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1 INTRODUCTION

[Performance Monitoring for Action \(PMA\)](#) uses innovative mobile technology to support low-cost, rapid-turnaround surveys that monitor key health and development indicators.

PMA surveys collect longitudinal data throughout a country at the household and health facility levels by female data collectors, known as resident enumerators, using mobile phones. The survey collects information from the same women and households over time for regular tracking of progress and for understanding the drivers of contraceptive use dynamics. The data are rapidly validated, aggregated, and prepared into tables and graphs, making results quickly available to stakeholders. PMA surveys can be integrated into national monitoring and evaluation systems using a low-cost, rapid-turnaround survey platform that can be adapted and used for various health data needs.

The PMA project is implemented by local partner universities and research organizations who train and deploy the cadres of female resident enumerators.

The purpose of this manual is to provide guidance on the analysis of **harmonized longitudinal data** for a panel of women age 15-49 surveyed by PMA and published in partnership with [IPUMS PMA](#). IPUMS provides census and survey products from around the world in an integrated format, making it easy to compare data from multiple countries. IPUMS PMA data are available free of charge, subject to terms and conditions: please [register here](#) to request access to the data featured in this guide.

PMA has also published a guide to cross-sectional analysis in both [English](#) and [French](#).

This manual provides reproducible coding examples in the statistical programming language [R](#). Each chapter also appears as a post on the IPUMS PMA [data analysis blog](#), where you'll find new content posted every two weeks.

Stata users: a companion manual for IPUMS PMA longitudinal analysis is also available with coding examples written in Stata.

1.1 IPUMS PMA DATA IN R

The first two chapters of this manual introduce new users to [PMA longitudinal data](#) and the [IPUMS PMA website](#), respectively. After demonstrating how to obtain an IPUMS PMA data extract, the remaining chapters feature extensive data analysis examples written in R.

To follow along, you'll need to download the appropriate version of R for your computer's operating system at <https://www.r-project.org/>. R is available at no cost and it runs on a wide variety of UNIX platforms, Windows, and MacOS. We also recommend downloading a free copy of [RStudio](#), an integrated development environment (IDE) designed to make your experience with R much easier.



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(GPL-2 | GPL-3)

Individual chapters may introduce one or two **R packages** that provide helpful functions for longitudinal survey analysis, in particular. Two packages we feature in *every* chapter are [ipumsr](#) and [tidyverse](#). You can install these and other packages featured in this guide like so:

```
install.packages("ipumsr")
install.packages("tidyverse")
```

The [ipumsr](#) package is designed to help R users import and explore data extracts downloaded from IPUMS. As we'll see, categorical variables from IPUMS appear as **labelled integers** represented in R by a number and a label:

```
# A tibble: 4 × 2
  COUNTRY                n
  <int+lbl>            <int>
1 1 [Burkina Faso]     8257
2 2 [Congo, Democratic Republic] 6090
3 7 [Kenya]           12605
4 9 [Nigeria]         3225
```



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(MPL-2.0)

The [tidyverse](#) is actually a collection of packages developed in-part by contributors at RStudio. These include:

- [ggplot2](#) for data visualisation
- [dplyr](#) for data manipulation
- [tidyr](#) for data tidying
- [readr](#) for data import
- [purrr](#) for functional programming
- [tibble](#) for tibbles, a modern re-imagining of data frames
- [stringr](#) for strings
- [forcats](#) for factors



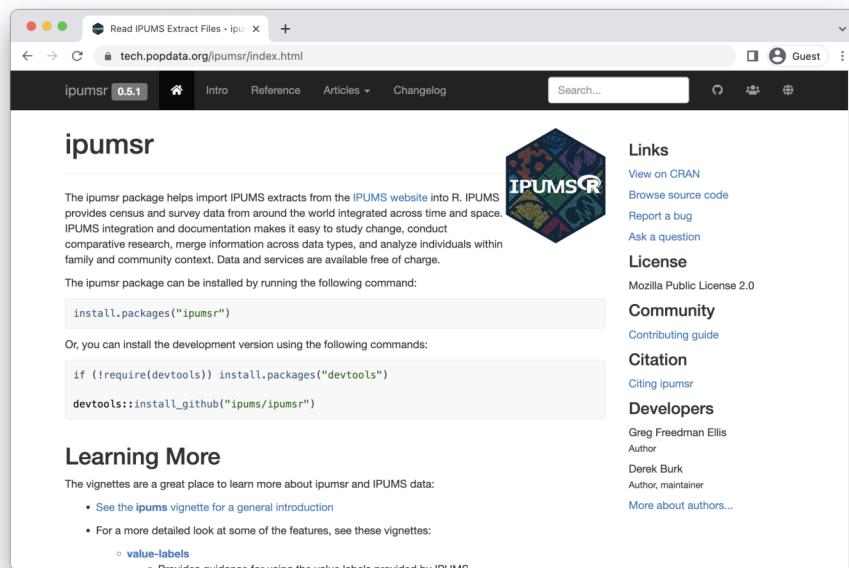
© RStudio, Inc.
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1.2 RESOURCES FOR R USERS

This manual focuses exclusively on longitudinal family planning data from IPUMS PMA, but the companion [data analysis blog](#) covers a wide range of topics like:

- A free [online course](#) for beginners
- New data announcements
- Data cleaning and reformatting
- Data analysis and visualization
- Spatial analysis
- Guides to PMA Service Delivery Point & Client Exit Interview data

Beyond the blog, it's important to know where to find **instructions and examples** for the R packages featured in this guide. Nearly all of these packages have a dedicated website with a homepage, reference page (documentation for individual functions), collection of articles (for general instructions), and changelog (for news about updates). The [ipumsr](#) page is a great place to start:



Finally, if you're looking for a more general introduction to R, we strongly recommend the following **free resources**:

- [R for Data Science](#) for beginners
- [Advanced R](#) for a deeper dive
- [RSpatial](#) for analysis with spatial data
- [ggplot2](#) for data visualization
- [R Markdown: The Definitive Guide](#) for producing annotated code, word documents, presentations, web pages, and more
- [R-bloggers](#) for regular news and tutorials

1.3 PMA BACKGROUND

Dating back to 2013, the original PMA survey design included high-frequency, **cross-sectional** samples of women and service delivery points collected from eleven countries participating in [Family Planning 2020](#) (FP2020) - a global partnership that supports the rights of women and girls to decide for themselves whether, when, and how many children they want to have. These surveys were designed to monitor annual progress towards [FP2020 goals](#) via population-level estimates for several [core indicators](#).

Beginning in 2019, PMA surveys were redesigned under a renewed partnership called [Family Planning 2030](#) (FP2030). These new surveys have been refocused on reproductive and sexual health indicators, and they feature a **longitudinal panel** of women of childbearing age. This design will allow researchers to measure contraceptive dynamics and changes in women's fertility intentions over a **three year period** via annual in-person interviews.¹

Questions on the redesigned survey cover topics like:

- awareness, perception, knowledge, and use of contraceptive methods
- perceived quality and side effects of contraceptive methods among current users
- birth history and fertility intentions
- aspects of health service provision
- domains of empowerment

¹In addition to these three in-person surveys, PMA also conducted telephone interviews with panel members focused on emerging issues related to the COVID-19 pandemic in 2020. These telephone surveys are already available for several countries - see our series on [PMA COVID-19 surveys](#) for details.

1.4 SAMPLING

PMA panel data includes a mixture of **nationally representative** and **sub-nationally representative** samples. The panel study consists of three data collection phases, each spaced one year apart.

As of this writing, IPUMS PMA has released data from the first *two* phases for four countries where Phase 1 data collection began in 2019; IPUMS PMA has released data from only the *first* phase for three countries where Phase 1 data collection began in August or September 2020. Phase 3 data collection and processing is currently underway.

Sample	Phase 1 Data Collection*	Now Available from IPUMS PMA		
		Phase 1	Phase 2	Phase 3
Burkina Faso	Dec 2019 - Mar 2020	x	x	
Cote d'Ivoire	Sep 2020 - Dec 2020	x		
DRC - Kinshasa	Dec 2019 - Feb 2020	x	x	
DRC - Kongo Central	Dec 2019 - Feb 2020	x	x	
India - Rajasthan	Aug 2020 - Oct 2020	x		
Kenya	Nov 2019 - Dec 2019	x	x	
Nigeria - Kano	Dec 2019 - Jan 2020	x	x	
Nigeria - Lagos	Dec 2019 - Jan 2020	x	x	
Uganda	Sep 2020 - Oct 2020	x		

*Each data collection phase is spaced one year apart

PMA uses a multi-stage clustered sample design, with stratification at the urban-rural level or by sub-region. Sample clusters - called enumeration areas (EAs) - are provided by the national statistics agency in each country.² These EAs are sampled using a *probability proportional to size* (PPS) method relative to the population distribution in each stratum.

Resident enumerators are women over age 21 living in (or near) each EA who hold at least a high school diploma.

²Displaced GPS coordinates for the centroid of each EA are available for most samples [by request](#) from PMA. IPUMS PMA provides shapefiles for PMA countries [here](#).

At Phase 1, 35 household dwellings were selected at random within each EA. Resident enumerators visited each dwelling and invited one household member to complete a [Household Questionnaire](#)³ that includes a census of all household members and visitors who stayed there during the night before the interview. Female household members and visitors aged 15-49 were then invited to complete a subsequent Phase 1 [Female Questionnaire](#).⁴

One year later, resident enumerators visited the same dwellings and administered a Phase 2 Household Questionnaire. A panel member in Phase 2 is any woman still age 15-49 who could be reached for a second Female Questionnaire, either because:

- she still lived there, or
- she had moved elsewhere within the study area,⁵ but at least one member of the Phase 1 household remained and could help resident enumerators locate her new dwelling.⁶

Additionally, resident enumerators administered the Phase 2 Female Questionnaire to *new* women in sampled households who:

- reached age 15 after Phase 1
- joined the household after Phase 1
- declined the Female Questionnaire at Phase 1, but agreed to complete it at Phase 2

SAMEDWELLING
indicates whether a Phase 2 female respondent resided in her Phase 1 dwelling or a new one.

PANELWOMAN
indicates whether a Phase 2 household member completed the Phase 1 Female Questionnaire.

³Questionnaires administered in each country may vary from this Core Household Questionnaire - [click here](#) for details.

⁴Questionnaires administered in each country may vary from this Core Female Questionnaire - [click here](#) for details.

⁵The “study area” is area within which resident enumerators should attempt to find panel women that have moved out of their Phase 1 dwelling. This may extend beyond the woman’s original EA as determined by in-country administrators - see [PMA Phase 2 and Phase 3 Survey Protocol](#) for details.

⁶In cases where no Phase 1 household members remained in the dwelling at Phase 2, women from the household are considered lost to follow-up (LTFU). A panel member is also considered LTFU if a Phase 2 Household Questionnaire was not completed, if she declined to participate, or if she was deceased or otherwise unavailable.

When you select the new **Longitudinal** sample option at checkout, you'll be able to include responses from every available phase of the study. These samples are available in either "long" format (responses from each phase will be organized in separate rows) or "wide" format (responses from each phase will be organized in columns).

The screenshot shows a web browser window for 'IPUMS PMA: select samples'. The URL is pma.ipums.org/pma-action/samples. The page title is 'SELECT SAMPLES'. It features the IPUMS PMA logo and navigation links for HOME, SELECT DATA, MY DATA, and SUPPORT. A note says variable documentation can be filtered by dataset. It allows selecting datasets for browsing, with 'Long' being selected. A red arrow points to the 'Long' radio button. A 'SUBMIT SAMPLE SELECTIONS' button is visible. Below the selection area, there's a section for 'FAMILY PLANNING - PERSON' with a 'Documentation' link and checkboxes for 'All Samples (long)', 'Burkina Faso', and '2020 - 2021'.

In addition to following up with women in the panel over time, PMA also adjusted sampling so that a cross-sectional sample could be produced concurrently with each data collection phase. These samples mainly overlap with the data you'll obtain for a particular phase in the longitudinal sample, except that replacement households were drawn from each EA where more than 10% of households from the previous phase were no longer there. Conversely, panel members who were located in a new dwelling at Phase 2 will not be represented in the cross-sectional sample drawn from that EA. These adjustments ensure that population-level indicators may be derived from cross-sectional samples in a given year, even if panel members move or are lost to follow-up.

CROSS SECTION indicates whether a household member in a longitudinal sample is also included in the cross-sectional sample for a given year (every person in a cross-sectional sample is included in the longitudinal sample).

You'll find PMA cross-sectional samples dating back to 2013 if you select the **Cross-sectional** sample option at checkout.

The screenshot shows a web browser window for 'IPUMS PMA: select samples'. The URL is pma.ipums.org/pma-action/samples. The page has a dark header with the IPUMS PMA logo and navigation links for LOG IN, REGISTER, GLOBAL HEALTH, and IPUMS.ORG. Below the header, there's a 'SELECT SAMPLES' section. A red arrow points to the 'Cross-sectional' radio button, which is selected. To the right of the radio buttons is a 'SUBMIT SAMPLE SELECTIONS' button. Below the selection buttons is a 'FAMILY PLANNING - PERSON' section with a 'All Samples' checkbox and a timeline of years from 2015 to 2021, with 2021 being the most recent.

1.5 SURVEY DESIGN ELEMENTS

Throughout this guide, we'll demonstrate how to incorporate PMA sampling weights and information about its stratified cluster sampling procedure into your analysis. To do so, we'll rely on tools from the [svyrr](#) package.⁷

You can install or update svyrr like so:

```
install.packages("svyrr")
```

To use svyrr and other tidyverse packages in an R session, load them with the [library](#) function:

```
library(svyrr)
library(ipumsr)
library(tidyverse)
```

We'll demonstrate how to obtain an IPUMS PMA data extract in the next chapter. For now, let's assume that we've got a wide-format⁸ data extract loaded into R as an object named dat. In this example, we'll feature data collected from the first two phases of the Burkina Faso panel. These data will be organized in a tidy table - a [tibble](#) - that looks like this:

```
dat
```

```
# A tibble: 5,212 × 138
  SAMPLE_1      SAMPLE_2      COUNTRY YEAR_1 YEAR_2 HHID_1 HHID_2 RESP0...¹ RESP0...² ELIGI...³
  <int+lbl>     <int+lbl>     <int+lbl> <int>  <int> <chr>  <chr>  <int+lbl> <int+lbl> <int+lbl>
1 85409 [Burkin... 85412 [Bur... 1 [Bur... 2019  2021 85420... 85420... 0 [No]  0 [No]  1 [Yes...
2 85409 [Burkin... 85412 [Bur... 1 [Bur... 2019  2021 85420... 85420... 0 [No]  1 [Yes] 1 [Yes...
3 85409 [Burkin... 85412 [Bur... 1 [Bur... 2019  2021 85420... 85420... 0 [No]  0 [No]  1 [Yes...
# ... with 5,209 more rows, 128 more variables: ELIGIBLE_2 <int+lbl>, LINENO_1 <int>,
#   LINENO_2 <int>, STRUCTURNO_1 <dbl+lbl>, STRUCTURNO_2 <dbl+lbl>, HNUM_1 <dbl>,
#   HNUM_2 <dbl>, EAID_1 <dbl>, EAID_2 <dbl>, ENUMID_1 <dbl+lbl>, ENUMID_2 <dbl+lbl>,
#   CONSENTFQ_1 <int+lbl>, CONSENTFQ_2 <int+lbl>, AVAILABLEFQ_1 <int+lbl>,
#   AVAILABLEFQ_2 <int+lbl>, FQACQUAINTED_1 <int+lbl>, FQACQUAINTED_2 <int+lbl>,
#   VISITNUMFQ_1 <int+lbl>, VISITNUMFQ_2 <int+lbl>, RESULTFQ_1 <int+lbl>,
#   RESULTFQ_2 <int+lbl>, CROSS_SECTION_1 <int+lbl>, CROSS_SECTION_2 <int+lbl>, ...
```

⁷The svyrr package is a [tidy](#) implementation of the popular [survey](#) package for R, authored by Dr. Thomas Lumley. For thorough discussion of the types of weights available in both R and Stata, we recommend [this blog post](#) by Dr. Lumley.

⁸As we will see in Chapter 2, IPUMS PMA publishes longitudinal data in both “wide” (one row per woman) and “long” (one row per phase) format.

1.5.1 Survey Weights

Whether you intend to work with a new **Longitudinal** or **Cross-sectional** data extract, you'll find the same set of sampling weights available for all PMA Family Planning surveys dating back to 2013:

- **HQWEIGHT** can be used to generate cross-sectional population estimates from questions on the Household Questionnaire.¹⁰
- **FQWEIGHT** can be used to generate cross-sectional population estimates from questions on the Female Questionnaire.¹¹
- **EAWEIGHT** can be used to compare the selection probability of a particular household with that of its EA.

A fourth Family Planning survey weight, **POPWT**, is currently available only for **Cross-sectional** data extracts.⁹

Additionally, PMA created a new weight, **PANELWEIGHT**, which should be used in longitudinal analyses spanning multiple phases, as it adjusts for loss to follow-up. **PANELWEIGHT** is available only for **Longitudinal** data extracts.

For example, suppose we wanted to estimate the proportion of reproductive age women in Burkina Faso who were using contraception at the time of data collection for both Phase 1 and Phase 2. In a cross-sectional or “long” longitudinal extract, you’ll find this information in the variable **CP**. In the “wide” extract featured here, you’ll find it in **CP_1** for Phase 1, and in **CP_2** for Phase 2.

```
dat %>% count(CP_1, CP_2)
```

Variable names in a “wide” extract have a numeric suffix for their data collection phase. **CP_1** is the Phase 1 version of **CP**, while **CP_2** comes from Phase 2.

```
# A tibble: 5 × 3
  CP_1          CP_2      n
  <int+lbl>    <int+lbl> <int>
1 0 [No]        0 [No]    2589
2 0 [No]        1 [Yes]   821
3 1 [Yes]       0 [No]    556
4 1 [Yes]       1 [Yes]   1241
5 99 [NIU (not in universe) or missing] 0 [No]     5
```

⁹POPWT can be used to estimate population-level counts - [click here](#) or view [this video](#) for details.

¹⁰HQWEIGHT reflects the [calculated selection probability](#) for a household in an EA, normalized at the population-level. Users intending to estimate population-level indicators for *households* should restrict their sample to one person per household via [LINENO](#) - see [household weighting guide](#) for details.

¹¹FQWEIGHT adjusts HQWEIGHT for female non-response within the EA, normalized at the population-level - see [female weighting guide](#) for details.

The `srvyr` package provides two functions we'll need to obtain our population estimate. The first, `as_survey_design`, allows us to specify `PANELWEIGHT` as a sampling weight. The second, `survey_mean`, uses that weight in an estimating function; in this case, we'll get the estimated proportion where `CP_1` and `CP_2` both have the value 1 [Yes] after removing missing / NIU responses with `CP_1 < 90 & CP_2 < 90`.

In subsequent chapters, we'll use `vartype = "ci"` to include a 95% confidence interval set by `level = 0.95` any time we calculate a population estimate. For discrete variables, we'll also include `proportion = TRUE` and `prop_method = "logit"`. In practice, there are large number of ways to calculate a confidence interval for a proportion.¹² The `srvyr` package includes several options for `prop_method`,¹³ but we'll use these settings because:

1. they ensure that each proportion's confidence interval only includes values between 0% and 100%,
2. they will include the real-world population proportion close to 95% of the time,
3. the `logit` method yields a relatively narrow interval compared with other options, and
4. these intervals will match the default intervals reported by Stata and SPSS survey proportion functions.

```
dat %>%
  as_survey_design(weight = PANELWEIGHT) %>%
  filter(CP_1 < 90 & CP_2 < 90) %>%
  summarise(
    survey_mean(
      CP_1 * CP_2,
      vartype = "ci",
      level = 0.95,
      proportion = TRUE,
      prop_method = "logit"
    )
  )

# A tibble: 1 × 3
  coef `_low` `_upp`
  <dbl>   <dbl>   <dbl>
1 0.188   0.174   0.203
```

`coef` shows the estimated population proportion

`_low` and `_upp` show the lower and upper bounds of a 95% confidence interval

¹²See Dean & Pagano [-@Dean-Pagano] for discussion.

¹³See `svyciprop` for a complete list of methods.

1.5.2 Sample Clusters

You can also provide information about sample clusters via `as_survey_design`. In general, we expect households selected from the same EA to share certain characteristics, such that some degree of variation seen in a variable of interest may be non-random at the EA-level. To compensate, you may wish to expand the standard errors produced by `survey_mean` by providing EA identifiers in `EAID`.

Here, we include `id = EAID_1`.¹⁴ Compared with our original estimate, notice that the 95% confidence interval for our contraceptive use estimate is wider when we provide information about the clustered sample design - these are “cluster-robust” standard errors.

```
dat %>%
  as_survey_design(weight = PANELWEIGHT, id = EAID_1) %>%
  filter(CP_1 < 90 & CP_2 < 90) %>%
  summarise(
    survey_mean(
      CP_1 * CP_2,
      vartype = "ci",
      level = 0.95,
      proportion = TRUE,
      prop_method = "logit"
    )
  )

# A tibble: 1 × 3
  coef `_low` `_upp`
  <dbl>  <dbl>  <dbl>
1 0.188   0.163   0.215
```

¹⁴As we'll see in an upcoming post, women are considered “lost to follow-up” if they moved outside the study area after Phase 1. Therefore, `EAID_1` and `EAID_2` are identical for all panel members: you can use either one to identify sample clusters.

1.5.3 Sample Strata

Finally, we'll also use `as_survey_design` to specify sample strata. For most samples, including Burkina Faso, this information is included in the variable `STRATA`. We'll include it here with `strata = STRATA_1`.¹⁵

```
dat %>%
  as_survey_design(weight = PANELWEIGHT, id = EAID_1, strata = STRATA_1) %>%
  filter(CP_1 < 90 & CP_2 < 90) %>%
  summarise(
    survey_mean(
      CP_1 * CP_2,
      vartype = "ci",
      level = 0.95,
      proportion = TRUE,
      prop_method = "logit"
    )
  )

# A tibble: 1 × 3
  coef `_low` `_upp`
  <dbl>  <dbl>  <dbl>
1 0.188  0.164  0.214
```

¹⁵As with `EAID`, you may use either `STRATA_1` or `STRATA_2` if your analysis is restricted to panel members.

The variable [STRATA](#) is *not available* for samples collected from DRC - Kinshasa or DRC - Kongo Central. If your extract includes any DRC sample, you'll need to amend this variable to include one unique numeric code for each of those regions.

For example, let's look at a different “wide” extract, `dat2`, containing all of the samples included in this data release. Notice that `STRATA_1` lists the sample strata for every [COUNTRY](#) *except* for DRC, where you see the value NA.

```
dat2 %>% count(COUNTRY, STRATA_1)
```

# A tibble: 27 × 3		
COUNTRY	STRATA_1	n
<int+lbl>	<int+lbl>	<int>
1 1 [Burkina Faso]	85401 [Urban, Burkina Faso]	3058
2 1 [Burkina Faso]	85402 [Rural, Burkina Faso]	2154
3 2 [Congo, Democratic Republic]	NA	3487
4 7 [Kenya]	40410 [Bungoma – urban, Kenya]	153
5 7 [Kenya]	40411 [Bungoma – rural, Kenya]	489
6 7 [Kenya]	40412 [Kakamega – urban, Kenya]	133
7 7 [Kenya]	40413 [Kakamega – rural, Kenya]	438
8 7 [Kenya]	40414 [Kericho – urban, Kenya]	249
9 7 [Kenya]	40415 [Kericho – rural, Kenya]	453
10 7 [Kenya]	40416 [Kiambu – urban, Kenya]	214
11 7 [Kenya]	40417 [Kiambu – rural, Kenya]	311
12 7 [Kenya]	40418 [Kilifi – urban, Kenya]	170
13 7 [Kenya]	40419 [Kilifi – rural, Kenya]	455
14 7 [Kenya]	40420 [Kitui – urban, Kenya]	153
15 7 [Kenya]	40421 [Kitui – rural, Kenya]	586
16 7 [Kenya]	40422 [Nairobi – urban, Kenya]	494
17 7 [Kenya]	40423 [Nandi – urban, Kenya]	260
18 7 [Kenya]	40424 [Nandi – rural, Kenya]	711
19 7 [Kenya]	40425 [Nyamira – urban, Kenya]	143
20 7 [Kenya]	40426 [Nyamira – rural, Kenya]	382
21 7 [Kenya]	40427 [Siaya – urban, Kenya]	130
22 7 [Kenya]	40428 [Siaya – rural, Kenya]	437
23 7 [Kenya]	40429 [West Pokot – urban, Kenya]	104
24 7 [Kenya]	40430 [West Pokot – rural, Kenya]	474
25 9 [Nigeria]	56606 [Lagos, Nigeria]	1089
26 9 [Nigeria]	56611 [Kano – Urban]	437
27 9 [Nigeria]	56612 [Kano – Rural]	561

Now let's see what happens when we try to produce population-level estimates with STRATA_1:

```
dat2 %>%
  as_survey_design(weight = PANELWEIGHT, id = EAID_1, strata = STRATA_1) %>%
  filter(CP_1 < 90 & CP_2 < 90) %>%
  group_by(COUNTRY, GEOCD, GEONG) %>%
  summarise(
    survey_mean(
      CP_1 * CP_2,
      vartype = "ci",
      level = 0.95,
      proportion = TRUE,
      prop_method = "logit"
    )
  )
```

```
Error in (function (object, ...) : missing values in `strata'
```

This fails because `as_survey_design` encounters NA values in STRATA_1. Fortunately, we can replace those values with numeric codes from the variable `GEOCD`:

```
dat2 %>% count(GEOCD)
```

```
# A tibble: 3 × 2
  GEOCD          n
  <int+lbl>     <int>
1 1 [Kinshasa]   1973
2 2 [Kongo Central] 1514
3 NA             14238
```

If GEOCD is not NA, we'll use its numeric code in place of STRATA_1. Otherwise, we'd like to leave STRATA_1 unchanged. However, because both variables include *value labels*, we'll first need remove them with `as.numeric`. To avoid confusion with the original variable STRATA_1, we'll call our new variable STRATA_RECODE.

```
dat2 <- dat2 %>%
  mutate(
    STRATA_RECODE = if_else(
      is.na(GEOCD),
      as.numeric(STRATA_1),
      as.numeric(GEOCD)
    )
  )
```

Notice that STRATA_RECODE replaces the NA values in STRATA_1, leaving its numeric values unchanged.

```
dat2 %>% count(GEOCD, STRATA_1, STRATA_RECODE)
```

	# A tibble: 28 × 4		
	GEOCD	STRATA_1	STRATA_RECODE
	<int+lbl>	<int+lbl>	<dbl> <int>
1	1 [Kinshasa]	NA	1 1973
2	2 [Kongo Central]	NA	2 1514
3	NA	40410 [Bungoma - urban, Kenya]	40410 153
4	NA	40411 [Bungoma - rural, Kenya]	40411 489
5	NA	40412 [Kakamega - urban, Kenya]	40412 133
6	NA	40413 [Kakamega - rural, Kenya]	40413 438
7	NA	40414 [Kericho - urban, Kenya]	40414 249
8	NA	40415 [Kericho - rural, Kenya]	40415 453
9	NA	40416 [Kiambu - urban, Kenya]	40416 214
10	NA	40417 [Kiambu - rural, Kenya]	40417 311
11	NA	40418 [Kilifi - urban, Kenya]	40418 170
12	NA	40419 [Kilifi - rural, Kenya]	40419 455
13	NA	40420 [Kitui - urban, Kenya]	40420 153
14	NA	40421 [Kitui - rural, Kenya]	40421 586
15	NA	40422 [Nairobi - urban, Kenya]	40422 494
16	NA	40423 [Nandi - urban, Kenya]	40423 260
17	NA	40424 [Nandi - rural, Kenya]	40424 711
18	NA	40425 [Nyamira - urban, Kenya]	40425 143
19	NA	40426 [Nyamira - rural, Kenya]	40426 382
20	NA	40427 [Siaya - urban, Kenya]	40427 130
21	NA	40428 [Siaya - rural, Kenya]	40428 437
22	NA	40429 [West Pokot - urban, Kenya]	40429 104
23	NA	40430 [West Pokot - rural, Kenya]	40430 474
24	NA	56606 [Lagos, Nigeria]	56606 1089
25	NA	56611 [Kano - Urban]	56611 437
26	NA	56612 [Kano - Rural]	56612 561
27	NA	85401 [Urban, Burkina Faso]	85401 3058
28	NA	85402 [Rural, Burkina Faso]	85402 2154

Now, we can use STRATA_RECODE with `as_survey_design` to obtain population estimates for each nationally representative or sub-nationally representative sample.

```
dat2 %>%
  as_survey_design(weight = PANELWEIGHT, id = EAID_1, strata = STRATA_RECODE) %>%
  filter(CP_1 < 90 & CP_2 < 90) %>%
  group_by(COUNTRY, GEOCD, GEONG) %>%
  summarise(
    survey_mean(
      CP_1 * CP_2,
      vartype = "ci",
      level = 0.95,
      proportion = TRUE,
      prop_method = "logit"
    )
  )
```

```
# A tibble: 6 × 6
# Groups:   COUNTRY, GEOCD [5]
  COUNTRY           GEOCD        GEONG     coef `_low` `_upp`
  <int+lbl>       <int+lbl>    <int+lbl>  <dbl>  <dbl>  <dbl>
1 1 [Burkina Faso] NA          NA      0.188  0.164  0.214
2 2 [Congo, Democratic Republic] 1 [Kinshasa] NA      0.320  0.288  0.353
3 2 [Congo, Democratic Republic] 2 [Kongo Central] NA      0.268  0.215  0.329
4 7 [Kenya]          NA          NA      0.366  0.350  0.382
5 9 [Nigeria]         NA          2 [Lagos]  0.293  0.259  0.330
6 9 [Nigeria]         NA          4 [Kano]   0.0537 0.0322 0.0880
```

1.6 INCLUSION CRITERIA FOR ANALYSIS

The remainder of this guide will feature code you can use to reproduce key indicators included in the **PMA Longitudinal Brief** for each sample. In many cases, you'll find separate reports available in English and French, and for both national and sub-national summaries. For reference, here are the highest-level population summaries available in English for each sample where Phase 2 IPUMS PMA data is currently available:

- [Burkina Faso](#)
- [DRC - Kinshasa](#)
- [DRC - Kongo Central](#)
- [Kenya](#)
- [Nigeria - Kano](#)
- [Nigeria - Lagos](#)

Panel data in these reports is limited to the *de facto* population of women who completed the Female Questionnaire in both Phase 1 and Phase 2. This includes women who slept in the household during the night before the interview for the Household Questionnaire. The *de jure* population includes women who are usual household members, but who slept elsewhere that night. We'll remove *de jure* cases recorded in the variable [RESIDENT](#).

For example, returning to our “wide” data extract for Burkina Faso, you can see the number of women who slept in the household before the Household Questionnaire for each phase reported in RESIDENT_1 and RESIDENT_2:

NA cases in
RESIDENT_2
represent women
who were lost to
follow-up in Phase
2.

```
dat %>% count(RESIDENT_1)
```

```
# A tibble: 3 × 2
  RESIDENT_1                n
  <int+lbl>                
  1 11 [Visitor, slept in hh last night]    106
  2 21 [Usual member, did not sleep in hh last night] 174
  3 22 [Usual member, slept in hh last night]   6510
```

```
dat %>% count(RESIDENT_2)
```

```
# A tibble: 5 × 2
  RESIDENT_2                n
  <int+lbl>                
  1 11 [Visitor, slept in hh last night]    74
  2 21 [Usual member, did not sleep in hh last night] 230
  3 22 [Usual member, slept in hh last night] 5993
  4 31 [Slept in hh last night, no response if usually lives in hh] 1
  5 NA                                     492
```

The *de facto* population is represented in codes 11 and 22. We'll use `filter` to include only those cases.

```
dat_2 <- dat %>%
  filter(
    RESIDENT_1 == 11 | RESIDENT_1 == 22,
    RESIDENT_2 == 11 | RESIDENT_2 == 22
  )

dat_2 %>% count(RESIDENT_1, RESIDENT_2)
```

```
# A tibble: 4 × 3
  RESIDENT_1             RESIDENT_2          n
  <int+lbl>            <int+lbl>        <int>
1 11 [Visitor, slept in hh last night] 11 [Visitor, slept in hh last night] 56
2 11 [Visitor, slept in hh last night] 22 [Usual member, slept in hh last ni... 39
3 22 [Usual member, slept in hh last night] 11 [Visitor, slept in hh last night] 17
4 22 [Usual member, slept in hh last night] 22 [Usual member, slept in hh last ni... 5855
```

Additionally, these reports only include women who completed (or partially completed) both Female Questionnaires. This information is reported in [RESULTFQ](#). In our “wide” extract, this information appears in [RESULTFQ_1](#) and [RESULTFQ_2](#): if you select the “Female Respondents” option at checkout, only women who completed (or partially completed) the Phase 1 Female Questionnaire will be included in your extract.

The screenshot shows a web browser window for the IPUMS PMA website. The title bar reads "IPUMS PMA: select samples". The URL is "pma.ipums.org/pma-action/samples". The page header includes "LOG IN | REGISTER | GLOBAL HEALTH" and "IPUMS.ORG". The main navigation menu has links for "HOME | SELECT DATA | MY DATA | SUPPORT". The main content area is titled "SELECT SAMPLES". A note says "Variable documentation on the web site can be filtered to display only material corresponding to chosen datasets ([more information](#) on this feature)." Another note says "You may select any of the below datasets for browsing. Please [log in](#) to see which samples you are authorized to include in extracts." There are two sets of radio buttons for selecting sample types: "Cross-sectional" (unchecked), "Longitudinal" (checked), "Long" (unchecked), and "Wide" (checked). To the right of these is a "SUBMIT SAMPLE SELECTIONS" button. Below this, under "FAMILY PLANNING - PERSON", there is a section for "Documentation" with checkboxes for "All Samples (wide)", "Burkina Faso", "Congo (Democratic Republic)", "Kenya", and "Nigeria", each with specific year ranges and notes. Under "Sample Members", there are four radio buttons: "Female Respondents" (checked), "Female Respondents and Household Members", "Female Respondents and Female Non-respondents", and "All Cases (Respondents and Non-respondents to Household and Female Questionnaires)". An arrow points to the "Female Respondents" button. At the bottom is another "SUBMIT SAMPLE SELECTIONS" button. A footer note at the bottom of the page reads "SUPPORTED BY THE BILL & MELINDA GATES FOUNDATION, DIAA, STAT/TRANSCEND, AND UNIVERSITY OF MINNESOTA".

We'll further restrict our sample by selecting only cases where RESULTFQ_2 shows that the woman also completed the Phase 2 questionnaire. Notice that, in addition to each of the value 1 through 10, there are several **non-response codes** numbered 90 through 99. You'll see similar values repeated across all IPUMS PMA variables, except that they will be left-padded to match the maximum width of a particular variable (e.g. 9999 is used for [INTFQYEAR](#), which represents a 4-digit year for the Female Interview).

```
dat %>% count(RESULTFQ_2)
```

# A tibble: 11 × 2	n
RESULTFQ_2 <int+lbl>	<int>
1 1 [Completed]	5491
2 2 [Not at home]	78
3 3 [Postponed]	22
4 4 [Refused]	66
5 5 [Partly completed]	12
6 7 [Respondent moved]	15
7 10 [Incapacitated]	19
8 95 [Not interviewed (female questionnaire)]	4
9 96 [Not interviewed (household questionnaire)]	192
10 99 [NIU (not in universe)]	399
11 NA	492

Possible **non-response codes** include:

- 95 Not interviewed (female questionnaire)
- 96 Not interviewed (household questionnaire)
- 97 Don't know
- 98 No response or missing
- 99 NIU (not in universe)

The value NA in an IPUMS extract indicates that a particular variable is not provided for a selected sample. In a “wide” **Longitudinal** extract, it may also signify that a particular person was not included in the data from a particular phase. Here, an NA appearing in RESULTFQ_2 indicates that a Female Respondent from Phase 1 was not found in Phase 2.

You can drop incomplete Phase 2 female responses as follows:

```
dat_3 <- dat %>% filter(RESULTFQ_2 == 1)
```

```
dat_3 %>% count(RESULTFQ_1, RESULTFQ_2)
```

```
# A tibble: 2 × 3
  RESULTFQ_1      RESULTFQ_2       n
  <int+lbl>      <int+lbl>     <int>
1 1 [Completed]    1 [Completed]  5487
2 5 [Partly completed] 1 [Completed]  4
```

Generally, we will combine both filtering steps together in a single function like so:

```
dat <- dat %>%
  filter(
    RESIDENT_1 == 11 | RESIDENT_1 == 22,
    RESIDENT_2 == 11 | RESIDENT_2 == 22,
    RESULTFQ_2 == 1
  )
```

In subsequent analyses, we'll use the remaining cases to show how PMA generates key indicators for **contraceptive use status** and **family planning intentions and outcomes**. The summary report for each country includes measures disaggregated by demographic variables like:

- MARSTAT - marital status
- EDUCATT and EDUCATTGEN - highest attended level of education¹⁶
- AGE - age
- WEALTHQ and WEALTHT - household wealth quintile or tertile¹⁷
- URBAN and SUBNATIONAL - geographic location¹⁸

¹⁶Levels in EDUCATT may vary by country; EDUCATTGEN recodes country-specific levels in four general categories.

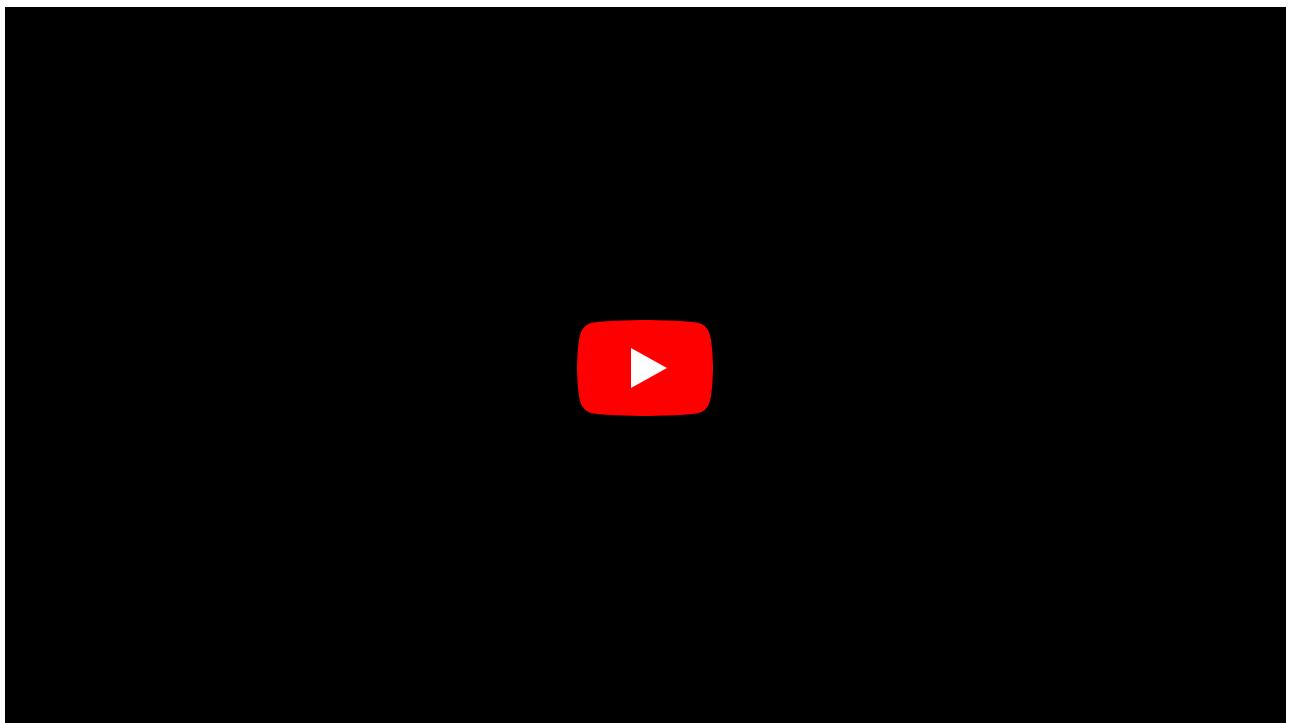
¹⁷Households are divided into quintiles/tertiles relative to the distribution of an asset SCORE weighted for all sampled households. For subnationally-representative samples (DRC and Nigeria), separate wealth distributions are calculated for each sampled region.

¹⁸SUBNATIONAL includes subnational regions for all sampled countries; country-specific variables are also available on the household - geography page.

2 POST 2

When we introduced new [harmonized panel data from PMA](#) in our last post, we mentioned that we've made big changes to the [IPUMS PMA website](#) making it easy to compare women's responses across each phase of data collection. This includes a new option allowing users to choose whether to organize panel data in either **long** or **wide** format. In this post, we'll practice building a data extract in both formats and discuss the advantages of each.

New users: make sure you [register](#) for a free IPUMS account! See our [user guide](#) for details.



2.1 GETTING STARTED

PMA panel data represent women aged 15-49 from sampled households in eight participating countries. IPUMS PMA makes it possible to combine data from multiple samples from the same unit of analysis: you'll need to select the **Family Planning** topic under the **Person** unit of analysis to begin browsing available samples and variables.

The screenshot shows the IPUMS PMA website interface. At the top, there is a navigation bar with links for LOG IN, REGISTER, GLOBAL HEALTH, and IPUMS. On the right, there is a 'DATA CART' section showing 0 VARIABLES and 0 SAMPLES. Below the navigation, the IPUMS PMA logo is displayed. In the center, there is a banner with the text 'PERFORMANCE MONITORING FOR ACTION' and links for HOME, SELECT DATA, MY DATA, and SUPPORT. A callout box highlights the current browse category: 'CURRENTLY BROWSING: "FAMILY PLANNING - PERSON"' with a 'CHANGE' link. Below this, there are three main selection buttons: 'SELECT SAMPLES' (purple), 'SELECT VARIABLES' (with dropdown menus for TOPICS and A-Z, and a SEARCH bar), and 'DISPLAY OPTIONS'. To the right of these buttons are 'HELP' and 'COUNTRY ABBREVIATIONS'. A note below the buttons says 'Select samples and variables to build a data extract.' At the bottom of the page, there is a footer with the text 'SUPPORTED BY: THE BILL & MELINDA GATES FOUNDATION, PMA, STAT/TRANSFER, AND UNIVERSITY OF MINNESOTA.' and 'COPYRIGHT © MINNESOTA POPULATION CENTER, UNIVERSITY OF MINNESOTA.'

IPUMS PMA: vars by group

LOG IN | REGISTER | GLOBAL HEALTH | IPUMS.ORG

Guest

DATA CART
YOUR DATA EXTRACT
0 VARIABLES
0 SAMPLES

SELECT SAMPLES
Select samples and variables

REVARIATIONS

CHOOSE THE TOPIC FOR DATA BROWSING

	FAMILY PLANNING	NUTRITION
PERSON	DESCRIPTION	DESCRIPTION
	CLIENT EXIT INTERVIEW	COVID-19
	DESCRIPTION	DESCRIPTION
SERVICE DELIVERY POINT	FAMILY PLANNING	NUTRITION
	DESCRIPTION	DESCRIPTION
INFANT	MATERNAL AND NEWBORN HEALTH	
	DESCRIPTION	

https://pma.ipums.org/pma-action/variables/group?unit_of_analysis=person

Check out our previous series on the [Nutrition](#), [Client Exit Interview](#), [COVID-19](#), and [Service Delivery Point](#) surveys you'll also find in the [unit of analysis](#) menu.

2.2 SAMPLE SELECTION

Once you've selected the **Family Planning** option, you'll next need to choose between cross-sectional or longitudinal samples. Cross-sectional samples are selected by default; these are nationally or sub-nationally representative samples collected each year dating backward as far as 2013.

Variable documentation on the web site can be filtered to display only material corresponding to chosen datasets ([more information](#) on this feature).

You may select any of the below datasets for browsing. Please [log in](#) to see which samples you are authorized to include in extracts.

