 176198173   10601 16621. 16621.  0.470
## 12 176198173   10601 16621. 16621.  0.470
## 13  34223066    9193  3723.  3723. -0.160
## 14   7766946    3053  2544.  2544.  0.160
## 15   7766946    3053  2544.  2544.  0.160
## 16  28770592    9193  3129.  3130. -0.140
## 17  18747118    9228  2031.  2032. -0.1000
## 18   3200000   12570   255.   255.  0.01
## 19   3721375   33380   111.   111. -0.01000
```

Transform GDP per capita data to long format, convert to $2018, and add cost & benefit columns.

```r
# Max cost +, to create a sequence for plotting
max_x <- max(cea_data$cost) + 50000000
seq_x <- seq(0, max_x, by = 100000)

# Convert GDP data to 2018 $
gdp_data <- gdp_data %>%
  gather(key = "year", value = "gdp_pc", -Country) %>%
  rename(country = Country) %>%
  mutate(year = as.numeric(year)) %>%
  # Convert currency
  left_join(currency_conv %>% rename(year = dollar_year),
            by = c("country", "year")) %>%
  mutate(gdp_pc = gdp_pc * currency_mult) %>%
  select(-currency_mult)

# Add cost and benefit columns to gdp_data to
#   draw the CEA threshold
gdp_data <- gdp_data %>%
  # Create rows for each analysis
  slice(rep(row_number(), length(seq_x))) %>%
  # Add a cost column, for plotting cost x-axis
  mutate(cost = unlist(sapply(seq_x, function(x) rep(x, nrow(gdp_data)), simplify = FALSE))) %>%
  # Add a number of benefit lines for plotting
  mutate(benefit_line = cost/gdp_pc,
         benefit_half_line = cost/gdp_pc/0.5,
         benefit_3_line = cost/gdp_pc/3,
         benefit_4_5_line = cost/gdp_pc/4.5)

# Convert to long data tibble
gdp_data <- gdp_data %>%
  gather(key = threshold, value = cea_line, benefit_line:benefit_4_5_line) %>%
  # Write clear headings for different thresholds
  mutate(threshold = ifelse(threshold == "benefit_line",
                            "1 x GDP\nper capita",
                            threshold)) %>%
  mutate(threshold = ifelse(threshold == "benefit_half_line",
                            "0.5 x GDP\nper capita",
                            threshold)) %>%
  mutate(threshold = ifelse(threshold == "benefit_3_line",
                            "3 x GDP\nper capita",
                            threshold)) %>%
  mutate(threshold = ifelse(threshold == "benefit_4_5_line",
                            "4.5 x GDP\nper capita",
                            threshold))
```

Convert the CEA data into 2018 US Dollars using WB deflator.

```r
# Combine CEA data and currency conversion data
cea_data <- left_join(cea_data, currency_conv, by = c("country", "dollar_year")) %>%
  # Convert all costs
  mutate(cost_for_horizon = cost_for_horizon * currency_mult,
         cost = cost * currency_mult,
         cea = cea * currency_mult,
         benefit = ifelse(
           grepl("Total healthcare cost averted|Out-of-pocket expenditure",
                 indicator),
           benefit * currency_mult,
           benefit))
```

Co-financing data

Clean co-financing data.

```
fund_data <-
  fund_data %>%
  # Rename columns so they are easier to work with.
  rename(country = Country, vaccine = Vaccine, year = Year,
         total = Total,
         domestic = `Domestic contribution ($)`,
         gavi = `Gavi contribution ($)`,
         domestic_p = `Domestic (%)`, gavi_p = `Gavi (%)`) %>%
  # Remove some columns that are unnecessary
  select(country:gavi_p) %>%
  # Remove rows with countries that are not part of the analysis (there are some
  #   unnecessary rows in the data that explain the data)
  filter(country %in% countries_model) %>%
  # Convert numbers to numeric
  mutate(year = as.numeric(year),
         total = as.numeric(gsub("\\,", "", total)),
         domestic = as.numeric(gsub("\\,", "", domestic)),
         gavi = as.numeric(gsub("\\,", "", gavi)),
         domestic_p = as.numeric(domestic_p)/100,
         gavi_p = as.numeric(gavi_p)/100) %>%
  # Convert currency using currency conversion table
  left_join(currency_conv %>% rename(year = dollar_year),
            by = c("country", "year")) %>%
  mutate(total = total * currency_mult,
         domestic = domestic * currency_mult,
         gavi = gavi * currency_mult) %>%
  select(-currency_mult) %>%
  # Some of the vaccine names differ between fund_data and cea_data;
  #   fix.
  mutate(vaccine = ifelse(grepl("DTP-Hep", vaccine),
                          "DTP-hep B",
                          vaccine)) %>%
  mutate(vaccine = ifelse(grepl("Yellow Fever", vaccine),
                          "Yellow Fever",
                          vaccine)) %>%
  mutate(vaccine = ifelse(grepl("Measles", vaccine),
                          "Measles",
                          vaccine)) %>%
  mutate(vaccine = ifelse(grepl("Pneumococcal", vaccine),
                          "PCV",
                          vaccine)) %>%
  mutate(vaccine = ifelse(grepl("Rota", vaccine),
                          "Rotavirus",
                          vaccine))
```

Combine CEA and funding data into a tibble

```
# Check what vaccines in CEA data are not in co-financing data
temp <- (cea_data %>% distinct(vaccine) %>% unlist) %in%
(fund_data %>% distinct(vaccine) %>% unlist)
(cea_data %>% distinct(vaccine) %>% unlist)[!temp]
```

```
## vaccine3
##    "BCG"
```

```
# Check what vaccines in co-financing data are not in CEA data
temp <- (fund_data %>% distinct(vaccine) %>% unlist) %in%
(cea_data %>% distinct(vaccine) %>% unlist)
(fund_data %>% distinct(vaccine) %>% unlist)[!temp]
```

```
##                vaccine6                 vaccine7                 vaccine8
##                  "MenA" "MR Follow up campaign"          "MenA Routine"
##                vaccine9
##                   "IPV"
```

```
# Combine CEA and co-financing data by country and vaccine.
#   Include all of the vaccines we have in the CEA analysis data,
#   but not ones we have only in the co-financing data.
data <- full_join(cea_data,
                  fund_data %>% rename(year_gavi = year),
                  by = c("country", "vaccine"))

# Add BCG vaccine, not supported by Gavi for plotting
BCG_data <- data %>%
  # Get BCG data; at this point only includes Levin et al 2007
  filter(vaccine == "BCG") %>%
  # Copy rows years to create years 2006-2018
  slice(rep(row_number(), length(2006:2018))) %>%
  arrange(indicator) %>%
  mutate(year_gavi = rep(2006:2018, 3)) %>%
  # Remove 2015 since do not have data
  filter(year_gavi != 2015)

# Add the BCG data
data <- data %>%
  # Remove the NA BCG data row
  filter(vaccine != "BCG") %>%
  # Add rest of BCG data
  rbind(BCG_data)
```

Clean combined data.

```
# Remove non-base-case
data <- data %>%
  # Include only DALY or YLL
  filter(grepl("DALY|YLL", indicator)) %>%
  # Filter years that do not have any Gavi data or only for
  #   a few countries and based on future projections
  #   First add a year for BCG, so plot despite no Gavi
  #   funding.
  mutate(year_gavi = ifelse(is.na(year_gavi) &
                              authors == "Levin et al. 2007" &
                              vaccine == "BCG",
                            2007,
                            year_gavi)) %>%
  filter(year_gavi < 2019) %>%
  # Only include base-case of Abbot et al. 2012
  #  and use earliest year of Gavi funding (since intervention is 2003-08).
  filter(!(authors == "Abbott et al. 2012" &
             (assumptions != "$5 per dose"))) %>%# | year_gavi != 2012))) %>%
  # Do not include the CEA with Gavi Subsidy accounted for
  #   and focus on health system perspective.
  filter(!(authors == "Nonvignon et al. 2018" &
             (grepl("Ghana only", assumptions) |
             !grepl("Health system", perspective)))) %>%
  # Use relevant Gavi data year for Krishnamoorthy et al. 2019
  #   based on paper intervention years
  # filter(!(authors == "Krishnamoorthy et al. 2019" &
  #            year_gavi != 2018)) %>%
  # Use the analysis with the 90% intervention coverage and year 2018
  #   for Gavi funding based on paper intervention years
  filter(!(authors == "Megiddo et al. 2018" &
             (grepl("Expanded coverage (90%)", assumptions)))) %>%
  # Do not include the CEA with Gavi subsidy accounted for
  filter(!(authors == "Debellut et al., 2019" &
             (assumptions == "Vaccine programme costs with Gavi subsidy"))) %>%
  # Remove rows with no co-financing data
  filter(!(is.na(total) & (!is.na(gavi) | !is.na(domestic)))) %>%
  # Add a column with vaccine and paper
  mutate(vaccine_cea_paper = paste0(vaccine, "\n", authors)) %>%
  # Remove columns that do not need for figures
  select(-cost_for_horizon, -benefit_for_horizon, -currency_mult)
```

DC model with data

In the following code, we use the CEA study data for costs and benefits. We use the DC model to calculate the split between domestic and donor funding.

