

# IPUMS PMA LONGITUDINAL ANALYSIS GUIDE

## For R Users



November 2022



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# PREFACE

This guide was commissioned and funded by the Family Planning Team at the Bill & Melinda Gates Foundation. The examples here are directly based on the companion [IPUMS PMA data analysis blog](#), with R examples developed by Matt Gunther and IPUMS PMA documentation by Devon Kristiansen under the management of Kathryn Grace, PhD and Elizabeth Heger Boyle, PhD at IPUMS PMA, University of Minnesota. The Stata version and statistical consulting were provided by Mia Yu and Dale Rhoda at [Biostat Global Consulting](#). These authors are grateful for helpful reviews & comments from Philip Anglewicz, PhD; Linnea Zimmerman, PhD, and Aisha Siewe at Johns Hopkins University. Thanks also to Caitlin Clary, PhD, Nina Brooks, PhD, and Finn Roberts for code contributions and review.

## Suggested Citation

Matt Gunther, Mia Yu, Dale Rhoda, and Devon Kristiansen. *IPUMS PMA Longitudinal Analysis Guide for R Users* (November 2022). Minneapolis, MN: IPUMS. [pma.ipums.org](http://pma.ipums.org)

## Source Code

This manual is open source. It was constructed from [R Markdown](#) files with the [pagedown](#) package for R.<sup>1</sup> These files are available on our [GitHub repository](#), where you will also find [.r](#) and [.do](#) files containing the code shown in this manual.

The IPUMS PMA data files referenced in this manual are also available at no cost, but you must register and adhere to terms of use at [pma.ipums.org/register](http://pma.ipums.org/register). Dataset access is granted only for non-commercial purposes. Users must register an account with IPUMS, request access to data from particular countries, and describe their intended use for the data. Users who have been approved for access to certain countries may submit justification to expand their access to other countries.

## La version française du formulaire d'inscription

## Hyperlinks

Hyperlinks to IPUMS PMA variable documentation, relevant R and Stata documentation, and various other resources are highlighted [in pink](#) throughout this manual. If the reader prefers a printed version, they are recommended to compile the manual from source files on our GitHub repository, changing the [pagedown](#) option described [here](#). **Warning:** this will add additional footnotes to the document, and may impact pagination.

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<sup>1</sup>[pagedown](#) © Xie, Yihui et al. (MIT)

## Acronyms

- BMGF - Bill & Melinda Gates Foundation
- CI - confidence interval
- CMC - century month code
- CONSORT - Consolidated Standards of Reporting Trials
- CRAN - The Comprehensive R Archive Network (statistical software)
- CSV - comma-separated values file format
- DEFF - design effect
- DEFT - root design effect (square root of DEFF)
- DRC - Democratic Republic of Congo
- EA - enumeration area
- FP - family planning
- FP2020 - Family Planning 2020
- FP2030 - Family Planning 2030
- GPS - global positioning system
- IPUMS - Integrated Public Use Microdata Series
- ISO - International Organization for Standardization
- IUD - intrauterine device
- LAM - lactational amenorrhea method of contraception
- NA - not available (R notation for a missing data element)
- NIU - not in universe
- PMA - Performance Monitoring for Action
- PPS - probability proportional to size
- SAS - statistical analysis system (statistical software)
- SPSS - statistical package for social sciences (statistical software)

# 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.<sup>2</sup>

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.

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<sup>2</sup>PMA data for individual countries is also available at no cost from [pmadata.org](#). Please note that the variable names, value labels, numeric codes, and other metadata featured in this guide have been altered by IPUMS PMA to facilitate comparison across countries.

## 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 [r-project.org](#). R is available at no cost and it runs on Windows, MacOS, and a wide variety of UNIX platforms. We also recommend downloading a free copy of [RStudio](#), an integrated development environment (IDE) designed to make your experience with R much easier.

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 require additional tools because they appear as **labelled integers** represented in R by a number and a label like this:

```
# 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
```

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

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



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© IPUMS  
(MPL-2.0)



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## Featured Data Extracts

In subsequent chapters, we will include instructions for requesting data extracts from IPUMS PMA that are identical those used in our analysis. These data are available at no cost, but you must register and adhere to terms of use at [pma.ipums.org/register](http://pma.ipums.org/register).

Each data extract that you request from IPUMS PMA is named with a unique number. For example, your very first extract will include a pair of files named `pma_00001.dat.gz` and `pma_00001.xml`. In this guide we reference seven data extracts, but your own file names may vary depending on the number of IPUMS PMA extracts you have requested previously.

- `pma_00001.dat.gz` and `pma_00001.xml`
- `pma_00002.dat.gz` and `pma_00002.xml`
- `pma_00003.dat.gz` and `pma_00003.xml`
- `pma_00004.dat.gz` and `pma_00004.xml`
- `pma_00005.dat.gz` and `pma_00005.xml`
- `pma_00006.dat.gz` and `pma_00006.xml`
- `pma_00007.dat.gz` and `pma_00007.xml`

As you follow along with each chapter, save each data extract in folder called `data` within your [R working directory](#).

## Working Directory

R users can identify their current working directory with the function `getwd` and change it with `setwd`. Files within the working directory can be found by R using the **relative path** from this locations. For example, we'll load our first data extract into R *assuming* that you have placed it in a folder called `data` within your [R working directory](#).

```
dat <- read_ipums_micro(  
  ddi = "data/pma_00001.xml",  
  data = "data/pma_00001.dat.gz"  
)
```

Rstudio users can find all of the code demonstrated in this guide in [this RStudio Project](#).<sup>3</sup> Simply open the file `pma-longitudinal.Rproj` and navigate to the `RMarkdown` file `r_users.Rmd` in RStudio - no need to set your own working directory!

---

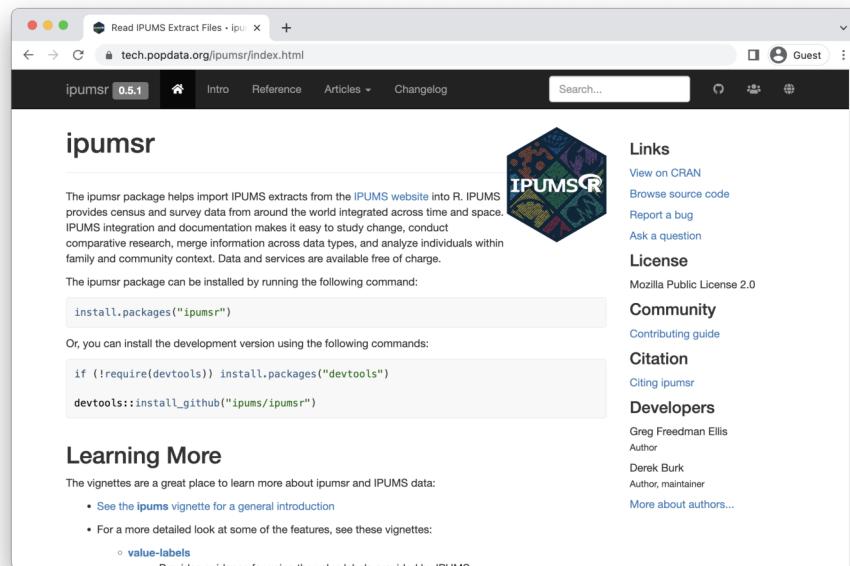
<sup>3</sup>Lean more about RStudio Projects [here](#).

## Learning More

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 change-log (for news about updates). The [ipumsr](#) page is a great place to start:

A screenshot of a web browser displaying the ipumsr package website. The URL in the address bar is "tech.popdata.org/ipumsr/index.html". The page has a dark header with the text "ipumsr 0.5.1" and navigation links for "Intro", "Reference", "Articles", and "Changelog". A search bar and a guest user icon are also present. The main content area features the title "ipumsr" in large letters, followed by a brief description of the package: "The ipumsr package helps import IPUMS extracts from the IPUMS website into R. IPUMS provides census and survey data from around the world integrated across time and space. IPUMS integration and documentation makes it easy to study change, conduct comparative research, merge information across data types, and analyze individuals within family and context. Data and services are available free of charge." Below this is a code block showing how to install the package: "install.packages("ipumsr")". Further down, another code block shows how to install the development version: "if (!require(devtools)) install.packages("devtools") devtools::install\_github("ipums/ipumsr")". To the right of the main content, there is a sidebar titled "Links" containing links to "View on CRAN", "Browse source code", "Report a bug", and "Ask a question". Other sections include "License" (Mozilla Public License 2.0), "Community" (Contributing guide), "Citation" (Citing ipumsr), and "Developers" (listing Greg Freedman Ellis as Author and Derek Burk as Author, maintainer, with a link to "More about authors...").

The ipumsr package helps import IPUMS extracts from the [IPUMS website](#) into R. IPUMS provides census and survey data from around the world integrated across time and space. IPUMS integration and documentation makes it easy to study change, conduct comparative research, merge information across data types, and analyze individuals within family and context. Data and services are available free of charge.

The ipumsr package can be installed by running the following command:

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

Or, you can install the development version using the following commands:

```
if (!require(devtools)) install.packages("devtools")
devtools::install_github("ipums/ipumsr")
```

### Learning More

The vignettes are a great place to learn more about ipumsr and IPUMS data:

- See the [ipums vignette](#) for a general introduction
- For a more detailed look at some of the features, see these vignettes:
  - [value-labels](#)
    - Provides guidance for using the value labels provided by IPUMS

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

## 1.2 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.<sup>4</sup>

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

---

<sup>4</sup>In 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 - the IPUMS PMA blog series on **PMA COVID-19 surveys** covers this topic in detail.

## 1.3 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.<sup>5</sup> 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.

<sup>5</sup>Displaced 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**<sup>6</sup> 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**.<sup>7</sup>

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,<sup>8</sup> but at least one member of the Phase 1 household remained and could help resident enumerators locate her new dwelling.<sup>9</sup>

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.

<sup>6</sup>Questionnaires administered in each country may vary from this **Core Household Questionnaire** - [click here](#) for details.

<sup>7</sup>Questionnaires administered in each country may vary from this **Core Female Questionnaire** - [click here](#) for details.

<sup>8</sup>The “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.

<sup>9</sup>In cases where no Phase 1 household members remained in the dwelling at Phase 2, women from the household are considered **lost to follow-up**. Chapter 3 covers this topic in detail.

When you select the new **Longitudinal** sample option from IPUMS PMA, 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 states: '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.' Below this, there are three radio button options: 'Cross-sectional' (unchecked), 'Longitudinal' (checked), and 'Wide' (unchecked). A red arrow points to the 'Longitudinal' radio button. To the right is a purple 'SUBMIT SAMPLE SELECTIONS' button. Below the radio buttons is a section titled 'FAMILY PLANNING - PERSON' containing a 'Documentation' link and two checkboxes: 'All Samples (long)' and 'Burkina Faso'. At the bottom right is a date range checkbox labeled '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 from IPUMS PMA.

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 states: '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.' Below this, there are two radio button options: 'Cross-sectional' (selected) and 'Longitudinal'. A red arrow points to the 'Cross-sectional' radio button. To the right is a purple 'SUBMIT SAMPLE SELECTIONS' button. A section titled 'FAMILY PLANNING - PERSON' contains a checkbox for 'All Samples' and a timeline from 2015 to 2021 with checkboxes for each year.

## 1.4 INCLUSION CRITERIA FOR ANALYSIS

Several chapters in this manual 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. In order to reproduce the findings from PMA reports, we'll remove *de jure* cases recorded in the variable **RESIDENT**.

For example, let's consider a **Wide** format data extract containing Phase 1 and Phase 2 respondents to the Female Questionnaire from Burkina Faso. We've downloaded such an extract and placed it in the data sub-folder of our R working directory. We'll load **ipumsr** and **tidyverse** together with our extract.

We will demonstrate how to request and download an IPUMS PMA data extract in Chapter 2.

```
library(ipumsr)
library(tidyverse)

dat <- read_ipums_micro(
  ddi = "data/pma_00001.xml",
  data = "data/pma_00001.dat.gz"
)
```

In a **Wide** format data extract, a numeric suffix indicates the data collection phase associated with each variable. So, you'll find the the number of women who slept in the household before the Household Questionnaire for each phase reported in **RESIDENT\_1** and **RESIDENT\_2**.

This extract includes 174 women who are not members of the *de facto* population because they did not sleep in the sampled household during the night before the Phase 1 interview:

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

```
# A tibble: 3 × 2
  RESIDENT_1                n
  <int+lbl>                <int>
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
```

The extract also includes 230 women who are not members of the *de facto* population because they did not sleep in the sampled household during the night before the Phase 2 interview:

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

```
# A tibble: 5 × 2
  RESIDENT_2                n
  <int+lbl>                <int>
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
```

Moreover, there are 492 NA values in `RESIDENT_2` representing women who were **lost to follow-up** after Phase 1. We will explain **loss to follow-up** in detail in Chapter 3.

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

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

```
defacto %>% 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, PMA 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 'IPUMS PMA: select samples'. The URL is [pma.ipums.org/pma-action/samples](https://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 states: '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.' Below this, there are two sections: 'FAMILY PLANNING - PERSON' and 'Sample Members'. Under 'FAMILY PLANNING - PERSON', there is a 'Documentation' section with checkboxes for 'All Samples (wide)', 'Burkina Faso', 'Congo (Democratic Republic)', 'Kenya', and 'Nigeria', each with specific year ranges. Under 'Sample Members', there are five options: 'Female Respondents' (selected), 'Female Respondents and Household Members', 'Female Respondents and Female Non-respondents', and 'All Cases (Respondents and Non-respondents to Household and Female Questionnaires)'. Each option has a small red arrow pointing to it from the left margin. At the bottom of the page, there is a 'SUBMIT SAMPLE SELECTIONS' button and a footer note: '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 PMA extract indicates that a particular variable is not provided for a selected sample. In a **Wide** 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:

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

completed %>% 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 %in% c(11, 22) & RESIDENT_2 %in% c(11, 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 dis-aggregated by demographic variables like:

- **MARSTAT** - marital status
- **EDUCATT** and **EDUCATTGEN** - highest attended level of education<sup>10</sup>
- **AGE** - age
- **WEALTHQ** and **WEALTHT** - household wealth quintile or tertile<sup>11</sup>
- **URBAN** and **SUBNATIONAL** - geographic location<sup>12</sup>

<sup>10</sup>Levels in **EDUCATT** may vary by country; **EDUCATTGEN** recodes country-specific levels in four general categories.

<sup>11</sup>Households are divided into quintiles/tertiles relative to the distribution of an asset **SCORE** weighted for all sampled households. For sub-nationally-representative samples (DRC and Nigeria), separate wealth distributions are calculated for each sampled region.

<sup>12</sup>**SUBNATIONAL** includes sub-national regions for all sampled countries; country-specific variables are also available on the **household - geography** page.

## 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. This section describes how to use survey weights, cluster IDs, and sample strata in R.

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.<sup>14</sup>
- **FQWEIGHT** can be used to generate cross-sectional population estimates from questions on the Female Questionnaire.<sup>15</sup>
- **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.<sup>13</sup>

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.

PMA sample clusters are identified by the variable **EAID**, while sample strata are identified by **STRATA**. We'll demonstrate how to use each of these survey design elements in R below.

<sup>13</sup>POPWT can be used to estimate population-level counts - [click here](#) or view [this video](#) for details.

<sup>14</sup>HQWEIGHT 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.

<sup>15</sup>FQWEIGHT adjusts HQWEIGHT for female non-response within the EA, normalized at the population-level - see [female weighting guide](#) for details.

## 1.5.1 Set survey design

Throughout this guide, we'll use tools from the `srvyr` package to incorporate survey design elements into our analyses.<sup>16</sup> You can install or update `srvyr` like so:

```
install.packages("srvyr")
```



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Ellis  
(GPL-2 | GPL-3)

Load `srvyr` for use in an R session with:

```
library(srvyr)
```

Let's return to the **Wide** data extract described in the previous section, which includes Phase 1 and Phase 2 **Female Respondents** from Burkina Faso. In the following example, we'll show how to use IPUMS PMA survey design elements 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** format longitudinal extract, you'd 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.

Here is how to count the *unweighted* number of sampled women using and not using contraception in both phases. (We drop 5 cases coded 99 for “NIU (not in universe)” in Phase 1).

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

```
# A tibble: 4 × 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
```

<sup>16</sup>The `srvyr` package is a `tidyverse` 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.

To estimate a population percentage, we'll need to tell `svydesign` that we are working with a sample survey dataset and specify the IPUMS PMA survey design elements. This is accomplished with `as_survey_design`: we use `PANELWEIGHT` as the sampling weight. We also use `EAID_1` to `id` the sample clusters,<sup>17</sup> and `STRATA_1` to represent sample strata.<sup>18</sup>

Summary functions like `survey_mean` use information from `as_survey_design` to derive weighted population estimates with cluster-adjusted standard errors. The argument `vartype = "ci"` reports a cluster-robust 95% confidence interval,<sup>19</sup> while `prop = TRUE` and `prop_method = "logit"` ensure that no estimated proportion includes values beyond 0% and 100%.<sup>20</sup>

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

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

`coef` shows the estimated population proportion

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

Using the survey design information for this sample, we estimate that about 18.8% of all reproductive age women in Burkina Faso were using contraception at the time both Phase 1 and Phase 2 data were collected. We're 95% certain that this value falls between 16.4% and 21.4%.

<sup>17</sup>As we'll see in Chapter 3, 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.

<sup>18</sup>As with `EAID`, you may use either `STRATA_1` or `STRATA_2` if your analysis is restricted to panel members

<sup>19</sup>The confidence level in `survey_mean` can be adjusted with `level` (e.g. `level = 0.99`)

<sup>20</sup>See `svyciprop` for a complete list of available adjustment methods.

## 1.5.2 Sample strata for DRC

Importantly, 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 <- read_ipums_micro(  
  ddi = "data/pma_00002.xml",  
  data = "data/pma_00002.dat.gz"  
)  
  
dat2 <- dat2 %>%  
  filter(  
    RESIDENT_1 %in% c(11, 22) & RESIDENT_2 %in% c(11, 22),  
    RESULTFQ_2 == 1,  
    CP_1 < 90 & CP_2 < 90  
)  
  
dat2 %>% filter(is.na(STRATA_1)) %>% count(COUNTRY, STRATA_1)
```

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) %>%  
  group_by(COUNTRY, GEOCD, GEONG) %>%  
  summarise(  
    survey_mean(  
      CP_1 * CP_2,  
      vartype = "ci",  
      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]    1967
2 2 [Kongo Central] 1511
3 NA              14227
```

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 `STRATARC` (for “strata recoded”).

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

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

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

# A tibble: 28 × 4		STRATARC	n
GEOCD	STRATA_1	<dbl>	<int>
1	1 [Kinshasa]	NA	1 1967
2	2 [Kongo Central]	NA	2 1511
3	NA	40410 [Bungoma - urban, Kenya]	40410 153
4	NA	40411 [Bungoma - rural, Kenya]	40411 488
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 213
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 585
15	NA	40422 [Nairobi - urban, Kenya]	40422 493
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 473
24	NA	56606 [Lagos, Nigeria]	56606 1088
25	NA	56611 [Kano - Urban]	56611 437
26	NA	56612 [Kano - Rural]	56612 561
27	NA	85401 [Urban, Burkina Faso]	85401 3053
28	NA	85402 [Rural, Burkina Faso]	85402 2154

Finally, we can use the updated survey design information to estimate the proportion of women who were using contraception at both Phase 1 and Phase 2 in every sample (including those from Kinshasa and Kongo Central).