Cross-sectional Longitudinal

SUBMIT SAMPLE SELECTIONS

FAMILY PLANNING - PERSON

All Samples

2021 2020 2019 2018 2017 2016 2015

Burkina Faso [2021 P2](#) [2020 P1](#) [2018 R6](#) [2017 R5](#) [2016b R4](#) [2015 R2](#)
 [2016a R3](#)

Congo (Democratic Republic) [2020 P2](#) i [2019b P1](#) i [2018b R7](#) i [2017b R6](#) i [2016b R5](#) i [2015c R4](#) i

Longitudinal samples are only available from 2019 onward, and they include all of the available phases for each sampled country (sub-nationally representative samples for DRC and Nigeria are listed separately). You'll only find longitudinal samples for countries where Phase 2 data has been made available; Phase 1 data for Cote d'Ivoire, India, and Uganda can currently be found under the Cross-sectional sample menu (Phase 2 data will be released soon!).

Annual cross-sectional samples are also available for each of the countries participating in the new PMA panel study. See our [last post](#) for details.

Clicking the Longitudinal button reveals options for either **long** or **wide** format. You'll find the same samples available in either case:

The screenshot shows a web browser window for the IPUMS PMA: select samples page. The URL is pma.ipums.org/pma-action/samples. The page title is "IPUMS PMA: select samples". The header includes links for LOG IN, REGISTER, GLOBAL HEALTH, and IPUMS.ORG. The main content area has a dark blue header with the IPUMS PMA logo and navigation links for HOME, SELECT DATA, MY DATA, and SUPPORT.

SELECT SAMPLES

Variable documentation on the web site can be filtered to display only material corresponding to chosen datasets ([more information](#) on this feature).

You may select any of the below datasets for browsing. Please [log in](#) to see which samples you are authorized to include in extracts.

Cross-sectional
 Longitudinal
 Long ⓘ
 Wide ⓘ

FAMILY PLANNING - PERSON

Documentation

All Samples (long) ⏵

Burkina Faso 2020 - 2021

Congo (Democratic Republic) 2019b - 2020b ⓘ
 2019a - 2020a ⓘ

Kenya 2019 - 2020

Nigeria 2019b - 2020b ⓘ
 2019a - 2020a ⓘ

Sample Members

Female Respondents
 Female Respondents and Household Members
 Female Respondents and Female Non-respondents
 All Cases (Respondents and Non-respondents to Household and Female Questionnaires)

SUBMIT SAMPLE SELECTIONS

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IPUMS PMA: select samples

pma.ipums.org/pma-action/samples

SELECT SAMPLES

Variable documentation on the web site can be filtered to display only material corresponding to chosen datasets ([more information](#) on this feature).

You may select any of the below datasets for browsing. Please [log in](#) to see which samples you are authorized to include in extracts.

Cross-sectional
 Longitudinal
 Long ⓘ
 Wide ⓘ

FAMILY PLANNING - PERSON

Documentation

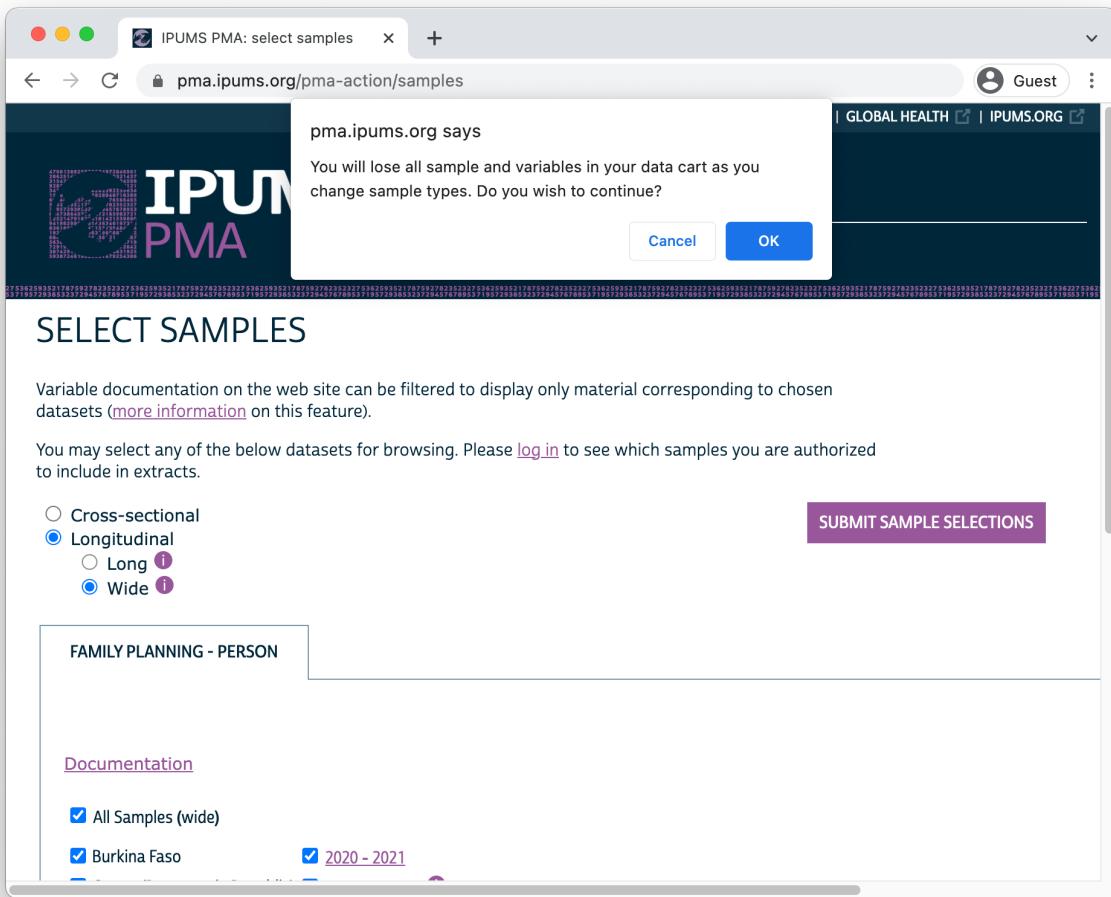
All Samples (wide) ←
 Burkina Faso 2020 - 2021
 Congo (Democratic Republic) 2019a - 2020b ⓘ
 Kenya 2019a - 2020a ⓘ
 Nigeria 2019b - 2020b ⓘ
 2019a - 2020a ⓘ

Sample Members

Female Respondents
 Female Respondents and Household Members
 Female Respondents and Female Non-respondents
 All Cases (Respondents and Non-respondents to Household and Female Questionnaires)

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Important: if you decide to change formats after selecting variables, your Data Cart will be emptied and you'll need to begin again from scratch.



After you've selected one of the available longitudinal formats, choose one or more samples listed below. There are also several Sample Members options listed:

- **Female Respondents** only includes women who completed *all or part* of a Female Questionnaire. This option selects all members of the panel study. In addition, it includes women who only participated in only one phase - we will demonstrate how to identify and drop these cases below.¹⁹
- **Female Respondents and Household Members** adds records for all other members of a Female Respondent's household. These household members did not complete the Female Questionnaire, but were listed on the household roster provided by the

¹⁹Women who completed all or part of the Female Questionnaire in *more than one phase* of the study are considered panel members. Women who completed it only at Phase 1 are included in a longitudinal extract, but they are not panel members. Likewise, women who completed it for the first time at Phase 2 are included, but are not panel members if they 1) will reach age 50 before Phase 3, or 2) declined the invitation to participate again in Phase 3.

respondent to a Household Questionnaire. Basic demographic variables are available for each household member, as are common wealth, water, sanitation, and other variables shared for all members of the same household.

- **Female Respondents and Female Non-respondents** includes all women who were eligible to participate in a Female Questionnaire. Eligible women are those age 15-49 who were listed on the roster collected in a Household Questionnaire. If an eligible woman declined the Female Questionnaire or was not available, variables associated with that questionnaire will be coded “Not interviewed (female questionnaire)”.
- **All Cases** includes all members listed on the household roster from a Household Questionnaire. If the Household Questionnaire was declined or if no respondent was available, any panel member appearing in other phases of the study will be coded “Not interviewed (household questionnaire)” for variables associated with the missing Household Questionnaire.

PANELWOMAN
indicates whether an individual is a member of the panel study.

RESULTFQ indicates whether an individual completed the Female Questionnaire.

RESIDENT indicates whether an individual is included in the *de facto* population.

ELIGIBLE indicates whether an individual was eligible for the female questionnaire.

RESULTHQ indicates whether a member of the individual’s household completed the Household Questionnaire.

The screenshot shows the 'IPUMS PMA: select samples' interface. At the top, there's a header bar with the title and a guest user indicator. Below the header is a navigation bar with back, forward, and search icons, followed by the URL 'pma.ipums.org/pma-action/samples'. The main content area has a left sidebar titled 'Documentation' and a right panel for selecting samples.

Sample Selections:

- All Samples (wide)** (checked)
- Burkina Faso** (checked)
- Congo (Democratic Republic)** (checked)
- Kenya** (checked)
- Nigeria** (checked)
- 2020 - 2021** (checked)
- 2019b - 2020b** ⓘ (checked)
- 2019a - 2020a** ⓘ (checked)
- 2019 - 2020** (checked)
- 2019b - 2020b** ⓘ (checked)
- 2019a - 2020a** ⓘ (checked)

Sample Members: A red oval highlights this section.

- Female Respondents
- Female Respondents and Household Members
- Female Respondents and Female Non-respondents
- All Cases (Respondents and Non-respondents to Household and Female Questionnaires)

Buttons:

- SUBMIT SAMPLE SELECTIONS** (purple button)

Footer:

- SUPPORTED BY: [THE BILL & MELINDA GATES FOUNDATION](#), [PMA](#), [STAT/TRANSFER](#), AND [UNIVERSITY OF MINNESOTA](#).
- COPYRIGHT © MINNESOTA POPULATION CENTER, UNIVERSITY OF MINNESOTA.

After you've selected samples and sample members for your extract, click the "Submit Sample Selections" button to return to the main data browsing menu.

2.3 VARIABLE SELECTION

You can browse IPUMS PMA variables by topic or alphabetically by name, or you can [search](#) for a particular term in a variable name, label, value labels, or description.

The screenshot shows the IPUMS PMA website interface. At the top, there's a navigation bar with links for LOG IN, REGISTER, GLOBAL HEALTH, and IPUMS.ORG. On the right, there's a 'DATA CART' section showing 0 VARIABLES and 6 SAMPLES, with a 'VIEW CART' button. The main content area has a header 'PERFORMANCE MONITORING FOR ACTION' and navigation links for HOME, SELECT DATA, MY DATA, and SUPPORT. A message box says 'CURRENTLY BROWSING: "FAMILY PLANNING - PERSON"' with a 'CHANGE' link. Below this is a 'SELECT VARIABLES' section with a 'TOPICS' dropdown set to 'A-Z'. The 'FAMILY PLANNING' topic is selected, showing its sub-topics: FERTILITY PREFERENCES, SEXUAL BEHAVIOR, CURRENT OR RECENT FAMILY PLANNING USE, PREVIOUS FAMILY PLANNING USE, EVER OR FIRST USE OF FAMILY PLANNING, DISCONTINUATION OF FAMILY PLANNING, NOT USING FAMILY PLANNING, FUTURE FAMILY PLANNING USE, FAMILY PLANNING ADVERTISEMENT, FAMILY PLANNING KNOWLEDGE, FAMILY PLANNING ACCESS, ATTITUDE TOWARDS FAMILY PLANNING, INFLUENCES ON FP, CONTRACEPTIVE ACCEPTABILITY, and CONTRACEPTIVE CALENDAR. To the left of this menu, there's a 'SAMPLES' section with a 'CHANGE SAMPLES' button. On the right, there are 'HELP' and 'COUNTRY ABBREVIATIONS' links. The bottom of the page has a footer with copyright information and a 'javascript:void(0);' link.

In this example, we'll select the [Discontinuation of Family Planning](#) topic. The availability of each associated variable is shown in a table containing all of the samples we've selected.

- X indicates that the variable is available for *all phases*
- / indicates that the variable is available for *one phase*
- – indicates that the variable is not available for *any phase*

You can click the + button to add a variable to your cart, or click a variable name to learn more.

The screenshot shows the IPUMS PMA website interface. At the top, there's a navigation bar with links for LOG IN, REGISTER, GLOBAL HEALTH, and IPUMS.ORG. On the right, it says "Guest" and "DATA CART YOUR DATA EXTRACT 0 VARIABLES 6 SAMPLES". Below the header, there's a banner for "PERFORMANCE MONITORING FOR ACTION" with links to HOME, SELECT DATA, MY DATA, and SUPPORT. A "VIEW CART" button is also present.

In the center, a box displays "CURRENTLY BROWSING: 'FAMILY PLANNING - PERSON'" with a "CHANGE" link. Below this, there are three tabs: "CHANGE SAMPLES", "SELECT VARIABLES" (which is active), and "DISPLAY OPTIONS". Under "SELECT VARIABLES", there are dropdown menus for TOPICS and A-Z, and a search bar.

A note below the tabs says "AN 'X' INDICATES THE VARIABLE IS AVAILABLE IN THAT DATASET." The main content area features a table titled "DISCONTINUATION OF FAMILY PLANNING VARIABLES" with a "TOP" link. The table has columns for "Add to cart", "Variable", "Variable Label", "Type", and several longitudinal samples (BURKF, CONDR, KENYA, NIGERA). The "Variable" column lists variables like FPSTOPMO, FPSTOPYR, and FPIMPREMOVEYR, each with a detailed description and availability status across the samples.

At the bottom of the page, there's a footer with "SUPPORTED BY: THE BILL & MELINDA GATES FOUNDATION, PMA, STAT/TRANSFER, AND UNIVERSITY OF MINNESOTA." and "COPYRIGHT © MINNESOTA POPULATION CENTER, UNIVERSITY OF MINNESOTA."

Let's take a look at the variable [PREGNANT](#). You'll find the variable name and label shown at the top of the page. Below, you'll see several tabs beginning with the [CODES](#) tab. For discrete variables, this tab shows all of the available codes and value labels associated with each response. You'll also see the same X, /, and – symbols in a table indicating the availability of each response in each sample.

Screenshot of the IPUMS PMA website showing the "PREGNANT" variable page.

The page includes the IPUMS PMA logo, navigation links (LOG IN | REGISTER | GLOBAL HEALTH | IPUMS.ORG), and a "DATA CART" section indicating 0 VARIABLES and 6 SAMPLES.

Key sections on the page include:

- PREGNANT**: The main variable name.
- ADD TO CART** and **CHANGE SAMPLES** buttons.
- Codes and Frequencies** section.
- Category availability view** (selected) and **Case-count view (Unavailable for longitudinal samples)**.
- Female Respondents** (selected) and other options: Female Respondents and Household Members, Female Respondents and Female Non-respondents, All Cases (Respondents and Non-respondents to Household and Female Questionnaires).
- LONGITUDINAL SAMPLES** table:

Code Label	BURKF 20 - 21	COND 19a - 20a	COND 19b - 20b	KENYA 19 - 20	NIGERA 19a - 20a	NIGERA 19b - 20b
00 No	X	X	X	X	X	X
01 Yes	X	X	X	X	X	X
95 Not interviewed (female questionnaire)	-	-	-	-	-	-
96 Not interviewed (household questionnaire)	-	-	-	-	-	-
97 Don't know	X	X	X	X	X	X
98 No response	X	/	-	-	X	X
99 NIU (not in universe) or missing	-	-	-	-	-	-

Above, there are no responses for “Not interviewed (female questionnaire)” and “Not interviewed (household questionnaire)”; this is because only samples members included in a “Female Respondents” extract are displayed by default. If we instead choose “All Cases”, this variable will include those response options because we’ll include every person listed on the household roster (even if the Household or Female Questionnaire was not completed).

“Case-count view” is not available for longitudinal samples, where each sample includes data from multiple phases. For cross-sectional samples, this option shows the frequency of each response.

Screenshot of the IPUMS PMA website showing the variable "PREGNANT".

The page header includes the IPUMS PMA logo, navigation links for LOG IN, REGISTER, GLOBAL HEALTH, and IPUMS.ORG, and a guest status indicator.

The main content area shows the variable "PREGNANT" under the heading "PERFORMANCE MONITORING FOR ACTION". It includes links for HOME, SELECT DATA, MY DATA, and SUPPORT.

A "DATA CART" sidebar indicates 0 VARIABLES and 6 SAMPLES, with a "VIEW CART" button.

The variable details section shows "Pregnancy status" and "Group: Core demographics".

Filter tabs include CODES (selected), DESCRIPTION, COMPARABILITY, UNIVERSE, AVAILABILITY, and QUESTIONNAIRE TEXT.

Codes and Frequencies

Category availability view (radio button selected) vs Case-count view (Unavailable for longitudinal samples).

Sampling categories (radio buttons): Female Respondents, Female Respondents and Household Members, Female Respondents and Female Non-respondents, All Cases (Respondents and Non-respondents to Household and Female Questionnaires) (selected and highlighted with a red oval).

An 'X' indicates the category is available for that sample.

LONGITUDINAL SAMPLES						
Code	Label	BURKF	COND	COND	KENYA	NIGERA
		20 - 21	19a - 20a	19b - 20b	19 - 20	19a - 20a
00	No	X	X	X	X	X
01	Yes	X	X	X	X	X
95	Not interviewed (female questionnaire)	X	X	X	X	X
96	Not interviewed (household questionnaire)	X	X	X	X	X
97	Don't know	X	X	X	X	X
98	No response	X	/	.	X	X
99	NIU (not in universe) or missing	X	X	X	X	X

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The symbol / again indicates that a particular response is available for some - but not all - phases of the study. For PREGNANCY it indicates that one of the options was either unavailable or was not selected by any sample respondents in a particular phase. If a variable was not included in all phases of the study, all response options will be marked with this symbol. For example, consider the variable COVIDCONCERN, indicating the respondent's level of concern about becoming infected with COVID-19.

COVIDCONCERN

Concerned about getting infected
Group: [Perceptions around COVID](#)

CODES	DESCRIPTION	COMPARABILITY	UNIVERSE	AVAILABILITY	QUESTIONNAIRE TEXT

Codes and Frequencies

Category availability view
 Case-count view (Unavailable for longitudinal samples)

Female Respondents
 Female Respondents and Household Members
 Female Respondents and Female Non-respondents
 All Cases (Respondents and Non-respondents to Household and Female Questionnaires)

An 'X' indicates the category is available for that sample

LONGITUDINAL SAMPLES							
Code	Label	BURKF 20 - 21	COND 19a - 20a	COND 19b - 20b	KENYA 19 - 20	NIGERA 19a - 20a	NIGERA 19b - 20b
01	Not concerned	/	/	/	/	/	
02	A little concerned	/	/	/	/	/	
03	Concerned	/	/	/	/	/	
04	Very concerned	/	/	/	/	/	
05	Currently / previously infected with COVID-19	/	/	/	/	.	
95	Not interviewed (female questionnaire)	
96	Not interviewed (household questionnaire)	
98	No response or missing	/	/	/	.	/	
99	NIU (not in universe)	

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Because Phase 1 questionnaires were administered prior to the emergence of COVID-19, this variable only appeared on Phase 2 questionnaires. The symbol / indicates limited availability across phases.

You'll find a detailed description for each variable on the [DESCRIPTION](#) tab. This tab also indicates whether a particular question appeared on the Household or Female Questionnaire.

The screenshot shows a web browser window for the IPUMS PMA website. The URL is pma.ipums.org/pma-action/variables/PREGNANT#description_section. The page title is "IPUMS PMA: descr: PREGNANT". The top navigation bar includes links for LOG IN, REGISTER, GLOBAL HEALTH, and IPUMS.ORG. A "Guest" account is logged in. On the right, there's a "DATA CART" section showing 0 VARIABLES and 6 SAMPLES, with a "VIEW CART" button. The main content area is titled "PREGNANT" and includes a "PERFORMANCE MONITORING FOR ACTION" banner with links to HOME, SELECT DATA, MY DATA, and SUPPORT. Below this, there are buttons for ADD TO CART and CHANGE SAMPLES. A navigation bar at the bottom of the content area has tabs for CODES (selected), DESCRIPTION, COMPARABILITY, UNIVERSE, AVAILABILITY, and QUESTIONNAIRE TEXT. The "DESCRIPTION" tab is currently active, displaying the following text:

Description

PREGNANT indicates whether or not the woman was pregnant at the time of the interview.

The question associated with this variable was included in the female questionnaire.

The COMPARABILITY tab describes important differences between samples. Additionally, it may contain information about similar variables appearing in DHS samples provided by IPUMS DHS.

The screenshot shows a web browser window for the IPUMS PMA website. The URL is pma.ipums.org/pma-action/variables/PREGNANT#comparability_section. The page title is "IPUMS PMA: descr: PREGNANT". The top navigation bar includes links for LOG IN, REGISTER, GLOBAL HEALTH, and IPUMS.ORG. A "Guest" account is logged in. On the right, there's a "DATA CART" section showing 0 variables and 6 samples, with a "VIEW CART" button. The main content area is titled "PREGNANT" and shows the "COMPARABILITY" tab selected. Other tabs include CODES, DESCRIPTION, UNIVERSE, AVAILABILITY, and QUESTIONNAIRE TEXT. Below the tabs, the word "Comparability" is highlighted. A note states: "There are minor universe differences among samples; see the Universe tab for more details." A link to "Comparability with IPUMS-DHS" is provided. A note below it says: "PREGNANT in IPUMS-PMA is similar to the variable PREGNANT in IPUMS-DHS. There may be differences in questionnaire text or the variable's universe; see the Survey Text and Universe Tab of the IPUMS-DHS variable for more information." At the bottom, it says "SUPPORTED BY: THE BILL & MELINDA GATES FOUNDATION, PMA, STAT/TRANSFER, AND UNIVERSITY OF MINNESOTA." and "COPYRIGHT © MINNESOTA POPULATION CENTER, UNIVERSITY OF MINNESOTA."

The UNIVERSE tab describes selection criteria for this question. In this case, there are some differences between samples:

- In DRC samples, all women aged 15-49 received this question.
- For all other samples, the question was skipped if any such woman previously indicated that she was menopausal or had a hysterectomy.

The screenshot shows a web browser window for the IPUMS PMA website. The URL is pma.ipums.org/pma-action/variables/PREGNANT#universe_section. The page title is "IPUMS PMA: descr: PREGNANT". The top navigation bar includes links for LOG IN | REGISTER | GLOBAL HEALTH | IPUMS.ORG and a "Guest" account indicator. A "DATA CART" sidebar shows 0 VARIABLES and 6 SAMPLES, with a "VIEW CART" button.

The main content area is titled "PREGNANT". Below it, under "Pregnancy status", is the group "Core demographics". There are five tabs at the top of the content area: CODES, DESCRIPTION, COMPARABILITY, UNIVERSE (which is selected), AVAILABILITY, and QUESTIONNAIRE TEXT.

Universe

Burkina Faso 2020 Baseline/Phase 1 Longitudinal Survey: Women aged 15-49 who are not menopausal and have not had a hysterectomy.

Burkina Faso 2021 Phase 2 Longitudinal Survey: Women aged 15-49 who are not menopausal and have not had a hysterectomy.

Congo Democratic Republic (Kinshasa) 2019 Baseline/Phase 1 Longitudinal Survey: Women aged 15-49.

Congo Democratic Republic (Kongo Central) 2019 Baseline/Phase 1 Longitudinal Survey: Women aged 15-49.

Democratic Republic of the Congo (Kinshasa) 2020 Phase 2 Longitudinal Survey: Women aged 15-49.

Democratic Republic of the Congo (Kongo Central) 2020 Phase 2 Longitudinal Survey: Women aged 15-49.

Kenya 2019 Baseline/Phase 1 Longitudinal Survey: Women aged 15-49 who are not menopausal and have not had a hysterectomy.

Kenya 2020 Phase 2 Longitudinal Survey: Women aged 15-49 who are not menopausal and have not had a hysterectomy.

Nigeria 2019 (Kano) Baseline/Phase 1 Longitudinal Survey: Women aged 15-49 who are not menopausal and have not had a hysterectomy.

Nigeria 2019 (Lagos) Baseline/Phase 1 Longitudinal Survey: Women aged 15-49 who are not menopausal and have not had a hysterectomy.

Nigeria (Kano) 2020 Phase 2 Longitudinal Survey: Women aged 15-49 who are not menopausal and have not had a hysterectomy.

Nigeria (Lagos) 2020 Phase 2 Longitudinal Survey: Women aged 15-49 who are not menopausal and have not had a hysterectomy.

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The AVAILABILITY tab shows all other samples (including cross-sectional samples) where this variable is available.

The screenshot shows a web browser window for the IPUMS PMA website. The URL in the address bar is pma.ipums.org/pma-action/variables/PREGNANT#availability_section. The page title is "IPUMS PMA: descr: PREGNANT". The top navigation bar includes links for LOG IN, REGISTER, GLOBAL HEALTH, and IPUMS.ORG. A "Guest" account is logged in. On the right, there's a "DATA CART" section showing 0 VARIABLES and 6 SAMPLES, with a "VIEW CART" button.

The main content area is titled "PREGNANT". Below it, under "Pregnancy status", is a group labeled "Core demographics". There are five tabs: CODES, DESCRIPTION, COMPARABILITY, UNIVERSE, AVAILABILITY, and QUESTIONNAIRE TEXT. The AVAILABILITY tab is selected, displaying a list of countries and years:

- Burkina Faso: 2014-2018, 2020-2021
- Congo (Democratic Republic): 2013-2020
- Cote d'Ivoire: 2017-2018, 2020
- Ethiopia: 2014-2019
- Ghana: 2013-2017
- India: 2016-2018, 2020
- Indonesia: 2015-2016
- Kenya: 2014-2020
- Niger: 2015-2018
- Nigeria: 2014-2020
- Uganda: 2014-2020

At the bottom of the page, a footer notes: "SUPPORTED BY: THE BILL & MELINDA GATES FOUNDATION, PMA, STAT/TRANSFER, AND UNIVERSITY OF MINNESOTA." and "COPYRIGHT © MINNESOTA POPULATION CENTER, UNIVERSITY OF MINNESOTA."

Finally, you'll find the full text of each question on the [QUESTIONNAIRE TEXT](#) tab. Each phase of the survey is shown separately, and you may click the "view entire document: text" link to view the complete questionnaire for a particular sample in any given phase.

The screenshot shows a web browser window for the IPUMS PMA website. The URL is pma.ipums.org/pma-action/variables/PREGNANT#questionnaire_text_section. The page title is "IPUMS PMA: descr: PREGNANT". The top navigation bar includes links for LOG IN, REGISTER, GLOBAL HEALTH, and IPUMS.ORG. A "Guest" account is logged in. On the right, there is a "DATA CART" section showing 0 VARIABLES and 6 SAMPLES, with a "VIEW CART" button.

The main content area is titled "PREGNANT". It features a "Questionnaire Text" section with tabs for CODES, DESCRIPTION, COMPARABILITY, UNIVERSE, AVAILABILITY, and QUESTIONNAIRE TEXT. The QUESTIONNAIRE TEXT tab is selected, displaying the following text:

Questionnaire Text

Burkina Faso 2020 Congo (Democratic Republic) Kenya 2019 Nigeria 2019b
2019b
Burkina Faso 2021 Congo (Democratic Republic) Kenya 2020 Nigeria 2020a
2020a
Congo (Democratic Republic) Congo (Democratic Republic) Nigeria 2019a Nigeria 2020b
2019a 2020b

[Burkina Faso 2020](#) [top](#)

Questionnaire form [view entire document: text](#)

14. Are you pregnant now?

Yes
 No
 Unsure
 No response

[Burkina Faso 2021](#) [top](#)

Questionnaire form [view entire document: text](#)

14. Are you pregnant now?

Yes
 No
 Unsure
 No response

[Congo \(Democratic Republic\) 2019a](#) [top](#)

Use the buttons at the top of this page to add the variable to your Data Cart, or to “VIEW CART” and begin checkout.

MONITORING FOR ACTION

ELECT DATA | MY DATA | SUPPORT

DATA CART
YOUR DATA EXTRACT

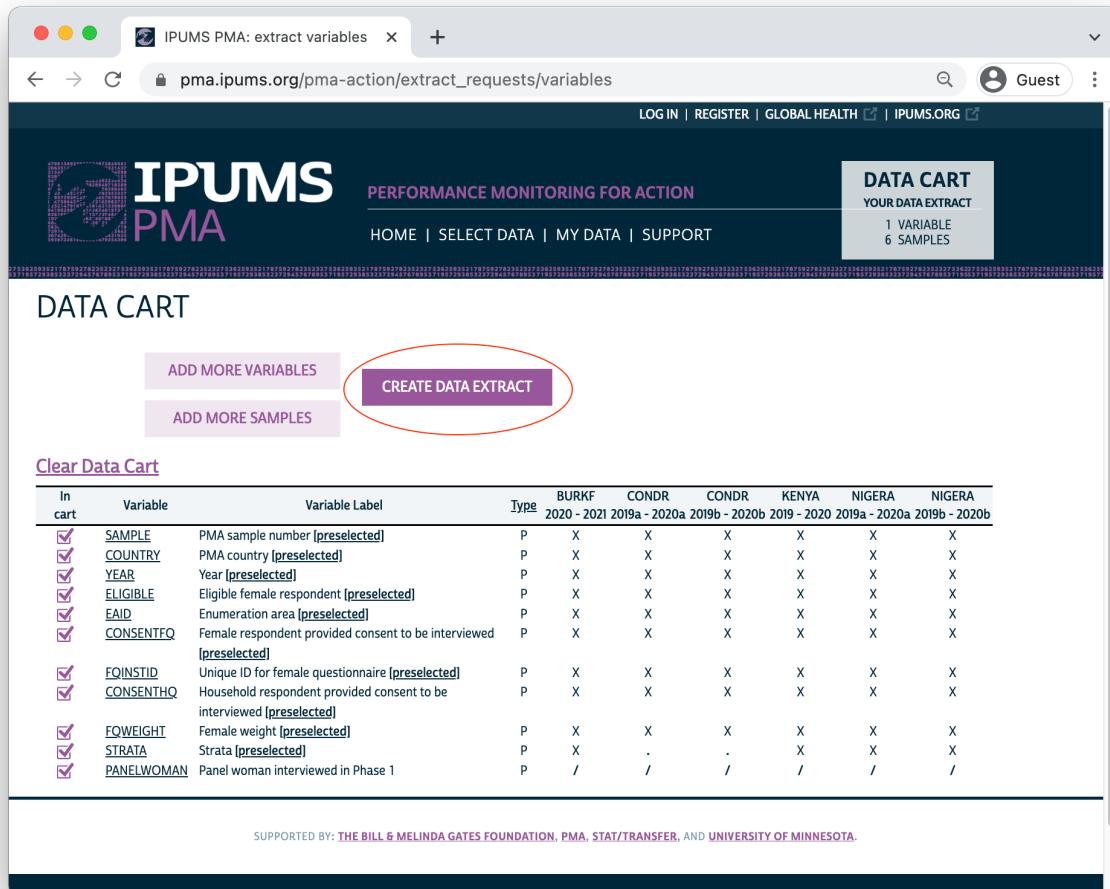
0 VARIABLES
6 SAMPLES

VIEW CART

ADD TO CART CHANGE SAMPLES

2.4 LOADING AN EXTRACT INTO R

Your Data Cart shows all of the variables you've selected, plus several “preselected” variables that will be automatically included in your extract. Click the “CREATE DATA EXTRACT” button to prepare your download.



The screenshot shows the IPUMS PMA Data Cart interface. At the top right, there's a "DATA CART" section indicating "1 VARIABLE" and "6 SAMPLES". Below this, the main title "DATA CART" is centered. Underneath it are three buttons: "ADD MORE VARIABLES", "CREATE DATA EXTRACT" (which is highlighted with a red oval), and "ADD MORE SAMPLES". A "Clear Data Cart" link is located just below the buttons. The main content area is a table titled "Clear Data Cart" with columns for "In cart", "Variable", "Variable Label", "Type", and six country codes: BURKF, CONDR, CONDR, KENYA, NIGERA, and NIGERA. The table lists various variables like SAMPLE, COUNTRY, YEAR, ELIGIBLE, EAID, CONSENTFO, FQINSTID, CONSENTHQ, FQWEIGHT, STRATA, and PANELWOMAN, each with a checked checkbox in the "In cart" column. The "CREATE DATA EXTRACT" button is located at the bottom of the table. At the very bottom of the page, there's a small note: "SUPPORTED BY: THE BILL & MELINDA GATES FOUNDATION, PMA, STAT/TRANSFER, AND UNIVERSITY OF MINNESOTA."

Before you submit an extract request, you'll have the opportunity to choose a “Data Format”. **R users should select Fixed-width text (.dat)** - you'll notice that data formatted for Stata, SPSS, and SAS are also available. CSV files are provided, but not recommended. (If you wish to change Sample Members, you may do so again here.)

IPUMS PMA: extract summary X +

Guest : pma.ipums.org/pma-action/extract_requests/summary?

LOG IN | REGISTER | GLOBAL HEALTH | IPUMS.ORG

IPUMS PMA

EXTRACT REQUEST ([HELP](#))

SAMPLES: 6 [\(show\)](#) [Change](#)

VARIABLES: 11 [\(show\)](#) [Change](#)

DATA FORMAT: .dat (fixed-width text) [Change](#)

STRUCTURE: Rectangular (longitudinal - long) [Change](#)

SAMPLE MEMBERS: Female Respondents [Change](#)

ESTIMATED SIZE: 11.2 MB

Describe your extract

SUBMIT EXTRACT

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The screenshot shows a web browser window titled "IPUMS PMA: extract options". The URL is "pma.ipums.org/pma-action/extract_requests/structure". The page header includes "LOG IN | REGISTER | GLOBAL HEALTH | IPUMS.ORG". The main content area has a dark blue header with the "IPUMS PMA" logo. Below it, a section titled "DATA FORMAT ([HELP](#))" contains a "Data Format" heading and a note about receiving Stata, SPSS, and SAS syntax files for fixed-width text (.dat) format. A list of file formats is shown with "Fixed-width text (.dat)" selected. A note below states "Data conversion supplied by [Stat/Transfer](#)". Another section titled "Sample Members" shows "Female Respondents" selected. At the bottom are "CANCEL" and "APPLY SELECTIONS" buttons. A copyright notice at the very bottom reads "COPYRIGHT © MINNESOTA POPULATION CENTER, UNIVERSITY OF MINNESOTA."

Click “APPLY SELECTIONS” to return to the previous screen. There, you may add a description and then proceed to the download page.

EXTRACT REQUEST ([HELP](#))

SAMPLES:	6	(show)	Change
VARIABLES:	11	(show)	Change
DATA FORMAT:	.dat (fixed-width text)		Change
STRUCTURE:	Rectangular (longitudinal - long)		Change
SAMPLE MEMBERS:	Female Respondents		Change
ESTIMATED SIZE:	11.2 MB		

Describe your extract

SUBMIT EXTRACT

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After a few moments, you'll receive an email indicating that your extract has been created. You'll need to obtain two files from the download page:

- Click the green “Download DAT” button to download the data file. You’ll receive a file with a number like “pma_00001.dat.gz”.
- Right click on “DDI” and click “Save link as”. You’ll receive a corresponding XML file like “pma_00001.xml”.

Extract Number	Date	Formatted Data	Fixed-width Text Files				Codebook	Revise Extract	Resubmit Extract	Description (click to edit)	Hide selections
			Data	SPSS	SAS	STATA	Basic			Show all	
20	2018-04-03	--	Download DAT	SPSS	SAS	STATA	Basic	DDI			
19	2018-03-23	--		--	--	--					
18	2017-10-25	--									
17	2017-10-18	--									
16	2017-09-26	--									
15	2017-09-22	--									

1) Click here to download the data.

2) Right click here to select the DDI.

Extract Number	Date	Formatted Data	Fixed-width Text Files				Codebook	Revise Extract	Resubmit Extract	Description (click to edit)	Hide selections
			Data	SPSS	SAS	STATA	Basic			Show all	
20	2018-04-03	--	Download DAT	SPSS	SAS	STATA	Basic				
19	2018-03-23	--		--	--	--					
18	2017-10-25	--	3) Then select "Save link as..." (or "Download Linked File") to save the DDI.								
17	2017-10-18	--									
16	2017-09-26	--									
15	2017-09-22	--									

3) Then select "Save link as..." (or "Download Linked File") to save the DDI.

→ Save link as...

Place both files in a folder that R can use as its [working directory](#). We **strongly recommend** using [RStudio projects](#) to manage all of the files and analysis scripts used for a particular research project. We'll place our files in a subfolder called “data” within our own RStudio project folder.

The [ipumsr](#) package offers the easiest way to import an IPUMS PMA extract into R. You can install it from [CRAN](#) like so:

```
install.packages("ipumsr")
```

After installation, you'll be able to load [ipumsr](#) and use the function `read_ipums_micro` to import your data extract. We'll now demonstrate loading both a **long** and a **wide** extract, and we'll take a brief look at the structure of each.

To do so, we'll use functions from the [tidyverse](#) family of R packages. You can install all of the tidyverse packages in a single step:

```
install.packages("tidyverse")
```

Once per session, you'll need to load the [ipumsr](#) and [tidyverse](#) packages into R.

```
library(ipumsr)
library(tidyverse)
```





2.5 LONG DATA STRUCTURE

We've downloaded a **long** data extract (Female Respondents only) and saved it in a folder called "data" in our working directory. We'll now load it into R as an object called `long`.

```
long <- read_ipums_micro(  
  ddi = "data/pma_00095.xml",  
  data = "data/pma_00095.dat.gz"  
)
```

In a **long** extract, data from each phase will be organized in *separate rows*. Here, responses from three panel members are shown:

```
long %>%  
  filter(FQINSTID %>% str_starts("011") | FQINSTID %>% str_starts("015")) %>%  
  arrange(FQINSTID) %>%  
  select(FQINSTID, PHASE, AGE, PANELWOMAN)
```

```
# A tibble: 6 × 4  
  FQINSTID          PHASE      AGE PANELWOMAN  
  <chr>            <int+lbl> <int+lbl> <int+lbl>  
1 011W5S0HN91I4H4I3T9JCMHB 1 [Baseline]    29     NA  
2 011W5S0HN91I4H4I3T9JCMHB 2 [First follow up] 30      1 [Yes]  
3 015NP6FJTIA98FYCBBBS1F0F7 1 [Baseline]    47     NA  
4 015NP6FJTIA98FYCBBBS1F0F7 2 [First follow up] 48      1 [Yes]  
5 015WYNN02WXHH6JA4HA9PL1MR 1 [Baseline]    20     NA  
6 015WYNN02WXHH6JA4HA9PL1MR 2 [First follow up] 21      1 [Yes]
```

Each panel member receives a unique ID shown in `FQINSTID`. The variable `PHASE` shows that each woman's responses to the Phase 1 Female Questionnaire appears in the first row, while her Phase 2 responses appear in the second. `AGE` shows each woman's age when she completed the Female Questionnaire for each phase.

`PANELWOMAN` indicates whether the woman completed all or part of the Female Questionnaire in a *prior* phase, and that she'd agreed to continue participating in the panel study at that time. The value `NA` appears in the rows for Phase 1, as `PANELWOMAN` was not included in Phase 1 surveys.

We mentioned above that you'll also include responses from some non-panel members when you request an extract with Female Respondents. These include women who did not complete all or part the Female Questionnaire in a prior phase, as indicated by `PANELWOMAN`. These women are not assigned a value for `FQINSTID` - instead, you'll find an empty string:

```
long %>% count(PHASE, PANELWOMAN, FQINSTID == "")
```

```
# A tibble: 3 × 4
  PHASE      PANELWOMAN `FQINSTID == ""`     n
  <int+lbl>    <int+lbl>  <lgl>           <int>
  1 1 [Baseline]      NA     FALSE          23591
  2 2 [First follow up] 0 [No]    TRUE          6586
  3 2 [First follow up] 1 [Yes]   FALSE         18194
```

For most longitudinal analysis applications, you'll need to drop non-panel members together with any women who did not fully complete the Phase 2 Female Questionnaire. We'll demonstrate using `group_by` to ensure that there is one row for every `FQINSTID` where `PHASE == 1` and another row where `PHASE == 2 & RESULTFQ == 1`.

```
long <- long %>%
  group_by(FQINSTID) %>%
  filter(any(PHASE == 1) & any(PHASE == 2 & RESULTFQ == 1)) %>%
  ungroup()
```

The [PMA Longitudinal Briefs](#) published for each sample also include only members of the *de facto* population. These are women who slept in the household during the night prior to the interview for each Household Questionnaire, such that `RESIDENT` takes the value 11 or 22. We'll use `group_by` again to include only *de facto* women from both phases.

```
long <- long %>%
  group_by(FQINSTID) %>%
  filter(all(RESIDENT %in% c(11, 22))) %>%
  ungroup()
```

Following these steps, you can check the size of each analytic sample like so:

```
long %>% count(COUNTRY, GEOCD, GEONG, PHASE)
```

	COUNTRY	GEOCD	GEONG	PHASE	n	
1 1	[Burkina Faso]	<int+lbl>	<int+lbl>	NA	1 [Baseline]	5212
2 1	[Burkina Faso]	NA	NA	2 [First follow u...]	5212	
3 2	[Congo, Democratic Republic]	1 [Kinshasa]	NA	1 [Baseline]	1973	
4 2	[Congo, Democratic Republic]	1 [Kinshasa]	NA	2 [First follow u...]	1973	
5 2	[Congo, Democratic Republic]	2 [Kongo Central]	NA	1 [Baseline]	1514	
6 2	[Congo, Democratic Republic]	2 [Kongo Central]	NA	2 [First follow u...]	1514	
7 7	[Kenya]	NA	NA	1 [Baseline]	6939	
8 7	[Kenya]	NA	NA	2 [First follow u...]	6939	
9 9	[Nigeria]	NA	2 [Lagos]	1 [Baseline]	1089	
10 9	[Nigeria]	NA	2 [Lagos]	2 [First follow u...]	1089	
11 9	[Nigeria]	NA	4 [Kano]	1 [Baseline]	998	
12 9	[Nigeria]	NA	4 [Kano]	2 [First follow u...]	998	

Reminder: samples for DRC and Nigeria are sub-nationally representative, so we'll show separate frequencies for each [GEOCD](#) and [GEONG](#).

2.6 WIDE DATA STRUCTURE

We've also downloaded a **wide** data extract (Female Respondents only) and saved it in the "data" folder in our working directory. We'll also load this extract into R as an object named `wide`.

```
wide <- read_ipums_micro(  
  ddi = "data/pma_00084.xml",  
  data = "data/pma_00084.dat.gz"  
)
```

In a **wide** extract, all of the responses from one woman appear in the *same row*. The IPUMS extract system appends a numeric suffix to each variable name corresponding with the phase from which it was drawn. Consider our three example panel members again:

```
wide %>%  
  filter(FQINSTID %>% str_starts("011") | FQINSTID %>% str_starts("015")) %>%  
  select(FQINSTID, AGE_1, AGE_2, PANELWOMAN_1, PANELWOMAN_2)
```

```
# A tibble: 3 × 5  
FQINSTID          AGE_1     AGE_2    PANELWOMAN_1 PANELWOMAN_2  
<chr>            <int+lbl> <int+lbl> <int+lbl>   <int+lbl>  
1 011W5S0HN91I4H4I3T9Jcmbhb 29        30       NA         1 [Yes]  
2 015NP6FJTIA98FYCBBBS1F0F7 47        48       NA         1 [Yes]  
3 015WYNN02WXHH6JA4HA9PL1MR 20        21       NA         1 [Yes]
```

Each panel member has one unique ID shown in `FQINSTID`. However, `AGE` is parsed into two columns: `AGE_1` shows each woman's age at Phase 1, and `AGE_2` shows her age at Phase 2.

As we've discussed, `PANELWOMAN` is not available for Phase 1, as it indicates whether the woman completed all or part of the Female Questionnaire in a *prior* phase. For this reason, all values in `PANELWOMAN_1` are NA. Most variables are copied once for each phase, even if they - like `PANELWOMAN_1` - are not available for all phases.

