Unmasking Seasonal Cycles in Human Fertility: How holiday sex and fertility cycles shape birth seasonality

Supplementary Materials

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This document contains additional text (Expanded Introduction, Results and Discussion), an overview of the Materials and Methods and the pdf-rendering of all analyses performed for the manuscript "Unmasking Seasonal Cycles in Human Fertility: How holiday sex and fertility cycles shape birth seasonality". The R markdown (.Rmd) files used to generate this pdf can be found on github (https://github.com/lasy/Seasonality-Public-Repo). Each section is a standalone Rmd file and can be run separately. The data for each section is available on the same github repository except for the sections "App data processing and filtering" and "App data aggregation" as the raw App data cannot be shared publicly to respect users' privacy and data ownership.

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Expanded Introduction

While only a few studies of birth seasonality have focused on countries outside of the Northern Hemisphere, the most extensive study to date revealed that throughout the 20th Century, births were highly heterogeneous in terms of amplitude and timing of the birth peak worldwide (*1–3*). In the Northern Hemisphere, there is a latitudinal gradient in the timing of the birth peak, with Northern countries having their peak earlier in the year compared to countries closer to the equator (*1*, *4*). In terms of birth amplitude, one study of countries in Sub-Saharan Africa found that modern-day birth seasonality in Guinea, Sierra Leone, Ivory Coast, and Nigeria ranged from 37-55%, relative to the mean; representing a three times higher amplitude than in the US (*4*, *5*). If birth seasonality has a tendency to be higher amplitude in the Southern Hemisphere (*5*, *6*), this may be due to environmental factors including more connection to the natural environment, less reliance on artificial light and time spent indoors, and/or limited ability to statistically detect seasonal patterns in Northern Hemisphere countries where populations typically have fewer births per year.

Expanded Results

Sexual Activity.

Time series analysis of the app (Fig 1b) data revealed striking increases in sexual activity on weekends and around holidays for all countries taken together (Fig 1c) and each country uniquely with respect to local holidays (Suppl. Figs. 21-26,78).

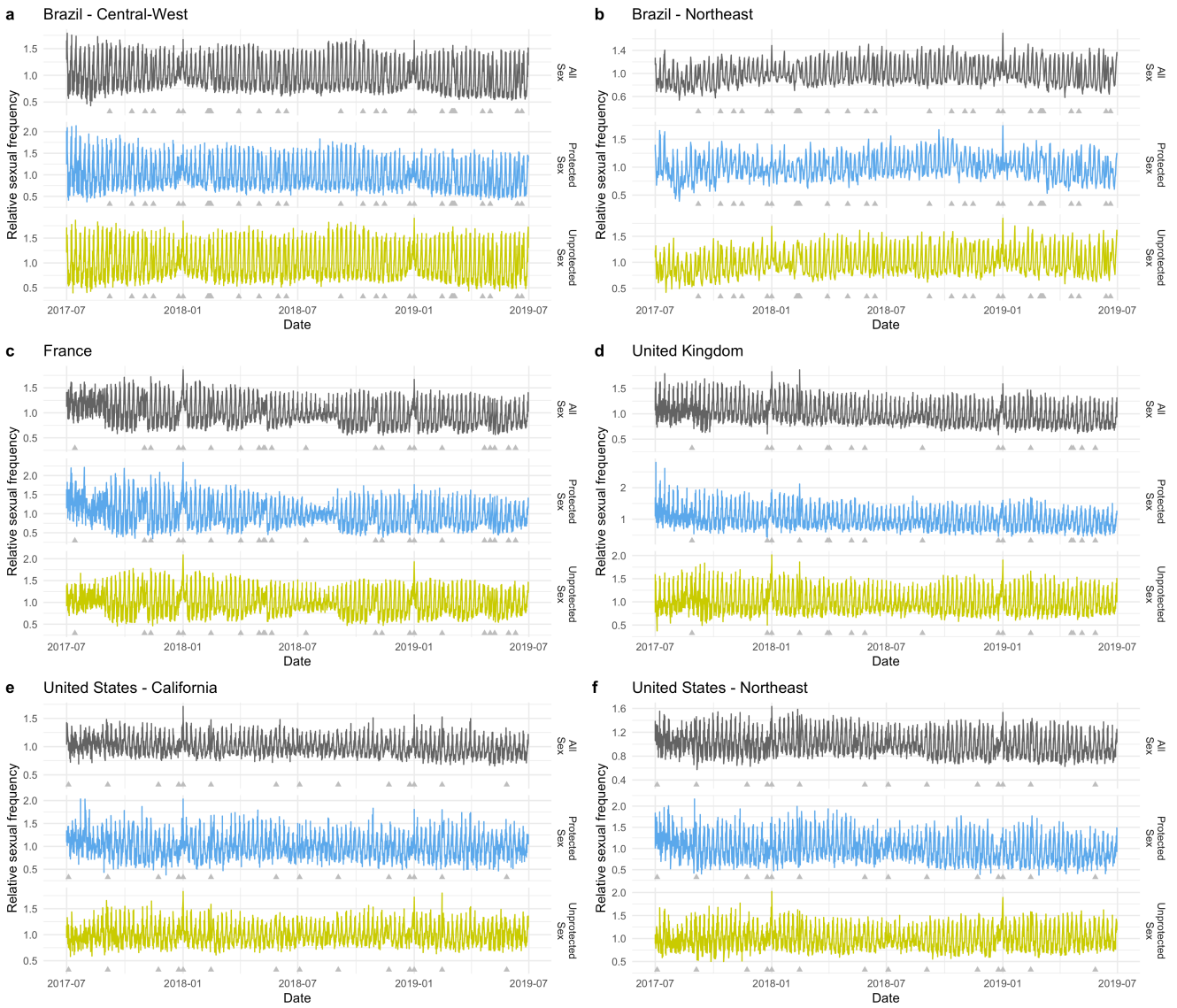


Figure 1: Time-series of the relative sexual activity for each study location and sex type (protected, unprotected, all). Gray triangles indicate local holidays.

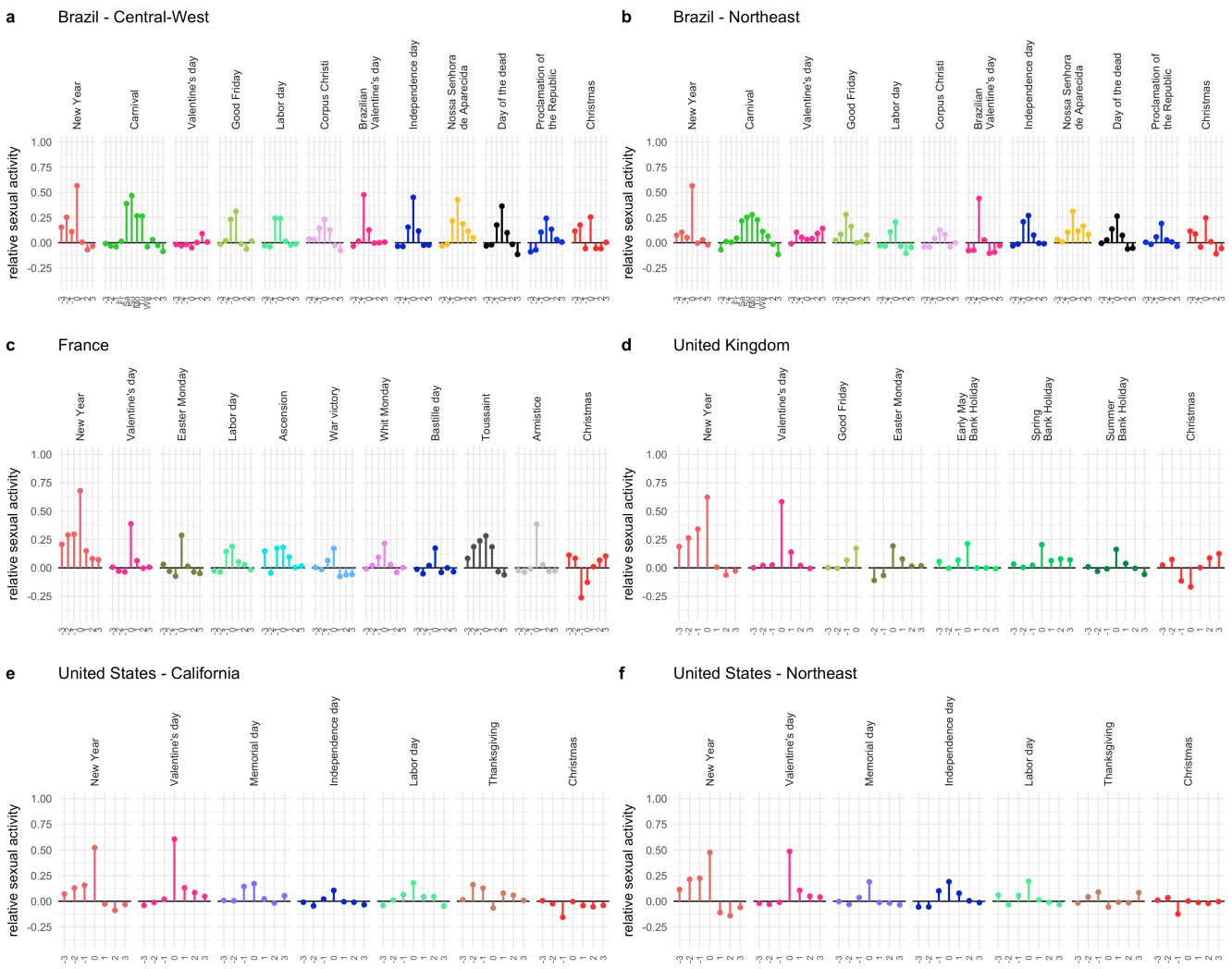


Figure 2: Relative sexual activity on and around local holidays for each study location.

The increased sexual activity on New Year was comparable to the increase in sexual activity measured in Brazil during Carnival and Valentine's Day in the US and UK. Brazil was the country in which sexual activity was consistently higher around holidays whereas, France, the US, and UK had much more variation in sexual activity among holidays. One pattern consistent among countries was decreased sexual activity in the three days before Christmas, which was followed by elevated sexual activity on Christmas and the three days after.

For France, we also observed higher sexual activity in the summer months, July and August, due to increases in weekday sexual activity in these months. A smaller increase in weekday sexual activity was also observed in the UK (Suppl. Fig. 4.17-18). We ensured the variation in sexual activity measured here was not a statistical artifact of app tracking fidelity due to individuals tracking more on weekends, holidays, and during the summer. We controlled for tracking frequency by contrasting the sexual frequency with other reported features such as exercise, long sleep (>9 hr sleep duration), breast pain, and menstrual bleeding. If the weekend effect were a statistical artifact, all features would be elevated on weekends. On weekends we observed that exercise was reduced, long sleep was reported more often, and there was no weekend effect on breast pain or bleeding (Suppl. Fig 5.1-5.6).

Mathematical Model.

In general, birth seasonality had a unique shape in each location. Some locations, like Brazil, had a distinct major peak and a minor peak (i.e., shoulder during the downswing). Other locations had more complex seasonal shapes. France and the UK had similar high frequency oscillations, with the major peak centered in the summer and punctuated by increases in Jan/Feb, July, and September. Seasonal births had the simplest shape in the US,

and were distinct for each location. California birth seasonality had a strikingly narrow peak, triangular in shape; while, the Northeastern US had a shallower upswing and a plateau at top, followed by a sharp decrease. Despite these location differences, these patterns are very consistent from year to year for a given location (Suppl. Fig. 70-75).

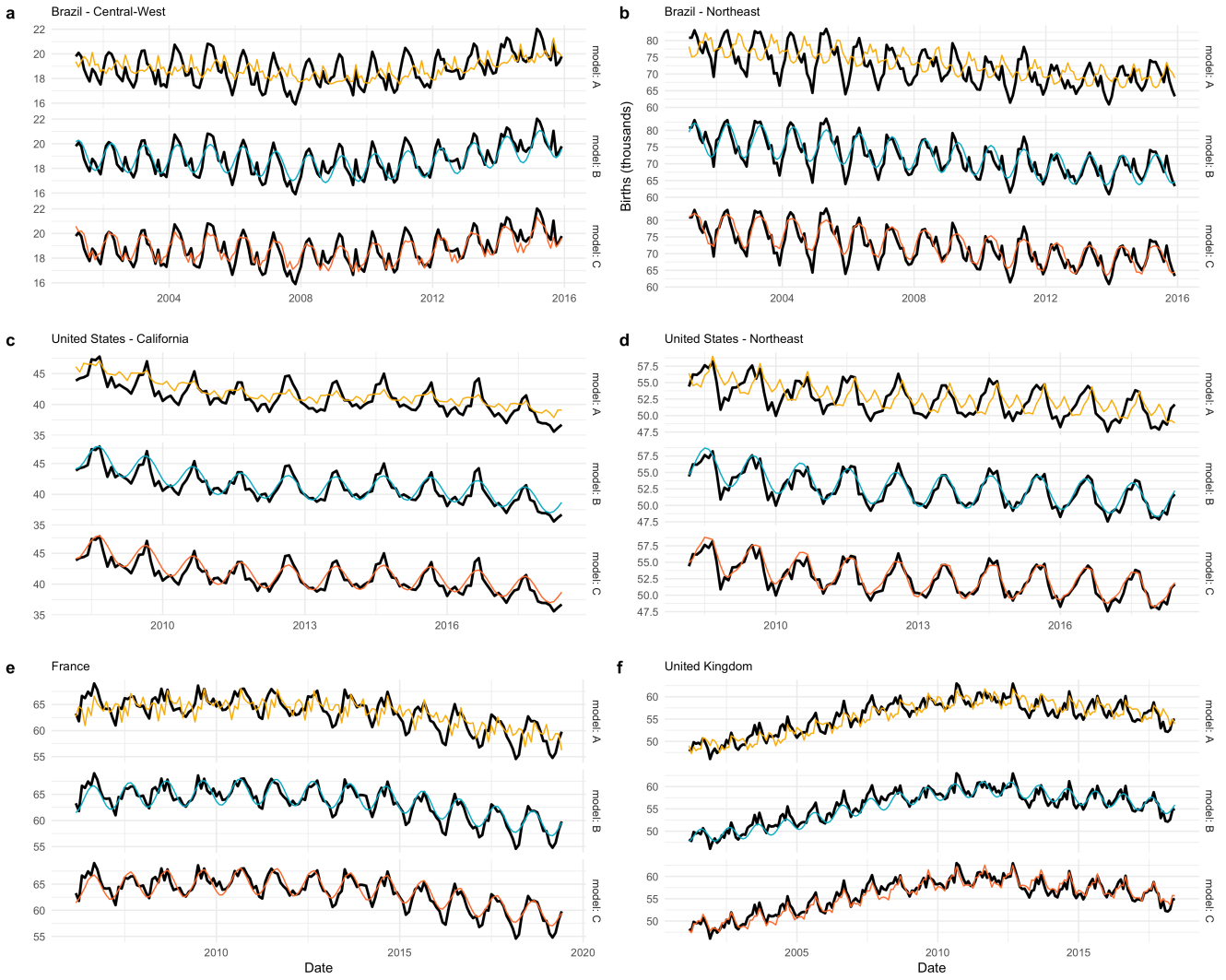


Figure 3: Time-series of births and simulated births with our three models for each location.

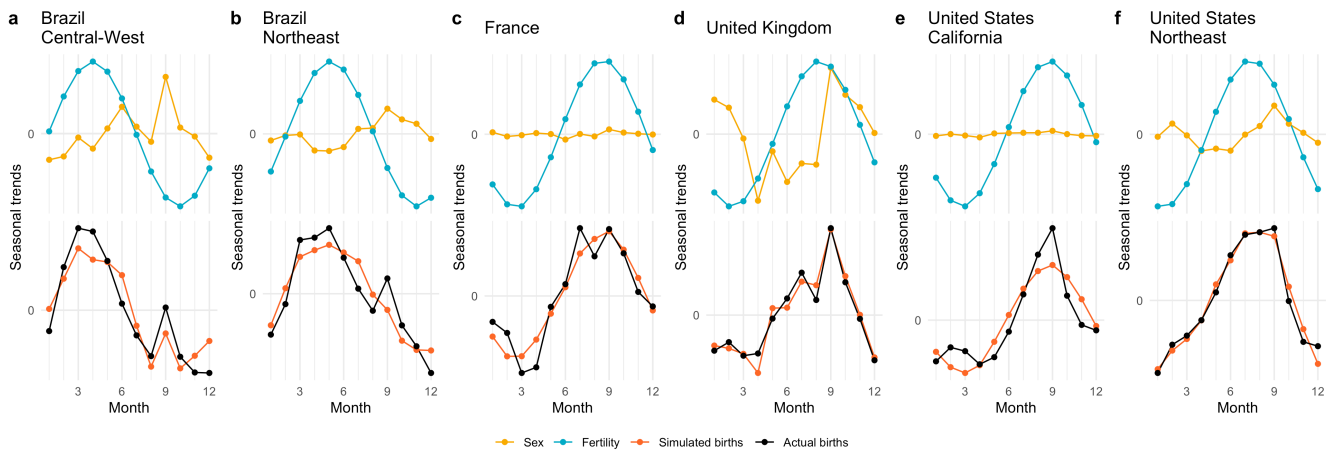


Figure 4: Relative contribution of sexual activity and fertility to the births seasonal trends for each location (output of model C).

In Brazil, the inclusion of seasonal/holiday sexual activity allowed Model C to capture the distinct shape of the major and minor peaks. The major peak in Brazil is driven by seasonal fertility, while the minor peak is driven by sexual activity surrounding the New Year holiday (Fig 3b & c). In the UK, seasonal fertility explains the overall seasonal pattern of births; but the September spike is driven by the New Year holiday. In the US Northeast, sexual activity allowed Model C to capture the non-sinusoidal peak and sharp decline in births after September. In France and California, however, Model C was penalized by the addition of seasonal sexual activity, because holiday sexual activity does not seem to result in elevated birth rates in these countries. Model results were robust to the type of sex (i.e., total sex, protected sex, and unprotected, see Supplementary Materials).

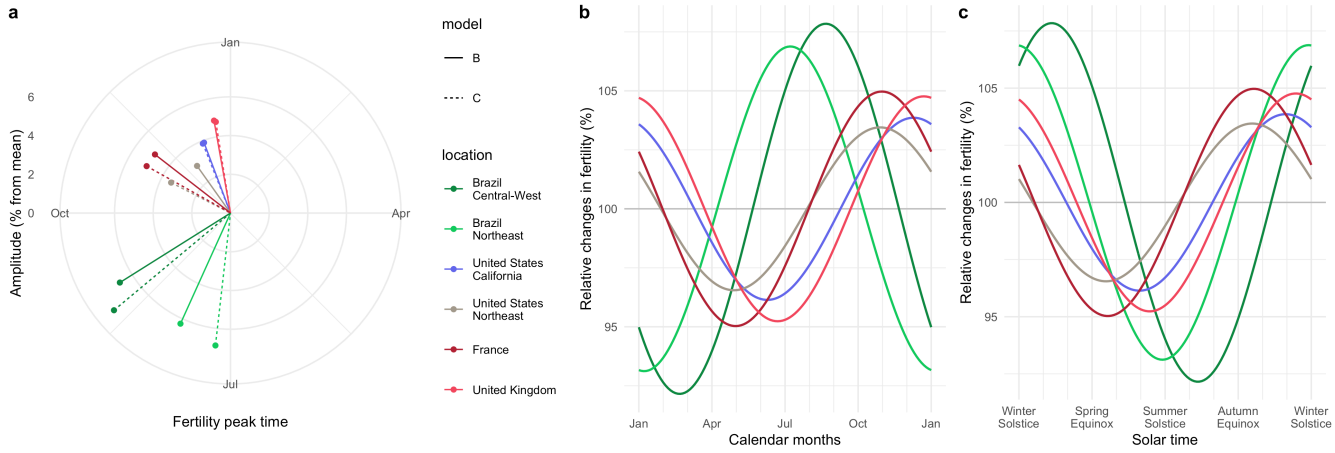


Figure 5: Fertility peak time and amplitude.(a) Polar plot of fertility peak time (calendar year) and amplitude; (b) Fertility curves for each location and (c) Fertility curves for each location relative to the solar time (equinoxes and solstices).

As for amplitude, the locations fell into three general categories of low, intermediate, and high amplitude seasonal fertility. The UK and France had the lowest amplitude seasonal fertility (half peak-trough difference < 4%). California and the Northeastern US had intermediate amplitude (< 6%) and Brazil had the highest amplitude (~8%). Although these are relatively low-amplitude fluctuations, compared to birth seasonality observed in some parts of the world, seasonal fertility is operating at a population-scale resulting in substantial differences in the number of births. In the lowest amplitude countries, UK and France, seasonal fertility results in roughly 3000-4000 more births in peak versus trough months (Fig. 3).

Expanded Discussion

Study Limitations

One limitation of our sexual activity data is that it originates from a self-selected, potentially biased population of app users that are typically young females. Data presented herein are aggregated over all age groups, all birth control types, and for unprotected sex, but our conclusions are robust to stratification by age and birth control use/type (see Supplementary Table 10). Our users consisted of individuals born between 1965-2004. While the demographics of menstrual app users may differ from those of the general population, smartphone ownership is likely a negligible source of bias in our data. Smartphone ownership rates among reproductive-age individuals are high in all locations studied, ranging from 85% in Brazil to 97% in France (*7*). Thus, our sample may offer a good approximation of sexual activity. Another limitation was that our data only covered two years. Thus, we could not fully quantify interactions between day-of-week and individual holidays; however, we were able to account for shifting holiday dates, such as Easter and Carnival, which differ by several weeks each year (Supplementary Fig 4.50). An interesting extension of this work would be to also include countries with different national holidays outside of the Judeo-Christian calendar. Within the countries we studied, one could also explore the effect of holidays that are not on the national calendar, such as Jewish, Muslim and Hindu holidays, that are celebrated by an increasing proportion of the population.