```
dat2 %>%
  as_survey_design(weight = PANELWEIGHT, id = EAID_1, strata = STRATARC) %>%
  group_by(COUNTRY, GEOCD, GEONG) %>%
  summarise(
    survey_mean(
      CP_1 * CP_2,
      vartype = "ci",
      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
```

## 2 LONGITUDINAL DATA EXTRACTS

This chapter provides a guided tour of the IPUMS PMA data extract system. While you may also access the original data directly from our partners at PMA, harmonized data from IPUMS have a few additional features. For instance, you can request an extract that:

- includes samples from multiple countries
- includes samples from multiple rounds of data collection
- are formatted in either **Long** or **Wide** format

IPUMS PMA also makes it easy to switch between multiple *units of analysis* covered in PMA surveys. In addition to the data featured in this guide, you'll find surveys representing:

- Service Delivery Points (SDPs)
- Client Exit Interviews conducted at SDPs
- Participants in special surveys covering topics like COVID-19, nutrition, and maternal & newborn health

To get started with a longitudinal data extract, you'll need to select the **Family Planning** topic under the **Person** unit of analysis.

Register here to access IPUMS PMA data at no cost. See our user guide for details.

A video tour of the longitudinal extract system is available here on the IPUMS PMA Youtube channel.

The screenshot shows the IPUMS PMA website at <https://pma.ipums.org/pma-action/variables/group>. The main heading is "CHOOSE THE TOPIC FOR DATA BROWSING". Below it, there's a grid of categories:

	FAMILY PLANNING	NUTRITION
PERSON	DESCRIPTION	DESCRIPTION
SERVICE DELIVERY POINT	FAMILY PLANNING DESCRIPTION	NUTRITION DESCRIPTION
INFANT	MATERNAL AND NEWBORN HEALTH DESCRIPTION	

A red oval highlights the "FAMILY PLANNING" button under the "PERSON" category. The URL at the bottom of the browser window is [https://pma.ipums.org/pma-action/variables/group?unit\\_of\\_analysis=person](https://pma.ipums.org/pma-action/variables/group?unit_of_analysis=person).

## 2.1 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.

The screenshot shows the IPUMS PMA website at [pma.ipums.org/pma-action/samples](https://pma.ipums.org/pma-action/samples). The top navigation bar includes links for LOG IN, REGISTER, GLOBAL HEALTH, and IPUMS.ORG. The main header features the IPUMS PMA logo and the text "PERFORMANCE MONITORING FOR ACTION". Below the header are links for HOME, SELECT DATA, MY DATA, and SUPPORT. The main content area is titled "SELECT SAMPLES". A note states: "Variable documentation on the web site can be filtered to display only material corresponding to chosen datasets ([more information](#) on this feature)." It says users can select any datasets for browsing and provides a link to log in. Two radio buttons are shown: "Cross-sectional" (selected) and "Longitudinal". A "SUBMIT SAMPLE SELECTIONS" button is located to the right. The "FAMILY PLANNING - PERSON" section contains a "All Samples" checkbox and a grid of checkboxes for years from 2015 to 2021. Below the grid, country-specific checkboxes are listed: Burkina Faso, Congo (Democratic Republic), and others for 2020, 2019, 2018, 2017, 2016, and 2015. Some options have small informational icons (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!).

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

**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.

The screenshot shows the 'SELECT SAMPLES' page of the IPUMS PMA website. At the top, there is a navigation bar with links for LOG IN, REGISTER, GLOBAL HEALTH, and IPUMS.ORG. Below the navigation is the IPUMS PMA logo and a menu bar with links for HOME, SELECT DATA, MY DATA, and SUPPORT. The main content area is titled 'SELECT SAMPLES'. It contains instructions about variable documentation and sample selection. A section for 'FAMILY PLANNING - PERSON' includes a 'Documentation' table with rows for All Samples (wide), Burkina Faso, Congo (Democratic Republic), Kenya, and Nigeria, each with specific survey years. Below this 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. A red arrow points to the 'All Samples (wide)' checkbox in the documentation table. A red circle highlights the 'Longitudinal' radio button in the sample selection section. A 'SUBMIT SAMPLE SELECTIONS' button is located at the bottom of both sections.

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.

The screenshot shows a web browser window titled "IPUMS PMA: select samples". The URL is "pma.ipums.org/pma-action/samples". The page has a sidebar on the left with "Documentation" and a main content area. In the main area, there are two sections: "Sample Members" and "SUBMIT SAMPLE SELECTIONS". A red oval highlights the "Sample Members" section. It contains four radio button options: "Female Respondents" (selected), "Female Respondents and Household Members", "Female Respondents and Female Non-respondents", and "All Cases (Respondents and Non-respondents to Household and Female Questionnaires)". Below the "Sample Members" section is a "SUBMIT SAMPLE SELECTIONS" button. At the bottom of the page, there is 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".

**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.<sup>21</sup>

**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)”.

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

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

<sup>21</sup>Women 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.

**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 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.

**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.

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.

**RESULTFQ** indicates whether an individual completed the Female Questionnaire.

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

## 2.2 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 for variable selection. At the top, there is a navigation bar with links for 'LOG IN | REGISTER | GLOBAL HEALTH | IPUMS.ORG'. On the right, a 'DATA CART' section indicates '0 VARIABLES' and '6 SAMPLES' with a 'VIEW CART' button. The main content area has a header 'CURRENTLY BROWSING: "FAMILY PLANNING - PERSON"' with a 'CHANGE' link. Below this is a 'SELECT VARIABLES' section with dropdown menus for 'TOPICS' (set to 'TECHNICAL'), 'A-Z' (set to 'FAMILY PLANNING'), and 'SEARCH' (with a magnifying glass icon). To the right of these are 'DISPLAY OPTIONS' and 'HELP' and 'COUNTRY ABBREVIATIONS' links. A sidebar on the left lists various topics: 'SAMPLES have been selected', followed by 'TECHNICAL', 'DEMOGRAPHICS (WOMEN)', 'FAMILY PLANNING' (which is currently selected), 'HEALTH', 'ABORTION', 'HOUSEHOLD', 'WATER AND SANITATION', and 'COVID-19'. Under 'FAMILY PLANNING', a list of sub-topics is shown: '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'. At the bottom of the page, there is a footer with the text 'MINNESOTA.' and a 'COPYRIGHT' section. A small 'javascript:void(0);' is visible at the very bottom left.

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 shows a DATA CART with 0 VARIABLES and 6 SAMPLES, and a VIEW CART button. Below the navigation, the IPUMS PMA logo is displayed. The main content area has a header for "CURRENTLY BROWSING: 'FAMILY PLANNING - PERSON'" with a CHANGE link. There are buttons for CHANGE SAMPLES, SELECT VARIABLES (TOPICS, A-Z, SEARCH), DISPLAY OPTIONS, and HELP (COUNTRY ABBREVIATIONS). A note says "AN 'X' INDICATES THE VARIABLE IS AVAILABLE IN THAT DATASET." The main feature is a table titled "DISCONTINUATION OF FAMILY PLANNING VARIABLES (TOP)" under the heading "LONGITUDINAL SAMPLES". The table includes columns for Add to cart, Variable, Variable Label, Type, and sample years: BURKF (2020-2021), CONDR (2019a-2020a), CONDR (2019b-2020b), KENYA (2019-2020), NIGERA (2019a-2020a), and NIGERA (2019b-2020b). The table lists variables like FPSTOPMO, EPIMPREMOVEYR, and EPIMPRMYYUNAVAIL, each with a brief description and availability status across the samples. At the bottom of the page, there's 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."

DISCONTINUATION OF FAMILY PLANNING VARIABLES (TOP)		LONGITUDINAL SAMPLES							
Add to cart	Variable	Variable Label	Type	BURKF 2020 - 2021	CONDR 2019a - 2020a	CONDR 2019b - 2020b	KENYA 2019 - 2020	NIGERA 2019a - 2020a	NIGERA 2019b - 2020b
	FPSTOPMO	Month stopped using most recent method	P	X	X	X	.	X	X
	FPSTOPYR	Year stopped using most recent method	P	X	X	X	.	X	X
	FPSTOPUSECMC	Date stopped using recent method of FP in century month	P	X	X	X	.	X	X
	FPIMPREMOVEYR	Tried to remove implant in past 12 months	P	X	/	/	X	/	/
	EPIMPRMTRYLOC	Location of implant removal attempt	P	X	/	/	/	-	-
	EPIMPRMYYCOST	Why implant not removed: Service cost	P	X	/	/	X	/	/
	EPIMPRMYYCOUND	Why implant not removed: Provider counseled against	P	X	/	/	X	/	/
	EPIMPRMYYCLOSED	Why implant not removed: Facility closed	P	X	/	/	X	/	/
	EPIMPRMYYOTH	Why implant not removed: Other	P	X	/	/	X	/	/
	EPIMPRMYYREFUSE	Why implant not removed: Provider refused	P	X	/	/	X	/	/
	EPIMPRMYYELSEWH	Why implant not removed: Referred elsewhere	P	X	/	/	X	/	/
	EPIMPRMYYRETURN	Why implant not removed: Told to return another day	P	X	/	/	X	/	/
	EPIMPRMYYTRAVEL	Why implant not removed: Travel cost	P	X	/	/	X	/	/
	EPIMPRMYYUNAVAIL	Why implant not removed: Qualified provider not available	P	X	/	/	X	/	/
	EPIMPRMYYUNSUCC	Why implant not removed: Failed attempt by provider	P	X	/	/	X	/	/

## 2.2.1 Codes

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.

“Case-count view” is not available for longitudinal samples. For cross-sectional samples, this option shows the frequency of each response.

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.ORG. A 'Guest' button is also present. 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'. Below it, there are buttons for 'ADD TO CART' and 'CHANGE SAMPLES'. A navigation bar below the title has tabs for CODES (which is selected), DESCRIPTION, COMPARABILITY, UNIVERSE, AVAILABILITY, and QUESTIONNAIRE TEXT. The 'CODES' tab is highlighted with a purple background. The main content area is titled 'Codes and Frequencies'. It includes a legend for 'Category availability view' with two options: 'Female Respondents' (selected) and 'Case-count view (Unavailable for longitudinal samples)'. Below this is a table titled 'LONGITUDINAL SAMPLES' with columns for BURKF, CONDR, CONDR, KENYA, NIGERA, and NIGERA. The rows represent different codes: 00 (No), 01 (Yes), 95 (Not interviewed (female questionnaire)), 96 (Not interviewed (household questionnaire)), 97 (Don't know), 98 (No response), and 99 (NIU (not in universe) or missing). The table uses X, /, and - symbols to indicate availability across the samples. The row for code 96 is highlighted with a red oval. At the bottom of the page, there is a footer with links to SUPPORTED BY: THE BILL & MELINDA GATES FOUNDATION, PMA, STAT/TRANSFER, and UNIVERSITY OF MINNESOTA. There is also a copyright notice: COPYRIGHT © MINNESOTA POPULATION CENTER, UNIVERSITY OF MINNESOTA.

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).

The screenshot shows the IPUMS PMA website interface. At the top, the IPUMS PMA logo is visible along with navigation links for LOGIN, REGISTER, GLOBAL HEALTH, and IPUMS.ORG. A 'DATA CART' section indicates 0 VARIABLES and 6 SAMPLES, with a 'VIEW CART' button. The main title is 'PREGNANT' under the heading 'Pregnancy status'. Below it, 'Group: Core demographics' is listed. A horizontal menu bar includes 'CODES' (which is selected), 'DESCRIPTION', 'COMPARABILITY', 'UNIVERSE', 'AVAILABILITY', and 'QUESTIONNAIRE TEXT'. The 'CODES' section contains a sub-section titled 'Codes and Frequencies' with a note: 'An 'X' indicates the category is available for that sample'. It lists several categories with radio buttons: 'Category availability view' (selected), '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)' (selected and highlighted with a red circle). Below this is a table titled 'LONGITUDINAL SAMPLES' showing availability across various countries and sample codes. The table includes columns for BURKF, CONDR, CONDR, KENYA, NIGERA, and NIGERA. Rows include codes 00 (No), 01 (Yes), 95 (Not interviewed (female questionnaire)), 96 (Not interviewed (household questionnaire)), 97 (Don't know), 98 (No response), and 99 (NIU (not in universe) or missing). The rows for 95 and 96 are also circled in red.

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

The screenshot shows the IPUMS PMA website interface. At the top, there is a navigation bar with links for LOG IN | REGISTER | GLOBAL HEALTH | IPUMS.ORG. On the right side of the header, there is a "DATA CART" section showing 0 VARIABLES and 6 SAMPLES, with a "VIEW CART" button. The main content area is titled "COVIDCONCERN". Below the title, there are buttons for "ADD TO CART" and "CHANGE SAMPLES". A sub-header says "Concerned about getting infected" and "Group: Perceptions around COVID". There is a legend at the top of the data table with tabs for CODES, DESCRIPTION, COMPARABILITY, UNIVERSE, AVAILABILITY, and QUESTIONNAIRE TEXT. The "CODES" tab is selected. The data table is titled "Codes and Frequencies" and includes a note: "An 'X' indicates the category is available for that sample". The table has a header row for "LONGITUDINAL SAMPLES" with columns for BURKF, CONDR, CONDR, KENYA, NIGERA, and NIGERA. The data rows show the following information:

Code	Label	BURKF 20 - 21	CONDR 19a - 20a	CONDR 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)	.	.	.	.	.	.

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.

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.

## 2.2.2 Variable Description

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](https://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 | IPUMS.ORG and a "Guest" account. A "DATA CART" sidebar shows 0 VARIABLES and 6 SAMPLES with a "VIEW CART" button. The main content area is titled "PREGNANT" and describes it as a "Pregnancy status". It includes buttons for "ADD TO CART" and "CHANGE SAMPLES". Below these are tabs for "CODES", "DESCRIPTION" (which is selected), "COMPARABILITY", "UNIVERSE", "AVAILABILITY", and "QUESTIONNAIRE TEXT". The "DESCRIPTION" tab contains 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.

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

## 2.2.3 Comparability Notes

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: desc: PREGNANT". The top navigation bar includes links for LOGIN | REGISTER | GLOBAL HEALTH | IPUMS.ORG and a "Guest" account indicator. A "DATA CART" section on the right shows "YOUR DATA EXTRACT" with "0 VARIABLES" and "6 SAMPLES", with a "VIEW CART" button. The main content area is titled "PREGNANT" and shows "Pregnancy status" under "Group: Core demographics". Below this, there are tabs for CODES, DESCRIPTION, COMPARABILITY, UNIVERSE, AVAILABILITY, and QUESTIONNAIRE TEXT. The "COMPARABILITY" tab is active, displaying the heading "Comparability" and the text: "There are minor universe differences among samples; see the Universe tab for more details." It also contains a section titled "Comparability with IPUMS-DHS" which states: "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 of the page, there is a footer note: "SUPPORTED BY: THE BILL & MELINDA GATES FOUNDATION, PMA, STAT/TRANSFER, AND UNIVERSITY OF MINNESOTA." and a copyright notice: "COPYRIGHT © MINNESOTA POPULATION CENTER, UNIVERSITY OF MINNESOTA."

## 2.2.4 Sample Universe

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" with "PERFORMANCE MONITORING FOR ACTION" below it. The top navigation bar includes links for LOGIN, REGISTER, GLOBAL HEALTH, and IPUMS. A "DATA CART" section on the right shows 0 VARIABLES and 6 SAMPLES with a "VIEW CART" button. The main content area is titled "PREGNANT" with "Pregnancy status" and "Group: Core demographics". Below this are tabs for CODES, DESCRIPTION, COMPARABILITY, UNIVERSE (which is selected), AVAILABILITY, and QUESTIONNAIRE TEXT. The "UNIVERSE" tab contains a section titled "Universe" which lists survey descriptions for various countries and years, specifying age (15-49) and non-menopausal status, except for DRC samples where all women aged 15-49 received the question. At the bottom of the page, there is a footer note about support from The Bill & Melinda Gates Foundation, PMA, STAT/TRANSFER, and the University of Minnesota, and a copyright notice for the Minnesota Population Center, University of Minnesota.

## 2.2.5 Availability Across Samples

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

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.ORG. On the right side of the header, there is a "DATA CART" section indicating 0 VARIABLES and 6 SAMPLES, with a "VIEW CART" button. Below the header, the IPUMS PMA logo is displayed, along with the text "PERFORMANCE MONITORING FOR ACTION" and links for HOME, SELECT DATA, MY DATA, and SUPPORT. The main content area is titled "PREGNANT". Underneath it, there are buttons for "ADD TO CART" and "CHANGE SAMPLES". A horizontal navigation bar below these buttons includes tabs for CODES, DESCRIPTION, COMPARABILITY, UNIVERSE, AVAILABILITY (which is currently selected), and QUESTIONNAIRE TEXT. The "AVAILABILITY" tab displays a list of countries and their survey years where the variable is available:

Country	Years
Burkina Faso	2014-2018, 2020-2021
Congo (Democratic Republic)	2013-2020
Côte 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, there is a footer note: "SUPPORTED BY: THE BILL & MELINDA GATES FOUNDATION, PMA, STAT/TRANSFER, AND UNIVERSITY OF MINNESOTA." and a copyright notice: "COPYRIGHT © MINNESOTA POPULATION CENTER, UNIVERSITY OF MINNESOTA."

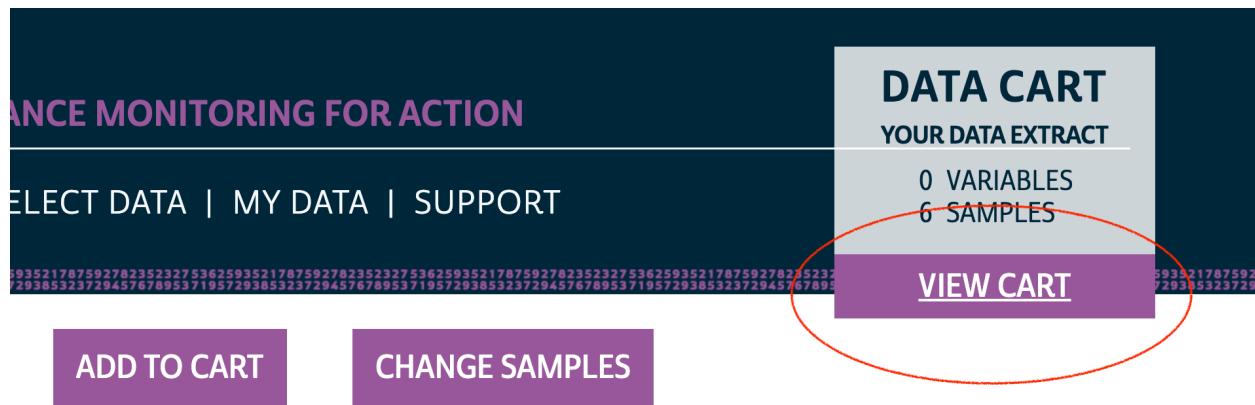
## 2.2.6 Questionnaire Text

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](https://pma.ipums.org/pma-action/variables/PREGNANT#questionnaire_text_section). The page title is "IPUMS PMA" and the sub-section is "PERFORMANCE MONITORING FOR ACTION". The top navigation bar includes links for LOG IN | REGISTER | GLOBAL HEALTH | IPUMS.ORG and a "Guest" button. A "DATA CART" section on the right shows "YOUR DATA EXTRACT", "0 VARIABLES", and "6 SAMPLES" with a "VIEW CART" button. The main content area is titled "PREGNANT" and shows a "Questionnaire Text" tab selected among other tabs like CODES, DESCRIPTION, COMPARABILITY, UNIVERSE, and AVAILABILITY. Below the tabs, there is a table of questionnaire items for Burkina Faso 2020, Congo (Democratic Republic) 2019a, and Nigeria 2019b. Each item includes a "view entire document: text" link. The "Burkina Faso 2020" section contains a question about pregnancy status with four response options: Yes, No, Unsure, and No response. The "Congo (Democratic Republic) 2019a" section also contains a similar question with the same response options. At the bottom of the page, there is a footer with a copyright notice: "© 2023 IPUMS. All rights reserved. IPUMS is a registered trademark of the University of Minnesota." and a link to "IPUMS.ORG".

## 2.2.7 Checkout

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



## 2.3 DATA FOR R USERS

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 area is titled "DATA CART" and contains three buttons: "ADD MORE VARIABLES", "CREATE DATA EXTRACT" (which is circled in red), and "ADD MORE SAMPLES". A "Clear Data Cart" link is also present. The central part of the screen displays a table of variables selected for the data extract. The columns include "In cart", "Variable", "Variable Label", "Type", and country codes for BURKF, CONDR, KENYA, NIGERA, and NIGERA. The "CREATE DATA EXTRACT" button is highlighted with a red oval.

In cart	Variable	Variable Label	Type	BURKF 2020 - 2021	CONDR 2019a - 2020a	CONDR 2019b - 2020b	KENYA 2019 - 2020	NIGERA 2019a - 2020a	NIGERA 2019b - 2020b
<input checked="" type="checkbox"/>	SAMPLE	PMA sample number [preselected]	P	X	X	X	X	X	X
<input checked="" type="checkbox"/>	COUNTRY	PMA country [preselected]	P	X	X	X	X	X	X
<input checked="" type="checkbox"/>	YEAR	Year [preselected]	P	X	X	X	X	X	X
<input checked="" type="checkbox"/>	ELIGIBLE	Eligible female respondent [preselected]	P	X	X	X	X	X	X
<input checked="" type="checkbox"/>	EALD	Enumeration area [preselected]	P	X	X	X	X	X	X
<input checked="" type="checkbox"/>	CONSENTFO	Female respondent provided consent to be interviewed [preselected]	P	X	X	X	X	X	X
<input checked="" type="checkbox"/>	FOINSTID	Unique ID for female questionnaire [preselected]	P	X	X	X	X	X	X
<input checked="" type="checkbox"/>	CONSENTHQ	Household respondent provided consent to be interviewed [preselected]	P	X	X	X	X	X	X
<input checked="" type="checkbox"/>	FOWEIGHT	Female weight [preselected]	P	X	X	X	X	X	X
<input checked="" type="checkbox"/>	STRATA	Strata [preselected]	P	X	.	.	X	X	X
<input checked="" type="checkbox"/>	PANELWOMAN	Panel woman interviewed in Phase 1	P	/	/	/	/	/	/

### 2.3.1 Select a Fixed-width File

Before you submit an extract request, you'll have the opportunity to choose a "Data Format". **R users should select a Fixed-width text file (.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.)

The screenshot shows a web browser window for the IPUMS PMA website. The title bar reads "IPUMS PMA: extract summary". The URL is "pma.ipums.org/pma-action/extract\_requests/summary?". The top right corner shows "Guest" and "LOG IN | REGISTER | GLOBAL HEALTH | IPUMS.ORG". The main content area has a dark header with the IPUMS PMA logo. Below it, the heading "EXTRACT REQUEST ([HELP](#))" is displayed. A series of input fields are shown, each with a "Change" link. The "DATA FORMAT" field is highlighted with a red circle around its "Change" link. The other fields include "SAMPLES: 6", "VARIABLES: 11", "STRUCTURE: Rectangular (longitudinal - long)", "SAMPLE MEMBERS: Female Respondents", and "ESTIMATED SIZE: 11.2 MB". Below these fields is a text area labeled "Describe your extract" with a placeholder text "Describe your extract". At the bottom is a purple "SUBMIT EXTRACT" button. A small copyright notice at the very bottom of the page reads "COPYRIGHT © MINNESOTA POPULATION CENTER, UNIVERSITY OF MINNESOTA."

Once the Fixed-width option is selected, you may add a description and then proceed to the download page.

### 2.3.2 Download

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\_0003.dat.gz.
- Right click on “DDI” and click “Save link as”. You’ll receive a corresponding XML file like pma\_0003.xml.

The screenshot shows a table of extracts. The first row is highlighted with a red box around the 'Download DAT' button. An arrow points to it with the text "1) Click here to download the data.". The second row is highlighted with a red box around the 'DDI' link. An arrow points to it with the text "2) Right click here to select the DDI." A third row is highlighted with a red box around the 'Save link as...' option in a context menu. An arrow points to it with the text "3) Then select 'Save link as...' (or 'Download Linked File') to save the DDI." The table columns include Extract Number, Date, Formatted Data, Fixed-width Text Files (Data, SPSS, SAS, STATA), Codebook, Revise Extract, Resubmit Extract, Description (click to edit), and Hide selections>Show all.

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 sub-folder called “data” within our own RStudio project folder.

Open RStudio (or R) and load the packages [ipumsr](#) and [tidyverse](#). If you are not using an RStudio project, you will need to change your working directory to match the location of your downloaded files.