You might expect the total length of a **wide** extract to be half the length of a corresponding **long** extract. This is not the case! A **wide** extract includes one row for each woman who completed all or part of the Female Questionnaire *for any phase* - you'll find placeholder columns for phases where the interview was not conducted.

```
wide %>%  
  filter(FQINSTID == "0C8VQU6B03BXLAVVZ8SB90EKQ") %>%  
  select(RESULTFQ_1, AGE_1, RESULTFQ_2, AGE_2)
```

```
# A tibble: 1 × 4
  RESULTFQ_1    AGE_1    RESULTFQ_2    AGE_2
  <int+lbl>    <int+lbl> <int+lbl>    <int+lbl>
1 1 [Completed] 31          2 [Not at home] 95 [Not interviewed (female questionnaire)]
```

In a **long** extract, rows for the missing phase are dropped. In this example, the woman was “not at home” for the Phase 2 Female Questionnaire. When we select a **long** extract containing only Female Respondents, her Phase 2 row is excluded automatically (it will be included if you request an extract containing Female Respondents and Female Non-respondents).

```
long %>%
  filter(FQINSTID == "0C8VQU6B03BXLAVVZ8SB90EKQ") %>%
  select(PHASE, RESULTFQ, AGE)
```

```
# A tibble: 1 × 3
  PHASE    RESULTFQ    AGE
  <int+lbl> <int+lbl> <int+lbl>
1 1 [Baseline] 1 [Completed] 31
```

Again: for most longitudinal analysis applications, you’ll need to remove cases where women were not interviewed for Phase 1 or where the Phase 2 Female Questionnaire was not completed:

```
wide <- wide %>% filter(RESULTFQ_2 == 1 & !is.na(RESULTFQ_1))
```

The *de facto* population appearing in [PMA Longitudinal Briefs](#) is defined in **wide** extracts by cases where the values 11 or 12 appear in *both* RESIDENT_1 and RESIDENT_2:

```
wide <- wide %>% filter(RESIDENT_1 %in% c(11, 22) & RESIDENT_2 %in% c(11, 22))
```

Following these steps, each analytic sample contains the same number of cases shown in the final **long** format extract above.

```
wide %>%
  group_by(COUNTRY, GEOCD, GEONG) %>%
  count()
```

```

# A tibble: 6 × 4
# Groups:   COUNTRY, GEOCD, GEONG [6]
  COUNTRY           GEOCD      GEONG     n
  <int+lbl>       <int+lbl>  <int+lbl> <int>
1 1 [Burkina Faso]    NA        NA     5212
2 2 [Congo, Democratic Republic] 1 [Kinshasa]    NA     1973
3 2 [Congo, Democratic Republic] 2 [Kongo Central] NA     1514
4 7 [Kenya]          NA        NA     6939
5 9 [Nigeria]        NA        2 [Lagos]  1089
6 9 [Nigeria]        NA        4 [Kano]   998

```

2.7 WHICH FORMAT IS BEST FOR ME?

The choice between **long** and **wide** formats ultimately depends on your research objectives.

Many data manipulation tasks, for example, are faster and easier to perform in the **wide** format. In the example above, we needed to identify women who completed a Female Questionnaire and were members of the *de facto* population in both phases. In the **long** format, we first had to group the data by FQINSTID with [group_by](#), thereby ensuring that a Phase 1 and Phase 2 check could be performed for each woman. In preparing for this post, this approach took about 36.5 seconds. By comparison, the same task was achieved without [group_by](#) in **wide** format in just 0.16 seconds. If your workflow requires multiple comparisons between phases, the **wide** format may be the best choice!

On the other hand, many of the longitudinal modeling packages available for R require data to be in a **long** format - this includes both the [survival](#) package for Cox regression and the [lme4](#) package for multilevel models. Users who prefer the **wide** format for data cleaning and exploration can manually switch to **long** format with help from [pivot_longer](#), for example:

```
wide %>% select(FQINSTID, AGE_1, PREGNANT_1, AGE_2, PREGNANT_2)
```

```
# A tibble: 17,725 × 5
#> FQINSTID          AGE_1    PREGNANT_1 AGE_2    PREGNANT_2
#> <chr>            <int+lbl> <int+lbl>  <int+lbl> <int+lbl>
#> 1 uuid:0005f6d7-b7cd-46f6-8a6f-5f051b6ab4a2 30      0 [No]    31      0 [No]
#> 2 uuid:0006cb76-09d1-4f2a-a92d-c12fcacf194b5 34      1 [Yes]   34      0 [No]
#> 3 uuid:00204481-5cae-4188-abb3-0367d0ed9c14 17      0 [No]    18      0 [No]
#> 4 uuid:002398f4-8f2d-4095-8019-c306d39cf2b9 29      0 [No]    29      0 [No]
#> 5 uuid:00407300-c1e6-4e24-ab8d-8af5e1ca85a6 25      0 [No]    25      0 [No]
#> 6 uuid:00413ed1-d176-44fb-a232-7e53c1db0958 32      0 [No]    32      0 [No]
#> 7 uuid:0048a052-66ff-4ed5-9fa9-fc72e6dab696 38      0 [No]    39      0 [No]
#> 8 uuid:004d80f0-90c6-4b77-bb4d-21d09c84fe74 38      0 [No]    38      0 [No]
#> 9 uuid:00504cf5-870c-4a02-aad7-ea5d47b135ff 33      0 [No]    34      0 [No]
#> 10 uuid:00534792-fb84-47b4-8606-e145d74cd089 24     0 [No]    25      0 [No]
#> 11 uuid:0058cbb8-9892-4a60-b9ed-fb556a21f862 29     0 [No]    30      0 [No]
#> 12 uuid:00682e93-0483-42b4-8f8d-2e0c36a26d37 16     0 [No]    17      0 [No]
#> 13 uuid:007699e0-d078-4a30-ace2-6de2cfaa571a 29     0 [No]    30      0 [No]
#> 14 uuid:00776552-ad8a-455b-93e0-ac9d066e2a85 22     0 [No]    23      0 [No]
#> 15 uuid:0084cafdf-e83f-45ee-9906-8a1d2d0b923a 28    0 [No]    29      0 [No]
#> 16 uuid:009dbdcf-f9f0-4cb6-94e2-e6a46fb23bd6 41    0 [No]    42      0 [No]
#> 17 uuid:00b89b1d-25e1-40f0-8e52-e06ce5525555 47    1 [Yes]   47      0 [No]
#> 18 uuid:00bf8df9-340f-454b-95b7-04921ef54c28 15    0 [No]    16      0 [No]
#> 19 uuid:00c8312a-561a-4855-840d-63a6fba578ae 22    0 [No]    22      0 [No]
#> 20 uuid:00f7a6fb-484e-4664-a646-79dd480ab43e 24    0 [No]    25      0 [No]
#> 21 uuid:00f834ef-fb10-4402-a609-f0f39f331f41 47    0 [No]    47      0 [No]
#> 22 uuid:01009c42-e131-4845-a746-93c98b892b57 47   0 [No]    47      0 [No]
#> 23 uuid:0105d2b2-e4f0-494a-81e2-1847d122cd80 37   0 [No]    38      0 [No]
#> 24 uuid:010fbcc4c-464d-41ab-b76c-bafa69eb18f4 36   0 [No]    37      0 [No]
#> 25 uuid:011ef212-8106-4893-8e37-de7c07c38f9c 43   0 [No]    44      0 [No]
#> 26 uuid:011f023e-baba-4bdb-bf41-749857749381 17   0 [No]    17      0 [No]
#> 27 uuid:0138720b-6145-484d-b1ac-347f39bc70af 22   0 [No]    22      0 [No]
#> 28 uuid:0147c5e0-1de8-49c2-bd35-f4e4ba639e35 35   0 [No]    36      0 [No]
#> 29 uuid:01702a75-7518-436d-a2e9-1aed8ff529f8 20   0 [No]    22      0 [No]
#> 30 uuid:01a47bc3-496a-4661-bf50-3069209621b5 33   1 [Yes]   34      0 [No]
# ... with 17,695 more rows
```

With `pivot_longer`, you can strip the suffix 1 or 2 from each variable, placing the result in a new column called PHASE. Then, we'll pivot each woman's age and pregnancy status from 2 wide columns into a single long one.

```
wide %>%
  select(FQINSTID, AGE_1, PREGNANT_1, AGE_2, PREGNANT_2) %>%
  pivot_longer(
    !FQINSTID,
    names_pattern = "(.*)([1-2])",
    names_to = c(".value", "PHASE")
  )
```

```
# A tibble: 35,450 × 4
#> FQINSTID          PHASE AGE PREGNANT
#> <chr>             <chr> <int+lbl> <int+lbl>
#> 1 uuid:0005f6d7-b7cd-46f6-8a6f-5f051b6ab4a2 1   30    0 [No]
#> 2 uuid:0005f6d7-b7cd-46f6-8a6f-5f051b6ab4a2 2   31    0 [No]
#> 3 uuid:0006cb76-09d1-4f2a-a92d-c12fcacf194b5 1   34    1 [Yes]
#> 4 uuid:0006cb76-09d1-4f2a-a92d-c12fcacf194b5 2   34    0 [No]
#> 5 uuid:00204481-5cae-4188-abb3-0367d0ed9c14 1   17    0 [No]
#> 6 uuid:00204481-5cae-4188-abb3-0367d0ed9c14 2   18    0 [No]
#> 7 uuid:002398f4-8f2d-4095-8019-c306d39cf2b9 1   29    0 [No]
#> 8 uuid:002398f4-8f2d-4095-8019-c306d39cf2b9 2   29    0 [No]
#> 9 uuid:00407300-c1e6-4e24-ab8d-8af5e1ca85a6 1   25    0 [No]
#> 10 uuid:00407300-c1e6-4e24-ab8d-8af5e1ca85a6 2  25    0 [No]
#> 11 uuid:00413ed1-d176-44fb-a232-7e53c1db0958 1  32    0 [No]
#> 12 uuid:00413ed1-d176-44fb-a232-7e53c1db0958 2  32    0 [No]
#> 13 uuid:0048a052-66ff-4ed5-9fa9-fc72e6dab696 1  38    0 [No]
#> 14 uuid:0048a052-66ff-4ed5-9fa9-fc72e6dab696 2  39    0 [No]
#> 15 uuid:004d80f0-90c6-4b77-bb4d-21d09c84fe74 1  38    0 [No]
#> 16 uuid:004d80f0-90c6-4b77-bb4d-21d09c84fe74 2  38    0 [No]
#> 17 uuid:00504cf5-870c-4a02-aad7-ea5d47b135ff 1  33    0 [No]
#> 18 uuid:00504cf5-870c-4a02-aad7-ea5d47b135ff 2  34    0 [No]
#> 19 uuid:00534792-fb84-47b4-8606-e145d74cd089 1  24    0 [No]
#> 20 uuid:00534792-fb84-47b4-8606-e145d74cd089 2  25    0 [No]
#> 21 uuid:0058cbb8-9892-4a60-b9ed-fb556a21f862 1  29    0 [No]
#> 22 uuid:0058cbb8-9892-4a60-b9ed-fb556a21f862 2  30    0 [No]
#> 23 uuid:00682e93-0483-42b4-8f8d-2e0c36a26d37 1  16    0 [No]
#> 24 uuid:00682e93-0483-42b4-8f8d-2e0c36a26d37 2  17    0 [No]
#> 25 uuid:007699e0-d078-4a30-ace2-6de2cfaa571a 1  29    0 [No]
#> 26 uuid:007699e0-d078-4a30-ace2-6de2cfaa571a 2  30    0 [No]
#> 27 uuid:00776552-ad8a-455b-93e0-ac9d066e2a85 1  22    0 [No]
#> 28 uuid:00776552-ad8a-455b-93e0-ac9d066e2a85 2  23    0 [No]
#> 29 uuid:0084cafde83f-45ee-9906-8a1d2d0b923a 1  28    0 [No]
#> 30 uuid:0084cafde83f-45ee-9906-8a1d2d0b923a 2  29    0 [No]
# ... with 35,420 more rows
```

Manipulating patterns in variable names with [pivot_longer](#) takes practice, and we imagine many users will find it easier to simply work with data in the **long** format from the beginning.

Fortunately, the updated IPUMS PMA extract system makes it easy to select the samples, sample members, and variables that matter to your particular research question. New choices for **long** and **wide** data formats save an additional data cleaning step, allowing you to jump into longitudinal analysis as quickly as possible.

For more examples using [pivot_longer](#), check out our posts on [contraceptive calendar](#) and [migration](#) data!

3 POST 3

When we introduced new [Family Planning Panel Data](#) from PMA last month, we mentioned that PMA uses a **multi-stage cluster sample design** for each phase of the panel study. This means you'll find data from a Household Questionnaire administered once each year, and you'll find data from a subsequent Female Questionnaire collected shortly afterward. Three years - or phases - of data will be collected in total.

Because data are collected through two questionnaires administered in three phases, there are several places where incomplete or missing data may indicate **loss to follow-up** - dropped cases from the original panel design. At the same time, PMA uses an **open panel design**, whereby women who move into the study area or reach participation age after Phase 1 are permitted to join the panel at any subsequent phase.

In this post, we'll cover these issues in detail. To illustrate, we'll be using a **wide format** data extract from [IPUMS PMA](#) that includes "All cases" from both currently available phases. In other words, we'll include every member of the household roster collected in the Household Questionnaire at the start of each phase (even if no Female Questionnaire was completed by that person).

To make our explanation easier to follow, we'll make use of a data visualization tool known in clinical research settings as a [CONSORT diagram](#).

Check out our [last post](#) for information on advantages of wide vs. long data extracts, and for details on case selection.

3.1 CONSORT DIAGRAM

A CONSORT diagram is a flowchart showing enrollment and attrition points, most typically in longitudinal studies. PMA publishes a CONSORT diagram together with the User Notes for each longitudinal sample. We'll consider the 6 samples for which harmonized Phase 1 and Phase 2 data are currently available:

- [Burkina Faso](#)
- [DRC - Kinshasa](#)
- [DRC - Kongo Central](#)
- [Kenya](#)
- [Nigeria - Lagos](#)
- [Nigeria - Kano](#)

We've constructed a multi-sample CONSORT diagram for this post using the [ggplot2](#) package for R, but we've hidden the source code for readers who might want to stay focused on our sample design discussion. In you're interested, click the "Show CONSORT diagram source code" button to follow along as we build our diagram below.

```

# load custom font
library(sysfonts)
library(showtext)
sysfonts::font_add(
  family = "cabrito",
  regular = ".../fonts/cabritosansnormregular-webfont.ttf"
)
showtext::showtext_auto()

# define consort function
consort <- function(dat){
  dat <- dat %>%
    ungroup() %>%
    arrange(pop, step, keep) %>%
    mutate(
      across(c(pop, label), ~as_factor(.x)),
      label = fct_rev(label),
      x = as.double(pop) %>% ifelse(keep, ., . + 0.19),
      y = as.double(label),
      x_line1 = ifelse(keep, x, x - 0.19), # start horiz line at origin
      x_line2 = ifelse(keep, x, x - 0.05), # end horiz line 0.05 before label
      y_line1 = ifelse(keep, y - 0.3, y),
      y_line2 = ifelse(keep, y - 1.7, y),
      across(
        starts_with("x"),
        ~case_when(
          step <= 6 & (is.na(samedw) | !keep) ~ .x, # leave as-is
          step == 9 ~ .x, # leave as-is
          keep & samedw ~ .x + 0.19, # right-side dwelling
          keep & !samedw ~ .x - 0.19, # left-side dwelling
          !keep ~ .x + .19, # dwelling discard
        )
      ),
      across(
        starts_with("x"), # flip dwelling discard
        ~case_when(!keep & !samedw ~ .x - 2*(.x - floor(.x)), T ~.x)
      ),
      x_line2 = case_when(
        step == 8 & keep & samedw ~ x_line2 - 0.13, # back to origin at step 8
        step == 8 & keep & !samedw ~ x_line2 + 0.13,
        TRUE ~ x_line2
      ),
      across(
        matches("line"),
        ~ifelse(keep & step == max(step), NA, .x) %>% # no lines at final step
        as.double()
      ),
      y = case_when(step == 9 ~ y - 1, TRUE ~ as.double(y)),
      y_line1 = ifelse(step == 6 & keep, y_line1 - 0.5, y_line1),
    )
}

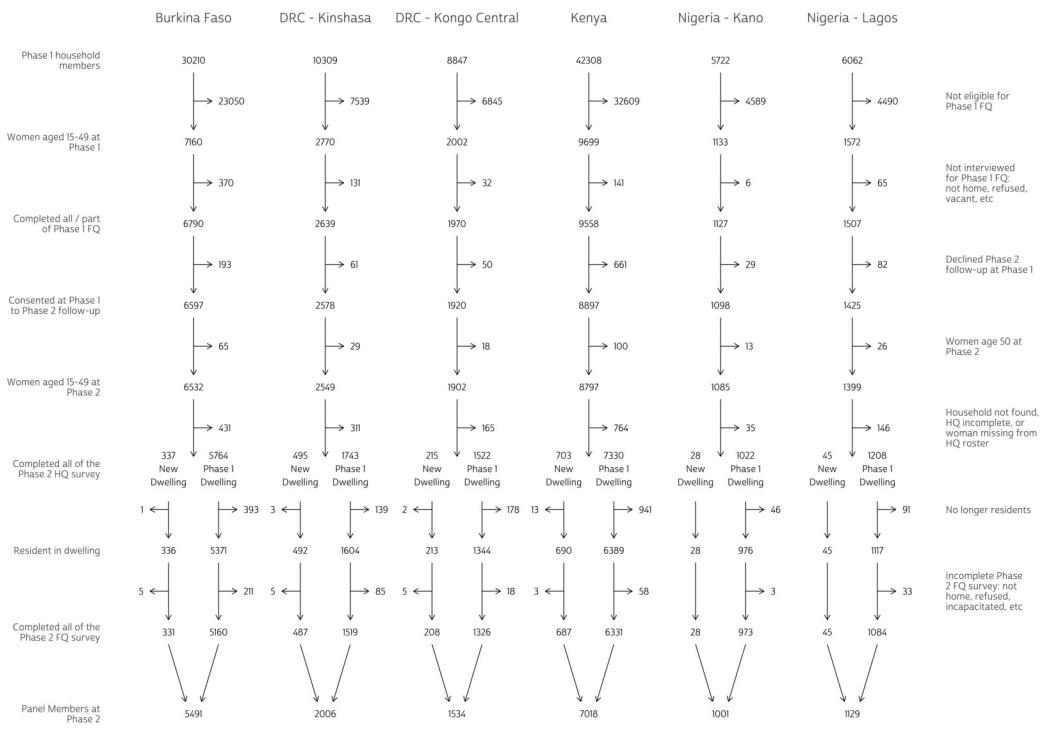
```

```

hjust = case_when(           keep ~ "center",           !keep & !samedw ~ "right",
  TRUE ~ "left"      )      )      dat %>%
ggplot(aes(x = x, y = y)) +      geom_text(
  aes(label = n, hjust = hjust),      size = 3,      family = "cabrito"
) +      geom_segment(      arrow = arrow(length = unit(0.008, "npc")),
  aes(x = x_line1, xend = x_line2, y = y_line1, yend = y_line2),      size = .3
) +      scale_x_continuous(      position = "top",      breaks = 1:6,
  labels = levels(dat$pop)      ) +      scale_y_continuous(
  breaks = if(max(dat$step) == 9){      seq(0, 2*max(dat$step)-1, by = 2)
} else if(max(dat$step) == 1){      1      } else {
  seq(0, 2*max(dat$step)-1, by = 2) + 1      },
  labels = dat %>% filter(keep) %>%
  count(label) %>% pull(label) %>% str_wrap(20),      sec.axis = sec_axis(
  trans = ~.,      breaks = if(max(dat$step) == 9){
    seq(3, 2*max(dat$step)-2, by = 2)      } else if(max(dat$step) == 1){
    NULL      } else {      seq(2, 2*max(dat$step)-1, by = 2)      },
  labels = if(max(dat$step) > 1){
    dat %>% filter(!keep) %>% count(label) %>%
    pull(label) %>% str_wrap(20)      } else {      NULL      }
),      expand = if(max(dat$step) > 4){      expansion(mult = 0.05)
} else {      expansion(mult = 0.3)      } +      theme_minimal() +
theme(      text = element_text(family = "cabrito"),
  axis.ticks = element_blank(),      axis.title = element_blank(),
  axis.text.x = element_text(size = 12),      panel.grid = element_blank(),
  panel.border = element_blank(),      plot.margin = margin(20, 100, 20, 100)
)      }

```

Warning: Removed 6 rows containing missing values (geom_segment).



3.2 SETUP

To get started, we'll need to request a **wide** longitudinal extract from the [IPUMS PMA data website](#). As shown above, we'll select all 6 of the available samples, and choose "All Cases (Respondents and Non-respondents to Household and Female Questionnaires)". Notice that *both phases* are included with each sample when you request a longitudinal extract.

The screenshot shows a web browser window for the IPUMS PMA website. The URL is pma.ipums.org/pma-action/samples. The page title is "IPUMS PMA: select samples". The header includes links for LOG IN, REGISTER, GLOBAL HEALTH, and IPUMS.ORG. Below the header, the IPUMS PMA logo and the text "PERFORMANCE MONITORING FOR ACTION" are displayed, along with links for HOME, SELECT DATA, MY DATA, and SUPPORT.

SELECT SAMPLES

Variable documentation on the web site can be filtered to display only material corresponding to chosen datasets ([more information](#) on this feature).

You may select any of the below datasets for browsing. Please [log in](#) to see which samples you are authorized to include in extracts.

Cross-sectional
 Longitudinal
 Long ⓘ
 Wide ⓘ

SUBMIT SAMPLE SELECTIONS

FAMILY PLANNING - PERSON

Documentation

All Samples (wide)
 Burkina Faso 2020 - 2021
 Congo (Democratic Republic) 2019b - 2020b ⓘ
 2019a - 2020a ⓘ
 Kenya 2019 - 2020
 Nigeria 2019b - 2020b ⓘ
 2019a - 2020a ⓘ

Sample Members

Female Respondents
 Female Respondents and Household Members
 Female Respondents and Female Non-respondents
 All Cases (Respondents and Non-respondents to Household and Female Questionnaires)

SUBMIT SAMPLE SELECTIONS

SUPPORTED BY: [THE BILL & MELINDA GATES FOUNDATION](#), [PMA](#), [STAT/TRANSFER](#), AND [UNIVERSITY OF MINNESOTA](#).

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Variables describing sample composition are located under the “Technical” topics heading. Our extract will contain all of the variables in the “Technical Variables” and “Longitudinal

Panel” subheadings shown:

CURRENTLY BROWSING: "FAMILY PLANNING - PERSON"
CHANGE

SELECT VARIABLES

TOPICS ▾ A-Z ▾ SEARCH 🔎

TECHNICAL ▾ TECHNICAL VARIABLES
DEMOCRAPHICS (WOMEN) ▾ WEIGHTS AND ESTIMATION
FAMILY PLANNING ▾ LONGITUDINAL PANEL
HEALTH
ABORTION
HOUSEHOLD
WATER AND SANITATION
COVID-19

DISPLAY OPTIONS

HELP ⓘ COUNTRY ABBREVIATIONS

DATA CART
YOUR DATA EXTRACT
48 VARIABLES
6 SAMPLES
VIEW CART

MINNESOTA POPULATION CENTER, UNIVERSITY OF MINNESOTA.

Once you’ve finished selecting variables and downloaded an extract, you’ll receive two files: an .xml DDI codebook, and a .dat.gz data file. We’ve saved both of these files in a folder called “data” in our R Working Directory, so we’ll load them into R together with the [tidyverse](#) and [ipumsr](#) packages.

```
library(ipumsr)
library(tidyverse)

dat <- read_ipums_micro(
  ddi = "data/pma_00086.xml",
  data = "data/pma_00086.dat.gz"
)
```

Need help
downloading an
IPUMS PMA data
extract? Check out
our [full](#)
[walkthrough](#).

When you first load your **wide** data extract into R, you’ll notice that most variable names are duplicated: the same variable will appear once with the suffix “1” for Phase 1 variables, and again with the suffix “2” for Phase 2 variables. For example, you’ll find two copies of [SAMPLE](#):

```
dat %>% count(SAMPLE_1)
```

```
# A tibble: 5 × 2
#> #> SAMPLE_1
#> #> <int+lbl> n
#> #> 1 18012 [Congo, Democratic Republic (Kinshasa and Kongo Central) 2019 Baseline] 19245
#> #> 2 40410 [Kenya 2019 Baseline] 42708
#> #> 3 56609 [Nigeria (Kano and Lagos) 2019 Baseline] 12000
#> #> 4 85409 [Burkina Faso 2019 Baseline] 30357
#> #> 5 NA 98687
```

dat %>% count(SAMPLE_2)

```
# A tibble: 5 × 2
#> #> SAMPLE_2
#> #> <int+lbl> n
#> #> 1 18015 [Congo, Democratic Republic (Kinshasa and Kongo Central) 2020 Phase 2] 23186
#> #> 2 40413 [Kenya 2020 Phase 2] 48975
#> #> 3 56612 [Nigeria (Kano and Lagos) 2020 Phase 2] 13227
#> #> 4 85412 [Burkina Faso 2021 Phase 2] 33931
#> #> 5 NA 83678
```

IPUMS PMA combines sub-nationally representative samples for DRC (Kinshasa and Kongo Central) and Nigeria (Kano and Lagos) with one SAMPLE code each. Here, we'll separate those samples and abbreviate country names to ensure that everything fits nicely in our graphics output. We'll also use the same recoded variable for Phase 1 and Phase 2 samples together. Let's call this variable pop (for "population of study").

We'll combine the COUNTRY name for each sample together with the DRC and Nigeria regions shown in GEOCD and GEONG, respectively.

```
# Preview country and region names
dat %>% count(COUNTRY, GEOCD, GEONG)
```

COUNTRY	GEOCD	GEONG	n
1 1 [Burkina Faso]	NA	NA	57990
2 2 [Congo, Democratic Republic]	1 [Kinshasa]	NA	20831
3 2 [Congo, Democratic Republic]	2 [Kongo Central]	NA	17625
4 7 [Kenya]	NA	NA	83645
5 9 [Nigeria]	NA	2 [Lagos]	11936
6 9 [Nigeria]	NA	4 [Kano]	10970

```

# Abbreviate "DRC" and combine `COUNTRY` with `GEOCD` and `GEONG`
dat <- dat %>%
  mutate(
    across(
      c(COUNTRY, GEOCD, GEONG),
      ~as_factor(.x) %>% as.character()
    ),
    COUNTRY = if_else(str_detect(COUNTRY, "Congo"), "DRC", COUNTRY),
    pop = case_when(
      !is.na(GEOCD) ~ paste(COUNTRY, "-", GEOCD),
      !is.na(GEONG) ~ paste(COUNTRY, "-", GEONG),
      TRUE ~ COUNTRY
    )
  )

dat %>% count(pop)

```

```

# A tibble: 6 × 2
  pop                  n
  <chr>              <int>
1 Burkina Faso        57990
2 DRC – Kinshasa     20831
3 DRC – Kongo Central 17625
4 Kenya                83645
5 Nigeria – Kano       10970
6 Nigeria – Lagos      11936

```

3.3 PHASE 1

Phase 1 marks the beginning of the PMA panel study (baseline). As we've mentioned, it consists of two separate questionnaires administered in stages: first, resident enumerators visited 35 household dwellings selected at random within each sample cluster, or [enumeration area](#). If a qualifying respondent was available, they were invited to complete a [Household Questionnaire²⁰](#) including a census of all household members and visitors who stayed there during the night before the interview. If this census included any women aged 15-49, the enumerator would later return to the household and invite each eligible woman to complete a [Female Questionnaire²¹](#) and participate in the three-year panel study.

We'll take a look at the inclusion criteria and missing data codes for each questionnaire, in turn.

²⁰Questionnaires administered in each country may vary from this Core Household Questionnaire - [click here](#) for details.

²¹Questionnaires administered in each country may vary from this Core Female Questionnaire - [click here](#) for details.

3.3.1 Household Questionnaire

In our **wide** data extract, each **PANELWOMAN** is a woman who completed all or part of the Phase 1 Female Questionnaire and agreed to participate in the longitudinal panel study: as a result, you'll find all of her Phase 1 responses and her Phase 2 responses together in *a single row*.

This is *not* the case for household members who are not, themselves, participants in the panel study. These household members are represented by *one row per phase*. For example, if a young child was listed on the Phase 1 Household Questionnaire, you'll find details about their age in **AGEHQ_1**, their sex in **SEX_1**, and their relationship to the head of household in **RELATE_1**. If you look in the same row for corresponding Phase 2 variables (**AGEHQ_2**, **SEX_2**, and **RELATE_2**), you'll find NA values even if the child still lived in the household at Phase 2: their Phase 2 data may be located in another row (with NA values listed for Phase 1), or it may not exist if the child was not listed on the Phase 2 household roster. It is not possible to link Phase 1 and Phase 2 responses for household members who were not participants in the panel study.

This explains why, for example, you'll see a large number of NA values in **RESULTHQ_1**, which gives the result of the Phase 1 Household Questionnaire.

```
dat %>% count(RESULTHQ_1)
```

# A tibble: 10 × 2	
	n
1	1 [Completed]
2	2 [Not at home]
3	3 [Postponed]
4	4 [Refused]
5	5 [Partly completed]
6	6 [Vacant or not a dwelling]
7	7 [Destroyed]
8	8 [Not found]
9	9 [Absent extended period]
10	NA

Close to half of the values in **RESULTHQ_1** are NA: these are household members for whom no linked Phase 2 data exists.

What about the other values in **RESULTHQ_1**? You'll notice a range of outcomes including:

- 1 - Completed
- 5 - Partly completed
- several other codes giving the reason why no household interview occurred

If no household interview occurred, PMA creates one row to represent the household in RESULTHQ_1. Otherwise, if the household roster was completed during the interview, PMA creates one row for each person on the roster.

In order to determine the proportion of households that completed all or part of the Household Questionnaire - or any other **household-level statistics** - you must count only one row per household. Each Phase 1 household receives a unique identifier in HHID_1 - this value is an empty string "" for household members included only in Phase 2. All Phase 1 households have a unique HHID_1, regardless of the outcome recorded in RESULTHQ_1.

Therefore, you can use group_by to find the RESULTHQ_1 outcome for each household via HHID_1. To obtain the proportion of Phase 1 households that completed all or part of the questionnaire, we'll first use filter to drop Phase 2 households with the value "". Then, we'll use slice to include only the first row in each household. Finally, we'll count the number of fully (code 1) or partly (code 5) completed questionnaires in RESULTHQ_1 - the base R function prop.table derives proportions for these counts.

```
dat %>%
  filter(HHID_1 != "") %>% # drop Phase 2 households
  group_by(HHID_1) %>%
  slice(1) %>% # include only the first row in each household
  ungroup() %>%
  count(RESULTHQ_1 %in% c(1, 5)) %>% # how many households completed all / part?
  mutate(prop = prop.table(n))
```

```
# A tibble: 2 × 3
`RESULTHQ_1 %in% c(1, 5)`     n    prop
<lgl>                      <int>  <dbl>
1 FALSE                      852  0.0365
2 TRUE                       22494 0.964
```

Conversely, it is often useful to exclude non-interviewed households when calculating **person-level statistics**. In the first row of our CONSORT diagram above, we drop these households before we count the total number of sampled Phase 1 household members.

```
dat %>%
  filter(RESULTHQ_1 %in% c(1, 5)) %>%
  count(pop)
```

Across samples,
96.4% of
households
completed all or
part of the Phase 1
Household
Questionnaire.

```

# A tibble: 6 × 2
  pop                  n
  <chr>             <int>
1 Burkina Faso      30210
2 DRC - Kinshasa    10309
3 DRC - Kongo Central 8847
4 Kenya              42308
5 Nigeria - Kano    5722
6 Nigeria - Lagos   6062

hh <- dat

# Step 1: Household members at Phase 1
hh <- hh %>% group_by(pop) %>% mutate(step = 1, keep = RESULTHQ_1 %in% c(1, 5))
hh_plot <- hh %>%
  filter(keep) %>%
  count(step, keep) %>%
  mutate(
    samedw = NA,
    label = "Phase 1 household members"
  )

consort(hh_plot)

```

Warning: Removed 6 rows containing missing values (geom_segment).

	Burkina Faso	DRC - Kinshasa	DRC - Kongo Central	Kenya	Nigeria - Kano	Nigeria - Lagos
Phase 1 household members	30210	10309	8847	42308	5722	6062

3.3.2 Female Questionnaire

IPUMS PMA uses a **non-response code** labeled “Not interviewed (household questionnaire)” for variables related to questions that were only relevant if the Household Questionnaire was fully or partly completed. This includes ELIGIBLE_1, which indicates whether a particular household member was a woman aged 15-49 at Phase 1, and therefore eligible for the Phase 1 Female Questionnaire. If the household was not interviewed, eligibility for the Female Questionnaire could not be determined.

```
dat %>% count(RESULTHQ_1, ELIGIBLE_1)
```

# A tibble: 12 × 3		
RESULTHQ_1	ELIGIBLE_1	n
<int+lbl>	<int+lbl>	<int>
1 1 [Completed]	0 [No]	79091
2 1 [Completed]	1 [Yes, eligible female respondent]	24320
3 2 [Not at home]	96 [Not interviewed (household questionnaire)]	210
4 3 [Postponed]	96 [Not interviewed (household questionnaire)]	8
5 4 [Refused]	96 [Not interviewed (household questionnaire)]	230
6 5 [Partly completed]	0 [No]	31
7 5 [Partly completed]	1 [Yes, eligible female respondent]	16
8 6 [Vacant or not a dwelling]	96 [Not interviewed (household questionnaire)]	95
9 7 [Destroyed]	96 [Not interviewed (household questionnaire)]	10
10 8 [Not found]	96 [Not interviewed (household questionnaire)]	3
11 9 [Absent extended period]	96 [Not interviewed (household questionnaire)]	296
12 NA	NA	98687

RESULTFQ_1 shows the result of the Female Questionnaire for eligible women. The **non-response code** “NIU (not in universe)” is used for household members who were not eligible.

```
dat %>% count(RESULTFQ_1)
```

# A tibble: 9 × 2		
RESULTFQ_1		n
<int+lbl>		<int>
1 1 [Completed]		23542
2 2 [Not at home]		427
3 3 [Postponed]		20
4 4 [Refused]		150
5 5 [Partly completed]		49
6 10 [Incapacitated]		145
7 96 [Not interviewed (household questionnaire)]		852
8 99 [NIU (not in universe)]		79124
9 NA		98687

You can calculate the proportion of eligible women who completed the Phase 1 Female Questionnaire like so:

```
dat %>%
  filter(ELIGIBLE_1 == 1) %>% # drops ineligible / Phase 2 household members
  count(RESULTFQ_1 %in% c(1, 5)) %>%
  mutate(prop = prop.table(n))

# A tibble: 2 × 3
`RESULTFQ_1 %in% c(1, 5)`   n    prop
<lgl>                      <int> <dbl>
1 FALSE                     745  0.0306
2 TRUE                      23591 0.969
```

Our CONSORT diagram shows the total number of women who were eligible to participate in the panel study at Phase 1, after excluding women who:

- were members of a household where no Phase 1 Household Questionnaire was administered
- were not eligible (aged 15-49)
- did not complete at least part of the Phase 1 Female Questionnaire

Across samples,
96.9% of eligible
women completed
the Phase 1 Female
Questionnaire.

```
dat %>%
  filter(RESULTFQ_1 %in% c(1, 5)) %>%
  count(pop)
```

```
# A tibble: 6 × 2
pop                  n
<chr>                <int>
1 Burkina Faso       6790
2 DRC – Kinshasa     2639
3 DRC – Kongo Central 1970
4 Kenya                 9558
5 Nigeria – Kano      1127
6 Nigeria – Lagos     1507
```

If you select a data extract with “Female Respondents” rather than “All cases”, you will receive only records for women who completed all or part of the Female Questionnaire in at least one phase. See

```
# Step 2: HH members Eligible at Phase 1
```

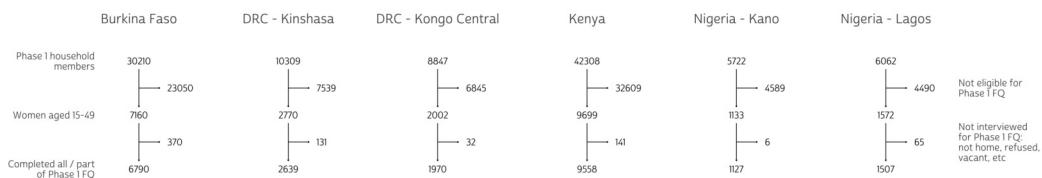
our [last post](#) for details.

```
hh <- hh %>% filter(keep) %>% mutate(step = 2, keep = ELIGIBLE_1 == 1)
hh_plot <- hh %>%
  count(step, keep) %>%
  mutate(label = if_else(
    keep,
    "Women aged 15-49",
    "Not eligible for Phase 1 FQ"
  )) %>%
  bind_rows(hh_plot)

# Step 3: Result of Phase 1 FQ
hh <- hh %>% filter(keep) %>% mutate(step = 3, keep = RESULTFQ_1 %in% c(1, 5))
hh_plot <- hh %>%
  count(step, keep) %>%
  mutate(label = if_else(
    keep,
    "Completed all / part of Phase 1 FQ",
    "Not interviewed for Phase 1 FQ: not home, refused, vacant, etc"
  )) %>%
  bind_rows(hh_plot)

consort(hh_plot)
```

Warning: Removed 6 rows containing missing values (geom_segment).



Enumerators invited these women to participate in Phase 2 of the panel study one year later. Only women who agreed to participate at that time are considered panel members at Phase 2, as shown in [PANELWOMAN_2](#).²²

Their responses to the panel invitation are recorded in [SURVEYWILLING_1](#). IPUMS PMA uses the **non-response code** “Not interviewed (female questionnaire)” to indicate women who were eligible, but not interviewed for the Female Questionnaire as shown in [RESULTFQ_1](#). Additionally, “No response or missing” is used for women who did not respond to the panel invitation.

²²Women who completed the Phase 1 Female Questionnaire but declined to participate in the panel were given an opportunity to join the panel again at Phase 2 (if eligible). They are not panel members as shown in [PANELWOMAN_2](#), but they may be listed as such in [PANELWOMAN_3](#) if they agree to participation in the panel going forward.

```
dat %>% count(SURVEYWILLING_1)
```

```
# A tibble: 7 × 2
  SURVEYWILLING_1      n
  <int+lbl>        <int>
1 0 [No]            1023
2 1 [Yes]           22515
3 95 [Not interviewed (female questionnaire)]    743
4 96 [Not interviewed (household questionnaire)]  852
5 98 [No response or missing]                  53
6 99 [NIU (not in universe)]                 79124
7 NA                98687
```

You should include “No response or missing” cases when calculating the proportion of Phase 1 female respondents who agreed to participate in the panel follow-up:

```
dat %>%
  filter(RESULTFQ_1 %in% c(1, 5)) %>% # Drops NIU and Not interviewed cases
  count(SURVEYWILLING_1) %>%
  mutate(prop = prop.table(n))
```

```
# A tibble: 3 × 3
  SURVEYWILLING_1      n     prop
  <int+lbl>        <int>   <dbl>
1 0 [No]            1023  0.0434
2 1 [Yes]           22515 0.954
3 98 [No response or missing] 53  0.00225
```

Across samples,
95.4% of women
who completed the
Phase 1 Female
Questionnaire
agreed to
participate in panel
follow-ups one year
later.

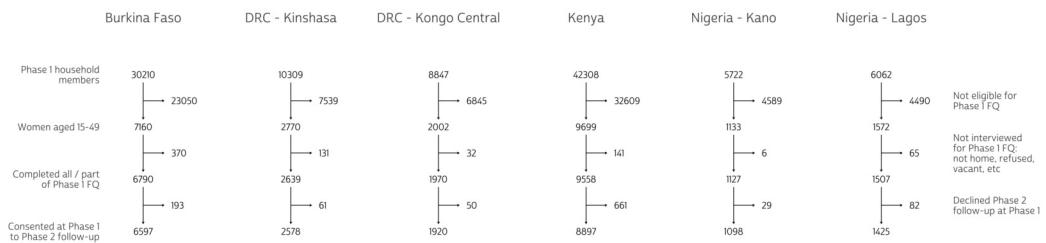
```

# Step 4: Willing to participate in Phase 2
hh <- hh %>% filter(keep) %>% mutate(step = 4, keep = SURVEYWILLING_1 == 1)
hh_plot <- hh %>%
  count(step, keep) %>%
  mutate(label = if_else(
    keep,
    "Consented at Phase 1 to Phase 2 follow-up",
    "Declined Phase 2 follow-up at Phase 1"
  )) %>%
  bind_rows(hh_plot)

consort(hh_plot)

```

Warning: Removed 6 rows containing missing values (geom_segment).



3.4 PHASE 2

Both questionnaires were administered again in Phase 2, approximately one year later. Resident enumerators visited the same dwellings where Phase 1 interviews occurred; if the woman's household had moved elsewhere within the study area,²³ enumerators used local contacts to find its new location. If found, they administered a Household Questionnaire including an updated household roster.

As we've mentioned, any woman aged 15-49 listed on the Phase 2 household roster was eligible to complete a Phase 2 Female Questionnaire. However, only women who completed all or part of a Phase 1 Female Questionnaire are considered members of the panel in [PANELWOMAN_2](#).

²³The “study area” is area within which resident enumerators should attempt to find panel women that have moved out of their Phase 1 dwelling. This may extend beyond the woman’s original EA as determined by in-country administrators - see [PMA Phase 2 and Phase 3 Survey Protocol](#) for details.

3.4.1 Household Questionnaire

Several variables are available to describe the [status of households](#) surveyed at Phase 2. As with Phase 1, [RESULTHQ_2](#) describes the result of the Phase 2 Household Questionnaire.

```
dat %>% count(RESULTHQ_2)
```

RESULTHQ_2	n
<int+lbl>	<int>
1 1 [Completed]	116955
2 2 [Not at home]	298
3 3 [Postponed]	15
4 4 [Refused]	425
5 5 [Partly completed]	16
6 6 [Vacant or not a dwelling]	861
7 7 [Destroyed]	227
8 8 [Not found]	209
9 9 [Absent extended period]	313
10 NA	83678

[SAMEDWELLING_2](#) indicates whether the Household Questionnaire was administered at the same physical dwelling from Phase 1, or whether the enumerator located the woman's household in a new dwelling.

```
dat %>% count(SAMEDWELLING_2)
```

SAMEDWELLING_2	n
<int+lbl>	<int>
1 0 [No]	7255
2 1 [Yes]	110973
3 95 [Not interviewed (female questionnaire)]	15
4 96 [Not interviewed (household questionnaire)]	19
5 99 [NIU (not in universe)]	1057
6 NA	83678

Each Phase 2 sample may also include new households that were not included in Phase 1, as indicated by [HHTYPE_2](#): these are replacement households drawn for enumeration areas where more than 10% of Phase 1 households were no longer present. They account for all of the **non-response code** shown in [SAMEDWELLING_2](#), as no prior dwelling was sampled.

```
dat %>% count(SAMEDWELLING_2, HHTYPE_2)
```

# A tibble: 6 × 3		
SAMEDWELLING_2	HHTYPE_2	n
<int+lbl>	<int+lbl>	<int>
1 0 [No]	3 [Panel woman followup]	7255
2 1 [Yes]	1 [Phase 1 Dwelling]	110973
3 95 [Not interviewed (female questionnaire)]	2 [Replacement cross-section]	15
4 96 [Not interviewed (household questionnaire)]	2 [Replacement cross-section]	19
5 99 [NIU (not in universe)]	2 [Replacement cross-section]	1057
6 NA	NA	83678

As mentioned above, it is not possible to link Phase 1 and Phase 2 records for household members who were not women participating in the panel study. However, the variable HHMEMSTAT_2 does describe whether a Phase 1 household member was listed on the household roster for Phase 2; if not, PMA creates a Phase 2 record for that person indicating whether they moved or were deceased.

```
dat %>% count(HHMEMSTAT_2)
```

# A tibble: 10 × 2		
HHMEMSTAT_2	n	
<int+lbl>	<int>	
1 1 [Still a resident in household]	84402	
2 2 [Moved within EA]	1155	
3 3 [Moved outside of EA]	4815	
4 4 [Moved out of household for school]	1117	
5 5 [Deceased]	437	
6 95 [Not interviewed (female questionnaire)]	213	
7 96 [Not interviewed (household questionnaire)]	2337	
8 97 [Don't know]	30	
9 99 [NIU (not in universe)]	24813	
10 NA	83678	

After excluding women who reached age 50 at Phase 2, our CONSORT diagram diverges to show whether panel members were found in their Phase 1 dwelling or a new one. Women whose household was not found in the study area are considered **lost to follow-up**, as are those where the Phase 2 Household Questionnaire was not completed.