Material and Methods: summary

We tested three hypotheses on birth seasonality by using sexual activity data collected from over 500,000 individuals, representing 180 million days of active tracking data. The data were collected from Clue, a women's health mobile phone app (Fig 1b, main text). Data was de-identified, users were informed that their data may be shared for scientific research and they may opt-out while still using the app. Since the app is specifically built for menstrual cycle tracking, we assume all users are female or menstruating individuals. We used data from individuals residing in the United States, United Kingdom, France, and Brazil, that represent a geographically and culturally diverse set of countries with a high number of users. We also collated time series of births for each country. Due to the size of the US and Brazil, US data were focused on two regions, California, which is a Western state, and the Northeast CDC Census Region, which includes 9 states on the Northeast Coast. Similarly, in Brazil, we focused on two culturally and geographically distinct Regions, the Central-West region, which includes the capital Brasilia, and the Northeast, which is on the Northern Atlantic Coast. Overall, we had six geographic locations for all analyses: UK, France, Central-West Brazil, Northeast Brazil, California, and the Northeastern U.S (Fig 1a, main text). The following are numbers of Clue users by location: UK (n = 133,387), France (n = 126,634), Central-West Brazil (n = 160,896), Northeast Brazil (n = 23,127), California (n = 39,330) and the Northeastern US (n = 51,780). Data were combined with mathematical models developed explicitly to test our hypotheses.

Clue Data

De-identified individual-level daily records were obtained from n = 535,154 Clue users. Each individual self-reported some combination of sexual activity, contraception use, menstruation and other sexual and reproductive health indicators daily. As with all tracking apps, however, there was variation in the fidelity with which users tracked. Overall, we obtained n = 55,110,476 daily records from July 2017- July 2019, representing a period of 180 million days of active tracking. Due to changes in tracking fidelity, we used a rolling window to identify periods of active tracking for each individual. Sexual activity was reported as three types: protected, unprotected or withdrawal sex.

For each geographic location and sex type, aggregated time-series of daily sexual activity were constructed. These time series represented the daily sex rate in the population as defined by the fraction of active users reporting a specific type of sex. Because these data are not ideal for estimating the absolute amount of sexual activity in a population (i.e., due to biases in app user demographics and variation in tracking fidelity), we computed the relative sexual activity by dividing the sex counts by the number of users that opened the app on each day (Fig 1c, main text). This allowed us to focus on variation around the mean, particularly variation tied to day-of-week, holidays, and seasons.

To infer how sexual activity is impacted by holidays, weekends, and season, we fitted a statistical model to our data to measure relative sexual activity. This model allowed us to predict sexual activity for any location and any given calendar day in the year, based on the day-of-week, month, and its proximity to a local holiday (Fig 2, main text). Due to the large sample size, we were able to fit this statistical model for all combinations of sex type as well as birth control categories (e.g., contraceptive pills, condoms, etc.) (see section 4.3.2). Since sexual activity was similar among groupings, here we present results based on unprotected sex reported by users of any age and any birth control category.

Our model was structured as follows: $\text{sex}[i,j] = \alpha_i\, \text{h}[i] + \beta_j\, \text{wdm}[j]$ where each 365 days of the year is defined by a specific combination of i and j. The first term represents the contribution of a specific holiday to sexual activity and the second term represents the contribution of weekday and month. Each holiday has its own coefficient because we did not want to assume that all holidays lead to the same increase or decrease in sexual activity. We assumed all holidays included in our models have a day off, with the exception of Valentine's Day and the Dia dos Namorados (i.e., Brazilian Valentine's Day). For holidays with a day off, we estimated a fixed amount of sexual activity in the first term and set the second term to its intercept value. Whereas, for Valentine's and Dia dos Namorados, relative sexual activity was estimated as the sum of the holiday contribution combined with the weekday and month effect. This accounted for the fact that these holidays fall on different days-of-the-week each year and don't lead to a day off. In addition, we assumed there are three days off before and after Christmas and New Year and estimated a fixed amount of sexual activity on these days. Refer to section 4.3.2 for the holiday dichotomy (i.e., holiday categorization based on whether each holiday results in a day off of work/school).

Birth Data

Time series of monthly live births were obtained for each geographical area. The US data were obtained from the CDC Wonder database, and span 2007 to 2018. Brazilian birth data were obtained from DATASUS and span the years 2000-2016. UK data are from the Office of National Statistics and span 2000-2018; while data from France were retrieved from the INSEE database for years 2005-2019. Due to variation in the number of days per calendar month, the time series were standardized to represent a typical 30-day month. We did this to ensure that seasonality in the time series was not an artifact of variation in days per month.

Mathematical Models

We translated each of the three birth seasonality hypotheses into a deterministic population-level mathematical model of conception and birth (Fig 3a, main text). In each model, daily conceptions were modeled as the product of daily sexual activity and daily fertility. Daily conception was then used to predict daily births (approx. 9 months into the future) using empirical distributions of gestation period for each country (Suppl. Fig. 17). We searched existing literature for data on the mean gestation periods.(*8–10*) Since the time series of births were monthly totals, we then aggregated simulated daily births to monthly. Parameters of each model were estimated by minimizing the sum of squared errors between simulations and data. For each model we calculated the likelihood and the AIC that includes a penalty for additional parameters. We then discriminated among models using AIC; depending on assumptions regarding seasonal fertility, models differed in parameters estimated.

Model A assumed variation in sexual activity entered as a time-varying variable in the model and constant fertility (Fig 3a, main text). The time-series of daily sexual activity were output from our statistical model fitted to the app data. Model B assumed constant sexual activity and seasonal variation in fertility expressed as a sinusoidal function with a period of 1 year (Fig 3a, main text). The phase and amplitude of this function was estimated for each geographical area. Model C assumed variation in both sexual activity and fertility (Fig 3a, main text), with seasonal sexual activity entered as a time-varying variable. In Model C we added a scaling factor for sexual activity that allowed for changes in amplitude. The sexual activity scaling factor, along with the phase and amplitude of seasonal fertility, was estimated for each geographical location for Model C. Lastly, the mean daily conception rate was calculated based on the long-term trend in the birth time series.

1 Birth Official Records: data processing

Monthly birth records were acquired for each geographical area of interest from national statistics offices (see below for details and links for each country). Here, we format the collected data so that they can be collated into a single table with the following attributes: source, country, area, lat, lon, year, month, month_num, date, births.

1.1 Brazil birth data

1.1.1 Data source

Data were downloaded on Feb 21, 2018 from

http://www2.datasus.gov.br/DATASUS/index.php?area=0205

The dataset holds monthly births for each Brazilian state.

```
BR_birth = read_csv(file = str_c(IO$birth_records_dir,"Brazil_monthly_births_by_states_2000_2017.csv"),
                    col_types = cols(
                      year = col_double(),
                      location = col_character(),
                      month = col_character(),
                      month.number = col_double(),
                      births = col_double(),
                      location.type = col_character()
                    )
)
```

1.1.2 Data aggregation per regions and formatting

The areas defined below correspond to the official Brazilian Regions.

```
brazil.dict.list = list(
  "North" = c("Acre", "Amapá", "Amazonas", "Pará", "Rondônia", "Roraima", "Tocantins"),
  "Northeast" = c("Alagoas", "Bahia", "Ceará", "Maranhão", "Paraíba", "Pernambuco", "Piauí", "Rio Grande do Norte", "Sergipe"),
  "Central-West" = c("Goiás", "Mato Grosso", "Mato Grosso do Sul", "Distrito Federal" ),
  "Southeast" = c("Espírito Santo", "Minas Gerais", "Rio de Janeiro", "São Paulo"),
  "South" = c("Paraná", "Rio Grande do Sul", "Santa Catarina")
)

brazil.dict = data.frame(region = rep(names(brazil.dict.list), lengths(brazil.dict.list)),
                         states = unlist(brazil.dict.list),
                         stringsAsFactors = FALSE)

brazil.dict.geo = rbind(
  data.frame(region = "North", lat = -3.129167, lon = -60.021389),
  data.frame(region = "Northeast", lat = -12.966667, lon = -38.516667),
  data.frame(region = "Central-West", lat = -15.779722, lon = -47.930556 ),
  data.frame(region = "Southeast", lat = -23.55, lon = -46.633333 ),
  data.frame(region = "South", lat = -25.433333, lon = -49.266667)
)
```

```
BR_birth = BR_birth %>%  mutate(
  source = "svs.aids.gov.br",
  country = "Brazil",
  state = location,
  area = brazil.dict$region[match(location,brazil.dict$states)],
  month_num = month.number,
```

```
  month_short = month,
  month = months[month_num],
  date = as.Date(str_c(year,"-",month_num,"-01")),
  lat = brazil.dict.geo$lat[match(area, brazil.dict.geo$region)],
  lon = brazil.dict.geo$lon[match(area, brazil.dict.geo$region)]
)  %>%  dplyr::select(all_of(columns_from_each_source), state)


# save(BR_birth, file = paste0(IO$out_Rdata,"BR_birth_data_by_states.Rdata"))

# aggregate by area

BR_birth = BR_birth %>%
  group_by(source, country, area, lat, lon, year, month, month_num, date) %>%
  dplyr::summarize(births = sum(births), .groups = "drop")%>%
  dplyr::select(all_of(columns_from_each_source))

#save(BR_birth, file = paste0(IO$out_Rdata,"BR_birth_data.Rdata"))
```

1.2 US birth data

1.2.1 Data source

The US data per states were downloaded on Feb 20, 2020 from the CDC Wonder website:

https://wonder.cdc.gov/natality.html

The dataset holds monthly births for each American state.

```
US_birth = read_tsv(file = str_c(IO$birth_records_dir,"US_monthly_births_2007_2018.txt"),
                    col_types = cols(
                      notes = col_skip(),
                      state = col_character(),
                      state_code = col_skip(),
                      year = col_integer(),
                      year_code = col_skip(),
                      month = col_character(),
                      month_num = col_integer(),
                      births = col_integer()
                    ))
```

1.2.2 Data aggregation per regions and formatting

Areas defined below correspond to the US census regions, except for California, which is kept separate from the "West" region to match with the areas available in the Clue App dataset.

```
US.dict.list = list(
  "Northeast" = c("Connecticut", "Maine", "Massachusetts", "New Hampshire", "Rhode Island", "Vermont",
                  "New Jersey", "New York","Pennsylvania"),
  "Midwest" = c("Indiana","Illinois","Michigan","Ohio","Wisconsin",
                "Iowa","Kansas","Minnesota","Missouri","Nebraska","North Dakota","South Dakota"),
  "South" = c("Delaware", "District of Columbia", "Florida", "Georgia", "Maryland",
              "North Carolina", "South Carolina", "Virginia", "West Virginia",
              "Alabama","Kentucky","Mississippi","Tennessee",
              "Arkansas","Louisiana","Oklahoma","Texas"),
  "West - without California" = c("Arizona","Colorado","Idaho","New Mexico",
                                  "Montana","Utah","Nevada","Wyoming",
                                  "Alaska","Hawaii","Oregon","Washington"),
```

```
  "California" = c("California")
)

US.dict = data.frame(region = rep(names(US.dict.list), lengths(US.dict.list)),
                     states = unlist(US.dict.list),
                     stringsAsFactors = FALSE)

US.dict.geo = rbind(
  data.frame(region = "Northeast", lat = 42, lon = -73),
  data.frame(region = "Midwest", lat = 42, lon = -90),
  data.frame(region = "South", lat = 33, lon = -88 ),
  data.frame(region = "West - without California", lat = 40, lon = -113 ),
  data.frame(region = "California", lat = 37, lon = -120)
)
```

```
US_birth = US_birth %>%
  mutate(source = "CDC",
         country = "United States",
         date = as.Date(str_c(year,"-",month_num,"-01")),
         area = US.dict$region[match(state, US.dict$state)],
         lat = US.dict.geo$lat[match(area, US.dict.geo$region)],
         lon = US.dict.geo$lon[match(area, US.dict.geo$region)]) %>%
  dplyr::select(all_of(columns_from_each_source), state)


#save(US_birth, file = paste0(IO$out_Rdata,"US_birth_data_by_states.Rdata"))

# aggregate by area

US_birth =
  US_birth %>%
  group_by(source, country, area, lat, lon, year, month, month_num, date) %>%
  dplyr::summarize(births = sum(births)) %>%
  dplyr::select(all_of(columns_from_each_source))
```

```
## `summarise()` has grouped output by 'source', 'country', 'area', 'lat', 'lon', 'year', 'month', 'month_num'. You can override using the `.groups` argument.
```

```
#save(US_birth, file = paste0(IO$out_Rdata,"US_birth_data.Rdata"))
```

1.3 UK birth data

1.3.1 Data source

UK data were downloaded in April 2020 from

https://www.ons.gov.uk/peoplepopulationandcommunity/birthsdeathsandmarriages/livebirths/datasets/birthcharacteristicsinenglandandwales

The dataset holds monthly data for England and Wales from 2000 to 2018.

```
UK_birth = read_csv(file = str_c(IO$birth_records_dir,"UK_monthly_births_england_and_wales.csv"),
                    col_types = cols(
                      Year = col_double(),
                      Total = col_number(),
                      January = col_number(),
                      February = col_number(),
                      March = col_number(),
                      April = col_number(),
                      May = col_number(),
                      June = col_number(),
```

```
                July = col_number(),
                August = col_number(),
                September = col_number(),
                October = col_number(),
                November = col_number(),
                December = col_number()
              ))
```

1.3.2 Data processing

```
UK_birth = UK_birth %>% select(-Total) %>% pivot_longer(cols = -Year, names_to = "Month",values_to = "births")

UK_birth = UK_birth %>% mutate(
  source = "ons.gov.uk",
  country = "United Kingdom",
  area = "",
  lat = 52,
  lon = -1,
  year = Year,
  month = Month,
  month_num =  match(Month,levels(month(1:12, label = TRUE, abbr = FALSE))),
  date = as.Date(str_c(year,"-",month_num,"-01"))
) %>%  select(all_of(columns_from_each_source))


#save(UK_birth, file = paste0(IO$out_Rdata,"UK_birth_data.Rdata"))
```

1.4 France birth data

1.4.1 Data source

The France births data were downloaded in April 2020 from the INSEE data portal (https://www.insee.fr/fr/statistiques/serie/000436391?idbank=000436391#Telechargement)

The dataset holds monthly births.

```
FR_birth = read_delim(file = str_c(IO$birth_records_dir,"France_birth_data.csv"), delim = ";",
                col_types = cols(
                  month = col_character(),
                  births = col_double(),
                  code = col_character()
                ))
```

1.4.2 Data processing

```
FR_birth = FR_birth %>%
  rename(date_month_chr = month)%>%
  mutate(
    source = "INSEE",
    country = "France",
    area = "",
    lat = 46.62012,
    lon = 2.452757,
    year = str_sub(date_month_chr, 1, 4) %>% as.numeric(),
    month_num =  str_sub(date_month_chr, 6, 7) %>% as.numeric(),
```

```
    month = months[month_num],
    date = as.Date(str_c(year,"-",month_num,"-01"))
  ) %>%
  select(all_of(columns_from_each_source)) %>%
  arrange(year, month_num)

#save(FR_birth, file = paste0(IO$out_Rdata,"FR_birth_data.Rdata"))
```

1.5 Collating datasets

```
birth = bind_rows(
  BR_birth,
  US_birth,
  UK_birth,
  FR_birth
)

# add country_area + arrange country by latitude (North to South)
birth = birth %>%
  ungroup() %>%
  dplyr::mutate(country_area = str_c(country, ifelse(area == "","",str_c(" - ",area)))) %>%
  arrange(desc(lat), country, year, month_num) %>%
  dplyr::mutate(country = factor(country))

save(birth, file = "../Data/2_births_processed/birth_data.Rdata")
write_csv(birth, file = "../Data/2_births_processed/birth_data.csv")
```

```
birth_summary = birth %>%
  group_by(source, country, country_area) %>%
  summarize(start_date = min(date),
            end_date = max(date),
            n = n()) %>%
  arrange(country) %>%
  as.data.frame()
```

```
## `summarise()` has grouped output by 'source', 'country'. You can override using the `.groups` argument.
```

```
kable(birth_summary, format = "pandoc", caption = "Summary of the official birth record dataset. 'n' is the number of data-point, i.e. of monthly birth record for each location.
```

Table 1: Summary of the official birth record dataset. 'n' is the number of data-point, i.e. of monthly birth record for each location.

source	country	country_area	start_date	end_date	n
svs.aids.gov.br	Brazil	Brazil - Central-West	2000-01-01	2016-06-01	198
svs.aids.gov.br	Brazil	Brazil - North	2000-01-01	2016-06-01	198
svs.aids.gov.br	Brazil	Brazil - Northeast	2000-01-01	2016-06-01	198
svs.aids.gov.br	Brazil	Brazil - South	2000-01-01	2016-06-01	198
svs.aids.gov.br	Brazil	Brazil - Southeast	2000-01-01	2016-06-01	198
INSEE	France	France	2005-01-01	2019-12-01	180
ons.gov.uk	United Kingdom	United Kingdom	2000-01-01	2018-12-01	228
CDC	United States	United States - California	2007-01-01	2018-12-01	144
CDC	United States	United States - Midwest	2007-01-01	2018-12-01	144
CDC	United States	United States - Northeast	2007-01-01	2018-12-01	144
CDC	United States	United States - South	2007-01-01	2018-12-01	144
CDC	United States	United States - West - without California	2007-01-01	2018-12-01	144

2 App (Clue) data processing and filtering

Please note: Due to data privacy and ownership regulations, the raw data provided by Clue is not publicly available. The processed and aggregated data, result of this section and the next one, is provided on the github repository (https://github.com/lasy/Seasonality-Public-Repo) within ../Data/4_clue_data_aggregated, such that subsequent analyses (i.e., after section 3.9) can be reproduced.

2.1 Dataset structure

The Clue dataset was provided in four tables:

- users: basic demographic information about the users.
- birth_control: users' birth control method as self-reported by users in their app profile. The table holds the type of birth control and the date at which they changed this option if they changed it. If they did not change their birth control in their app profile, the table provides the birth control self-reported by users when their first registered their app profile.
- cycles : cycles starts and ends. Provided in 20 files to keep each file at a reasonable size.
- tracking : time-series of the features tracked by the users. Provided in 20 files to keep each file at a reasonable size.

These tables were provided by Clue in csv files and we transformed into feather files (see package feather) to accelerate reading/writing operations.

2.2 Filtering for countries/areas of interest.

Each of the four tables are filtered so that they only contain the data for users of the six countries/areas of interest:

Brazil - Central-West, Brazil - Northeast, United States - California, United States - Northeast, France, United Kingdom

```
subset_folder = paste0(IO$r_Data,"Clue_US_BR_EU/input/")
if(!dir.exists(subset_folder)){dir.create(subset_folder, recursive = TRUE)}
```

```
selected_country_areas = dict$country_area$country_area
```

Filtering users table

```
users = read_feather(path = paste0(IO$r_Data,"Clue/input/users.feather"))
n_users_tot = nrow(users)


users = users %>% filter(country_area %in% selected_country_areas)
n_users_selected = nrow(users)

n_users_tot
```

```
## [1] 1256541
```

```
n_users_selected
```

```
## [1] 535154
```

```
(n_users_selected/n_users_tot) %>% round(.,2)
```

```
## [1] 0.43
```

```
write_feather(users, path = paste0(subset_folder, "users.feather"))
```

Filtering birth control table

```
BC = read_feather(path = paste0(IO$r_Data,"Clue/input/birth_control.feather"))
dim(BC)
```

```
## [1] 1474662       6
```

```
BC = BC %>% filter(user_id %in% users$user_id)
dim(BC)
```

```
## [1] 653452      6
```

```
write_feather(BC, path = paste0(subset_folder, "birth_control.feather"))
```

Filtering cycles table

```
input_folder = paste0(IO$r_Data,"Clue/input/cycles/")
files = list.files(input_folder)

output_folder = paste0(subset_folder, "cycles/")
if(!dir.exists(output_folder)){dir.create(output_folder)}

ok = foreach(file = files) %do% {
  cat(file %>% str_remove(.,"cycles00") %>%  str_remove(.,".feather")," | ")
  cycle = read_feather(path = str_c(input_folder,file))
  dim(cycle)
  cycle = cycle %>% filter(user_id %in% users$user_id)
  dim(cycle)
  write_feather(cycle, path = paste0(output_folder, file))
}
```

```
## 00  | 01  | 02  | 03  | 04  | 05  | 06  | 07  | 08  | 09  | 10  | 11  | 12  | 13  | 14  | 15  | 16  | 17  | 18  | 19  |
```

Filtering tracking table

```
input_folder = paste0(IO$r_Data,"Clue/input/tracking/")
files = list.files(input_folder)

output_folder = paste0(subset_folder, "tracking/")
if(!dir.exists(output_folder)){

  dir.create(output_folder)

  ok = foreach(file = files) %do% {
    cat(file,"\n")
    tracking = read_feather(path = str_c(input_folder,file))
    dim(tracking)
    tracking = tracking %>% filter(user_id %in% users$user_id)
    dim(tracking)
    write_feather(tracking, path = paste0(output_folder, file))
  }

}else{warning("Clue data: tracking table files filtered for country_area already existed. Filtering was NOT done at this execution.")}
```

```
## Warning: Clue data: tracking table files filtered for country_area already
## existed. Filtering was NOT done at this execution.
```

2.3 Dataset overview

User table

```
users = read_feather(path = paste0(IO$input_clue,"users.feather"))
```

The users table has 535154 rows (*i.e.* users) and 7 columns: user_id, birth_year_bin, country_area, height_bin, weight_bin, latest_birth_control, csv_file

```
df = table(country_area = users$country_area) %>% sort(decreasing = TRUE) %>% as.data.frame()
knitr::kable(df, format = "pandoc", caption = "Total number of app users in each area.")
```

Table 2: Total number of app users in each area.

country_area	Freq
Brazil - Central-West	160896
United Kingdom	133387
France	126634
United States - Northeast	51780
United States - California	39330
Brazil - Northeast	23127

```
df = df %>%  mutate(
  country_area_col = dict$country_area$country_area_col[match(country_area, dict$country_area$country_area)],
  country_area_wrapped = str_replace(country_area," - ","\n") %>% factor(.,levels = str_replace(dict$country_area$country_area," - ","\n"))
)
ggplot(df, aes(x = country_area_wrapped, y = Freq, fill = country_area_col))+
  geom_bar(stat = "identity")+
  xlab("")+ylab("Total # of users")+
  scale_fill_identity()
```