```
library(ipumsr)
library(tidyverse)
setwd("~/Downloads") # ONLY if not using an RStudio project (change as needed)
```

We'll now demonstrate loading both a long and a wide extract, and we'll take a brief look at the structure of each.

## 2.4 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`.

To load an IPUMS PMA extract into R, you'll need to reference *both* the DDI file *and* the fixed-width data file in the function `read_ipums_micro` from `ipumsr`.

```
long <- read_ipums_micro(  
  ddi = "data/pma_00003.xml",  
  data = "data/pma_00003.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 011W5S0HN91I4H4I3T9JCMBHB 1 [Baseline]    29     NA  
2 011W5S0HN91I4H4I3T9JCMBHB 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
```

Chapter 1 describes **Inclusion Criteria for Analysis** and shows how to identify women in a **Wide** extract who did not complete the Female Questionnaire in both phases. In **Long** format, we use **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 *de facto* population is identified where **RESIDENT** takes the value 11 or 22 in both rows.

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

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

# A tibble: 12 × 5				
	COUNTRY	GEOCD	GEONG	PHASE
	<int+lbl>	<int+lbl>	<int+lbl>	<int>
1	1 [Burkina Faso]	NA	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

## 2.5 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_00004.xml",  
  data = "data/pma_00004.dat.gz"  
)
```

In a **Wide** extract, all of the responses from one woman appear in the *same row*. The IPUMS PMA 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
```

The **Inclusion Criteria for Analysis** section in Chapter 1 shows how to identify members of the *de facto* population who completed the Female Questionnaire in both phases for a **Wide** extract. Those steps are repeated here:

```
wide <- wide %>%
  filter(
    RESIDENT_1 %in% c(11, 22) & RESIDENT_2 %in% c(11, 22),
    RESULTFQ_2 == 1
  )
```

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

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

```
# A tibble: 6 × 4
#>   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
```

## 2.6 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 used in Chapter 6 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:0058ccb8-9892-4a60-b9ed-fb556a21f862 29     0 [No]    30      0 [No]
12 uuid:00682e93-0483-42b4-8f8d-2e0c36a26d37 16     0 [No]    17      0 [No]
# ... with 17,713 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")
  )
```

We will revisit `pivot_longer` when analyzing PMA Contraceptive Calendar data in Chapter 6.

```
# 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]
# ... with 35,438 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 IPUMS PMA extract system makes it easy to select the samples, sample members, and variables that matter to your particular research question. Choices for **Long** and **Wide** data formats save an additional data cleaning step, allowing you to jump into longitudinal analysis as quickly as possible.

## 3 PANEL MEMBERSHIP

In Chapter 1, 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.

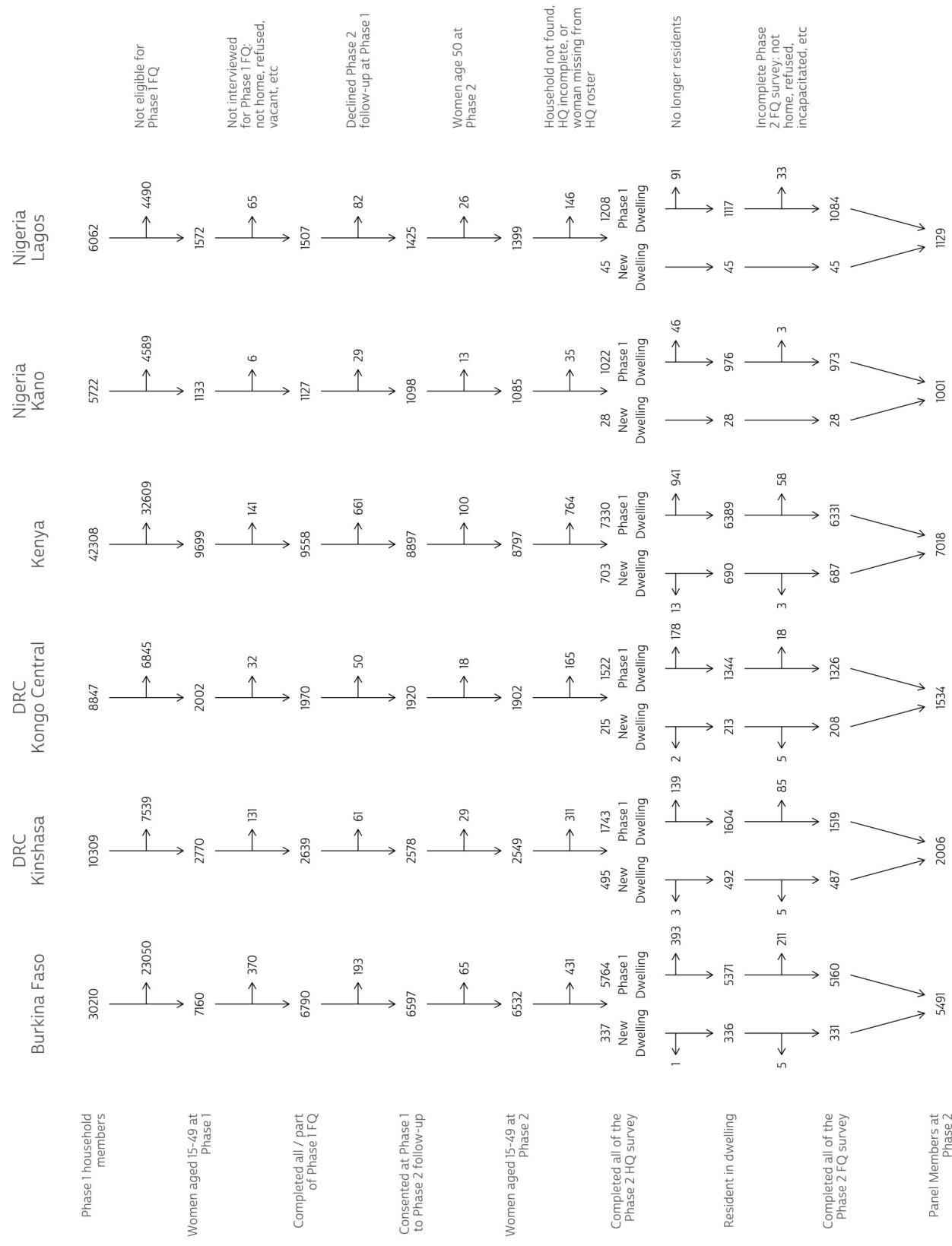
In Chapter 3, we'll cover these issues in detail. To illustrate, we'll be using a **Wide** format data extract from IPUMS PMA that includes **All cases** from both currently available phases. In other words, we'll include every member of the household roster collected in the Household Questionnaire at 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**. This type of 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, which you can find via the links below:

R code showing how to build a combined CONSORT diagram with **ggplot2** is available on the [IPUMS PMA data analysis blog](#).

- Burkina Faso
- DRC - Kinshasa
- DRC - Kongo Central
- Kenya
- Nigeria - Lagos
- Nigeria - Kano

We've constructed a single diagram showing all six samples available from IPUMS PMA, and we'll demonstrate how to identify cases for each level in turn:



## 3.1 CHAPTER SETUP

This chapter features a **Wide** longitudinal extract with all 6 of the available samples, including **All Cases** (Respondents and Non-respondents to Household and Female Questionnaires). As mentioned in Chapter 2, both phases are included with each sample when you request a longitudinal extract.

The screenshot shows the 'SELECT SAMPLES' page of the IPUMS PMA website. At the top, there is a navigation bar with links for LOG IN, REGISTER, GLOBAL HEALTH, and IPUMS.ORG. Below the header, the IPUMS PMA logo is displayed, along with links for HOME, SELECT DATA, MY DATA, and SUPPORT. The main section is titled 'SELECT SAMPLES'. It includes a note about variable documentation filtering and a message about selecting datasets. A radio button group allows users to choose between Cross-sectional, Longitudinal, Long, and Wide datasets. A 'SUBMIT SAMPLE SELECTIONS' button is located to the right of the dataset selection. Below this, a section titled 'FAMILY PLANNING - PERSON' contains a 'Documentation' table with checkboxes for various sample filters. The table includes columns for country and time period, with some entries including small informational icons. At the bottom of the page, there is a 'Sample Members' section with a radio button group for selecting female respondents or all cases. A final 'SUBMIT SAMPLE SELECTIONS' button is located at the bottom of this section. The footer of the page contains copyright information and support links.

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
<input checked="" type="checkbox"/> All Samples (wide)
<input checked="" type="checkbox"/> Burkina Faso <input checked="" type="checkbox"/> 2020 - 2021
<input checked="" type="checkbox"/> Congo (Democratic Republic) <input checked="" type="checkbox"/> 2019b - 2020b ⓘ <input checked="" type="checkbox"/> 2019a - 2020a ⓘ
<input checked="" type="checkbox"/> Kenya <input checked="" type="checkbox"/> 2019 - 2020
<input checked="" type="checkbox"/> Nigeria <input checked="" type="checkbox"/> 2019b - 2020b ⓘ <input checked="" type="checkbox"/> 2019a - 2020a ⓘ

**Sample Members**

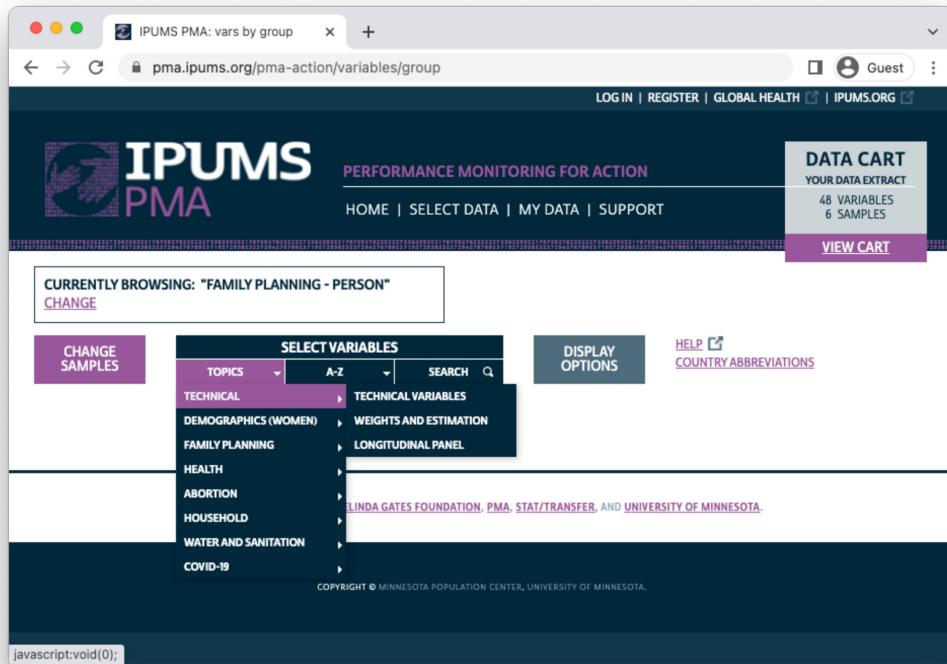
Female Respondents  
 Female Respondents and Household Members  
 Female Respondents and Female Non-respondents  
 All Cases (Respondents and Non-respondents to Household and Female Questionnaires)

**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:



The screenshot shows the IPUMS PMA website interface for selecting variables. At the top, there's a navigation bar with links for LOGIN, REGISTER, GLOBAL HEALTH, and IPUMS.ORG. On the left, there's a sidebar with a 'CHANGE SAMPLES' button and a list of topics: DEMOGRAPHICS (WOMEN), FAMILY PLANNING, HEALTH, ABORTION, HOUSEHOLD, WATER AND SANITATION, and COVID-19. The 'TOPICS' dropdown is set to 'TECHNICAL'. A 'SELECT VARIABLES' section shows 'TECHNICAL VARIABLES' as the current category, with 'WEIGHTS AND ESTIMATION' and 'LONGITUDINAL PANEL' listed below it. To the right, there are 'DISPLAY OPTIONS', 'HELP', and 'COUNTRY ABBREVIATIONS' links. A 'DATA CART' box in the top right corner indicates 48 VARIABLES and 6 SAMPLES. The bottom of the page has a copyright notice for the Minnesota Population Center, University of Minnesota, and the Linda Gates Foundation.

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 described in Chapter 1.

```
library(ipumsr)
library(tidyverse)

dat <- read_ipums_micro(
  ddi = "data/pma_00005.xml",
  data = "data/pma_00005.dat.gz"
)
```

We mentioned in Chapter 1 that variables in a **Wide** extract include a numeric suffix corresponding with a data collection phase. For example, you'll find two versions of **SAMPLE**: **SAMPLE\_1** represents the sample codes for Phase 1:

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

```
# A tibble: 5 × 2
  SAMPLE_1                               n
  <int+lbl>                            <int>
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
```

Whereas **SAMPLE\_2** represents the sample codes for Phase 2:

```
dat %>% count(SAMPLE_2)
```

```
# A tibble: 5 × 2
  SAMPLE_2                               n
  <int+lbl>                            <int>
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
```

We also mentioned in Chapter 1 that 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. Let's call this variable POP (for "population of interest").

- pop - Population of interest

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

```
# 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
```

## 3.2 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 Questionnaire<sup>22</sup>** 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 Questionnaire<sup>23</sup>** 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.

---

<sup>22</sup>Questionnaires administered in each country may vary from this Core Household Questionnaire - [click here](#) for details.

<sup>23</sup>Questionnaires administered in each country may vary from this Core Female Questionnaire - [click here](#) for details.

### 3.2.1 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 one row per household
  ungroup() %>%
  count(RESULTHQ_1 %in% c(1, 5)) %>%
  mutate(prop = prop.table(n))
```

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

```
# 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
```

It is also 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.

Total number of Phase 1 household members, per sample

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

```
# 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
```

### 3.2.2 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) %>% # drop if ineligible
  count(resultfq_1 %in% c(1, 5)) %>%
  mutate(prop = prop.table(n))
```

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

```
# 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

```
dat %>%
  filter(resultfq_1 %in% c(1, 5)) %>%
  count(POP)
```

Total number of  
eligible women, per  
sample, who  
completed all or  
part of the Phase 1  
Female  
Questionnaire

```
# 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
```

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](#).<sup>24</sup>

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.

Total number of women, per sample, who consented at Phase 1 to the Phase 2 follow-up

```
dat %>%
  filter(SURVEYWILLING_1 == 1) %>%
  count(POP)
```

```
# A tibble: 6 × 2
  POP                  n
  <chr>                <int>
1 Burkina Faso        6597
2 DRC - Kinshasa      2578
3 DRC - Kongo Central 1920
4 Kenya                 8897
5 Nigeria - Kano       1098
6 Nigeria - Lagos      1425
```

Make sure to include “No response or missing” cases in the denominator 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)) %>%
  count(SURVEYWILLING_1) %>%
  mutate(prop = prop.table(n))
```

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

```
# 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
```

<sup>24</sup>Women 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.

### **3.3 PHASE 2**

Both questionnaires were administered again in Phase 2, approximately one year after Phase 1. Resident enumerators visited the same dwellings where Phase 1 interviews occurred; if the woman's household had moved elsewhere within the study area,<sup>25</sup> 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**.

---

<sup>25</sup>The “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.

### 3.3.1 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)
```

```
# A tibble: 10 × 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)
```

```
# A tibble: 6 × 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		n
HHMEMSTAT_2		<int>
<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
```

### 3.3.2 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)
```

	# A tibble: 11 × 2	n
	RESULTFQ_2	<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))
```

	# A tibble: 2 × 3	n	prop
	PANELWOMAN_2	<int>	<dbl>
1	0 [No]	6576	0.266
2	1 [Yes]	18180	0.734

Across samples,  
73.4% of women  
completing the  
Phase 2 Female  
Questionnaire also  
did so at Phase 1.

26.6% are  
newcomers at  
Phase 2.

**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.

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
```

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

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.

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

Total number and proportion of potential panel members, per Phase 1 sample, that ultimately completed a Phase 2 Female Questionnaire

### 3.4 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](http://pmadata.org).

## 4 FAMILY PLANNING INDICATORS

In Chapter 4, we'll demonstrate how to calculate key family planning indicators appearing in the **PMA Longitudinal Brief** for each of the longitudinal samples currently available from IPUMS PMA. The brief for each sample is linked below.

- Burkina Faso
- DRC - Kinshasa
- DRC - Kongo Central
- Kenya
- Nigeria - Kano
- Nigeria - Lagos

Chapter 5 includes code you can use to reproduce the **alluvial plots** seen in these briefs.

Indicators calculated in this chapter 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

As we demonstrate how to calculate these indicators, we will also compare population estimates between subgroups within each sample. This chapter demonstrates how to conduct a **Rao-Scott chi-square test** for significant differences between subgroups, but we will primarily rely on an informal comparison of confidence intervals plotted on **grouped bar charts**. This approach facilitates visual comparisons for several indicators repeated for multiple samples in the same IPUMS PMA data extract, but we'll see that it produces somewhat conservative estimation of statistical difference compared to the chi-square test. We include both the formal and the informal-visual comparison, as each is useful in the appropriate context.

This chapter demonstrates how to build a single function capable of producing several similar bar charts for multiple indicators. To do so, we'll use the **ggplot2** package loaded with the **tidyverse** toolkit for R. If you installed **tidyverse** in Chapter 1, no additional installation is necessary to use **ggplot2**. If not, we recommend installing the **tidyverse** now:

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



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## 4.1 CHAPTER SETUP

Chapter 4 features a **Wide** longitudinal extract with all six of the available samples. Unlike Chapter 3, the data extract used in this chapter includes only **Female Respondents**.

The screenshot shows the 'SELECT SAMPLES' page of the IPUMS PMA website. At the top, there is a navigation bar with links for LOG IN, REGISTER, GLOBAL HEALTH, and IPUMS.ORG. Below the navigation is the IPUMS PMA logo and a 'PERFORMANCE MONITORING FOR ACTION' banner. The main section 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). 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 sample selection buttons. The first set, under 'FAMILY PLANNING - PERSON', includes 'Cross-sectional' (radio button), 'Longitudinal' (radio button selected), 'Long' (radio button with info icon), and 'Wide' (radio button selected). A 'SUBMIT SAMPLE SELECTIONS' button is to the right. The second set, under 'Sample Members', includes 'Female Respondents' (radio button selected), '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 at the bottom. At the very bottom, a footer notes: 'SUPPORTED BY: THE BILL & MELINDA GATES FOUNDATION, PMA, STAT/TRANSFER, AND UNIVERSITY OF MINNESOTA.'

Following the steps outlined in Chapter 2, you'll need to request a .dat (fixed-width) data extract with the following variables (preselected variables are included automatically).

- **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)

Download and save your extract in the data folder of your R working directory, and then load the following packages together with your extract.

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

dat <- read_ipums_micro(
  ddi = "data/pma_00006.xml",
  data = "data/pma_00006.dat.gz"
)
```

Chapter 1 describes **Inclusion Criteria for Analysis**: to summarise, we'll be focusing on members of the *de facto* population who participated in both phases of the panel study (excluding a small number of women marked “NIU (not in universe)” for a key measure of current contraceptive use recorded in **CP**).

```
dat <- dat %>%
  filter(
    RESIDENT_1 %in% c(11, 22) & RESIDENT_2 %in% c(11, 22),
    RESULTFQ_2 == 1,
    CP_1 < 90 & CP_2 < 90
  )
```

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 again 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()
  ))
```

We'll be using survey design information to derive population estimates throughout this chapter, so we'll also need to use **GEOCD** to update **STRATA\_1** for DRC samples. As in Chapter 1, we create **STRATARC** using unique numeric codes from **STRATA\_1**, except that we also include unique identifiers for each sampled region in **GEOCD**.

- **STRATARC** - Numeric codes for PMA sample strata (recoded for DRC samples)

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

Finally, Chapter 1 demonstrates how to use survey design information to estimate the proportion of women in each population **POP** who were using a contraceptive method both at Phase 1 and at Phase 2. Let's revisit that example again, expect that we'll now estimate the proportion of users and non-users alike:

```
cp_tbl <- dat %>%
  group_by(POP) %>%
  summarise(
    cur_data() %>%
    as_survey_design(weight = PANELWEIGHT, id = EAID_1, strata = STRATARC) %>%
    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
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

This table `cp_tbl` shows a population estimate for each row reported in the column `_coef`, while the columns `_low` and `_upp` report the limits of a 95% confidence interval. 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.

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

*Formal testing may also reveal significant differences between pairs of outcomes where these intervals overlap only slightly.* This informal comparison is well suited for data visualization, but it should not replace formal testing. Fortunately, you can adapt this code to replace (or complement) the output from `survey_mean` with a formal test.

## 4.2 SIGNIFICANCE TEST

Continuing with the previous example, we will now 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.<sup>26</sup> 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`. Elements of the chi-square test can be extracted `rowwise` like so:

```
dat %>%
  group_by(POP) %>%
  summarise(
    cur_data() %>%
      as_survey_design(weight = PANELWEIGHT, id = EAID_1, strata = STRATARC) %>%
      summarise(rao = svychisq(~CP_1 + CP_2, design = .) %>% list)
  ) %>%
  rowwise() %>%
  mutate(`F` = rao$statistic, p.value = rao$p.value, sig95 = p.value < 0.05)
```

```
# A tibble: 6 × 5
# Rowwise:
  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
```

For each POP, the `p.value` associated with our test falls below 0.05 (as indicated in `sig95`). This suggests that we may be at least 95% sure that the mean Phase 2 contraceptive use status for Phase 1 contraceptive users is not identical to the mean for non-users.

<sup>26</sup>The Rao-Scott second-order correction to Pearson's chi-square test is used to incorporate survey design information from `as_survey_design`. Wald-type chi-square tests are also available: see `svychisq` for details.