```
# Ochalek et al. 2018 proportion
ochalek_p <- 0.33

# Ghana data
ghana_data <-
  data %>%
  filter(country == "Ghana") %>%
  distinct(vaccine, cost, benefit)

# GDP per capita data
```

```r
ghana_gdppc <-
  gdp_data %>%
  filter(country == "Ghana") %>%
  distinct(year, gdp_pc)

# Run DC model
DCmodel_out <- DCmodel(
cost = ghana_data$cost,
benefit = ghana_data$benefit,
intervention = ghana_data$vaccine,
gdp_per_capita = rep(ghana_gdppc$gdp_pc, 5),
gdp_threshold_multiple = c(rep(ochalek_p, nrow(ghana_gdppc)),
                           rep(0.5, nrow(ghana_gdppc)),
                           rep(1, nrow(ghana_gdppc)),
                           rep(3, nrow(ghana_gdppc)),
                           rep(4.5, nrow(ghana_gdppc)))
)


# Print output
DCmodel_out %>%
  left_join(ghana_gdppc %>% rename(gdp_per_capita = gdp_pc),
            by = "gdp_per_capita") %>%
    # Remove rotavirus vaccines before 2012
    filter(!(intervention == "Rotavirus" & year < 2012)) %>%
  select(intervention, year, cer,
         gdp_threshold_multiple, threshold, domestic, donor) %>%
  print(n = nrow(DCmodel_out))
```