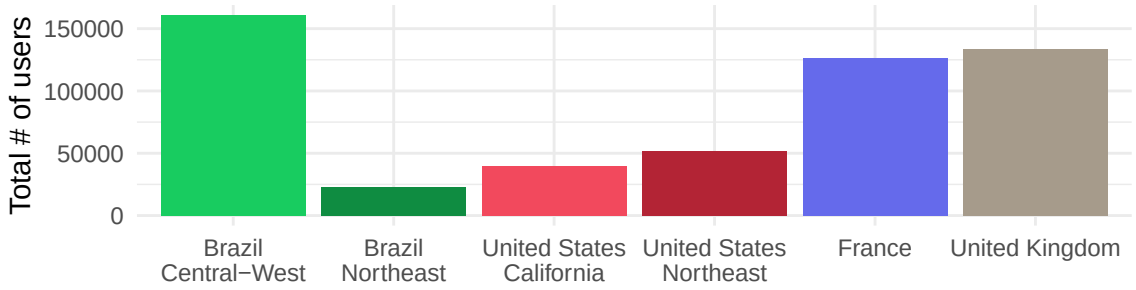


Figure 6: Total number of users in each considered area

```
kable(table(birth_year_bin = users$birth_year_bin) %>% as.data.frame(),
    format = "pandoc", caption = "Total number of app users in each birth year bin")
```

Table 3: Total number of app users in each birth year bin

birth_year_bin	Freq
1965-1969	138
1970-1974	4108
1975-1979	11335
1980-1984	26346
1985-1989	56642
1990-1994	97890
1995-1999	203964
2000-2004	134731

Birth control table

```
birth_control = read_feather(path = paste0(IO$input_clue,"birth_control.feather"))
```

The birth control table (birth_control) has 653452 rows (i.e. birth control at on-boarding and changes in birth control as declared by the users in their app profile) and 6 columns:

user_id, date, birth_control, pill_type, pill_regiment, csv_file

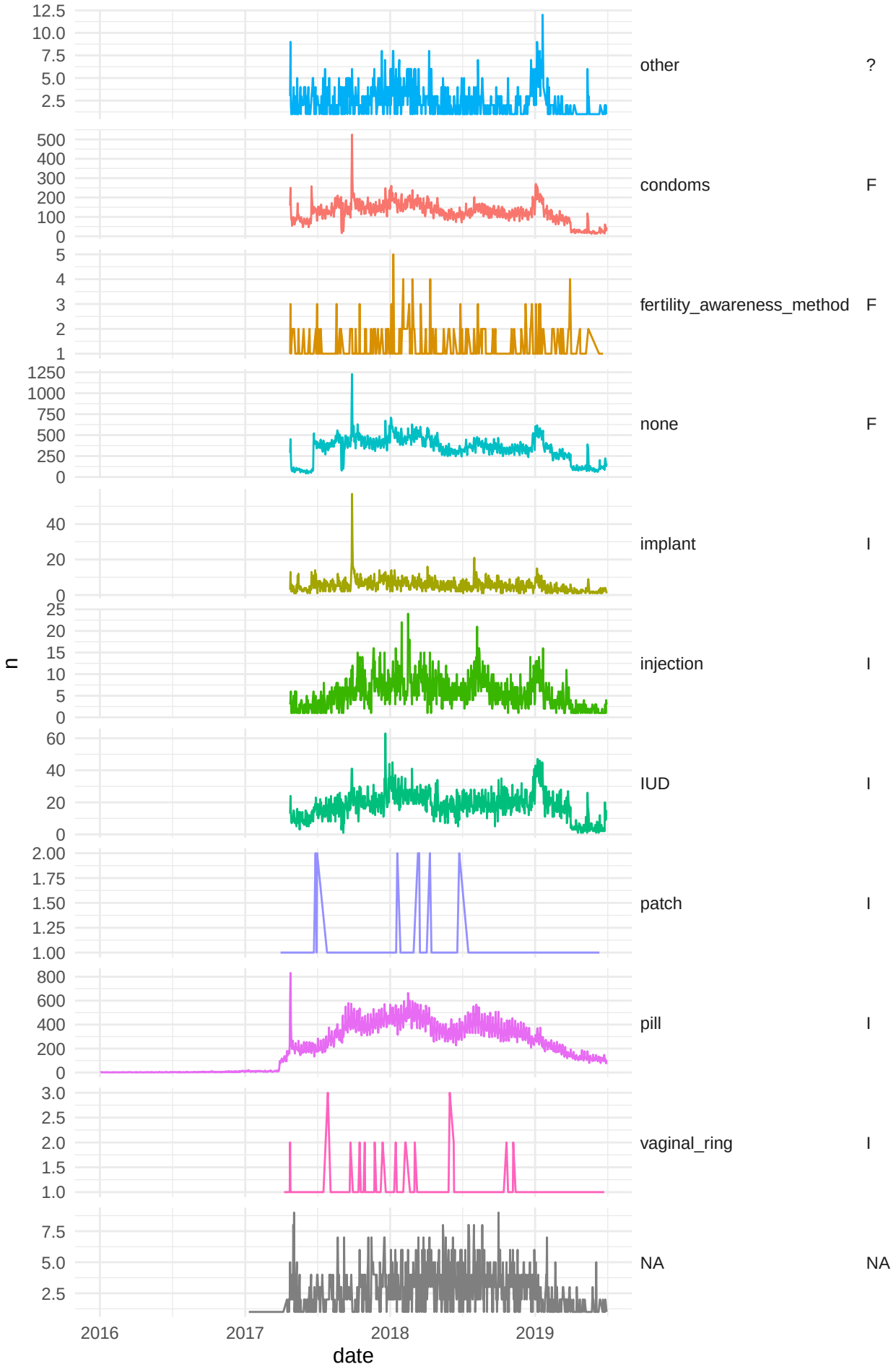
```
table(birth_control = birth_control$birth_control, useNA = "ifany") %>%
  sort(decreasing = TRUE) %>% as.data.frame() %>%
  kable(., format = "pandoc", caption = "Number of times users declared the following birth control in their app profile")
```

Table 4: Number of times users declared the following birth control in their app profile

birth_control	Freq
none	269275
pill	259114
condoms	97774
IUD	14466
injection	4388
implant	4188
NA	1930
other	1575
fertility_awareness_method	465
vaginal_ring	166
patch	111

```
ggplot(
  birth_control %>%
    group_by(date, birth_control) %>%
    summarize(n = n(), .groups = "drop") %>%
    left_join(., dict$BC_all %>% select(birth_control, type), by = "birth_control"),
  aes(x = date, y = n, col = birth_control)
) +
  geom_line() +
  facet_grid(type + birth_control ~ . , scale = "free") +
  guides(col = FALSE)  +
  theme(strip.text.y = element_text(angle = 0, hjust = 0))
```

```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.
```


n
date
2016
2017
2018
2019
other
?
condoms
F
fertility_awareness_method
F
none
F
implant
I
injection
I
IUD
I
patch
I
pill
I
vaginal_ring
I
NA
NA

Cycle table

The cycles table is split in several files due to their large size. Here, we load one the these files and describe the dataset based on this file.

```
cycles_00 = read_feather(path = paste0(IO$input_clue,"cycles/cycles0000.feather"))
```

The cycles tables have the following 11 columns:

user_id, cycle_nb, cycle_start, cycle_end, cycle_length, period_start, period_end, period_length, neg_preg_test, pos_preg_test, latest_preg_test

This cycles file has a total of 287684 cycles for 206001 users.

If we extrapolate from this number, we expect the total number of cycles to be 20 x 287684 = 5753680.

```
ggplot(cycles_00, aes(x = cycle_length))+
  geom_histogram(binwidth = 1)+ xlab("cycle length")+
  scale_x_continuous(breaks = seq(0,98, by = 7), limits = c(0,98))
```

```
## Warning: Removed 7954 rows containing non-finite values (stat_bin).
```

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

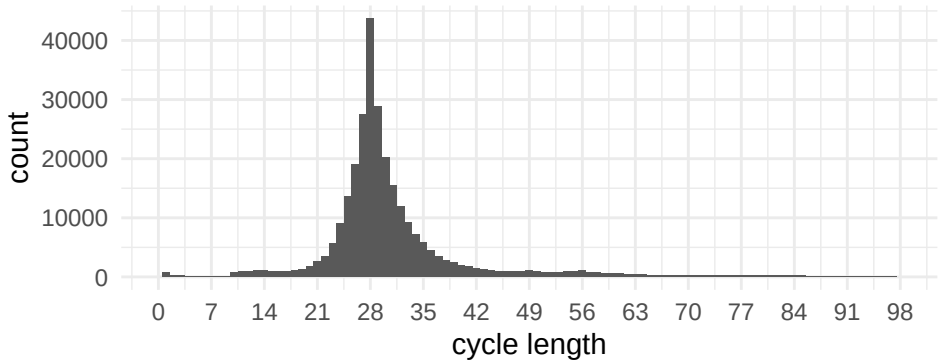


Figure 7: Histogram of the cycle lengths

Note that the cycles table is not further used in this analysis as the sex logs were aggregated at the population level, independent of the cycles in which they were logged.

Tracking table

The tracking table holds the daily logs of the app users.

```
tracking_folder = paste0(IO$input_clue,"tracking/")
files = list.files(tracking_folder)

tracking = read_feather(path = paste0(tracking_folder,files[1]))
```

The tracking table has 5 columns:

user_id, date, category, type, number.

Similarly to the cycles table, the tracking table is split into 20 files to keep each file at a reasonable size.

This particular files has 9988623 rows. If we extrapolate for the number of files, that means 1.9977246×10^8 total logs.

The tracking features are grouped into categories (each category has max 4 items, which are displayed together on the logging screen of the App).

Based on this particular file, the frequency of each of these category goes as follow:

Table 5: Number of times each category has been logged by users (based on 1/20 file of the tracking table)

category	Freq
ANY	55150040
period	26442340
pill_hbc	22555040
emotion	18209600
pain	13216120
sleep	12567280
energy	12401400
mental	9326160
sex	7276740
social	6805780
digestion	5863620
poop	4711880
fluid	2455920
exercise	1255880
weight	780540
medication	415640
ailment	229380
iud	52600
injection_hbc	25780
bbt	25340
test	5200
patch_hbc	180

Given that Clue did not provide data for all the tracking option they offer in the app, they additionally provided a "ANY" category, which tells us if anything was tracked in the app on that day. Note that for the categories displayed in the table above, all tracking data were provided, but some categories of the App, such as "doctor appointment" or "party" were not included in the dataset provided to the research team.

In section 2.10, we provide examples of users' time-series.

2.4 Data processing and filtering: WORKFLOW

- users table data augmentation (1)
  - split Country and Area into two distinct columns
  - estimate BMI from the weight and height bins
- Defining user batches: the tracking files provided by Clue did not ensure that the whole time-series of a user was held in a single file. Each user was thus assigned to a batch and the tracking table files are re-organized such that each file would contain the full time-series of users of a given batch. The users' features are also added to the tracking table at this step.
- users table data augmentation (2) : information from the tracking table is aggregated at the user level and added to the users table.
  - Dates of their first and last log in the app
  - Number of days they logged features in the app
  - Total number of logs
  - Total number of sex logs
- Label user's time-series (tracking table) with their **birth control** (from the birth_control table).

- Label user's time-series (tracking table) as **active** or **not active**. A user was considered active if they logged any feature in the app in a 42-day window. If that was the case, they were considered active for the whole 42-day window. 42 was chosen from 42 = 1.5*28, with 28 being the mode of cycle length distribution.

2.5 Users table data augmentation (1)

```
countries_areas = users$country_area %>% str_split_fixed(., " - ", n = 2)
users$country = countries_areas[,1]
users$area = countries_areas[,2]

write_feather(users, path = paste0(IO$output_clue, "users.feather"))
```

```
users$height_bin = factor(users$height_bin, levels = dict$height$bin)
users$weight_bin = factor(users$weight_bin, levels = dict$weight$bin)
heigh_mean = dict$height$mean[match(users$height_bin,dict$height$bin)]
weight_mean = dict$weight$mean[match(users$weight_bin,dict$weight$bin)]
users$est_mean_bmi = weight_mean/((heigh_mean/100)^2)

write_feather(users, path = paste0(IO$output_clue, "users.feather"))
```

```
ggplot(users, aes(x = est_mean_bmi))+
  geom_histogram(binwidth = 2)+
  facet_grid(country_area ~ ., scale = "free_y")+
  theme(strip.text.y = element_text(angle = 0, hjust = 0),
        strip.background.y = element_rect(fill = "gray90", color = NA))
```

```
## Warning: Removed 153517 rows containing non-finite values (stat_bin).
```

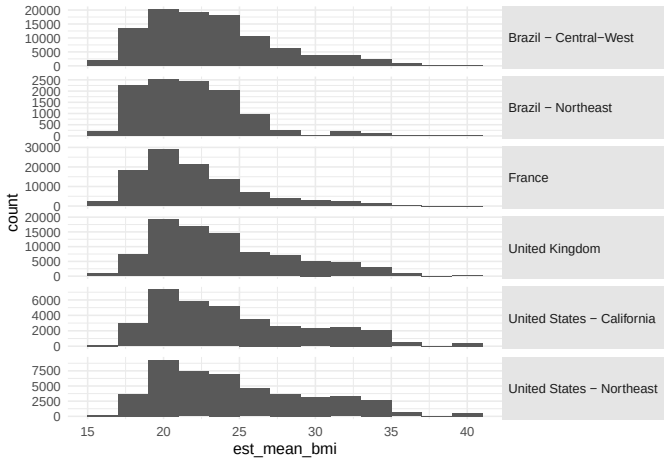


Figure 8: Histogram of the user's estimated BMI for each country/area. For each user, their BMI is estimated based on their 5kg-weight and 5cm-height bins.

2.6 Defining user batches

```
# maximum number of users per batch
max_batch_size = 5000

# computing the number of batches given the total number of users and the minimum number of batches.
n_batch = max(par$min_n_batches, ceiling(nrow(users)/max_batch_size))

# effective batch size
batch_size = ceiling(nrow(users)/n_batch)
```

```
users$batch = rep(1:n_batch, each = batch_size)[1:nrow(users)] # assigning a batch to each user
write_feather(users, path = paste0(IO$output_clue, "users.feather"))
ok = file.copy(from = paste0(IO$output_clue, "users.feather"), to = paste0(IO$tmp_clue, "users_with_batches.feather"))
```

```
# for each tracking file:
#   we read it,
#   assign each user to its batch
#   for each batch present in this file, we split the original tracking file and write them separately on disk
# for each user, we keep in the user table, the names of the original files in which its data were contained.
# Most users only have 1 file, but some can have many.


tracking_folder = paste0(IO$input_clue,"tracking/")
files = list.files(tracking_folder)

tmp_folder = paste0(IO$tmp_clue,"tracking_split_in_batches/")
tmp_final_folder = paste0(IO$tmp_clue,"tracking_in_batches/")


# Given its long execution time, we only execute this code if the folder in which the splitted files by batch are stored does NOT exist.
# To reset, one needs to "manually" delete the folder.
if((!file.exists(tmp_final_folder)) & (!file.exists(tmp_folder))){
 dir.create(tmp_folder,recursive = TRUE)

 cl = makeCluster(par$n_cores)
 registerDoParallel(cl)

 tic()
 users_original_file_ids = foreach(file = files, .combine = rbind, .packages = c("feather","stringr")) %dopar%
 {
  tracking = read_feather(path = paste0(tracking_folder, file))
  dim(tracking)
  tracking$batch = users$batch[match(tracking$user_id, users$user_id)]
  if(nrow(tracking)>0){
   for(b in unique(tracking$batch)){
    tracking_batch = tracking[which(tracking$batch == b),]
    new_file_name = gsub(".feather",paste0("_batch_",b,".feather"),file)
    write_feather(tracking_batch, path = paste0(tmp_folder, new_file_name ))
   }
   users_original_file_ids = data.frame(user_id = unique(tracking$user_id), original_file_id = str_extract(file,"\\d{4}"))
  }else{  users_original_file_ids = data.frame(user_id = character(), original_file_id = character())}
  return(users_original_file_ids)
 }
 toc()
 stopImplicitCluster()

 users_o_f = aggregate(original_file_id ~ user_id ,users_original_file_ids, function(x)  paste0(sort(x), collapse = ","))
 colnames(users_o_f) = c("user_id","original_tracking_files")
 write_feather(users_o_f, path = paste0(IO$tmp_clue,"original_tracking_files_per_users.feather"))
}else{
 warning("App data processing: spliting in batches is NOT done at this execution. Re-using results from a previous execution.")
}
```

```
## Warning: App data processing: spliting in batches is NOT done at this execution.
## Re-using results from a previous execution.
```

```
input_folder = paste0(IO$tmp_clue,"tracking_split_in_batches/")
output_folder = paste0(IO$output_clue,"tracking/")
```

```
# Similarly, we only execute this code if the folder does not exist.
# To re-execute this code, one needs to "manually" delete the folder.
if(!dir.exists(tmp_final_folder)){
  dir.create(tmp_final_folder,recursive = TRUE)

  # First we delete any existing tracking files in the output folder to avoid mess.
  if(file.exists(output_folder)){unlink(output_folder, recursive = TRUE)} ;dir.create(output_folder,recursive = TRUE)

  batches = unique(users$batch)
  ok = foreach(b = batches) %do% {
    cat("\t",b,"||\t")
    all_files = list.files(input_folder)
    files = all_files[grep(paste0("_batch_",b,"\\."),all_files)]

    cl = makeCluster(par$n_cores)
    registerDoParallel(cl)
    tracking = foreach(file  = files, .combine = rbind, .packages = "feather") %dopar%{tracking = read_feather(path = paste0(input_folder, file));return(tracking)}
    stopImplicitCluster()

    cols_to_add = c("birth_year_bin","country_area","height_bin","weight_bin", "est_mean_bmi")
    m = match(tracking$user_id, users$user_id)
    for(col_to_add in cols_to_add){
      eval(parse(text = paste0("tracking$",col_to_add," = users$",col_to_add,"[m]")))
    }
    o = order(tracking$user_id, tracking$date, tracking$category, tracking$type, tracking$number)
    tracking = tracking[o,]

    new_file_name = paste0("tracking_",b,".feather")
    write_feather(tracking, path = paste0(output_folder, new_file_name ))
    ok = file.copy(from = paste0(output_folder, new_file_name ), to = paste0(tmp_final_folder, new_file_name), overwrite = TRUE)
  }
}else{
  warning("App data processing: re-assembling in batches is NOT done at this execution. Re-using results from a previous execution.")
}
```

```
## Warning: App data processing: re-assembling in batches is NOT done at this
## execution. Re-using results from a previous execution.
```

2.7 Users table data augmentation (2)

Information from the tracking table is aggregated at the user level and added to the users table:

* Dates of their first and last log in the app

* Number of days they logged features in the app

* Total number of logs

* Total number of sex logs

```
if(!file.exists(paste0(IO$tmp_clue, "users_agg.feather"))){

  tracking_folder = paste0(IO$output_clue,"tracking/")
  files = list.files(tracking_folder)

  cl = makeCluster(par$n_cores)
  registerDoParallel(cl)

  tic()
```

```
 users_agg = foreach(file = files, .combine = rbind, .packages = c("feather","stringr", "plyr")) %dopar%
 {
  tracking = read_feather(path = paste0(tracking_folder, file))
  users_agg = ddply(tracking,
                    .(user_id),
                    summarize,
                    first_obs = min(date),
                    last_obs = max(date),
                    n_obs_day = length(unique(date)),
                    n_obs = sum(category != "ANY"),
                    n_sex = sum(category == "sex"),
                    n_mucus =  sum(category == "fluid"),
                    n_temp = sum(category == "bbt")
  )
  return(users_agg)
 }
 toc()
 stopImplicitCluster()

 write_feather(users_agg, path = paste0(IO$tmp_clue, "users_agg.feather"))

}else{
 warning("App data processing: tracking aggregation at the user level is NOT done at this iteration. Re-using results from a previous execution.")
}
```

```
## Warning: App data processing: tracking aggregation at the user level is NOT done
## at this iteration. Re-using results from a previous execution.
```

```
users_agg = read_feather(path = paste0(IO$tmp_clue, "users_agg.feather"))

cols_to_add = setdiff(colnames(users_agg),"user_id")
m = match(users$user_id, users_agg$user_id)
for(col_to_add in cols_to_add){eval(parse(text = paste0("users$",col_to_add," = users_agg$",col_to_add,"[m]")))}
users$n_days = as.numeric(users$last_obs - users$first_obs)

write_feather(users, path = paste0(IO$output_clue, "users.feather"))
ok = file.copy(from = paste0(IO$output_clue, "users.feather"), to = paste0(IO$tmp_clue, "users_augmented.feather"))
```

2.8 Users birth control

In this section, we label the user's time-series (tracking table) with the **birth control** the user declared in their app profile (from the birth_control table). If a user changed birth control (and thus have multiple entries at different dates in the birth_control table), their time-series are labeled with these different birth control.