## 4.3 DATA VISUALIZATION

We'll use simple **grouped bar charts** to show population estimates for each proportion calculated throughout the remainder of this chapter. We'll 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),
      ~.x %>% as_factor() %>% fct_relevel("No", "Yes")
    )
  )
```

Next, we'll use `ggplot2` to build the plot. 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`.<sup>27</sup>

```
theme_pma <- theme_minimal() %+replace%
  theme(
    text = element_text(family = "cabrito", size = 42),
    plot.title = element_text(size = 72, 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 = 48, angle = 0),
    axis.title.y = element_text(angle = 0, margin = margin(r = 10), lineheight = 0.3),
    panel.spacing = unit(1, "lines")
  )
```

Because we'll be constructing the same type of plot for each indicator, we'll wrap this theme together with several `ggplot2` functions we'll want to reuse every time we make a plot. This prevents copy/paste errors and eliminates redundant code. We'll call our custom function `pma_bars`.

---

<sup>27</sup>This manual uses the proprietary font `cabrito sans`, which is implemented in figures via the `showtext` package for R. You can purchase a license to use `cabrito sans`, or substitute with a font of your choice.

We'll design `pma_bars` to include all of the following `ggplot2` functions:

- `theme_pma` created above
- `labs` for plot labels (passed from function arguments)
- `scale_x_continuous` formatting for continuous x-axis labels
- `scale_y_discrete` formatting for discrete y-axis labels
- `geom_bar` for grouped bars
- `geom_errorbar` for error bars
- `scales::label_percent` to format proportions as percentages<sup>28</sup>

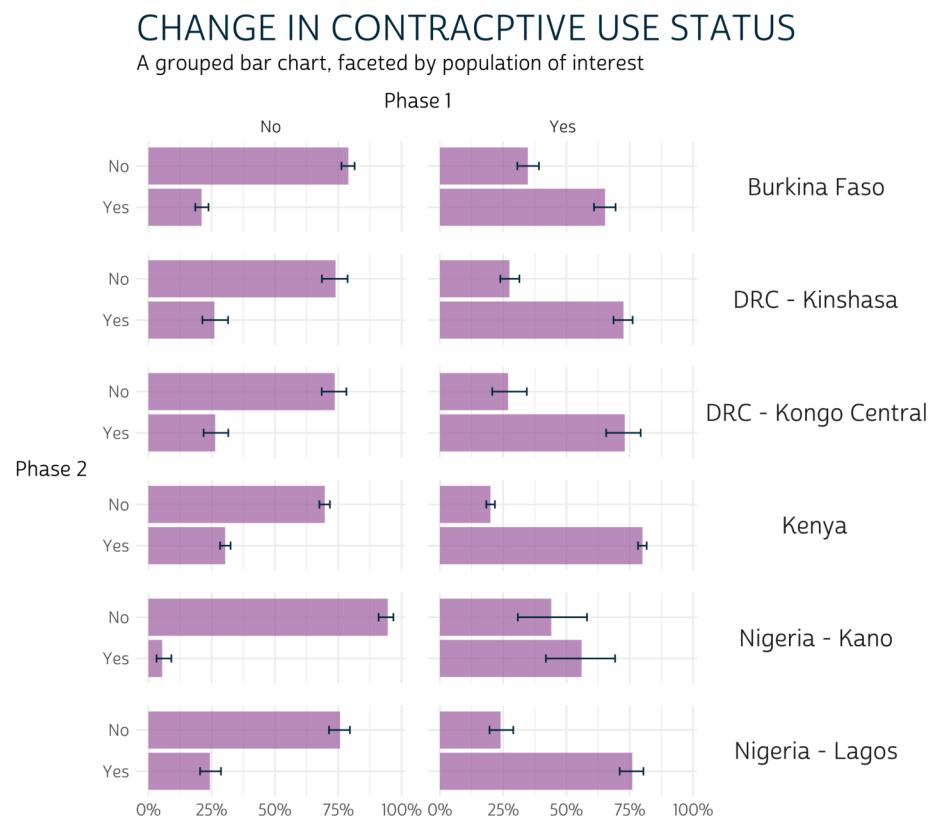
```
pma_bars <- function(  
  title = NULL,      # an optional title  
  subtitle = NULL,    # an optional subtitle  
  xaxis = NULL,      # an optional label for the x-axis (displayed above)  
  yaxis = NULL       # an optional label for the y-axis (displayed left)  
{  
  components <- list(  
    theme_pma,  
    labs(  
      title = toupper(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"  
    )  
  )  
}
```

---

<sup>28</sup>`scales` is installed, but not loaded, with the `tidyverse`.

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"
  )
```



## 4.4 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(
    cur_data() %>%
      as_survey_design(weight = PANELWEIGHT, id = EAID_1, strata = STRATARC) %>%
      group_by(FPSTATUS_1, FPSTATUS_2) %>%
      summarise(survey_mean(vartype = "ci", prop = TRUE, prop_method = "logit"))
  )
```

This new version of cp\_tbl includes the labels we assigned to FPSTATUS\_1 and FPSTATUS\_2. The first dozen rows are shown below.

```
cp_tbl
```

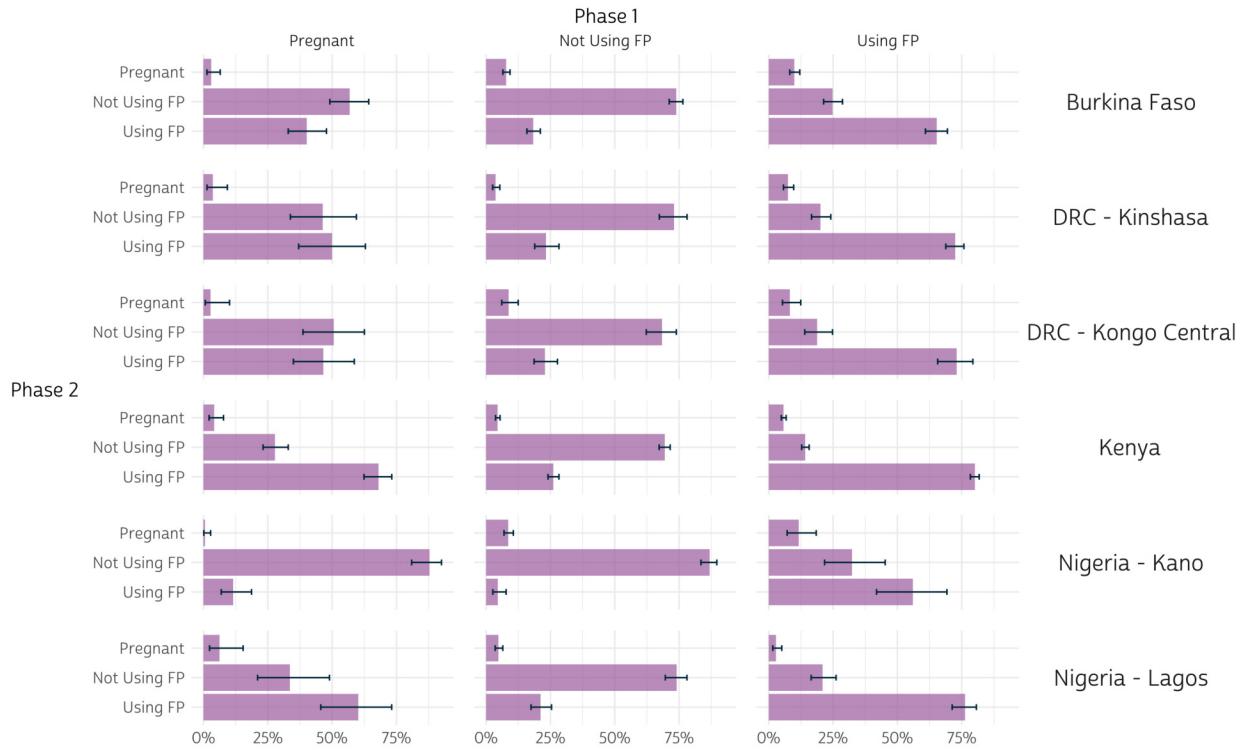
```
# A tibble: 54 × 6
# Groups:   POP [6]
  POP          FPSTATUS_1    FPSTATUS_2     coef `_low` `_upp`
  <chr>        <fct>       <fct>        <dbl>  <dbl>  <dbl>
  1 Burkina Faso Pregnant    Pregnant    0.0302 0.0137 0.0652
  2 Burkina Faso Pregnant    Not Using FP 0.568  0.491  0.642 
  3 Burkina 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
 11 DRC – Kinshasa Pregnant Not Using FP 0.464  0.338  0.594 
 12 DRC – Kinshasa Pregnant Using FP     0.500  0.370  0.629 
# ... with 42 more rows
```

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",
    yaxis = "Phase 2"
  )
```

## CHANGE IN CONTRACEPTIVE USE OR NON-USE

Percent women age 15-49 who changed contraceptive use 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 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 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:

- intrauterine devices (IUDs)
- implants
- male sterilization
- female sterilization

Short-acting methods include:

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

Traditional methods include:

- rhythm
- withdrawal
- other traditional

Women who were using no method are “NIU (not in universe)”.

```
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_FPCURREFFMETHRC` - Contraceptive method type (4 categories)

```
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(
    cur_data() %>%
      as_survey_design(weight = PANELWEIGHT, id = EAID_1, strata = STRATARC) %>%
      group_by(CAT_FPCURREFFMETHRC_1, CAT_FPCURREFFMETHRC_2) %>%
      summarise(survey_mean(vartype = "ci", prop = TRUE, prop_method = "logit"))
  )

```

`meth_tbl`

```
# A tibble: 95 × 6
# Groups:   POP [6]
  POP          CAT_FPCURREFFMETHRC_1 CAT_FPCURREFFMETHRC_2     coef  `_low` `upp`
  <chr>        <fct>              <fct>                  <dbl>  <dbl>  <dbl>
1 Burkina Faso long-acting       long-acting           0.680   0.629   0.727
2 Burkina Faso long-acting       short-acting         0.0658  0.0448  0.0955
3 Burkina Faso long-acting       traditional          0.00611 0.00325 0.0115
4 Burkina Faso long-acting       none                0.248   0.196   0.308
5 Burkina Faso short-acting     long-acting          0.0584  0.0367  0.0917
6 Burkina Faso short-acting     short-acting        0.465   0.405   0.526
7 Burkina Faso short-acting     traditional          0.0328  0.0205  0.0519
8 Burkina Faso short-acting     none                0.444   0.382   0.507
9 Burkina Faso traditional      long-acting          0.0635  0.0215  0.174
10 Burkina Faso traditional     short-acting        0.217   0.121   0.357
11 Burkina Faso traditional     traditional          0.302   0.178   0.464
12 Burkina Faso traditional     none                0.418   0.289   0.558
# ... with 83 more rows
```

And, 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",
    yaxis = "Phase 2"
  )
```

## CHANGE IN CONTRACEPTIVE METHOD TYPE

Percent of women age 15-49 who changed contraceptive method or use status



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.

## 4.6 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).

## 4.6.1 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(
    cur_data() %>%
      as_survey_design(weight = PANELWEIGHT, id = EAID_1, strata = STRATARC) %>%
      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 CONTRACEPTIVE USE STATUS, BY AGE AT PHASE 2")
```

## CHANGE IN CONTRACEPTIVE USE STATUS, BY AGE AT PHASE 2



## 4.6.2 Education level

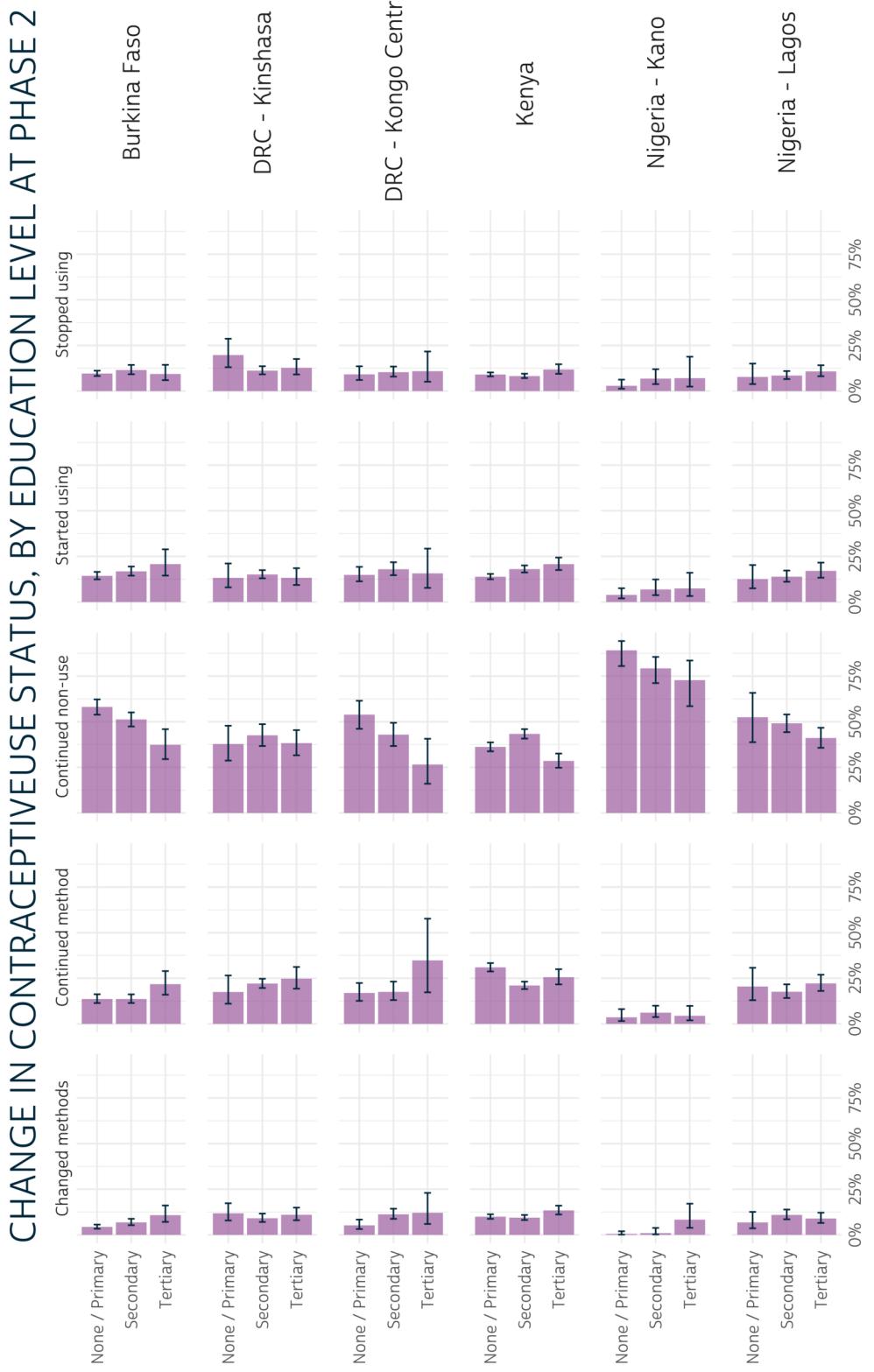
The variable `EDUCATTGEN` standardizes educational categories across countries (see `EDUCATT` for country-specific codes). To match PMA reports, we'll recode `EDUCATTGEN` into just three groups:

- `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(
    cur_data() %>%
      as_survey_design(weight = PANELWEIGHT, id = EAID_1, strata = STRATARC) %>%
      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 CONTRACEPTIVEUSE STATUS, BY EDUCATION LEVEL AT PHASE 2")
```



### 4.6.3 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".

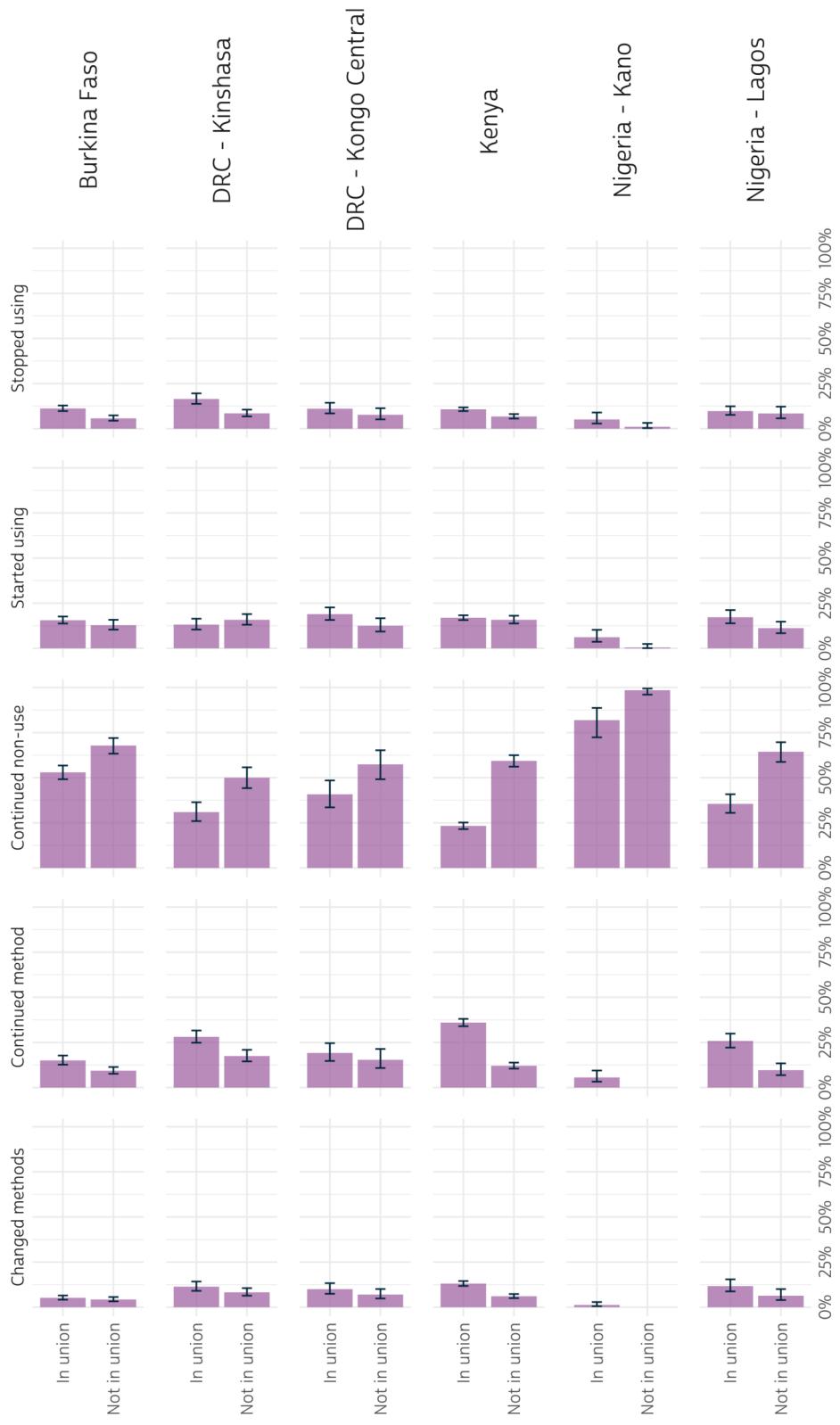
- CAT\_MARSTAT\_2 - Phase 2 marital status (2 categories)

```
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(
    cur_data() %>%
      as_survey_design(weight = PANELWEIGHT, id = EAID_1, strata = STRATARC) %>%
      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 AT PHASE 2")
```

## CHANGE IN CONTRACEPTIVE METHOD TYPE, BY MARITAL STATUS AT PHASE 2



#### 4.6.4 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(
    cur_data() %>%
      as_survey_design(weight = PANELWEIGHT, id = EAID_1, strata = STRATARC) %>%
      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 AT PHASE 2")
```

## CHANGE IN CONTRACEPTIVE METHOD TYPE, BY PARITY AT PHASE 2



## 4.7 OUTCOMES FOR PHASE 1 NON-USERS

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)
```