The variable HHPANELP2_2 indicates whether any woman who completed the Phase 1 Female Questionnaire was living in the dwelling at Phase 2. Women who were no longer residents of the household are also considered **lost to follow-up**.

```
dat %>% count(HHPANELP2_2)
```

```
# A tibble: 3 × 2
HHPANELP2_2      n
<int+lbl> <int>
1 0 [No]     29587
2 1 [Yes]    89732
3 NA        83678
```

```

# Step 5: Aged out
hh <- hh %>% filter(keep) %>% mutate(step = 5, keep = AGE_1 < 49)
hh_plot <- hh %>%
  count(step, keep) %>%
  mutate(label = if_else(
    keep,
    "Women aged 15–49 at Phase 2",
    "Women age 50 at Phase 2"
  )) %>%
  bind_rows(hh_plot)

# Step 6: Same dwelling
hh <- hh %>%
  filter(keep) %>%
  mutate(
    step = 6,
    keep = RESULTHQ_2 %in% 1,
    samedw = SAMEDWELLING_2 %in% 1
  ) %>%
  group_by(pop, samedw)
hh_plot <- hh %>%
  mutate(samedw = ifelse(!keep, TRUE, samedw)) %>%
  count(step, keep) %>%
  mutate(
    n = case_when(
      keep & samedw ~ paste(n, "Phase 1", "Dwelling", sep = "\n"),
      keep & !samedw ~ paste(n, "New", "Dwelling", sep = "\n"),
      !keep ~ as.character(n)
    ),
    label = if_else(
      keep,
      "Completed all of the Phase 2 HQ survey",
      "Household not found, HQ incomplete, or woman missing from HQ roster"
    )
  ) %>%
  bind_rows(hh_plot %>% mutate(n = as.character(n)))

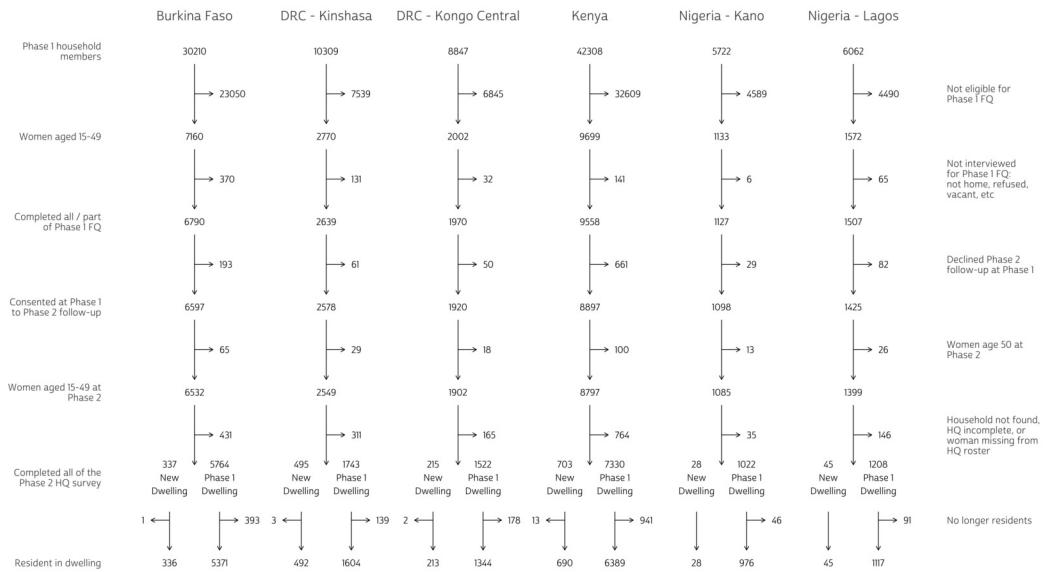
# Step 7: Resident in dwelling
hh <- hh %>% filter(keep) %>% mutate(step = 7, keep = HHMEMSTAT_2 %in% c(1, 99))
hh_plot <- hh %>%
  count(step, keep) %>%
  mutate(
    n = as.character(n),
    label = if_else(
      keep,
      "Resident in dwelling",
      "No longer residents"
    )
  ) %>%

```

`bind_rows(hh_plot)`

`consort(hh_plot)`

Warning: Removed 12 rows containing missing values (geom_segment).



3.4.2 Female Questionnaire

Finally, eligible women who were found in a household at Phase 2 were invited to complete a Female Questionnaire. `RESULTFQ_2` indicates the result of the Phase 2 Female Questionnaire both for panel members and women who were otherwise eligible to participate.

```
dat %>% count(RESULTFQ_2)
```

RESULTFQ_2	n
<int+lbl>	<int>
1 1 [Completed]	24756
2 2 [Not at home]	343
3 3 [Postponed]	40
4 4 [Refused]	278
5 5 [Partly completed]	24
6 7 [Respondent moved]	57
7 10 [Incapacitated]	241
8 95 [Not interviewed (female questionnaire)]	9
9 96 [Not interviewed (household questionnaire)]	2337
10 99 [NIU (not in universe)]	91234
11 NA	83678

You can find the proportion of women who completed the Phase 2 Female Questionnaire that were also available at Phase 1 (i.e. panel members) like so:

```
dat %>%
  filter(RESULTFQ_2 == 1) %>%
  count(PANELWOMAN_2) %>%
  mutate(prop = prop.table(n))
```

PANELWOMAN_2	n	prop
<int+lbl>	<int>	<dbl>
1 0 [No]	6576	0.266
2 1 [Yes]	18180	0.734

Wide data extracts make it particularly easy to combine Phase 1 and Phase 2 variables for the same woman. Note that potential panel members were identified at Phase 1: they are women who agreed to participate in `SURVEYWILLING_1` and were under age 49 in `AGE_1`. In order to calculate the proportion of potential panel members who ultimately completed the Female Questionnaire at Phase 2, you must include Phase 1 female respondents for whom no Phase 2 data exists.

Across samples, Phase 1 data are available for 73.4% of women who completed the Phase 2 Female Questionnaire.

26.6% of these women are newcomers at Phase 2.

These cases are marked NA in `RESULTFQ_2`, so they are easily included like so:

```
dat %>%
  filter(SURVEYWILLING_1 == 1 & AGE_1 < 49) %>%
  count(RESULTFQ_2 == 1) %>%
  mutate(prop = prop.table(n))
```

```
# A tibble: 3 × 3
`RESULTFQ_2 == 1`     n    prop
<lgl>                 <int>  <dbl>
1 FALSE                2452  0.110
2 TRUE                 18180 0.817
3 NA                   1632  0.0733
```

The final row of our CONSORT diagram shows the total number of completed Phase 2 Female Questionnaires for each sample. The totals below match the results reported in each of the PMA User Guides published for individual samples.

Across samples,
81.7% of potential
panel members
completed the
Phase 2 Female
Questionnaire.

```
dat %>%
  group_by(pop) %>%
  # denominator: potential panel members at Phase 1
  filter(SURVEYWILLING_1 == 1 & AGE_1 < 49) %>%
  # numerator: did a potential panel member complete Phase 2 FQ?
  count(final = RESULTFQ_2 == 1) %>%
  mutate(prop = prop.table(n)) %>%
  # drop members who did not compete Phase 2 FQ / no record in Phase 2
  filter(final) %>%
  select(-final)
```

```
# A tibble: 6 × 3
# Groups:   pop [6]
pop                  n    prop
<chr>                <int>  <dbl>
1 Burkina Faso        5491  0.841
2 DRC – Kinshasa      2006  0.787
3 DRC – Kongo Central 1534  0.807
4 Kenya                7018  0.798
5 Nigeria – Kano       1001  0.923
6 Nigeria – Lagos      1130  0.808
```

```

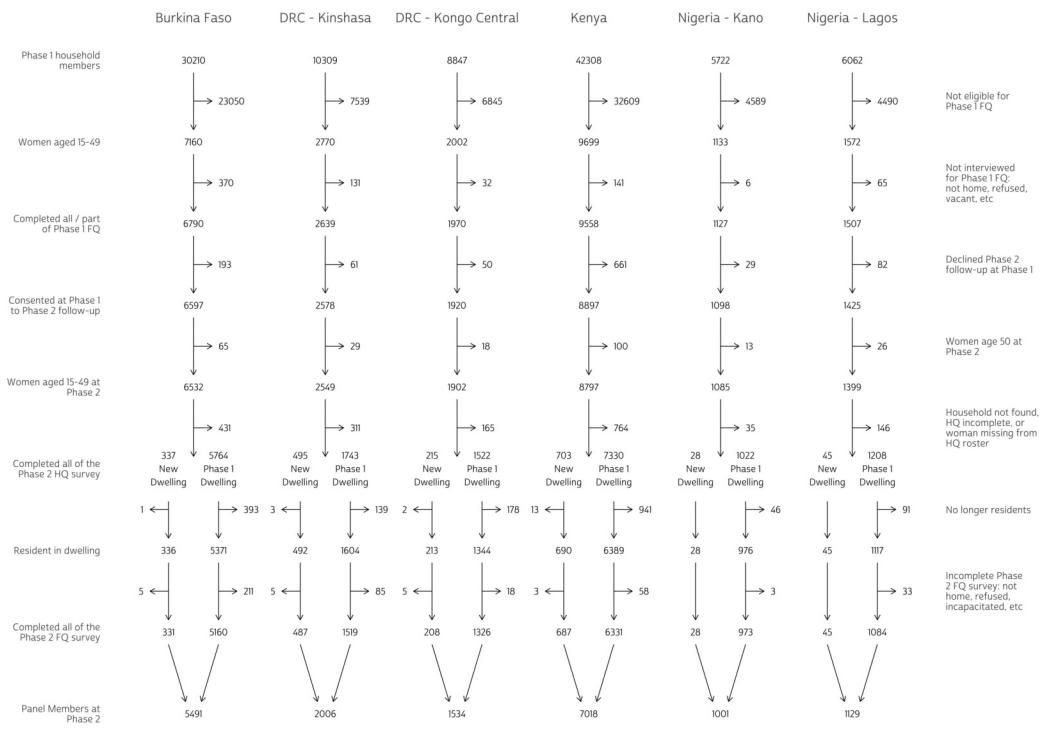
# Step 8: Result of Phase 2 FQ
hh <- hh %>% filter(keep) %>% mutate(step = 8, keep = RESULTFQ_2 == 1)
hh_plot <- hh %>%
  count(step, keep) %>%
  mutate(
    n = as.character(n),
    label = if_else(
      keep,
      "Completed all of the Phase 2 FQ survey",
      "Incomplete Phase 2 FQ survey: not home, refused, incapacitated, etc"
    )
  ) %>%
  bind_rows(hh_plot)

# Step 9: Final diagram
hh <- hh %>% filter(keep) %>% mutate(step = 9, keep = TRUE)
hh_plot <- hh %>%
  group_by(pop) %>%
  count(step, keep) %>%
  mutate(
    n = as.character(n),
    label = "Panel Members at Phase 2"
  ) %>%
  bind_rows(hh_plot)

consort(hh_plot)

```

Warning: Removed 6 rows containing missing values (geom_segment).



3.5 SUMMARY

There are ultimately several causes of **loss to follow-up** that may occur at different time points throughout the panel study. An individual is considered **lost to follow-up** if:

1. The household moved out of the Phase 1 dwelling, and the new dwelling could not be located within the study area
2. The Phase 2 Household Questionnaire was not completed (a respondent refused, was not available, etc)
3. A panel member from the household was no longer a resident (deceased, moved, or status unknown)
4. A panel member did not complete a Phase 2 Household Questionnaire (she refused, was not available, etc)

At the same time, the **open panel design** allows new participants to complete a Female Questionnaire at any phase. These women are not panel members at Phase 2, but they may become panel members at Phase 3 if they are eligible and agree to complete a forthcoming Phase 3 Female Questionnaire. Women can join the panel at Phase 2, for example, if they:

1. Reach age 15 only after Phase 1 interviews were completed
2. Move into a household sampled at Phase 2

For more details on sample design, check out the IPUMS PMA [sample notes](#) and User Guides published for individual samples at [pmadata.org](#).

4 POST 4

We've mentioned in previous posts in [this series](#) that data from the new [PMA panel study](#) gives researchers an important tool for understanding how women's family planning demand and utilization changes over time. In particular, PMA surveys cover topics like:

- pregnancy intentions and outcomes
- current use of long-acting, short-acting, and traditional contraceptives
- discontinuation of family planning
- intentions for future use of family planning
- unmet need for family planning
- partner's support for use of family planning

IPUMS PMA recently released **harmonized data** from four of the participating countries where the first two phases of data collection in this three-year panel study have already been completed. In this post, we'll demonstrate how to use an [IPUMS PMA data extract](#) to calculate and compare key family planning indicators across multiple samples.

Our partners at PMA have published indicators for each of these samples, individually. Phase 2 panel results summaries are available for:

- [Burkina Faso](#)
- [DRC - Kinshasa](#)
- [DRC - Kongo Central](#)
- [Kenya](#)
- [Nigeria - Kano](#)
- [Nigeria - Lagos](#)

Here, we'll share code you can use to reproduce the findings in each report, and we'll demonstrate one simple approach to visualizing indicators across samples with [ggplot2](#), a popular graphics package included in the [tidyverse](#) toolkit for R.

Interested in building the [alluvial plots](#) seen in these reports? Join us again in two weeks, when we'll dig into the [ggalluvial](#) package!

4.1 SETUP

To get started, you'll need to load three main packages:

- [tidyverse](#), which includes [ggplot2](#) and other data manipulation tools
- [ipumsr](#) for working with IPUMS data
- [srvyr](#) for use of survey design information (survey weights and sample cluster IDs)

```
library(tidyverse)  
library(ipumsr)  
library(srvyr)
```

[srvyr](#) brings
[tidyverse](#) syntax to
the popular [survey](#)
package.

We'll feature data organized in **wide format** for each of the six samples currently available from IPUMS PMA. You'll find the "wide" option under the "Longitudinal" sample button on our [Select Samples](#) page.

IPUMS PMA also
publishes panel
data in **long format**.
Check out our
complete [guide to
longitudinal data
extracts](#) for details.

The screenshot shows a web browser window for the IPUMS PMA website at pma.ipums.org/pma-action/samples. The page title is "IPUMS PMA: select samples". The header includes links for LOG IN, REGISTER, GLOBAL HEALTH, and IPUMS.ORG. The main navigation bar has links for HOME, SELECT DATA, MY DATA, and SUPPORT. The main content area is titled "SELECT SAMPLES". It contains a note about variable documentation filtering and a message about selecting datasets for browsing. A "SUBMIT SAMPLE SELECTIONS" button is visible. Below this, there are two sections: "FAMILY PLANNING - PERSON" and "Documentation". The "Documentation" section lists various sample types and years, many of which are checked. At the bottom, there is a "Sample Members" section with radio buttons for "Female Respondents", "Female Respondents and Household Members", "Female Respondents and Female Non-respondents", and "All Cases (Respondents and Non-respondents to Household and Female Questionnaires)". Another "SUBMIT SAMPLE SELECTIONS" button is located here. At the very bottom, there is a footer note about support from The Bill & Melinda Gates Foundation, PMA, STAT/TRANSFER, and the University of Minnesota.

Notice that, under “Sample Members”, we’ve selected the button for “Female Respondents”. This excludes records for all household members who are not, themselves, members of the

panel study. You'll find one row for each woman who completed all or part of the Female Questionnaire for at least one phase of the study.

Add the following variables to your Data Cart, then click the [View Cart](#) button to begin checkout ([preselected](#) variables are added automatically).

For details on panel enrollment and loss to follow-up, see our [panel membership](#) guide.

- [RESULTFQ](#) - Result of female questionnaire
- [PANELWEIGHT](#) - Phase 2 female panel weight
- [RESIDENT](#) - Household residence / membership
- [AGE](#) - Age in female questionnaire
- [PREGNANT](#) - Pregnancy status
- [BIRTHEVENT](#) - Number of birth events
- [EDUCATTGEN](#) - Highest level of school attended (4 categories)
- [MARSTAT](#) - Marital status
- [GEOCD](#) - Province, DRC
- [GEONG](#) - State, Nigeria
- [CP](#) - Contraceptive user
- [FPCURREFFMETHRC](#) - Most effective current FP method
- [UNMETYN](#) - Total unmet need
- [FPPARTSUPPORT](#) - Husband / partner would be supportive of FP use
- [FPPLANVAL](#) - When will start using FP method in the future - value
- [FPPLANWHEN](#) - When will start using FP method in the future - unit
- [COUNTRY](#) - PMA country (preselected)
- [EAID](#) - Enumeration area (preselected)

Before completing checkout, make sure that you've selected the dat data format (fixed-width text).

The screenshot shows a web browser window for the IPUMS PMA website. The URL is pma.ipums.org/pma-action/extract_requests/summary?. The page title is "IPUMS PMA". The main heading is "EXTRACT REQUEST ([HELP](#))". Below it is a table of extract details:

SAMPLES:	6	(show)	Change
VARIABLES:	28	(show)	Change
DATA FORMAT:	.dat (fixed-width text)	Change	←
STRUCTURE:	Rectangular (longitudinal - wide)	Change	
SAMPLE MEMBERS:	Female Respondents	Change	
ESTIMATED SIZE:	26.0 MB		

Below the table is a text input field labeled "Describe your extract" with a placeholder text area. At the bottom is a purple "SUBMIT EXTRACT" button.

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Finally, you'll need to download 2 files: an `xml` metadata file and a `dat.gz` compressed data file. We've saved both of these files in the “data” folder in R's working directory, so we'll import both to create a dataframe called `dat`:

```
dat <- read_ipums_micro(  
  ddi = "data/pma_00106.xml",  
  data = "data/pma_00106.dat.gz"  
)
```

4.2 POPULATIONS OF INTEREST

We've mentioned in previous posts that PMA samples are only valid for the [de facto](#) population: these are women who slept in the household during the night before the interview for the Household Questionnaire in both phases. These women are coded either 11 or 22 in both RESIDENT_1 and RESIDENT_2.

```
dat <- dat %>% filter(RESIDENT_1 %in% c(11, 22) & RESIDENT_2 %in% c(11, 22))
```

We also mentioned in our [sample membership guide](#) that women who completed the Phase 1 Female Questionnaire may have been [lost to follow-up](#) at Phase 2. As a reminder, we'll need to drop any cases where RESULTFQ_2 is not coded 1 for "completed".

```
dat <- dat %>% filter(RESULTFQ_2 == 1)
```

Additionally, a small number of women in each sample elected not to respond to key questions regarding current use of contraceptives. These cases are coded 90 and above, as shown on the [CP](#) Codes tab. In a [wide](#) extract, these cases can be identified with CP_1 and CP_2.

```
dat <- dat %>% filter(CP_1 < 90, CP_2 < 90)
```

Finally, recall that only the Burkina Faso and Kenya samples are [nationally representative](#). Samples from DRC represent regions identified by [GEOCD](#), while samples from Nigeria represent regions identified by [GEONG](#). In order to distinguish each population of interest, we'll define a custom variable POP that shows each sample's [COUNTRY](#) label concatenated with each of these regions where appropriate.

- POP - Population of interest

```
dat <- dat %>%
  mutate(POP = case_when(
    !is.na(GEOCD) ~ paste("DRC -", as_factor(GEOCD)),
    !is.na(GEONG) ~ paste("Nigeria -", as_factor(GEONG)),
    TRUE ~ as_factor(COUNTRY) %>% as.character()
  ))
```

The remaining sample size for each population of interest is simply a [count](#) of each level in POP.

```
dat %>% count(POP)
```

```
# A tibble: 6 × 2
  POP                  n
  <chr>              <int>
1 Burkina Faso      5207
2 DRC - Kinshasa    1967
3 DRC - Kongo Central 1511
4 Kenya               6934
5 Nigeria - Kano     998
6 Nigeria - Lagos   1088
```

4.3 POPULATION INFERENCE

We'll use the [svy](#) package to incorporate survey design information into each of the population estimates calculated below. This includes [PANELWEIGHT](#), which represents the calculated inverse selection probability for all panel members, adjusted for loss to follow-up.

You might remember from [earlier posts](#) that PMA surveys are collected within spatially-defined **sample clusters**. We'll also include identifying numbers for each cluster as survey design information via [EAID](#). Here, we'll use clusters identified in EAID_1.²⁴

Most PMA samples are also collected within separate strata indicated by [STRATA](#). We've [previously noted](#) that STRATA is *not available* for samples collected from DRC - Kinshasa and DRC - Kongo Central, so we demonstrated how to create placeholder codes for those samples in a variable we called [STRATA_RECODE](#). To review: STRATA_RECODE uses unique numeric codes from STRATA, except that it also includes unique identifiers for each sampled region in GEOCD.

```
dat <- dat %>%
  mutate(
    STRATA_RECODE = if_else(
      is.na(GEOCD),
      as.numeric(STRATA_1),
      as.numeric(GEOCD)
    )
  )

dat %>% count(STRATA_1, GEOCD, STRATA_RECODE)
```

²⁴Because women are considered “lost to follow-up” if they moved outside the study area, EAID_1 and EAID_2 are identical for all panel members; you can use either one to identify sample clusters.

	# A tibble: 28 × 4	STRATA_1	GEOCD	STRATA_RECODE	n
		<int+lbl>	<int+lbl>	<dbl>	<int>
1	40410 [Bungoma - urban, Kenya]	NA		40410	153
2	40411 [Bungoma - rural, Kenya]	NA		40411	488
3	40412 [Kakamega - urban, Kenya]	NA		40412	133
4	40413 [Kakamega - rural, Kenya]	NA		40413	438
5	40414 [Kericho - urban, Kenya]	NA		40414	249
6	40415 [Kericho - rural, Kenya]	NA		40415	453
7	40416 [Kiambu - urban, Kenya]	NA		40416	213
8	40417 [Kiambu - rural, Kenya]	NA		40417	311
9	40418 [Kilifi - urban, Kenya]	NA		40418	170
10	40419 [Kilifi - rural, Kenya]	NA		40419	455
11	40420 [Kitui - urban, Kenya]	NA		40420	153
12	40421 [Kitui - rural, Kenya]	NA		40421	585
13	40422 [Nairobi - urban, Kenya]	NA		40422	493
14	40423 [Nandi - urban, Kenya]	NA		40423	260
15	40424 [Nandi - rural, Kenya]	NA		40424	711
16	40425 [Nyamira - urban, Kenya]	NA		40425	143
17	40426 [Nyamira - rural, Kenya]	NA		40426	382
18	40427 [Siaya - urban, Kenya]	NA		40427	130
19	40428 [Siaya - rural, Kenya]	NA		40428	437
20	40429 [West Pokot - urban, Kenya]	NA		40429	104
21	40430 [West Pokot - rural, Kenya]	NA		40430	473
22	56606 [Lagos, Nigeria]	NA		56606	1088
23	56611 [Kano - Urban]	NA		56611	437
24	56612 [Kano - Rural]	NA		56612	561
25	85401 [Urban, Burkina Faso]	NA		85401	3053
26	85402 [Rural, Burkina Faso]	NA		85402	2154
27	NA	1 [Kinshasa]		1	1967
28	NA	2 [Kongo Central]		2	1511

The `svydesign` function allows us to pass the information in PANELWEIGHT, EAID_1, and STRATA_RECODE to other package functions like `survey_mean`. We'll also demonstrate how to use this information in formal significance tests within each sample via `svychisq`.

Let's begin with a simple example. The variable `CP` indicates whether a woman was currently using any family planning method. The variables `CP_1` and `CP_2` in our `wide` extract represent responses collected at Phase 1 and Phase 2, respectively. With help from `svydesign`, we'll obtain a population-level estimate of the proportion of women who were using a method at Phase 2, given their status at Phase 1.

Check out [this post](#) for more information on PMA survey design and the `svydesign` package.

```

cp_tbl <- dat %>%
  group_by(POP) %>%
  summarise(
    .groups = "keep",
    cur_data() %>%
      as_survey_design(weight = PANELWEIGHT, id = EAID_1, strata = STRATA_RECODE) %>%
      group_by(CP_1, CP_2) %>%
      summarise(survey_mean(vartype = "ci", prop = TRUE, prop_method = "logit")))
  )
}

cp_tbl

```

POP	CP_1	CP_2	coef	`_low`	`_upp`
	<int+lbl>	<int+lbl>	<dbl>	<dbl>	<dbl>
1 Burkina Faso	0 [No]	0 [No]	0.790	0.763	0.815
2 Burkina Faso	0 [No]	1 [Yes]	0.210	0.185	0.237
3 Burkina Faso	1 [Yes]	0 [No]	0.347	0.306	0.391
4 Burkina Faso	1 [Yes]	1 [Yes]	0.653	0.609	0.694
5 DRC – Kinshasa	0 [No]	0 [No]	0.739	0.685	0.787
6 DRC – Kinshasa	0 [No]	1 [Yes]	0.261	0.213	0.315
7 DRC – Kinshasa	1 [Yes]	0 [No]	0.275	0.239	0.314
8 DRC – Kinshasa	1 [Yes]	1 [Yes]	0.725	0.686	0.761
9 DRC – Kongo Central	0 [No]	0 [No]	0.736	0.685	0.782
10 DRC – Kongo Central	0 [No]	1 [Yes]	0.264	0.218	0.315
11 DRC – Kongo Central	1 [Yes]	0 [No]	0.270	0.207	0.343
12 DRC – Kongo Central	1 [Yes]	1 [Yes]	0.730	0.657	0.793
13 Kenya	0 [No]	0 [No]	0.697	0.676	0.717
14 Kenya	0 [No]	1 [Yes]	0.303	0.283	0.324
15 Kenya	1 [Yes]	0 [No]	0.200	0.183	0.217
16 Kenya	1 [Yes]	1 [Yes]	0.800	0.783	0.817
17 Nigeria – Kano	0 [No]	0 [No]	0.946	0.910	0.968
18 Nigeria – Kano	0 [No]	1 [Yes]	0.0544	0.0321	0.0905
19 Nigeria – Kano	1 [Yes]	0 [No]	0.440	0.308	0.581
20 Nigeria – Kano	1 [Yes]	1 [Yes]	0.560	0.419	0.692
21 Nigeria – Lagos	0 [No]	0 [No]	0.757	0.713	0.796
22 Nigeria – Lagos	0 [No]	1 [Yes]	0.243	0.204	0.287
23 Nigeria – Lagos	1 [Yes]	0 [No]	0.240	0.196	0.290
24 Nigeria – Lagos	1 [Yes]	1 [Yes]	0.760	0.710	0.804

Here, we first use `group_by` to divide the data extract into individual samples defined by `POP`. We then reference each of these samples as `cur_data` inside a summary function defined by `summarise` - this ensures that the population estimates obtained from our combined data extract are identical to those you would obtain if you downloaded one extract for each sample and analyzed them separately.

Within `summarise`, we use `as_survey_design` to specify information about the design of each sample, and we then use a second `group_by` to identify each of our variables of interest, `CP_1` and `CP_2`. Finally, we use a second `summarise` function to calculate a `svy` summary statistic: in this case, we use `survey_mean` to estimate proportions in the population.

The population estimate for each row appears in the column `_coef`. Looking at row 1, we would estimate that 79% of women aged 15-49 in Burkina Faso used *no method* both at Phase 1 and again at Phase 2. The columns `_low` and `_upp` report the limits of a 95% confidence interval: 76.3% and 81.5%.

Comparing these confidence intervals gives us an informal, conservative way to test for a significant difference between outcomes for each POP: if the intervals for any pair of outcomes in the same sample include no common values, we'll say that a significant difference exists. *Formal testing may also reveal significant differences between pairs of outcomes where these intervals overlap only slightly.* Our approach is well suited for data visualization, but it should not replace formal testing. Fortunately, you can adapt our code to replace (or complement) the output from `survey_mean`.

You may change the confidence interval to, for example, 99% by setting `level = 0.99` in `survey_mean`.

For example, here we demonstrate how to calculate a Rao-Scott chi-square test for significant differences between the estimated population proportions for each POP and the proportions we would *expect* to observe if Phase 2 outcomes were statistically independent from Phase 1 conditions.²⁵ Because we're interested in just one summary statistic per sample, we no longer need to `group_by` `CP_1` and `CP_2`; instead, we'll use the formula `~CP_1 + CP_2` in the function `svychisq`.

```
rao_tbl <- dat %>%
  group_by(POP) %>%
  summarise(
    .groups = "keep",
    cur_data() %>%
      as_survey_design(weight = PANELWEIGHT, id = EAID_1, strata = STRATA_RECODE) %>%
      summarise(rao = svychisq(~CP_1 + CP_2, design = .) %>% list)
  )
rao_tbl
```

²⁵The Rao-Scott second-order correction to Pearson's chi-square test is used to incorporate survey design information from `as_survey_design`, reflecting weighted population estimates. Wald-type chi-square tests are also available: see `svychisq` for details.

```
# A tibble: 6 × 2
# Groups:   POP [6]
  POP                  rao
  <chr>                <list>
1 Burkina Faso        <htest>
2 DRC – Kinshasa      <htest>
3 DRC – Kongo Central <htest>
4 Kenya                 <htest>
5 Nigeria – Kano       <htest>
6 Nigeria – Lagos      <htest>
```

Our new summary column `rao` contains output for each sample's test in a [list](#). From here, you can extract output elements [rowwise](#) by name like so:

```
rao_tbl %>%
  rowwise() %>%
  mutate(
    `F` = rao$statistic,
    p.value = rao$p.value,
    sig95 = p.value < 0.05
  )
```

```
# A tibble: 6 × 5
# Rowwise: POP
  POP                  rao          F    p.value sig95
  <chr>                <list>     <dbl>    <dbl> <lgl>
1 Burkina Faso        <htest>  468.  4.62e- 50 TRUE
2 DRC – Kinshasa      <htest>  216.  4.80e- 21 TRUE
3 DRC – Kongo Central <htest>  123.  9.43e- 16 TRUE
4 Kenya                 <htest> 1140. 8.58e-102 TRUE
5 Nigeria – Kano       <htest>  89.2 2.23e-  9 TRUE
6 Nigeria – Lagos      <htest> 204.  2.85e- 19 TRUE
```

4.4 VISUALIZATION

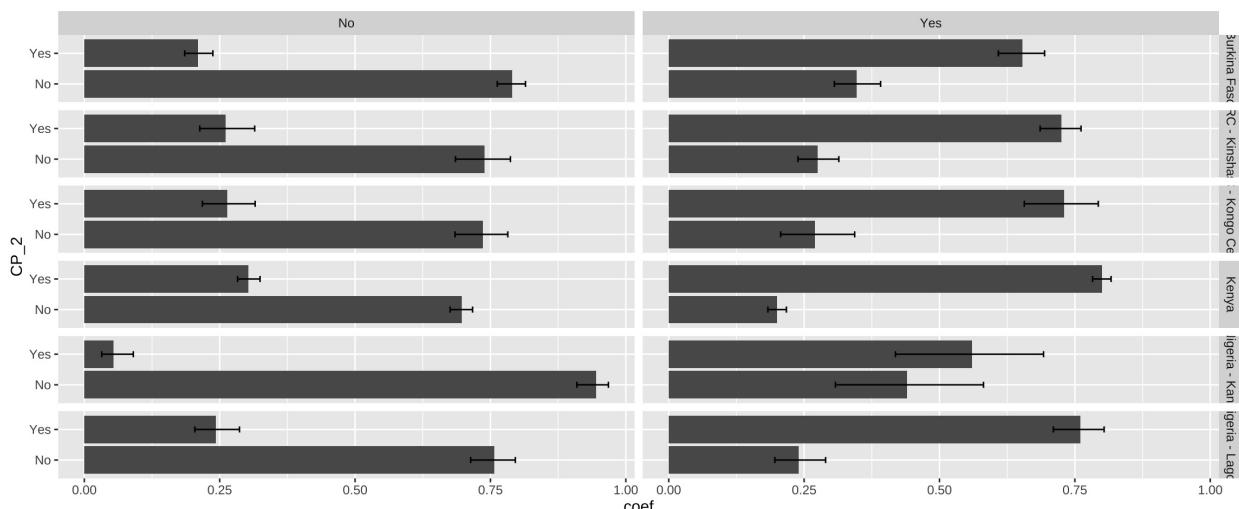
We'll use simple **grouped bar charts** to show population estimates for each proportion below. A grouped bar chart differs from the **stacked bar charts** shown in PMA reports in that each response is plotted along an axis (rather than stacked together in a single bar). We'll show **grouped bar charts** here so that we can also include **error bars** representing a 95% confidence interval for each proportion.

For example, let's plot the estimates created in `cp_tbl` above. As a preliminary step, we'll recode `CP_1` and `CP_2` with `as_factor` and sort their levels with `fct_relevel`. This ensures that the *value labels* for each variable will be printed on our plot.

```
cp_tbl <- cp_tbl %>%
  mutate(
    across(
      c(CP_1, CP_2),
      ~as_factor(.x) %>% fct_relevel("No", "Yes")
    )
  )
```

Next, we'll use `ggplot2` to build the plot. Because our data includes multiple samples, we'll use `facet_grid` to plot all summary data in multiple panels. The functions `geom_bar` and `geom_errorbar` plot the grouped bars and error bars, respectively. A baseline plot should look something like this:

```
cp_tbl %>%
  ggplot(aes(x = coef, y = CP_2)) +
  facet_grid(rows = vars(POP), cols = vars(CP_1)) +
  geom_bar(stat = "identity") +
  geom_errorbar(aes(xmin = `_low`, xmax = `_upp`), width = 0.2)
```



One of the powerful features of `ggplot2` is that you can use [pre-built themes](#) to customize this baseline layout. We'll build on `theme_minimal` to create our own `theme_pma` (with custom fonts incorporated by the `sysfonts` and `showtext` packages). [Feel free to use our theme, or tweak it to create your own!](#)

```
library(showtext)

sysfonts::font_add(
  family = "cabrito",
  regular = ".../fonts/cabritosansnormregular-webfont.ttf"
)
showtext::showtext_auto()

theme_pma <- theme_minimal() %>%
  theme(
    text = element_text(family = "cabrito", size = 13),
    plot.title = element_text(size = 22, color = "#00263A",
                               hjust = 0, margin = margin(b = 5)),
    plot.subtitle = element_text(hjust = 0, margin = margin(b = 10)),
    strip.background = element_blank(),
    strip.text.y = element_text(size = 16, angle = 0),
    panel.spacing = unit(1, "lines"),
    axis.title.y = element_text(angle = 0, margin = margin(r = 10))
  )
```

Throughout this post, we'll be repeating the same functions to create grouped bars, error bars, and labels for our plot. In order to avoid repeating ourselves each time, we'll combine these functions together with `theme_pma` in a single function called `pma_bars`.

```

pma_bars <- function(  

  title = NULL,      # an optional title  

  subtitle = NULL,    # an optional subtitle  

  xaxis = NULL,      # an optional label for the x-axis (displayed above)  

  yaxis = NULL       # an optional label for the y-axis (displayed left)  

){  

  components <- list(  

    if(exists("theme_pma")){theme_pma},  

    labs(  

      title = title,  

      subtitle = subtitle,  

      y = str_wrap(yaxis, 10),  

      x = NULL,  

      fill = NULL  

    ),  

    scale_x_continuous(  

      position = 'bottom',  

      sec.axis = sec_axis(trans = ~., name = xaxis, breaks = NULL),  

      labels = scales::label_percent()  

    ),  

    scale_y_discrete(limits = rev),  

    geom_bar(stat = "identity", fill = "#98579BB0"),  

    geom_errorbar(  

      aes(xmin = `_low`, xmax = `_upp`),  

      width = 0.2,  

      color = "#00263A"  

    )  

  )
}

```

Going forward, we'll incorporate pma_bars together with a [ggplot](#) and [facet](#) function for a given set of variables like so:

```

cp_tbl %>%
  ggplot(aes(x = coef, y = CP_2)) +
  facet_grid(rows = vars(POP), cols = vars(CP_1)) +
  pma_bars(  

    title = "Change in Contraceptive Use Status",  

    subtitle = "A grouped bar chart, faceted by population of interest",  

    xaxis = "Phase 1",  

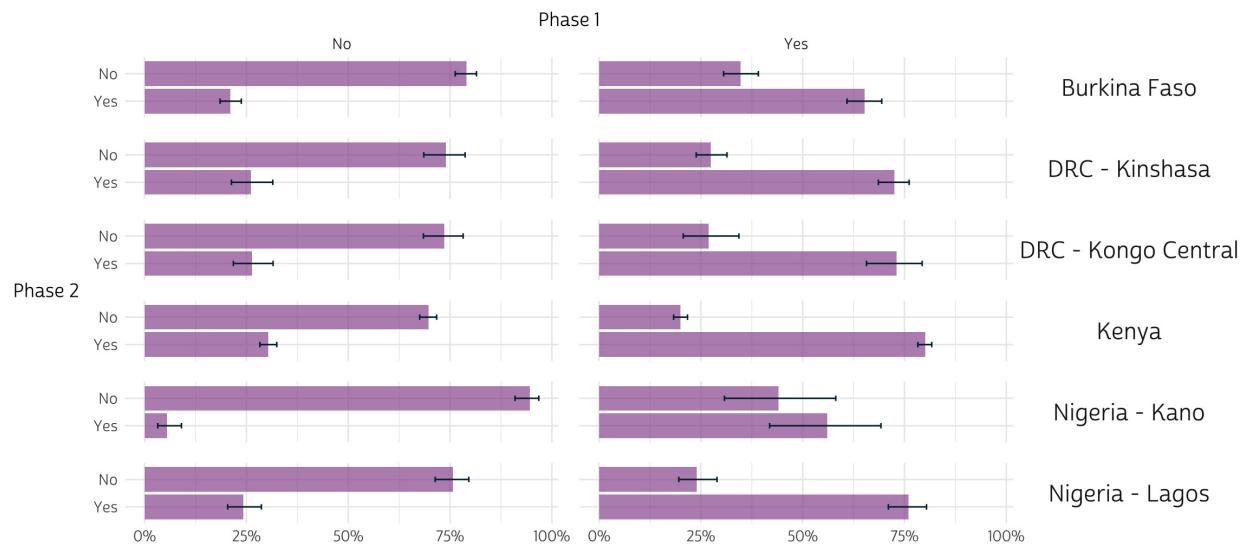
    yaxis = "Phase 2"  

  )

```

Change in Contraceptive Use Status

A grouped bar chart, faceted by population of interest



4.5 KEY INDICATORS

4.5.1 Contraceptive Use or Non-Use

Let's continue our examination of [CP](#). In the PMA reports for each sample linked above, you'll notice that women who were pregnant at either phase are distinguished from women who reported use or non-use in CP_1 or CP_2. We'll identify these women in the variable [PREGNANT](#), and then we'll create a combined indicator called FPSTATUS.

- FPSTATUS - Pregnant, using contraception, or using no contraception

```
dat <- dat %>%
  mutate(
    FPSTATUS_1 = case_when(
      PREGNANT_1 == 1 ~ "Pregnant",
      CP_1 == 1 ~ "Using FP",
      CP_1 == 0 ~ "Not Using FP"
    ),
    FPSTATUS_2 = case_when(
      PREGNANT_2 == 1 ~ "Pregnant",
      CP_2 == 1 ~ "Using FP",
      CP_2 == 0 ~ "Not Using FP"
    ),
    across(
      c(FPSTATUS_1, FPSTATUS_2),
      ~.x %>% fct_relevel("Pregnant", "Not Using FP", "Using FP")
    )
  )
```

We'll now revise cp_tbl to include information from FPSTATUS_1 and FPSTATUS_2. This will help us answer key questions like:

- Are women who were pregnant at Phase 1 more likely to use or not use family planning at Phase 2?
- Are women who were using (or not using) contraception at Phase 1 likely to maintain the same status at Phase 2?

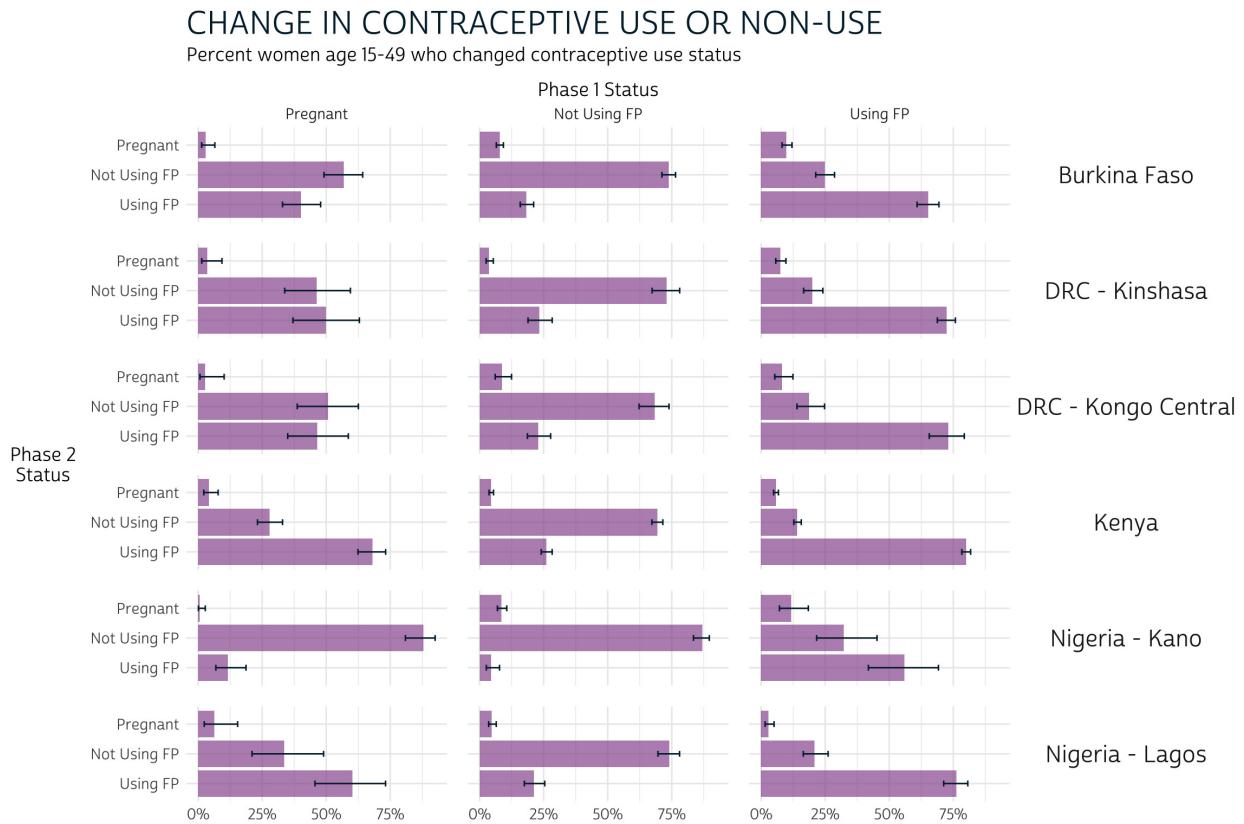
```
cp_tbl <- dat %>%
  group_by(POP) %>%
  summarise(
    .groups = "keep",
    cur_data() %>%
      as_survey_design(weight = PANELWEIGHT, id = EAID_1, strata = STRATA_RECODE) %>%
      group_by(FPSTATUS_1, FPSTATUS_2) %>%
      summarise(survey_mean(vartype = "ci", prop = TRUE, prop_method = "logit"))
  )
```

Next, we'll plot cp_tbl with pma_bars:

```

cp_tbl %>%
  ggplot(aes(x = coef, y = FPSTATUS_2)) +
  facet_grid(cols = vars(FPSTATUS_1), rows = vars(POP)) +
  pma_bars(
    "CHANGE IN CONTRACEPTIVE USE OR NON-USE",
    "Percent women age 15-49 who changed contraceptive use status",
    xaxis = "Phase 1 Status",
    yaxis = "Phase 2 Status"
  )

```



To reiterate: comparing the error bars within each of these 18 panels gives us an informal, but conservative test for significant difference. We'll say that a significant difference occurs where two pairs of error bars **do not overlap** (but additional testing may be necessary to determine whether a significant difference occurs where error bars overlap only slightly). A few observations:

- For women who were pregnant at Phase 1, there is usually no apparent difference between using and not using family planning at Phase 2. Kenya and Nigeria - Kano are the exception: in Kenya, pregnant women at Phase 1 were appear more likely to be using FP at Phase 2, while the opposite is true in Kano.
- Overall, non-pregnant women at Phase 1 appeared more likely to maintain the same status (use or non-use) at Phase 2 than they were to switch or become pregnant.