Note that the birth control feature was introduced into the app around April 2017. Thus users who started tracking with the app before that date do not have an entry for their data before that date. In addition, some users do not declare their birth control at on-boarding but do so later. Altogether, when birth control information is missing, it is replaced by "undefined".

```
BC = birth_control
BC = BC %>%
 arrange(user_id, date) %>%
 mutate(birth_control = birth_control %>% replace_na("undefined"))

write_feather(BC, path = paste0(IO$output_clue, "birth_control.feather"))
```

```
BC = read_feather(path = paste0(IO$output_clue,"birth_control.feather"))

input_folder = paste0(IO$tmp_clue,"tracking_in_batches/")
```

```
output_folder = paste0(IO$output_clue,"tracking/")
tmp_folder = paste0(IO$tmp_clue, "tracking_with_user_defined_birth_control/")

if(!dir.exists(tmp_folder)){

  dir.create(tmp_folder)
  files = list.files(input_folder)

  cl = makeCluster(par$n_cores)
  registerDoParallel(cl)

  tic()
  catch =
    foreach(file = files,
            .combine = rbind,
            .packages = c("feather","stringr", "plyr","tidyverse")
    ) %dopar% {

      tracking = read_feather(path = paste0(input_folder, file))

      # creating a table (BC_exp) that has one row per user and date that is found either in the tracking table or in the BC table. This table thus have one row per user and dat
        BC_exp = full_join(
          BC %>%
            filter(user_id %in% unique(tracking$user_id)) %>%
            select(-csv_file, -pill_type, -pill_regiment) %>%
            distinct(),
          tracking %>%
            select(user_id, date) %>%
            distinct(),
          by = c("user_id", "date")
        ) %>%
        arrange(user_id, date, birth_control) %>%
        group_by(user_id) %>%
        mutate(
          birth_control =
            replace_NAs_with_latest_value(birth_control) %>%
            replace_na("undefined")
        )

      tracking = tracking %>%
        left_join(.,
                  BC_exp,
                  by = c("user_id", "date"))

      write_feather(tracking, path = paste0(output_folder,file))
      file.copy(from = paste0(output_folder,file), to = paste0(tmp_folder,file), overwrite = TRUE)
    }
  toc()
  stopImplicitCluster()
}else{
  warning("App data processing: adding birth control to tracking table is NOT done at this execution. Re-using results from a previous execution.")
}
```

```
## Warning: App data processing: adding birth control to tracking table is NOT done
## at this execution. Re-using results from a previous execution.
```

2.9 Identifying active use of the app

User's time-series (tracking table) are labeled with **active** or **not active** labels. A user was considered active if they open and logged any feature in the app twice in a 42-day window. If that was the case, they were considered active for the whole 42-day window. 42 was chosen from 42 = 1.5*28, with 28 being the mode of cycle length distribution. A user can transition several times between "active" and "inactive" use of the App.

```
input_folder = paste0(IO$output_clue,"tracking/")
files = list.files(input_folder)

output_folder = paste0(IO$tmp_clue, "active_tracking/")
if(!dir.exists(output_folder)){

 dir.create(output_folder)

 time_vec = seq(min(users$first_obs), max(users$last_obs), by = 1)

 cl = makeCluster(par$n_cores)
 registerDoParallel(cl)
 tic()
 ok =
  foreach(file = files,
          .packages = c("dplyr", "feather", "tidyr")) %dopar%
  {
    # we load the tracking table
    tracking = read_feather(path = paste0(input_folder, file))

    # we keep the dates at which users logged smth in the app
    any_tracking = tracking %>% filter(. , category == "ANY")  %>%
      select(user_id, date, birth_control) %>%
      mutate(tracking_days = 1)

    # we create a data.frame that has one row for each calendar day from the first to the last log
    tmp = expand_grid(
      user_id = unique(tracking$user_id),
      date = time_vec)

    # we join this tmp table with the table that has active tracking.
    active_tracking = full_join(tmp,any_tracking, by = c("user_id","date"))

    # tracking_days is zero when there were no entries in the tracking table
    active_tracking = active_tracking %>%
      mutate(tracking_days = tracking_days %>% replace_na(0))
    # we keep the BC info
    active_tracking = active_tracking %>%
      group_by(user_id) %>%
      mutate(birth_control = birth_control %>% replace_NAs_with_latest_value)
    # we check for any active tracking in 42 days window
    active_tracking = active_tracking %>%  group_by(user_id) %>%
      mutate(tracking = data.table::frollsum(tracking_days,
                                             fill = 0,
                                             n = 42,
                                             align = "right") >= 2)

    # only keep the necessary columns.
    active_tracking = active_tracking %>%
      select(user_id, date, birth_control, tracking)

    ###
```

```
    # compressed table
    # (we compress the active tracking table to speed up IO operations)
    active_tracking  = active_tracking %>%
      group_by(user_id, birth_control) %>%
      mutate(transition = diff(c(0, tracking))) %>%
      group_by(user_id) %>%
      mutate(stretch_num = cumsum(transition == 1)) %>%
      group_by(user_id, birth_control, stretch_num, tracking) %>%
      mutate(stretch_length = sum(tracking)) %>%
      ungroup()

    compressed_tracking = active_tracking %>% filter(transition == 1) %>%
      select(user_id, date, birth_control, stretch_num, stretch_length) %>%
      dplyr::rename(start_date = date)

    file_name = paste0("active_",file)
    write_feather(compressed_tracking, path = paste0(output_folder,file_name))
  }
 toc()
 stopImplicitCluster()

}else{
  warning("App data processing: identification of active use is NOT done at this execution. Re-using results from a previous execution.")
}
```

```
## Warning: App data processing: identification of active use is NOT done at this
## execution. Re-using results from a previous execution.
```

2.10 Examples of individual users time-series

```
input_folder = paste0(IO$output_clue,"tracking/")
files = list.files(input_folder)
file = files[1]

tracking = read_feather(path = paste0(input_folder, file)) # we load the tracking table
```

```
plot_user_timeseries = function(tracking, u){

 dat = tracking %>% filter(user_id == u) %>%
  mutate(rel_date = (date - min(date)) %>% as.numeric()) %>%
  arrange(rel_date) %>%
  mutate(category = factor(category, levels = c("ANY", unique(feature_dict$category) %>% as.character())),
         type_col = feature_dict$color[match(type, feature_dict$type)] %>%  replace_na("black"))

 g = ggplot(dat, aes(x = rel_date, y = type, col = type_col))
 g = g +
  geom_point()+
  xlab("days from 1st log in the App")+ ylab("")+
  scale_color_identity()+
  facet_grid(category ~ ., scale = "free_y", space = "free", switch = "y")+
  theme(strip.placement = "outside",
        strip.background.y = element_rect(fill = "gray80", color = NA),
        strip.text.y.left = element_text(angle = 0, hjust = 1))
 g

}
```

```
u = c("dd1de61df75ded8f4dbbb0be30f27d2b8c658b4f")

plot_user_timeseries(tracking = tracking, u = u)
```

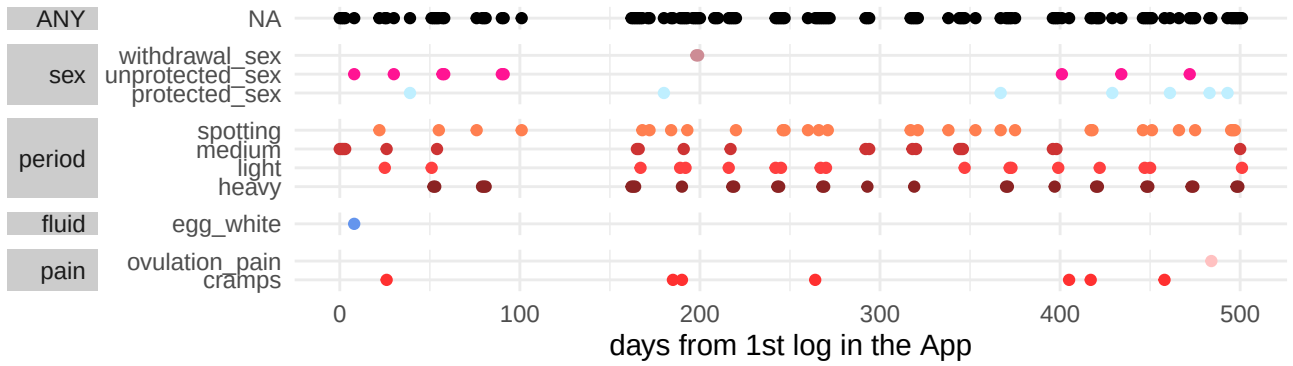


Figure 9: Example of a user tracking time-series (1)

```
# u = sample(tracking$user_id, 1)
# u = "b2f86085f009a8d1bc9691b782b6ffc1308871af"
u = "e12d958dc494c3c2a3aa2d42be6683f96bdd90e7"

plot_user_timeseries(tracking = tracking, u = u)
```

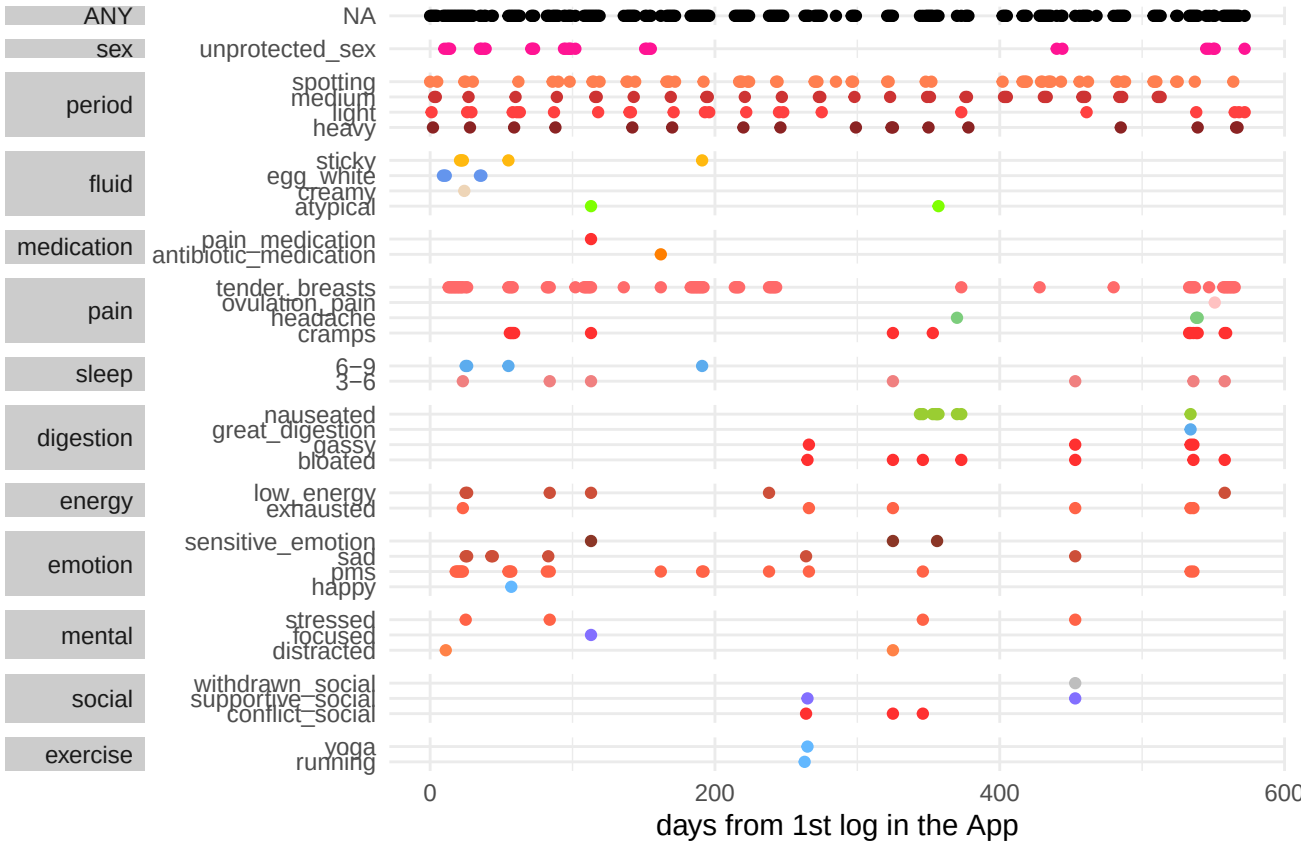


Figure 10: Example of a user tracking time-series (2)

Table 6: Total duration of active tracking and number of days tracked in the app.

number_of_days_of_observation	55110476.0
total_duration_of_active_tracking_in_days	180721915.0
number_of_years_of_observation	150987.6
total_duration_of_active_tracking_in_years	495128.5

2.11 Dataset characteristics

```
# Directory with the tracking tables
input_folder = paste0(IO$output_clue,"tracking/")
files = list.files(input_folder)

# Directory with the active tracking tables
input_active_tracking = paste0(IO$tmp_clue,"active_tracking/")

# file on which the tracking_duration_stats are saved
tds_file = str_c(IO$tmp_clue, "tracking_duration_stats.feather")

if(!file.exists(tds_file)){

  tracking_duration_stats = purrr::map_dfr(
    files,
    .f = function(file){
      tracking = read_feather(str_c(input_folder, file))
      active_tracking =  read_feather(str_c(input_active_tracking, "active_", file))
      data.frame(file = file,
                 number_of_days_of_observation = tracking %>% select(user_id, date) %>% distinct() %>% nrow(),
                 total_duration_of_active_tracking = active_tracking$stretch_length %>% sum())
    })
  write_feather(tracking_duration_stats, path = tds_file)
}else{
  tracking_duration_stats = read_feather(path = tds_file)
}

tracking_duration_stats_summary = tracking_duration_stats %>%
  summarise(number_of_days_of_observation = sum(number_of_days_of_observation),
            total_duration_of_active_tracking_in_days = sum(total_duration_of_active_tracking)) %>%
  mutate(number_of_years_of_observation = number_of_days_of_observation/365,
         total_duration_of_active_tracking_in_years = total_duration_of_active_tracking_in_days/365)
```

```
kable(t(tracking_duration_stats_summary),
      format = "latex",
      booktabs = T,
      caption = "Total duration of active tracking and number of days tracked in the app.")
```

3 App data aggregation: constructing population-wide time-series

In this section, the App users logs are aggregated in population-wide time-series.

```
# Loading the users table
users = read_feather(path = paste0(IO$output_clue, "users.feather"))
```

```
# defining the date-range for which we will build the aggregated table.
# starts with the first observation of the first user in this dataset and ends with the last day a feature was logged by any user.
time_vec = seq(min(users$first_obs), max(users$last_obs), by = 1)
range(time_vec)
```

```
## [1] "2016-01-01" "2019-06-30"
```

3.1 Aggregating variables

We will aggregate at the following levels:

- **country/area** (6): Brazil - Central-West, Brazil - Northeast, United States - California, United States - Northeast, France, United Kingdom
- **age**. Users are grouped into 2 age categories: the younger users (<= 23 years old) and the older (> 23 years old). This age limit (23 years old) is approximately the median age of the app users (we do not have an exact median value given that the birth year of users was given in 5-year bins).
- **birth control**. Birth control methods are grouped into three categories:
  - **F** (for potentially **f**ertile) for birth control methods, such as "condoms" or "fertility awareness method", where unprotected sex could lead to a pregnancy.
  - **I** (for **i**nfertile) for birth control methods, such as IUDs or the pill, where unprotected sex does not potentially lead to a pregnancy.
  - **?** (for unknown) when the birth control method is not specified by the user.

Table 7: Types of birth control available to users in the Clue profile and their classification into F or I type.

birth_control	type	type_descr
none	F	Potentially fertile, and thus fecundable with unprotected sex
fertility_awareness_method	F	Potentially fertile, and thus fecundable with unprotected sex
condoms	F	Potentially fertile, and thus fecundable with unprotected sex
pill	I	Infertile due to contaceptive
vaginal_ring	I	Infertile due to contaceptive
IUD	I	Infertile due to contaceptive
patch	I	Infertile due to contaceptive
injection	I	Infertile due to contaceptive
implant	I	Infertile due to contaceptive
vaginal_ring	I	Infertile due to contaceptive
other	?	NA
undefined	?	NA

3.2 Aggregation

We aggregate and build time-series counting:

- the number of active users
- the number of sex logs: protected sex, unprotected sex, all sex
- the number of logs for each control feature (see section 5): medium flow bleeding (period), exercise,

tender breasts (pain), sleeping more than 9h.

```
# Directory with the tracking tables
input_folder = paste0(IO$output_clue,"tracking/")
files = list.files(input_folder)

# Directory with the active tracking tables
input_active_tracking = paste0(IO$tmp_clue,"active_tracking/")

# Directory where the aggregated table will be stored
indicators_folder = paste0(IO$output_clue, "pop_indicators/")
if(!dir.exists(indicators_folder)){dir.create(indicators_folder)}

# We only run this code if the file containing the aggregated table does not exists.
if(!file.exists(paste0(indicators_folder, "tracking_pop_agg.feather"))){

 tic()
 tracking_pop_agg = foreach(file = files,
                            .combine = rbind,
                            .packages = c("dplyr","tidyverse")) %do% {
  cat("\t",file,"\t||")

  # tracking table
  tracking = read_feather(path = paste0(input_folder, file))

  # aggregating variables
  tracking$BC = dict$BC_all$type[match(tracking$birth_control, dict$BC_all$birth_control)]
  birth_year_bins = data.frame(birth_year_bin = unique(tracking$birth_year_bin))
  birth_year_bins = birth_year_bins %>%
    mutate(birth_year_bin_mid = (
      as.numeric(str_sub(birth_year_bin,1,4)) +
        as.numeric(str_sub(birth_year_bin,6,9))
    )/2
    )

  tracking = tracking %>% mutate(
    birth_year_bin_mid = birth_year_bins$birth_year_bin_mid[
      match(birth_year_bin, birth_year_bins$birth_year_bin)],
    date_r = year(date),
    age = date_r - birth_year_bin_mid,
    age_cat = cut(age, breaks = c(-Inf, 23, Inf), labels = c("<= 23", "> 23")))


  # active tracking
  active_tracking_compressed = read_feather(path = paste0(input_active_tracking,"active_",file))
  active_tracking = expand_compressed_tracking(active_tracking_compressed)


  # tracking during active tracking period
  tracking_full = tracking
  tracking = inner_join(active_tracking %>% select(user_id, date),
                        tracking %>% select(user_id, date, category, type, number,
                                            country_area, BC, age_cat),
                        by = c("user_id", "date"))

  # variables aggregates
  tracking_pop_agg_this_file = tracking %>%
    group_by(date, country_area, BC, age_cat) %>%
    dplyr::summarise(
```

```
    n_prot_sex = sum((category == "sex") & (type == "protected_sex"), na.rm = TRUE),
    n_unprot_sex = sum((category == "sex") & (type == "unprotected_sex"), na.rm = TRUE),
    n_wd_sex = sum((category == "sex") & (type == "withdrawal_sex"), na.rm = TRUE),
    n_exercise = sum(category == "exercise", na.rm = TRUE),
    n_long_sleep = sum((category == "sleep")&(type == ">9"), na.rm = TRUE),
    n_bleeding = sum((category == "period")&(type != "spotting"), na.rm = TRUE),
    n_medium_bleeding = sum((category == "period") & (type == "medium"), na.rm = TRUE),
    n_breast_pain = sum((category == "pain") & (type == "tender_breasts"), na.rm = TRUE),
    n_pill_taken = sum((category == "pill_hbc") & (type == "taken"), na.rm = TRUE),
    n_any = sum(category == "ANY", na.rm = TRUE),
    n_pain = sum(category == "pain", na.rm = TRUE),
    n_emotion = sum(category == "emotion", na.rm = TRUE),
    .groups = "drop"
  )

 # adding total sex
 tracking_pop_agg_this_file = tracking_pop_agg_this_file %>%
  mutate(n_sex = n_prot_sex + n_unprot_sex + n_wd_sex)

 ### counting the number of active users
 # aggregating variables
 m = match(active_tracking$birth_control, dict$BC_all$birth_control)
 active_tracking$BC = dict$BC_all$type[m] %>% replace_na("?")
 #active_tracking =  active_tracking %>%  filter(BC %in% c("F","I"))
 active_tracking = active_tracking %>% mutate(
  birth_year_bin = users$birth_year_bin[match(user_id, users$user_id)],
  birth_year_bin_mid = birth_year_bins$birth_year_bin_mid[
    match(birth_year_bin, birth_year_bins$birth_year_bin)],
  date_r = year(date),
  age = date_r - birth_year_bin_mid,
  age_cat = cut(age, breaks = c(-Inf, 23, Inf), labels = c("<= 23", "> 23"))
 )
 active_tracking$country_area = tracking$country_area[match(active_tracking$user_id, tracking$user_id)]
 active_tracking = active_tracking %>% filter(!is.na(country_area))

 # total number of users
 active_tracking_agg = active_tracking %>%
  group_by(date, country_area, BC, age_cat) %>%
  summarize(n_users = sum(tracking, na.rm = TRUE),
            .groups = "drop")

 # We then need to join the feature aggregation with the # of active users
 tmp = dplyr::full_join(
  x = active_tracking_agg,
  y = tracking_pop_agg_this_file,
  by = c("date","country_area","BC", "age_cat")
  ) %>%
  arrange(country_area, BC, age_cat, date) %>%
  replace_na(
    list(n_users = 0,
         n_prot_sex = 0, n_unprot_sex = 0, n_wd_sex= 0, n_sex = 0,
          n_exercise = 0, n_long_sleep = 0, n_bleeding = 0, n_medium_bleeding = 0,
          n_breast_pain = 0, n_pain = 0, n_pill_taken = 0, n_emotion = 0, n_any = 0)) %>%
  mutate(filename = file)

 return(tmp)
}
toc()
```

```
 tracking_pop_agg_not_aggregated_by_file = tracking_pop_agg
 write_feather(tracking_pop_agg_not_aggregated_by_file,
           path = paste0(indicators_folder, "tracking_pop_agg_not_aggregated_by_file.feather"))


 tic()
 # sum the results from all files
 tmp = tracking_pop_agg_not_aggregated_by_file %>%
  group_by(date, country_area, BC, age_cat) %>%
  summarise(across(starts_with("n_"), sum, na.rm = TRUE)) %>%
  arrange(country_area, BC, age_cat, date)
 # expand to have one row per possible date
 tmp2 = expand.grid(date = time_vec, country_area = unique(tmp$country_area),
                BC = unique(tmp$BC), age_cat = unique(tmp$age_cat))

 tmp3 = dplyr::full_join(tmp, tmp2, by = c("date","country_area","BC","age_cat")) %>%
  arrange(country_area, BC, age_cat, date) %>%
  replace_na(., list(n_users = 0,
                   n_prot_sex = 0, n_unprot_sex = 0, n_wd_sex= 0, n_sex = 0,
                   n_exercise = 0, n_long_sleep = 0,
                   n_bleeding = 0, n_medium_bleeding = 0,
                   n_breast_pain = 0, n_pain = 0, n_pill_taken = 0, n_emotion = 0,
                   n_any = 0)) %>%
  ungroup()

 # final table
 tracking_pop_agg = tmp3

 # save the results
 write_feather(tracking_pop_agg, path = paste0(indicators_folder, "tracking_pop_agg.feather"))
 toc()

}else{
  warning("The aggregation was not executed at this rendering. Loading data from a previous execution.")
  tracking_pop_agg = read_feather(path = paste0(indicators_folder, "tracking_pop_agg.feather"))
}
```

```
## Warning: The aggregation was not executed at this rendering. Loading data from a
## previous execution.
```

3.3 Additional categories

In addition to the 2 age categories and the 3 BC categories, a category (all) is created for both of these variables to include all users.