## 4.7.1 Unmet need

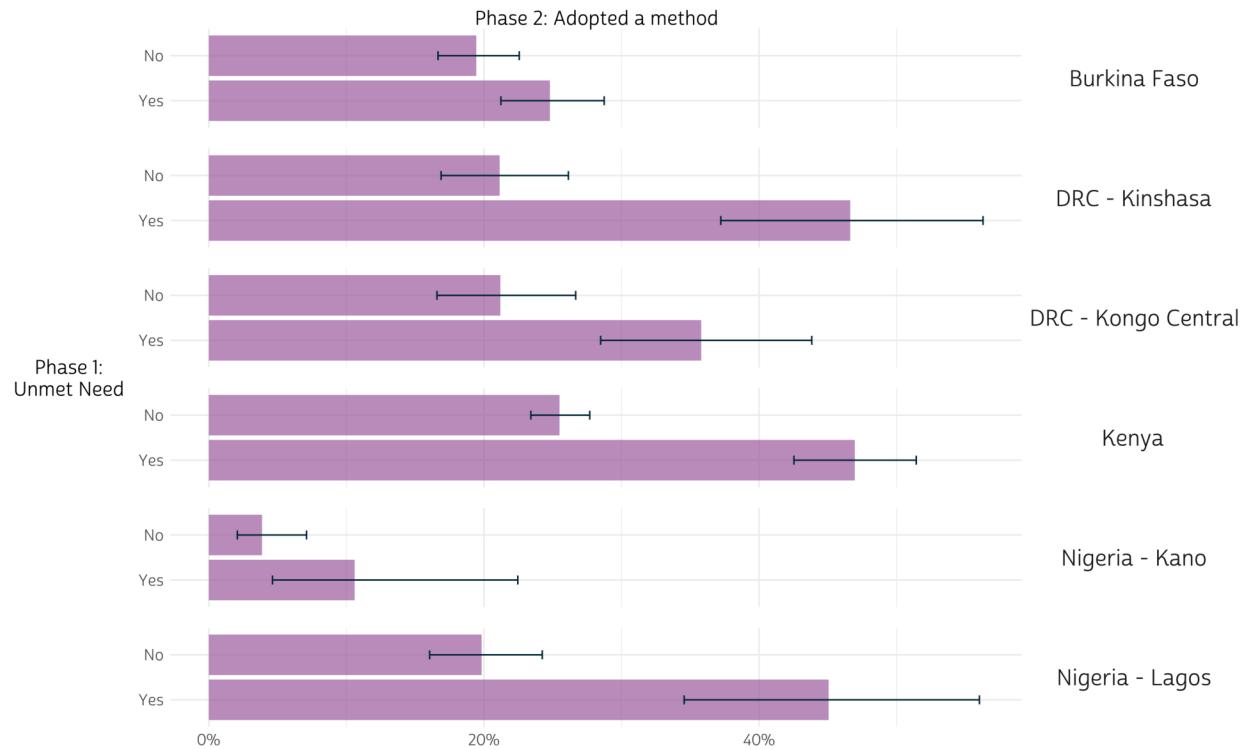
PMA defines unmet need for family planning according to each woman's fertility preferences, current use of family planning methods, and risk factors for pregnancy. Women may have "unmet need" for birth spacing (e.g. pregnant women whose pregnancy was mistimed) or for limiting births (e.g. pregnant women 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(
    cur_data() %>%
      as_survey_design(weight = PANELWEIGHT, id = EAID_1, strata = STRATARC) %>%
      group_by(UNMETYN_1, CP_2) %>%
      summarise(survey_mean(vartype = "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"
  )
```

## UNMET NEED FOR FAMILY PLANNING

Percent of women age 15-49 who were not using a method at Phase 1



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 - Kano.

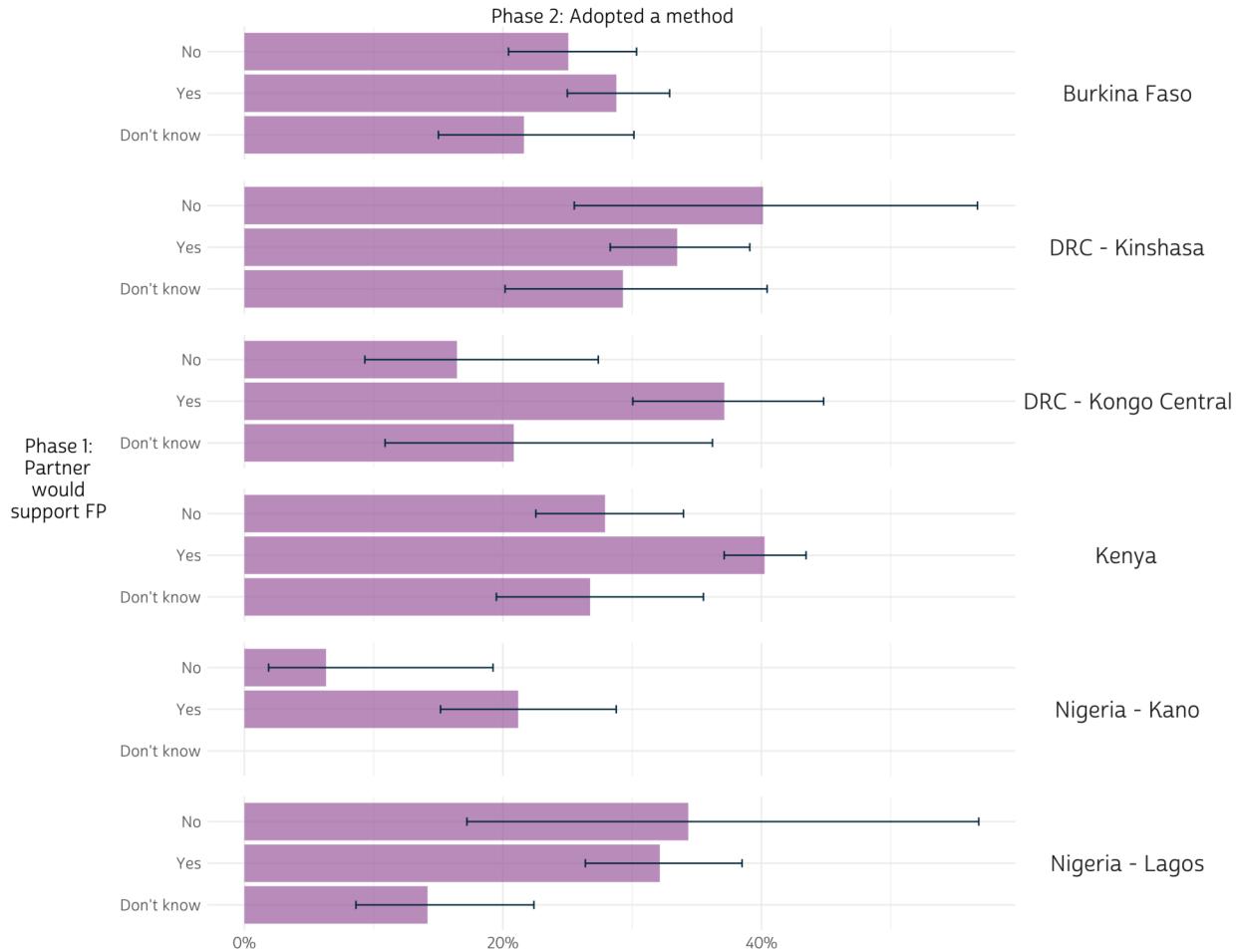
## 4.7.2 Partner support

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(
    cur_data() %>%
    as_survey_design(weight = PANELWEIGHT, id = EAID_1, strata = STRATARC) %>%
    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"
  )
```

## PARTNER SUPPORT FOR FAMILY PLANNING

Percent of women age 15-49 who were not using a method at Phase 1



We've included responses for women who were unsure whether their partner would or would not support future use of FP ("Don't 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.

Setting aside women who answered "Don't know", women with Phase 1 partner support in DRC - Kongo Central and Kenya ("Yes") were more likely to adopt a method than those without ("No"). 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).

### 4.7.3 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	n
FPPLANWHEN_1	<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

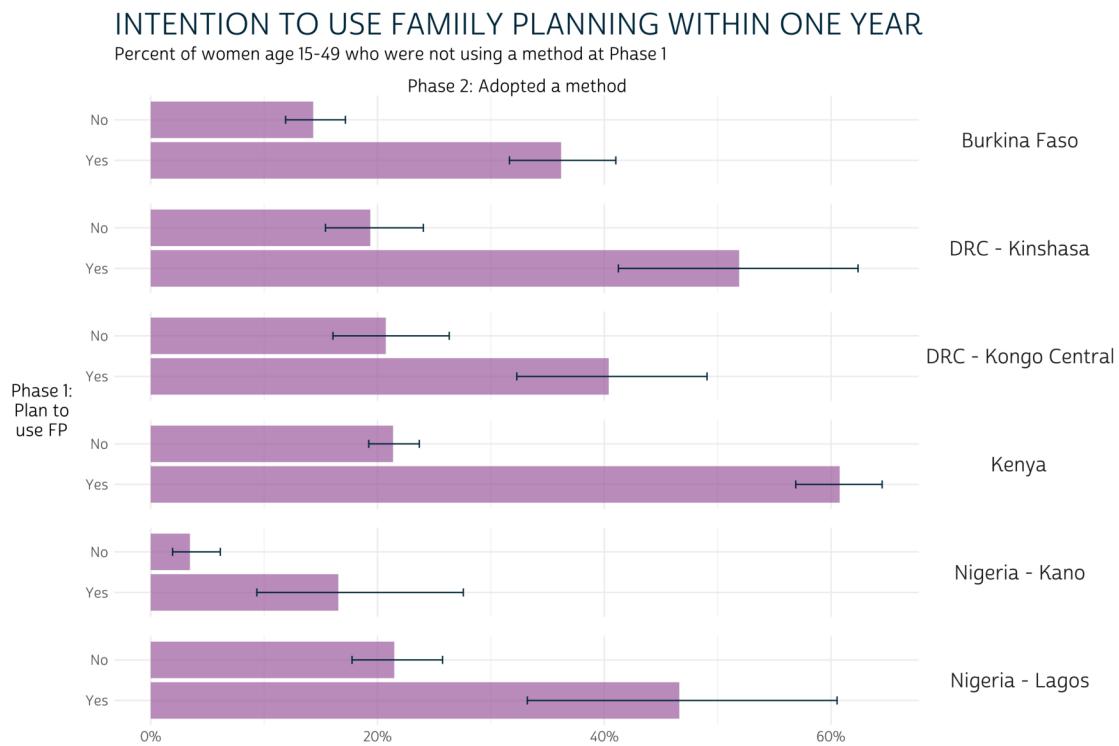
```
dat <- dat %>%
  mutate(
    FPPLANR_1 = case_when(
      FPPLANWHEN_1 == 1 & FPPLANVAL_1 <= 12 ~ "Yes", # Within 12 months
      FPPLANWHEN_1 == 2 & FPPLANVAL_1 == 1 ~ "Yes", # Within 1 year
      FPPLANWHEN_1 %in% c(3, 4) ~ "Yes", # Soon / now or after current pregnancy
      TRUE ~ "No" # Includes 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(
    cur_data() %>%
      as_survey_design(weight = PANELWEIGHT, id = EAID_1, strata = STRATARC) %>%
      group_by(FPPLANRYR_1, CP_2) %>%
      summarise(survey_mean(vartype = "ci", prop = TRUE, prop_method = "logit"))
  ) %>%
  filter(CP_2 == 1) %>%
  ggplot(aes(x = coef, y = FPPLANRYR_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.

## 4.8 LIMITATIONS

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 using graphical confidence interval overlap as a substitute for hypothesis tests 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 proportions in a complex survey sample.

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 Chapter 5, we'll show how to create **alluvial plots**, like those shown in the first two pages of each PMA report.

## 5 ADVANCED DATA VISUALIZATION

In Chapter 4, we demonstrated how to calculate key family planning indicators and plot our estimates in a way that allows the reader to compare confidence intervals for each population.

Chapter 5 digs into some of the other data visualization tools that are commonly used for two-phase panel data: this will include color-coded crosstabs - or **heatmaps** - and **alluvial plots** resembling those shown in the PMA Longitudinal Brief for each panel survey.

R users can build heatmaps with the same `ggplot2` package featured in Chapter 4, but alluvial plots are a bit more challenging. To make things easier, we'll build ours with `ggalluvial`, an extension package for `ggplot2` that includes tools designed specifically for alluvial plots.<sup>29</sup>

---

<sup>29</sup> `ggalluvial` © Cory Brunson et al. (GPL-3)

## 5.1 CHAPTER SETUP

In addition to `ggalluvial`, we'll also load three packages featured throughout this manual: `tidyverse`, `ipumsr`, and `srvyr`.

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

This chapter features the same data extract showcased in Chapter 4, which includes all six of the available samples. It is organized in **Wide** format with only **Female Respondents** selected. This chapter focuses on the following variables included in that extract:

- `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)

Recall that our analysis in Chapter 4 concerned only *de facto* panel members who completed all or part of the Female Questionnaire in both Phase 1 and Phase 2. We also excluded women who are marked “NIU (not in universe)” for a key question concerning current contraceptive use (`CP`). As a reminder, you can load the extract into R and select relevant cases like so:

```
# import the data extract and metadata files
dat <- read_ipums_micro(
  ddi = "data/pma_00006.xml",
  data = "data/pma_00006.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)
  )
```

Additionally, we will reference four variables created in Chapter 4:

- POP - Population of interest
- STRATARC - Numeric codes for PMA sample strata (recoded for DRC samples)
- FPSTATUS\_1 - Pregnant, using contraception, or using no contraception at Phase 1
- FPSTATUS\_2 - Pregnant, using contraception, or using no contraception at Phase 2

These variables were created like so:

```
# 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
    STRATARC = 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")
    )
  )
```

## 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 in Chapter 4. We made this chart in basically two steps.

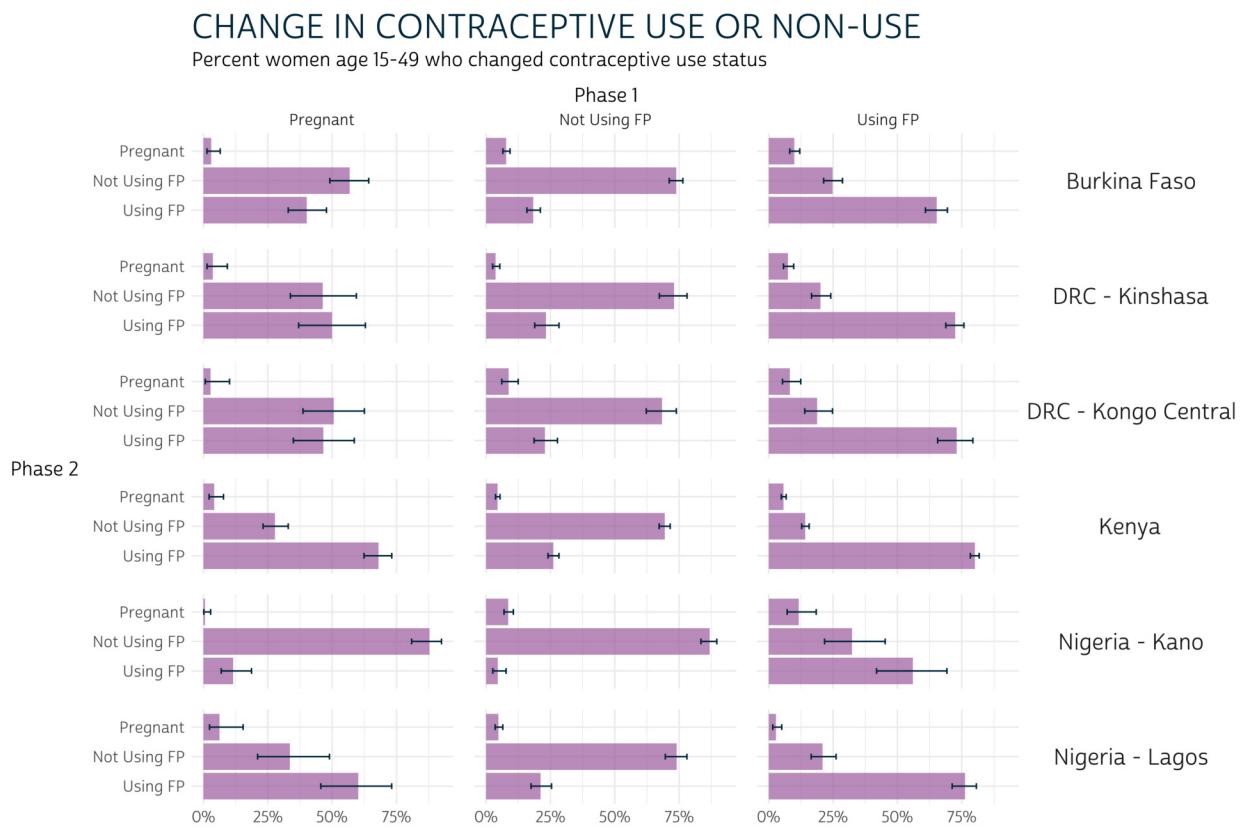
First, we used `svyr` to build a summary table that incorporates survey weights from `PANELWEIGHT` and generates a 95% confidence interval for each estimate. We used `EAID_1` to generate the cluster-robust standard errors underlying each confidence interval, and we stratified standard error estimation by `STRATARC`.

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 = STRATARC) %>%
      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
```

The **grouped bar chart** made in Chapter 4 plots the estimated values in `coef` together with the confidence interval represented by `_low` and `_upp`. This chart is useful because it packs a lot of information into a single, reader-friendly graphic. However, we also mentioned at the end of Chapter 4 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.

## 5.3 HEATMAPS

Let's return to `status_tbl`, but this time we'll plot it as a `heatmap` with `color` and `alpha` (transparency) aesthetics. As in Chapter 4, we'll design a function that combines several `ggplot2` tools we'll recycle in each plot.<sup>30</sup>

```
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_minimal() %>% replace% theme(
      text = element_text(family = "cabrito", size = 42, lineheight = 0.3),
      plot.title = element_text(size = 64, color = "#00263A",
                                hjust = 0, margin = margin(b = 5)),
      plot.subtitle = element_text(hjust = 0, margin = margin(b = 10)),
      axis.text = element_text(size = 28),
      strip.text.x = element_text(margin = margin(t = 10, b = 10)),
      strip.text.y = element_text(angle = 0),
      strip.background = element_blank(),
      axis.title.y = element_text(angle = 0, margin = margin(l = 20), hjust = 1),
      axis.title.y.right = element_text(angle = 0),
      axis.title.x.bottom = element_text(margin = margin(t = 20)),
      panel.grid = element_blank(),
      panel.spacing = unit(1, "lines"),
      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)
  )
}
```

A simple `heatmap` can be built with rectangles from `geom_tile` and text labels from `geom_text`. We'll also 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.

---

<sup>30</sup>This manual uses the proprietary font `cabrito sans`, which is implemented in figures via the `showtext` package for R. You can purchase a license to use `cabrito sans`, or substitute with a font of your choice.

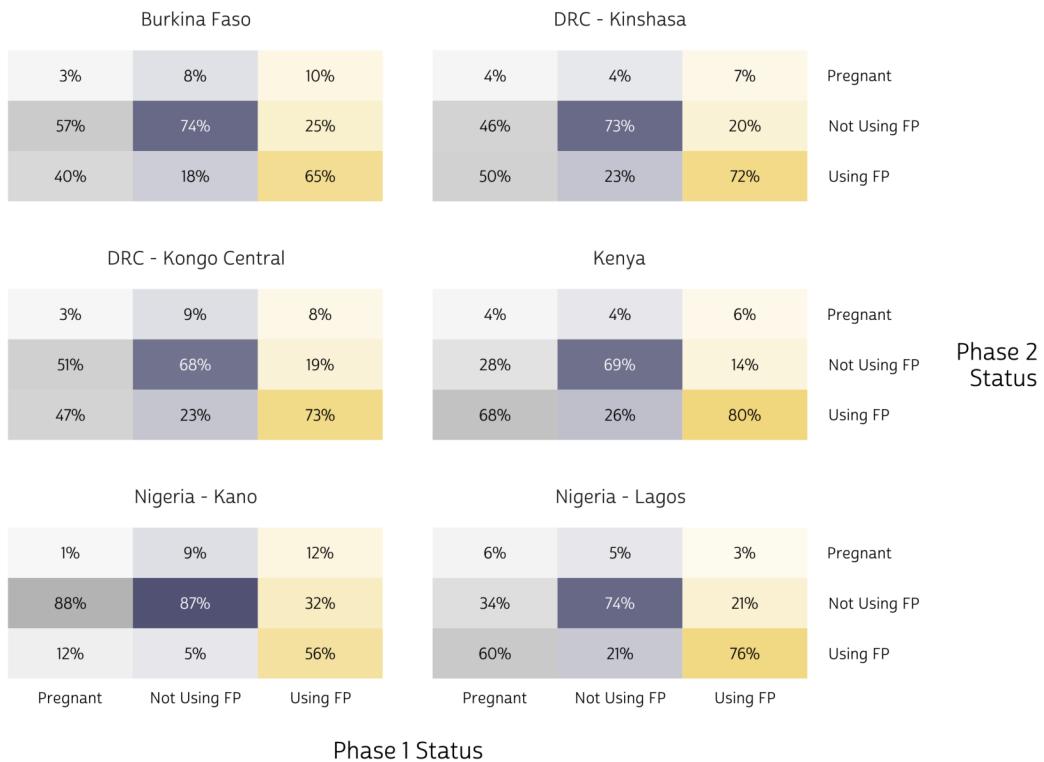
```

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 - compared with our bar chart - it's much easier to 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.

First, we use `group_by(FPSTATUS_1)` to make the column margins and `join` them to `status_tbl`. (Note that we set `vartype = NULL` because we won't be able to include confidence intervals on our heatmap.)

```
status_tbl <- dat %>%
  group_by(POP) %>%
  summarise(
    cur_data() %>%
    as_survey_design(weight = PANELWEIGHT, id = EAID_1, strata = STRATARC) %>%
    group_by(FPSTATUS_1) %>%
    summarise(cols = survey_mean(prop = TRUE, prop_method = "logit", vartype = NULL))
  ) %>%
  full_join(status_tbl, ., by = c("POP", "FPSTATUS_1"))
```

We use `full_join`, but both `left_join` and `right_join` would work equally well in this case.

Next, we use `group_by(FPSTATUS_2)` to add row margins to `status_tbl`.

```
status_tbl <- dat %>%
  group_by(POP) %>%
  summarise(
    cur_data() %>%
    as_survey_design(weight = PANELWEIGHT, id = EAID_1, strata = STRATARC) %>%
    group_by(FPSTATUS_2) %>%
    summarise(rows = survey_mean(prop = TRUE, prop_method = "logit", vartype = NULL))
  ) %>%
  full_join(status_tbl, ., by = c("POP", "FPSTATUS_2"))
```

The column margins now appear in `cols`, while the row margins appear in `rows`.