```
## # A tibble: 465 x 7
##     intervention  year    cer gdp_threshold_mul~ threshold  domestic  donor
##     <chr>        <dbl>  <dbl>              <dbl>     <dbl>     <dbl>  <dbl>
##   1 Measles       2001   3397               0.33       388  5276800  4.09e7
##   2 DTP-hep B     2001   2665               0.33       388 13980804  8.21e7
##   3 Yellow Fever  2001    176               0.33       388  4719371. 0.
##   4 BCG           2001 154221               0.33       388    62080  2.46e7
##   5 Measles       2002   3397               0.33       396  5385600  4.08e7
##   6 DTP-hep B     2002   2665               0.33       396 14269068  8.18e7
##   7 Yellow Fever  2002    176               0.33       396  4719371. 0.
##   8 BCG           2002 154221               0.33       396    63360  2.46e7
##   9 Measles       2003   3397               0.33       407  5535200  4.07e7
##  10 DTP-hep B     2003   2665               0.33       407 14665431  8.14e7
##  11 Yellow Fever  2003    176               0.33       407  4719371. 0.
##  12 BCG           2003 154221               0.33       407    65120  2.46e7
##  13 Measles       2004   3397               0.33       419  5698400  4.05e7
##  14 DTP-hep B     2004   2665               0.33       419 15097827  8.09e7
##  15 Yellow Fever  2004    176               0.33       419  4719371. 0.
##  16 BCG           2004 154221               0.33       419    67040  2.46e7
##  17 Measles       2005   3397               0.33       433  5888800  4.03e7
##  18 DTP-hep B     2005   2665               0.33       433 15602289  8.04e7
##  19 Yellow Fever  2005    176               0.33       433  4719371. 0.
##  20 BCG           2005 154221               0.33       433    69280  2.46e7
##  21 Measles       2006   3397               0.33       449  6106400  4.01e7
##  22 DTP-hep B     2006   2665               0.33       449 16178817  7.99e7
##  23 Yellow Fever  2006    176               0.33       449  4719371. 0.
##  24 BCG           2006 154221               0.33       449    71840  2.46e7
##  25 Measles       2007   3397               0.33       456  6201600  4.00e7
##  26 DTP-hep B     2007   2665               0.33       456 16431048  7.96e7
##  27 Yellow Fever  2007    176               0.33       456  4719371. 0.
##  28 BCG           2007 154221               0.33       456    72960  2.46e7
##  29 Measles       2008   3397               0.33       485  6596000  3.96e7
##  30 DTP-hep B     2008   2665               0.33       485 17476005  7.86e7
##  31 Yellow Fever  2008    176               0.33       485  4719371. 0.
##  32 BCG           2008 154221               0.33       485    77600  2.46e7
##  33 Measles       2009   3397               0.33       496  6745600  3.94e7
##  34 DTP-hep B     2009   2665               0.33       496 17872368  7.82e7
##  35 Yellow Fever  2009    176               0.33       496  4719371. 0.
##  36 BCG           2009 154221               0.33       496    79360  2.46e7
##  37 Measles       2010   3397               0.33       522  7099200  3.91e7
##  38 DTP-hep B     2010   2665               0.33       522 18809226  7.72e7
##  39 Yellow Fever  2010    176               0.33       522  4719371. 0.
##  40 BCG           2010 154221               0.33       522    83520  2.46e7
##  41 Measles       2011   3397               0.33       581  7901600  3.83e7
##  42 DTP-hep B     2011   2665               0.33       581 20935173  7.51e7
##  43 Yellow Fever  2011    176               0.33       581  4719371. 0.
##  44 BCG           2011 154221               0.33       581    92960  2.46e7
##  45 Rotavirus     2012    113               0.33       620  2105497. 0.
##  46 Rotavirus     2012    387               0.33       620  4931933. 0.
##  47 Measles       2012   3397               0.33       620  8432000  3.78e7
##  48 DTP-hep B     2012   2665               0.33       620 22340460  7.37e7
##  49 Yellow Fever  2012    176               0.33       620  4719371. 0.
##  50 Rotavirus     2012    215               0.33       620  7183815. 0.
##  51 BCG           2012 154221               0.33       620    99200  2.46e7
##  52 Rotavirus     2013    113               0.33       650  2105497. 0.
##  53 Rotavirus     2013    387               0.33       650  4931933. 0.
##  54 Measles       2013   3397               0.33       650  8840000  3.74e7
##  55 DTP-hep B     2013   2665               0.33       650 23421450  7.26e7
##  56 Yellow Fever  2013    176               0.33       650  4719371. 0.
##  57 Rotavirus     2013    215               0.33       650  7183815. 0.
##  58 BCG           2013 154221               0.33       650   104000  2.46e7
##  59 Rotavirus     2014    113               0.33       654  2105497. 0.
##  60 Rotavirus     2014    387               0.33       654  4931933. 0.
##  61 Measles       2014   3397               0.33       654  8894400  3.73e7
##  62 DTP-hep B     2014   2665               0.33       654 23565582  7.25e7
##  63 Yellow Fever  2014    176               0.33       654  4719371. 0.
##  64 Rotavirus     2014    215               0.33       654  7183815. 0.
##  65 BCG           2014 154221               0.33       654   104640  2.46e7
##  66 Rotavirus     2015    113               0.33       653  2105497. 0.
##  67 Rotavirus     2015    387               0.33       653  4931933. 0.
##  68 Measles       2015   3397               0.33       653  8880800  3.73e7
##  69 DTP-hep B     2015   2665               0.33       653 23529549  7.25e7
##  70 Yellow Fever  2015    176               0.33       653  4719371. 0.
##  71 Rotavirus     2015    215               0.33       653  7183815. 0.
##  72 BCG           2015 154221               0.33       653   104480  2.46e7
##  73 Rotavirus     2016    113               0.33       661  2105497. 0.
##  74 Rotavirus     2016    387               0.33       661  4931933. 0.
##  75 Measles       2016   3397               0.33       661  8989600  3.72e7
##  76 DTP-hep B     2016   2665               0.33       661 23817813  7.22e7
##  77 Yellow Fever  2016    176               0.33       661  4719371. 0.    
##  78 Rotavirus     2016    215               0.33       661  7183815. 0.    
##  79 BCG           2016 154221               0.33       661   105760  2.46e7
##  80 Rotavirus     2017    113               0.33       699  2105497. 0.    
##  81 Rotavirus     2017    387               0.33       699  4931933. 0.    
##  82 Measles       2017   3397               0.33       699  9506400  3.67e7
##  83 DTP-hep B     2017   2665               0.33       699 25187067  7.09e7
##  84 Yellow Fever  2017    176               0.33       699  4719371. 0.    
##  85 Rotavirus     2017    215               0.33       699  7183815. 0.    
##  86 BCG           2017 154221               0.33       699   111840  2.46e7
##  87 Rotavirus     2018    113               0.33       727  2105497. 0.    
##  88 Rotavirus     2018    387               0.33       727  4931933. 0.    
##  89 Measles       2018   3397               0.33       727  9887200  3.63e7
##  90 DTP-hep B     2018   2665               0.33       727 26195991  6.98e7
##  91 Yellow Fever  2018    176               0.33       727  4719371. 0.    
##  92 Rotavirus     2018    215               0.33       727  7183815. 0.    
##  93 BCG           2018 154221               0.33       727   116320  2.46e7
##  94 Measles       2001   3397               0.5        589  8010400  3.82e7
##  95 DTP-hep B     2001   2665               0.5        589 21223437  7.48e7
##  96 Yellow Fever  2001    176               0.5        589  4719371. 0.    
##  97 BCG           2001 154221               0.5        589    94240  2.46e7
##  98 Measles       2002   3397               0.5        600  8160000  3.80e7
##  99 DTP-hep B     2002   2665               0.5        600 21619800  7.44e7
## 100 Yellow Fever  2002    176               0.5        600  4719371. 0.    
## 101 BCG           2002 154221               0.5        600    96000  2.46e7
## 102 Measles       2003   3397               0.5        616  8377600  3.78e7
## 103 DTP-hep B     2003   2665               0.5        616 22196328  7.38e7
## 104 Yellow Fever  2003    176               0.5        616  4719371. 0.    
## 105 BCG           2003 154221               0.5        616    98560  2.46e7
## 106 Measles       2004   3397               0.5        635  8636000  3.76e7
## 107 DTP-hep B     2004   2665               0.5        635 22880955  7.32e7
## 108 Yellow Fever  2004    176               0.5        635  4719371. 0.    
## 109 BCG           2004 154221               0.5        635   101600  2.46e7
## 110 Measles       2005   3397               0.5        655  8908000  3.73e7
## 111 DTP-hep B     2005   2665               0.5        655 23601615  7.24e7
## 112 Yellow Fever  2005    176               0.5        655  4719371. 0.    
## 113 BCG           2005 154221               0.5        655   104800  2.46e7
## 114 Measles       2006   3397               0.5        680  9248000  3.69e7
## 115 DTP-hep B     2006   2665               0.5        680 24502440  7.15e7
## 116 Yellow Fever  2006    176               0.5        680  4719371. 0.    
## 117 BCG           2006 154221               0.5        680   108800  2.46e7
## 118 Measles       2007   3397               0.5        691  9397600  3.68e7
## 119 DTP-hep B     2007   2665               0.5        691 24898803  7.11e7
## 120 Yellow Fever  2007    176               0.5        691  4719371. 0.    
## 121 BCG           2007 154221               0.5        691   110560  2.46e7
## 122 Measles       2008   3397               0.5        735  9996000  3.62e7
## 123 DTP-hep B     2008   2665               0.5        735 26484255  6.96e7
## 124 Yellow Fever  2008    176               0.5        735  4719371. 0.    
## 125 BCG           2008 154221               0.5        735   117600  2.46e7
## 126 Measles       2009   3397               0.5        752 10227200  3.60e7
## 127 DTP-hep B     2009   2665               0.5        752 27096816  6.89e7
## 128 Yellow Fever  2009    176               0.5        752  4719371. 0.    
## 129 BCG           2009 154221               0.5        752   120320  2.46e7
## 130 Measles       2010   3397               0.5        791 10757600  3.54e7
## 131 DTP-hep B     2010   2665               0.5        791 28502103  6.75e7
## 132 Yellow Fever  2010    176               0.5        791  4719371. 0.
## 133 BCG           2010 154221               0.5        791   126560  2.45e7
## 134 Measles       2011   3397               0.5        880 11968000  3.42e7
## 135 DTP-hep B     2011   2665               0.5        880 31709040  6.43e7
## 136 Yellow Fever  2011    176               0.5        880  4719371. 0.
## 137 BCG           2011 154221               0.5        880   140800  2.45e7
## 138 Rotavirus     2012    113               0.5        940  2105497. 0.
## 139 Rotavirus     2012    387               0.5        940  4931933. 0.
## 140 Measles       2012   3397               0.5        940 12784000  3.34e7
## 141 DTP-hep B     2012   2665               0.5        940 33871020  6.22e7
## 142 Yellow Fever  2012    176               0.5        940  4719371. 0.
## 143 Rotavirus     2012    215               0.5        940  7183815. 0.
## 144 BCG           2012 154221               0.5        940   150400  2.45e7
## 145 Rotavirus     2013    113               0.5        985  2105497. 0.
## 146 Rotavirus     2013    387               0.5        985  4931933. 0.
## 147 Measles       2013   3397               0.5        985 13396000  3.28e7
## 148 DTP-hep B     2013   2665               0.5        985 35492505  6.06e7
## 149 Yellow Fever  2013    176               0.5        985  4719371. 0.
## 150 Rotavirus     2013    215               0.5        985  7183815. 0.
## 151 BCG           2013 154221               0.5        985   157600  2.45e7
## 152 Rotavirus     2014    113               0.5        991  2105497. 0.
## 153 Rotavirus     2014    387               0.5        991  4931933. 0.
## 154 Measles       2014   3397               0.5        991 13477600  3.27e7
## 155 DTP-hep B     2014   2665               0.5        991 35708703  6.03e7
## 156 Yellow Fever  2014    176               0.5        991  4719371. 0.
## 157 Rotavirus     2014    215               0.5        991  7183815. 0.
## 158 BCG           2014 154221               0.5        991   158560  2.45e7
## 159 Rotavirus     2015    113               0.5        990  2105497. 0.
## 160 Rotavirus     2015    387               0.5        990  4931933. 0.
## 161 Measles       2015   3397               0.5        990 13464000  3.27e7
## 162 DTP-hep B     2015   2665               0.5        990 35672670  6.04e7
## 163 Yellow Fever  2015    176               0.5        990  4719371. 0.
## 164 Rotavirus     2015    215               0.5        990  7183815. 0.
## 165 BCG           2015 154221               0.5        990   158400  2.45e7
## 166 Rotavirus     2016    113               0.5       1001  2105497. 0.
## 167 Rotavirus     2016    387               0.5       1001  4931933. 0.
## 168 Measles       2016   3397               0.5       1001 13613600  3.26e7
## 169 DTP-hep B     2016   2665               0.5       1001 36069033  6.00e7
## 170 Yellow Fever  2016    176               0.5       1001  4719371. 0.
## 171 Rotavirus     2016    215               0.5       1001  7183815. 0.
## 172 BCG           2016 154221               0.5       1001   160160  2.45e7
## 173 Rotavirus     2017    113               0.5       1059  2105497. 0.
## 174 Rotavirus     2017    387               0.5       1059  4931933. 0.
## 175 Measles       2017   3397               0.5       1059 14402400  3.18e7
## 176 DTP-hep B     2017   2665               0.5       1059 38158947  5.79e7
## 177 Yellow Fever  2017    176               0.5       1059  4719371. 0.
## 178 Rotavirus     2017    215               0.5       1059  7183815. 0.
## 179 BCG           2017 154221               0.5       1059   169440  2.45e7
## 180 Rotavirus     2018    113               0.5       1101  2105497. 0.
## 181 Rotavirus     2018    387               0.5       1101  4931933. 0.
## 182 Measles       2018   3397               0.5       1101 14973600  3.12e7
## 183 DTP-hep B     2018   2665               0.5       1101 39672333  5.64e7
## 184 Yellow Fever  2018    176               0.5       1101  4719371. 0.
## 185 Rotavirus     2018    215               0.5       1101  7183815. 0.
## 186 BCG           2018 154221               0.5       1101   176160  2.45e7
## 187 Measles       2001   3397               1         1177 16007200  3.02e7
## 188 DTP-hep B     2001   2665               1         1177 42410841  5.36e7
## 189 Yellow Fever  2001    176               1         1177  4719371. 0.
## 190 BCG           2001 154221               1         1177   188320  2.45e7
## 191 Measles       2002   3397               1         1200 16320000  2.99e7
## 192 DTP-hep B     2002   2665               1         1200 43239600  5.28e7
## 193 Yellow Fever  2002    176               1         1200  4719371. 0.
## 194 BCG           2002 154221               1         1200   192000  2.45e7
## 195 Measles       2003   3397               1         1232 16755200  2.94e7
## 196 DTP-hep B     2003   2665               1         1232 44392656  5.17e7
## 197 Yellow Fever  2003    176               1         1232  4719371. 0.
## 198 BCG           2003 154221               1         1232   197120  2.45e7
## 199 Measles       2004   3397               1         1269 17258400  2.89e7
## 200 DTP-hep B     2004   2665               1         1269 45725877  5.03e7
## 201 Yellow Fever  2004    176               1         1269  4719371. 0.
## 202 BCG           2004 154221               1         1269   203040  2.45e7
## 203 Measles       2005   3397               1         1311 17829600  2.84e7
## 204 DTP-hep B     2005   2665               1         1311 47239263  4.88e7
## 205 Yellow Fever  2005    176               1         1311  4719371. 0.
## 206 BCG           2005 154221               1         1311   209760  2.45e7
## 207 Measles       2006   3397               1         1359 18482400  2.77e7
## 208 DTP-hep B     2006   2665               1         1359 48968847  4.71e7
## 209 Yellow Fever  2006    176               1         1359  4719371. 0.
## 210 BCG           2006 154221               1         1359   217440  2.45e7
## 211 Measles       2007   3397               1         1382 18795200  2.74e7
## 212 DTP-hep B     2007   2665               1         1382 49797606  4.62e7
## 213 Yellow Fever  2007    176               1         1382  4719371. 0.
## 214 BCG           2007 154221               1         1382   221120  2.45e7
## 215 Measles       2008   3397               1         1470 19992000  2.62e7
## 216 DTP-hep B     2008   2665               1         1470 52968510  4.31e7
## 217 Yellow Fever  2008    176               1         1470  4719371. 0.
## 218 BCG           2008 154221               1         1470   235200  2.44e7
## 219 Measles       2009   3397               1         1503 20440800  2.58e7
## 220 DTP-hep B     2009   2665               1         1503 54157599  4.19e7
## 221 Yellow Fever  2009    176               1         1503  4719371. 0.
## 222 BCG           2009 154221               1         1503   240480  2.44e7
## 223 Measles       2010   3397               1         1582 21515200  2.47e7
## 224 DTP-hep B     2010   2665               1         1582 57004206  3.90e7
## 225 Yellow Fever  2010    176               1         1582  4719371. 0.
## 226 BCG           2010 154221               1         1582   253120  2.44e7
## 227 Measles       2011   3397               1         1761 23949600  2.22e7
## 228 DTP-hep B     2011   2665               1         1761 63454113  3.26e7
## 229 Yellow Fever  2011    176               1         1761  4719371. 0.
## 230 BCG           2011 154221               1         1761   281760  2.44e7
## 231 Rotavirus     2012    113               1         1880  2105497. 