3.3.1 BC = all

```
tracking_pop_agg_BC_all = tracking_pop_agg %>%
  select(-BC) %>%
  group_by(country_area, age_cat, date) %>%
  summarize(across(starts_with("n_"), sum), .groups = "drop") %>%
  mutate(BC = "all") %>%
  select(all_of(colnames(tracking_pop_agg)))

tmp = bind_rows(tracking_pop_agg, tracking_pop_agg_BC_all)
```

```
tracking_pop_agg = tmp


# ggplot(tmp, aes(x = date, y = n_users, col = BC, linetype = age_cat)) +
#   geom_line() +
#   facet_grid(country_area ~ ., scale = "free")
```

3.3.2 Filtering out the category of unknown birth-control

Note that while we will not perform analyses specifically on that group of users, they are still included in the group BC = all, i.e. the group that include all users of the app, regardless of their birth control.

```
tracking_pop_agg = tracking_pop_agg %>%
  filter(BC != "?")
```

3.3.3 Age = all

```
tracking_pop_agg = tracking_pop_agg %>%
  mutate(age_cat = age_cat %>% as.character())

tracking_pop_agg_age_all = tracking_pop_agg %>%
  select(-age_cat) %>%
  group_by(country_area, BC, date) %>%
  summarize(across(starts_with("n_"), sum), .groups = "drop") %>%
  mutate(age_cat = "all") %>%
  select(all_of(colnames(tracking_pop_agg)))

tmp = bind_rows(tracking_pop_agg, tracking_pop_agg_age_all)

tracking_pop_agg = tmp

# ggplot(tmp, aes(x = date, y = n_users, col = BC, linetype = age_cat)) +
#   geom_line() +
#   facet_grid(country_area ~ ., scale = "free")
```

We check that all categories have 3.5 years (3.5*365 = 1277) of data

```
tracking_pop_agg %>%
  group_by(country_area, BC, age_cat) %>%
  summarize(n = n(), .groups = "drop") %>%
  as.data.frame() %>%
  select(n) %>% unlist() %>% unique()
```

```
## [1] 1277
```

```
write_feather(tracking_pop_agg, path = paste0(indicators_folder, "tracking_pop_agg_with_all_BC_and_age.feather"))
```

3.4 Filtering time-series to keep series with sufficient number of users.

The number of app users increase over time in each location.

```
ggplot(tracking_pop_agg %>%
       mutate(category =
              str_c("BC: ", BC," - age cat.: ", age_cat)),
     aes(x = date, y = n_users, col = category)) +
  geom_line() +
  facet_grid(country_area ~ ., scale = "free")
```

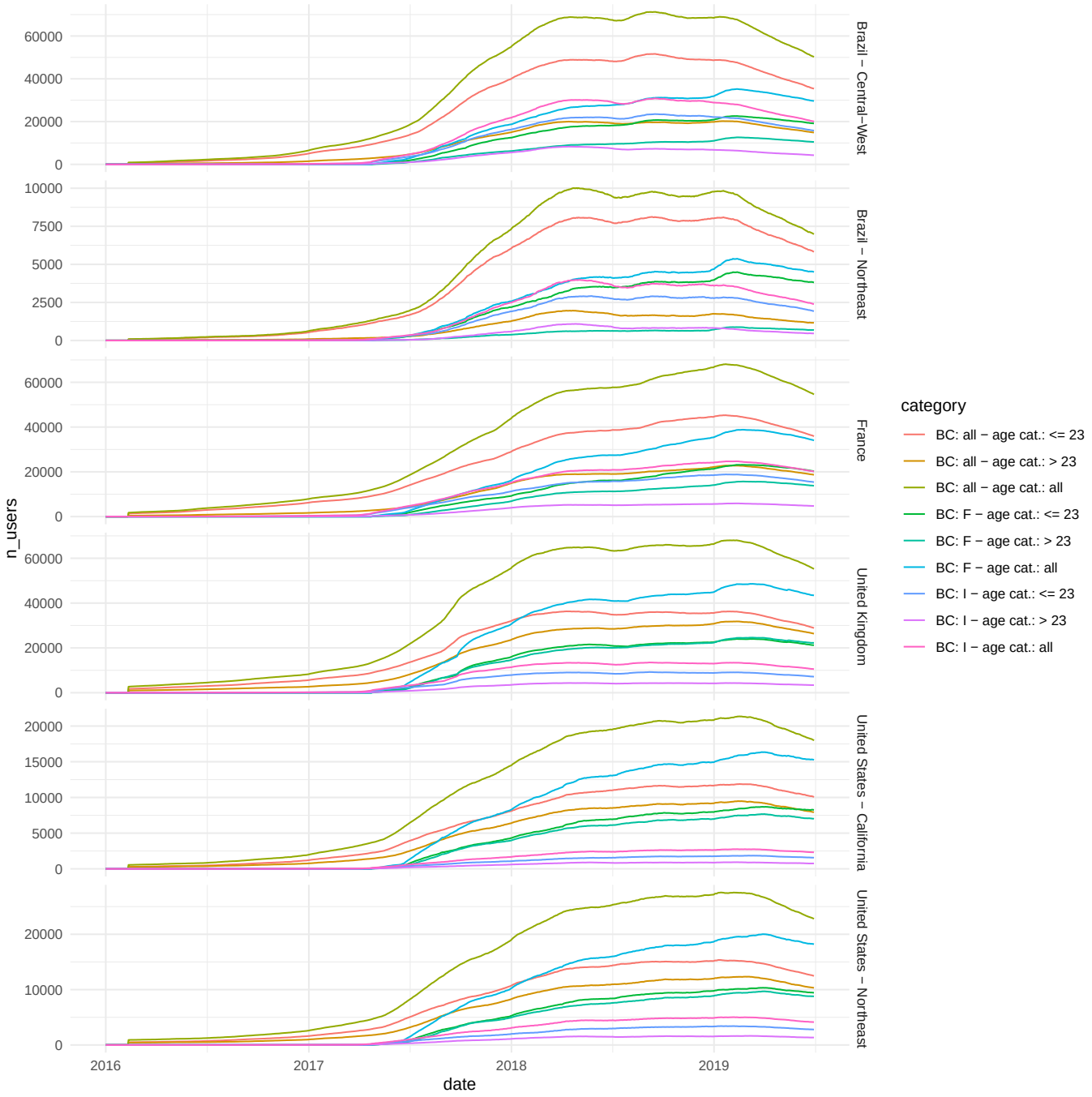


Figure 11: Number of app users over time (unflitered data).

To ensure reliable estimation of our sexual activity indicators, we filter for the last two years of data and remove any category for future analysis if the number of users in that category is lower than 1000 users at any time-point.

```
tracking_pop_agg = tracking_pop_agg %>%
  filter(date >= as.Date("2017-07-01")) %>%
  group_by(country_area, BC, age_cat) %>%
  mutate(has_less_than_1000_users = any(n_users < 1000)) %>%
  filter(!has_less_than_1000_users) %>%
  select(-has_less_than_1000_users)
```

```r
df = tracking_pop_agg %>%
  group_by(country_area, age_cat, BC) %>%
  summarize(min_n = min(n_users),
            max_n = max(n_users),
            median_n = median(n_users),
            .groups = "drop") %>%
  ungroup() %>%
  mutate(age_cat = age_cat %>% factor(., levels = c("all","<= 23","> 23")),
         BC = BC %>% factor(., levels = c("all", "F","I"))) %>%
  filter(!is.na(age_cat)) %>%
  arrange(country_area, age_cat, BC)


kable(df, format = "pandoc", caption = "Minimum, maximum and median number of users in each category")
```

Table 8: Minimum, maximum and median number of users in each category

country_area	age_cat	BC	min_n	max_n	median_n
Brazil - Central-West	all	all	18437	71254	65366.0
Brazil - Central-West	all	F	2861	35220	27684.5
Brazil - Central-West	all	I	4658	30802	27184.0
Brazil - Central-West	<= 23	all	13753	51623	46325.0
Brazil - Central-West	<= 23	F	1855	22592	18162.0
Brazil - Central-West	<= 23	I	3633	23507	20409.0
Brazil - Central-West	> 23	all	4684	20224	18960.0
Brazil - Central-West	> 23	F	1006	12634	9522.5
Brazil - Central-West	> 23	I	1025	8295	6507.5
Brazil - Northeast	all	all	1953	10014	9118.0
Brazil - Northeast	<= 23	all	1674	8121	7456.0
France	all	all	18483	68109	57423.5
France	all	F	2633	38829	27436.5
France	all	I	4798	24707	20799.5
France	<= 23	all	14013	45297	38224.0
France	<= 23	F	1824	23153	16156.5
France	<= 23	I	4024	18857	15641.0
France	> 23	all	4470	22812	19076.0
United Kingdom	all	all	21653	68043	63630.0
United Kingdom	all	F	4552	48609	41421.0
United Kingdom	all	I	3284	13513	12770.5
United Kingdom	<= 23	all	13526	36331	34989.0
United Kingdom	<= 23	F	2549	24006	21286.0
United Kingdom	<= 23	I	2431	9238	8660.5
United Kingdom	> 23	all	8127	31826	28575.0
United Kingdom	> 23	F	2003	24611	20144.0
United States - California	all	all	6406	21355	19212.5
United States - California	all	F	1317	16354	13062.0
United States - California	<= 23	all	3916	11881	10719.5
United States - California	> 23	all	2490	9486	8476.0
United States - Northeast	all	all	8177	27551	24754.0
United States - Northeast	all	F	1442	20016	15975.5
United States - Northeast	all	I	1001	5022	4424.0
United States - Northeast	<= 23	all	5017	15367	13953.0
United States - Northeast	> 23	all	3160	12341	10786.0

```r
write_feather(tracking_pop_agg, path = paste0(indicators_folder, "tracking_pop_agg_with_all_BC_and_age_filtered.feather"))
```

3.5 App user engagement over time.

Early adopters, i.e. users who started using the app early in time, tend to be more engaged with a technology. We investigate if this is the case in our data by looking at the relative frequency of reporting any feature in the app over time.

```
ggplot(tracking_pop_agg %>%
       mutate(category =
              str_c("BC: ", BC," - age cat.: ", age_cat)),
     aes(x = date, y = n_any/n_users, col = age_cat)) +
 #geom_hline(yintercept = c(0,1), col = "black") +
 geom_line() +
 facet_grid(country_area ~ BC)
```

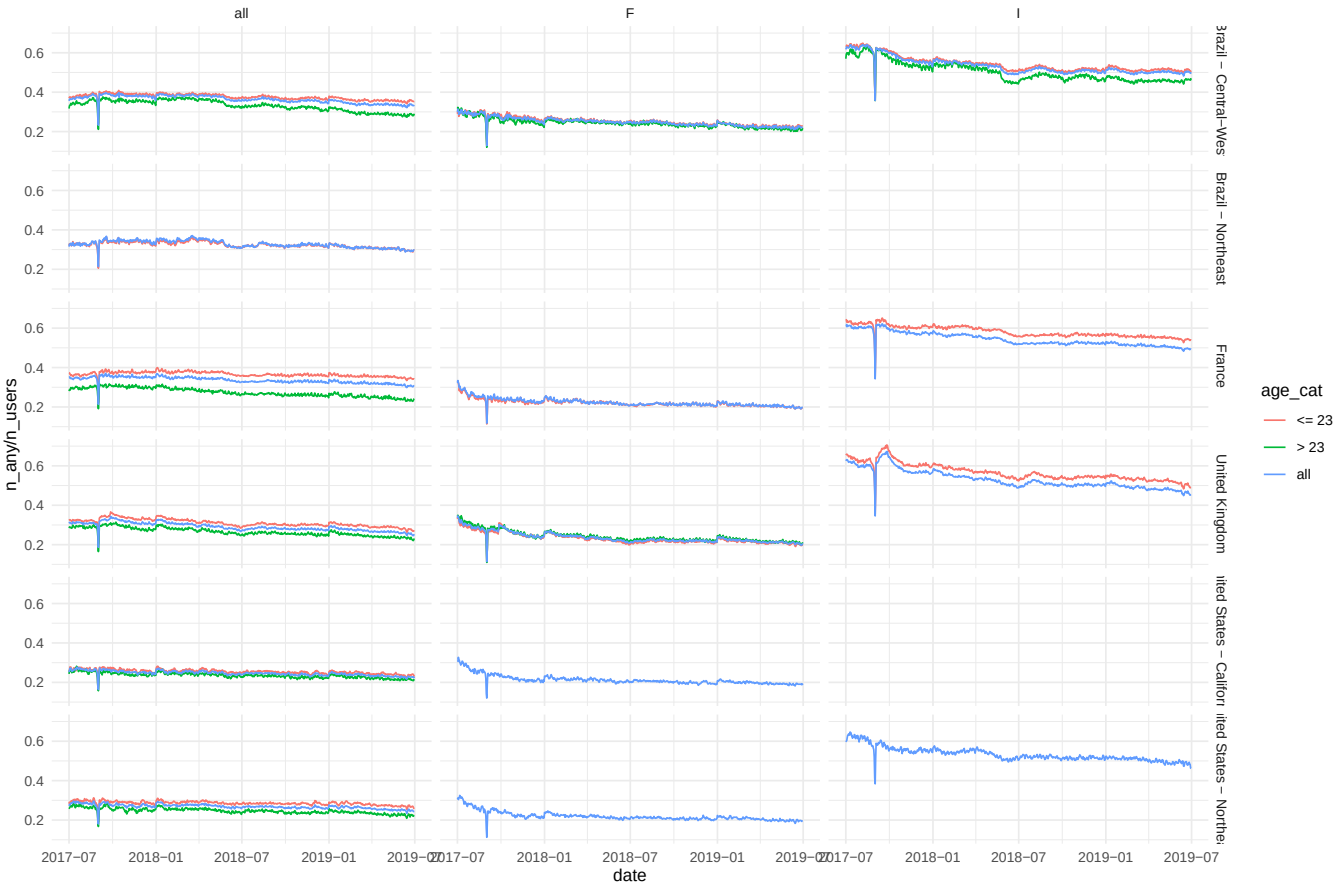


Figure 12: Reporting frequency of users over time and per user category.

From this visualization, we see that new features introduced into the app, such as allowing users to declare their birth control (groups "F" and "I") and let them set up reminders to log their birth control pill intake for example, influence the reporting behavior of early adopters of these new features. This has an impact on how the relative frequency of sexual activity is computed.

We also see that there were probably a day or two during which the app users likely experienced technical difficulties with the app as we see a consistent dip in reporting in August 2017.

3.6 Computing the relative sexual frequency and adjusting for changes in reporting frequency.

Given that $f(t)$ is the true frequency of sexual activity of the app users at time t, i.e. $f(t) = \frac{s_{true}(t)}{N(t)}$ where $s_{true}(t)$ is the true number of sexual intercourse of the app users at time t and $N(t)$ is the number of users of the app

at time t. However, we have access to $s_{reported}(t)$, i.e. the number of sexual intercourse reported into the app by users, with $s_{reported}(t) = s_{true}(t) * p(t)$ where $p(t)$ is the probability that users will report their sexual activity into the app. $p(t)$ is thus the joint probability that users will open the app at time t (event A) and that they will report a sexual intercourse into the app (event S): $p(t) = P(A \cap S, t) = P(A, t)\ P(S|A, t)$. From our data, we can estimate $P(A, t)$, which is the engagement rate of users with the app because we can compute the ratio between the number of logs of *any* feature into the app at time t and the number of users at time t. If we assume that the probability of users to report sexual intercourse once they have already open the app is constant over time, e.g. that users may be more likely to open the app on week-ends but not to decide to report sex on week-ends once the app is already open, then we can write $p(t)$ as $p(t) = P(A, t)p_0$, and we can estimate $P(A, t)$ as $P(A, t) = \frac{n_{any}(t)}{N(t)}$.

Altogether, the true frequency of sexual intercourse can be computed as:

$$f_t = \frac{s_{true}(t)}{N(t)} \tag{1}$$

$$= \frac{s_{reported}(t)}{p(t)} \frac{1}{N(t)} \tag{2}$$

$$= \frac{s_{reported}(t)}{p_0 n_{any}(t)} \frac{N(t)}{N(t)} \tag{3}$$

$$= \frac{s_{reported}(t)}{p_0 n_{any}(t)} \tag{4}$$

$$\tag{5}$$

Unfortunately, we do not have any way to estimate p_0, i.e. the probability that app users report sexual intercourse in the app. However, since we assumed that this probability is stable over time, we can compute the **relative frequency of sexual intercourse** $x(t)$.

We define the relative frequency of sexual intercourse $x(t)$ as the variation of the frequency of sexual intercourse around its mean value. In other words, the sexual activity frequency is expressed in terms of its mean value and the temporal variations around this reference value: $f(t) = f_0 x(t)$.

We can estimate $x(t)$ from our app data as:

$$\hat{x}(t) = \frac{s_{reported}(t)}{n_{any}(t)} \frac{1}{X_0} \tag{6}$$

$$\tag{7}$$

where X_0 is a normalizing factor such that the mean of $\hat{x}(t)$ is equal to 1.

We make the same assumptions for tree of our four control features (sleep, breast pain and exercise) but not to compute the relative frequency of 'medium bleeding' as logging periods are the primary reason Clue users use the app and this likely does not depend on user engagement with the app but rather whether they are currently actively using the app or not (which we account for in the n_users variable which counts the number of active users).

```
tracking_pop_agg = tracking_pop_agg %>%
  group_by(country_area, BC, age_cat) %>%
  mutate(x_sex = n_sex/n_any,
         x_sex = x_sex /mean(x_sex, na.rm = TRUE),

         x_prot_sex = n_prot_sex/n_any,
         x_prot_sex = x_prot_sex/mean(x_prot_sex, na.rm = TRUE),

         x_unprot_sex = n_unprot_sex/n_any,
         x_unprot_sex = x_unprot_sex/mean(x_unprot_sex, na.rm = TRUE),
```

```
      x_long_sleep = n_long_sleep/n_any,
      x_long_sleep = x_long_sleep/mean(x_long_sleep, na.rm = TRUE),

      x_exercise = n_exercise/n_any,
      x_exercise = x_exercise/mean(x_exercise, na.rm = TRUE),

      x_breast_pain = n_breast_pain/n_any,
      x_breast_pain = x_breast_pain/mean(x_breast_pain, na.rm = TRUE),

      x_medium_bleeding = n_medium_bleeding/n_users,
      x_medium_bleeding = x_medium_bleeding/
        mean(x_medium_bleeding, na.rm = TRUE)
      )
```

```
for_comparison =
  tracking_pop_agg %>%
      filter(age_cat == "all") %>%
      group_by(country_area, BC) %>%
      mutate(r_sex = n_sex/n_users,
             r_sex = r_sex/mean(r_sex, na.rm = TRUE)) %>%
  select(country_area, BC, date, x_sex, r_sex) %>%
  pivot_longer(., cols = c(x_sex, r_sex),
               names_to = "relative_sexual_activity",
               values_to = "x") %>%
  mutate(relative_sexual_activity =
           ifelse(relative_sexual_activity == "x_sex",
                  "adjusted for changes in reporting behavior",
                  "non adjusted for changes in reporting behavior"))


ggplot(for_comparison,
       aes(x = date, y = x, col = relative_sexual_activity)) +
  geom_hline(yintercept = 1, col = "gray40")+
  geom_line(alpha = 0.5) +
  facet_grid(country_area ~ BC) +
  scale_color_manual("",values = c("steelblue","tomato")) +
  theme(legend.position = "bottom",
        strip.text.y = element_text(angle = 0, hjust = 0))
```

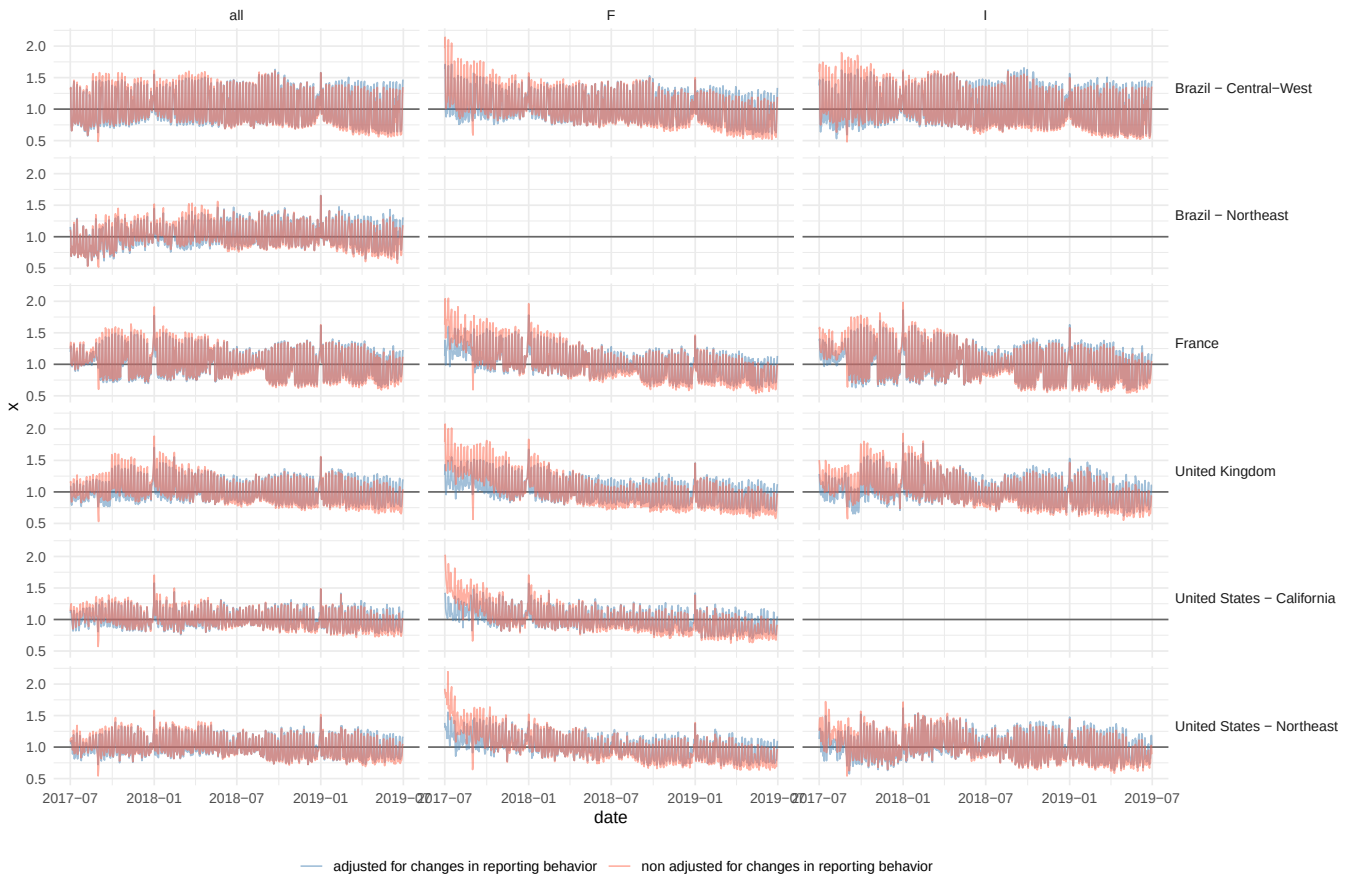


Figure 13: Comparing relative sexual activity when adjusting (or not) for changes in reporting behavior

From this visualization, we can see that adjusting for reporting behavior changes help in removing or attenuating upward biases at the start of time-series and downward biases at the end of time-series. It also successfully adjust for the dip in reporting due to technical difficulties in August 2017. Residuals "early" adopters effects are found, despite adjustments, at the start of time-series, especially in those where the number of users is lower.