```
status_tbl
```

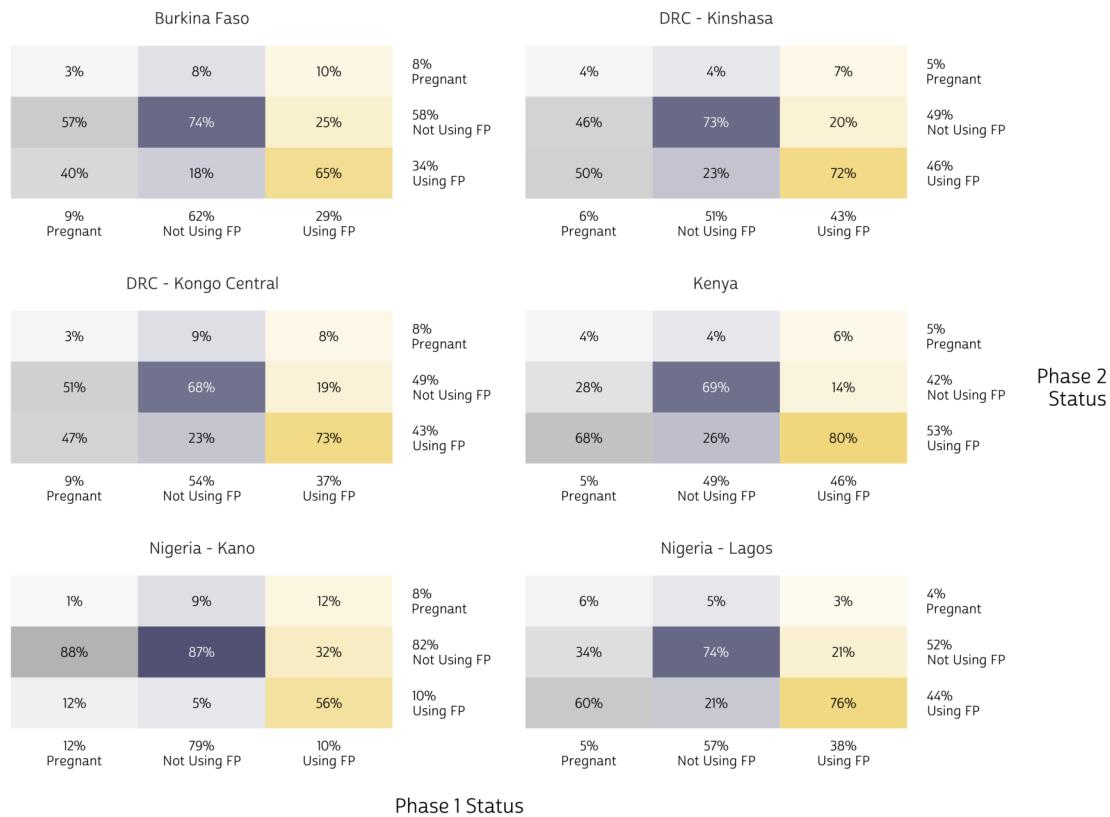
```
# A tibble: 54 × 8
# Groups:   POP [6]
  POP          FPSTATUS_1  FPSTATUS_2      coef `_low` `_upp`  cols  rows
  <chr>        <fct>     <fct>       <dbl>  <dbl>  <dbl>  <dbl>  <dbl>
  1 Burkina Faso Pregnant  Pregnant  0.0302  0.0137  0.0652  0.0879  0.0799
  2 Burkina Faso Pregnant  Not Using 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
```

Now, we can simply `paste` these values together with the original labels from `FPSTATUS_1` and `FPSTATUS_2`.

```
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: 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 = STRATARC) %>%
      group_by(interact(FPSTATUS_1, FPSTATUS_2)) %>%
      summarise(joint = survey_mean(prop = TRUE, prop_method = "logit", var_type = "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 all columns, indicating that the percentages sum for 100% for each population.

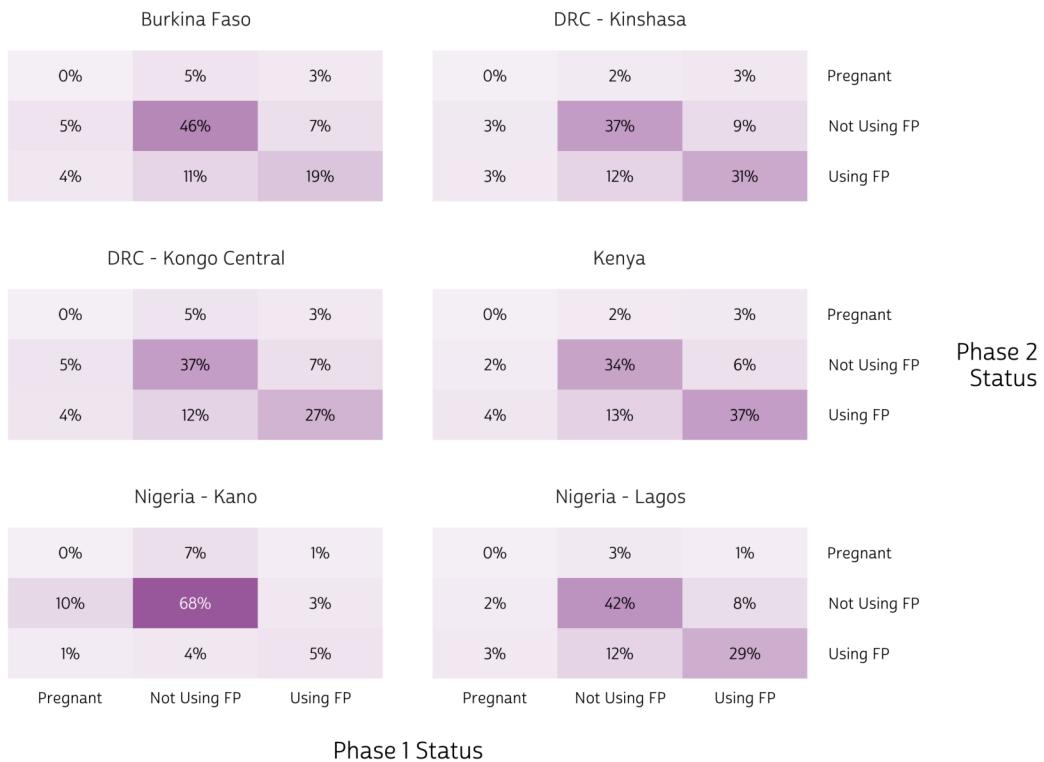
```

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 layout options in a function we'll call `pma_alluvial`:

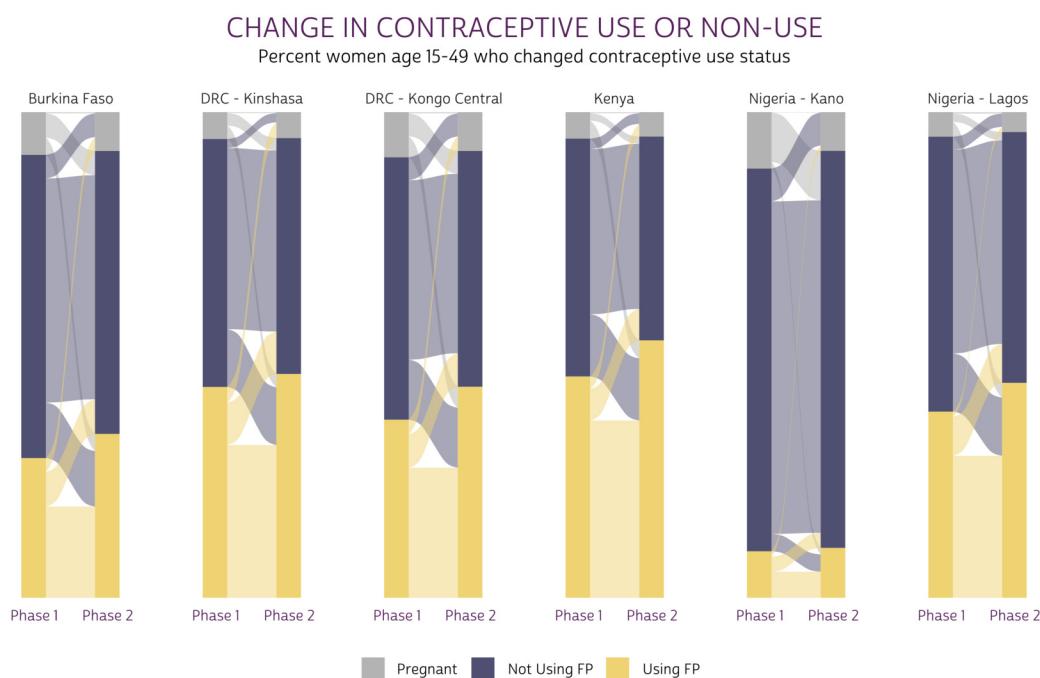
```
pma_alluvial <- function(
  title = NULL,      # an optional title
  subtitle = NULL,   # an optional subtitle
  xaxis = NULL,      # an optional label for the x-axis (displayed below)
  yaxis = NULL        # an optional label for the y-axis (displayed left)
){
  components <- list(
    theme_minimal() %+replace% theme(
      text = element_text(family = "cabrito", size = 42, lineheight = 0.3),
      plot.title = element_text(size = 64, color = "#541E5A",
                                 hjust = 0.5, mar = margin(b = 5)),
      plot.subtitle = element_text(hjust = 0.5, margin = margin(b = 20)),
      strip.background = element_blank(),
      strip.text.x = element_text(margin = margin(b = 5)),
      axis.text.x = element_text(color = "#541E5A", margin = margin(t = 5, b = 10)),
      axis.text.y = element_blank(),
      panel.spacing = unit(1, "lines"),
      plot.margin = margin(0, 100, 0, 100),
      legend.position = "bottom",
      legend.title = element_blank(),
      legend.spacing.x = unit(10, "pt"),
      panel.grid = 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



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.

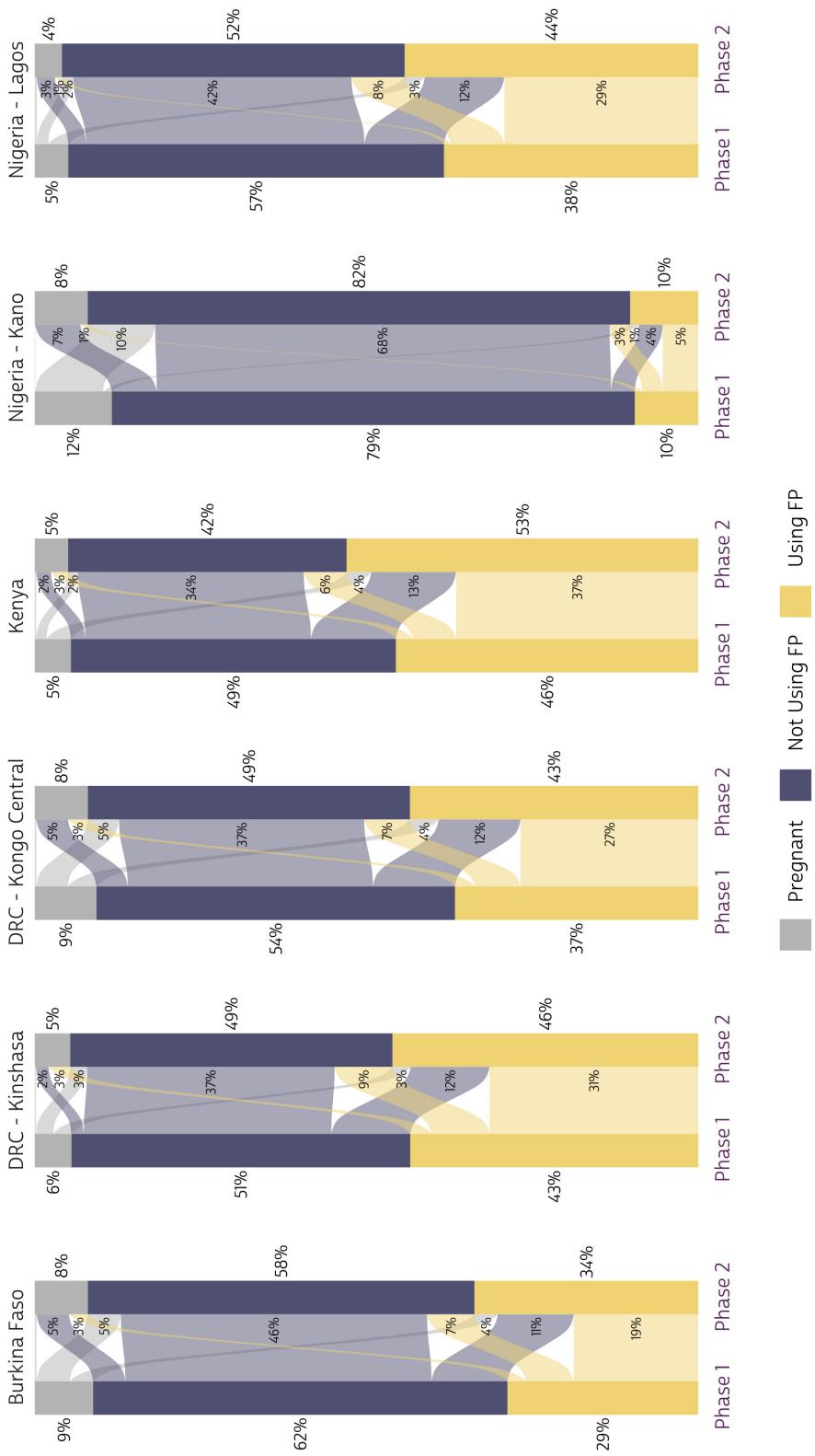
Values may not add to 100% due to rounding (values rounded to 0% are not labelled).

```
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 = 8         # use a slightly smaller font
)
```

Now, it's easy to identify the proportion of women at each phase *and* the proportion who switched or maintained their status between phases.

## CHANGE IN CONTRACEPTIVE USE OR NON-USE

Percent women age 15-49 who changed contraceptive use status



## 6 CONTRACEPTIVE CALENDAR

As we've seen, PMA panel surveys represent annual interviews that will ultimately include three phases of data collection. Most questions will be repeated for a total of three observations each spaced one year apart. However, some data in PMA panel surveys are reported *monthly* up to three years prior to the interview in each phase. These data are provided as a comma-delimited character string known as the **Contraceptive Calendar**.

Chapter 6 includes code you can use to parse and analyze data from the **Contraceptive Calendar**. These data are particularly exciting because they offer researchers an opportunity to explore longitudinal analysis techniques like **survival** to model the duration of events like:

- continuous use (or non-use) of a contraceptive method
- birth spacing
- pregnancies leading to birth or termination

To demonstrate, we'll 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. In R, this type of analysis is facilitated by the **survival** package, which can be installed from CRAN like so:

```
install.packages("survival")
```



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Therneau et al.  
(LGPL >=2)

The term "survival analysis" refers to the probability that a person "survives" a particular condition for a given period of time, most commonly in clinical research settings. In the social sciences, this type of analysis is also known as "event history", "time-to-event", or "duration" analysis. We use the term "survival" in order to match the terminology used in the R package featured in this chapter.

There are many additional R packages available for plotting Time-to-Event curves showing the probability of survival over time.<sup>31</sup> Here, we will show how to construct these figures with the same **ggplot2** toolkit featured in previous chapters.

---

<sup>31</sup>For example, see **ggsurvfit**.

## 6.1 CHAPTER SETUP

Two calendar variables are available for each country in the PMA panel study. The main calendar - which we refer to as the **Contraceptive Calendar** - is named as follows:

- CALENDARBF
- 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

For example, consider a woman sampled in Kenya who gave birth during the month of the interview following 8 prior months of pregnancy. If she had used the pill every month up until the month she became pregnant, her string in **CALENDARKE** would look like this:

B,P,P,P,P,P,P,P,7

The second calendar is the **Discontinuation Calendar**, and it gives the *reason why* a woman stopped using a contraceptive method for each month following an episode of continuous use. This calendar is represented by the following variables:

- CALENDARBFWHY
- CALENDARCDWHY
- CALENDARKEWHY
- CALENDARNGWHY

Like the **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

Returning to our example, if the same woman reported that she stopped using the pill because she wanted to become pregnant, her string in `r_link(CALENDARKEWHY)` would look like this:

.....,3,.....

Note that the length of the string is padded by blank values before and after the only month in which this woman stopped using the pill. This ensures that *all calendars in the same sample contain the same number of values* including blanks. Women who were interviewed one month before the final interviews were collected, for example, will always have a blank value for the left-most space on their calendar.

However, calendars from *different samples may be different lengths*. In this chapter, we'll demonstrate how to work with a data extract containing multiple samples. We will use tools from the `tidyverse` package to **separate** the comma-delimited string into multiple columns, and then reshape the columns into rows with `pivot_longer`. `tidyverse` is included in the `tidyverse` toolkit for R. Following these steps, you'll be able to merge and analyze data from calendars collected in multiple countries covering a range of different dates.



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All six of the currently available longitudinal samples are included in the data extract featured in this chapter (**Female Respondents** only). We've selected a **wide** format extract, so that the variables from each phase appear together in the same row. For example, the Kenya contraceptive calendar from Phase 1 is named **CALENDARKE\_1**, while the Kenya contraceptive calendar from Phase 2 is named **CALENDARKE\_2**.

We've selected all of the calendar variables listed above, 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
- **COUNTRYSTR** - Country two-letter ISO code
- **INTFQMON & INTFQYEAR** - Date of Female Questionnaire interview
- **FPCURREFFMETHRC** - Most effective current family planning method (recoded<sup>32</sup>)
- **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

We'll load the data extract into R together with each of the packages we'll feature in this post. Then, \*Inclusion Criteria for Analysis\*\* described in Chapter 1, we'll drop cases for women who did not complete the Female Questionnaire or were not members of the *de facto* population in both phases.

---

<sup>32</sup>The 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.

```

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

dat <- read_ipums_micro(
  ddi = "data/pma_00007.xml",
  data = "data/pma_00007.dat.gz") %>%
  filter(RESULTFQ_2 == 1, RESIDENT_1 %in% c(11, 22) & RESIDENT_2 %in% c(11, 22))

```

In order to make this chapter a bit easier to follow, we're going to omit survey design information - weights and identifiers for samples clusters and strata - featured in previous chapters. R users can find several functions adapted from the `survival` package in the `survey` package, but we recommend that beginners start with the basics before confronting complex survey design.<sup>33</sup>

We'll instead organize results by country (combining sub-national samples for Nigeria and the DRC, which use the same calendar variables). Two-letter ISO codes for each country are available in the variable `COUNTRYSTR_1`; we'll extract these codes with `zap_labels` to make a new variable called `CNTRY`.<sup>34</sup> In graphics, we'll switch these ISO codes for readable country names extracted from the value labels in `COUNTRY`.

Use `zap_labels` to remove all labels from an IPUMS variable.

- `CNTRY` - Country two-letter ISO code

```

dat <- dat %>%
  mutate(
    CNTRY = COUNTRYSTR_1 %>% zap_labels,
    COUNTRY = COUNTRY %>%
      as_factor %>%
      fct_recode("DRC" = "Congo, Democratic Republic")
  )

dat %>% count(CNTRY, COUNTRY)

```

<sup>33</sup>The survival function `survfit` used to fit a Kaplan-Meier curve in the Analysis section of this chapter is analogous to the `survey` function `svykm`, except that the latter incorporates complex survey information. For simplicity, the confidence intervals shown in this chapter do not account for cluster sampling, and may be narrower as a result.

<sup>34</sup>The same ISO codes are also available in `COUNTRYSTR_2`.

```
# A tibble: 4 × 3
  CNTRY COUNTRY      n
  <chr> <fct>     <int>
1 BF    Burkina Faso 5212
2 CD    DRC          3487
3 KE    Kenya         6939
4 NG    Nigeria       2087
```

Finally, we'll also create a short ID number for each woman, making it easier for the reader to follow the same individual's responses throughout several reformatting steps. **This is for display purposes only** - in practice, the 41-character variable `FQINSTID` should be used as a unique identifier for each panel member.

- `ID` - Short ID for each panel member (for display only)

```
dat <- dat %>% rowid_to_column("ID")
```

## 6.2 CENTURY MONTH CODES (CMC)

As shown above, we'll be referencing several variables representing **dates** in this chapter. 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))  
}
```

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

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.

```
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()
```

# A tibble: 6 × 4		PANELBIRTHYR_2	PANELBIRTHCMC_2	n
		<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	15074

## 6.3 CALENDAR LENGTH

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

This is because the width of each calendar variable differs according to 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.

You can find the precise range of dates included in each calendar on the [description tab](#) for each country's calendar variable. Here, for example, we see that the Kenya Phase 1 sample includes dates from January 2017 to the month of the interview, and that its Phase 2 sample includes dates from January 2018 to the month of the interview. Note: the two calendars overlap between January 2018 and the Phase 1 interview.

The screenshot shows a web browser window for the IPUMS PMA website ([pma.ipums.org/pma-action/variables/CALENDARKE#description\\_section](https://pma.ipums.org/pma-action/variables/CALENDARKE#description_section)). The page title is "CALENDARKE". The header includes the IPUMS PMA logo, navigation links for "HOME | SELECT DATA | MY DATA | SUPPORT", and a "LOG IN | REGISTER | GLOBAL HEALTH" link. A "DATA CART" sidebar indicates "0 VARIABLES" and "6 SAMPLES" with a "VIEW CART" button. The main content area has tabs for "CODES", "DESCRIPTION" (which is selected), "COMPARABILITY", "UNIVERSE", "AVAILABILITY", and "QUESTIONNAIRE TEXT". The "DESCRIPTION" tab contains the following text:

**Description**

CALENDARKE contains retrospective contraceptive calendar data for 3 years prior to the female interview for Kenya. These data are contained in a comma delimited reading from right to left chronologically. For Kenya 2019, this variable represents the 3 years prior to the female interview, starting in January 2017 going to the month of the interview (either November or December 2019). For Kenya 2020, this variable represents 3 years prior to the female interview, starting in January 2018 going to the month of the interview (either November or December 2020). See the Codes tab for a list of the codes and meanings. Our [user note on calendar data](#) contains Stata code to convert this string variable into wide or long form numeric variables.

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

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

Start Contraceptive Calendar

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

All women in the same sample were asked to recall events dating backward to a common start date (always in January, as shown above). However, the length of each woman's calendar will vary depending on the date of her interview. Interviews were collected over a period of months shown in the table below.

Stop Contraceptive Calendar

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

To determine the precise length of each woman's calendar, we'll need to create variables for the CMC date of its first month in CALSTART\_1 and CALSTART\_2, and also for the CMC date of its last month in CALSTOP\_1 and CALSTOP\_2.

- CALSTART\_1 - CMC for a woman's first calendar month in Phase 1
- CALSTOP\_1 - CMC for a woman's last calendar month in Phase 1
- CALSTART\_2 - CMC for a woman's first calendar month in Phase 2
- CALSTOP\_2 - CMC for a woman's last calendar month in Phase 2

We'll manually set CALSTART\_1 and CALSTART\_2 like so:

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

CALSTOP\_1 and CALSTOP\_2 can be copied directly from the dates we made above for INTFQCMC\_1 and INTFQCMC\_2.

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

## 6.4 FORMATTING CALENDAR STRINGS

Now that we know the appropriate dates for each value in all calendar variables, we'll begin separating each string into columns. As a first step, we'll want to use `pivot_longer` to align all of the calendars assigned to different countries. Let's call our reformatted data frame `cals`. For now, it will only include `ID`, `CNTRY`, and all variables that start with `CAL`.

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

Notice that the first few rows of our dataset represent women from Burkina Faso. Their values for variables like `CALENDARKE_1` are blank; only the variables for Burkina Faso contain comma-delimited values.