0.
## 232 Rotavirus     2012    387               1         1880  4931933. 0.
## 233 Measles       2012   3397               1         1880 25568000  2.06e7
## 234 DTP-hep B     2012   2665               1         1880 67742040  2.83e7
## 235 Yellow Fever  2012    176               1         1880  4719371. 0.
## 236 Rotavirus     2012    215               1         1880  7183815. 0.
## 237 BCG           2012 154221               1         1880   300800  2.44e7
## 238 Rotavirus     2013    113               1         1971  2105497. 0.
## 239 Rotavirus     2013    387               1         1971  4931933. 0.
## 240 Measles       2013   3397               1         1971 26805600  1.94e7
## 241 DTP-hep B     2013   2665               1         1971 71021043  2.50e7
## 242 Yellow Fever  2013    176               1         1971  4719371. 0.
## 243 Rotavirus     2013    215               1         1971  7183815. 0.
## 244 BCG           2013 154221               1         1971   315360  2.44e7
## 245 Rotavirus     2014    113               1         1982  2105497. 0.
## 246 Rotavirus     2014    387               1         1982  4931933. 0.
## 247 Measles       2014   3397               1         1982 26955200  1.92e7
## 248 DTP-hep B     2014   2665               1         1982 71417406  2.46e7
## 249 Yellow Fever  2014    176               1         1982  4719371. 0.
## 250 Rotavirus     2014    215               1         1982  7183815. 0.
## 251 BCG           2014 154221               1         1982   317120  2.44e7
## 252 Rotavirus     2015    113               1         1980  2105497. 0.
## 253 Rotavirus     2015    387               1         1980  4931933. 0.
## 254 Measles       2015   3397               1         1980 26928000  1.93e7
## 255 DTP-hep B     2015   2665               1         1980 71345340  2.47e7
## 256 Yellow Fever  2015    176               1         1980  4719371. 0.
## 257 Rotavirus     2015    215               1         1980  7183815. 0.
## 258 BCG           2015 154221               1         1980   316800  2.44e7
## 259 Rotavirus     2016    113               1         2002  2105497. 0.
## 260 Rotavirus     2016    387               1         2002  4931933. 0.
## 261 Measles       2016   3397               1         2002 27227200  1.90e7
## 262 DTP-hep B     2016   2665               1         2002 72138066  2.39e7
## 263 Yellow Fever  2016    176               1         2002  4719371. 0.
## 264 Rotavirus     2016    215               1         2002  7183815. 0.
## 265 BCG           2016 154221               1         2002   320320  2.44e7
## 266 Rotavirus     2017    113               1         2118  2105497. 0.
## 267 Rotavirus     2017    387               1         2118  4931933. 0.
## 268 Measles       2017   3397               1         2118 28804800  1.74e7
## 269 DTP-hep B     2017   2665               1         2118 76317894  1.97e7
## 270 Yellow Fever  2017    176               1         2118  4719371. 0.
## 271 Rotavirus     2017    215               1         2118  7183815. 0.
## 272 BCG           2017 154221               1         2118   338880  2.43e7
## 273 Rotavirus     2018    113               1         2202  2105497. 0.
## 274 Rotavirus     2018    387               1         2202  4931933. 0.
## 275 Measles       2018   3397               1         2202 29947200  1.62e7
## 276 DTP-hep B     2018   2665               1         2202 79344666  1.67e7
## 277 Yellow Fever  2018    176               1         2202  4719371. 0.
## 278 Rotavirus     2018    215               1         2202  7183815. 0.
## 279 BCG           2018 154221               1         2202   352320  2.43e7
## 280 Measles       2001   3397               3         3532 46193653. 0.
## 281 DTP-hep B     2001   2665               3         3532 96045852. 0.
## 282 Yellow Fever  2001    176               3         3532  4719371. 0.
## 283 BCG           2001 154221               3         3532   565120  2.41e7
## 284 Measles       2002   3397               3         3601 46193653. 0.
## 285 DTP-hep B     2002   2665               3         3601 96045852. 0.
## 286 Yellow Fever  2002    176               3         3601  4719371. 0.
## 287 BCG           2002 154221               3         3601   576160  2.41e7
## 288 Measles       2003   3397               3         3696 46193653. 0.
## 289 DTP-hep B     2003   2665               3         3696 96045852. 0.
## 290 Yellow Fever  2003    176               3         3696  4719371. 0.
## 291 BCG           2003 154221               3         3696   591360  2.41e7
## 292 Measles       2004   3397               3         3808 46193653. 0.
## 293 DTP-hep B     2004   2665               3         3808 96045852. 0.
## 294 Yellow Fever  2004    176               3         3808  4719371. 0.
## 295 BCG           2004 154221               3         3808   609280  2.41e7
## 296 Measles       2005   3397               3         3932 46193653. 0.
## 297 DTP-hep B     2005   2665               3         3932 96045852. 0.
## 298 Yellow Fever  2005    176               3         3932  4719371. 0.
## 299 BCG           2005 154221               3         3932   629120  2.40e7
## 300 Measles       2006   3397               3         4078 46193653. 0.
## 301 DTP-hep B     2006   2665               3         4078 96045852. 0.
## 302 Yellow Fever  2006    176               3         4078  4719371. 0.
## 303 BCG           2006 154221               3         4078   652480  2.40e7
## 304 Measles       2007   3397               3         4147 46193653. 0.
## 305 DTP-hep B     2007   2665               3         4147 96045852. 0.
## 306 Yellow Fever  2007    176               3         4147  4719371. 0.
## 307 BCG           2007 154221               3         4147   663520  2.40e7
## 308 Measles       2008   3397               3         4411 46193653. 0.
## 309 DTP-hep B     2008   2665               3         4411 96045852. 0.
## 310 Yellow Fever  2008    176               3         4411  4719371. 0.
## 311 BCG           2008 154221               3         4411   705760  2.40e7
## 312 Measles       2009   3397               3         4509 46193653. 0.
## 313 DTP-hep B     2009   2665               3         4509 96045852. 0.
## 314 Yellow Fever  2009    176               3         4509  4719371. 0.
## 315 BCG           2009 154221               3         4509   721440  2.40e7
## 316 Measles       2010   3397               3         4746 46193653. 0.
## 317 DTP-hep B     2010   2665               3         4746 96045852. 0.
## 318 Yellow Fever  2010    176               3         4746  4719371. 0.
## 319 BCG           2010 154221               3         4746   759360  2.39e7
## 320 Measles       2011   3397               3         5283 46193653. 0.
## 321 DTP-hep B     2011   2665               3         5283 96045852. 0.
## 322 Yellow Fever  2011    176               3         5283  4719371. 0.
## 323 BCG           2011 154221               3         5283   845280  2.38e7
## 324 Rotavirus     2012    113               3         5639  2105497. 0.
## 325 Rotavirus     2012    387               3         5639  4931933. 0.
## 326 Measles       2012   3397               3         5639 46193653. 0.
## 327 DTP-hep B     2012   2665               3         5639 96045852. 0.
## 328 Yellow Fever  2012    176               3         5639  4719371. 0.
## 329 Rotavirus     2012    215               3         5639  7183815. 0.
## 330 BCG           2012 154221               3         5639   902240  2.38e7
## 331 Rotavirus     2013    113               3         5912  2105497. 0.
## 332 Rotavirus     2013    387               3         5912  4931933. 0.
## 333 Measles       2013   3397               3         5912 46193653. 0.
## 334 DTP-hep B     2013   2665               3         5912 96045852. 0.
## 335 Yellow Fever  2013    176               3         5912  4719371. 0.
## 336 Rotavirus     2013    215               3         5912  7183815. 0.
## 337 BCG           2013 154221               3         5912   945920  2.37e7
## 338 Rotavirus     2014    113               3         5945  2105497. 0.
## 339 Rotavirus     2014    387               3         5945  4931933. 0.
## 340 Measles       2014   3397               3         5945 46193653. 0.
## 341 DTP-hep B     2014   2665               3         5945 96045852. 0.
## 342 Yellow Fever  2014    176               3         5945  4719371. 0.
## 343 Rotavirus     2014    215               3         5945  7183815. 0.
## 344 BCG           2014 154221               3         5945   951200  2.37e7
## 345 Rotavirus     2015    113               3         5939  2105497. 0.
## 346 Rotavirus     2015    387               3         5939  4931933. 0.
## 347 Measles       2015   3397               3         5939 46193653. 0.
## 348 DTP-hep B     2015   2665               3         5939 96045852. 0.
## 349 Yellow Fever  2015    176               3         5939  4719371. 0.
## 350 Rotavirus     2015    215               3         5939  7183815. 0.
## 351 BCG           2015 154221               3         5939   950240  2.37e7
## 352 Rotavirus     2016    113               3         6007  2105497. 0.
## 353 Rotavirus     2016    387               3         6007  4931933. 0.
## 354 Measles       2016   3397               3         6007 46193653. 0.
## 355 DTP-hep B     2016   2665               3         6007 96045852. 0.
## 356 Yellow Fever  2016    176               3         6007  4719371. 0.
## 357 Rotavirus     2016    215               3         6007  7183815. 0.
## 358 BCG           2016 154221               3         6007   961120  2.37e7
## 359 Rotavirus     2017    113               3         6353  2105497. 0.
## 360 Rotavirus     2017    387               3         6353  4931933. 0.
## 361 Measles       2017   3397               3         6353 46193653. 0.
## 362 DTP-hep B     2017   2665               3         6353 96045852. 0.
## 363 Yellow Fever  2017    176               3         6353  4719371. 0.
## 364 Rotavirus     2017    215               3         6353  7183815. 0.
## 365 BCG           2017 154221               3         6353  1016480  2.37e7
## 366 Rotavirus     2018    113               3         6607  2105497. 0.
## 367 Rotavirus     2018    387               3         6607  4931933. 0.
## 368 Measles       2018   3397               3         6607 46193653. 0.
## 369 DTP-hep B     2018   2665               3         6607 96045852. 0.
## 370 Yellow Fever  2018    176               3         6607  4719371. 0.
## 371 Rotavirus     2018    215               3         6607  7183815. 0.
## 372 BCG           2018 154221               3         6607  1057120  2.36e7
## 373 Measles       2001   3397               4.5       5297 46193653. 0.
## 374 DTP-hep B     2001   2665               4.5       5297 96045852. 0.
## 375 Yellow Fever  2001    176               4.5       5297  4719371. 0.
## 376 BCG           2001 154221               4.5       5297   847520  2.38e7
## 377 Measles       2002   3397               4.5       5402 46193653. 0.
## 378 DTP-hep B     2002   2665               4.5       5402 96045852. 0.
## 379 Yellow Fever  2002    176               4.5       5402  4719371. 0.
## 380 BCG           2002 154221               4.5       5402   864320  2.38e7
## 381 Measles       2003   3397               4.5       5545 46193653. 0.
## 382 DTP-hep B     2003   2665               4.5       5545 96045852. 0.
## 383 Yellow Fever  2003    176               4.5       5545  4719371. 0.
## 384 BCG           2003 154221               4.5       5545   887200  2.38e7
## 385 Measles       2004   3397               4.5       5712 46193653. 0.
## 386 DTP-hep B     2004   2665               4.5       5712 96045852. 0.
## 387 Yellow Fever  2004    176               4.5       5712  4719371. 0.
## 388 BCG           2004 154221               4.5       5712   913920  2.38e7
## 389 Measles       2005   3397               4.5       5898 46193653. 0.
## 390 DTP-hep B     2005   2665               4.5       5898 96045852. 0.
## 391 Yellow Fever  2005    176               4.5       5898  4719371. 0.
## 392 BCG           2005 154221               4.5       5898   943680  2.37e7
## 393 Measles       2006   3397               4.5       6117 46193653. 0.
## 394 DTP-hep B     2006   2665               4.5       6117 96045852. 0.
## 395 Yellow Fever  2006    176               4.5       6117  4719371. 0.
## 396 BCG           2006 154221               4.5       6117   978720  2.37e7
## 397 Measles       2007   3397               4.5       6221 46193653. 0.
## 398 DTP-hep B     2007   2665               4.5       6221 96045852. 0.
## 399 Yellow Fever  2007    176               4.5       6221  4719371. 0.
## 400 BCG           2007 154221               4.5       6221   995360  2.37e7
## 401 Measles       2008   3397               4.5       6617 46193653. 0.
## 402 DTP-hep B     2008   2665               4.5       6617 96045852. 0.
## 403 Yellow Fever  2008    176               4.5       6617  4719371. 0.
## 404 BCG           2008 154221               4.5       6617  1058720  2.36e7
## 405 Measles       2009   3397               4.5       6764 46193653. 0.
## 406 DTP-hep B     2009   2665               4.5       6764 96045852. 0.
## 407 Yellow Fever  2009    176               4.5       6764  4719371. 0.
## 408 BCG           2009 154221               4.5       6764  1082240  2.36e7
## 409 Measles       2010   3397               4.5       7119 46193653. 0.
## 410 DTP-hep B     2010   2665               4.5       7119 96045852. 0.
## 411 Yellow Fever  2010    176               4.5       7119  4719371. 0.
## 412 BCG           2010 154221               4.5       7119  1139040  2.35e7
## 413 Measles       2011   3397               4.5       7924 46193653. 0.
## 414 DTP-hep B     2011   2665               4.5       7924 96045852. 0.
## 415 Yellow Fever  2011    176               4.5       7924  4719371. 0.
## 416 BCG           2011 154221               4.5       7924  1267840  2.34e7
## 417 Rotavirus     2012    113               4.5       8458  2105497. 0.
## 418 Rotavirus     2012    387               4.5       8458  4931933. 0.
## 419 Measles       2012   3397               4.5       8458 46193653. 0.
## 420 DTP-hep B     2012   2665               4.5       8458 96045852. 0.
## 421 Yellow Fever  2012    176               4.5       8458  4719371. 0.
## 422 Rotavirus     2012    215               4.5       8458  7183815. 0.
## 423 BCG           2012 154221               4.5       8458  1353280  2.33e7
## 424 Rotavirus     2013    113               4.5       8867  2105497. 0.
## 425 Rotavirus     2013    387               4.5       8867  4931933. 0.
## 426 Measles       2013   3397               4.5       8867 46193653. 0.
## 427 DTP-hep B     2013   2665               4.5       8867 96045852. 0.
## 428 Yellow Fever  2013    176               4.5       8867  4719371. 0.
## 429 Rotavirus     2013    215               4.5       8867  7183815. 0.
## 430 BCG           2013 154221               4.5       8867  1418720  2.33e7
## 431 Rotavirus     2014    113               4.5       8918  2105497. 0.
## 432 Rotavirus     2014    387               4.5       8918  4931933. 0.
## 433 Measles       2014   3397               4.5       8918 46193653. 0.
## 434 DTP-hep B     2014   2665               4.5       8918 96045852. 0.
## 435 Yellow Fever  2014    176               4.5       8918  4719371. 0.
## 436 Rotavirus     2014    215               4.5       8918  7183815. 0.
## 437 BCG           2014 154221               4.5       8918  1426880  2.32e7
## 438 Rotavirus     2015    113               4.5       8908  2105497. 0.
## 439 Rotavirus     2015    387               4.5       8908  4931933. 0.
## 440 Measles       2015   3397               4.5       8908 46193653. 0.
## 441 DTP-hep B     2015   2665               4.5       8908 96045852. 0.
## 442 Yellow Fever  2015    176               4.5       8908  4719371. 0.
## 443 Rotavirus     2015    215               4.5       8908  7183815. 0.
## 444 BCG           2015 154221               4.5       8908  1425280  2.33e7
## 445 Rotavirus     2016    113               4.5       9010  2105497. 0.
## 446 Rotavirus     2016    387               4.5       9010  4931933. 0.
## 447 Measles       2016   3397               4.5       9010 46193653. 0.
## 448 DTP-hep B     2016   2665               4.5       9010 96045852. 0.
## 449 Yellow Fever  2016    176               4.5       9010  4719371. 0.
## 450 Rotavirus     2016    215               4.5       9010  7183815. 0.
## 451 BCG           2016 154221               4.5       9010  1441600  2.32e7
## 452 Rotavirus     2017    113               4.5       9530  2105497. 0.
## 453 Rotavirus     2017    387               4.5       9530  4931933. 0.
## 454 Measles       2017   3397               4.5       9530 46193653. 0.
## 455 DTP-hep B     2017   2665               4.5       9530 96045852. 0.
## 456 Yellow Fever  2017    176               4.5       9530  4719371. 0.
## 457 Rotavirus     2017    215               4.5       9530  7183815. 0.
## 458 BCG           2017 154221               4.5       9530  1524800  2.32e7
## 459 Rotavirus     2018    113               4.5       9910  2105497. 0.
## 460 Rotavirus     2018    387               4.5       9910  4931933. 0.
## 461 Measles       2018   3397               4.5       9910 46193653. 0.
## 462 DTP-hep B     2018   2665               4.5       9910 96045852. 0.
## 463 Yellow Fever  2018    176               4.5       9910  4719371. 0.
## 464 Rotavirus     2018    215               4.5       9910  7183815. 0.
## 465 BCG           2018 154221               4.5       9910  1585600  2.31e7
```

In the following code, we use the CEA study benefits but use data from Gavi reports on costs (this does not include many of the costs that are in the CEA studies). We use the DC model to calculate the split between domestic and donor funding.