We will adjust for that when modeling sexual activity by giving a weight proportional to the number of users at each time-point (see next section).

3.7 Formatting to long format

Given that the aggregated time-series with sex and control features logs will be used in different files, we save them separately. Additionally, we transform both tables to a "long format" such that the type of sex (protected, unprotected, all) or the type of control feature becomes a column on which we can aggregate or group.

3.7.1 For sexual behavior

```
clue_sex_agg = tracking_pop_agg %>%
  select(country_area, BC, age_cat, date,
         n_users, n_any,
         n_sex, n_prot_sex, n_unprot_sex,
         x_sex, x_prot_sex, x_unprot_sex) %>%
  rename(n_all_sex = n_sex,
         x_all_sex = x_sex) %>%
  pivot_longer(cols = c(n_all_sex, n_prot_sex, n_unprot_sex,
                        x_all_sex, x_prot_sex, x_unprot_sex),
               names_to = c(".value","sex_type"),
```

```
          names_pattern = "(.)_(.*)")

head(clue_sex_agg)
```

country_area	BC	age_cat	date	n_users	n_any	sex_type	n	x
Brazil - Central-West	F	<= 23	2017-07-01	1855	540	all_sex	118	1.629741
Brazil - Central-West	F	<= 23	2017-07-01	1855	540	prot_sex	47	2.019502
Brazil - Central-West	F	<= 23	2017-07-01	1855	540	unprot_sex	39	1.483521
Brazil - Central-West	F	<= 23	2017-07-02	1898	588	all_sex	141	1.788431
Brazil - Central-West	F	<= 23	2017-07-02	1898	588	prot_sex	53	2.091408
Brazil - Central-West	F	<= 23	2017-07-02	1898	588	unprot_sex	43	1.502152

```
nrow(clue_sex_agg) == nrow(tracking_pop_agg)*3
```

```
## [1] TRUE
```

3.7.2 For control features

```
control_features_agg = tracking_pop_agg %>%
  select(country_area, BC, age_cat, date,
         n_users, n_any,
         n_medium_bleeding, n_long_sleep, n_exercise, n_breast_pain,
         x_medium_bleeding, x_long_sleep, x_exercise, x_breast_pain) %>%
  pivot_longer(cols = (starts_with("n_") | starts_with("x_")) &
                 !(starts_with("n_users") | starts_with("n_any")) ,
               names_to = c(".value","control_features"),
               names_pattern = "(.)_(.*)")

head(control_features_agg)
```

country_area	BC	age_cat	date	n_users	n_any	control_features	n	x
Brazil - Central-West	F	<= 23	2017-07-01	1855	540	medium_bleeding	78	0.9314015
Brazil - Central-West	F	<= 23	2017-07-01	1855	540	long_sleep	44	1.4138076
Brazil - Central-West	F	<= 23	2017-07-01	1855	540	exercise	15	0.7948971
Brazil - Central-West	F	<= 23	2017-07-01	1855	540	breast_pain	66	1.0652881
Brazil - Central-West	F	<= 23	2017-07-02	1898	588	medium_bleeding	92	1.0736874
Brazil - Central-West	F	<= 23	2017-07-02	1898	588	long_sleep	61	1.8000472

```
#nrow(control_features_agg) == nrow(tracking_pop_agg)*4
```

3.8 Visualizations of the aggregated time-series

We visualize here the aggregated time-series for each country-area and for users of any birth-control (BC = "all") and of any age (age_cat = "all").

```
A = clue_sex_agg %>%
  filter(BC == "all",
         age_cat == "all",
         sex_type == "all_sex") %>%
  mutate(country_area_col = dict$country_area$country_area_col[match(country_area, dict$country_area$country_area)])
```

```
ggplot(A, aes(x = date, y = n_users, col = country_area_col))+
  geom_line()+
  scale_color_identity(
    "Location",
    guide = "legend",
    breaks = dict$country_area$country_area_col,
    labels = dict$country_area$country_area)+
  ylab("# of active users")
```

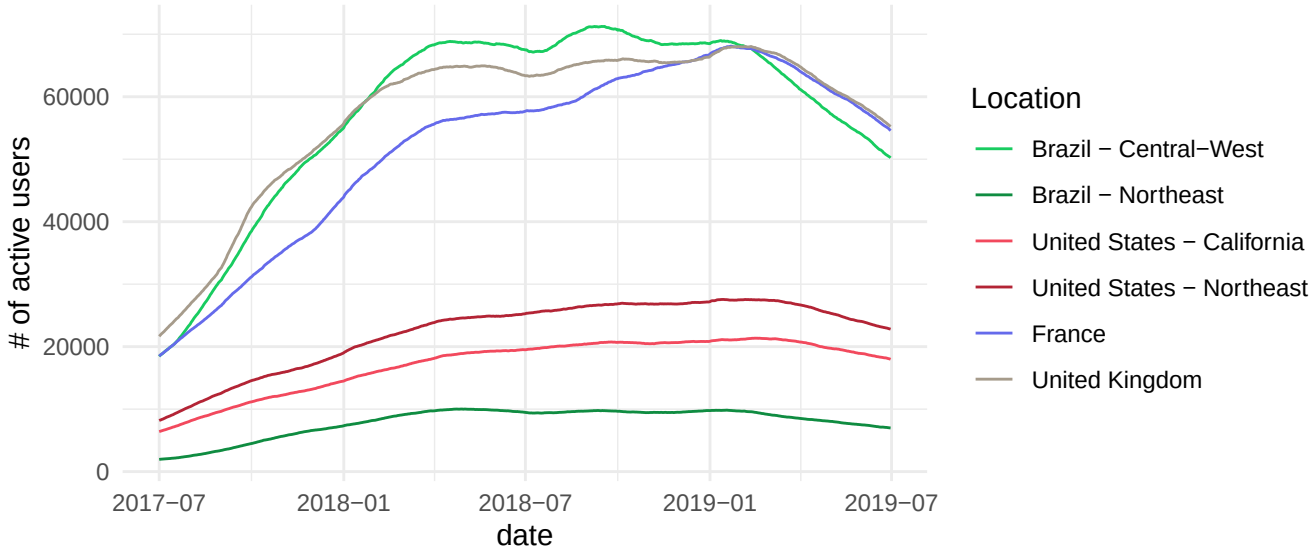


Figure 14: Number of active users at each time-point for each location

```
ggplot(A, aes(x = date, y = n, col = country_area_col))+
  geom_line()+
  scale_color_identity(
    "Location",
    guide = "legend",
    breaks = dict$country_area$country_area_col,
    labels = dict$country_area$country_area) +
  guides(col = FALSE)+
  ylab("# of sexual intercourses logged")
```

```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.
```

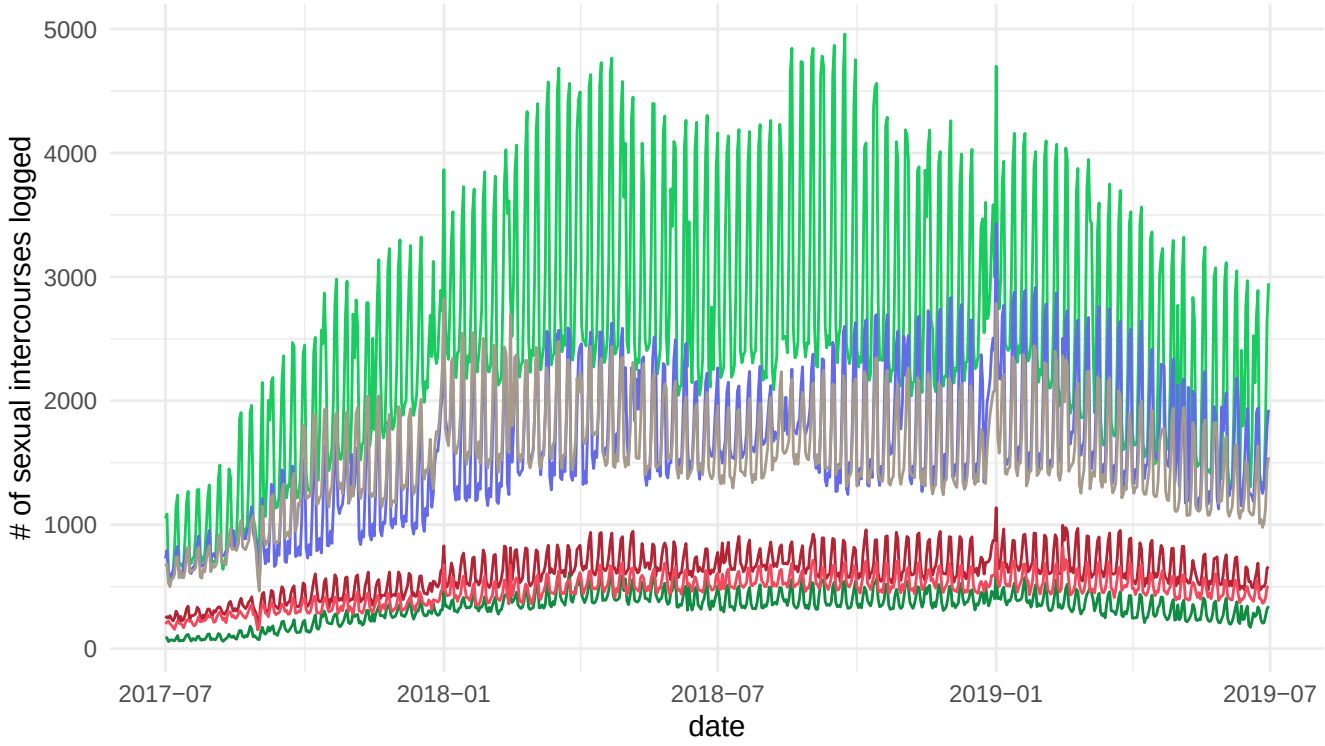


Figure 15: Number of sex logs at each time-point

```
ggplot(A, aes(x = date, y = x, col = country_area_col))+
  geom_line()+
  scale_color_identity(
    "Location",
    guide = "legend",
    breaks = dict$country_area$country_area_col,
    labels = dict$country_area$country_area) +  guides(col = FALSE)+
  ylab("# of sex / # of active users")
```

```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.
```

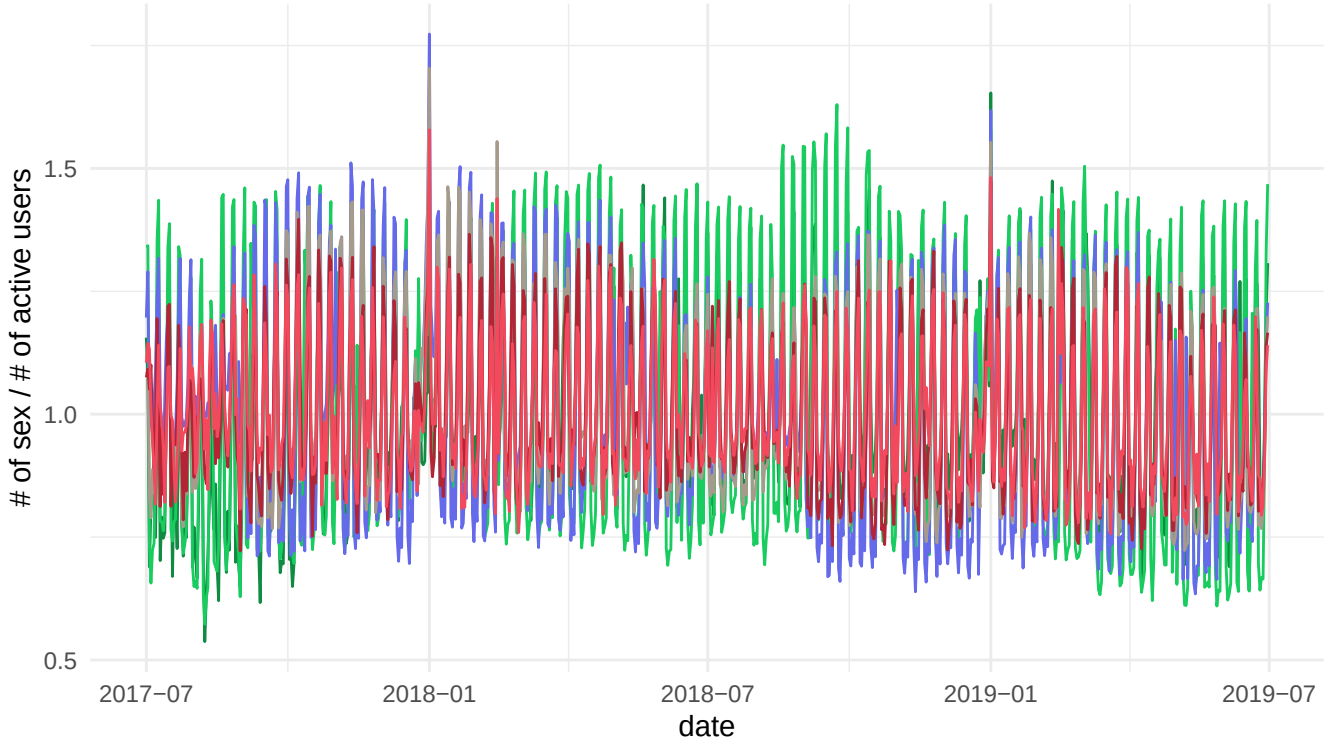


Figure 16: Relative number of sex logs at each time-point

3.9 Saving and exporting aggregated time-series

```
write_feather(
  clue_sex_agg,
  path =
    "../Data/4_clue_data_aggregated/aggregated_sex_counts_clue_July2017-June2019_incl.feather"
  )

write_feather(
  control_features_agg,
  path =
    "../Data/4_clue_data_aggregated/aggregated_control_features_counts_clue_July2017-June2019_incl.feather"
  )


write_csv(
  clue_sex_agg,
  file =
    "../Data/4_clue_data_aggregated/aggregated_sex_counts_clue_July2017-June2019_incl.csv"
  )


write_csv(
  control_features_agg,
  file = "../Data/4_clue_data_aggregated/aggregated_control_features_counts_clue_July2017-June2019_incl.csv"
  )
```

4 Birth Models

4.1 Mathematical Models

Mathematical model for number of births:

$$C(t) = f(t)S(t) \tag{8}$$

$$B(t) = \int_{t-max(G)}^{t-min(G)} d^G(\tau)\,(1 - l(\tau))\,C(\tau)d\tau \tag{9}$$

where

$C(t)$ = number of conceptions at time t;

$f(t)$ is the fertility at time t (= the odds of a conception from a sexual intercourse);

$S(t)$ the number of sexual intercourses at time t;

$B(t)$ is the number of births at time t;

G is the gestation duration (i.e. the duration of a pregnancy)

$d^G(t)$ is the probability density of the gestation duration and;

$l(t)$ is the pregnancy loss rate at time t (= the fraction of pregnancies ending up in a loss).

This model can be rewritten as

$$B(t) = \int_{t-max(G)}^{t-min(G)} d^G(\tau)\,(1 - l(\tau))\,f(\tau)\,S(\tau)d\tau \tag{10}$$

$$\implies B(t) = \int_{t-max(G)}^{t-min(G)} d^G(\tau)\,F(\tau)\,S(\tau)\,d\tau \tag{11}$$

Where $F(\tau)$ is a function combining fertility and loss rate.

In discrete time-steps, the model becomes:

$$B_t = \sum_{\tau=t-max(G)}^{t-min(G)} d_\tau\,F_\tau\,S_\tau \tag{12}$$

We will assume that the gestation duration follows a normal distribution around the average distribution duration $\bar{G}$ of standard deviation = σ_G days:

$$G \sim \mathcal{N}(\bar{G}, \sigma_G) = d_\tau \tag{13}$$

4.1.1 Comparing actual births with simulated births records from the sex reports of the app users.

In this study, we will compare the actual monthly birth records B_t^m (m stands for *measured*) with simulated births B_t^e (e stands from *estimated*) from the sexual behavior of the app users (S_t) while making different assumptions on the fertility F_t (see Models A, B & C below).

4.1.2 Births, fertility and sexual behavior expressed as relative changes around their average value.

Because we have data for a small fraction of the population (the app users) and because we don't know how many of the app users are never reporting sexual intercourses, we cannot extrapolate the absolute number of births from the number of sexual intercourses reported in the app. However, we can compare the relative changes throughout the year in reported sexual intercourse with the relative variations in births.

Two approaches are possible to compare the relative changes:

1. expressing B_t, S_t and F_t as a variation around a mean value.

I.e. $X_t = \bar{X}\,(1 + \tilde{X}_t)$

The model becomes

$$B_t = \sum_{\tau=t-max(G)}^{t-min(G)} d_\tau\, F_\tau\, S_\tau \tag{14}$$

$$= \sum_{\tau=t-max(G)}^{t-min(G)} d_\tau\, \bar{F}\,(1+\tilde{F}_\tau)\,\bar{S}\,(1+\tilde{S}_\tau) \tag{15}$$

$$= \bar{F}\bar{S} \sum_{\tau=t-max(G)}^{t-min(G)} d_\tau\,(1+\tilde{F}_\tau)\,(1+\tilde{S}_\tau) \tag{16}$$

$$= E \sum_{\tau=t-max(G)}^{t-min(G)} d_\tau\,(1+\tilde{F}_\tau)\,(1+\tilde{S}_\tau) \tag{17}$$

where E is a scaling factor that reflects how the relative variations in sexual intercourse translates into births.

2. expressing B_t and S_t as the fraction of the total number of yearly births or sexual intercourses: $X_t = \mathbf{X}\,x(t)$ where **X** is the total number of births or sexual intercourses in the population.

In this case, the model becomes

$$B_t = \sum_{\tau=t-max(G)}^{t-min(G)} d_\tau\, F_\tau\, S_\tau \tag{18}$$

$$= \sum_{\tau=t-max(G)}^{t-min(G)} d_\tau\, \mathbf{F}\, F_\tau\, \mathbf{S}\, s_\tau \tag{19}$$

$$= \mathbf{S} \sum_{\tau=t-max(G)}^{t-min(G)} d_\tau\, F_\tau\, s_\tau \tag{20}$$

$$= E_2 \sum_{\tau=t-max(G)}^{t-min(G)} d_\tau\, F_\tau\, s_\tau \tag{21}$$

where $E_2 = \mathbf{S}$ is a scaling factor.

Note that we have the equivalence: $(1 + \tilde{S}_t) = 365 * s_t$ over a non-leap year (for leap year, the multiplicative factor is 366).

In our implementation, we chose the first approach:

$$B_t = E \sum_{\tau=t-max(G)}^{t-min(G)} d_\tau \left(1 + \tilde{F}_\tau\right)\left(1 + \tilde{S}_\tau\right) \tag{22}$$

4.1.3 Model A: Constant Fertility, Varying Sexual Behavior.

In **model A**, we assume that f and l (and thus F) are constant (not seasonal): seasonal patterns in births are driven by seasonal patterns in sexual intercourses.

We can thus simplify to:

$$B_t = E \sum_{\tau=t-max(G)}^{t-min(G)} d_\tau \left(1 + \tilde{S}_\tau\right) \tag{23}$$

4.1.4 Model B: Varying fertility, Constant Sexual Behavior

In **model B**, we assume that seasonal variations in birth is only driven by varying fertility and that variations in sex does not contribute to the seasonal variations ($S_t = \bar{S}$):

$$B_t = E \sum_{\tau=t-max(G)}^{t-min(G)} d_\tau \left(1 + \tilde{F}_\tau\right) \tag{24}$$

$$\text{with } \tilde{F}_\tau = \alpha \cos(\omega \left(\tau - T\right)) \tag{25}$$

$$\text{and } \omega = \frac{2\pi}{P} \tag{26}$$

Where

α is the relative amplitude of the fertility variation,

T is the time of peak fertility,

ω is the frequency of the sine curve and

P the period (i.e. 12 months or 365 days).

4.1.5 Model C: Varying fertility, Varying Sexual Behavior

In **model C**, we assume that both varying fertility and sexual behavior drive births rhythms.

$$B_t = E \sum_{\tau=t-max(G)}^{t-min(G)} d_\tau \left(1 + \tilde{F}_\tau\right)\left(1 + \beta\tilde{S}_\tau\right) \tag{27}$$

$$\text{with } \tilde{F} = \alpha \cos(\omega \left(t - T\right)) \tag{28}$$

$$\text{and } \omega = \frac{2\pi}{P} \tag{29}$$

Where

α is the relative amplitude of the fertility variation,

β is the relative amplitude of the variations in sexual activity,

T is the time of the year with peak fertility,

ω is the frequency of the sine curve and

P the period (i.e. 12 months or 365 days).