```
cals %>% select(ID, CNTRY, CALENDARKE_1, CALENDARBF_1)
```

Our goal is to reduce the number of variables in `cals` so that we only need to work with one calendar for *all* countries. We'll "pivot" `cals` in two steps. First, we'll merge data from each Phase one column per country. Second, we'll merge data from each country into a finally, unified column.

## 6.4.1 Merge Phases

We'll use `pivot_longer` to reorganize our **wide format** data into **long format**, with one row per Phase of the panel study. This procedure strips the numeric suffix from each calendar variable: we'll store this information in a new column called `PHASE`. Notice that the argument `cols` selects every column that `starts_with` the prefix "CAL".

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

For example, let's return to those first few rows of data representing women from Burkina Faso. The variables `CALENDARKE_1` and `CALENDARBE_1` we previewed above are replaced with a new variable `PHASE` and a pair of variables named `CALENDARKE` and `CALENDARBF`.

```
cals %>% select(ID, CNTRY, PHASE, CALENDARKE, CALENDARBF)
```

```
# A tibble: 35,450 × 5
  ID CNTRY PHASE CALENDARKE CALENDARBF
  <int> <chr> <chr> <chr+lbl> <chr+lbl>
1 1 BF 1     ""      ",,,,,,,,,,0,0,0,0,0,0,0,0,0,0,B,P,P,P,P,P...
2 1 BF 2     ""      ",,,,,,,,,,3,3,3,3,3,3,0,0,0,0,0,0,0,0,0,0,0,0...
3 2 BF 1     ""      ",,,,,,,,,,P,P,P,P,P,P,0,0,0,0,0,0,0,3,3,3...
4 2 BF 2     ""      ",,,,,,,,,,5,5,5,5,5,5,5,5,5,B,P,P,P,P,P,P...
5 3 BF 1     ""      ",,,,,,,,,,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0...
6 3 BF 2     ""      ""
7 4 BF 1     ""      ",,,,,,,,,,0,0,0,5,5,5,5,5,5,5,5,5,5,0,0,0,0...
8 4 BF 2     ""      ",,,,,,,,,,0,0,0,0,0,0,0,0,0,0,0,0,0,0,5,5,5...
9 5 BF 1     ""      ",,,,,,,,,,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0...
10 5 BF 2     ""      ""
# ... with 35,440 more rows
```

We've applied similar changes to variables for the **Discontinuation Calendar**.

```
cals %>% select(ID, CNTRY, PHASE, CALENDARKEWHY, CALENDARBFWHY)
```

```
# A tibble: 35,450 × 5
  ID CNTRY PHASE CALENDARKEWHY CALENDARBFWHY
  <int> <chr> <chr> <chr+lbl>    <chr+lbl>
1 1 BF   1     "       "....."
2 1 BF   2     "       "....."
3 2 BF   1     "       ".....,6,....."
4 2 BF   2     "       ".....,6,....."
5 3 BF   1     "       "....."
6 3 BF   2     "       "....."
7 4 BF   1     "       ".....,1,....."
8 4 BF   2     "       ".....,12,....."
9 5 BF   1     "       "....."
10 5 BF  2     "       "....."
# ... with 35,440 more rows
```

And, because our CALSTART and CALSTOP variables were also named with the prefix “CAL”, they been pivoted as well.

```
cals %>% select(ID, CNTRY, PHASE, CALSTART, CALSTOP)
```

```
# A tibble: 35,450 × 5
  ID CNTRY PHASE CALSTART CALSTOP
  <int> <chr> <chr>   <dbl>   <dbl>
1 1 BF   1      1417    1442
2 1 BF   2      1417    1453
3 2 BF   1      1417    1441
4 2 BF   2      1417    1453
5 3 BF   1      1417    1441
6 3 BF   2      1417    1453
7 4 BF   1      1417    1441
8 4 BF   2      1417    1452
9 5 BF   1      1417    1441
10 5 BF  2      1417    1453
# ... with 35,440 more rows
```

## 6.4.2 Merge Countries

We'll now pivot a second time, leaving only two columns representing data collected from all four countries: we'll call the **Contraceptive Calendar** FPSTATUS, and we'll call the **Discontinuation Calendar** WHYSTOP. The suffix labeling the country for each variable will be stripped and placed in a new column, CNTRY\_CAL.

- FPSTATUS - Calendar string derived from the main Contraceptive Calendar
- WHYSTOP - Calendar string derived from the Discontinuation 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("CNTRY_CAL", ".value"),
    values_to = "CALENDAR_STRING"
  )
```

Notice that each woman now occupies *eight rows*: that's four country calendars per phase.

```
cals
```

```
# A tibble: 141,800 × 8
  ID CNTRY PHASE CALSTART CALSTOP CNTRY_CAL FPSTATUS      WHYSTOP
  <int> <chr> <chr>   <dbl>   <dbl> <chr> <chr+lbl> <chr+lbl>
1 1   BF    1       1417   1442 KE    ""               ""
2 1   BF    1       1417   1442 NG    ""               ""
3 1   BF    1       1417   1442 BF    ",,,,...,0,0,0,0,0,... ,,,,..."
4 1   BF    1       1417   1442 CD    ""               ""
5 1   BF    2       1417   1453 KE    ""               ""
6 1   BF    2       1417   1453 NG    ""               ""
7 1   BF    2       1417   1453 BF    ",,,,...,3,3,3,3,3,... ,,,,..."
8 1   BF    2       1417   1453 CD    ""               ""
9 2   BF    1       1417   1441 KE    ""               ""
10 2   BF   1       1417   1441 NG    ""               ""
# ... with 141,790 more rows
```

We'll remove extra rows where the two-letter ISO code in CNTRY does not match the value in our new variable CNTRY\_CAL. Finally, leaves all women with only two rows each.

```
cals <- cals %>%
  filter(CNTRY_CAL == CNTRY) %>%
  select(-CNTRY_CAL)
```

cals

```
# A tibble: 35,450 × 7
  ID CNTRY PHASE CALSTART CALSTOP FPSTATUS WHYSTOP
  <int> <chr> <chr>   <dbl>   <dbl> <chr+lbl> <chr+lbl>
1     1 BF    1        1417    1442 ",,,,,,,,,,0,0,0,0,0,0,0,0,0,..." ",,,,,,"
2     1 BF    2        1417    1453 ",,,,,,,,,,3,3,3,3,3,0,0,0,0,..." ",,,,,,"
3     2 BF    1        1417    1441 ",,,,,,,,,,P,P,P,P,P,P,0,0,0,..." ",,,,,,"
4     2 BF    2        1417    1453 ",,,,,,,,,,5,5,5,5,5,5,5,5,B,..." ",,,,,,"
5     3 BF    1        1417    1441 ",,,,,,,,,,0,0,0,0,0,0,0,0,0,..." "''"
6     3 BF    2        1417    1453 "''"
7     4 BF    1        1417    1441 ",,,,,,,,,,0,0,0,5,5,5,5,5,5,..." ",,,,,,"
8     4 BF    2        1417    1452 ",,,,,,,,,,0,0,0,0,0,0,0,0,0,..." ",,,,,,"
9     5 BF    1        1417    1441 ",,,,,,,,,,0,0,0,0,0,0,0,0,0,..." ",,,,,,"
10    5 BF    2        1417    1453 "''"
# ... with 35,440 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.

### 6.4.3 Blank Strings

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 [universe tab](#) explains why some cases are "NIU (not in universe)".

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: 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 (Kenya)". It has buttons for "ADD TO CART" and "CHANGE SAMPLES". Below these are 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.  
At the bottom of the page, there is a footer with links to "SUPPORTED BY" (The Bill & Melinda Gates Foundation, PMA, Stat/Transfer, and University of Minnesota) and "COPYRIGHT © MINNESOTA POPULATION CENTER, UNIVERSITY OF MINNESOTA".

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.

About 1 in every 5 calendars in our dataset `cals` is blank "" for one of the two reasons mentioned above.

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

```
# A tibble: 2 × 3
`FPSTATUS == ""` n    prop
<lgl>           <int> <dbl>
1 FALSE          28173 0.795
2 TRUE           7277  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 neither started nor stopped 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.

- CALMISSING - Indicates whether a blank calendar cannot be completed from other variables

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"))
```

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(
    CALMISSING = FPSTATUS == "" & WHYSTOP == "" & {
      PREGNANT == 1 | if_any(ends_with("CMC"), ~!is.na(.x) & .x >= CALSTART)
    }
  )
```

Let's use `glimpse` to take a closer look at the data collected for the woman row 6, whose Phase 2 `FPSTATUS` calendar is an empty string.

```
cals %>% slice(6) %>% glimpse()
```

```
Rows: 1
Columns: 17
$ ID              <int> 3
$ PHASE           <chr> "2"
$ KID1STBIRTHCMC <dbl> NA
$ FPBEGINUSECMC  <dbl> NA
$ LASTBIRTHCMC   <dbl> NA
$ OTHERBIRTHCMC  <dbl> NA
$ PANELBIRTHCMC  <dbl> NA
$ PREGENDCMC     <dbl> NA
$ PANELPREGENDCMC <dbl> NA
$ PREGNANT        <int+lbl> 0
$ FPCURREFFMETHRC <int+lbl> 999
$ CNTRY           <chr> "BF"
$ CALSTART        <dbl> 1417
$ CALSTOP         <dbl> 1453
$ FPSTATUS         <chr+lbl> ""
$ WHYSTOP          <chr+lbl> ""
$ CALMISSING       <lgl> FALSE
```

We know that this woman has never given birth because all of the `CMC` variables related to birth are `NA`; moreover, `PREGNANT == 0` indicates that she is not currently pregnant. She also has not used contraception, as indicated by `FPCURREFFMETHRC` and `FPBEGINUSECMC`. So, we have marked `CALMISSING = FALSE` because it's safe to auto-complete her calendar with the value `0` for every month between `CALSTART` and `CALSTOP`.

On the other hand, consider the woman in row 10, whose Phase 2 FPSTATUS calendar is also an empty string.

```
cals %>% slice(10) %>% glimpse()
```

```
Rows: 1
Columns: 17
$ ID              <int> 5
$ PHASE           <chr> "2"
$ KID1STBIRTHCMC <dbl> 1366
$ FPBEGINUSECMC  <dbl> NA
$ LASTBIRTHCMC   <dbl> 1422
$ OTHERBIRTHCMC  <dbl> NA
$ PANELBIRTHCMC  <dbl> NA
$ PREGENDCMC    <dbl> NA
$ PANELPREGENDCMC <dbl> NA
$ PREGNANT        <int+lbl> 0
$ FPCURREFFMETHRC <int+lbl> 999
$ CNTRY           <chr> "BF"
$ CALSTART        <dbl> 1417
$ CALSTOP         <dbl> 1453
$ FPSTATUS         <chr+lbl> ""
$ WHYSTOP         <chr+lbl> ""
$ CALMISSING      <lgl> TRUE
```

You can see in LASTBIRTHCMC that she gave birth in month 1422, 5 months after we'd hope to see reported events beginning in CALSTART == 1417. We have flagged this row with CALMISSING == TRUE 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.

Counting the number of women flagged by CALMISSING we see that we'll now be able to reduce the number of missing calendars from 1 in 5 cases 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      28173 0.795
2 FALSE      TRUE       5816  0.164
3 TRUE       TRUE       1461  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.

- CALDUR - Duration of a woman's calendar (in months)

```
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
  ))
```

Returning to our example, row 6 is now completed with the value 0, excluding the first month (we leave this blank because this woman's interview was one month before the final month of Phase 2 data collection in Burkina Faso). Row 10 is left unchanged.

```
cals
```

```
# A tibble: 35,450 × 6
  ID PHASE CNTRY CALSTART FPSTATUS          WHYSTOP
  <int> <chr> <chr>    <dbl> <chr>          <chr+l>
1 1     1 1      BF      1417 ",,,,,,,,,,0,0,0,0,0,0,0,0,0,0,B,P,P,... ",,,,,,,
2 1     1 2      BF      1417 ",,,,,,,,,,3,3,3,3,3,0,0,0,0,0,0,0,0,... ",,,,,,,
3 2     2 1      BF      1417 ",,,,,,,,,P,P,P,P,P,P,P,0,0,0,0,0,0,0,3... ",,,,,,,
4 2     2 2      BF      1417 ",,,,,,,,,,5,5,5,5,5,5,5,5,5,5,B,P,P,P,... ",,,,,,,
5 3     3 1      BF      1417 ",,,,,,,,,,0,0,0,0,0,0,0,0,0,0,0,0,0,... """
6 3     3 2      BF      1417 ",0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,... """
7 4     4 1      BF      1417 ",,,,,,,,,,0,0,0,5,5,5,5,5,5,5,5,5,5,0,... ",,,,,,,
8 4     4 2      BF      1417 ",,,,,,,,,,0,0,0,0,0,0,0,0,0,0,0,0,0,... ",,,,,,,
9 5     5 1      BF      1417 ",,,,,,,,,,0,0,0,0,0,0,0,0,0,0,0,0,0,... ",,,,,,,
10 5    5 2      BF      1417 """
# ... with 35,440 more rows
```

#### 6.4.4 Split 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: 70,900 × 6
  ID PHASE CNTRY CALSTART name      value
  <int> <chr> <chr>   <dbl> <chr>    <chr+lbl>
1 1     1     BF     1417 FPSTATUS ",,,,,,,,,,0,0,0,0,0,0,0,0,0,B,P,P...
2 1     1     BF     1417 WHYSTOP  ",,,,,,,,,,,,""
3 1     2     BF     1417 FPSTATUS ",,,,,,,,,,3,3,3,3,3,3,0,0,0,0,0,0,0,0...
4 1     2     BF     1417 WHYSTOP  ",,,,,,,,,,,,""
5 2     1     BF     1417 FPSTATUS ",,,,,,,,,,P,P,P,P,P,P,0,0,0,0,0,0,0,0...
6 2     1     BF     1417 WHYSTOP  ",,,,,,,,,,,6,,,""
7 2     2     BF     1417 FPSTATUS ",,,,,,,,,,5,5,5,5,5,5,5,5,B,P,P,P...
8 2     2     BF     1417 WHYSTOP  ",,,,,,,,,,,6,,,""
9 3     1     BF     1417 FPSTATUS ",,,,,,,,,,0,0,0,0,0,0,0,0,0,0,0,0,0,0...
10 3    1     BF     1417 WHYSTOP  """
# ... with 70,890 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.<sup>35</sup> 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
```

<sup>35</sup>Here, 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).

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.

```
# Create one column for every month in the longest calendar
cals <- cals %>%
  separate(value, into = paste0("cal", 1:48), sep = ",", fill = "left", )

cals

# A tibble: 70,900 × 53
  ID PHASE CNTRY CALSTART name    cal48 cal47 cal46 cal45 cal44 cal43 cal42
  <int> <chr> <chr>   <dbl> <chr>   <chr> <chr> <chr> <chr> <chr> <chr>
  1     1 1     BF      1417 FPSTATUS <NA>  <NA>  <NA>  <NA>  <NA>  <NA>
  2     1 1     BF      1417 WHYSTOP  <NA>  <NA>  <NA>  <NA>  <NA>  <NA>
  3     1 2     BF      1417 FPSTATUS ""   ""   ""   ""   ""   ""   ""
  4     1 2     BF      1417 WHYSTOP  ""   ""   ""   ""   ""   ""   ""
  5     2 1     BF      1417 FPSTATUS <NA>  <NA>  <NA>  <NA>  <NA>  <NA>
  6     2 1     BF      1417 WHYSTOP  <NA>  <NA>  <NA>  <NA>  <NA>  <NA>
  7     2 2     BF      1417 FPSTATUS ""   ""   ""   ""   ""   ""   ""
  8     2 2     BF      1417 WHYSTOP  ""   ""   ""   ""   ""   ""   ""
  9     3 1     BF      1417 FPSTATUS <NA>  <NA>  <NA>  <NA>  <NA>  <NA>
 10    3 1     BF      1417 WHYSTOP  <NA>  <NA>  <NA>  <NA>  <NA>  <NA>
# ... with 70,890 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 use `across` to convert blank values `""` to `NA` as well.

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

## 6.4.5 One Row per Month

Finally, we'll want to use `pivot_longer` one more time, reorganizing the data for each month into a separate row. This will allow us to label each month with the correct CMC value, and to align overlapping calendars collected in Phase 1 and Phase 2.

Here, we place each month into a single column temporarily called `value`. The label shown 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: 3,403,200 × 7
  ID PHASE CNTRY CALSTART name      MONTH value
  <int> <chr> <chr>     <dbl> <chr>     <chr> <chr>
1 1     1     BF        1417 FPSTATUS 48     <NA>
2 1     1     BF        1417 FPSTATUS 47     <NA>
3 1     1     BF        1417 FPSTATUS 46     <NA>
4 1     1     BF        1417 FPSTATUS 45     <NA>
5 1     1     BF        1417 FPSTATUS 44     <NA>
6 1     1     BF        1417 FPSTATUS 43     <NA>
7 1     1     BF        1417 FPSTATUS 42     <NA>
8 1     1     BF        1417 FPSTATUS 41     <NA>
9 1     1     BF        1417 FPSTATUS 40     <NA>
10 1    1     BF        1417 FPSTATUS 39    <NA>
# ... with 3,403,190 more rows
```

From `MONTH` and `CALSTART`, we'll derive `CALCMC` to mark the CMC for each `value`.

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

```
cals
```

```
# A tibble: 3,403,200 × 8
  ID PHASE CNTRY CALSTART name    MONTH value CALCMC
  <int> <chr> <chr>     <dbl> <chr>   <chr> <dbl>
1 1 1 BF 1417 FPSTATUS 48 <NA> 1464
2 1 1 BF 1417 FPSTATUS 47 <NA> 1463
3 1 1 BF 1417 FPSTATUS 46 <NA> 1462
4 1 1 BF 1417 FPSTATUS 45 <NA> 1461
5 1 1 BF 1417 FPSTATUS 44 <NA> 1460
6 1 1 BF 1417 FPSTATUS 43 <NA> 1459
7 1 1 BF 1417 FPSTATUS 42 <NA> 1458
8 1 1 BF 1417 FPSTATUS 41 <NA> 1457
9 1 1 BF 1417 FPSTATUS 40 <NA> 1456
10 1 1 BF 1417 FPSTATUS 39 <NA> 1455
# ... with 3,403,190 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 %>% print(n = 40)

# A tibble: 769,636 × 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 769,596 more rows

```

## 6.5 ANALYSIS

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.](#).

Here, we'd like to highlight just one way that the PMA panel design might help researchers understand patterns in the calendar data. In previous chapters, we saw that IPUMS PMA includes variables indicating whether women had **unmet need** or **plans to adopt** a contraceptive method in each phase. We'll now examine these variables at Phase 1, and use the **Contraceptive Calendar** data from Phase 2 to test whether either factor influences the adoption rate of contraceptive methods reported one year later.

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 Chapter 4 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,  
    FPPLANRYR_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)  
    )  
  )
```

Also in Chapter 4, we demonstrated how to create a `theme` for graphics built with `ggplot2`. We'll do so again here, creating `theme_pma`.

```
theme_pma <- theme_minimal() %>replace%
  theme(
    text = element_text(family = "cabrito", size = 42),
    plot.title = element_text(size = 72, 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(angle = 0),
    panel.spacing = unit(1, "lines"),
    axis.title.y = element_blank(),
    axis.title.x = element_text(margin = margin(t = 10)),
    legend.title = element_blank()
  )
```

Before we begin our analysis, let's check 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 %>%
  group_by(COUNTRY) %>%
  count(UNMETYN_1, FPPLANYR_1) %>%
  mutate(
    prop = prop.table(n),
    UNMETYN_1 = UNMETYN_1 %>% if_else("Unmet Need", "No Unmet Need"),
    FPPLANYR_1 = FPPLANYR_1 %>% if_else("Plans", "No Plans"),
  ) %>%
  ggplot(aes(x = UNMETYN_1, y = FPPLANYR_1)) +
  geom_tile(fill = "#98579BB0", aes(alpha = prop)) +
  geom_text(aes(label = scales::percent(prop, 0.1))) +
  facet_wrap(vars(COUNTRY), scales = "free") +
  labs(
    title = "Non-users: Unmet Need and Plans to Adopt a Method within 1 Year",
    subtitle = "Percentage among sampled women not using a method at Phase 1",
    x = NULL
  ) +
  theme_pma %>replace%
  theme(panel.grid = element_blank(), legend.position = "none")
```

### Non-users: Unmet Need and Plans to Adopt a Method within 1 Year

Percentage among sampled women not using a method at Phase 1



As you can see, a majority of Phase 1 nonusers in each country had 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 women who planned to adopt a method would be *most likely* to adopt one within the year, but also that 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 %>% select(ID, FPSTATUS_2, CALCMC), by = "ID") %>%
  filter(
    CALCMC >= INTFQCMC_1,
    !if_any(c(FPSTATUS_2, UNMETYN_1, FPPLANYR_1), is.na)
  )
```

## 6.5.1 Right-censoring

A key concept in survival analysis is the idea of **right-censoring**, which refers to cases where the event of interest happens after the last observation point (or not at all). It's important that we identify these cases now so that we don't mistake them for women who first adopted a method during the month of the Phase 2 interview.