4.5.2 Contraceptive Method Type

PMA surveys also ask contraceptive users to indicate which method they are currently using at each phase of the study. If a woman reports using more than one method, [FPCURREFFMETH](#) shows her most *effective* currently used method. These responses are combined with detailed information about use of the lactational amenorrhea method (LAM), emergency contraception, or injectable type in [FPCURREFFMETHRC](#). PMA reports use [FPCURREFFMETHRC](#) to determine whether each woman's most effective current method is a short-acting, long-acting, or traditional method.

Long-acting methods include:

- IUDs
- implants
- male sterilization
- female sterilization

Short-acting methods include:

- injectables (intramuscular and subcutaneous)
- the pill
- emergency contraception
- male condoms
- female condoms
- LAM
- diaphragm
- foam/jelly
- standard days method

Traditional methods include:

- rhythm
- withdrawal
- other traditional

These methods are coded sequentially by group in [FPCURREFFMETHRC](#). Women who are “NIU (not in universe)” were using no method.

```
dat %>% count(FPCURREFFMETHRC_1)
```

```
# A tibble: 19 × 2
#> #>   FPCURREFFMETHRC_1      n
#> #>   <int+lbl>        <int>
#> #> 1 101 [Female Sterilization]    198
#> #> 2 102 [Male Sterilization]      1
#> #> 3 111 [Implants]                2248
#> #> 4 112 [IUD]                     226
#> #> 5 121 [Injectables (3 months)] 1412
#> #> 6 123 [Injectables (Sayana Press)] 296
#> #> 7 131 [Pill]                    547
#> #> 8 132 [Emergency Contraception] 243
#> #> 9 141 [Male condom]             791
#> #> 10 142 [Female condom]          1
#> #> 11 151 [Diaphragm]              1
#> #> 12 152 [Foam]                  1
#> #> 13 160 [Standard Days/Cycle Beads Method] 70
#> #> 14 170 [Lactational amenorrhea method (LAM)] 24
#> #> 15 210 [Rhythm]                 569
#> #> 16 220 [Withdrawal]              351
#> #> 17 240 [Other traditional]       153
#> #> 18 998 [No response or missing]    1
#> #> 19 999 [NIU (not in universe)]     10572
```

We'll use `across` to recode the Phase 1 and Phase 2 versions of `FPCURREFFMETHRC` simultaneously. We'll also attach the prefix `CAT` to each variable, indicating that we've created "categorized" versions of each.

- `CAT_FPSFPCURREFFMETHRC_1` - Phase 1 contraceptive method type
- `CAT_FPSFPCURREFFMETHRC_2` - Phase 2 contraceptive method type

```
dat <- dat %>%
  mutate(
    across(
      c(FPCURREFFMETHRC_1, FPCURREFFMETHRC_2),
      ~case_when(
        .x < 120 ~ "long-acting",
        .x < 200 ~ "short-acting",
        .x < 900 ~ "traditional",
        TRUE ~ "none") %>%
        fct_relevel("long-acting", "short-acting", "traditional", "none"),
      .names = "CAT_{.col}"
    )
  )
```

Next, we'll generate population estimates for our derived variables, `CAT_FPCURREFFMETHRC_1` and `CAT_FPCURREFFMETHRC_2`.

```

meth_tbl <- dat %>%
  group_by(POP) %>%
  summarise(
    .groups = "keep",
    cur_data() %>%
      as_survey_design(weight = PANELWEIGHT, id = EAID_1, strata = STRATA_RECODE) %>%
      group_by(CAT_FPCURREFFMETHRC_1, CAT_FPCURREFFMETHRC_2) %>%
      summarise(survey_mean(vartype = "ci", prop = TRUE, prop_method = "logit"))
  )

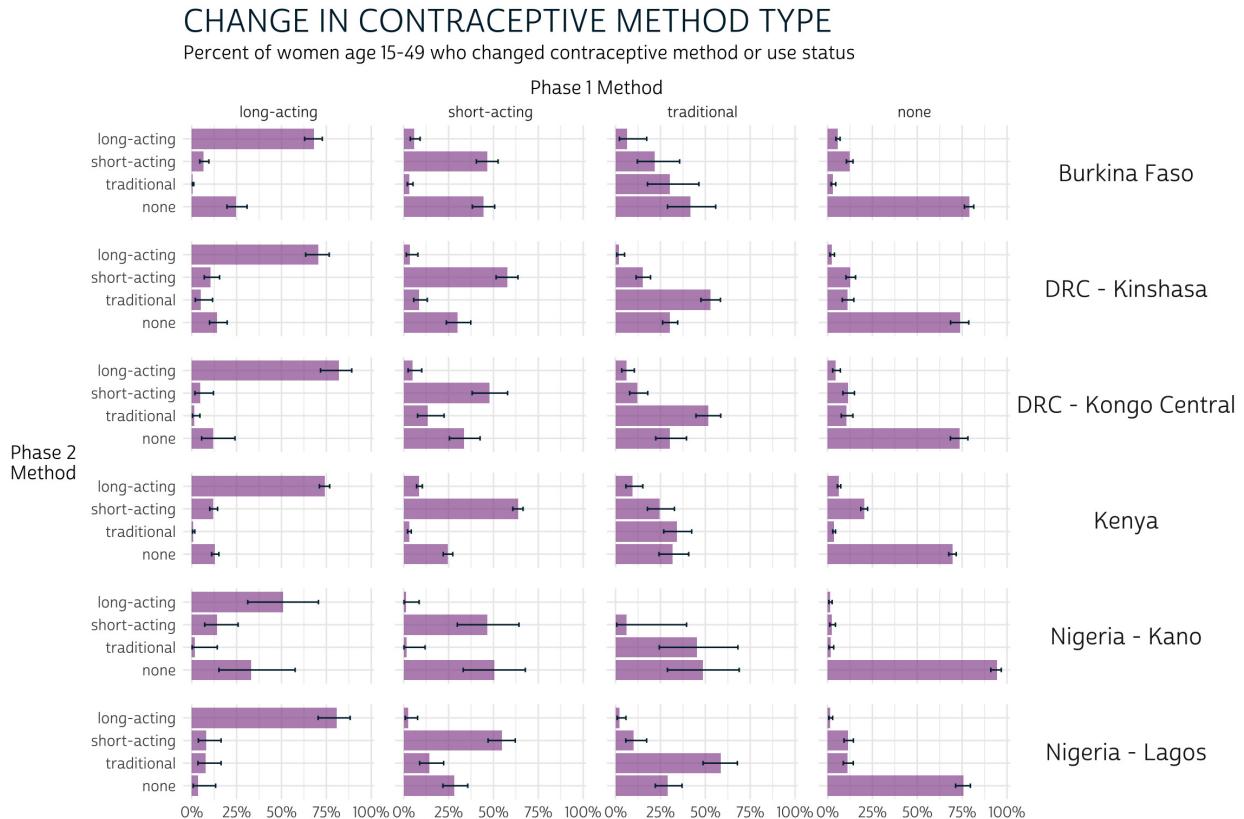
```

We'll again use pma_bars to plot the results.

```

meth_tbl %>%
  ggplot(aes(x = coef, y = CAT_FPCURREFFMETHRC_2)) +
  facet_grid(cols = vars(CAT_FPCURREFFMETHRC_1), rows = vars(POP)) +
  pma_bars(
    "CHANGE IN CONTRACEPTIVE METHOD TYPE",
    "Percent of women age 15-49 who changed contraceptive method or use status",
    xaxis = "Phase 1 Method",
    yaxis = "Phase 2 Method"
  )

```



What do we learn from this plot? Let's consider each column in turn:

- Users of “long-acting” methods at Phase 1 appear more likely to have used “long-acting” methods at Phase 2 than to have changed status (except perhaps in Kano, where the intervals for “long-acting” and “none” overlap at Phase 2).
- Users of “short-acting” methods at Phase 1 appeared generally likely to use them again at Phase 2, but some samples show that women are equally likely to be using “none” at Phase 2. A difference between these two outcomes is visually apparent only in Kinshasa, Kenya, and Lagos (where women were more likely to be using “short-acting” methods than “none”).
- The status of Phase 1 “traditional” users is generally unclear at Phase 2. In Kinshasa, Kongo Central, and Lagos, these women seem most likely to remain “traditional” users at Phase 2. Elsewhere, there are no clear trends.
- Users of “none” at Phase 1 were clearly most likely to remain as such at Phase 2.

4.5.3 Contraceptive Dynamics by Subgroup

We can also use [FPCURREFFMETHRC](#) to see whether women switched methods, stopped using any method, started using any method, or made no changes. Let's summarize this information as CHG_FPCURR:

- CHG_FPCURR - Change in contraceptive use between Phase 1 and Phase 2

```
dat <- dat %>%
  mutate(
    CHG_FPCURR = case_when(
      FPCURREFFMETHRC_1 > 900 & FPCURREFFMETHRC_2 > 900 ~ "Continued non-use",
      FPCURREFFMETHRC_1 > 900 ~ "Started using",
      FPCURREFFMETHRC_2 > 900 ~ "Stopped using",
      FPCURREFFMETHRC_1 != FPCURREFFMETHRC_2 ~ "Changed methods",
      FPCURREFFMETHRC_1 == FPCURREFFMETHRC_2 ~ "Continued method"
    )
  )
```

PMA reports disaggregate the outcomes captured in CHG_FPCURR by age, marital status, education level, and parity (number of live childbirths).

4.5.3.1 Age

We'll use PMA's categorization of AGE_2 to examine differences between women in three categories.

- CAT_AGE_2 - Phase 2 age (3 categories)

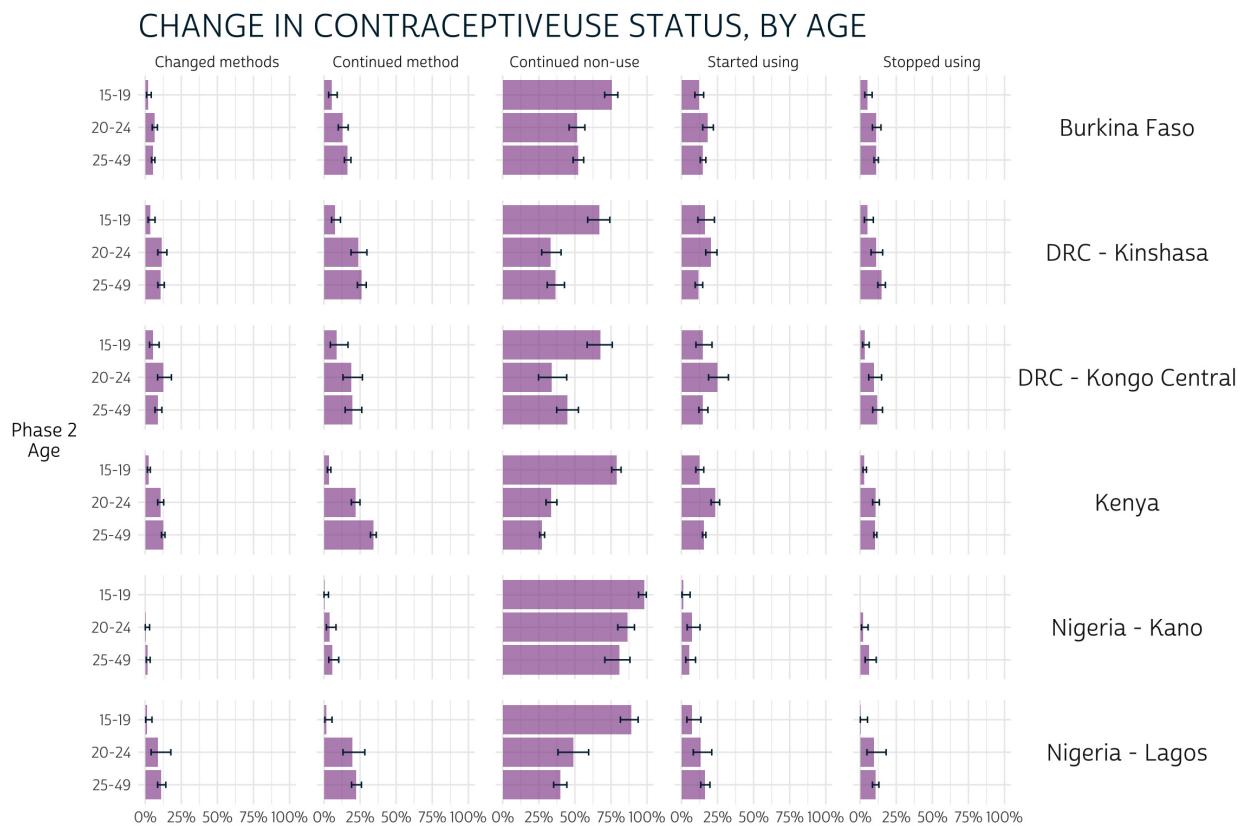
```
dat <- dat %>%
  mutate(
    CAT_AGE_2 = case_when(
      AGE_2 < 20 ~ "15-19",
      AGE_2 < 25 ~ "20-24",
      TRUE ~ "25-49"
    )
  )
```

Plotting CAT_AGE_2 on the y-axis allows us to compare confidence intervals across age groups. For example, notice that women aged 15-19 in every population seem more likely to continue non-use than women who are aged 20-24 or 25-49 (column 3).

```

dat %>%
  group_by(POP) %>%
  summarise(
    .groups = "keep",
    cur_data() %>%
      as_survey_design(weight = PANELWEIGHT, id = EAID_1, strata = STRATA_RECODE) %>%
      group_by(CAT_AGE_2, CHG_FPCURR) %>%
      summarise(survey_mean(vartype = "ci", prop = TRUE, prop_method = "logit"))
  ) %>%
  ggplot(aes(x = coef, y = CAT_AGE_2)) +
  facet_grid(cols = vars(CHG_FPCURR), rows = vars(POP)) +
  pma_bars(
    "CHANGE IN CONTRACEPTIVEUSE STATUS, BY AGE",
    yaxis = "Phase 2 Age"
  )

```



4.5.3.2 Education level

The variable [EDUCATTGEN](#) standardizes educational categories across countries (see [EDUCATT](#) for country-specific codes). To match PMA reports, we'll recode [EDUCATTGEN](#) into just three groups:

- CAT_EDUCATTGEN_2 - Phase 2 education level (3 categories)

```

dat <- dat %>%
  mutate(
    CAT_EDUCATTGEN_2 = case_when(
      EDUCATTGEN_2 < 3 ~ "None / Primary",
      EDUCATTGEN_2 == 3 ~ "Secondary",
      EDUCATTGEN_2 == 4 ~ "Tertiary"
    )
  )

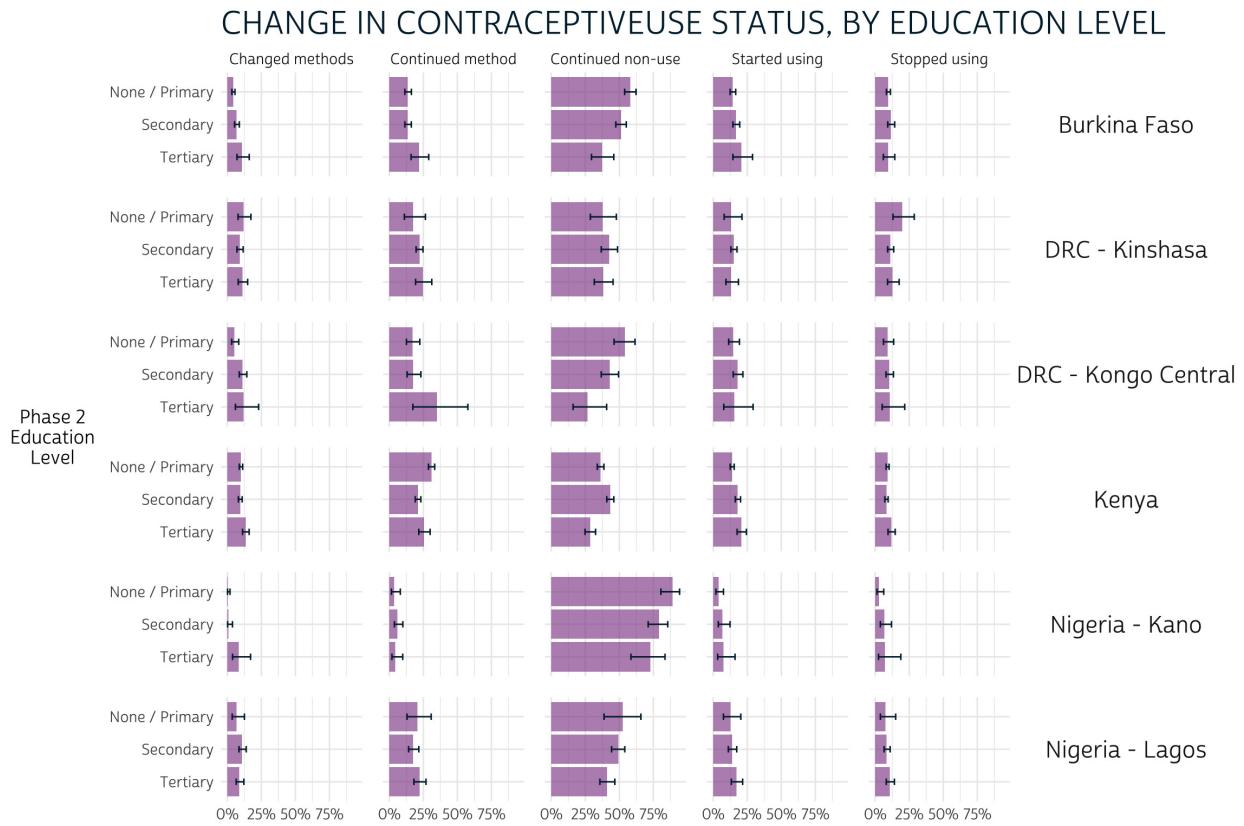
```

As with age, we'll plot CAT_EDUCATTGEN_2 on the y-axis. There aren't many clear takeaways here: confidence intervals overlap in each column for almost every education level, so visual inspection reveals no clear significant differences:

```

dat %>%
  filter(EDUCATTGEN_2 < 90) %>% # drop if missing
  group_by(POP) %>%
  summarise(
    .groups = "keep",
    cur_data() %>%
      as_survey_design(weight = PANELWEIGHT, id = EAID_1, strata = STRATA_RECODE) %>%
      group_by(CAT_EDUCATTGEN_2, CHG_FPCURR) %>%
      summarise(survey_mean(vartype = "ci", prop = TRUE, prop_method = "logit"))
  ) %>%
  ggplot(aes(x = coef, y = CAT_EDUCATTGEN_2)) +
  facet_grid(cols = vars(CHG_FPCURR), rows = vars(POP)) +
  pma_bars(
    "CHANGE IN CONTRACEPTIVE USE STATUS, BY EDUCATION LEVEL",
    yaxis = "Phase 2 Education Level"
  )

```



4.5.3.3 Marital status

The variable [MARSTAT](#) indicates each woman’s marital / partnership status. PMA considers women “in union” to be those who are currently married (code 21) or currently living with their partner (code 22). Otherwise, women who were never married, divorced / separated, or widowed are considered “not in union”.

- CAT_MARSTAT_2 - Phase 2 marital status (2 categories)

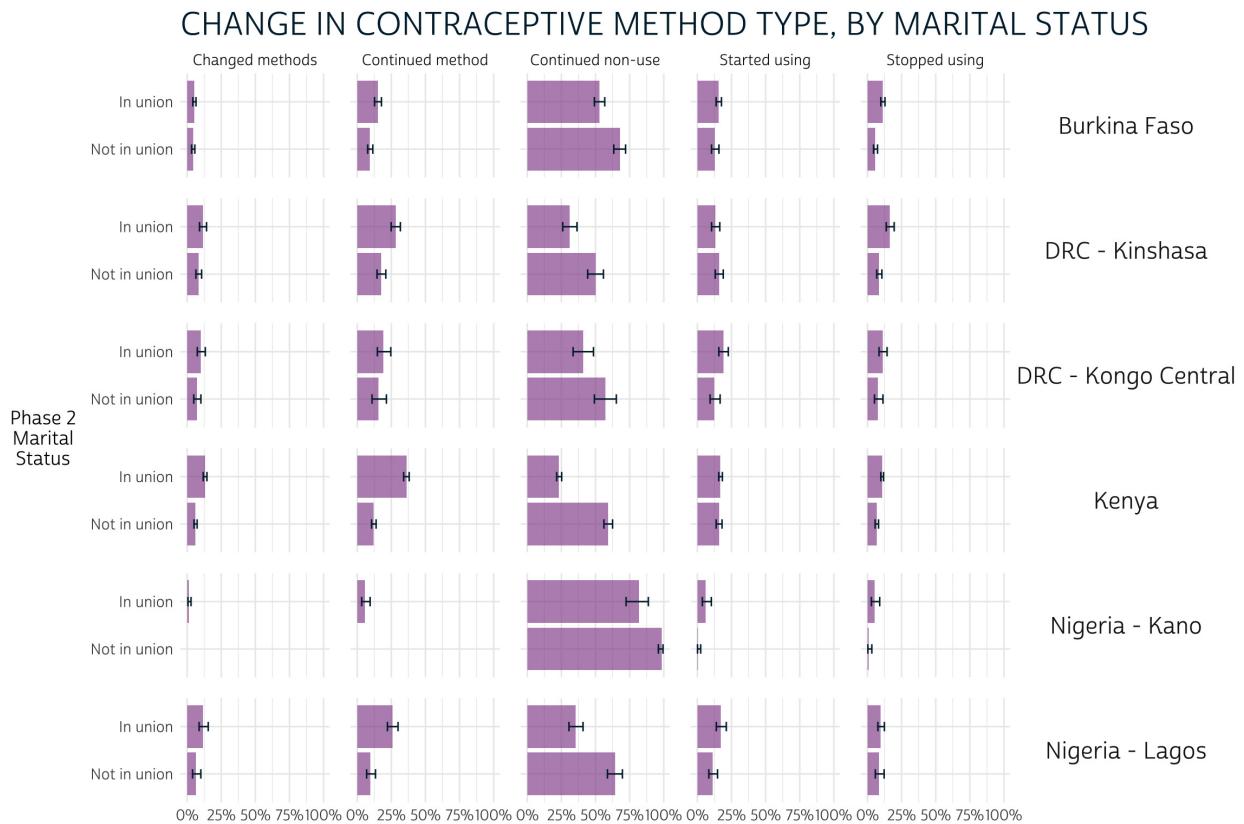
```
dat <- dat %>%
  mutate(
    CAT_MARSTAT_2 = case_when(
      MARSTAT_2 %in% 21:22 ~ "In union",
      TRUE ~ "Not in union"
    )
  )
```

Here, we see that women who were *not* in a union at Phase 2 were significantly more likely to continue non-use of contraception compared to married / partnered women in each population. On the other hand, women who *were* in a union mainly appeared more likely to continue using the same method, or perhaps to change methods (most clearly in Kenya).

```

dat %>%
  group_by(POP) %>%
  summarise(
    .groups = "keep",
    cur_data() %>%
      as_survey_design(weight = PANELWEIGHT, id = EAID_1, strata = STRATA_RECODE) %>%
      group_by(CAT_MARSTAT_2, CHG_FPCURR) %>%
      summarise(survey_mean(vartype = "ci", prop = TRUE, prop_method = "logit"))
  ) %>%
  ggplot(aes(x = coef, y = CAT_MARSTAT_2)) +
  facet_grid(cols = vars(CHG_FPCURR), rows = vars(POP)) +
  pma_bars(
    "CHANGE IN CONTRACEPTIVE METHOD TYPE, BY MARITAL STATUS",
    yaxis = "Phase 2 Marital Status"
  )
)

```



4.5.3.4 Parity

Parity refers to the number of times a women has given live birth (excluding stillbirths). This information is recorded in the IPUMS variable [BIRTHEVENT](#), in which the values 0 and 99 (not in universe) can both be interpreted as “none”.

- CAT_BIRTHEVENT_2 - Phase 2 number of live births (4 categories)

```

dat <- dat %>%
  mutate(
    CAT_BIRTHEVENT_2 = case_when(
      BIRTHEVENT_2 %in% c(0, 99) ~ "None",
      BIRTHEVENT_2 %in% c(1, 2) ~ "One-two",
      BIRTHEVENT_2 %in% c(3, 4) ~ "Three-four",
      BIRTHEVENT_2 >= 5 ~ "Five +") %>%
    fct_relevel("None", "One-two", "Three-four", "Five +")
  )

```

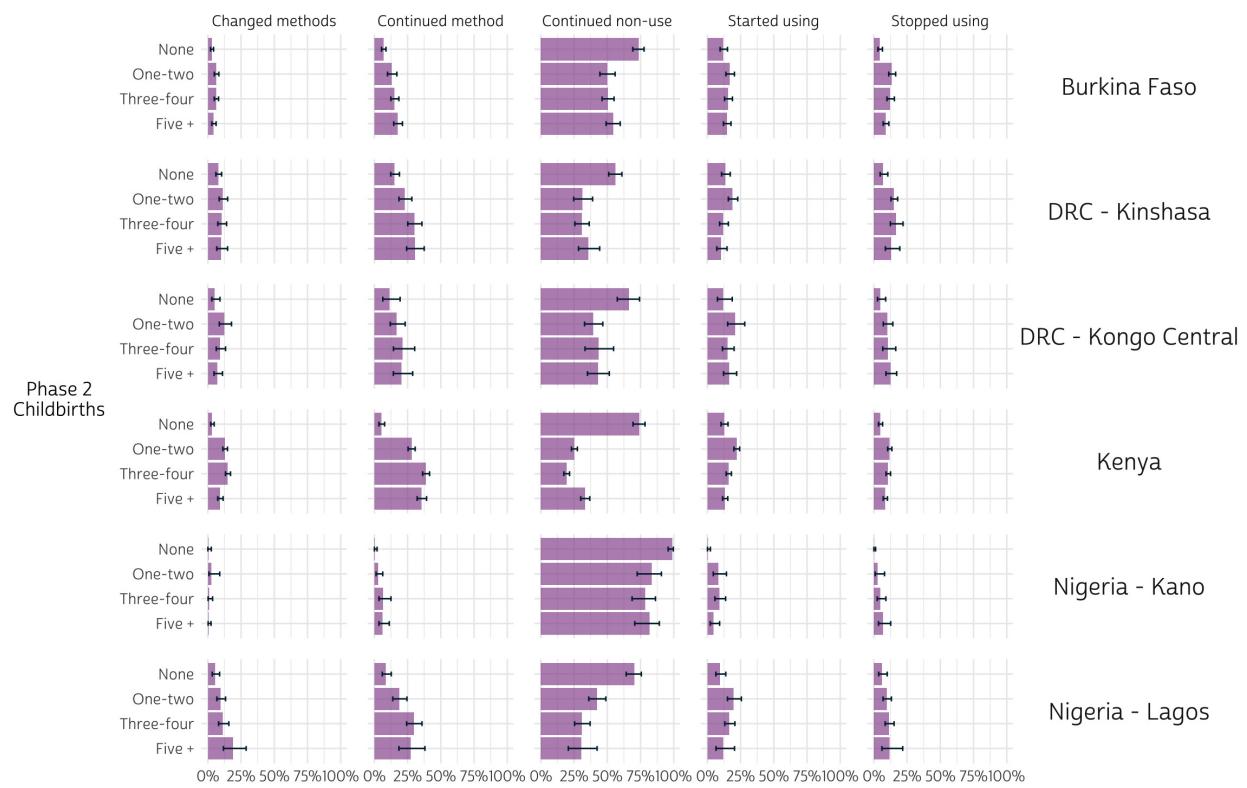
There are few clear patterns related to parity, except that women who have never given birth are also more likely to continue non-use of contraception between phases.

```

dat %>%
  filter(BIRTHEVENT_2 != 98) %>% # drops 2 missing cases (code 98)
  group_by(POP) %>%
  summarise(
    .groups = "keep",
    cur_data() %>%
      as_survey_design(weight = PANELWEIGHT, id = EAID_1, strata = STRATA_RECODE) %>%
      group_by(CAT_BIRTHEVENT_2, CHG_FPCURR) %>%
      summarise(survey_mean(vartype = "ci", prop = TRUE, prop_method = "logit"))) %>%
  ggplot(aes(x = coef, y = CAT_BIRTHEVENT_2)) +
  facet_grid(cols = vars(CHG_FPCURR), rows = vars(POP)) +
  pma_bars(
    "CHANGE IN CONTRACEPTIVE METHOD TYPE, BY PARITY",
    yaxis = "Phase 2 Childbirths"
  )

```

CHANGE IN CONTRACEPTIVE METHOD TYPE, BY PARITY



4.5.4 Other Panel Dynamics

The final page in each PMA report covers family planning dynamics related to unmet need, partner support, and plans for future use of family planning methods. In each case, we'll be focusing on women who were *not* using any method at Phase 1. We'll show how each of these dynamics impacts the likelihood that Phase 1 non-users would have adopted any family planning method at Phase 2.

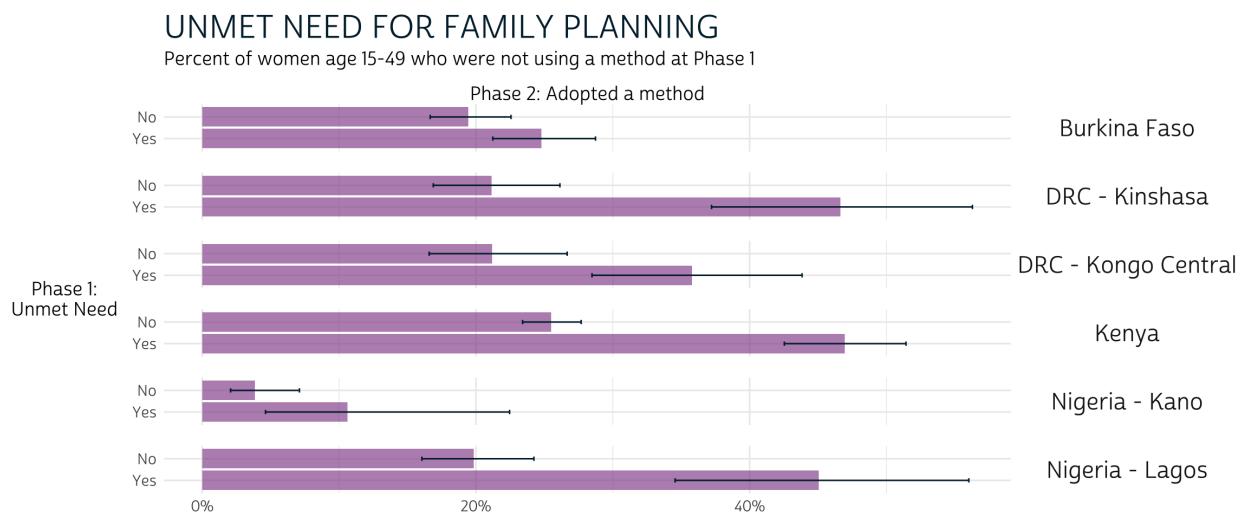
```
dat <- dat %>% filter(CP_1 == 0)
```

4.5.4.1 Unmet need

PMA defines unmet need for family planning according to each woman's fertility preferences, current use of family planning methods, and risk factors for pregnancy. Women may have "unmet need" for birth spacing (e.g. pregnant women whose pregnancy was mistimed) or for limiting births (e.g. pregnant women whose pregnancy was unwanted), while women are considered "not at risk" if they are not sexually active or cannot become pregnant. The variable UNMETNEED provides detailed information on types of need for each woman, and on related variables that were used to calculate unmet need.

The binary variable UNMETYN recodes UNMETNEED as either "Unmet need", or "No unmet need". We'll reword these labels only slightly to minimize the amount of repeated text on our plot:

```
dat %>%
  mutate(UNMETYN_1 = if_else(UNMETYN_1 == 1, "Yes", "No")) %>%
  group_by(POP) %>%
  summarise(
    .groups = "keep",
    cur_data() %>%
      as_survey_design(weight = PANELWEIGHT, id = EAID_1, strata = STRATA_RECODE) %>%
      group_by(UNMETYN_1, CP_2) %>%
      summarise(survey_mean(var_type = "ci", prop = TRUE, prop_method = "logit"))
  ) %>%
  filter(CP_2 == 1) %>%
  ggplot(aes(x = coef, y = UNMETYN_1)) +
  facet_grid(rows = vars(POP)) +
  pma_bars(
    "UNMET NEED FOR FAMILY PLANNING",
    "Percent of women age 15-49 who were not using a method at Phase 1",
    xaxis = "Phase 2: Adopted a method",
    yaxis = "Phase 1: Unmet Need"
  )
```



Overall, these results suggest that non-users with unmet need for family planning at Phase 1 were more likely to adopt a method at Phase 2 compared to non-users who had none (e.g. women who were not sexually active, could not become pregnant, etc.). However, formal testing is needed to determine whether these trends were statistically significant in Burkina Faso and Nigeria - Lagos.

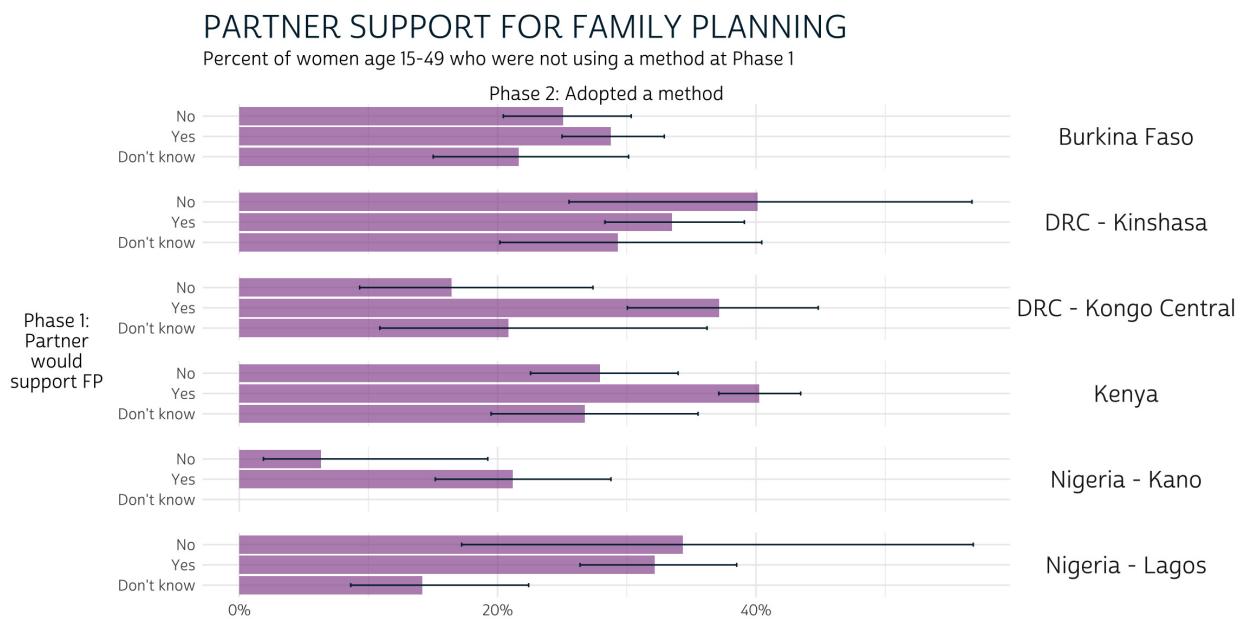
4.5.4.2 Partner support

Women who were not using family planning and not pregnant at Phase 1 were asked whether they thought their husband / partner would be supportive of use of family planning in the future. These results are recorded in [FPPARTSUPPORT](#). We'll exclude non-partnered women here, as they are "NIU (not in universe)".

```

dat %>%
  filter(FPPARTSUPPORT_1 %in% c(0, 1, 97)) %>%
  mutate(FPPARTSUPPORT_1 = FPPARTSUPPORT_1 %>% as_factor) %>%
  group_by(POP) %>%
  summarise(
    .groups = "keep",
    cur_data() %>%
      as_survey_design(weight = PANELWEIGHT, id = EAID_1, strata = STRATA_RECODE) %>%
      group_by(FPPARTSUPPORT_1, CP_2) %>%
      summarise(survey_mean(vartype = "ci", prop = TRUE, prop_method = "logit"))
  ) %>%
  filter(CP_2 == 1) %>%
  ggplot(aes(x = coef, y = FPPARTSUPPORT_1)) +
  facet_grid(rows = vars(POP)) +
  pma_bars(
    "PARTNER SUPPORT FOR FAMILY PLANNING",
    "Percent of women age 15–49 who were not using a method at Phase 1",
    xaxis = "Phase 2: Adopted a method",
    yaxis = "Phase 1: Partner would support FP"
  )
)

```



We've included responses for women who were unsure whether their partner would or would not support future use of FP ("Dont know"), but Phase 2 outcomes for these women were usually not visually distinct from those who answered "Yes" or "No". Formal testing is needed to determine whether any significant differences exist.

Meanwhile, women with Phase 1 partner support in DRC - Kongo Central and Kenya were more likely to adopt a method than not. Outcomes for women in other populations are not

visibly different based on partner support, one way or the other (again, formal testing may prove otherwise).

4.5.4.3 Intentions

Lastly, we'll demonstrate the impact of women's plans for future family planning use at Phase 1. The variable `FPUSPLAN` indicates whether women had plans for future use *at any point* in the future, but here we'll consider whether women had plans to adopt a method *within the next year* to correspond with the timing of Phase 2 surveys.

There are two variables that describe the approximate time when women said they would adopt a family planning method (if at all). `FPPLANVAL` contains a raw number that should be matched with a *unit* of time (months, years) or a categorical response ("soon / now", "after the birth of this child") in `FPPLANWHEN`:

```
dat %>% count(FPPLANWHEN_1)
```

```
# A tibble: 7 × 2
  FPPLANWHEN_1          n
  <int+lbl>        <int>
1 1 [Months]         932
2 2 [Years]          3039
3 3 [Soon / Now]     685
4 4 [After the birth of this child] 338
5 97 [Don't know]    893
6 98 [No response or missing]   18
7 99 [NIU (not in universe)] 4668
```

We'll create `FPPLANR_1` to indicate whether each woman planned to use family planning within a year's time at Phase 1.

- `FPPLANR_1` - Phase 1 plans to use FP within one year

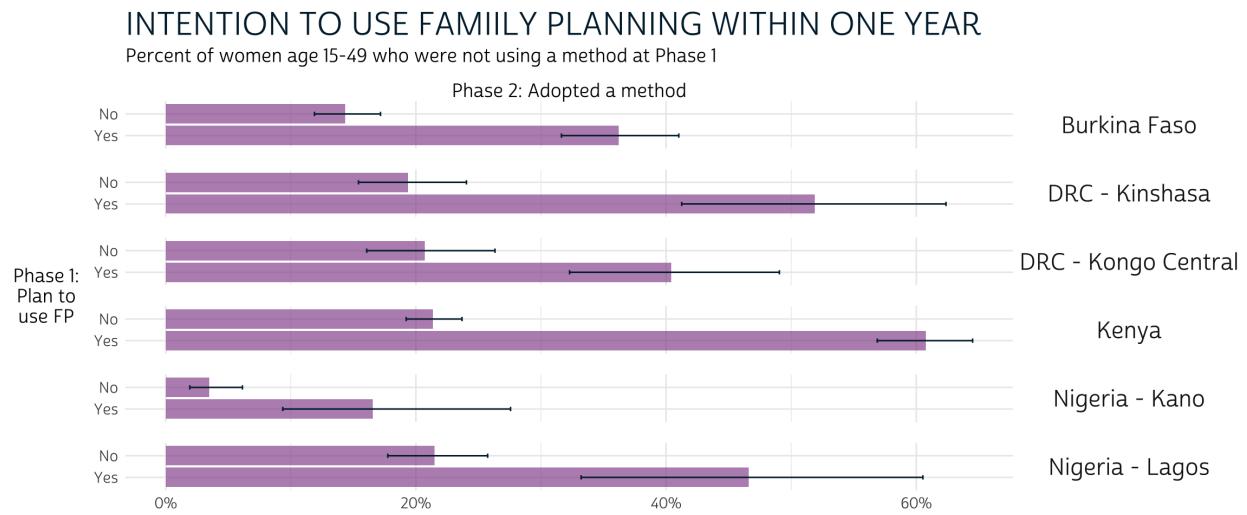
```
dat <- dat %>%
  mutate(
    FPPLANR_1 = case_when(
      FPPLANWHEN_1 == 1 & FPPLANVAL_1 <= 12 ~ "Yes", # Within 12 months
      FPPLANWHEN_1 == 2 & FPPLANVAL_1 == 1 ~ "Yes", # Within 1 year
      FPPLANWHEN_1 %in% c(3, 4) ~ "Yes", # Soon / now or after current pregnancy
      TRUE ~ "No" # Includes date unknown, no response, or no intention (FPUSPLAN)
    )
  )
```

Our final plot shows the difference in FP adoption between women who planned to do so within the year, compared with women with no such plans.

```

dat %>%
  group_by(POP) %>%
  summarise(
    .groups = "keep",
    cur_data() %>%
      as_survey_design(weight = PANELWEIGHT, id = EAID_1, strata = STRATA_RECODE) %>%
      group_by(FPPLANYR_1, CP_2) %>%
      summarise(survey_mean(vartype = "ci", prop = TRUE, prop_method = "logit"))
  ) %>%
  filter(CP_2 == 1) %>%
  ggplot(aes(x = coef, y = FPPLANYR_1)) +
  facet_grid(rows = vars(POP)) +
  pma_bars(
    "INTENTION TO USE FAMILY PLANNING WITHIN ONE YEAR",
    "Percent of women age 15-49 who were not using a method at Phase 1",
    xaxis = "Phase 2: Adopted a method",
    yaxis = "Phase 1: Plan to use FP"
  )
)

```



In every population, Phase 1 non-users who planned to adopt a method by Phase 2 were significantly more likely to do so. However, a significant *majority* of Phase 1 non-users with plans to adopt a method actually did so only in Kenya, where the 95% confidence interval for “Yes” responses includes only proportions greater than the 50% threshold. In fact, women who adopted a method at Phase 2 represent a significant *minority* of Phase 1 non-users who planned to do so in Burkina Faso, DRC - Kongo Central, and Nigeria - Kano.

4.6 WRAP-UP

As we've seen, **grouped bar charts** give us a simple way to identify clear differences between Phase 2 outcomes for subgroups defined by baseline family planning conditions or key demographic features. Additionally, when we **facet** populations of interest on the same axis, we can easily compare differences between subgroups for many samples in a single figure.

One drawback to this approach is that it's more conservative than formal statistical tests. We are not able to easily spot differences near the conventional 95% certainty threshold.

However, we demonstrated how you can adapt our code to conduct formal hypothesis tests like the [Rao-Scott chi-square test](#) for weighted proportions.

Another drawback to this approach is that we've been unable to showcase estimates for the proportion of responses at any *one* phase of the study. For example, in our last figure, we estimated that about 35% of women who *planned to use* contraception within the year at Phase 1 did so at Phase 2; our figure does not show how many women planned to use contraception within the year *as a share of the Phase 1 population*.

To better understand the change over time relative to the size of each subgroup in our analysis, we'll turn to a slightly more complicated data visualization method. In our next post, we'll show how to create **alluvial plots**, like those shown in the first two pages of each PMA report.