Note that this model does not make assumptions on the underlying biological causes of fertility. The variations in fertility may originate from variation in female fertility (either in the conception rate or the loss rate) or in male fertility or both.

4.1.6 Model parameters

Each model has some parameters which need to be fixed or estimated.

4.1.6.1 Scaling factor E, which is the average daily birth rate, is computed from the births records themselves:

- First the monthly births are normalized by the number of days in each month (we re-scale the births as if each month had a duration of 30 days).
- Then the moving average of these normalized monthly births is computed over a period of 12 months
- Finally, this moving average is divided by 30 to obtain the average daily births and values are extrapolated to obtain a smooth variation of the daily births over the years with available data.

4.1.6.2 Fertility and sexual activity parameters There are two fertility parameters α and T

α is the relative amplitude of the fertility cosine curve. It can take values between 0 and 1 as a relative amplitude larger than one would lead to negative values ($\tilde{F} = \bar{F}\,(1 + \alpha\cos(\omega\,(t - T)))$. T is the peak time of fertility, i.e. when the cos takes its maximal value. Time is expressed as "fraction of the year", to T also takes its value in [0,1].

There is one parameter to adjust the relative amplitude of the sexual activity: β.

These three parameters are estimated so that they minimize the sum of square of the residuals (SSR) between the simulated births and the actual birth records:

$$\text{SSR} = \sum_t (B_t^m - B_t^e)^2$$

Where B_t^m (m for measured) are the birth records at time t and B_t^e (e for estimated) are the simulated births at time t.

We use the function `optim` with `method = "L-BFGS-B"` for the optimization of these parameters.

4.1.6.3 Gestation duration.

4.1.6.3.1 Average gestational duration While the average gestational age at birth (gestational duration) is of approximately 9 months (38 weeks), differences in gestational age at birth were found in different countries (*9*).

In (*9*), gestational age at birth in France was of 39.4 weeks, of 39.6 weeks in the UK and of 39 weeks in the US (California excluded).

These differences can be explained by different preterm birth rates, consistently found higher in the US than in most European countries (*10*, *11*), or by delivery choices (e.g. planned C-sections) and most common method for the evaluation of the gestational age (e.g. estimation by ultrasounds or based on the last menstrual period).

Here we fixed the average gestation duration ($\bar{G}$) to a given value for each considered country based on the existing literature, when available, or, for Brazil, based on the alignment of the high-frequency fluctuations in the birth curve with the sexual behavior peaks (See section 4.8).

```r
G_table = dict$country_area %>% mutate(G = c(37.5,37.5,37.5,37.5,38,38.5)) %>% select(country_area, G)

write_feather(G_table, path = str_c(IO$out_Rdata,"Gestation_par_table.feather"))

kable(G_table, format = "pandoc", caption = "Average gestation duration (in weeks) for each considered area")
```

Table 9: Average gestation duration (in weeks) for each considered area

country_area	G
Brazil - Central-West	37.5
Brazil - Northeast	37.5
United States - California	37.5
United States - Northeast	37.5
France	38.0
United Kingdom	38.5

4.1.6.3.2 Variability of gestational duration In normal, non pre-term births, the natural gestational age at birth was found to show important variation (*8*). Following the data presented in (*8*), the standard deviation of the gestational duration was set to σ_G = 10 days.

```r
t = seq(30*7, 45*7)

d = foreach(ca = G_table$country_area, .combine = bind_rows) %do% {
  this_ca = G_table %>% filter(country_area == ca)
  res = this_ca[rep(1,length(t)),]
  res = res %>% mutate(t = t, d = dnorm(t, mean = this_ca$G*7, sd = Gsd0), G = this_ca$G*7)
  res
}

br = seq(min(t), max(t), by = 14)

d = d %>%
  mutate(country_area_wrapped = str_replace(country_area, " - ","\n"),
         country_area_col = dict$country_area$country_area_col[match(country_area, dict$country_area$country_area)])

g_d = ggplot(d, aes(x = t, y = d, fill = country_area_col))+
  geom_area(alpha = 0.6)+
  geom_vline(aes(xintercept = G, col = country_area_col))+
  scale_color_identity()+
  scale_fill_identity()+
  scale_x_continuous(breaks = br , labels = br/7)+
  scale_y_continuous(breaks = NULL)+
  xlab("G, gestation duration\n(weeks)")+
  ylab(expression(paste("Density, d",tau)))+  #expression(paste("Value is ", sigma,",", R^{2},'=0.6'))
  facet_grid(country_area_wrapped ~ ., scale = "free")+
  theme(strip.text.y = element_text(angle = 0, hjust = 0))
g_d
```

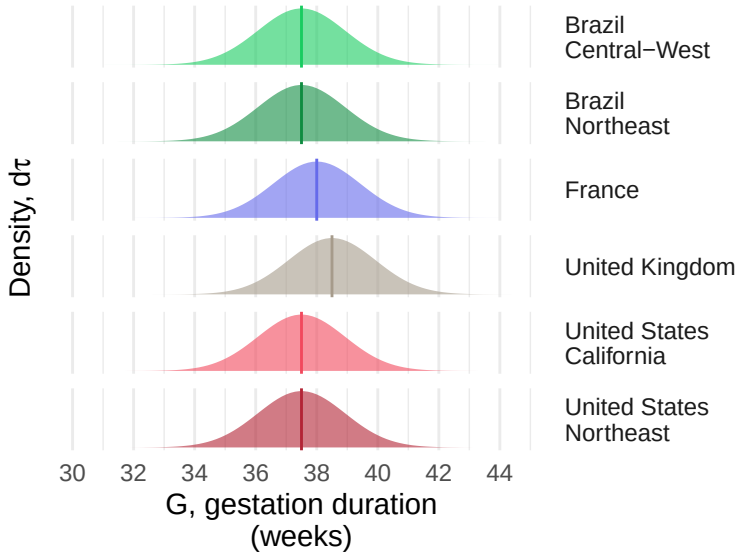


Figure 17: Gestation duration density for each considered location.

4.2 Workflow

For each user category (i.e. country/area, age group and birth control type)

and each type of sex (protected, unprotected, sum of both sex type):

1. **Sexual behavior**
    a. Model the sexual behavior as a combination of a weekly trend, a seasonal trend and a holiday response
2. **Overall births trend (average daily birth)**
    a. Correct for the number of days in each month
    b. Compute the average daily birth for each country/area (the scaling factor E)
3. **Optimize the model parameters** (α, β and T) for each birth model (A, B or C); i.e. minimize the SSR from several initial values of the parameters by:
    a. Predicting the daily sexual behavior from the weekdays-seasons-holidays model for the time-window which have births records available.
    b. Simulating the daily births
    c. Aggregating as a monthly time-series
    d. SSR: Computing the difference (the residuals) between the simulated and actual births.
4. **Simulate monthly births** with the optimized parameters
5. **Determine best birth model (A, B or C)**
    a. By comparing the SSR and the AIC (Akaike Information Criteria) for each model
    b. By performing a **seasonal decomposition** to compare the seasonal trends of the actual and simulated births.

4.3 Sexual behavior: modelling relative changes

```
clue_sex_agg =
  read_feather(
    "../Data/4_clue_data_aggregated/aggregated_sex_counts_clue_July2017-June2019_incl.feather")
str(clue_sex_agg)
```

```
## tibble [76,650 x 9] (S3: tbl_df/tbl/data.frame)
##  $ country_area: chr [1:76650] "Brazil - Central-West" "Brazil - Central-West" "Brazil - Central-West" "Brazil - Central-West" ...
##  $ BC          : chr [1:76650] "F" "F" "F" "F" ...
##  $ age_cat     : chr [1:76650] "<= 23" "<= 23" "<= 23" "<= 23" ...
##  $ date        : Date[1:76650], format: "2017-07-01" "2017-07-01" ...
##  $ n_users     : num [1:76650] 1855 1855 1855 1898 1898 ...
##  $ n_any       : num [1:76650] 540 540 540 588 588 588 583 583 583 551 ...
##  $ sex_type    : chr [1:76650] "all_sex" "prot_sex" "unprot_sex" "all_sex" ...
##  $ n           : num [1:76650] 118 47 39 141 53 43 80 29 25 74 ...
##  $ x           : num [1:76650] 1.63 2.02 1.48 1.79 2.09 ...
```

These data hold daily sex counts aggregated by geographic area and birth control type from the sex logs of the users of the menstrual cycle tracking app Clue as well as the relative sexual activity frequency computed from the sex counts and adjusted for the changes in reporting behavior.

The preparation of these data from the raw logs can be found in section 2 (file 2_app_data_processing_and_filtering.Rmd) while the aggregation and the adjustments have been done in section 3 (file 3_app_data_aggregation.Rmd).

The relative sexual frequency ($x(d)$) correspond to $(1 + \tilde{S(t)})$ in the model described above.

```
A = clue_sex_agg %>%
  filter(BC == "all",
         age_cat == "all",
         sex_type == "all_sex") %>%
  mutate(country_area_col = dict$country_area$country_area_col[match(country_area, dict$country_area$country_area)])


ggplot(A, aes(x = date, y = x, col = country_area_col))+
  geom_line()+
  scale_color_identity()+
  guides(col = FALSE)+
  ylab("detrended relative sex")+
  facet_grid(country_area ~ .)+
  theme(strip.text.y = element_text(angle = 0, hjust = 0))
```

```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.
```

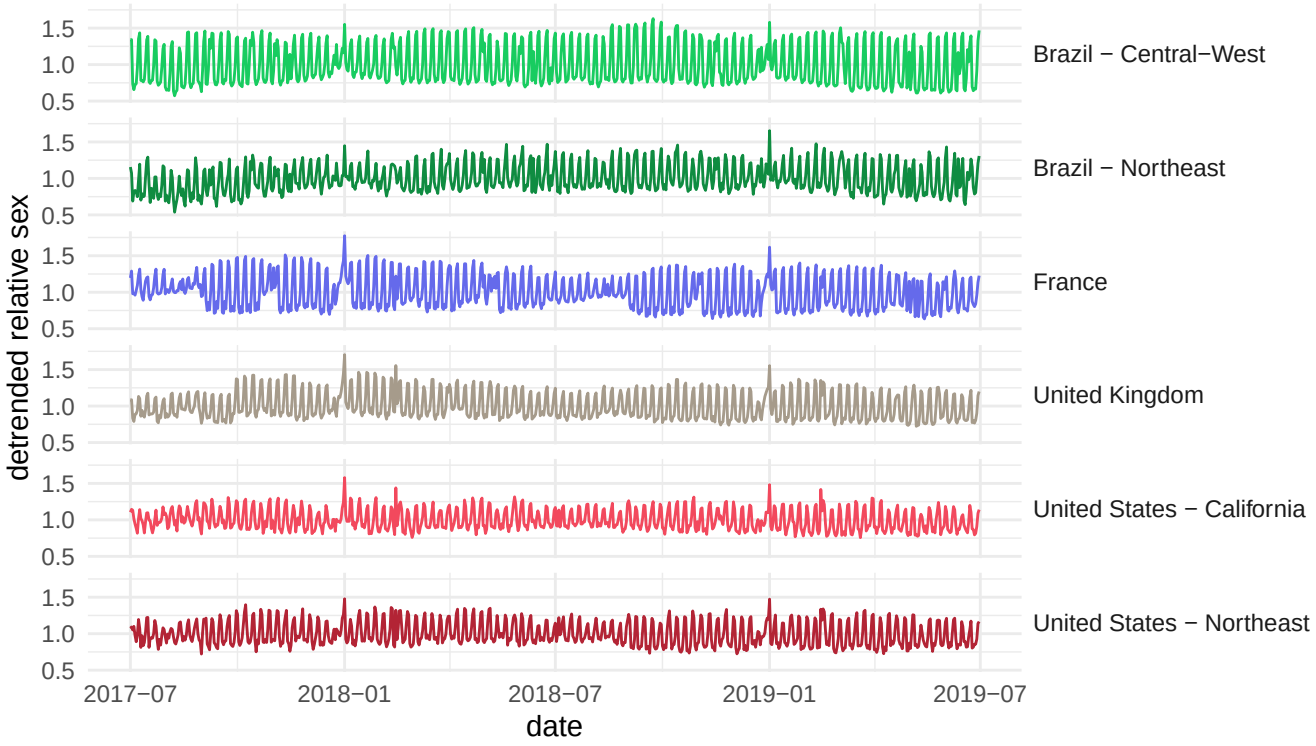


Figure 18: Relative changes in sexual behavior (all users of all age group on any birth control type, all sex).

```
ggplot(A %>%
       mutate(year = year(date) %>% factor(),
              day_of_the_year = yday(date)),
     aes(x = day_of_the_year, y = x, col = year))+
 geom_line()+
 ylab("detrended relative sex")+
 facet_grid(country_area ~ .)+
 theme(strip.text.y = element_text(angle = 0, hjust = 0))
```

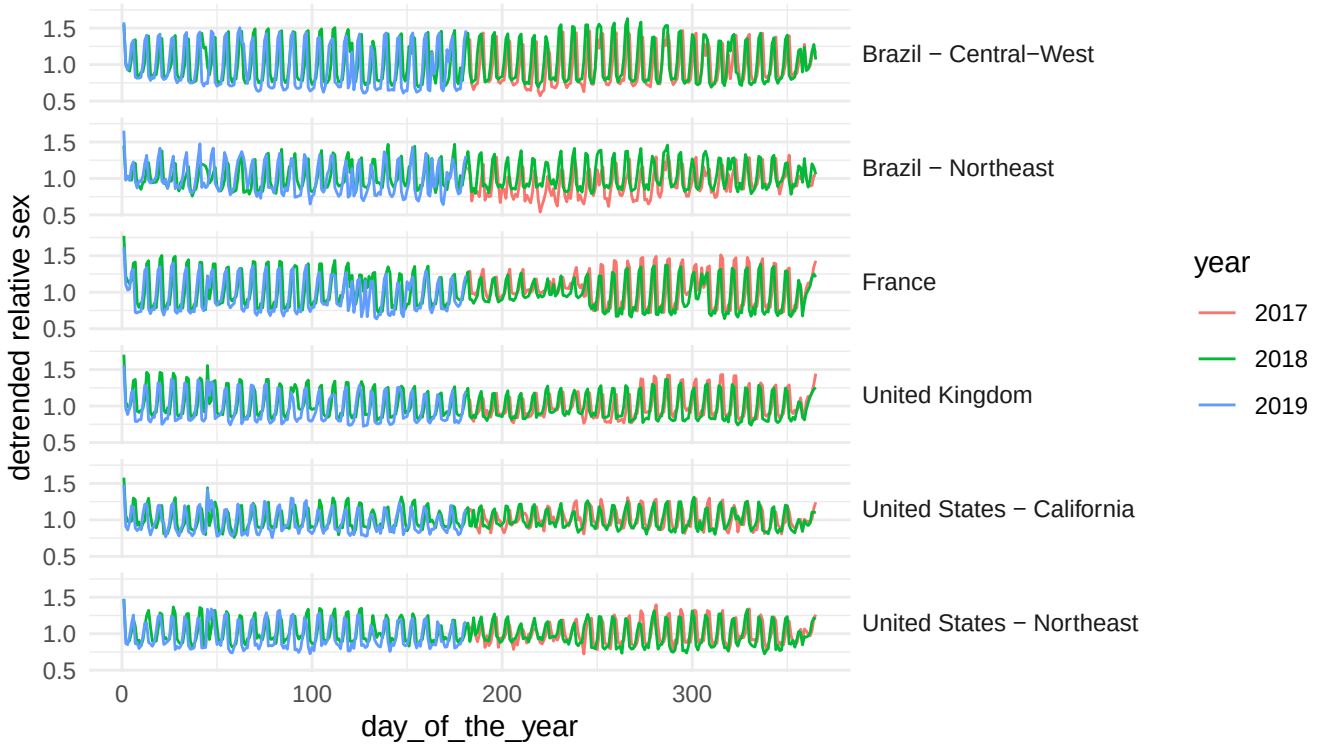


Figure 19: Relative changes in sexual behavior throughout the year (all users of all age group on any birth control type, all sex - two years of data overlapped).

4.3.1 Comparing sexual activity by sex type.

Here we visualize the relative sexual activity and compare by sex type for each location.

```
g = ggplot(clue_sex_agg %>% filter(BC == "all", age_cat == "all"),
       aes(x = date, y = x, col = sex_type)) +
  geom_line(alpha = 0.5)+
  facet_grid(country_area ~ .)

g
```

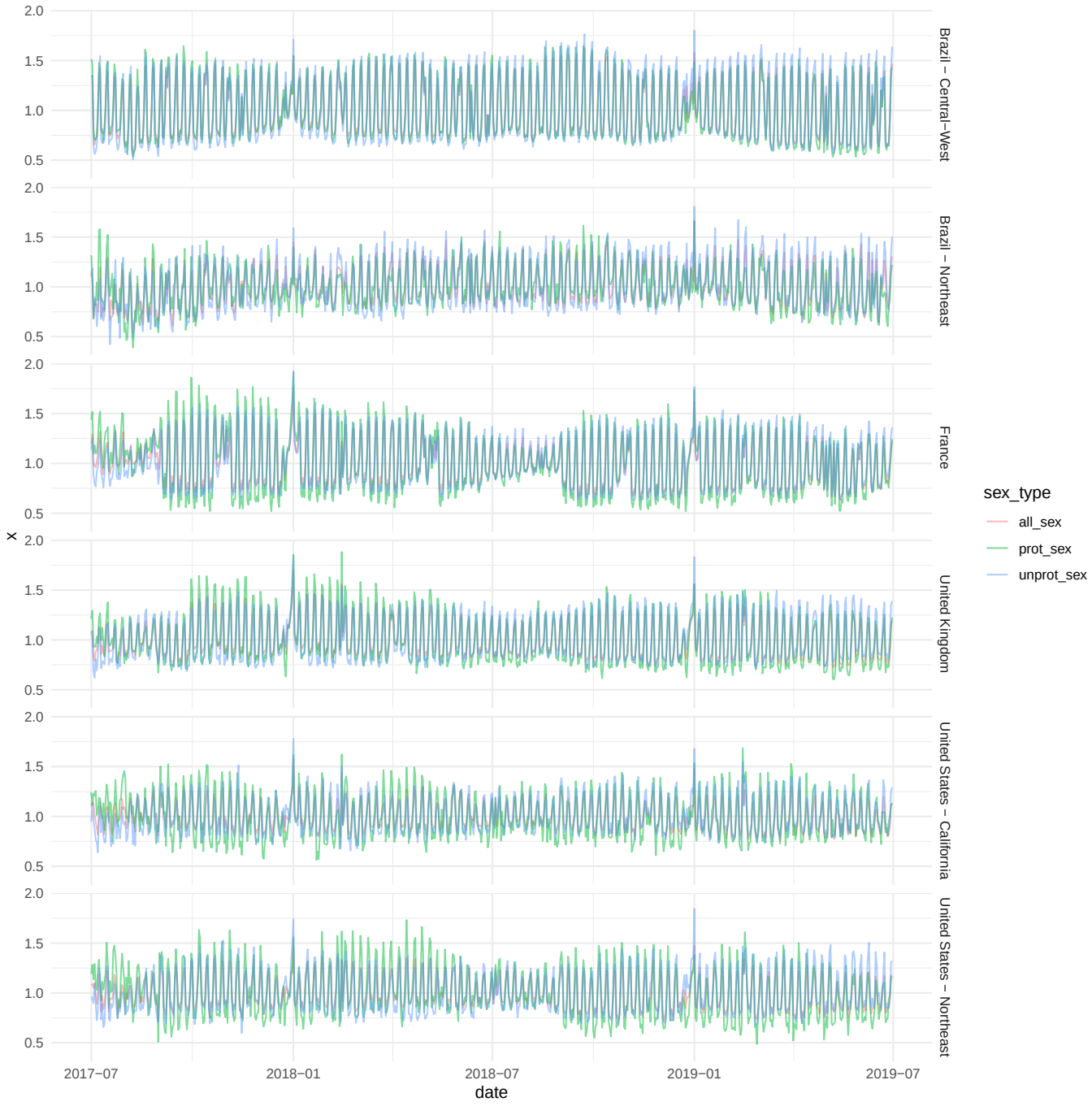


Figure 20: Comparing sexual activity by sex type for all users of each location

```
for(ca in unique(clue_sex_agg$country_area)){
  g = ggplot(clue_sex_agg %>% filter(country_area == ca),
             aes(x = date, y = x, col = sex_type)) +
    geom_line()+
    facet_grid(BC + age_cat ~ .) +
    ggtitle(ca)

  print(g)
}
```

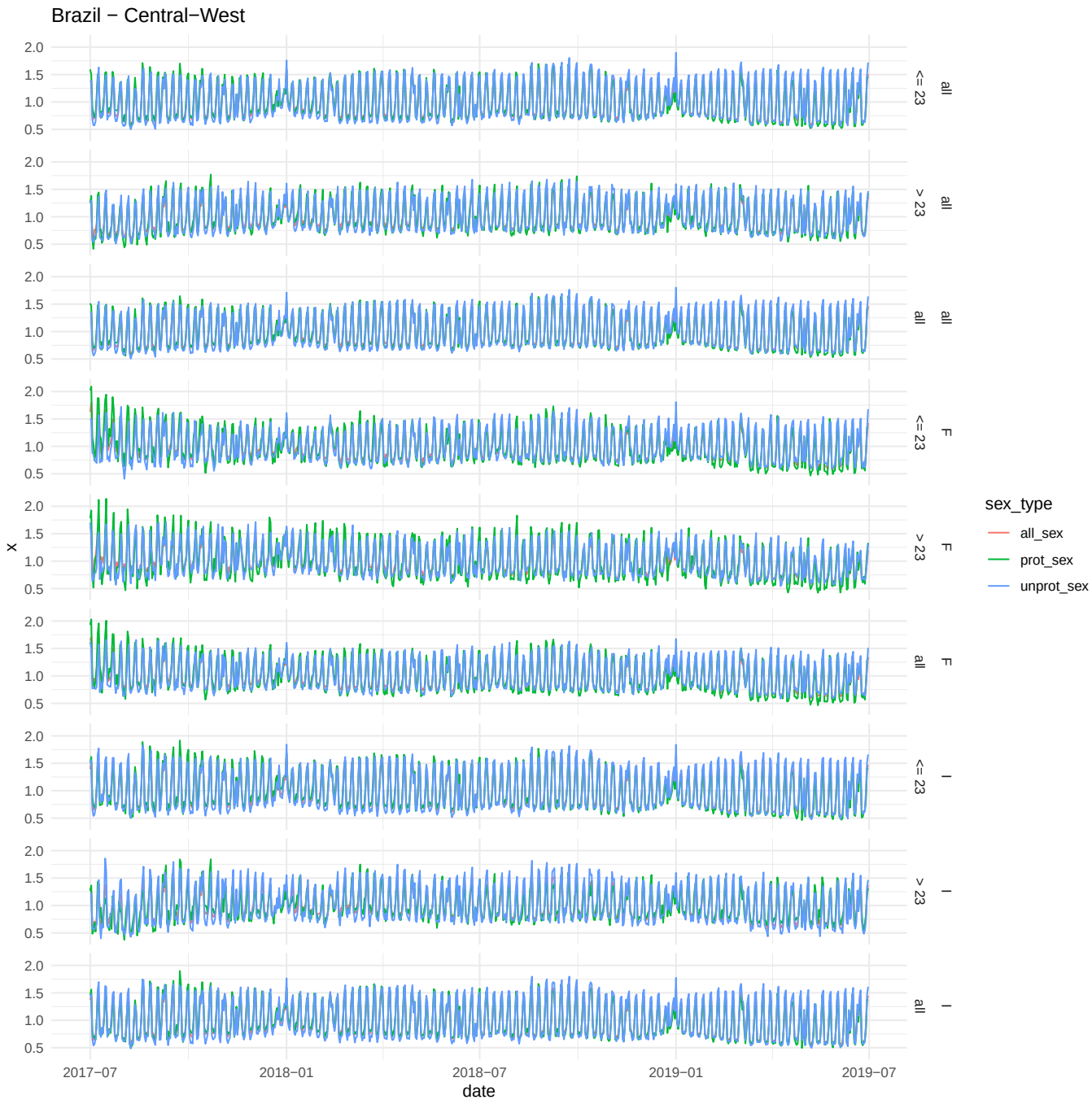


Figure 21: Comparing sexual activity by sex type for each location and user group.