```r
# Ghana data
ghana_data <-
  data %>%
  filter(country == "Ghana") %>%
  distinct(vaccine, cost = total, benefit)

# GDP per capita data
ghana_gdppc <-
  gdp_data %>%
  filter(country == "Ghana") %>%
  distinct(year, gdp_pc)

# Run DC model
DCmodel_out <- DCmodel(
cost = ghana_data$cost,
benefit = ghana_data$benefit,
intervention = ghana_data$vaccine,
gdp_per_capita = rep(ghana_gdppc$gdp_pc, 5),
gdp_threshold_multiple = c(rep(ochalek_p, nrow(ghana_gdppc)),
                           rep(0.5, nrow(ghana_gdppc)),
                           rep(1, nrow(ghana_gdppc)),
                           rep(3, nrow(ghana_gdppc)),
                           rep(4.5, nrow(ghana_gdppc)))
)

# Donor financing is 0 in all rows since the total amount
#   is missing many costs included in CEAs. We only pring
#   out rows in which donor co-financing is higher than 0
#   here.
DCmodel_out %>%
  left_join(ghana_gdppc %>% rename(gdp_per_capita = gdp_pc),
            by = "gdp_per_capita") %>%
  # Remove rotavirus vaccins befow 2012
    filter(!(intervention == "Rotavirus" & year < 2012)) %>%
  select(intervention, year, cer,
         gdp_threshold_multiple, threshold, domestic, donor) %>%
  filter(donor > 0)
```