5 POST 5

In our last post, we demonstrated [how to calculate](#) key indicators for women's family planning status with new [panel surveys](#) from our partners at [PMA](#). When you download PMA data from [IPUMS PMA](#), you can include multiple samples together in the same data extract. Currently, Phase 1 and Phase 2 data are available for six samples, and we've devoted much of [this series](#) to reproducing and synthesizing the major findings published in individual [PMA reports](#) for each sample:

- [Burkina Faso](#)
- [DRC - Kinshasa](#)
- [DRC - Kongo Central](#)
- [Kenya](#)
- [Nigeria - Kano](#)
- [Nigeria - Lagos](#)

Now that we've learned how to compare population-level estimates for indicators in each population with [grouped bar charts](#), we'd like to dig into some of the other data visualization tools that are commonly used for two-phase panel data. We'll quickly recap our approach to building bar charts, and then we'll explore color-coded crosstabs - or [heatmaps](#) - followed by [alluvial plots](#) built with [ggalluvial](#), an extension to the [ggplot2](#) package for R.

5.1 SETUP

In addition to [ggalluvial](#), we'll also showcase just a few of the helpful functions in [scales](#), a package devoted to making axes, labels, and legends easier to read (in particular, we'll use [percent](#) to transform proportions into percentages labeled with the % symbol). You'll need those two packages, plus the three packages we've already used at length in this series: [tidyverse](#), [ipumsr](#), and [srvyr](#).

```
library(tidyverse)
library(ipumsr)
library(srvyr)
library(ggalluvial)
library(scales)
```

As a reminder, our last post featured a [wide format](#) data extract with “Female Respondents” only (other household members not participating in the panel study are excluded). If you’re following along with this series, you can use the same extract again in this post; if not, you’ll need to build a new extract that contains all of the variables we’ll use here ([preselected](#) variables are added automatically):

- [RESULTFQ](#) - Result of female questionnaire
- [PANELWEIGHT](#) - Phase 2 female panel weight
- [RESIDENT](#) - Household residence / membership
- [PREGNANT](#) - Pregnancy status
- [GEOCD](#) - Province, DRC
- [GEONG](#) - State, Nigeria
- [CP](#) - Contraceptive user
- [COUNTRY](#) - PMA country (preselected)
- [EAID](#) - Enumeration area (preselected)

Today’s analysis will focus on three [recoded](#) variables we derived in our last post:

- [POP](#) - Population of interest
- [FPSTATUS_1](#) - Pregnant, using contraception, or using no contraception at Phase 1
- [FPSTATUS_2](#) - Pregnant, using contraception, or using no contraception at Phase 2

Finally, our analysis dropped cases for women who only completed one of the two Female Questionnaires, were not members of the *de facto* population, or skipped critical questions regarding current use of family planning. If you’d like a refresher on the steps we took to load, filter, and recode data from our previous post, click the button below:

```

# import the data extract and metadata files
dat <- read_ipums_micro(
  ddi = "data/pma_00106.xml",
  data = "data/pma_00106.dat.gz"
)

# inclusion criteria for analysis
dat <- dat %>%
  filter(
    RESULTFQ_2 == 1, # must have completed Phase 1 FQ
    RESIDENT_1 %in% c(11, 22) & # must be de facto population (both phases)
      RESIDENT_2 %in% c(11, 22),
    CP_1 < 90 & CP_2 < 90 # must answer "current FP use" question (both phases)
  )

# custom variables: `POP` and `FPSTATUS`
dat <- dat %>%
  mutate(
    # Population of interest (country + region, where applicable)
    POP = case_when(
      !is.na(GEOCD) ~ paste("DRC -", as_factor(GEOCD)),
      !is.na(GEONG) ~ paste("Nigeria -", as_factor(GEONG)),
      TRUE ~ as_factor(COUNTRY) %>% as.character()
    ),
    # strata: includes placeholder values for DRC regions
    STRATA_RECODE = if_else(
      is.na(GEOCD),
      as.numeric(STRATA_1),
      as.numeric(GEOCD)
    ),
    # Family planning use-status at Phase 1
    FPSTATUS_1 = case_when(
      PREGNANT_1 == 1 ~ "Pregnant",
      CP_1 == 1 ~ "Using FP",
      CP_1 == 0 ~ "Not Using FP"
    ),
    # Family planning use-status at Phase 2
    FPSTATUS_2 = case_when(
      PREGNANT_2 == 1 ~ "Pregnant",
      CP_2 == 1 ~ "Using FP",
      CP_2 == 0 ~ "Not Using FP"
    ),
    # Create factors to control order of display in graphics output
    across(
      c(FPSTATUS_1, FPSTATUS_2),
      ~.x %>% fct_relevel("Pregnant", "Not Using FP", "Using FP")
    )
  )

```

One more thing: our blog uses a particular font, layout, and color scheme that we've incorporated into a [custom theme](#) we call theme_pma. Feel free to use our theme, tweak it, or create your own. In case you're interested, we've included the code necessary to create our theme below (you'll need the [showtext](#) package to load a custom font).

```
# Custom font
library(showtext)
sysfonts::font_add(
  family = "cabrito",
  regular = ".../fonts/cabritosansnormregular-webfont.ttf"
)
showtext::showtext_auto()
update_geom_defaults("text", list(family = "cabrito", size = 4))

# Theme
theme_pma <- theme_minimal() %>%
  theme(
    text = element_text(family = "cabrito", size = 13),
    plot.title = element_text(size = 22, color = "#00263A",
      hjust = 0, margin = margin(b = 5)),
    plot.subtitle = element_text(hjust = 0, margin = margin(b = 10)),
    strip.background = element_blank(),
    strip.text.y = element_text(size = 16, angle = 0),
    panel.spacing = unit(1, "lines"),
    axis.title.y = element_text(angle = 0, margin = margin(r = 10))
  )
```

5.2 GROUPED BAR CHARTS

Now let's revisit the **grouped bar chart** we made to compare FPSTATUS_1 and FPSTATUS_2 for each population POP. We made this chart in basically two steps.

First, we used [svy](#) to build a summary table that incorporates survey weights from [PANELWEIGHT](#) and generates a 95% confidence interval for each estimate. We used [EAID_1](#) to generate the cluster-robust standard errors underlying each confidence interval, and we stratified standard error estimation by [STRATA_RECODE](#).

Notice that we [group_by](#) FPSTATUS_1 and FPSTATUS_2 here. When we do this, [survey_mean](#) estimates the proportion of outcomes represented by the variable that appears *last*, which is FPSTATUS_2. The proportions sum to 1.0 for each combination of POP and FPSTATUS_1: in other words, we obtain the proportion of FPSTATUS_2 *on the condition* that women from a given POP held a particular status represented by FPSTATUS_1. For this reason, this is known as a **conditional distribution**.

```
status_tbl <- dat %>%
  group_by(POP) %>%
  summarise(
    .groups = "keep",
    cur_data() %>%
      as_survey_design(weight = PANELWEIGHT, id = EAID_1, strata = STRATA_RECODE) %>%
      group_by(FPSTATUS_1, FPSTATUS_2) %>%
      summarise(survey_mean(prop = TRUE, prop_method = "logit", vartype = "ci"))
  )
status_tbl
```

```
# A tibble: 54 × 6
# Groups:   POP [6]
  POP          FPSTATUS_1   FPSTATUS_2      coef `_low` `_upp`
  <chr>        <fct>       <fct>        <dbl>  <dbl>  <dbl>
  1 Burkina Faso Pregnant   Pregnant     0.0302 0.0137 0.0652
  2 Burkina Faso Pregnant   Not Using FP 0.568  0.491  0.642 
  3 Burkina Faso Pregnant   Using FP    0.401  0.329  0.478 
  4 Burkina Faso Not Using FP Pregnant    0.0779 0.0651 0.0929
  5 Burkina Faso Not Using FP Not Using FP 0.739  0.711  0.765 
  6 Burkina Faso Not Using FP Using FP    0.183  0.158  0.211 
  7 Burkina Faso Using FP    Pregnant    0.0993 0.0815 0.121 
  8 Burkina Faso Using FP    Not Using FP 0.248  0.213  0.287 
  9 Burkina Faso Using FP    Using FP    0.653  0.609  0.694 
 10 DRC – Kinshasa Pregnant Pregnant    0.0367 0.0140 0.0930
# ... with 44 more rows
```

As a second step, we plotted each conditional distribution as a series of grouped bar charts arranged in [facets](#) by POP. Because we wanted to recycle the same layout for several similar

variables, we wrapped all of the necessary [ggplot2](#) tools together in a custom function called `pma_bars`.

```
pma_bars <- function(  
  title = NULL,      # an optional title  
  subtitle = NULL,    # an optional subtitle  
  xaxis = NULL,      # an optional label for the x-axis (displayed above)  
  yaxis = NULL       # an optional label for the y-axis (displayed left)  
) {  
  components <- list(  
    theme_pma,  
    labs(  
      title = title,  
      subtitle = subtitle,  
      y = str_wrap(yaxis, 10),  
      x = NULL,  
      fill = NULL  
    ),  
    scale_x_continuous(  
      position = 'bottom',  
      sec.axis = sec_axis(trans = ~., name = xaxis, breaks = NULL),  
      labels = scales::label_percent()  
    ),  
    scale_y_discrete(limits = rev),  
    geom_bar(stat = "identity", fill = "#98579BB0"),  
    geom_errorbar(  
      aes(xmin = `_low`, xmax = `_upp`),  
      width = 0.2,  
      color = "#00263A"  
    )  
  )  
}  
  
status_tbl %>%  
  ggplot(aes(x = coef, y = FPSTATUS_2)) +  
  facet_grid(cols = vars(FPSTATUS_1), rows = vars(POP)) +  
  pma_bars(  
    "CHANGE IN CONTRACEPTIVE USE OR NON-USE",  
    "Percent women age 15–49 who changed contraceptive use status",  
    xaxis = "Phase 1 Status",  
    yaxis = "Phase 2 Status"  
)
```

CHANGE IN CONTRACEPTIVE USE OR NON-USE

Percent women age 15-49 who changed contraceptive use status



5.3 HEATMAPS

We love this bar chart because it packs a lot of information into a single, reader-friendly graphic. However, we mentioned that it has some considerable drawbacks. Most importantly, we weren't able to include information from the **marginal distribution** in each phase.

A marginal distribution for `FPSTATUS_1` would indicate the likelihood that a woman began the survey period pregnant, using family planning, or not using family planning. Likewise the marginal distribution for `FPSTATUS_2` estimates the likelihood that a woman would hold any such status at Phase 2, *independently of* her status at Phase 1. We call these distributions “marginal” because they’re usually included in the row or column margins of a crosstab.

Let’s return to `status_tbl`, but this time we’ll plot it as a crosstab with `color` and `alpha` (transparency) aesthetics. This type of crosstab is usually called a **heatmap**. First, we’ll again wrap a few cosmetic layout options into a custom function we’ll call `pma_heatmap`.

For consistency,
`pma_heatmap` uses
the same color
scheme shown in
the first figure of
each PMA report.

```

pma_heatmap <- function(
  title = NULL,      # an optional title
  subtitle = NULL,   # an optional subtitle
  xaxis = NULL,      # an optional label for the x-axis (displayed below)
  yaxis = NULL       # an optional label for the y-axis (displayed right)
){
  components <- list(
    theme_pma %>% replace% theme(
      axis.text = element_text(size = 10),
      strip.text.x = element_text(size = 16,
                                   margin = margin(t = 10, b = 10)),
      axis.title.y.right = element_text(angle = 0, margin = margin(l = 10)),
      axis.title.x.bottom = element_text(margin = margin(t = 20)),
      panel.grid = element_blank(),
      legend.position = "none"
    ),
    labs(
      title = title,
      subtitle = subtitle,
      x = xaxis,
      y = str_wrap(yaxis, 10),
    ),
    scale_fill_manual(values = c(
      "Pregnant" = "#B4B3B3",
      "Not Using FP" = "#4E4F71",
      "Using FP" = "#EFD372"
    )),
    scale_color_manual(values = c("black", "white")),
    scale_y_discrete(position = "right", limits = rev)
  )
}

```

The plot, itself, is built with rectangles from [geom_tile](#) and text labels from [geom_text](#). Both of these require a pair of x and y-coordinates, so we'll specify them globally in a [ggplot](#) function.

Then, we tell [geom_tile](#) to use one fill color for each type of response in `FPSTATUS_1`: this makes it easy for the reader to see that the totals in each tile sum to 100% in columns (not rows). The alpha aesthetic uses the value in `coef` to control the transparency of each color (by default, our minimum value `0` would be 100% transparent).

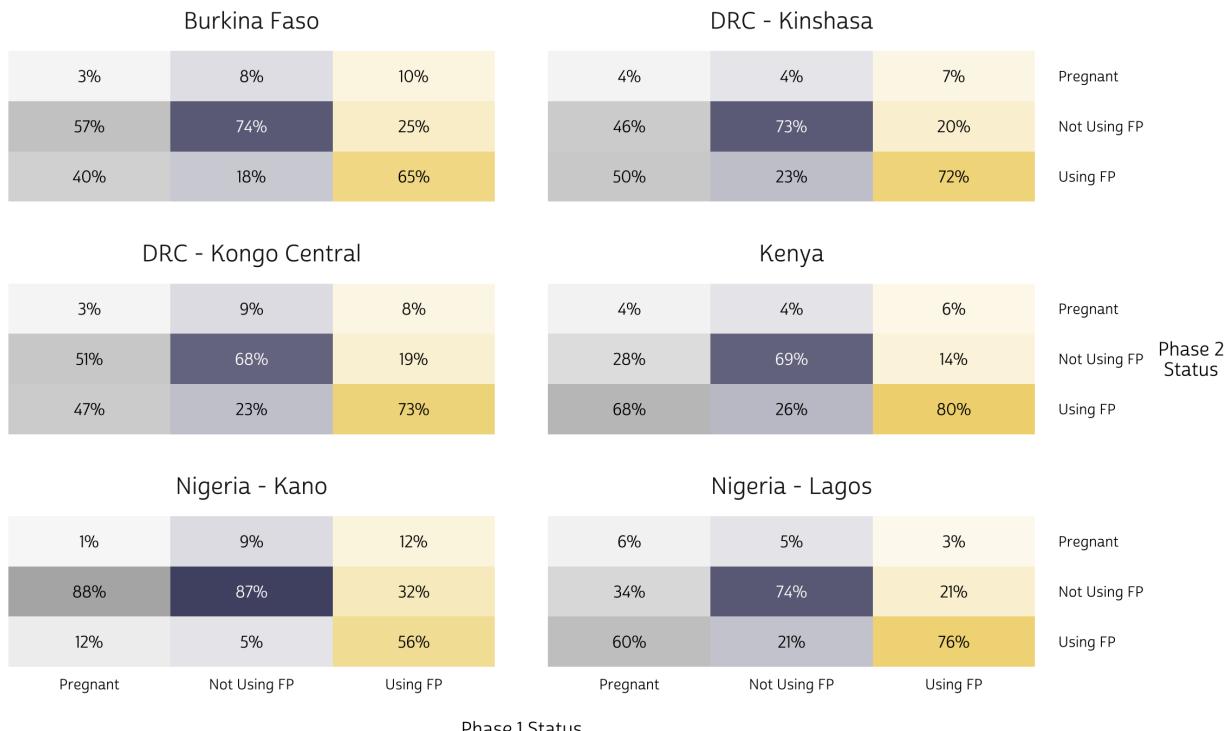
The aesthetics in [geom_text](#) include `label` and `color`. Only `label` is really necessary: it tells the function to use the value in `coef` as a text label, except that we use [percent](#) to stylize each number as a percentage rounded to the nearest integer. We're also including `color` to switch the font color from black to white for purple tiles where `coef` is higher than `0.5`: black text would be too hard to read here.

Finally, `facet_wrap` plots each POP separately. We use `nrow = 3` to specify three rows, and we use `scales = "fixed"` to save a bit of space: the labels for `FPSTATUS_1` and `FPSTATUS_2` are printed only once in the row and column margins for the entire plot.

```
status_tbl %>%
  ggplot(aes(x = FPSTATUS_1, y = FPSTATUS_2)) +
  geom_tile(aes(fill = FPSTATUS_1, alpha = coef)) +
  geom_text(aes(
    label = scales::percent(coef, 1),
    color = coef > 0.5 & FPSTATUS_1 == "Not Using FP" # white vs black text
  )) +
  facet_wrap(~POP, nrow = 3, scales = "fixed") +
  pma_heatmap(
    "CHANGE IN CONTRACEPTIVE USE OR NON-USE",
    "Percent women age 15-49 who changed contraceptive use status",
    xaxis = "Phase 1 Status",
    yaxis = "Phase 2 Status"
  )
)
```

CHANGE IN CONTRACEPTIVE USE OR NON-USE

Percent women age 15-49 who changed contraceptive use status



The nice thing about this heatmap layout is that we *can* easily include data from the marginal distribution of `FPSTATUS_1` and `FPSTATUS_2`. To do so, we'll first need to add them to `status_tbl`. Note: because our heatmap is not well-suited for comparing confidence intervals, we'll omit them in `survey_mean` with the argument `vartype = NULL`.

```

col_margins <- dat %>%
  group_by(POP) %>%
  summarise(
    .groups = "keep",
    cur_data() %>%
      as_survey_design(weight = PANELWEIGHT, id = EAID_1, strata = STRATA_RECODE) %>%
      group_by(FPSTATUS_1) %>%
      summarise(cols = survey_mean(prop = TRUE, prop_method = "logit", vartype = NULL))
  )

row_margins <- dat %>%
  group_by(POP) %>%
  summarise(
    .groups = "keep",
    cur_data() %>%
      as_survey_design(weight = PANELWEIGHT, id = EAID_1, strata = STRATA_RECODE) %>%
      group_by(FPSTATUS_2) %>%
      summarise(rows = survey_mean(prop = TRUE, prop_method = "logit", vartype = NULL))
  )

status_tbl <- status_tbl %>% right_join(col_margins) %>% right_join(row_margins)

status_tbl

```

```

# A tibble: 54 × 8
# Groups:   POP [6]
  POP        FPSTATUS_1  FPSTATUS_2      coef `_low` `_upp`    cols    rows
  <chr>     <fct>       <fct>        <dbl>  <dbl>  <dbl>  <dbl>  <dbl>
1 Burkina Faso Pregnant    Pregnant    0.0302 0.0137 0.0652 0.0879 0.0799
2 Burkina Faso Pregnant    Not Using FP 0.568  0.491  0.642  0.0879 0.583 
3 Burkina Faso Pregnant    Using FP    0.401  0.329  0.478  0.0879 0.337 
4 Burkina Faso Not Using FP Pregnant    0.0779 0.0651 0.0929 0.624  0.0799
5 Burkina Faso Not Using FP Not Using FP 0.739  0.711  0.765  0.624  0.583 
6 Burkina Faso Not Using FP Using FP    0.183  0.158  0.211  0.624  0.337 
7 Burkina Faso Using FP    Pregnant    0.0993 0.0815 0.121  0.288  0.0799
8 Burkina Faso Using FP    Not Using FP 0.248  0.213  0.287  0.288  0.583 
9 Burkina Faso Using FP    Using FP    0.653  0.609  0.694  0.288  0.337 
10 DRC – Kinshasa Pregnant Pregnant   0.0367 0.0140 0.0930 0.0552 0.0533
# ... with 44 more rows

```

To keep things simple, we've named the marginal distribution for `FPSTATUS_1` "cols", and the marginal distribution for `FPSTATUS_2` "rows". Ultimately, we think it's clearest to [paste](#) these values (as percentages) together with the original labels from `FPSTATUS_1` and `FPSTATUS_2` (the symbol `\n` represents a line break). We'll also transform each character string into a [factor](#), which ensures that the values will be plotted in the same order that they appear in our table.

Finally, we switch from `scales = "fixed"` to `scales = "free"`. This time, we'll want to print the row and column margins for each `POP` separately.

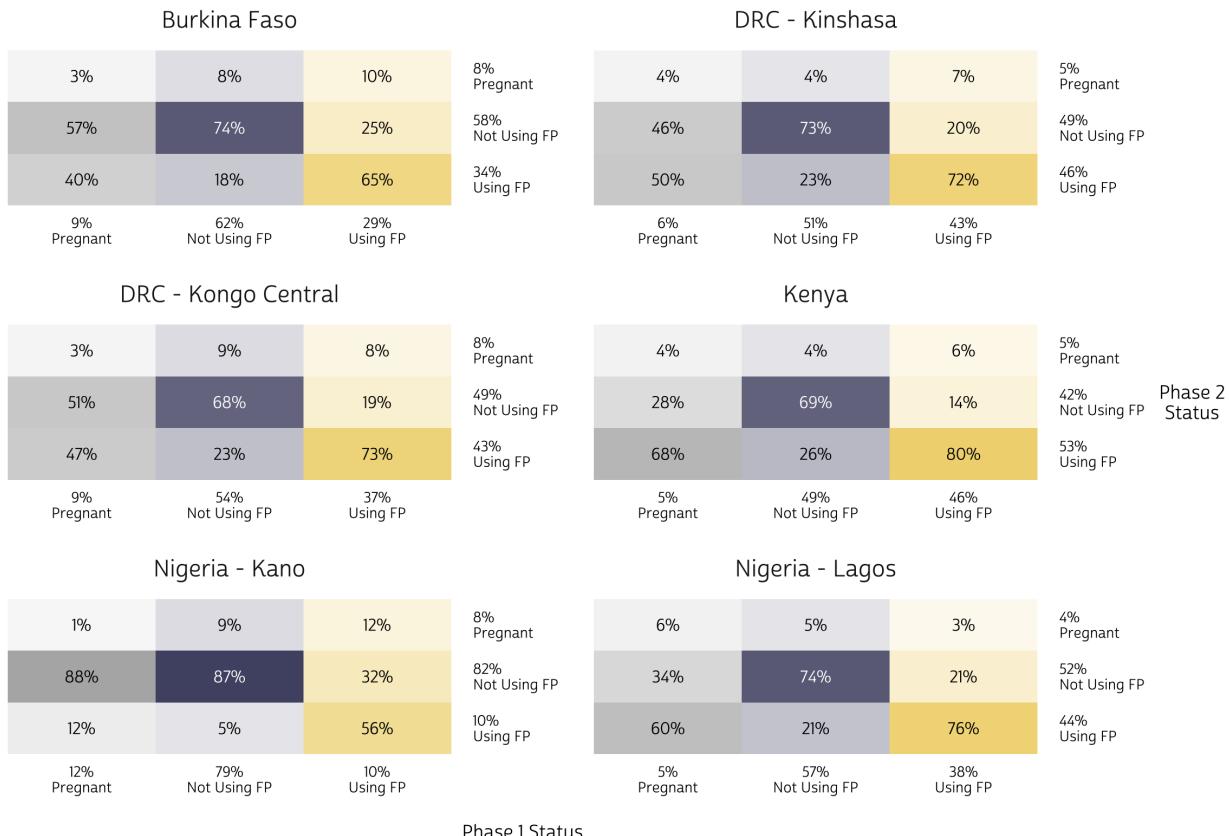
```

status_tbl %>%
  ggplot(aes(
    x = paste0(scales::percent(cols, 1), "\n", FPSTATUS_1) %>% as_factor,
    y = paste0(scales::percent(rows, 1), "\n", FPSTATUS_2) %>% as_factor
  )) +
  geom_tile(aes(fill = FPSTATUS_1, alpha = coef)) +
  geom_text(aes(
    label = scales::percent(coef, 1),
    color = coef > 0.5 & FPSTATUS_1 == "Not Using FP"
  )) +
  facet_wrap(~POP, nrow = 3, scales = "free") +
  pma_heatmap(
    "CHANGE IN CONTRACEPTIVE USE OR NON-USE",
    "Percent women age 15-49 who changed contraceptive use status",
    xaxis = "Phase 1 Status",
    yaxis = "Phase 2 Status"
  )
)

```

CHANGE IN CONTRACEPTIVE USE OR NON-USE

Percent women age 15-49 who changed contraceptive use status



The information contained in our heatmap is similar to what we saw in our bar chart, except for two things:

1. There are no error bars on our heatmap. If we wanted to include information about the confidence interval for each estimation, we would have to include [text symbols](#).
2. While both plots show information about the conditional distribution of FPSTATUS_2 given a starting point in FPSTATUS_1, only the heatmap includes the marginal distribution of each variable in its row and column margins.

The marginal distribution may provide crucial information about the conditional distribution that we would otherwise miss. Consider Burkina Faso, where both users and non-users of family planning at Phase 1 were generally most likely to maintain their status at Phase 2. The marginal distribution adds additional information: non-users comprise a larger share of the overall population at Phase 1.

In certain contexts, you may want to combine information from the Phase 1 marginal distribution together with the conditional distribution of outcomes at Phase 2. To continue with our example from Burkina Faso, you might report that - because non-users represent about 62% of the population, only about 11% of the population adopted family planning at Phase 2 following non-use at Phase 1. That is: 18% of 62% is 11%.

In contrast with the conditional distribution, this type of distribution describes the share of the population that experiences some combination of Phase 1 and Phase 2 outcomes *without* assuming a particular starting point at Phase 1. It's known as a **joint distribution** because it gives the probability that two events will happen together (in sequence). Let's return to our summary table, status_tbl:

```
status_tbl
```

```
# A tibble: 54 × 8
# Groups:   POP [6]
  POP      FPSTATUS_1  FPSTATUS_2    coef `_low` `_upp`  cols  rows
  <chr>    <fct>     <fct>       <dbl>  <dbl>  <dbl>  <dbl>  <dbl>
1 Burkina Faso Pregnant  Pregnant  0.0302 0.0137 0.0652 0.0879 0.0799
2 Burkina Faso Pregnant  Not Using FP 0.568  0.491  0.642  0.0879 0.583 
3 Burkina Faso Pregnant  Using FP   0.401  0.329  0.478  0.0879 0.337 
4 Burkina Faso Not Using FP Pregnant  0.0779 0.0651 0.0929 0.624  0.0799
5 Burkina Faso Not Using FP Not Using FP 0.739  0.711  0.765  0.624  0.583 
6 Burkina Faso Not Using FP Using FP   0.183  0.158  0.211  0.624  0.337 
7 Burkina Faso Using FP   Pregnant  0.0993 0.0815 0.121  0.288  0.0799
8 Burkina Faso Using FP   Not Using FP 0.248  0.213  0.287  0.288  0.583 
9 Burkina Faso Using FP   Using FP   0.653  0.609  0.694  0.288  0.337 
10 DRC – Kinshasa Pregnant Pregnant 0.0367 0.0140 0.0930 0.0552 0.0533
# ... with 44 more rows
```

To find the estimated joint distribution for each combination of FPSTATUS_1 and FPSTATUS_2, you could simply multiply each value in cols by the value in coef:

```
status_tbl %>% mutate(joint = cols * coef)
```

```

# A tibble: 54 × 9
# Groups:   POP [6]
  POP          FPSTATUS_1    FPSTATUS_2      coef `_low` `_upp`  cols  rows  joint
  <chr>        <fct>       <fct>        <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>
1 Burkina Faso Pregnant    Pregnant     0.0302 0.0137 0.0652 0.0879 0.0799 0.00266
2 Burkina Faso Pregnant    Not Using FP 0.568  0.491  0.642  0.0879 0.583  0.0499
3 Burkina Faso Pregnant    Using FP     0.401  0.329  0.478  0.0879 0.337  0.0353
4 Burkina Faso Not Using FP Pregnant    0.0779 0.0651 0.0929 0.624  0.0799 0.0486
5 Burkina Faso Not Using FP Not Using FP 0.739  0.711  0.765  0.624  0.583  0.461
6 Burkina Faso Not Using FP Using FP     0.183  0.158  0.211  0.624  0.337  0.114
7 Burkina Faso Using FP     Pregnant    0.0993 0.0815 0.121  0.288  0.0799 0.0286
8 Burkina Faso Using FP     Not Using FP 0.248  0.213  0.287  0.288  0.583  0.0713
9 Burkina Faso Using FP     Using FP     0.653  0.609  0.694  0.288  0.337  0.188
10 DRC – Kinshasa Pregnant Pregnant   0.0367 0.0140 0.0930 0.0552 0.0533 0.00203
# ... with 44 more rows

```

In practice, you'll usually want to let `svy` calculate a confidence interval for each joint probability. To do so, we'll add an `interact` function listing the variables in `group_by` that we want to model jointly.

```

joint_tbl <- dat %>%
  group_by(POP) %>%
  summarise(
    .groups = "keep",
    cur_data() %>%
      as_survey_design(weight = PANELWEIGHT, id = EAID_1, strata = STRATA_RECODE) %>%
      group_by(interact(FPSTATUS_1, FPSTATUS_2)) %>%
      summarise(joint = survey_mean(prop = TRUE, prop_method = "logit", vartype = "ci"))
  )

```

joint_tbl

```

# A tibble: 54 × 6
# Groups:   POP [6]
  POP          FPSTATUS_1    FPSTATUS_2      joint joint_low joint_upp
  <chr>        <fct>       <fct>        <dbl>     <dbl>      <dbl>
1 Burkina Faso Pregnant    Pregnant    0.00266  0.00120  0.00587
2 Burkina Faso Pregnant    Not Using FP 0.0499   0.0404   0.0615 
3 Burkina Faso Pregnant    Using FP     0.0353   0.0291   0.0427 
4 Burkina Faso Not Using FP Pregnant   0.0486   0.0402   0.0588 
5 Burkina Faso Not Using FP Not Using FP 0.461    0.428    0.495  
6 Burkina Faso Not Using FP Using FP    0.114    0.100    0.130  
7 Burkina Faso Using FP     Pregnant   0.0286   0.0228   0.0357 
8 Burkina Faso Using FP     Not Using FP 0.0713   0.0613   0.0829 
9 Burkina Faso Using FP     Using FP    0.188    0.164    0.214  
10 DRC – Kinshasa Pregnant Pregnant   0.00203  0.000794 0.00515
# ... with 44 more rows

```

Now, the values in `joint` sum to `1.0` for each `POP`. Returning to our heatmap, we'll want to use the same color for every column, indicating that the percentages sum for 100% for each population.

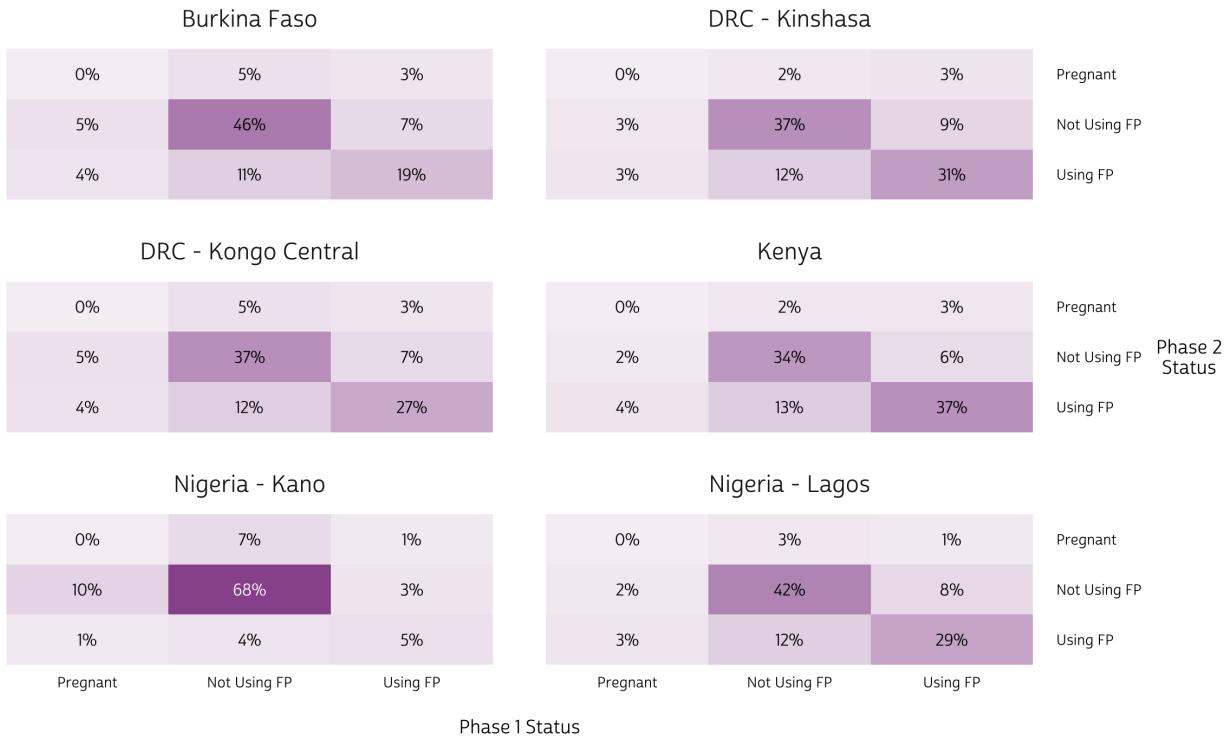
```

joint_tbl %>%
  ggplot(aes(x = FPSTATUS_1, y = FPSTATUS_2)) +
  geom_tile(aes(alpha = joint), fill = "#98579B") +
  geom_text(aes(
    label = scales::percent(joint, 1),
    color = joint > 0.5 & FPSTATUS_1 == "Not Using FP"
  )) +
  facet_wrap(~POP, nrow = 3, scales = "fixed") +
  pma_heatmap(
    "CHANGE IN CONTRACEPTIVE USE OR NON-USE",
    "Percent women age 15–49 who changed contraceptive use status",
    xaxis = "Phase 1 Status",
    yaxis = "Phase 2 Status"
  )

```

CHANGE IN CONTRACEPTIVE USE OR NON-USE

Percent women age 15-49 who changed contraceptive use status



Information provided by the joint distribution nuances our story a bit further. To continue with our examination of Burkina Faso: we knew that family planning users and non-users at Phase 1 were each most likely to maintain, rather than switch their status at Phase 2. However, it's now clear that *continuous non-users* (non-users at both Phase 1 and Phase 2) represent a near-majority of the population.

5.4 ALLUVIAL PLOTS

Alluvial plots are an especially popular way to visualize longitudinal data, in part, because they combine information from each of the three distributions we've discussed. They also make it possible to show data from more than two variables (we'll use them again when Phase 3 data become available). You'll find alluvial plots on the first two pages of the PMA report for each sample.

In an alluvial plot, the marginal distribution of responses for each variable are usually plotted in vertical stacks. The [ggalluvial](#) package authors refer to these stacks as "strata", and they may be layered onto a [ggplot](#) with [geom_stratum](#). In our case, the strata will show the marginal distribution of women in FPSTATUS_1 and FPSTATUS_2.

The **joint distribution** for any pair of variables is plotted in horizontal splines called "alluvia", which bridge the space between any given pair of strata. Alluvia are plotted with [geom_flow](#).

Finally, we'll use color to map each alluvium with an originating stratum from FPSTATUS_1. This will help the reader visualize the conditional distribution of FPSTATUS_2 responses given a starting point in FPSTATUS_1.

To begin, let's revisit `joint_tbl`, which only contains the joint distribution for FPSTATUS_1 and FPSTATUS_2. In fact, [ggalluvial](#) will calculate the marginal distribution for both variables automatically if we reshape `joint_tbl` with [pivot_longer](#) like so:

```
joint_tbl <- joint_tbl %>%
  rowid_to_column("alluvium") %>%
  pivot_longer(
    c(FPSTATUS_1, FPSTATUS_2),
    names_to = "x",
    values_to = "stratum"
  ) %>%
  mutate(x = ifelse(x == "FPSTATUS_1", "Phase 1", "Phase 2")) %>%
  arrange(x, alluvium)

joint_tbl
```

```

# A tibble: 108 × 7
# Groups:   POP [6]
  alluvium POP      joint joint_low joint_upp x      stratum
  <int> <chr>     <dbl>    <dbl>    <dbl> <chr> <fct>
1     1 Burkina Faso 0.00266  0.00120  0.00587 Phase 1 Pregnant
2     2 Burkina Faso 0.0499   0.0404   0.0615  Phase 1 Pregnant
3     3 Burkina Faso 0.0353   0.0291   0.0427  Phase 1 Pregnant
4     4 Burkina Faso 0.0486   0.0402   0.0588  Phase 1 Not Using FP
5     5 Burkina Faso 0.461    0.428    0.495   Phase 1 Not Using FP
6     6 Burkina Faso 0.114    0.100    0.130   Phase 1 Not Using FP
7     7 Burkina Faso 0.0286   0.0228   0.0357  Phase 1 Using FP
8     8 Burkina Faso 0.0713   0.0613   0.0829  Phase 1 Using FP
9     9 Burkina Faso 0.188    0.164    0.214   Phase 1 Using FP
10    10 DRC - Kinshasa 0.00203 0.000794 0.00515 Phase 1 Pregnant
# ... with 98 more rows

```

Here, we create the column `alluvium` to hold the original row number for each of the 56 combinations of `POP`, `FPSTATUS_1`, and `FPSTATUS_2`. When we [pivot_longer](#), we repeat the value in `joint` once for each end of the same `alluvium`. The values in `stratum` describe the strata to which each `alluvium` is attached, and `x` indicates whether the stratum is located in the Phase 1 or Phase 2 stack.

As with our heatmap, we'll want to define some custom fonts, color, and layout options adapted from `theme_pma`. We'll bundle these together in a function called `pma_alluvial` - feel free to use, adjust, or omit this function for your own purposes.

For consistency,
`pma_alluvial` uses
the same color
scheme shown in
the first alluvial plot
in each PMA report.

```

pma_alluvial <- function(
  title = NULL,      # an optional title
  subtitle = NULL,   # an optional subtitle
  xaxis = NULL,      # an optional label for the x-axis (displayed below)
  yaxis = NULL        # an optional label for the y-axis (displayed left)
){
  components <- list(
    theme_pma %+replace% theme(
      plot.title = element_text(size = 22, color = "#541E5A",
                                  hjust = 0.5, mar = margin(b = 5)),
      plot.subtitle = element_text(hjust = 0.5, margin = margin(b = 20)),
      axis.text.x = element_text(color = "#541E5A",
                                  margin = margin(t = 5, b = 10)),
      strip.text.x = element_text(size = 13, margin = margin(b = 5)),
      plot.margin = margin(0, 100, 0, 100),
      legend.position = "bottom",
      legend.title = element_blank(),
      legend.spacing.x = unit(10, "pt"),
      panel.grid = element_blank(),
      axis.text.y = element_blank()
    ),
    labs(
      title = title,
      subtitle = subtitle,
      x = xaxis,
      y = str_wrap(yaxis, 10),
    ),
    scale_fill_manual(values = c(
      "Pregnant" = "#B4B3B3",
      "Not Using FP" = "#4E4F71",
      "Using FP" = "#EFD372"
    )),
    scale_y_continuous(expand = c(0, 0))
  )
}

```

We'll start by mapping common aesthetics in a [ggplot](#) function. We'll map the values in `x` onto our x-axis, and we'll map the values in `joint` onto the y-axis. The remaining aesthetics are specific to the functions from [ggalluvial](#): we'll use `stratum` to build vertical strata and to define colors mapped with “fill”. We also use the identifying numbers in `alluvium` to organize responses into alluvia.

The remaining functions are straightforward, since they mainly use information passed from [ggplot](#). We make only one small modification to [geom_stratum](#): setting `size = 0` removes border lines that appear around each stratum, by default.

```

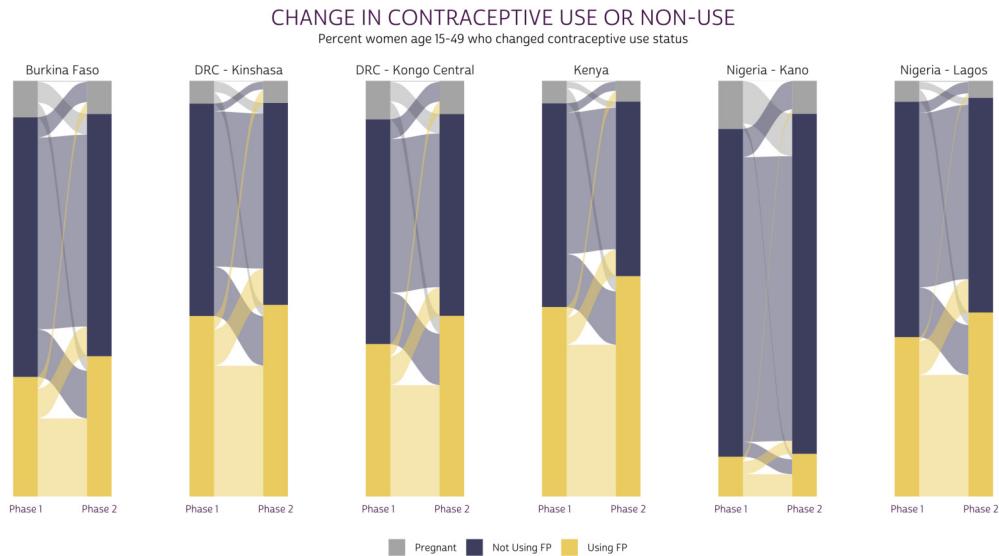
status_alluvial <- joint_tbl %>%
  ggplot(aes(
    x = x,
    y = joint,
    fill = stratum,
    stratum = stratum,
    alluvium = alluvium
  )) +
  geom_flow() +
  geom_stratum(size = 0) +
  facet_wrap(~POP, scales = "free_x", nrow = 1) +
  pma_alluvial(
    "CHANGE IN CONTRACEPTIVE USE OR NON-USE",
    "Percent women age 15-49 who changed contraceptive use status",
    )

```

status_alluvial

Warning: `spread_()` was deprecated in tidyverse 1.2.0.
Please use `spread()` instead.

Warning: The `.` argument of `group_by()` is deprecated as of dplyr 1.0.0.

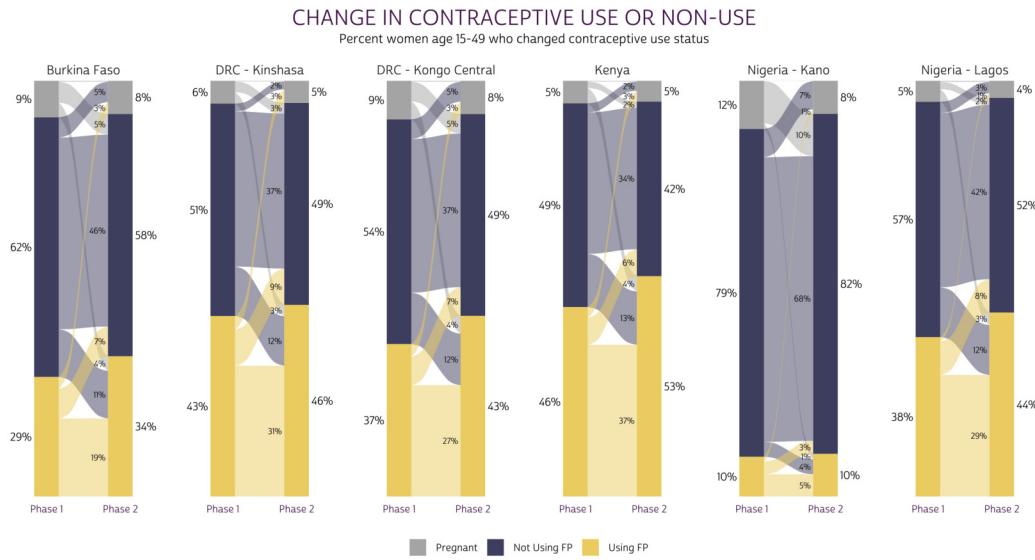


Of course, you should always include either y-axis gridlines or text labels for the probabilities shown on a plot like this one. We find it clearer to include the latter, which we'll build with [geom_text](#).

