

# Package: mindthegap (via r-universe)

September 12, 2024

**Title** Mind the Gap: 90-90-90 Trends and ART Coverage Gaps

**Version** 1.1.2

**Description** Package to pull UNAIDS estimates as well as plot trends in UNAIDS 90-90-90 goals and ART coverage gap by country.

**License** MIT + file LICENSE

**Encoding** UTF-8

**LazyData** true

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.2

**URL** <https://github.com/USAID-OHA-SI/mindthegap>,  
<https://usaid-oha-si.github.io/mindthegap>,  
<https://usaid-oha-si.github.io/mindthegap/>

**BugReports** <https://github.com/USAID-OHA-SI/mindthegap/issues>

**Imports** magrittr, dplyr, tidyr, glue, googlesheets4, readr, forcats, scales, ggplot2, stringr, tidyselect, piggyback, lifecycle, ggtext, gt, gtExtras, cli

**Suggests** googledrive, gridExtra, devtools, knitr, usethis, rmarkdown, kableExtra, systemfonts, tibble

**Remotes** USAID-OHA-SI/gophr, USAID-OHA-SI/glamr, USAID-OHA-SI/glitr, USAID-OHA-SI/gagglr

**VignetteBuilder** knitr

**Depends** R (>= 2.10)

**Repository** <https://usaid-oha-si.r-universe.dev>

**RemoteUrl** <https://github.com/USAID-OHA-SI/mindthegap>

**RemoteRef** HEAD

**RemoteSha** 89a56d3b0e16b455015385c9969db5549c823861

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base_plot	<i>95's Table Plot</i>
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## Description

This function creates a summary table showing OU progress toward the 95-95-95's

## Usage

```
base_plot(sel_base, sel_cntry)
```

## Arguments

sel_base	Returns one of 2 table types eg "PLHIV", "Relative"
sel_cntry	PEPFAR country to visualize (list OU name)

## Value

df\_tt

## Examples

```
## Not run:
base_plot(sel_base = "PLHIV", sel_cntry = "Lesotho")
base_plot(sel_base = "Relative", sel_cntry = "Lesotho")

## End(Not run)
```

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epi_plot	<i>Epidemic Control Plot</i>
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**Description**

This function creates epidemic control curves for "ALL PEPFAR" or selected OU's

**Usage**

```
epi_plot(sel_cntry = c("All PEPFAR"))
```

**Arguments**

sel_cntry	PEPFAR country to visualize ("ALL PEPFAR" as default or list OU names)
df	UNAIDS based data frame

**Value**

Epidemic control plot showing trends in new infections and total deaths to HIV population

**Examples**

```
## Not run:  
epi_plot()  
epi_plot(sel_cntry = "Lesotho")  
epi_plot(sel_cntry = c("South Africa", "Zambia", "Kenya", "Malawi"))  
epi_plot(sel_cntry = "USA") #breaks with non-PEPFAR countries  
  
## End(Not run)
```

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load_data	<i>Load data for viz</i>
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**Description**

Deprecated

**Usage**

```
load_data(usaid_email = NULL)
```

**Arguments**

usaid_email	USAID email to store file on GDrive
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**Examples**

```
## Not run:  
  load_data("twhitmore@usaid.gov")  
## End(Not run)
```

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munge_unaids	<i>Cleaning UNAIDS Data</i>
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**Description**

(Updated July 2023)

This function fetches and cleans UNAIDS Estimates/Test and Treat Data

**Usage**

```
munge_unaids(return_type, indicator_type)
```

**Arguments**

`return_type` Returns either 'HIV Estimates' or 'HIV Test & Treat' Data  
`indicator_type` Returns either 'Integer' or 'Percent' indicator values

**Value**

df

**Examples**

```
## Not run:  
  munge_unaids(return_type = "HIV Test & Treat", indicator_type = "Percent")  
## End(Not run)
```

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pull_estimates	<i>Pull clean UNAIDS HIV Estimates</i>
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**Description**

Pull clean UNAIDS estimates data. Wrapper around pull\_unaids.

**Usage**

```
pull_estimates(pepfar_only = TRUE)
```

**Arguments**

pepfar\_only filters dataset to only PEPFAR countries if TRUE (default = TRUE)

**Value**

df

**Examples**

```
## Not run:  
pull_estimates()  
  
## End(Not run)
```

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*pull\_testtreat*      *Pull clean UNAIDS HIV Test & Treat*

---

**Description**

Pull clean UNAIDS 2022 (1990-2022) HIV Test & Treat data. Wrapper around pull\_unaids.

**Usage**

```
pull_testtreat(pepfar_only = TRUE)
```

**Arguments**

pepfar\_only filters dataset to only PEPFAR countries if TRUE (default = TRUE)

**Value**

df

**Examples**

```
## Not run:  
pull_testtreat()  
  
## End(Not run)
```

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pull_unaids	<i>Pull clean UNAIDS HIV Estimates and Test &amp; Treat Data</i>
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**Description**

Pull clean UNAIDS estimates

**Usage**

```
pull_unaids(data_type, pepfar_only = TRUE)
```

**Arguments**

data_type	returns one of 2 available data set types eg "HIV Estimates", "HIV Test & Treat" (or both if missing)
pepfar_only	filters dataset to only PEPFAR countries if TRUE (default = TRUE)

**Value**

df

**Examples**

```
## Not run:  
pull_unaids(data_type = "HIV Estimates", pepfar_only = TRUE)  
  
## End(Not run)
```

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source_note	<i>UNAIDS Source Info</i>
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**Description**

Returns UNAIDS Source info for consistent sourcing notes

**Usage**

```
source_note
```

**Format**

An object of class character of length 1.

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unaids\_hdrs

*Generate UNAIDS headers*

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**Description**

Generate UNAIDS headers

**Usage**

unaids\_hdrs()

**Value**

list of headers

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