First, we'll want to identify the earliest month in which each woman reported using a method, if she did so at all. To do this, we'll begin by identifying months of contraceptive USE as those where FPSTATUS\_2 contains any value other than 0, B, P, or T.

```
nonusers <- nonusers %>% mutate(USE = !FPSTATUS_2 %in% c("0", "B", "P", "T"))  
  
nonusers
```

```
# A tibble: 116,948 × 8  
  ID COUNTRY    INTFQCMC_1 UNMETYN_1 FPPLANYR_1 FPSTATUS_2 CALCMC USE  
  <int> <fct>      <dbl> <lgl>     <lgl>     <chr>      <dbl> <lgl>  
1 1 Burkina Faso 1442 FALSE TRUE 3 1453 TRUE  
2 1 Burkina Faso 1442 FALSE TRUE 3 1452 TRUE  
3 1 Burkina Faso 1442 FALSE TRUE 3 1451 TRUE  
4 1 Burkina Faso 1442 FALSE TRUE 3 1450 TRUE  
5 1 Burkina Faso 1442 FALSE TRUE 3 1449 TRUE  
6 1 Burkina Faso 1442 FALSE TRUE 3 1448 TRUE  
7 1 Burkina Faso 1442 FALSE TRUE 0 1447 FALSE  
8 1 Burkina Faso 1442 FALSE TRUE 0 1446 FALSE  
9 1 Burkina Faso 1442 FALSE TRUE 0 1445 FALSE  
10 1 Burkina Faso 1442 FALSE TRUE 0 1444 FALSE  
11 1 Burkina Faso 1442 FALSE TRUE 0 1443 FALSE  
12 1 Burkina Faso 1442 FALSE TRUE 0 1442 FALSE  
13 2 Burkina Faso 1441 FALSE FALSE 5 1452 TRUE  
14 2 Burkina Faso 1441 FALSE FALSE 5 1451 TRUE  
15 2 Burkina Faso 1441 FALSE FALSE 5 1450 TRUE  
# ... with 116,933 more rows
```

Above, we can see that 6 months pass before the woman with ID == 1 adopts a method (code 3 for implant). However, some women *never* adopt a method before the Phase 2 interview. These cases are right-censored.

Ultimately, we'll want to include only one row for each woman in our analysis. For those who adopted a method, we'll need to find the earliest month of USE. For right-censored cases, we'll include only the month of the Phase 2 interview.

We begin by numbering each month in a variable call M0, counting upward from 0 for the Phase 1 interview. We'll then create an exact copy of M0 called USEM0 that is NA for months of non-USE.

```

nonusers <- nonusers %>%
  mutate(
    MO = CALCMC - INTFQCMC_1,
    USEMO = case_when(USE ~ MO)
  ) %>%
  select(-c(CALCMC, INTFQCMC_1))

```

nonusers

```

# A tibble: 116,948 × 8
  ID COUNTRY UNMETYN_1 FPPLANRYR_1 FPSTATUS_2 USE     MO USEMO
  <int> <fct>   <lgl>    <lgl>    <chr>    <lgl> <dbl> <dbl>
1 1 Burkina Faso FALSE TRUE     3 TRUE     11 11
2 1 Burkina Faso FALSE TRUE     3 TRUE     10 10
3 1 Burkina Faso FALSE TRUE     3 TRUE      9 9
4 1 Burkina Faso FALSE TRUE     3 TRUE      8 8
5 1 Burkina Faso FALSE TRUE     3 TRUE      7 7
6 1 Burkina Faso FALSE TRUE     3 TRUE      6 6
7 1 Burkina Faso FALSE TRUE     0 FALSE     5 NA
8 1 Burkina Faso FALSE TRUE     0 FALSE     4 NA
9 1 Burkina Faso FALSE TRUE     0 FALSE     3 NA
10 1 Burkina Faso FALSE TRUE     0 FALSE     2 NA
11 1 Burkina Faso FALSE TRUE     0 FALSE     1 NA
12 1 Burkina Faso FALSE TRUE     0 FALSE     0 NA
13 2 Burkina Faso FALSE FALSE     5 TRUE     11 11
14 2 Burkina Faso FALSE FALSE     5 TRUE     10 10
15 2 Burkina Faso FALSE FALSE     5 TRUE      9 9
# ... with 116,933 more rows

```

The minimum value in `USEMO` is the month of adoption, and we'll flag this month with a variable called `ADOPT`. However, if *no method was adopted* we'll need to flag the maximum value in `MO` with both `ADOPT` and an additional variable indicating that the case is right-censored. This final variable, which we'll call `RC`, helps functions in the `survival` package distinguish women who never adopted a method before Phase 2.

Finally, we'll now drop every row except for those matching `ADOPT`. This leaves one row for each woman in `nonusers`.

```

nonusers <- nonusers %>%
  group_by(ID) %>%
  mutate(
    ADOPT = ifelse(any(USE), min(USEMO, na.rm = T), max(MO)),
    RC = case_when(ADOPT == MO ~ !USE)
  ) %>%
  filter(ADOPT == MO)

```

nonusers

```
# A tibble: 9,213 × 10
# Groups:   ID [9,213]
  ID COUNTRY UNMETYN_1 FPPLAN_YR_1 FPSTA...¹ USE MO USEMO ADOPT RC
  <int> <fct>    <lgl>    <lgl>    <chr>  <lgl> <dbl> <dbl> <dbl> <lgl>
1     1 Burkina Faso FALSE    TRUE      3 TRUE     6     6     6 FALSE
2     2 Burkina Faso FALSE   FALSE      5 TRUE     3     3     3 FALSE
3     3 Burkina Faso FALSE   FALSE      0 FALSE    12    NA    12 TRUE
4     6 Burkina Faso FALSE   FALSE      0 FALSE    12    NA    12 TRUE
5     7 Burkina Faso FALSE   FALSE      0 FALSE    11    NA    11 TRUE
6     8 Burkina Faso TRUE    FALSE      0 FALSE    11    NA    11 TRUE
7    13 Burkina Faso FALSE   TRUE      5 TRUE     0     0     0 FALSE
8    16 Burkina Faso FALSE   FALSE      5 TRUE     8     8     8 FALSE
9    17 Burkina Faso FALSE   TRUE      0 FALSE    11    NA    11 TRUE
10   18 Burkina Faso FALSE   FALSE      0 FALSE    11    NA    11 TRUE
11   21 Burkina Faso FALSE   FALSE      0 FALSE    11    NA    11 TRUE
12   22 Burkina Faso FALSE   FALSE      0 FALSE    12    NA    12 TRUE
13   26 Burkina Faso FALSE   FALSE      0 FALSE    11    NA    11 TRUE
14   28 Burkina Faso FALSE   FALSE      0 FALSE    12    NA    12 TRUE
15   29 Burkina Faso FALSE   FALSE      0 FALSE    13    NA    13 TRUE
# ... with 9,198 more rows, and abbreviated variable name `¹FPSTATUS_2`
```

Above, only the women with IDs 1, 2, 13, and 16 ultimately adopted a method before Phase 2. All other visible cases are right-censored.

## 6.5.2 Survival Models

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, the function `survfit` reports the likelihood that a baseline non-user would have adopted any family planning method at 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.<sup>36</sup> Notice the function `Surv(M0, !RC)`: this indicates that the event of interest occurs in month `M0`, but only if the case is not right-censored `!RC`.

```
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",
    UNMETYN_1 & !FPPLANYR_1 ~ "Unmet Need, No Plan",
    !UNMETYN_1 & FPPLANYR_1 ~ "No Unmet Need, Plan",
    !UNMETYN_1 & !FPPLANYR_1 ~ "No Unmet Need, No Plan"
  )) %>%
  # 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 `CNTRY` for the figure
  mutate(across(where(is.list), ~map(.x, broom::tidy)))
```

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 `UNMETYN_1=FALSE` and `UNMETYN_1=TRUE` in the column labelled `strata`.

```
adopt_models %>%
  select(COUNTRY, unmet) %>%
  unnest(unmet) %>%
  filter(strata == "UNMETYN_1=FALSE") %>%
  select(-strata)
```

---

<sup>36</sup>`broom` is installed, but not loaded, with the `tidyverse`.

```
# A tibble: 59 × 9
# ... with 44 more rows, and abbreviated variable names `¹conf.high`, `²conf.low`
# ... with 44 more rows, and abbreviated variable names `¹conf.high`, `²conf.low`
```

COUNTRY	time	n.risk	n.event	n.censor	estimate	std.error	conf...¹	conf...²
<fct>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
1 Burkina Faso	0	2249	158	0	0.930	0.00580	0.940	0.919
2 Burkina Faso	1	2091	20	0	0.921	0.00618	0.932	0.910
3 Burkina Faso	2	2071	21	0	0.912	0.00657	0.923	0.900
4 Burkina Faso	3	2050	25	0	0.900	0.00701	0.913	0.888
5 Burkina Faso	4	2025	27	0	0.888	0.00747	0.902	0.875
6 Burkina Faso	5	1998	22	0	0.879	0.00784	0.892	0.865
7 Burkina Faso	6	1976	28	0	0.866	0.00829	0.880	0.852
8 Burkina Faso	7	1948	26	0	0.855	0.00870	0.869	0.840
9 Burkina Faso	8	1922	30	0	0.841	0.00916	0.857	0.826
10 Burkina Faso	9	1892	37	0	0.825	0.00972	0.841	0.809
11 Burkina Faso	10	1855	35	97	0.809	0.0102	0.826	0.793
12 Burkina Faso	11	1723	27	907	0.797	0.0107	0.813	0.780
13 Burkina Faso	12	789	5	687	0.792	0.0111	0.809	0.775
14 Burkina Faso	13	97	3	71	0.767	0.0212	0.800	0.736
15 Burkina Faso	14	23	0	23	0.767	0.0212	0.800	0.736

Among non-users who had no unmet need at Phase 1, the column `n.risk` shows the total number of women 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 2249 women in the Phase 1 Burkina Faso sample who were not using family planning and had no unmet need. Among these, `n.event` shows that 158 adopted a family planning method less than one month after the interview: this leaves 93.0% of the group remaining before one full month had passed.

Note that column `n.censor` shows the number of right-censored cases at each month in `time`. For example, 97 cases in Burkina Faso are right-censored after 10 months: these are the women interviewed in the earliest month of Phase 2 data collection (December 2020). 23 cases in Burkina Faso are right-censored after 14 months: these are women interviewed in the last month (April 2020).

Let's look at non-users who *did* have unmet need at Phase 1.

```
adopt_models %>%
  select(COUNTRY, unmet) %>%
  unnest(unmet) %>%
  filter(strata == "UNMETYN_1=TRUE") %>%
  select(-strata)
```

```
# A tibble: 58 × 9
# ... with 43 more rows, and abbreviated variable names `¹conf.high`, `²conf.low`
# ... with 43 more rows, and abbreviated variable names `¹conf.high`, `²conf.low`
```

COUNTRY	time	n.risk	n.event	n.censor	estimate	std.error	conf...¹	conf...²
<fct>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
1 Burkina Faso	0	632	86	0	0.864	0.0158	0.891	0.838
2 Burkina Faso	1	546	15	0	0.840	0.0173	0.869	0.812
3 Burkina Faso	2	531	6	0	0.831	0.0180	0.860	0.802
4 Burkina Faso	3	525	9	0	0.816	0.0189	0.847	0.787
5 Burkina Faso	4	516	6	0	0.807	0.0195	0.838	0.777
6 Burkina Faso	5	510	13	0	0.786	0.0207	0.819	0.755
7 Burkina Faso	6	497	11	0	0.769	0.0218	0.803	0.737
8 Burkina Faso	7	486	12	0	0.75	0.0230	0.785	0.717
9 Burkina Faso	8	474	11	0	0.733	0.0240	0.768	0.699
10 Burkina Faso	9	463	15	0	0.709	0.0255	0.745	0.674
11 Burkina Faso	10	448	8	21	0.696	0.0263	0.733	0.661
12 Burkina Faso	11	419	11	257	0.678	0.0275	0.715	0.642
13 Burkina Faso	12	151	1	135	0.673	0.0283	0.712	0.637
14 Burkina Faso	13	15	1	12	0.629	0.0746	0.727	0.543
15 Burkina Faso	14	2	0	2	0.629	0.0746	0.727	0.543

Here, we begin with 632 non-users who had unmet need at Phase 1. 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.

### 6.5.3 Data Visualization

We'll produce a Time-to-Event plot by inverting the probabilities reported in event and its accompanying confidence interval.<sup>37</sup> This plot uses `geom_step` to draw a step-wise function, and `geom_rect` to create a shaded confidence interval for each step.

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.

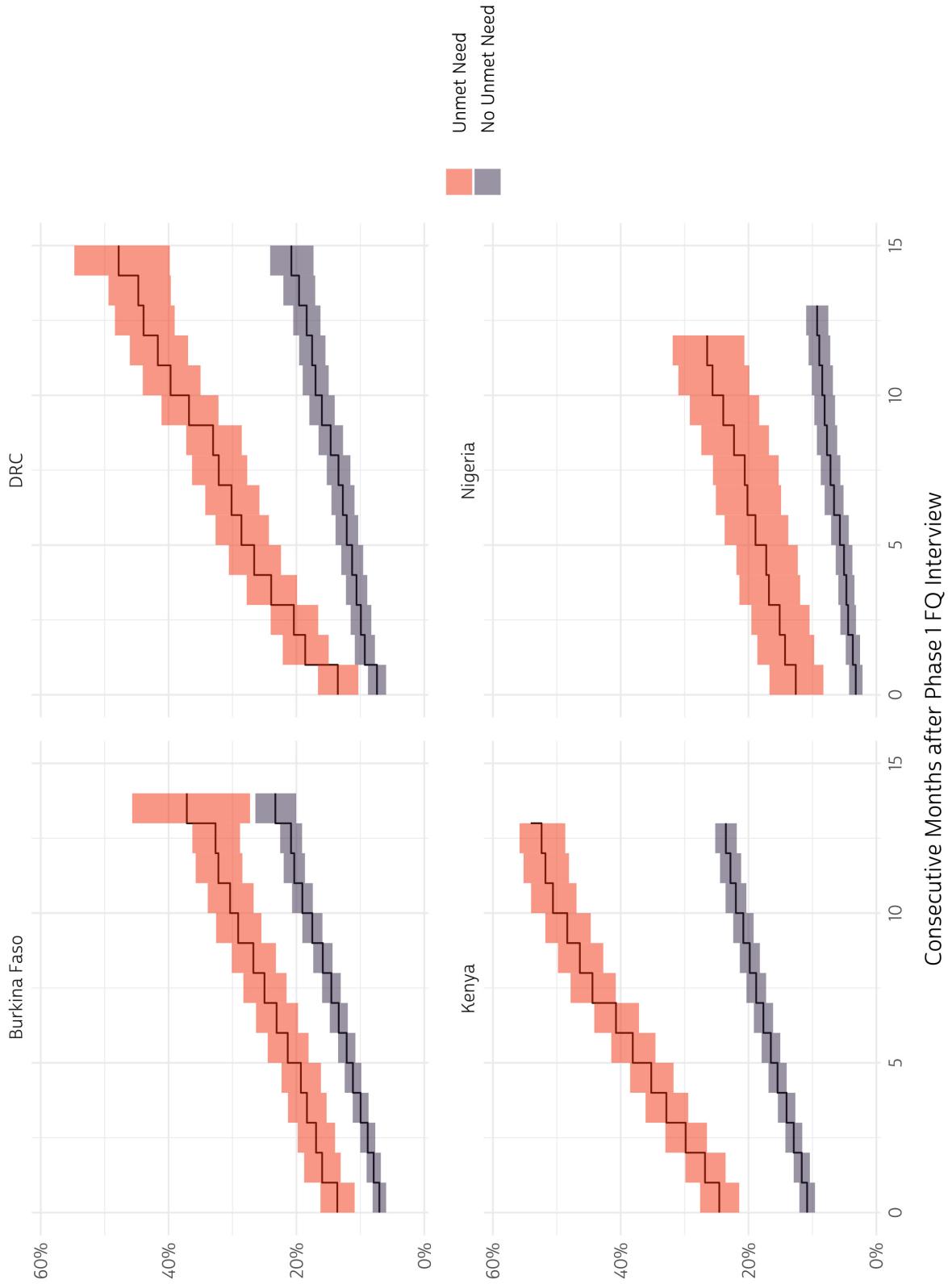
```
adopt_models %>%
  unnest(unmet) %>%
  group_by(COUNTRY, strata) %>%
  mutate(
    strata = if_else(strata %>% str_detect("TRUE"), "Unmet Need", "No Unmet Need"),
    across(where(is.double) & !time, ~1-.x),
    xmax = if_else(time == max(time), time, time + 1) # horizontal ci shading
  ) %>%
  ggplot(aes(x = 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"
  ) +
  theme_pma

# ggsave("images/km1.png", width = 11, height = 8.5, units = "in", bg = "white")
knitr::include_graphics("images/km1.png")
```

---

<sup>37</sup>The so-called “Time-to-Event” plot is an inverted case the Kaplan Meier curve, depicting increased risk over time rather than decreased survival. The same `survival` function can be used to produce either plot.

# Predicted Time to FP Adoption by Phase 1 Unmet Status



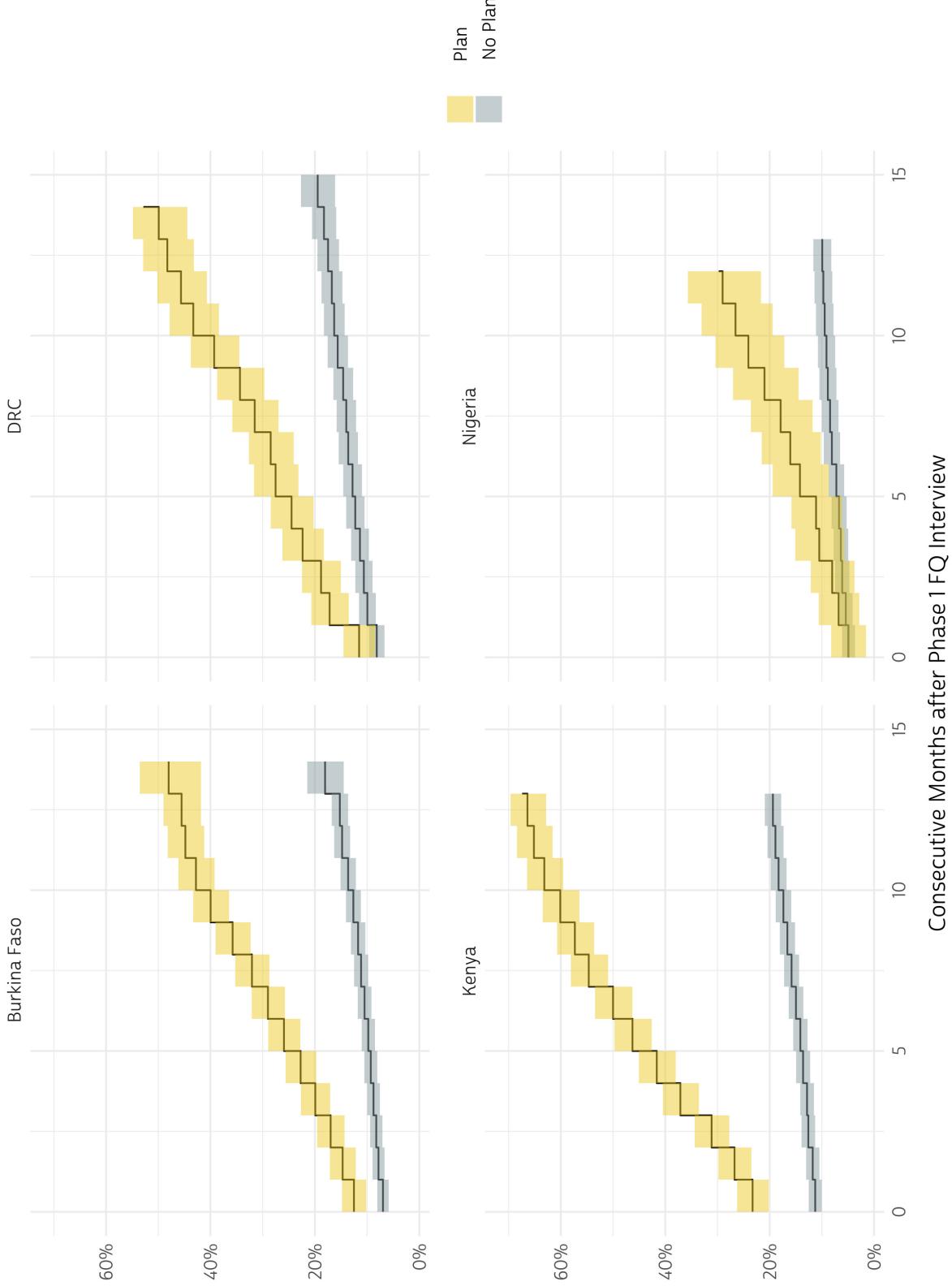
Let's now consider how the adoption rate might be influenced to by `FPPLAN1YR_1`.

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).

```
adopt_models %>%
  unnest(plan) %>%
  group_by(COUNTRY, strata) %>%
  mutate(
    strata = if_else(strata %>% str_detect("TRUE"), "Plan", "No Plan"),
    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("Plan" = "#EBCC2A", "No Plan" = "#899DA4")) +
  labs(
    title = "Predicted Time to FP Adoption by Intentions Within 1 Year of Phase 1",
    x = "Consecutive Months after Phase 1 FQ Interview"
  ) +
  theme_pma

# ggsave("images/km2.png", width = 11, height = 8.5, units = "in", bg = "white")
knitr:::include_graphics("images/km2.png")
```

# Predicted Time to FP Adoption by Intentions Within 1 Year of Phase 1



Finally, let's consider the interaction reported in INTERACT\_1.

The interaction between UNMETYN\_1 and FPPLANRYR\_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.

```
adopt_models %>%
  unnest(interact) %>%
  group_by(COUNTRY, strata) %>%
  mutate(
    strata = str_remove(strata, ".*="),
    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, Plan" = "#98579B",
    "Unmet Need, No Plan" = "#00263A",
    "No Unmet Need, Plan" = "#CCBA72",
    "No Unmet Need, No Plan" = "#81A88D"
  )) +
  labs(
    title = "Predicted Time to FP Adoption by Phase 1 Intentions and Unmet Need",
    x = "Consecutive Months after Phase 1 FQ Interview"
  ) +
  theme_pma

# ggsave("images/km3.png", width = 11, height = 8.5, units = "in", bg = "white")
knitr::include_graphics("images/km3.png")
```

# Predicted Time to FP Adoption by Phase 1 Intentions and Unmet Need