```
## # A tibble: 4 x 7
##   intervention  year   cer gdp_threshold_multip~ threshold domestic   donor
##   <chr>        <dbl> <dbl>                 <dbl>     <dbl>    <dbl>   <dbl>
## 1 DTP-hep B     2001   422                  0.33       388 13980804  1.24e6
## 2 DTP-hep B     2002   422                  0.33       396 14269068  9.47e5
## 3 DTP-hep B     2003   422                  0.33       407 14665431  5.50e5
## 4 DTP-hep B     2004   422                  0.33       419 15097827  1.18e5
```

Figures

All Ghana figure

```r
# Add plotting themes.
library(ggthemes)

# Extract Ghana data
data_ghana <- data %>%
  rename(year = year_gavi) %>%
  filter(country == "Ghana" &
           grepl("DALY|YLL", indicator)) %>%
  select(vaccine_cea_paper, indicator, cost, benefit, cea, year, total,
         domestic, gavi, domestic_p, gavi_p, s_year, e_year, vaccine, perspective) %>%
  # Data for 2018 only on BCG which is not supported
  filter(year < 2018)

# Max axes
max_ghana_x <- data_ghana %>%
  summarise(max(cost)) %>% unlist %>%
  roundUp + 10000000
max_ghana_y <- data_ghana %>%
  summarise(max(benefit)) %>% unlist %>%
  roundUp

# Select relevant GDP data (depending on which years have data
#   for Ghana)
gdp_data_ghana <- left_join(data_ghana %>% select(year),
                            gdp_data %>% filter(country == "Ghana"),
                            by = "year") %>%
  # Data for 2018 only on BCG which is not supported
  filter(year < 2018)

# Plot legend lables
legend_lables <- data_ghana %>%
  distinct(vaccine_cea_paper) %>%
  unlist %>% sort



# Plot Ghana
p1 <- ggplot() +
  # Facet by year and threshold
  facet_grid(year~threshold, scales = "free") +
  # Threshold line
  geom_line(data = gdp_data_ghana %>%
              filter(country == "Ghana") %>%
              filter(cost < max_ghana_x),
            mapping = aes(x = cost/1000000, y = cea_line/1000), linetype = 2) +
  # Costs and effectiveness point
  geom_point(data = data_ghana,
             mapping = aes(x = cost/1000000, y = benefit/1000,
                           color = vaccine_cea_paper,
                           shape = vaccine_cea_paper),
             size = 2.5) +
  # Arrow based on the proportion of Gavi support relative to domestic
  geom_segment(data = data_ghana,
               aes(x = cost/1000000, xend = (cost - gavi)/1000000,
                   y = benefit/1000, yend = benefit/1000),
               arrow = arrow(length = unit(0.1, "cm"))) +
  # x-axis name and $ formatting
  scale_x_continuous(name = "Cost (in millions USD 2018)",
                     labels = scales::dollar) +
  # y-axis name and formatting
  scale_y_continuous(name ="DALYs averted (in thousdands)",
                     labels = scales::comma) +
  # Remove color/shape legend name
  # Display color legend in two rows and remove shape legend
  # Set colors and shapes
  guides(color = guide_legend(nrow = 2, byrow = TRUE)) +
  scale_color_manual(name = "",
                     labels = legend_lables,
                     values = gdocs_pal()(7)) +

  scale_shape_manual(name = "",
                     labels = legend_lables,
                     values = c(15, 16, 18, 17, 17, 17, 7)) +
  # Change theme of plot
  theme_fivethirtyeight() +
  theme(legend.position = "bottom",
        axis.title = element_text(),
        plot.caption = element_text(hjust = 0))

# Save figure
ggsave("figures/ghana_all.png", p1, dpi = 300,
       width = 8*2.5, height = 10*2.5, units = "cm")
```

```
## Warning: Removed 44 rows containing missing values (geom_segment).
```

```
# Create and save figure with appendix caption
p1 +
  # Add a caption
  labs(caption = paste(
    "Figure A1. Gavi contribution to vaccines in Ghana.",
    "Columns differ by cost-effectiveness thresholds, represented by the dashed black line;",
    "Rows differ by the year of Gavi funding (years missing are due to lack of data);",
    "Points represent costs and benefits are extracted from cost-effectiveness (CE) studies;",
    "Arrows represent financing by Gavi (CE studies typically include costs not covered by Gavi",
    "such as distribution costs).",
    sep = "\n"))
```

```
## Warning: Removed 44 rows containing missing values (geom_segment).
```

```
ggsave("figures/A1_ghana_all_appendix_caption.png", dpi = 300,
       width = 8*2.5, height = 10*2.5, units = "cm")
```

```
## Warning: Removed 44 rows containing missing values (geom_segment).
```

All cross country figure 1 x GDP

```r
# Get years that include non-Ghana countries
years_include <- data %>%
  filter(country != "Ghana") %>% distinct(year_gavi) %>% unlist

# All country data
data_all_countries <-
  data %>%
  rename(year = year_gavi) %>%
  filter(grepl("DALY|YLL", indicator)) %>%
  filter(year %in% years_include) %>%
  select(country, vaccine_cea_paper, indicator, cost, benefit, cea, year, total,
         domestic, gavi, domestic_p, gavi_p, s_year, e_year, vaccine, perspective) %>%
  # Data for 2018 only on BCG which is not supported
  #   Also remove 2015 for which there is very limited data
  filter(year < 2018 & year != 2015) %>%
  # Add population data
  left_join(population_data, by = c("country", "year")) %>%
  # Convert values to per 100,000 population
  mutate(cost = cost/population*100000,
         benefit = benefit/population*100000,
         gavi = gavi/population*100000,
         domestic = domestic/population*100000)

# Max axes
max_all_countries_x <- data_all_countries %>%
  summarise(max(cost)) %>% unlist %>%
  roundUp + 10
max_all_countries_y <- data_all_countries %>%
  summarise(max(benefit)) %>% unlist %>%
  roundUp

# GDP data selct
gdp_data_all_countries <-
  left_join(data_all_countries %>% select(year, country),
            gdp_data,
            by = c("year", "country")) %>%
  filter(year %in% years_include) %>%
  # Data for 2018 only on BCG which is not supported
  #   Also remove 2015 for which there is very limited data
  filter(year < 2018 & year != 2015)

# Plot legend lables
legend_lables <- data_all_countries %>%
  distinct(vaccine_cea_paper) %>%
  unlist %>% sort

# Plot all countries using 1 X GDP per capita threshold
p2 <- ggplot() +
  # Facet by country and year
  facet_grid(year~country, scales = "free") +
  # Threshold line
  geom_line(data = gdp_data_all_countries %>%
              filter(threshold == "1 x GDP\nper capita") %>%
              filter(cost < max_all_countries_x),
            mapping = aes(x = cost/1000, y = cea_line), linetype = 2) +
  # Costs and effectiveness point
  geom_point(data = data_all_countries,
             mapping = aes(x = cost/1000, y = benefit,
                           color = vaccine_cea_paper,
                           shape = vaccine_cea_paper),
             size = 2.5) +
  # Arrow based on the proportion of Gavi support relative to domestic
  geom_segment(data = data_all_countries,
               aes(x = cost/1000, xend = (cost - gavi)/1000,
                   y = benefit, yend = benefit),
               arrow = arrow(length = unit(0.1, "cm"))) +
  # x-axis name and $ formatting
  scale_x_continuous(name = "Cost per 100,000 people (in thousands USD 2018)",
                     labels = scales::dollar) +
  # y-axis name and formatting
  scale_y_continuous(name ="DALYs averted per 100,000 people",
                     labels = scales::comma) +
  # Remove color/shape legend name
  # Display color legend in two rows and remove shape legend
  # Set colors and shapes
  guides(color = guide_legend(nrow = 2, byrow = TRUE)) +
  scale_color_manual(name = "",
                     labels = legend_lables,
                     values = gdocs_pal()(10)) +

  scale_shape_manual(name = "",
                     labels = legend_lables,
                     values = c(15, 16, 18,  13, 13, 13, 17, 17, 17, 7)) +
  # Display color legend in 4 columns
  # Change theme of plot
  theme_fivethirtyeight() +
  theme(legend.position = "bottom",
        axis.title = element_text(),
        axis.text.x = element_text(angle = 45),
        plot.caption = element_text(hjust = 0))

# Save figure
ggsave("figures/all_country_compare_1GDP.png", p2, dpi = 300,
       width = 8*2.5, height = 10*2.5, units = "cm")
```

```
## Warning: Removed 5 rows containing missing values (geom_segment).
```

```r
p2 + labs(
  caption = paste(
    "Figure A2. Gavi contribution to vaccines in Ghana, Angola, India, Kenya, and Senegal.",
    "The dashed black line is the 1 x GDP cost-effectiveness threshold;",
    "Points represent costs and benefits are extracted from cost-effectiveness (CE) studies;",
    "Arrows represent financing by Gavi (CE studies typically include costs not covered by Gavi",
    "such as distribution costs).",
    sep = "\n"))
```

```
## Warning: Removed 5 rows containing missing values (geom_segment).
```

```
# Create and save figure with appendix caption
ggsave("figures/A2_all_country_compare_1GDP.png", dpi = 300,
       width = 8*2.5, height = 10*2.5, units = "cm")
```

```
## Warning: Removed 5 rows containing missing values (geom_segment).
```

All cross country figure 0.5 x GDP