These labels are a bit tricky, but the basic idea is that you use `stat = "stratum"` to label strata, and `stat = "flow"` to label alluvia. Then, you use `after_stat` to build labels from statistics that `ggalluvial` uses to construct the plot - check out [this list](#) of available statistics for details. We'll use the `prop` statistic to obtain *both* the marginal and joint probabilities for each outcome (we'll leave the conditional probabilities unlabeled, but you could adjust this code to include them here).

```
status_alluvial +
  geom_text(
    stat = "stratum",    # label strata
    aes(label = ifelse(
      x == 1, # labels the strata for Phase 1, otherwise blank """
      scales::percent(after_stat(prop), 1),
      """
    )),
    nudge_x = -0.2,    # nudge a bit to the left
    hjust = "right",  # right-justify
  ) +
  geom_text(
    stat = "stratum",    # label strata
    aes(label = ifelse(
      x == 2, # labels the strata for Phase 2, otherwise blank """
      scales::percent(after_stat(prop), 1),
      """
    )),
    nudge_x = 0.2,     # nudge a bit to the right
    hjust = "left",   # left-justify
  ) +
  geom_text(
    stat = "flow",     # label alluvia
    aes(label = ifelse(
      after_stat(flow) == "to" & # only label the destination (right-side)
      after_stat(prop) >= 0.01, # hide if 0%
      scales::percent(after_stat(prop), 1),
      """
    )),
    nudge_x = -0.2,    # nudge a bit to the left
    hjust = "right",  # right-justify
    size = 3          # use a slightly smaller font
  )
```

Values may not add to 100% due to rounding (values rounded to 0% are not labelled).



Now, it's easy to identify the proportion of women at each phase *and* the proportion who switched or maintained their status between phases. If possible, we recommend aligning alluvial plots for every sample in a single row as shown: this allows the readers to visually compare the relative size of strata and alluvia across samples.

5.5 NEXT STEPS

So far in [this series](#), we've covered topics related to:

- [Data availability](#)
- [Instructions of obtaining data](#)
- [Sample design](#)
- [Key family planning indicators](#)
- [Data Visualization](#)

In two weeks, we'll be wrapping up this introduction to PMA Panel Data with an update on a topic we first covered last year: the [contraceptive calendar](#) section of the Female Questionnaire. As we'll see, the calendar adds a different temporal dimension to the panel study: it represents the contraceptive use, non-use, and pregnancy status of women recalled on a *monthly basis* for several months prior the interview. We'll show how to parse these data from string-format, and how to merge responses obtained at Phase 1 and Phase 2 for each woman.

6 POST 6

We're wrapping up our introduction to the new [PMA Panel Surveys](#) this week with an update to a topic we first introduced [one year ago](#) when [IPUMS PMA](#) released Phase 1 data from Burkina Faso, DRC, Kenya, and Nigeria. With the release of Phase 2 data from these countries this spring, it's now possible to combine monthly [contraceptive calendar](#) data collected at multiple timepoints, each covering partially overlapping periods in the reproductive health history of every panel member.

The contraceptive calendar data are particularly exciting because they offer researchers an opportunity to explore longitudinal analysis techniques that are otherwise not feasible with the first two phases of panel observations. For example, we'll demonstrate how you might use [survival analysis](#) to test whether women with [unmet need](#) or [plans to adopt](#) a family planning method at Phase 1 were quicker to begin using one in the months between Phase 1 and Phase 2. Additionally, because calendar data are collected once *per phase*, there are unique opportunities to study the reliability of self-reporting for the same month recalled at different times [@Anglewicz2022-mx].

In this post, we'll share code you can use to parse and analyze calendar data collected in each phase in a data extract containing multiple samples. We'll use the [survival](#) package for R to model "time-to-event" for adoption of a family planning method for women who were not using one on the day of the Phase 1 interview. Finally, we'll use [ggplot2](#) to build a Kaplan-Meier curve for the cumulative incidence of adoption over each month between the Phase 1 and Phase 2 interviews.

Newcomers to the contraceptive calendar should check out our [previous blog post](#), including video from a workshop from the [2021 Population Association of America](#) annual meeting.

6.1 SETUP

Over on the contraceptive calendar [variable group page](#), you'll find two types of calendars for every sample:

The screenshot shows a web browser window for the IPUMS PMA website. The URL is pma.ipums.org/pma-action/variables/group?id=fem_cal. The page title is "IPUMS PMA" and "PERFORMANCE MONITORING FOR ACTION". The top right corner shows a "DATA CART" with "0 VARIABLES" and "6 SAMPLES", and a "VIEW CART" button. The main content area has a header "CURRENTLY BROWSING: 'FAMILY PLANNING - PERSON'" with a "CHANGE" link. Below this are "SELECT VARIABLES" and "DISPLAY OPTIONS" sections. A note says "AN 'X' INDICATES THE VARIABLE IS AVAILABLE IN THAT DATASET." A table titled "CONTRACEPTIVE CALENDAR VARIABLES" lists variables like CALENDARKE, CALENDARKEWHY, CALENDARNG, CALENDARNGWHY, CALENDARBE, CALENDARBFWHY, CALENDARCD, and CALENDARCDWHY, along with their variable labels and availability across datasets (BURKF, CONDR, KENYA, NIGERA). At the bottom, it says "SUPPORTED BY: THE BILL & MELINDA GATES FOUNDATION, PMA, STAT/TRANSFER, AND UNIVERSITY OF MINNESOTA." and "COPYRIGHT © MINNESOTA POPULATION CENTER, UNIVERSITY OF MINNESOTA."

# CONTRACEPTIVE CALENDAR VARIABLES TOP		LONGITUDINAL SAMPLES							
Add to cart	Variable	Variable Label	Type	BURKF 2020 - 2021	COND 2019a - 2020a	COND 2019b - 2020b	KENYA 2019 - 2020	NIGERA 2019a - 2020a	NIGERA 2019b - 2020b
+	CALENDARKE	Contraceptive calendar (Kenya)	P	.	.	.	X	.	.
+	CALENDARKEWHY	Contraceptive calendar - why stopped using (Kenya)	P	.	.	.	X	.	.
+	CALENDARNG	Contraceptive calendar (Nigeria)	P	X	X
+	CALENDARNGWHY	Contraceptive calendar - why stopped using (Nigeria)	P	X	X
+	CALENDARBE	Contraceptive calendar (Burkina Faso)	P	X
+	CALENDARBFWHY	Contraceptive calendar - why stopped using (Burkina Faso)	P	X
+	CALENDARCD	Contraceptive calendar (DRC)	P	.	X	X	.	.	.
+	CALENDARCDWHY	Contraceptive calendar - why stopped using (DRC)	P	.	X	X	.	.	.

We refer to the main calendar as the “contraceptive calendar”, and it includes the following variables:

- [CALENDARBE](#)
- [CALENDARCD](#)
- [CALENDARKE](#)
- [CALENDARNG](#)

This calendar represents contraceptive use, pregnancy, pregnancy termination, and birth information for each month preceding the interview for the Female Questionnaire in a particular phase of the panel study. Women are asked to recall their status for each month in the calendar period, and their responses are recorded in a single comma delimited string with the following codes:

- B - Birth
- P - Pregnant
- T - Pregnancy ended
- 0 - No family planning method used
- 1 - Female Sterilization
- 2 - Male Sterilization
- 3 - Implant
- 4 - IUD
- 5 - Injectables
- 7 - Pill
- 8 - Emergency Contraception
- 9 - Male Condom
- 10 - Female Condom
- 11 - Diaphragm
- 12 - Foam / Jelly
- 13 - Standard Days / Cycle beads
- 14 - LAM
- 30 - Rhythm method
- 31 - Withdrawal
- 39 - Other traditional methods

The second calendar is the “discontinuation calendar”, and it gives the reason why a woman stopped using a family planning method for each month following an episode of continuous use. This calendar is represented by the following variables:

- CALENDARBFWHY
- CALENDARCDWHY
- CALENDARKEWHY
- CALENDARNGWHY

Like the main contraceptive calendar, the discontinuation calendar is a single comma delimited string. It contains the following codes for months when a method was discontinued (and is blank otherwise):

- 1 - Infrequent sex / husband away
- 2 - Became pregnant while using
- 3 - Wanted to become pregnant
- 4 - Husband / partner disapproved
- 5 - Wanted more effective method
- 6 - Side effects / health concerns
- 7 - Lack of access / too far

- 8 - Costs too much
- 9 - Inconvenient to use
- 10 - Up to God / fatalistic
- 11 - Difficult to get pregnant / menopausal
- 12 - Marital dissolution / separation
- 96 - Other

We've created a data extract containing all of the eight calendar variables, plus these additional variables that we'll need for our analysis:

- RESULTFQ - Result of female questionnaire
- FQINSTID - Unique ID for female questionnaire
- RESIDENT - Household residence / membership
- COUNTRY - Country of residence
- INTFQMON & INTFQYEAR - Date of Female Questionnaire interview
- FPCURREFFMETHRC - Most effective current family planning method (recoded²⁶)
- PREGNANT - Current pregnancy status
- UNMETYN - Total unmet need
- FPPLANVAL - When will start using FP method in the future - value
- FPPLANWHEN - When will start using FP method in the future - unit
- KID1STBIRTHMO & KID1STBIRTHYR - Date of first childbirth
- LASTBIRTHMO & LASTBIRTHYR - Date of most recent childbirth
- PANELBIRTHMO & PANELBIRTHYR - Date of childbirth during the panel study
- OTHERBIRTHMO & OTHERBIRTHYR - Date of any other childbirth during the calendar period
- PREGENDMO & PREGENDYR - Date of most recent pregnancy termination (miscarriage, abortion, or stillbirth)
- PANELPREGENDMO & PANELPREGENDYR - Date of pregnancy termination during the panel study (miscarriage, abortion, or stillbirth)
- FPBEGINUSEMO & FPBEGINUSEYR - Date of adoption for currently used family planning method

Our extract contains data from all available longitudinal samples.²⁷ As in [previous posts](#), we've selected "Female Respondents" organized in wide format: **each row** represents the Phase 1 and Phase 2 responses for **one female respondent**. Variables from the Phase 1 questionnaire are named with the suffix _1 (e.g. CALENDARKE_1), while variables from the Phase 2 questionnaire are named with the suffix _2 (e.g. CALENDARKE_2).

²⁶The related variable FPCURREFFMETH reports the most effective method reported by each woman. In FPCURREFFMETHRC, these responses are combined with detailed information about her use of the lactational amenorrhea method (LAM), emergency contraception, or specific types of injectable methods.

²⁷Burkina Faso, Kenya, DRC (Kinshasa and Kongo Central), and Nigeria (Kano and Lagos)

We'll load the data extract into R together with each of the packages we'll feature in this post. Then, we'll drop cases for women who did not fully complete the Female Questionnaire or were not members of the *de facto* population in both phases.

Finally, we'll modify two variables to make this post a bit easier to read. First, we'll transform COUNTRY into a factor containing a two-letter ISO country code for each sample.²⁸ Second, we'll generate a short ID for each woman based on her location in the dataframe: **this is for display purposes only** - we recommend that users adopt FQINSTID for their own analyses.

```
library(ipumsr)
library(tidyverse)
library(survival)

dat <- read_ipums_micro(
  ddi = "data/pma_00111.xml",
  data = "data/pma_00111.dat.gz"
)

dat <- dat %>%
  filter(
    RESULTFQ_1 == 1 & RESULTFQ_2 == 1,
    RESIDENT_1 %in% c(11, 22) &
      RESIDENT_2 %in% c(11, 22)
  ) %>%
  mutate(COUNTRY = COUNTRY %>% as_factor %>% recode(
    "Burkina Faso" = "BF",
    "Congo, Democratic Republic" = "CD",
    "Kenya" = "KE",
    "Nigeria" = "NG"
  )) %>%
  rowid_to_column("ID")
```

Note: there are two regionally representative samples each from DRC and Nigeria. We'll combine samples from the same country here, as both use the same variables for the contraceptive calendar.



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(LGPL >=2)

²⁸COUNTRYSTR also contains ISO codes for each country, but it contains blank values for women with responses from only one phase.

6.2 CENTURY MONTH CODES (CMC)

As shown above, we'll be referencing several variables representing **dates** in this post. Generally, IPUMS PMA publishes every date with two variables: one representing the month (e.g. [INTFQMON](#)) and one representing the year (e.g. [INTFQYEAR](#)). Sometimes, you'll notice a third variable representing dates with a **century month code (CMC)**: each CMC represents the number of months that have passed between a given date and January 1900. CMC dates are particularly useful for calculating the time between events because they replace two variables (with different units) with one simple integer.

Some CMC variables are available directly from IPUMS PMA (e.g. [INTFQCMC](#)), but we'll create our own CMC variables for all of the dates we'll reference in this post. CMC dates are simply calculated as follows:

$$CMC = Month + 12 * (Year - 1900)$$

Because all or part of a date may be **missing** (the month or year), and because certain dates may be **NIU (not in universe)** (e.g. “date of most recent childbirth” for women who have never given birth), we'll need to consider specific circumstances where we should use the value **NA** in a CMC variable.

In the contraceptive calendar, we'll be measuring the time between events in *months*. Therefore, it would be insufficient to include cases where a woman only reported the *year* in which an event occurred. We'll create a function that generates **NA** values if the numeric code representing a month is **90** or higher (all valid months are coded 1 through 12), and if a year is **9000** or higher (all valid years are in the 1900s or 2000s). Otherwise, we'll use the CMC formula to calculate the appropriate CMC value for each date.

Let's call this function `make_cmc`:

```
make_cmc <- function(mo, yr){  
  case_when(mo < 90 & yr < 9000 ~ mo + 12*(yr - 1900))  
}
```

You can apply `make_cmc` to any combination of variables representing the month and year for a date. We'll create one CMC for each date in our data extract.

With [`case_when`](#), any “case” not explicitly covered by `mo < 90 & yr < 9000` is assigned the value **NA**.

```

dat <- dat %>%
  mutate(
    INTFQCMC_1 = make_cmc(INTFQMON_1, INTFQYEAR_1),
    INTFQCMC_2 = make_cmc(INTFQMON_2, INTFQYEAR_2),
    KID1STBIRTHCMC_1 = make_cmc(KID1STBIRTHMO_1, KID1STBIRTHYR_1),
    KID1STBIRTHCMC_2 = make_cmc(KID1STBIRTHMO_2, KID1STBIRTHYR_2),
    LASTBIRTHCMC_1 = make_cmc(LASTBIRTHMO_1, LASTBIRTHYR_1),
    LASTBIRTHCMC_2 = make_cmc(LASTBIRTHMO_2, LASTBIRTHYR_2),
    OTHERBIRTHCMC_1 = make_cmc(OTHERBIRTHMO_1, OTHERBIRTHYR_1),
    OTHERBIRTHCMC_2 = make_cmc(OTHERBIRTHMO_2, OTHERBIRTHYR_2),
    PANELBIRTHCMC_1 = make_cmc(PANELBIRTHMO_1, PANELBIRTHYR_1),
    PANELBIRTHCMC_2 = make_cmc(PANELBIRTHMO_2, PANELBIRTHYR_2),
    PREGENDCMC_1 = make_cmc(PREGENDMO_1, PREGENDYR_1),
    PREGENDCMC_2 = make_cmc(PREGENDMO_2, PREGENDYR_2),
    PANELPREGENDCMC_1 = make_cmc(PANELPREGENDMO_1, PANELPREGENDYR_1),
    PANELPREGENDCMC_2 = make_cmc(PANELPREGENDMO_2, PANELPREGENDYR_2),
    FPBEGINUSECMC_1 = make_cmc(FPBEGINUSEMO_1, FPBEGINUSEYR_1),
    FPBEGINUSECMC_2 = make_cmc(FPBEGINUSEMO_2, FPBEGINUSEYR_2)
  )

```

Let's check our work. For example, consider how we've handled PANELBIRTHCMC_2 - the date of a woman's childbirth that happened during the panel study. If we count the dates by PANELBIRTHMO_2 and use `tail` to examine the last few rows, we see that one woman reported code 97 indicating that she did not know the precise month of birth. Meanwhile, there were 15,064 cases coded 99 indicating that they were **NIU (not in universe)** (no birth occurred during the panel study). We've coded both of these case types with the value NA; all other values follow the CMC formula to count the number of months between January 1900 and the month of birth.

```

dat %>%
  count(PANELBIRTHMO_2, PANELBIRTHYR_2, PANELBIRTHCMC_2) %>%
  tail()

```

	PANELBIRTHMO_2	PANELBIRTHYR_2	PANELBIRTHCMC_2	n
	<int+lbl>	<int+lbl>	<dbl>	<int>
1	12 [December]	2017	1416	1
2	12 [December]	2018	1428	13
3	12 [December]	2019	1440	99
4	12 [December]	2020	1452	90
5	97 [Don't know]	2017	NA	1
6	99 [NIU (not in universe)]	9999 [NIU (not in universe)]	NA	15064

6.3 MERGING COUNTRY CALENDARS

You may be wondering: why does IPUMS PMA publish a separate calendar variable for *each country*?

In fact, the width of each calendar variable differs by the number of months women were asked to recall in a particular sample. This, in turn, depends on the range of dates in which women were interviewed for the Female Questionnaire in a particular phase.

6.3.1 Start and Stop Dates

You can find the precise range of dates included in each calendar on the [description tab](#) for each country's calendar variable.

The screenshot shows a web browser window for the IPUMS PMA website. The URL is pma.ipums.org/pma-action/variables/CALENDARKE#description_section. The page title is "IPUMS PMA: descr: CALENDARKE". The header includes the IPUMS PMA logo, navigation links (LOG IN | REGISTER | GLOBAL HEALTH | IPUMS.ORG), and a "DATA CART" section indicating 0 VARIABLES and 6 SAMPLES with a "VIEW CART" button. The main content area is titled "CALENDARKE" and describes it as a contraceptive calendar for Kenya. It includes tabs for CODES, DESCRIPTION (which is selected), COMPARABILITY, UNIVERSE, AVAILABILITY, and QUESTIONNAIRE TEXT. The DESCRIPTION tab contains text about the variable, mentioning it contains retrospective contraceptive calendar data for 3 years prior to the female interview for Kenya, starting in January 2017 for 2019 and 2018. It also notes the variable represents 3 years prior to the interview for Kenya 2020, starting in January 2018. A note states to see the Codes tab for code meanings. At the bottom, there is a footer with copyright information: "SUPPORTED BY: THE BILL & MELINDA GATES FOUNDATION, PMA, STAT/TRANSFER, AND UNIVERSITY OF MINNESOTA." and "COPYRIGHT © MINNESOTA POPULATION CENTER, UNIVERSITY OF MINNESOTA".

The first month in each country's calendar is listed below:

Country	Phase 1	Phase 2
Burkina Faso	Jan 2018	Jan 2018
DRC	Jan 2017	Jan 2018
Kenya	Jan 2017	Jan 2018
Nigeria	Jan 2017	Jan 2018

Before we can merge calendars for multiple samples, we'll need to determine the correct beginning and ending points for each woman's calendar. First, we'll create CALSTART_1 and CALSTART_2 to record the CMC date for the first month.

```
dat <- dat %>%
  mutate(
    CALSTART_1 = if_else(COUNTRY == "BF", 2018, 2017),
    CALSTART_2 = 2018,
    across(c(CALSTART_1, CALSTART_2), ~12*(.x - 1900) + 1)
  )
```

Next, we'll create CALSTOP_1 and CALSTOP_2 to record the CMC date we created in INTFQCMC_1 and INTFQCMC_2. These dates cover a range of months in each sample.

Country	Phase 1	Phase 2
Burkina Faso	Dec 2019 - Mar 2020	Dec 2020 - Apr 2021
DRC	Dec 2019 - Feb 2020	Dec 2020 - Mar 2021
Kenya	Nov 2019 - Dec 2019	Nov 2020 - Dec 2020
Nigeria	Dec 2019 - Jan 2020	Dec 2020 - Feb 2021

```
dat <- dat %>%
  mutate(
    CALSTOP_1 = INTFQCMC_1,
    CALSTOP_2 = INTFQCMC_2
  )
```

Now, let's take a look at the calendar variables we want to merge. You'll only find responses in the calendar for the country in which a woman resides. The other calendars in her row will appear as an empty character string, the value "". For example, notice that the variable CALENDARKE_1 is blank for these women from Burkina Faso:

```
dat %>%
  filter(COUNTRY == "BF") %>%
  select(ID, COUNTRY, CALENDARBF_1, CALENDARKE_1)
```

```

# A tibble: 5,208 × 4
  ID COUNTRY CALENDARBF_1                               CALEN...¹
  <int> <fct>   <chr+lbl>                           <chr+lbl>
1 1 BF      ,,,0,0,0,0,0,0,0,0,0,0,B,P,P,P,P,P,P,P,0,... ""
2 2 BF      ,,,,P,P,P,P,P,P,0,0,0,0,0,0,0,3,3,3,3,3,3,... ""
3 3 BF      ,,,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,... ""
4 4 BF      ,,,0,0,0,5,5,5,5,5,5,5,5,5,5,5,5,0,0,0,0,0,0,... ""
5 5 BF      ,,,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,... ""
6 6 BF      ,,,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,... ""
7 7 BF      ,,,0,0,0,0,0,0,0,0,0,0,0,0,0,0,T,P,P,P,P,P,0,... ""
8 8 BF      ,,,B,P,P,P,P,P,P,0,0,0,0,0,0,0,0,0,0,0,0,... ""
9 9 BF      ,,,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,... ""
10 10 BF     ,,,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,... ""
# ... with 5,198 more rows, and abbreviated variable name `¹CALENDARKE_1`

```

6.3.2 Pivot Country Calendars

We'll want to use `pivot_longer` to reformat `dat` so that *each calendar variable appears in a separate row*, including calendars collected in different phases of the panel study. Let's call our reformatted data frame `cals`. For now, it will only include `ID`, `COUNTRY`, and all variables that start with `CAL`.

```
cals <- dat %>% select(ID, COUNTRY, starts_with("CAL"))
```

We'll “pivot” `cals` in two steps. First, we'll strip the numeric suffix from each calendar variable: we'll store this information in a new column called `PHASE`. All of the calendar variables from the same phase will then be stored in a separate row (resulting in two rows per woman).

```
cals <- cals %>%
  pivot_longer(
    cols = starts_with("CAL"),
    names_pattern = "(.*)_(.*)",
    names_to = c(".value", "PHASE")
  )
```

```
cals
```

```
# A tibble: 35,424 × 13
  ID COUNTRY PHASE CALEN...¹ CALEN...² CALEN...³ CALEN...⁴ CALEN...⁵ CALEN...⁶ CALEN...⁷
  <int> <fct>   <chr> <chr+lbl> <chr+lbl> <chr+lbl> <chr+lbl> <chr+lbl> <chr+lbl>
1 1 BF     1      ",,,"    ",,,"    ",,,"    ",,,"    ",,,"    ",,,"    ",,,"
2 1 BF     2      ",,,"    ",,,"    ",,,"    ",,,"    ",,,"    ",,,"    ",,,"
3 2 BF     1      ",,,"    ",,,"    ",,,"    ",,,"    ",,,"    ",,,"    ",,,"
4 2 BF     2      ",,,"    ",,,"    ",,,"    ",,,"    ",,,"    ",,,"    ",,,"
5 3 BF     1      ",,,"    ",,,"    ",,,"    ",,,"    ",,,"    ",,,"    ",,,"
6 3 BF     2      ",,,"    ",,,"    ",,,"    ",,,"    ",,,"    ",,,"    ",,,"
7 4 BF     1      ",,,"    ",,,"    ",,,"    ",,,"    ",,,"    ",,,"    ",,,"
8 4 BF     2      ",,,"    ",,,"    ",,,"    ",,,"    ",,,"    ",,,"    ",,,"
9 5 BF     1      ",,,"    ",,,"    ",,,"    ",,,"    ",,,"    ",,,"    ",,,"
10 5 BF    2      ",,,"    ",,,"    ",,,"    ",,,"    ",,,"    ",,,"    ",,,"
```

... with 35,414 more rows, 3 more variables: CALENDARCDWHY <chr+lbl>,
CALSTART <dbl>, CALSTOP <dbl>, and abbreviated variable names ¹CALENDARBF,
²CALENDARBFWHY, ³CALENDARKE, ⁴CALENDARKEWHY, ⁵CALENDARNG, ⁶CALENDARNGWHY,
⁷CALENDARCD

Before we “pivot” a second time, we'll want to identify suffixes that we can again strip and use as new column names (just as we did with `_1` and `_2` when we created `PHASE`). Let's use `FPSTATUS` for the main contraceptive calendar, and `WHYSTOP` for the discontinuation calendar. When we `pivot_longer` again, these suffixes will appear as two new columns containing each type of calendar.

```

cals <- cals %>%
  rename_with(
    ~paste0(.x, "FPSTATUS"),
    .cols = starts_with("CALENDAR") & !ends_with("WHY")
  ) %>%
  rename_with(
    ~paste0(.x, "STOP"),
    .cols = starts_with("CALENDAR") & ends_with("WHY")
  ) %>%
  pivot_longer(
    cols = starts_with("CALENDAR"),
    names_pattern = "CALENDAR(..)(.*)",
    names_to = c("COUNTRY_CAL", ".value"),
    values_to = "CALENDAR_STRING"
  )

```

Now, each woman occupies eight rows (4 country calendars per phase). We've also stripped the 2-letter country code from each calendar name to create COUNTRY_CAL: this indicates the country associated with each calendar.

```
cals
```

```
# A tibble: 141,696 × 8
  ID COUNTRY PHASE CALSTART CALSTOP COUNTRY_CAL FPSTATUS      WHYSTOP
  <int> <fct>   <chr>   <dbl>   <dbl> <chr>       <chr+lbl>      <chr+lbl>
1 1   BF      1        1417    1442  BF          ",,,,,,,,,0,0,0,0,... ",,,,,,,
2 1   BF      1        1417    1442  KE          ",,,"                      ",,,"
3 1   BF      1        1417    1442  NG          ",,,"                      ",,,"
4 1   BF      1        1417    1442  CD          ",,,"                      ",,,"
5 1   BF      2        1417    1453  BF          ",,,,,,,,,,3,3,3,3,... ",,,,,
6 1   BF      2        1417    1453  KE          ",,,"                      ",,,"
7 1   BF      2        1417    1453  NG          ",,,"                      ",,,"
8 1   BF      2        1417    1453  CD          ",,,"                      ",,,"
9 2   BF      1        1417    1441  BF          ",,,,,,,,,,P,P,P,P,... ",,,,,
10 2   BF     1        1417    1441  KE          ",,,"                      ",,,"
```

... with 141,686 more rows

Lastly, we can drop any row where COUNTRY does not match the value in COUNTRY_CAL:

```

cals <- cals %>%
  filter(COUNTRY_CAL == COUNTRY) %>%
  select(-COUNTRY_CAL)

cals

```

```

# A tibble: 35,424 × 7
  ID COUNTRY PHASE CALSTART CALSTOP FPSTATUS          WHYSTOP
  <int> <fct>   <chr>   <dbl>    <dbl> <chr+lbl>          <chr+lbl>
1     1 BF      1        1417     1442 ",,,,,,,,,,0,0,0,0,0,0,0,0,... ",,,,,,,
2     1 BF      2        1417     1453 ",,,,,,,,,,3,3,3,3,3,3,0,0,... ",,,,,,,
3     2 BF      1        1417     1441 ",,,,,,,,,,P,P,P,P,P,P,0,0,... ",,,,,,,
4     2 BF      2        1417     1453 ",,,,,,,,,,5,5,5,5,5,5,5,5,... ",,,,,,,
5     3 BF      1        1417     1441 ",,,,,,,,,,0,0,0,0,0,0,0,0,... """
6     3 BF      2        1417     1453 """
7     4 BF      1        1417     1441 ",,,,,,,,,,0,0,0,5,5,5,5,5,... ",,,,,,,
8     4 BF      2        1417     1452 ",,,,,,,,,,0,0,0,0,0,0,0,0,... ",,,,,,,
9     5 BF      1        1417     1441 ",,,,,,,,,,0,0,0,0,0,0,0,0,... ",,,,,,,
10    5 BF      2        1417     1453 """
# ... with 35,414 more rows

```

We're nearly ready to split each string into more usable variables for our analysis. But, before we do so: you might notice that there are still some calendars represented by empty character strings "" (see `FPSTATUS` in rows 6 and 10 above). These are cases where calendar data are not available.

6.4 DATA AVAILABILITY

There are two reasons why a woman's calendar might be unavailable.

First, these women might be **NIU (not in universe)**, as described on the IPUMS PMA [universe tab](#) for each country's contraceptive calendar. Generally, NIU cases are women who reported no qualifying event during the calendar period: a blank string could indicate that she was never pregnant and never adopted or discontinued a family planning method in any month during that period.

The screenshot shows a web browser window for the IPUMS PMA website. The URL is pma.ipums.org/pma-action/variables/CALENDARKE#universe_section. The page title is "IPUMS PMA" and the subtitle is "PERFORMANCE MONITORING FOR ACTION". The main content area is titled "CALENDARKE" and describes it as a "Contraceptive calendar (Kenya)". Below this are buttons for "ADD TO CART" and "CHANGE SAMPLES". A horizontal navigation bar includes "HOME", "SELECT DATA", "MY DATA", and "SUPPORT". On the right, there is a "DATA CART" section showing "0 VARIABLES" and "6 SAMPLES", with a "VIEW CART" button. The main content area has tabs for "CODES", "DESCRIPTION", "COMPARABILITY", "UNIVERSE" (which is selected), "AVAILABILITY", and "QUESTIONNAIRE TEXT". The "UNIVERSE" tab contains the following text:

Universe

Women aged 15-49 who are pregnant, or have used family planning, given birth, or had a pregnancy end within the past 3 years, excluding women who started using their current family planning method more than 3 years ago.

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Second, a blank might reflect **missing data**, like the duration of a pregnancy or an episode of continuous contraceptive use. Contraceptive calendars **do not contain missing values for individual months**, so you'll find the complete calendar missing if data from any one month was missing.

The **universe tab** explains why some cases are **NIU (not in universe)**.

Currently, about 1 in every 5 calendars is blank "" for one of these two reasons.

```
cals %>% count(FPSTATUS == "") %>% mutate(prop = prop.table(n))
```

```
# A tibble: 2 × 3
`FPSTATUS == ""`    n  prop
<lgl>                <int> <dbl>
1 FALSE              28153 0.795
2 TRUE               7271 0.205
```

In some research applications, you might want to complete the empty calendars for women who were NIU. For example: if a woman used the contraceptive pill from the beginning of the calendar period continuously through the day of the interview, her calendar is currently blank because she did not adopt or discontinue using the pill in that time span. You might want to fill her calendar with the value 7 repeated once for every month between CALSTART and CALSTOP.

Similarly, we can complete all calendars for women who never used a family planning method and were never pregnant during the calendar period: in this case, we'll repeat the value 0.

Note, however, that it is *not* possible to complete calendars for women who experienced birth or pregnancy termination during the calendar period. If these calendars are blank, we cannot determine the duration of the pregnancy or whether any family planning method was used prior to the pregnancy. We'll flag these cases with a new variable we'll call CALMISSING.

We'll begin by attaching all of the CMC variables we created above (except INTFQCMC) along with the variables [PREGNANT](#) and [FPCURREFFMETHRC](#). In order to match the format of `cals`, we'll again use [pivot_longer](#) to create separate rows for the dates collected from each PHASE.

```
cals <- dat %>%
  select(
    ID, matches("CMC") & !matches("INTFQ"),
    starts_with("PREGNANT"), starts_with("FPCURREFFMETHRC"),
  ) %>%
  pivot_longer(
    !ID,
    names_pattern = "(.*)_(.*)",
    names_to = c(".value", "PHASE")
  ) %>%
  full_join(cals, by = c("ID", "PHASE"))

cals
```

```

# A tibble: 35,424 × 16
   ID PHASE KID1STB...¹ FPBEG...² LASTB...³ OTHER...⁴ PANEL...⁵ PREGE...⁶ PANEL...⁷ PREGN...⁸
   <int> <chr>    <dbl>    <dbl>    <dbl>    <dbl>    <dbl>    <dbl>    <dbl> <int+lbl>
1     1 1        1314      NA      1430      NA      NA      NA      NA  0 [No]
2     1 2        1314     1448     1430     1430     1430      NA      NA  0 [No]
3     2 1        NA       NA      1390      NA      NA      NA      NA  1 [Yes]
4     2 2        NA       1444     1443      NA     1443      NA      NA  0 [No]
5     3 1        NA       NA      NA       NA      NA      NA      NA  0 [No]
6     3 2        NA       NA      NA       NA      NA      NA      NA  0 [No]
7     4 1        1324     1428     1406      NA      NA      NA      NA  0 [No]
8     4 2        1324      NA     1406      NA      NA      NA      NA  0 [No]
9     5 1        1366      NA     1422      NA      NA      NA      NA  0 [No]
10    5 2        1366      NA     1422      NA      NA      NA      NA  0 [No]
# ... with 35,414 more rows, 6 more variables: FPCURREFFMETHRC <int+lbl>,
#   COUNTRY <fct>, CALSTART <dbl>, CALSTOP <dbl>, FPSTATUS <chr+lbl>,
#   WHYSTOP <chr+lbl>, and abbreviated variable names ¹KID1STBIRTHCMC,
#   ²FPBEGINUSECMC, ³LASTBIRTHCMC, ⁴OTHERBIRTHCMC, ⁵PANELBIRTHCMC, ⁶PREGENDCMC,
#   ⁷PANELPREGENDCMC, ⁸PREGNANT

```

Now, we'll create `CALMISSING` to indicate whether women with an empty value "" in `FPSTATUS` were *actually* pregnant or adopted a family planning method at some point during the calendar period. In other words: we'll test whether any one of our CMC variables shows an event that occurred after `CALSTART`, but is not recorded in `FPSTATUS`. Likewise, this check will determine whether any such women are *currently* pregnant.

```

cals <- cals %>%
  mutate(
    .after = PHASE,
    CALMISSING = FPSTATUS == "" & WHYSTOP == "" & {
      PREGNANT == 1 | if_any(ends_with("CMC"), ~!is.na(.x) & .x >= CALSTART)
    }
  ) %>%
  relocate(CALSTART, .after = CALMISSING)

cals

```

```
# A tibble: 35,424 × 17
   ID PHASE CALMISS...¹ CALST...² KID1S...³ FPBEG...⁴ LASTB...⁵ OTHER...⁶ PANEL...⁷ PREGE...⁸
   <int> <chr> <lgl>     <dbl>    <dbl>    <dbl>    <dbl>    <dbl>    <dbl>
1     1 1 FALSE      1417    1314     NA     1430     NA     NA     NA
2     1 2 FALSE      1417    1314    1448    1430    1430    1430    NA
3     2 1 FALSE      1417     NA     NA    1390     NA     NA     NA
4     2 2 FALSE      1417     NA    1444    1443     NA    1443    NA
5     3 1 FALSE      1417     NA     NA     NA     NA     NA     NA
6     3 2 FALSE      1417     NA     NA     NA     NA     NA     NA
7     4 1 FALSE      1417    1324    1428    1406     NA     NA     NA
8     4 2 FALSE      1417    1324     NA    1406     NA     NA     NA
9     5 1 FALSE      1417    1366     NA    1422     NA     NA     NA
10    5 2 TRUE       1417    1366     NA    1422     NA     NA     NA
# ... with 35,414 more rows, 7 more variables: PANELPREGENDCMC <dbl>,
#   PREGNANT <int+lbl>, FPCURREFFMETHRC <int+lbl>, COUNTRY <fct>,
#   CALSTOP <dbl>, FPSTATUS <chr+lbl>, WHYSTOP <chr+lbl>, and abbreviated
#   variable names ¹CALMISSING, ²CALSTART, ³KID1STBIRTHCMC, ⁴FPBEGINUSECMC,
#   ⁵LASTBIRTHCMC, ⁶OTHERBIRTHCMC, ⁷PANELBIRTHCMC, ⁸PREGENDCMC
```

You can see in this output, for example, that the woman in row 10 (`ID == 5` and `PHASE == 2`) should have a calendar starting in month 1417. She tells us in `LASTBIRTHCMC` that she gave birth in month 1422, 5 months after the calendar period began, but the string we would expect to find in `FPSTATUS` is blank. We have flagged this row with `CALMISSING` because we won't be able to reconstruct her `FPSTATUS` calendar without knowing exactly when she became pregnant for this birth, or whether she was using a family planning method in any month prior.

On the other hand, women with blank `FPSTATUS` calendars who were *not* flagged with `CALMISSING` have not given birth or switched family planning methods during the calendar period. We can assume that they have held their current status between `CALSTART` and `CALSTOP`.

Prior to this procedure, 1 in 5 rows in `cals` contained an empty `FPSTATUS` calendar. With help from `CALMISSING`, we'll now be able to reduce the proportion of empty calendars to less than 1 in 20.

```
cals %>% count(CALMISSING, FPSTATUS == "") %>% mutate(prop = prop.table(n))

# A tibble: 3 × 4
  CALMISSING `FPSTATUS == ""` n    prop
  <lgl>        <lgl>     <int> <dbl>
1 FALSE        FALSE      28153 0.795
2 FALSE        TRUE       5811  0.164
3 TRUE         TRUE       1460  0.0412
```

We'll now complete the blank calendars for women who were not flagged by `CALMISSING`. First, we'll recode `FPCURREFFMETHRC` to match the values used in the calendar:

```

cals <- cals %>%
  mutate(
    FPCURREFFMETHRC = FPCURREFFMETHRC %>%
      zap_labels() %>%
      # NA if "No response or missing" (1 case)
      na_if(998) %>%
      # Note: 5 is used twice, and 6 is not used
      recode(
        "999" = 0, "101" = 1, "102" = 2, "111" = 3, "112" = 4, "121" = 5,
        "123" = 5, "131" = 7, "132" = 8, "141" = 9, "142" = 10, "151" = 11,
        "152" = 12, "160" = 13, "170" = 14, "210" = 30, "220" = 31, "240" = 39
      )
  )

```

Then, we'll create CALDUR to calculate the duration (in months) of each woman's calendar.

```
cals <- cals %>% mutate(CALDUR = CALSTOP - CALSTART + 1)
```

Finally, we'll complete each empty string in FPSTATUS for women not flagged by CALMISSING (leaving it the same otherwise). To clean-up, we'll also drop any variables that are no longer needed.

```

cals <- cals %>%
  mutate(FPSTATUS = if_else(
    # If `FPSTATUS` is blank and `CALMISSING` is FALSE...
    FPSTATUS == "" & !CALMISSING,
    # Repeat "," and the value in `FPCURREFFMETHRC` as many times as `CALDUR`:
    str_c(",", FPCURREFFMETHRC) %>% str_dup(CALDUR),
    # Otherwise, recycle `FPSTATUS` as a character string:
    as.character(FPSTATUS)
  )) %>%
  select(-c(
    ends_with("CMC"), CALDUR, CALSTOP,
    CALMISSING, PREGNANT, FPCURREFFMETHRC
  ))

```

6.5 SPLITTING MONTHS INTO COLUMNS

We've now completed as many of the blank calendars as we can, so it's time to transform each calendar string into variables that will be usable in survival analysis.

We'll begin with another `pivot_longer` function to position FPSTATUS and WHYSTOP together in a single column. Notice the temporary column name describes the type of calendar that appears in the temporary column value.

```
cals <- cals %>% pivot_longer(c("FPSTATUS", "WHYSTOP"))
```

```
cals
```

```
# A tibble: 70,848 × 6
  ID PHASE CALSTART COUNTRY name      value
  <int> <chr>    <dbl> <fct>   <chr>    <chr+lbl>
1 1     1 1       1417 BF    FPSTATUS ",,,,,,,,,,0,0,0,0,0,0,0,0,0,0,0,B,P...
2 1     1 1       1417 BF    WHYSTOP  ",,,,,,,,,,,," 
3 1     1 2       1417 BF    FPSTATUS ",,,,,,,,,,3,3,3,3,3,3,0,0,0,0,0,0,0...
4 1     1 2       1417 BF    WHYSTOP  ",,,,,,,,,,,," 
5 2     2 1       1417 BF    FPSTATUS ",,,,,,,,,,P,P,P,P,P,P,P,0,0,0,0,0,0...
6 2     2 1       1417 BF    WHYSTOP  ",,,,,,,,,,,6,,," 
7 2     2 2       1417 BF    FPSTATUS ",,,,,,,,,,5,5,5,5,5,5,5,5,5,B,P,P...
8 2     2 2       1417 BF    WHYSTOP  ",,,,,,,,,,,6... 
9 3     3 1       1417 BF    FPSTATUS ",,,,,,,,,,0,0,0,0,0,0,0,0,0,0,0,0,0...
10 3    3 1       1417 BF   WHYSTOP  "" 
# ... with 70,838 more rows
```

Now, we'll use `separate` to split each string into several columns. You can manually specify the maximum number of columns you'll need to hold all of the calendars in your data extract, or you can let R determine the `max` length of each string.²⁹ We'll call this number `ncols`.

```
# How many columns would be needed for the single longest calendar?
ncols <- max(str_count(cals$value, ","), na.rm = TRUE) + 1
ncols
```

```
[1] 48
```

In `separate`, we tell R to split each string into 48 columns: if any given calendar has fewer than 48 values, we fill the left-most columns with the value NA as needed.

²⁹Here, we're counting the number of commas in each string, so we add +1 (e.g. 0,0,0 has two commas, but three responses).

```

# Create one column for every month in the longest calendar
cals <- cals %>%
  separate(value, into = paste0("cal", 1:53), sep = ",", fill = "left", )

cals

# A tibble: 70,848 × 53
  ID PHASE CALSTART COUNTRY name   cal48 cal47 cal46 cal45 cal44 cal43 cal42
  <int> <chr>    <dbl> <fct>   <chr>  <chr>  <chr>  <chr>  <chr>  <chr>  <chr>
  1     1 1       1417 BF      FPSTA... <NA>  <NA>  <NA>  <NA>  <NA>  <NA>
  2     1 1       1417 BF      WHYST... <NA>  <NA>  <NA>  <NA>  <NA>  <NA>
  3     1 2       1417 BF      FPSTA... ""    ""    ""    ""    ""    ""    ""
  4     1 2       1417 BF      WHYST... ""    ""    ""    ""    ""    ""    ""
  5     2 1       1417 BF      FPSTA... <NA>  <NA>  <NA>  <NA>  <NA>  <NA>
  6     2 1       1417 BF      WHYST... <NA>  <NA>  <NA>  <NA>  <NA>  <NA>
  7     2 2       1417 BF      FPSTA... ""    ""    ""    ""    ""    ""    ""
  8     2 2       1417 BF      WHYST... ""    ""    ""    ""    ""    ""    ""
  9     3 1       1417 BF      FPSTA... <NA>  <NA>  <NA>  <NA>  <NA>  <NA>
 10    3 1       1417 BF      WHYST... <NA>  <NA>  <NA>  <NA>  <NA>  <NA>
# ... with 70,838 more rows, and 41 more variables: cal41 <chr>, cal40 <chr>,
#   cal39 <chr>, cal38 <chr>, cal37 <chr>, cal36 <chr>, cal35 <chr>,
#   cal34 <chr>, cal33 <chr>, cal32 <chr>, cal31 <chr>, cal30 <chr>,
#   cal29 <chr>, cal28 <chr>, cal27 <chr>, cal26 <chr>, cal25 <chr>,
#   cal24 <chr>, cal23 <chr>, cal22 <chr>, cal21 <chr>, cal20 <chr>,
#   cal19 <chr>, cal18 <chr>, cal17 <chr>, cal16 <chr>, cal15 <chr>,
#   cal14 <chr>, cal13 <chr>, cal12 <chr>, cal11 <chr>, cal10 <chr>, ...