```
# Plot all countries using 0.5 X GDP per capita threshold
p3 <- ggplot() +
  # Facet by country and year
  facet_grid(year~country, scales = "free") +
  # Threshold line
  geom_line(data = gdp_data_all_countries %>%
              filter(threshold == "0.5 x GDP\nper capita") %>%
              filter(cost < max_all_countries_x),
            mapping = aes(x = cost/1000, y = cea_line), linetype = 2) +
  # CCosts and effectiveness point
  geom_point(data = data_all_countries,
             mapping = aes(x = cost/1000, y = benefit,
                           color = vaccine_cea_paper,
                           shape = vaccine_cea_paper),
             size = 2.5) +
  # Arrow based on the proportion of Gavi support relative to domestic
  geom_segment(data = data_all_countries,
               aes(x = cost/1000, xend = (cost - gavi)/1000,
                   y = benefit, yend = benefit),
               arrow = arrow(length = unit(0.1, "cm"))) +
  # x-axis name and $ formatting
  scale_x_continuous(name = "Cost per 100,000 people (in thousands USD 2018)",
                     labels = scales::dollar) +
  # y-axis name and formatting
  scale_y_continuous(name ="DALYs averted per 100,000 people",
                     labels = scales::comma) +
  # Remove color/shape legend name
  # Display color legend in four rows and remove shape legend
  # Set colors and shapes
  guides(color = guide_legend(nrow = 2, byrow = TRUE)) +
  scale_color_manual(name = "",
                     labels = legend_lables,
                     values = gdocs_pal()(10)) +

  scale_shape_manual(name = "",
                     labels = legend_lables,
                     values = c(15, 16, 18,  13, 13, 13, 17, 17, 17, 7)) +
  # Display color legend in 4 columns
  # Change theme of plot
  theme_fivethirtyeight() +
  theme(legend.position = "bottom",
        axis.title = element_text(),
        axis.text.x = element_text(angle = 45),
        plot.caption = element_text(hjust = 0))

# Save figure
ggsave("figures/all_country_compare_05GDP.png", p2, dpi = 300,
       width = 8*2.5, height = 10*2.5, units = "cm")
```

```
## Warning: Removed 5 rows containing missing values (geom_segment).
```

```
p2 + labs(
  caption = paste(
    "Figure A2. Gavi contribution to vaccines in Ghana, Angola, India, Kenya, and Senegal.",
    "The dashed black line is the 0.5 x GDP cost-effectiveness threshold;",
    "Points represent costs and benefits are extracted from cost-effectiveness (CE) studies;",
    "Arrows represent financing by Gavi (CE studies typically include costs not covered by Gavi",
    "such as distribution costs).",
    sep = "\n"))
```

```
## Warning: Removed 5 rows containing missing values (geom_segment).
```

```
# Create and save figure with appendix caption
ggsave("figures/A2_all_country_compare_05GDP.png", dpi = 300,
       width = 8*2.5, height = 10*2.5, units = "cm")
```

```
## Warning: Removed 5 rows containing missing values (geom_segment).
```

Ghana 1 x GDP 2012-2016 (most data for these years)

```
# Plot legend lables
legend_lables <- data_ghana %>%
  distinct(vaccine_cea_paper) %>%
  unlist %>% sort

# Plot Ghana
p4 <- ggplot() +
  # Facet by year and threshold
  facet_wrap(year~., scales = "free", ncol = 2) +
  # Threshold line
  geom_line(data = gdp_data_ghana %>%
              filter(country == "Ghana") %>%
              filter(cost < max_ghana_x) %>%
              filter(threshold == "1 x GDP\nper capita") %>%
              filter(year %in% 2012:2016),
            mapping = aes(x = cost/1000000, y = cea_line/1000), linetype = 2) +
  # Costs and effectiveness point
  geom_point(data = data_ghana %>%
               filter(year %in% 2012:2016),
             mapping = aes(x = cost/1000000, y = benefit/1000,
                           color = vaccine_cea_paper,
                           shape = vaccine_cea_paper),
             size = 4.5) +
  # Arrow based on the proportion of Gavi support relative to domestic
  geom_segment(data = data_ghana %>%
                 filter(year %in% 2012:2016),
               aes(x = cost/1000000, xend = (cost - gavi)/1000000,
                   y = benefit/1000, yend = benefit/1000),
               arrow = arrow(length = unit(0.2, "cm")),
               size = 1) +
  # x-axis name and $ formatting
  scale_x_continuous(name = "Cost (in millions USD 2018)",
                     labels = scales::dollar) +
  # y-axis name and formatting
  scale_y_continuous(name ="DALYs averted (in thousdands)",
                     labels = scales::comma) +
  # Remove color/shape legend name
  # Display color legend in two rows and remove shape legend
  # Set colors and shapes
  guides(color = guide_legend(nrow = 2, byrow = TRUE)) +
  scale_color_manual(name = "",
                     labels = legend_lables,
                     values = gdocs_pal()(7)) +
  scale_shape_manual(name = "",
                     labels = legend_lables,
                     values = c(15, 16, 18, 17, 17, 17, 7)) +
  # Change theme of plot
  theme_fivethirtyeight() +
  theme(legend.position = "bottom",
        axis.title = element_text(),
        plot.caption = element_text(hjust = 0),
        text = element_text(size = 16))

# Save figure
ggsave("figures/ghana_x1gdp.png", p4, dpi = 300,
       width = 8.5*2.5, height = 10*2.5, units = "cm")
```

```
## Warning: Removed 4 rows containing missing values (geom_segment).
```

```
# Create and save figure with appendix caption
p4 +
  # Add a caption
  labs(caption = paste(
    "Figure 1. Gavi contribution to vaccines in Ghana.",
    "The dashed black line is the 0.5 x GDP-based cost-effectiveness threshold;",
    "Each plot represents a different year of Gavi co-financing;",
    "Points represents costs and benefits extracted from cost-effectiveness (CE) studies;",
    "Arrows represent financing by Gavi (CE studies typically include costs not covered by Gavi",
    "such as distribution costs).",
    sep = "\n"))
```

```
## Warning: Removed 4 rows containing missing values (geom_segment).
```

```
ggsave("figures/A3_ghana_x1gdp_appendix_caption.png", dpi = 300,
       width = 8*2.5, height = 10*2.5, units = "cm")
```

```
## Warning: Removed 4 rows containing missing values (geom_segment).
```

Country comparison 1 x GDP per capita

```
# Plot legend lables
legend_lables <- data_all_countries %>%
  distinct(vaccine_cea_paper) %>%
  unlist %>% sort

# Plot all countries using 1 X GDP per capita threshold
p5 <- ggplot() +
  # Facet by country and year
  facet_grid(year~country, scales = "free") +
  # Threshold line
  geom_line(data = gdp_data_all_countries %>%
              filter(threshold == "1 x GDP\nper capita") %>%
              filter(cost < max_all_countries_x) %>%
              filter(year %in% c(2014, 2017)),
            mapping = aes(x = cost/1000, y = cea_line), linetype = 2) +
  # Costs and effectiveness point
  geom_point(data = data_all_countries %>%
              filter(year %in% c(2014, 2017)),
             mapping = aes(x = cost/1000, y = benefit,
                           color = vaccine_cea_paper,
                           shape = vaccine_cea_paper),
             size = 4.5) +
  # Arrow based on proportion of Gavi support relative to deomestic
  geom_segment(data = data_all_countries %>%
              filter(year %in% c(2014, 2017)),
               aes(x = cost/1000, xend = (cost - gavi)/1000,
                   y = benefit, yend = benefit),
               arrow = arrow(length = unit(0.2, "cm"))) +
  # x-axis name and $ formatting
  scale_x_continuous(name = "Cost per 100,000 people (in thousands USD 2018)",
                     labels = scales::dollar) +
  # y-axis name and formatting
  scale_y_continuous(name ="DALYs averted per 100,000 people",
                     labels = scales::comma) +
  # Remove color/shape legend name
  # Display color legend in four rows and remove shape legend
  # Set colors and shapes
  guides(color = guide_legend(nrow = 2, byrow = TRUE)) +
  scale_color_manual(name = "",
                     labels = legend_lables,
                     values = gdocs_pal()(10)) +
  scale_shape_manual(name = "",
                     labels = legend_lables,
                     values = c(15, 16, 18,  13, 13, 13, 17, 17, 17, 7)) +
  # Display color legend in 4 columns
  # Change theme of plot
  theme_fivethirtyeight() +
  theme(legend.position = "bottom",
        axis.title = element_text(),
        axis.text.x = element_text(angle = 45),
        plot.caption = element_text(hjust = 0),
        text = element_text(size = 16))

# Save figure
ggsave("figures/country_compare_1GDP.png", p5, dpi = 300,
       width = 11*2.5, height = 9*2.5, units = "cm")
```

```
## Warning: Removed 2 rows containing missing values (geom_segment).
```

```
p5 + labs(
  caption = paste(
    "Figure 2. Gavi contribution to vaccines in Ghana, Angola, India, Kenya, and Senegal.",
    "The dashed black line is the 1 x GDP cost-effectiveness threshold;",
    "Points represent costs and benefits are extracted from cost-effectiveness (CE) studies;",
    "Arrows represent financing by Gavi (CE studies typically include costs not covered by Gavi",
    "such as distribution costs).",
    sep = "\n"))
```

```
## Warning: Removed 2 rows containing missing values (geom_segment).
```

```
# Create and save figure with appendix caption
ggsave("figures/A5_country_compare_1GDP.png", dpi = 300,
       width = 8*2.5, height = 10*2.5, units = "cm")
```

```
## Warning: Removed 2 rows containing missing values (geom_segment).
```

Gavi co-financing Ghana