```

As you can see, this produced 48 columns named `cal48` to `cal1`, where `cal1` is the earliest month in chronological time. You'll notice some blank strings for women whose calendar included empty placeholders (e.g. ,,,,...,3,3,3,...). We'll now use [across](#) to convert blank strings `""` to `NA` as well.

```

cals <- cals %>%
  mutate(across(
    starts_with("cal", ignore.case = FALSE),
    ~na_if(.x, ""))
)

```

cals

```
# A tibble: 70,848 × 53
  ID PHASE CALSTART COUNTRY name    cal48 cal47 cal46 cal45 cal44 cal43 cal42
  <int> <chr>   <dbl> <fct>   <chr>  <chr>  <chr>  <chr>  <chr>  <chr>  <chr>
1     1 1      1417 BF    FPSTA... <NA>  <NA>  <NA>  <NA>  <NA>  <NA>
2     1 1      1417 BF    WHYST... <NA>  <NA>  <NA>  <NA>  <NA>  <NA>
3     1 2      1417 BF    FPSTA... <NA>  <NA>  <NA>  <NA>  <NA>  <NA>
4     1 2      1417 BF    WHYST... <NA>  <NA>  <NA>  <NA>  <NA>  <NA>
5     2 1      1417 BF    FPSTA... <NA>  <NA>  <NA>  <NA>  <NA>  <NA>
6     2 1      1417 BF    WHYST... <NA>  <NA>  <NA>  <NA>  <NA>  <NA>
7     2 2      1417 BF    FPSTA... <NA>  <NA>  <NA>  <NA>  <NA>  <NA>
8     2 2      1417 BF    WHYST... <NA>  <NA>  <NA>  <NA>  <NA>  <NA>
9     3 1      1417 BF    FPSTA... <NA>  <NA>  <NA>  <NA>  <NA>  <NA>
10    3 1      1417 BF    WHYST... <NA>  <NA>  <NA>  <NA>  <NA>  <NA>
# ... with 70,838 more rows, and 41 more variables: cal41 <chr>, cal40 <chr>,
#   cal39 <chr>, cal38 <chr>, cal37 <chr>, cal36 <chr>, cal35 <chr>,
#   cal34 <chr>, cal33 <chr>, cal32 <chr>, cal31 <chr>, cal30 <chr>,
#   cal29 <chr>, cal28 <chr>, cal27 <chr>, cal26 <chr>, cal25 <chr>,
#   cal24 <chr>, cal23 <chr>, cal22 <chr>, cal21 <chr>, cal20 <chr>,
#   cal19 <chr>, cal18 <chr>, cal17 <chr>, cal16 <chr>, cal15 <chr>,
#   cal14 <chr>, cal13 <chr>, cal12 <chr>, cal11 <chr>, cal10 <chr>, ...
```

We'll now [pivot_longer](#) again, placing each month into a single column temporarily called `value`. The label in `name` describes whether a particular value originated in the `FPSTATUS` or `WHYSTOP` calendar. We strip the numeric suffix from each column to create `MONTH`, which indicates the sequential month associated with each `value`.

```
cals <- cals  %>%
  pivot_longer(
    starts_with("cal", ignore.case = FALSE),
    names_to = "MONTH",
    names_prefix = "cal"
  )

cals
```

```
# A tibble: 3,400,704 × 7
  ID PHASE CALSTART COUNTRY name    MONTH value
  <int> <chr>   <dbl> <fct>   <chr>   <chr> <chr>
1 1     1       1417 BF     FPSTATUS 48     <NA>
2 1     1       1417 BF     FPSTATUS 47     <NA>
3 1     1       1417 BF     FPSTATUS 46     <NA>
4 1     1       1417 BF     FPSTATUS 45     <NA>
5 1     1       1417 BF     FPSTATUS 44     <NA>
6 1     1       1417 BF     FPSTATUS 43     <NA>
7 1     1       1417 BF     FPSTATUS 42     <NA>
8 1     1       1417 BF     FPSTATUS 41     <NA>
9 1     1       1417 BF     FPSTATUS 40     <NA>
10 1    1       1417 BF     FPSTATUS 39    <NA>
# ... with 3,400,694 more rows
```

From MONTH and CALSTART, we'll derive CALCMC to mark the *calendar* month for each value.

```
cals <- cals %>%
  mutate(CALCMC = CALSTART + as.integer(MONTH) - 1)

cals
```

```
# A tibble: 3,400,704 × 8
  ID PHASE CALSTART COUNTRY name    MONTH value  CALCMC
  <int> <chr>   <dbl> <fct>   <chr>   <chr> <dbl>
1 1     1       1417 BF     FPSTATUS 48     <NA>   1464
2 1     1       1417 BF     FPSTATUS 47     <NA>   1463
3 1     1       1417 BF     FPSTATUS 46     <NA>   1462
4 1     1       1417 BF     FPSTATUS 45     <NA>   1461
5 1     1       1417 BF     FPSTATUS 44     <NA>   1460
6 1     1       1417 BF     FPSTATUS 43     <NA>   1459
7 1     1       1417 BF     FPSTATUS 42     <NA>   1458
8 1     1       1417 BF     FPSTATUS 41     <NA>   1457
9 1     1       1417 BF     FPSTATUS 40     <NA>   1456
10 1    1       1417 BF     FPSTATUS 39    <NA>   1455
# ... with 3,400,694 more rows
```

Finally, we'll use [pivot_wider](#) to align the months for each available calendar, and then arrange each woman's calendar by CALCMC. If any month includes no value from either Phase 1 or Phase 2, we'll use [filter](#) to remove it from our data frame (these are placeholder values for future months).

In its final format, `cals` contains one row for every month covered by the contraceptive calendar from either Phase 1 or Phase 2. You'll notice that the two calendars contain overlapping months, as with the dates between CALCMC 1417 and 1442 for the first woman shown below.

```
cals <- cals %>%
  select(ID, PHASE, CALCMC, name, value) %>%
  pivot_wider(
    names_from = c(name, PHASE),
    values_from = value
  ) %>%
  filter(!(is.na(FPSTATUS_1) & FPSTATUS_2 == "")) %>%
  arrange(ID, desc(CALCMC))

cals
```

```
# A tibble: 769,071 × 6
  ID CALCMC FPSTATUS_1 WHYSTOP_1 FPSTATUS_2 WHYSTOP_2
  <int>   <dbl> <chr>      <chr>      <chr>      <chr>
1     1    1453 <NA>       <NA>       3          <NA>
2     1    1452 <NA>       <NA>       3          <NA>
3     1    1451 <NA>       <NA>       3          <NA>
4     1    1450 <NA>       <NA>       3          <NA>
5     1    1449 <NA>       <NA>       3          <NA>
6     1    1448 <NA>       <NA>       3          <NA>
7     1    1447 <NA>       <NA>       0          <NA>
8     1    1446 <NA>       <NA>       0          <NA>
9     1    1445 <NA>       <NA>       0          <NA>
10    1    1444 <NA>       <NA>       0          <NA>
11    1    1443 <NA>       <NA>       0          <NA>
12    1    1442 0          <NA>       0          <NA>
13    1    1441 0          <NA>       0          <NA>
14    1    1440 0          <NA>       0          <NA>
15    1    1439 0          <NA>       0          <NA>
16    1    1438 0          <NA>       0          <NA>
17    1    1437 0          <NA>       0          <NA>
18    1    1436 0          <NA>       0          <NA>
19    1    1435 0          <NA>       0          <NA>
20    1    1434 0          <NA>       0          <NA>
21    1    1433 0          <NA>       0          <NA>
22    1    1432 0          <NA>       0          <NA>
23    1    1431 0          <NA>       0          <NA>
24    1    1430 B          <NA>       B          <NA>
25    1    1429 P          <NA>       P          <NA>
26    1    1428 P          <NA>       P          <NA>
27    1    1427 P          <NA>       P          <NA>
28    1    1426 P          <NA>       P          <NA>
29    1    1425 P          <NA>       P          <NA>
30    1    1424 P          <NA>       P          <NA>
31    1    1423 P          <NA>       P          <NA>
32    1    1422 P          <NA>       0          <NA>
33    1    1421 0          <NA>       0          <NA>
34    1    1420 0          <NA>       0          <NA>
35    1    1419 0          <NA>       0          <NA>
36    1    1418 0          <NA>       0          <NA>
37    1    1417 0          <NA>       0          <NA>
38    2    1452 <NA>       <NA>       5          <NA>
39    2    1451 <NA>       <NA>       5          <NA>
40    2    1450 <NA>       <NA>       5          <NA>
# ... with 769,031 more rows
```

6.6 ANALYSIS

We mentioned at the beginning of this post that there are many ways to work with the contraceptive calendar data once you've formatted it this way. For example, we just saw that the FPSTATUS_1 and FPSTATUS_2 columns are a *nearly* perfect match for the woman marked ID == 1: she reports that she used no method of contraception between month 1417 until month 1421. Then, in Phase 1 she recalled that she became pregnant in month 1422; in Phase 2, she instead recalled that she became pregnant in month 1423. In both phases, she reports that she gave birth in month 1430, and then returned to using no family planning method.

We encourage researchers to explore sources of **recall bias** that may account for discrepancies between the Phase 1 and Phase 2 calendars. Generally, we assume that individuals remember events more reliably when they are in recent memory, but this may not always be true! For more on the reliability of responses in contraceptive calendars across PMA samples, we strongly recommend checking out work by Anglewicz et al. [-@Anglewicz2022-mx].

Here, we'd like to highlight just one way that the PMA panel design might help researchers understand patterns in the calendar data. When we introduced the Phase 1 contraceptive calendars [one year ago](#), we mentioned that Phase 2 calendars would allow researchers to compare the rate of adoption for women who were using no method at Phase 1; we also suggested that you might compare adoption rates for women with [unmet need](#) or [plans to adopt](#) a method within the next year. Let's now check to see whether these factors had any effect on the monthly contraceptive use status for each month between Phase 1 and Phase 2.

First, we'll need to identify women who were not using any family planning method at Phase 1. These are cases where [FPCURREFFMETHRC_1](#) is coded 999 for **NIU (not in universe)**. We'll drop any other cases from our original data frame dat, and we'll call this new data frame nonusers.

```
nonusers <- dat %>% filter(FPCURREFFMETHRC_1 == 999)
```

We'll follow steps in a [previous post](#) to identify women who meet the PMA criteria for "unmet need" in [UNMETYN_1](#), and also those who planned to adopt a family planning method within one year at Phase 1 as shown in [FPPLANVAL_1](#) and [FPPLANWHEN_1](#).

```
nonusers <- nonusers %>%  
  mutate(  
    UNMETYN_1 = UNMETYN_1 == 1,  
    FPPLANR_1 = case_when(  
      FPPLANWHEN_1 == 1 & FPPLANVAL_1 <= 12 ~ TRUE, # Within 12 months  
      FPPLANWHEN_1 == 2 & FPPLANVAL_1 == 1 ~ TRUE, # Within 1 year  
      FPPLANWHEN_1 %in% c(3, 4) ~ TRUE, # Soon / now, after current pregnancy  
      TRUE ~ FALSE # Includes date unknown, no response, or no intention (FPUSPLAN)  
    )  
  )
```

In that same post, we shared code you can use to create a custom [theme](#) for graphics built with [ggplot2](#). We named our theme `theme_pma`; if you'd like to review the code for our graphics theme, click the button below.

```
library(showtext)

sysfonts::font_add(
  family = "cabrito",
  regular = ".../fonts/cabritosansnormregular-webfont.ttf"
)
showtext::showtext_auto()
update_geom_defaults("text", list(family = "cabrito", size = 4))

theme_pma <- theme_minimal() %>%
  theme(
    text = element_text(family = "cabrito", size = 13),
    plot.title = element_text(size = 22, color = "#00263A",
                               hjust = 0, margin = margin(b = 5)),
    plot.subtitle = element_text(hjust = 0, margin = margin(b = 10)),
    strip.background = element_blank(),
    strip.text.y = element_text(size = 16, angle = 0),
    panel.spacing = unit(1, "lines"),
    axis.title.y = element_text(angle = 0, margin = margin(r = 10)),
    axis.title.x = element_text(margin = margin(t = 10))
  )
```

Before we begin our analysis, let's see the proportion of nonusers in each country who had unmet need or plans to adopt a family planning method within one year at Phase 1.

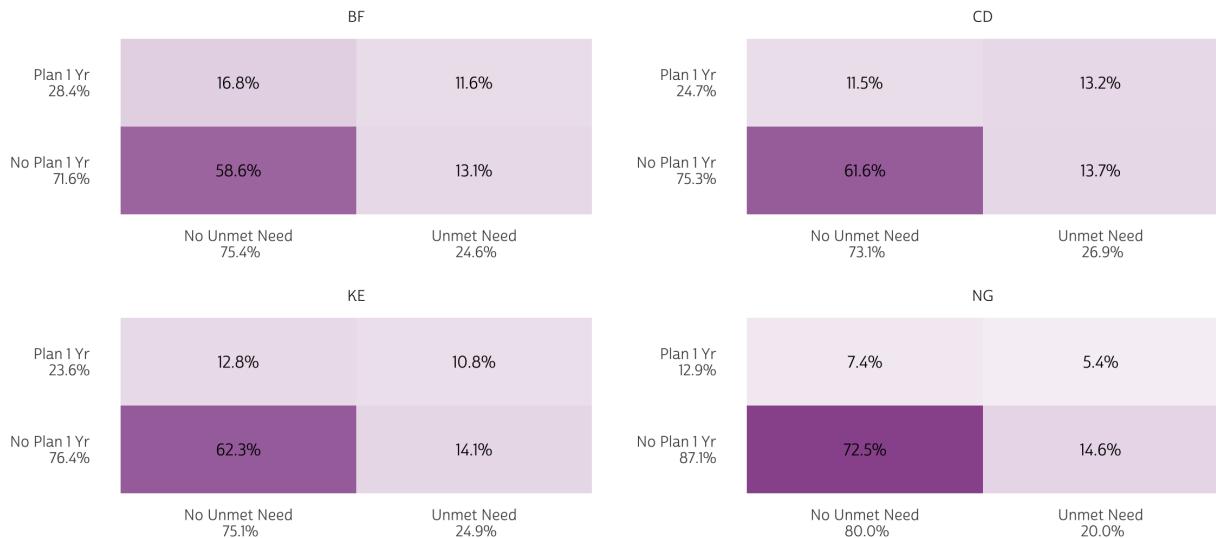
```

nonusers %>%
  count(COUNTRY, UNMETYN_1, FPPLANYR_1) %>%
  mutate(
    UNMETYN_1 = if_else(UNMETYN_1, "Unmet Need\n", "No Unmet Need\n"),
    FPPLANYR_1 = if_else(FPPLANYR_1, "Plan 1 Yr\n", "No Plan 1 Yr\n")
  ) %>%
  group_by(COUNTRY) %>%
  mutate(prop = prop.table(n), tot = sum(n)) %>% # joint percentages
  group_by(COUNTRY, UNMETYN_1) %>%
  mutate(propcol = sum(n)/tot) %>% # column margins
  group_by(COUNTRY, FPPLANYR_1) %>%
  mutate(proprow = sum(n)/tot) %>% # row margins
  ungroup() %>%
  mutate(
    propcol = paste(UNMETYN_1, scales::percent(propcol, .1)),
    proprow = paste(FPPLANYR_1, scales::percent(proprow, .1)),
    proplbl = scales::percent(prop, .1)
  ) %>%
  ggplot(aes(x = propcol, y = proprow)) +
  geom_tile(fill = "#98579BB0", aes(alpha = prop)) +
  facet_wrap(vars(COUNTRY), scales = "free") +
  geom_text(aes(label = proplbl)) +
  labs(
    title = "Non-users: Unmet Need and Intentions to Adopt a Method within 1 Year",
    subtitle = "Percentage among sampled women not currently using any method at Phase 1",
    x = NULL, y = NULL
  ) +
  theme_pma %+replace%
  theme(panel.grid = element_blank(), legend.position = "none")

```

Non-users: Unmet Need and Intentions to Adopt a Method within 1 Year

Percentage among sampled women not currently using any method at Phase 1



As you can see, a majority of Phase 1 nonusers in each country had both no unmet need and no plans to adopt a method within the next year. We might expect these women to be *least likely* to adopt a method within the subsequent months covered by the Phase 2 contraceptive calendar. Conversely, we might expect that women who planned to adopt a method within the year would be *most likely* to adopt a method during the calendar period, but this might be mitigated by factors related to unmet need.

Let's now attach the contraceptive calendar data from Phase 2 to nonusers. We'll exclude months before INTFQCMC_1 and women we identified with CALMISSING (where all values in FPSTATUS_2 are now NA). Finally, we'll exclude women for whom either UNMETYN_1 or FPPLANYR_1 is missing, NIU, or otherwise coded NA.

```
nonusers <- nonusers %>%
  select(ID, COUNTRY, INTFQCMC_1, UNMETYN_1, FPPLANYR_1) %>%
  full_join(cals, ., by = "ID") %>%
  filter(
    CALCMC >= INTFQCMC_1,
    !if_any(c(FPSTATUS_2, UNMETYN_1, FPPLANYR_1), is.na)
  )
```

The next several steps will help us remove every month for each woman *except* for the last consecutive month in which she was not using a family planning method after the Phase 1 interview. For those who were still not using a method by the date of the Phase 2 interview, we might say she “survived” the full observation period. We'll use the [survival](#) package to model the likelihood that a woman would have progressed through each month of the calendar without adopting a family planning method.

First, we'll classify every month in each woman's calendar with a new variable USE indicating whether she used any family planning method that month. We'll then create M0 to count the number of months that have passed between each month and the earliest month in CALCMC.

```
nonusers <- nonusers %>%
  transmute(
    ID, COUNTRY, CALCMC,
    FPSTATUS_2, UNMETYN_1, FPPLANYR_1,
    M0 = CALCMC - INTFQCMC_1,
    USE = !FPSTATUS_2 %in% c("0", "B", "P", "T")
  )

nonusers
```

```
# A tibble: 116,860 × 8
  ID COUNTRY CALCMC FPSTATUS_2 UNMETYN_1 FPPLANYR_1    MO USE
  <int> <fct>    <dbl> <chr>      <lgl>     <lgl>    <dbl> <lgl>
1 1 BF        1453 3 FALSE      TRUE      11 TRUE
2 1 BF        1452 3 FALSE      TRUE      10 TRUE
3 1 BF        1451 3 FALSE      TRUE      9 TRUE
4 1 BF        1450 3 FALSE      TRUE      8 TRUE
5 1 BF        1449 3 FALSE      TRUE      7 TRUE
6 1 BF        1448 3 FALSE      TRUE      6 TRUE
7 1 BF        1447 0 FALSE      TRUE      5 FALSE
8 1 BF        1446 0 FALSE      TRUE      4 FALSE
9 1 BF        1445 0 FALSE      TRUE      3 FALSE
10 1 BF       1444 0 FALSE      TRUE      2 FALSE
11 1 BF       1443 0 FALSE      TRUE      1 FALSE
12 1 BF       1442 0 FALSE      TRUE      0 FALSE
13 2 BF       1452 5 FALSE     FALSE      11 TRUE
14 2 BF       1451 5 FALSE     FALSE      10 TRUE
15 2 BF       1450 5 FALSE     FALSE      9 TRUE
16 2 BF       1449 5 FALSE     FALSE      8 TRUE
17 2 BF       1448 5 FALSE     FALSE      7 TRUE
18 2 BF       1447 5 FALSE     FALSE      6 TRUE
19 2 BF       1446 5 FALSE     FALSE      5 TRUE
20 2 BF       1445 5 FALSE     FALSE      4 TRUE
# ... with 116,840 more rows
```

Next, we'll create `USEMO` to copy the month recorded in `MO` for each month of `USE` (otherwise, `case_when` assigns the value `NA`). If there are any months of `USE` for an individual woman, we'll identify the first such month with `ADOPT`; if there are no cases of `USE`, `ADOPT` will record the last month in `MO`. Finally we'll use `RC` to indicate whether `ADOPT` is “right censored” - these are cases where `ADOPT` is the last month in `MO`.

```
nonusers <- nonusers %>%
  group_by(ID) %>%
  mutate(
    USEMO = case_when(USE ~ MO),
    ADOPT = ifelse(any(USE), min(USEMO, na.rm = T), max(MO)),
    RC = case_when(ADOPT == MO ~ !USE)
  ) %>%
  ungroup()
```

nonusers

```
# A tibble: 116,860 × 11
  ID COUNTRY CALCMC FPSTATUS_2 UNMETYN_1 FPPLANYR_1    M0 USE  USEMO ADOPT RC
  <int> <fct>   <dbl> <chr>     <lgl>    <lgl>    <dbl> <lgl> <dbl> <dbl> <lgl>
1 1 BF      1453 3 FALSE    TRUE      11 TRUE    11 6 NA
2 1 BF      1452 3 FALSE    TRUE      10 TRUE    10 6 NA
3 1 BF      1451 3 FALSE    TRUE      9  TRUE    9 6 NA
4 1 BF      1450 3 FALSE    TRUE      8  TRUE    8 6 NA
5 1 BF      1449 3 FALSE    TRUE      7  TRUE    7 6 NA
6 1 BF      1448 3 FALSE    TRUE      6  TRUE    6 6 FALSE
7 1 BF      1447 0 FALSE    TRUE      5 FALSE   NA 6 NA
8 1 BF      1446 0 FALSE    TRUE      4 FALSE   NA 6 NA
9 1 BF      1445 0 FALSE    TRUE      3 FALSE   NA 6 NA
10 1 BF     1444 0 FALSE    TRUE      2 FALSE   NA 6 NA
11 1 BF     1443 0 FALSE    TRUE      1 FALSE   NA 6 NA
12 1 BF     1442 0 FALSE    TRUE      0 FALSE   NA 6 NA
13 2 BF      1452 5 FALSE   FALSE     11 TRUE    11 3 NA
14 2 BF      1451 5 FALSE   FALSE     10 TRUE    10 3 NA
15 2 BF      1450 5 FALSE   FALSE     9  TRUE    9 3 NA
16 2 BF      1449 5 FALSE   FALSE     8  TRUE    8 3 NA
17 2 BF      1448 5 FALSE   FALSE     7  TRUE    7 3 NA
18 2 BF      1447 5 FALSE   FALSE     6  TRUE    6 3 NA
19 2 BF      1446 5 FALSE   FALSE     5  TRUE    5 3 NA
20 2 BF      1445 5 FALSE   FALSE     4  TRUE    4 3 NA
# ... with 116,840 more rows
```

Notice, for example, that the first month of use for `ID == 1` occurs in month 6. Hence, `ADOPT == 6` and, because she adopted a method before the end of the calendar, `RC == FALSE`.

Finally, we'll now drop every row except for those matching `ADOPT`. This leaves one row for each woman in nonusers.

```
nonusers <- nonusers %>% filter(ADOPT == M0)
```

```
nonusers
```

```
# A tibble: 9,206 × 11
  ID COUNTRY CALCMC FPSTATUS_2 UNMETYN_1 FPPLANYR_1    MO USE  USEMO ADOPT RC
  <int> <fct>   <dbl> <chr>     <lgl>    <lgl>    <dbl> <lgl> <dbl> <dbl> <lgl>
1 1 BF      1448 3 FALSE     TRUE      6 TRUE     6 6 FALSE
2 2 BF      1444 5 FALSE     FALSE     3 TRUE     3 3 FALSE
3 3 BF      1453 0 FALSE     FALSE     12 FALSE    NA 12 TRUE
4 6 BF      1453 0 FALSE     FALSE     12 FALSE    NA 12 TRUE
5 7 BF      1452 0 FALSE     FALSE     11 FALSE    NA 11 TRUE
6 8 BF      1452 0 TRUE      FALSE     11 FALSE    NA 11 TRUE
7 13 BF     1441 5 FALSE     TRUE      0 TRUE     0 0 FALSE
8 16 BF     1449 5 FALSE     FALSE     8 TRUE     8 8 FALSE
9 17 BF     1452 0 FALSE     TRUE     11 FALSE    NA 11 TRUE
10 18 BF    1452 0 FALSE     FALSE     11 FALSE    NA 11 TRUE
11 21 BF    1452 0 FALSE     FALSE     11 FALSE    NA 11 TRUE
12 22 BF    1453 0 FALSE     FALSE     12 FALSE    NA 12 TRUE
13 26 BF    1452 0 FALSE     FALSE     11 FALSE    NA 11 TRUE
14 28 BF    1453 0 FALSE     FALSE     12 FALSE    NA 12 TRUE
15 29 BF    1454 0 FALSE     FALSE     13 FALSE    NA 13 TRUE
16 30 BF    1445 3 FALSE     TRUE      4 TRUE     4 4 FALSE
17 31 BF    1453 0 FALSE     FALSE     12 FALSE    NA 12 TRUE
18 32 BF    1454 0 FALSE     FALSE     13 FALSE    NA 13 TRUE
19 33 BF    1452 P TRUE      TRUE     11 FALSE    NA 11 TRUE
20 34 BF    1452 B TRUE      FALSE     11 FALSE    NA 11 TRUE
# ... with 9,186 more rows
```

We'll now fit three survival models predicting the duration of continuous non-use for the women in nonusers: one model for `UNMETYN_1`, one for `FPPLANYR_1`, and one for their interaction effect, which we'll call `INTERACT_1`. For each model, `survfit` reports the likelihood that a baseline non-user would have adopted any family planning method for each month in the calendar period. We'll run each model separately for each country, and we'll use `broom::tidy` to create a tidy summary table for each model.

```

adopt_models <- nonusers %>%
  # Create a variable capturing the interaction between intentions and unmet need
  mutate(INTERACT_1 = case_when(
    UNMETYN_1 & FPPLANYR_1 ~ "Unmet Need, Plan 1 Yr",
    UNMETYN_1 & !FPPLANYR_1 ~ "Unmet Need, No Plan 1 Yr",
    !UNMETYN_1 & FPPLANYR_1 ~ "No Unmet Need, Plan 1 Yr",
    !UNMETYN_1 & !FPPLANYR_1 ~ "No Unmet Need, No Plan 1 Yr"
  )) %>%
  # Separate survival models for each country
  group_by(COUNTRY) %>%
  summarise(
    unmet = survfit(Surv(M0, !RC) ~ UNMETYN_1, data = cur_group()) %>% list,
    plan = survfit(Surv(M0, !RC) ~ FPPLANYR_1, data = cur_group()) %>% list,
    interact = survfit(Surv(M0, !RC) ~ INTERACT_1, data = cur_group()) %>% list
  ) %>%
  # Tidy the output and relabel `COUNTRY` for the figure
  mutate(
    across(where(is.list), ~map(.x, broom::tidy)),
    COUNTRY = COUNTRY %>% recode(
      "BF" = "Burkina Faso",
      "CD" = "DRC",
      "KE" = "Kenya",
      "NG" = "Nigeria"
    )
  )
)

```

Let's start with the model featuring UNMETYN_1. If you `unnest` the unmet model output, you'll see a separate row for each month reported for women with "No Unmet Need" and "Unmet Need".

```

m_unmet <- adopt_models %>%
  unnest(unmet) %>%
  mutate(strata = if_else(
    str_detect(strata, "TRUE"), "Unmet Need", "No Unmet Need"
  )) %>%
  relocate(strata, .after = COUNTRY)

m_unmet

```

```

# A tibble: 117 × 12
  COUNTRY strata   time n.risk n.event n.cen...¹ estim...² std.e...³ conf....⁴ conf....⁵ plan
  interact
  <fct>    <chr>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>
<list>    <list>
  1 Burkina Fa... No Un...     0     2245     157      0   0.930  0.00579   0.941   0.920
<tibble> <tibble>
  2 Burkina Fa... No Un...     1     2088      20      0   0.921  0.00617   0.932   0.910
<tibble> <tibble>
  3 Burkina Fa... No Un...     2     2068      21      0   0.912  0.00656   0.924   0.900
<tibble> <tibble>
  4 Burkina Fa... No Un...     3     2047      25      0   0.901  0.00701   0.913   0.888
<tibble> <tibble>
  5 Burkina Fa... No Un...     4     2022      27      0   0.889  0.00747   0.902   0.876
<tibble> <tibble>
  6 Burkina Fa... No Un...     5     1995      22      0   0.879  0.00784   0.892   0.865
<tibble> <tibble>
  7 Burkina Fa... No Un...     6     1973      27      0   0.867  0.00827   0.881   0.853
<tibble> <tibble>
  8 Burkina Fa... No Un...     7     1946      26      0   0.855  0.00868   0.870   0.841
<tibble> <tibble>
  9 Burkina Fa... No Un...     8     1920      30      0   0.842  0.00915   0.857   0.827
<tibble> <tibble>
 10 Burkina Fa... No Un...    9     1890      37      0   0.825  0.00971   0.841   0.810
<tibble> <tibble>
 11 Burkina Fa... No Un...   10     1853      35     97   0.810  0.0102    0.826   0.794
<tibble> <tibble>
 12 Burkina Fa... No Un...   11     1721      27    906   0.797  0.0107    0.814   0.781
<tibble> <tibble>
 13 Burkina Fa... No Un...   12     788       5    687   0.792  0.0110    0.809   0.775
<tibble> <tibble>
 14 Burkina Fa... No Un...   13      96       3     70   0.767  0.0214    0.800   0.736
<tibble> <tibble>
 15 Burkina Fa... No Un...   14      23       0     23   0.767  0.0214    0.800   0.736
<tibble> <tibble>
 16 Burkina Fa... Unmet...   0     632       86      0   0.864  0.0158    0.891   0.838
<tibble> <tibble>
 17 Burkina Fa... Unmet...   1     546       15      0   0.840  0.0173    0.869   0.812
<tibble> <tibble>
 18 Burkina Fa... Unmet...   2     531        6      0   0.831  0.0180    0.860   0.802
<tibble> <tibble>
 19 Burkina Fa... Unmet...   3     525        9      0   0.816  0.0189    0.847   0.787
<tibble> <tibble>
 20 Burkina Fa... Unmet...   4     516        6      0   0.807  0.0195    0.838   0.777
<tibble> <tibble>
# ... with 97 more rows, and abbreviated variable names ¹n.censor, ²estimate, ³std.error,
# ⁴conf.high,
# ⁵conf.low

```

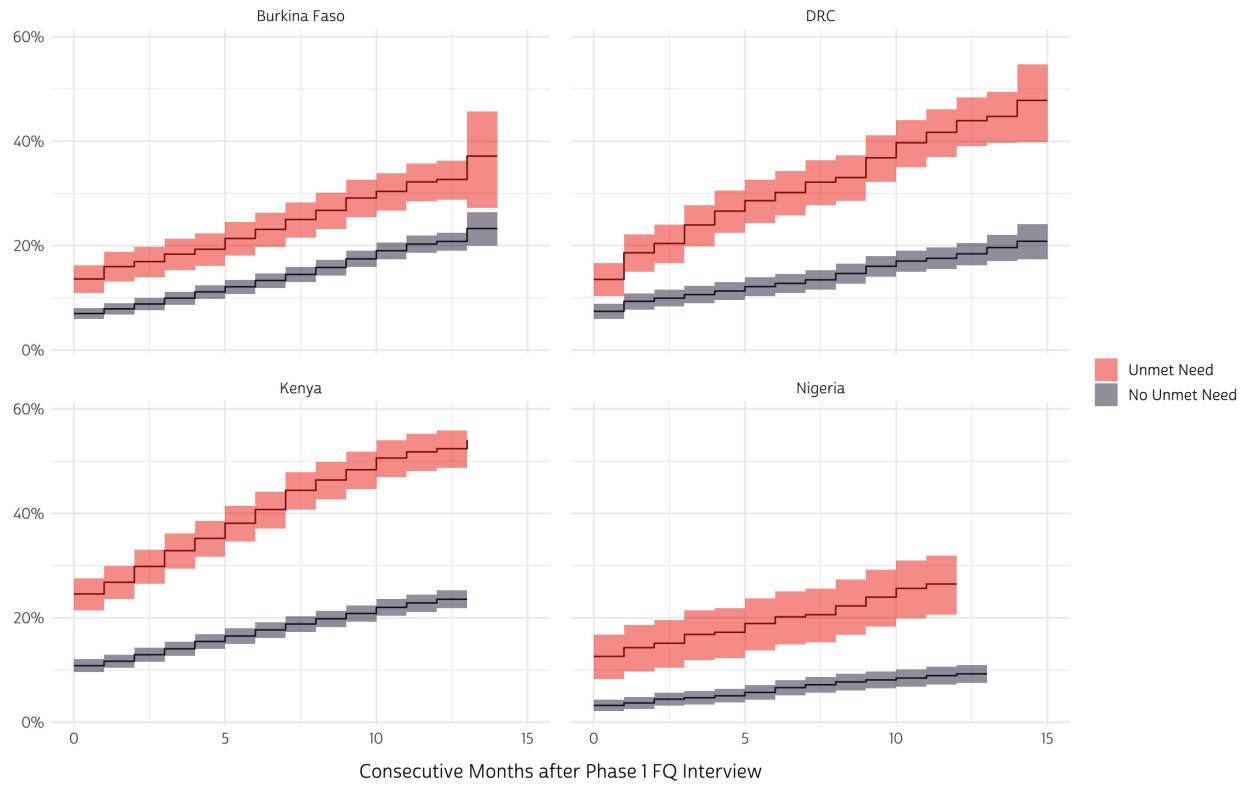
The column `n.risk` shows the total number of non-users remaining after the number of months passed in `time`. The column `estimate` shows the estimated probability that a randomly selected woman would remain in `n.risk` by that month (`conf.high` and `conf.low` report a 95% confidence interval by default). For example, row 1 shows that there were 2245 women in the Phase 1 Burkina Faso sample who were not using family planning did not meet PMA criteria for “unmet need”. Among these, `n.event` shows that 157 adopted a family planning method less than one month after the interview: this leaves 93.0% of the group remaining before one month had passed.

Below that, row 16 shows that there were 632 women in the Phase 1 Burkina Faso sample who were not using family planning, but *did* meet PMA criteria for “unmet need”. Among these, `n.event` shows that 86 adopted a family planning method less than one month after the interview: this leaves 86.4% of the group remaining before one month had passed.

We'll produce a “time-to-event” plot by inverting the probabilities reported in `event` and its accompanying confidence interval. This plot uses `geom_step` to draw a step-wise function, and `geom_rect` to create a shaded confidence interval for each step.

```
m_unmet %>%
  group_by(COUNTRY, strata) %>%
  mutate(
    across(where(is.double) & !time, ~1-.x),
    xmax = if_else(time == max(time), time, time + 1), # horizontal ci shading
  ) %>%
  ggplot(aes(x = time, y = estimate, fill = strata)) +
  geom_step() +
  geom_rect(
    aes(xmin = time, xmax = xmax, ymin = conf.low, ymax = conf.high),
    alpha = 0.5,
    color = 0
  ) +
  facet_wrap(~COUNTRY) +
  scale_y_continuous(labels = scales::label_percent()) +
  scale_fill_manual(values = c(
    "Unmet Need" = "#F2300E",
    "No Unmet Need" = "#352749"
  )) +
  labs(
    title = "Predicted Time to FP Adoption by Phase 1 Unmet Need Status",
    x = "Consecutive Months after Phase 1 FQ Interview", y = NULL, fill = NULL
  ) +
  theme_pma
```

Predicted Time to FP Adoption by Phase 1 Unmet Need Status



In general, we see evidence that non-users with unmet need at Phase 1 were significantly quicker to adopt a method compared to women with no unmet need in each country.

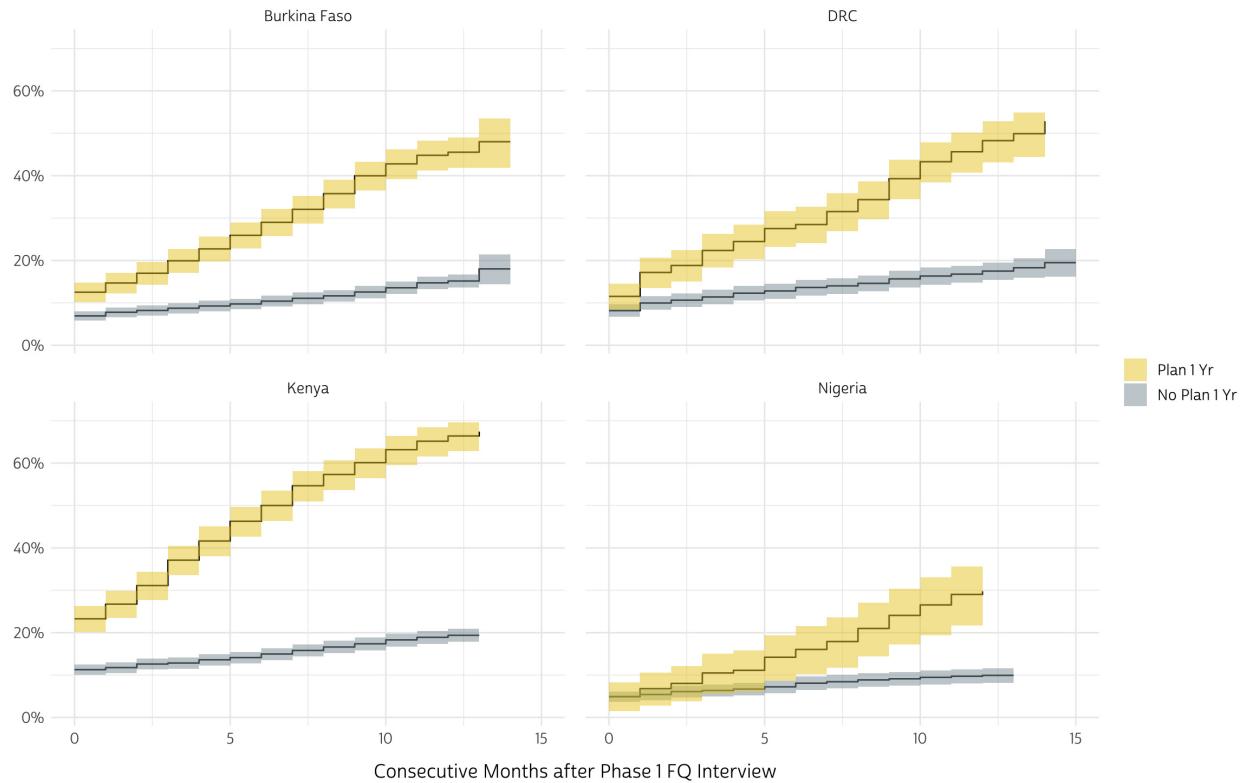
Let's now consider how the adoption rate might be influenced to by FPPLANYR_1.

```

adopt_models %>%
  unnest(plan) %>%
  mutate(strata = if_else(
    str_detect(strata, "TRUE"), "Plan 1 Yr", "No Plan 1 Yr"
  )) %>%
  group_by(COUNTRY, strata) %>%
  mutate(
    across(where(is.double) & !time, ~1-.x),
    xmax = if_else(time == max(time), time, time + 1),
  ) %>%
  ggplot(aes(x = time, y = estimate, fill = strata)) +
  geom_step() +
  geom_rect(
    aes(xmin = time, xmax = xmax, ymin = conf.low, ymax = conf.high),
    alpha = 0.5,
    color = 0
  ) +
  facet_wrap(~COUNTRY) +
  scale_y_continuous(labels = scales::label_percent()) +
  scale_fill_manual(values = c(
    "Plan 1 Yr" = "#EBCC2A",
    "No Plan 1 Yr" = "#899DA4"
  )) +
  labs(
    title = "Predicted Time to FP Adoption by Intentions Within 1 Year of Phase 1",
    x = "Consecutive Months after Phase 1 FQ Interview", y = NULL, fill = NULL
  ) +
  theme_pma

```

Predicted Time to FP Adoption by Intentions Within 1 Year of Phase 1



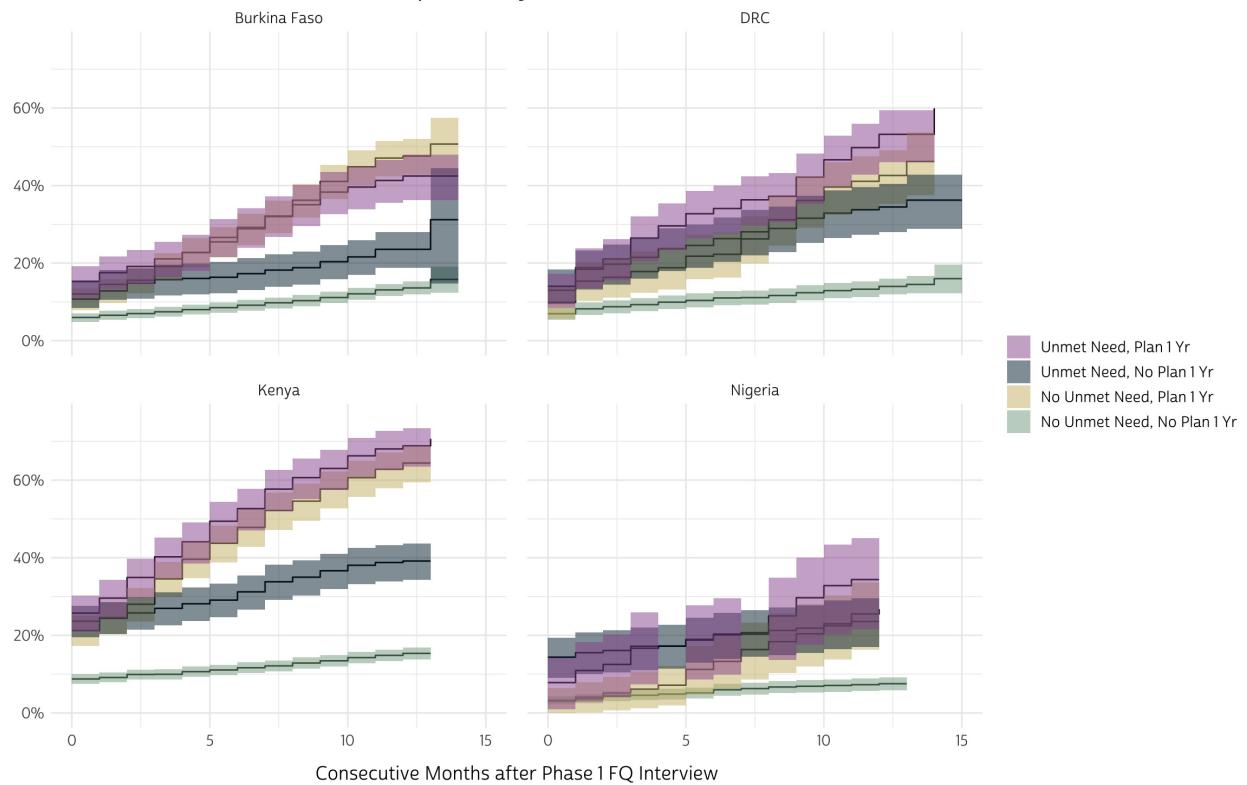
Here, we see that women who planned to adopt a method within 1 year following the Phase 1 interview were significantly quicker to begin using one compared to women who had no such plans (except within the first few months for women in Nigeria, where this difference was not statistically significant). Finally, let's consider the interaction reported in `INTERACT_1`.

```

adopt_models %>%
  unnest(interact) %>%
  group_by(COUNTRY, strata) %>%
  mutate(
    across(where(is.double) & !time, ~1-.x),
    xmax = if_else(time == max(time), time, time + 1),
    strata = str_remove(strata, ".*=")
  ) %>%
  ggplot(aes(x = time, y = estimate, fill = strata)) +
  geom_step() +
  geom_rect(
    aes(xmin = time, xmax = xmax, ymin = conf.low, ymax = conf.high),
    alpha = 0.5,
    color = 0
  ) +
  facet_wrap(~COUNTRY) +
  scale_y_continuous(labels = scales::label_percent()) +
  scale_fill_manual(values = c(
    "Unmet Need, Plan 1 Yr" = "#98579B",
    "Unmet Need, No Plan 1 Yr" = "#00263A",
    "No Unmet Need, Plan 1 Yr" = "#CCBA72",
    "No Unmet Need, No Plan 1 Yr" = "#81A88D"
  )) +
  labs(
    title = "Predicted Time to FP Adoption by Phase 1 Intentions and Unmet Need",
    x = "Consecutive Months after Phase 1 FQ Interview", y = NULL, fill = NULL
  ) +
  theme_pma

```

Predicted Time to FP Adoption by Phase 1 Intentions and Unmet Need



The interaction between UNMETYN_1 and FPPLAN1YR_1 seems to confirm at least one of our hypotheses: non-users who had no unmet need and no plans to adopt a method within the year were significantly slower to do so (again, except for the first few months shown in Nigeria). Women without plans to adopt a method were also somewhat slower to adopt a method if they experienced unmet need, but there are considerable differences in the strength of this finding across countries and over the length of the calendar period. Overall, women who planned to adopt a method were significantly quicker to do so, but the mitigating effects of unmet need are generally unclear.

We hope this preliminary analysis serves as an entry point for your own exploration of the contraceptive calendar data included in each PMA panel survey. Stay tuned here for updates in the coming months, when we'll return to the calendar to see how rainfall, temperature, and other climate shocks impact monthly family planning behavior.