```
financing_ghana_plot_data <-
  fund_data %>%
  filter(country == "Ghana" & !is.na(gavi)) %>%
  select(vaccine, year, domestic, gavi) %>%
  gather(key = source, value = amount, domestic:gavi) %>%
  mutate(source = gsub("gavi", "Gavi", source)) %>%
  mutate(source = gsub("domestic", "Domestic", source))

p6 <- ggplot(data = financing_ghana_plot_data,
       mapping = aes(x = factor(year), y = amount/1000000, fill = source)) +
  facet_wrap(vaccine~.) +
  geom_bar(stat = "identity", position = "dodge") +
  # x-axis name and $ formatting
  scale_x_discrete(name = "Year") +
  # y-axis name and formatting
  scale_y_continuous(name ="Funding in 2018 US Dollars",
                     labels = scales::dollar_format(prefix = "$", suffix = "M")) +
  # Remove fill legend title
  # Display color legend in four rows and remove shape legend
  # Set colors and shapes
  scale_fill_discrete(name = "Source") +
  # Change theme of plot
  theme_fivethirtyeight() +
  theme(legend.position = "bottom",
        axis.title = element_text(),
        plot.caption = element_text(hjust = 0),
        axis.text.x = element_text(angle = 45))

# Save figure
ggsave("figures/ghana_gavi_cofinancing.png", p6, dpi = 300,
       width = 6*2.5, height = 6*2.5, units = "cm")

p6 + labs(
  caption = paste(
    "Figure 1. Gavi co-financing of vaccines in Ghana.",
    "Source of data: Gavi Alliance Annual Progress Reports.",
    "DTP-hep B: dephtheria, tetanus, pertusis, and hepatitus B vaccine.",
    "MenA: Meningococcal vaccine.",
    "PCV: Pneumocaloccal conjugage vaccine.",
    sep = "\n"))
```

```
# Create and save figure with appendix caption
ggsave("figures/A6_ghana_gavi_cofinancing.png.png", dpi = 300,
       width = 9*2.5, height = 6*2.5, units = "cm")
```

Gavi co-financing All

```
financing_plot_data <-
  fund_data %>%
  filter(!is.na(gavi) & (year %in% 2012:2018)) %>%
  select(country, vaccine, year, domestic, gavi) %>%
  gather(key = source, value = amount, domestic:gavi) %>%
  mutate(source = gsub("gavi", "Gavi", source)) %>%
  mutate(source = gsub("domestic", "Domestic", source))

p7 <- ggplot(data = financing_plot_data,
       mapping = aes(x = factor(year), y = amount/1000000, fill = source)) +
  facet_wrap(vaccine~country, scales = "free") +
  geom_bar(stat = "identity", position = "dodge") +
  # x-axis name and $ formatting
```

```r
  scale_x_discrete(name = "Year") +
  # y-axis name and formatting
  scale_y_continuous(name ="Funding in 2018 US Dollars",
                     labels = scales::dollar_format(prefix = "$", suffix = "M")) +
  # Remove fill legend title
  # Display color legend in four rows and remove shape legend
  # Set colors and shapes
  scale_fill_discrete(name = "Source") +
  # Change theme of plot
  theme_fivethirtyeight() +
  theme(legend.position = "bottom",
        axis.title = element_text(),
        plot.caption = element_text(hjust = 0),
        axis.text.x = element_text(angle = 45))

# Save figure
ggsave("figures/all_gavi_cofinancing.png", p7, dpi = 300,
       width = 10*2.5, height = 10*2.5, units = "cm")

p6 + labs(
  caption = paste(
    "Figure 1. Gavi co-financing of vaccines",
    "Source of data: Gavi Alliance Annual Progress Reports.",
    "DTP-hep B: dephtheria, tetanus, pertusis, and hepatitus B vaccine.",
    "MenA: Meningococcal vaccine.",
    "PCV: Pneumocaloccal conjugage vaccine.",
    sep = "\n"))
```

```r
# Create and save figure with appendix caption
ggsave("figures/A7_all_gavi_cofinancing.png", dpi = 300,
       width = 8*2.5, height = 10*2.5, units = "cm")
```

Reproduce figure from Morton et al 2018

```r
threshold_data <- tibble(
  cost = 0:90,
  benefit = 0:90,
)

interventions_data <- tibble(
  cost = c(40, 80, 70, 90,
           20, 10, 40, 55, 15),
  benefit = c(10, 40, 50, 70,
              30, 40, 50, 80, 75),
  country_funded = c(rep(FALSE, 4),
                     rep(TRUE, 5))
)

library(grid)
library(pBrackets)
library(ggpubr)
```

```
## Warning: package 'ggpubr' was built under R version 3.6.3

## Loading required package: magrittr

##
## Attaching package: 'magrittr'

## The following object is masked from 'package:purrr':
##
##     set_names

## The following object is masked from 'package:tidyr':
##
##     extract
```

```
bracketsGrob <- function(...){
l <- list(...)
e <- new.env()
e$l <- l
  grid:::recordGrob(  {
    do.call(grid.brackets, l)
  }, e)
}

b1 <- bracketsGrob(0.79, 0.38, 0.41, 0.38, h=0.05, lwd=1, col="red")

ggplot() +
  geom_line(data = threshold_data,
            mapping = aes(x = cost, y = benefit),
            linetype = 2,
            size = 1) +
  geom_segment(data = interventions_data %>% filter(country_funded == FALSE),
               mapping = aes(x = cost, xend = benefit + 1, y = benefit, yend = benefit),
               arrow = arrow(length = unit(0.2, "cm")),
               size = 1) +
  annotation_custom(b1) +
  annotate("text", label = "Subsidy", x = 60, y = 30, color = "red", size = 6) +
  annotate("text", label = "Country funded\nprojects", x = 20, y = 60, hjust = 0,
           size = 6) +
  annotate("text", label = "Country rejected\nprojects", x = 60, y = 15, hjust = 0,
           size = 6) +
  annotate("text", label = "v[0]/c[0]", x = 95, y = 95, parse = TRUE, size = 6) +
  geom_point(data = interventions_data,
             mapping = aes(x = cost, y = benefit,
                           color = country_funded,
                           shape = country_funded),
             size = 4) +
  scale_color_manual(name = "", values = c("red", "darkgreen")) +
  scale_shape_manual(name = "", values = c("circle", "square")) +
  scale_x_continuous(name = "Costs", expand = c(0, 0), limits = c(0,100)) +
  scale_y_continuous(name = "Country Benefits", expand = c(0, 0), limits = c(0,100)) +
  theme_classic() +
  theme(legend.position = "none",
        axis.line = element_line(arrow = arrow(length = unit(0.4, "cm"))),
        axis.text = element_blank(),
        axis.ticks = element_blank(),
        text = element_text(size = 16))
```

```
ggsave("figures/donor_funding_reporduce_morton18.png", dpi = 300,
       width = 7*2.5, height = 6*2.5, units = "cm")
```

Tables

Ghana Gavi co-financing table

```r
table_out <- fund_data %>%
  filter(country == "Ghana") %>%
  filter(!is.na(gavi)) %>%
  mutate(domestic = paste(scales::dollar(signif(domestic, 3)),
                          " (", scales::percent(domestic_p, accuracy = 1), ")",
                          sep = ""),
         gavi = paste(scales::dollar(signif(gavi, 3)),
                          " (", scales::percent(gavi_p, accuracy = 1), ")",
                          sep = ""),
         total = scales::dollar(signif(total, 3))) %>%
  arrange(vaccine, year) %>%
  select(Vaccine = vaccine, Year = year,
         `Domestic support (%)` = domestic,
         `Gavi support (%)` = gavi, Total = total)
write_csv(table_out, "tables/csv_format/ghana_gavi_cofinancing.csv")
```

Gavi CEA table

```r
table_out <-
  cea_data  %>%
  filter(grepl("DALY|YLL", indicator)) %>%
  # Only include base-case of Abbot et al. 2012
  #  and use earliest year of Gavi funding (since intervention is 2003-08).
  filter(!(authors == "Abbott et al. 2012" &
             (assumptions != "$5 per dose"))) %>%# | year_gavi != 2012))) %>%
  # Do not include the CEA with Gavi Subsidy accounted for
  #   and focus on health system perspective.
  filter(!(authors == "Nonvignon et al. 2018" &
             (grepl("Ghana only", assumptions) |
             !grepl("Health system", perspective)))) %>%
  # Use relevant Gavi data year for Krishnamoorthy et al. 2019
  #   based on paper intervention years
  # filter(!(authors == "Krishnamoorthy et al. 2019" &
  #            year_gavi != 2018)) %>%
  # Use the analysis with the 90% intervention coverage and year 2018
  #   for Gavi funding based on paper intervention years
  filter(!(authors == "Megiddo et al. 2018" &
             (grepl("Expanded coverage (90%)", assumptions)))) %>%
  # Do not include the CEA with Gavi subsidy accounted for
  filter(!(authors == "Debellut et al., 2019" &
             (assumptions == "Vaccine programme costs with Gavi subsidy"))) %>%
  # Remove comma from authors column
  mutate(authors = gsub(",", "", authors)) %>%
  # Convert to dollars
  mutate(cost = scales::dollar(signif(cost, 3)),
         benefit = scales::comma(signif(benefit, 3)),
         cea = scales::dollar(signif(cea, 3)),
         year = as.numeric(gsub(".*\\. ", "", authors))) %>%
  arrange(country, vaccine, year) %>%
  select(Country = country, Vaccine = vaccine, Indicator = indicator,
         Costs = cost, Benefits = benefit, CER = cea, Perspective = perspective,
         Source = authors)
write_csv(table_out, "tables/csv_format/cea_table.csv")
```