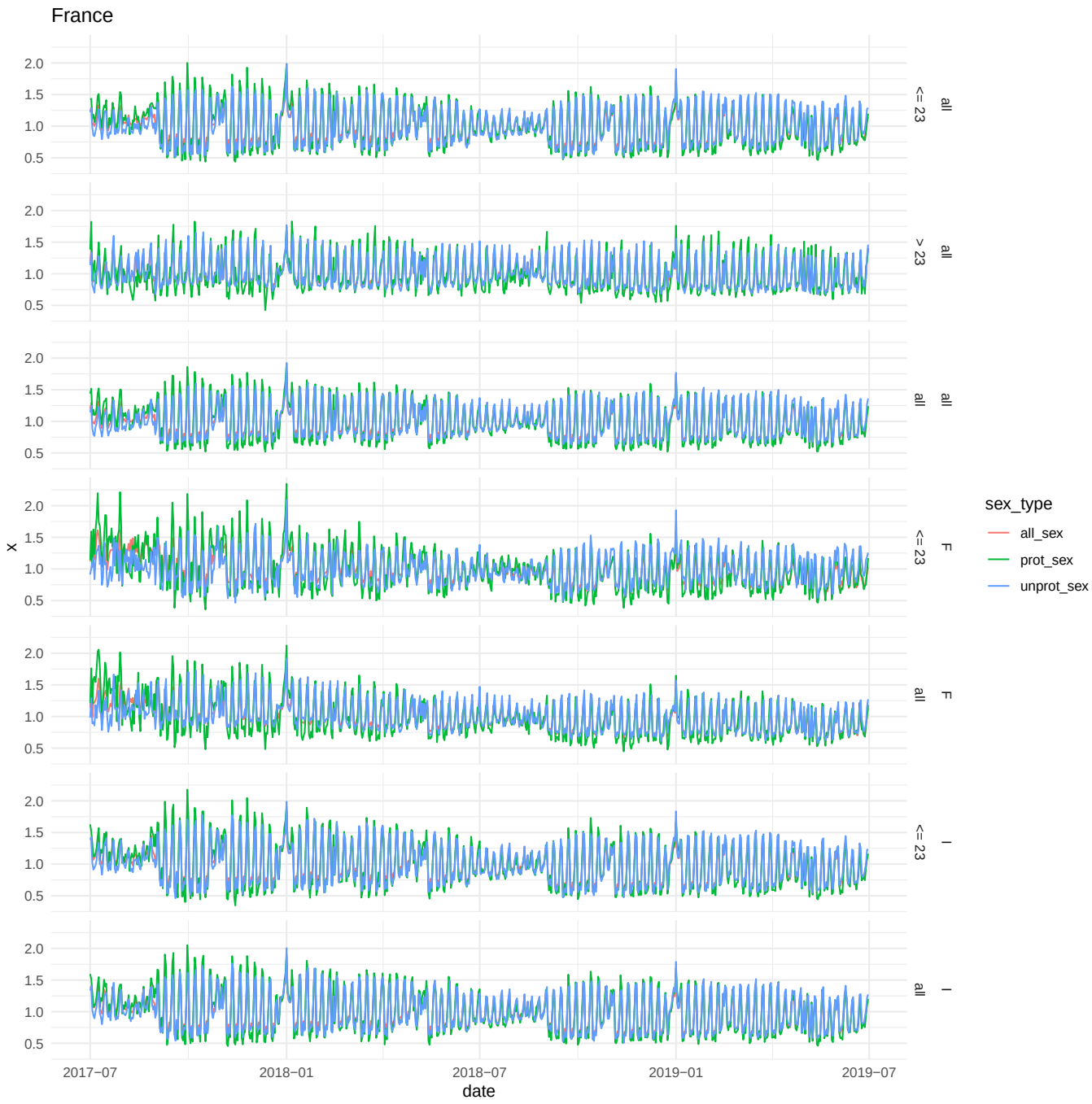


Figure 22: Comparing sexual activity by sex type for each location and user group.

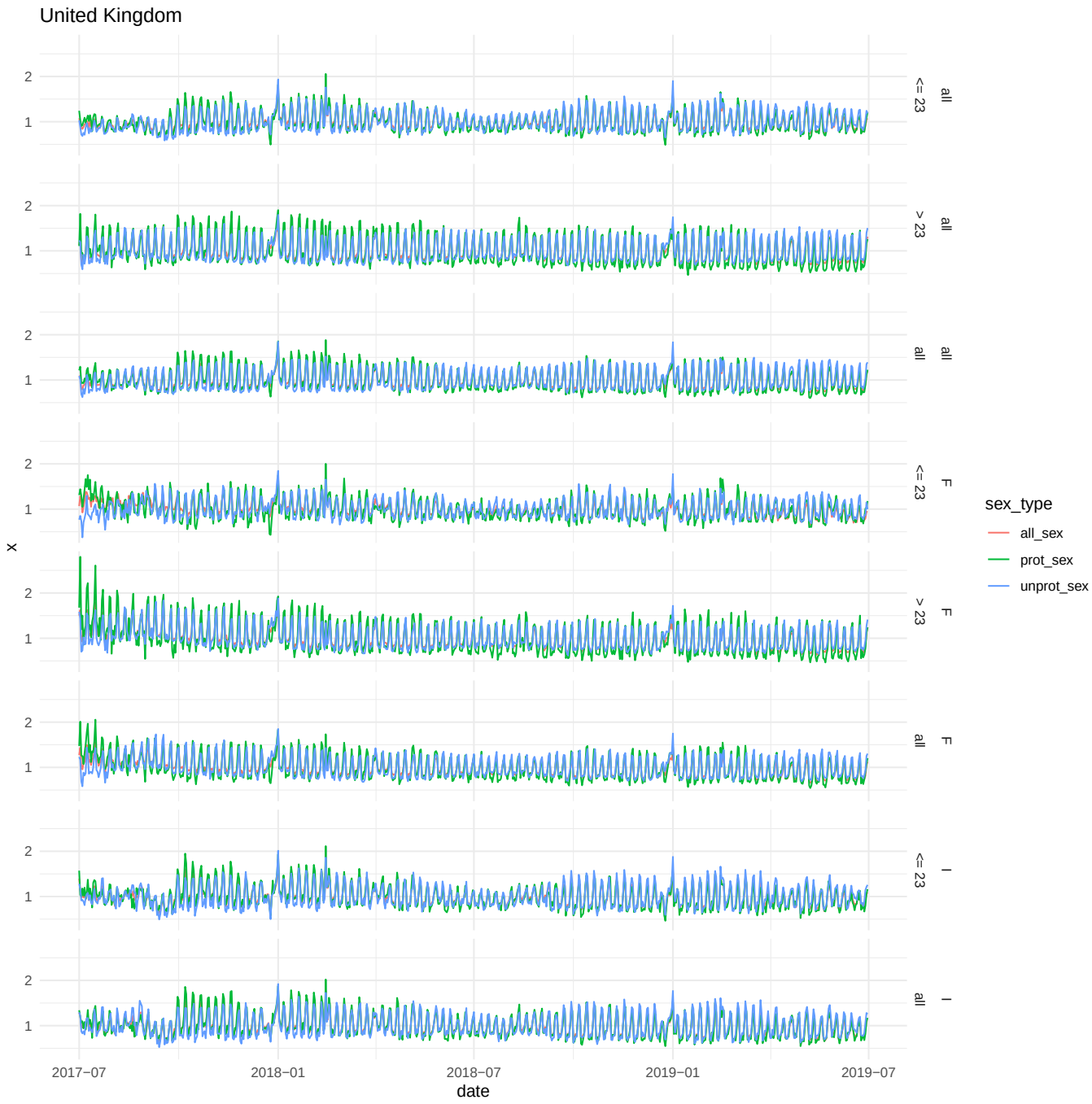


Figure 23: Comparing sexual activity by sex type for each location and user group.

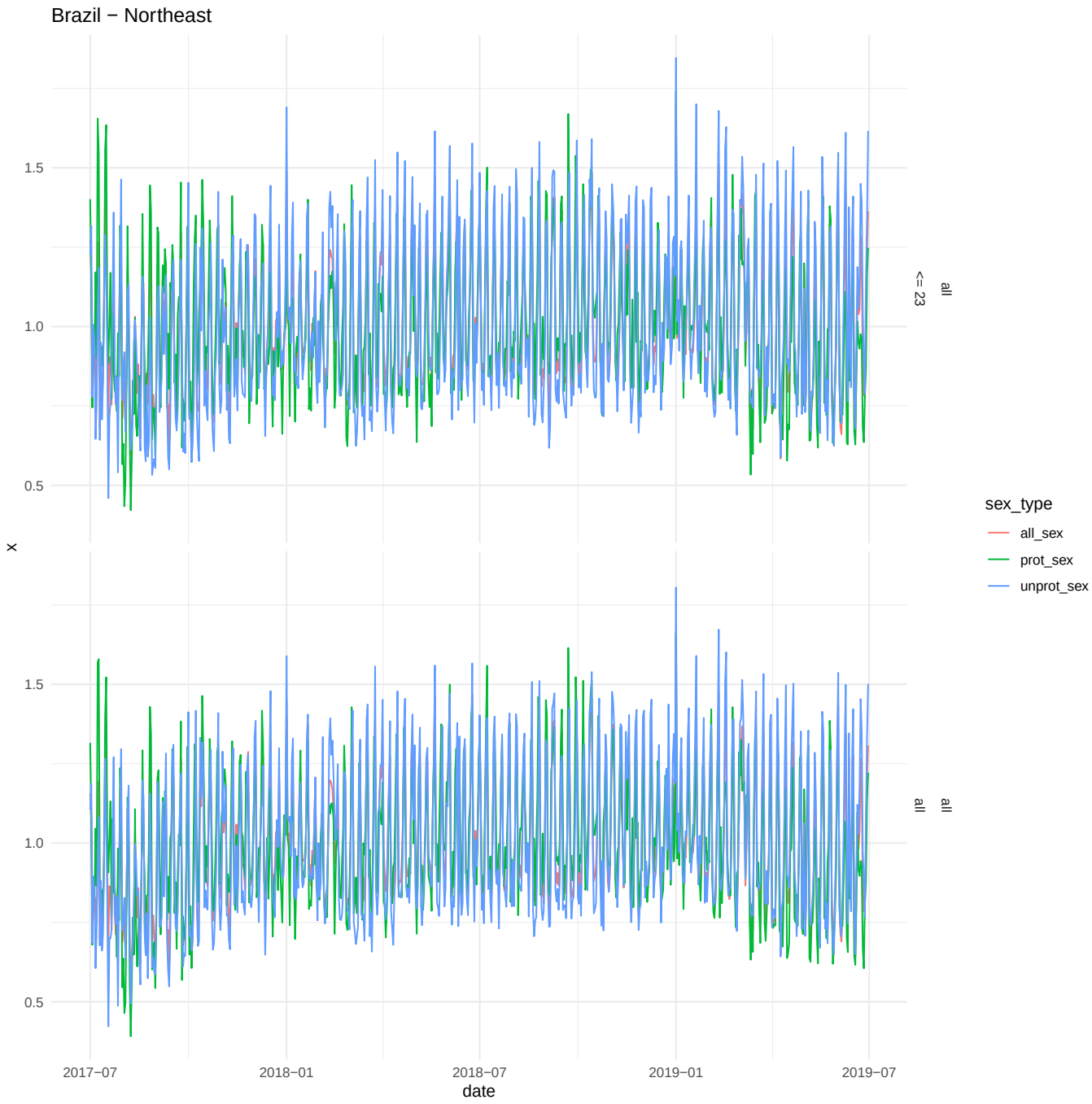


Figure 24: Comparing sexual activity by sex type for each location and user group.

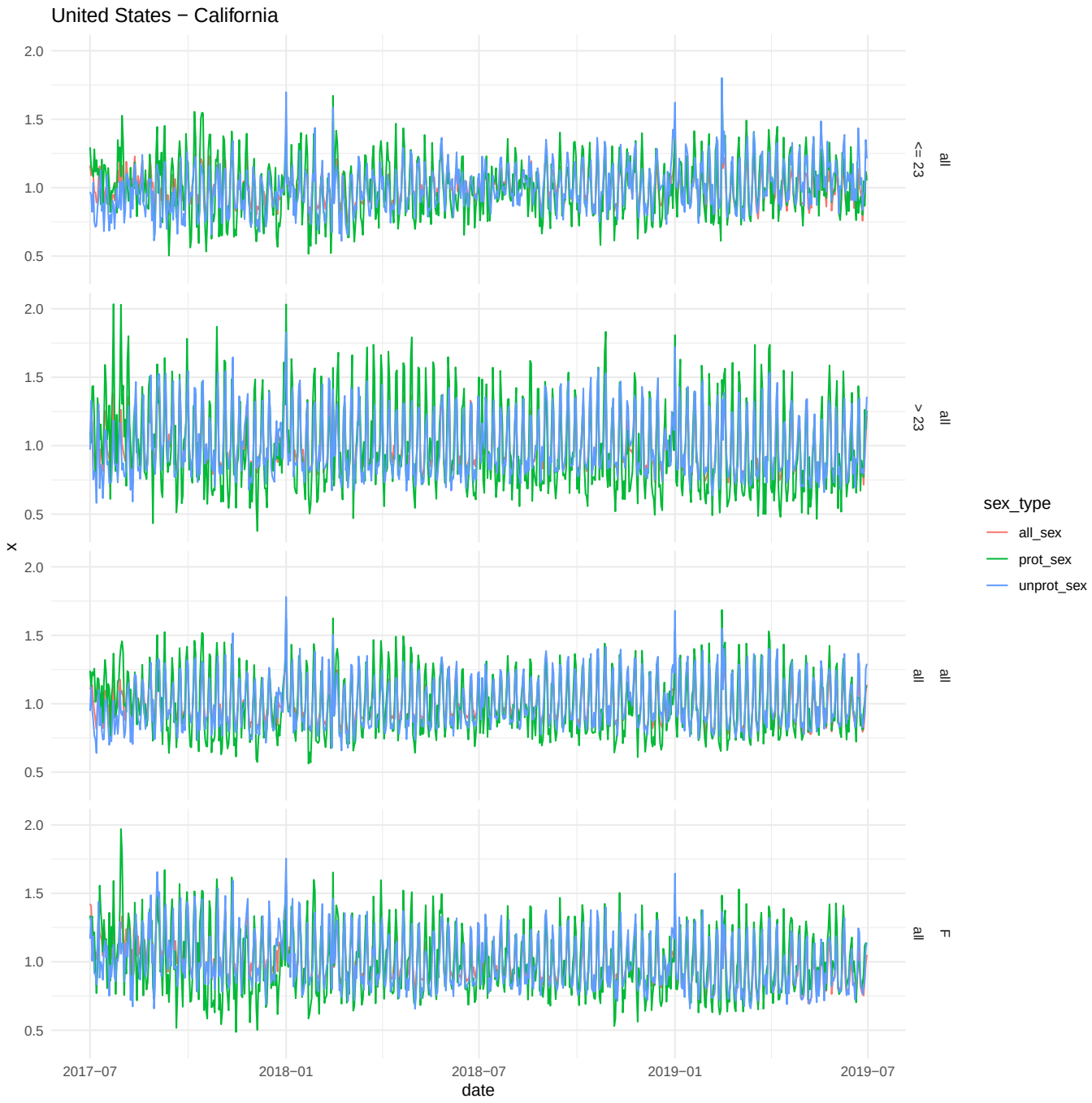


Figure 25: Comparing sexual activity by sex type for each location and user group.

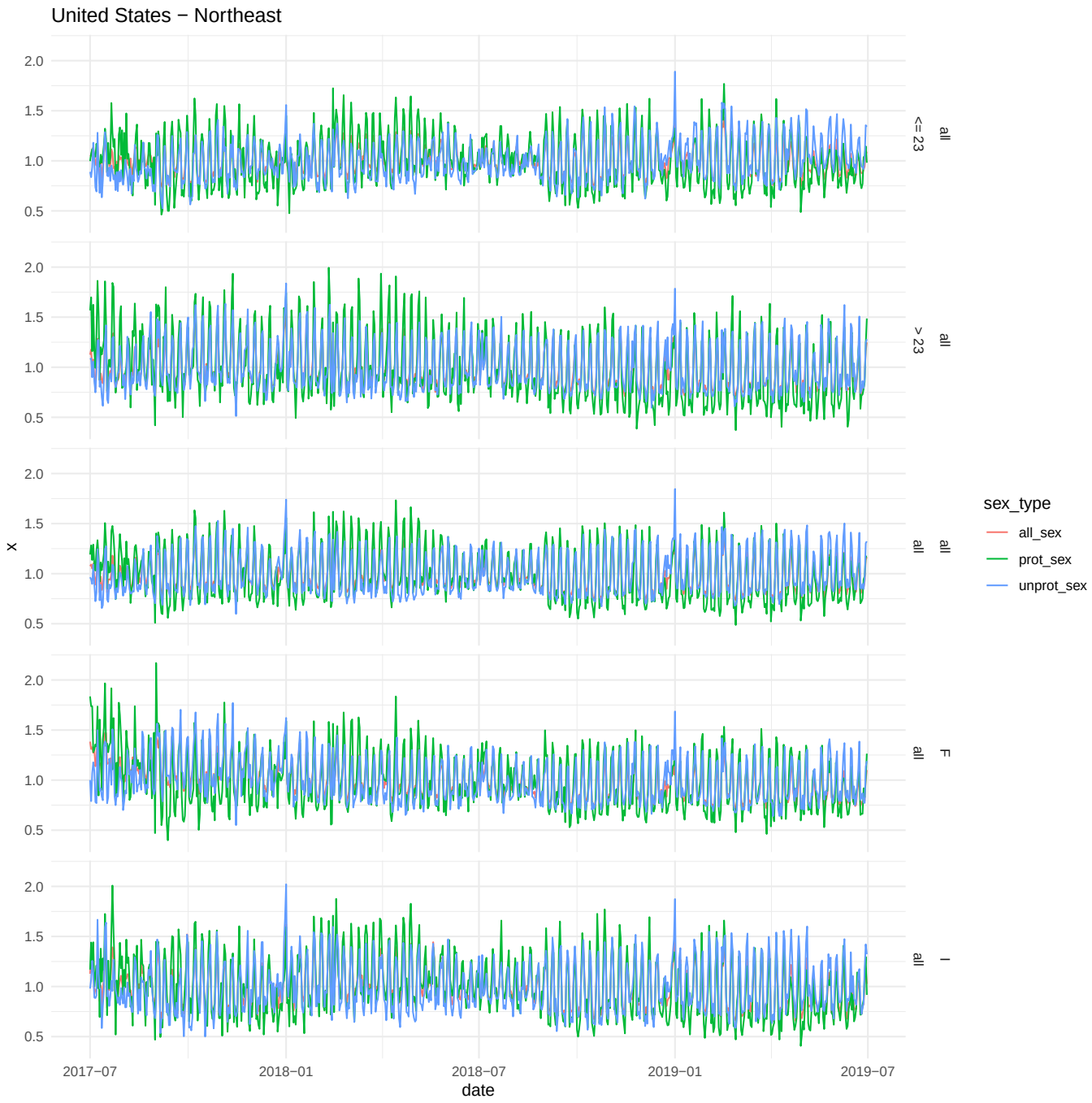


Figure 26: Comparing sexual activity by sex type for each location and user group.

```
M = clue_sex_agg %>%
  filter(BC == "all", age_cat == "all", sex_type == "all_sex") %>%
  mutate(month = month(date),
         year = year(date),
         year_month = year + (month-1)/12) %>%
  group_by(country_area, year_month) %>%
  summarize(x = mean(x),
            .groups = "drop")

g = ggplot(M, aes(x = year_month, y = x)) +
  geom_hline(yintercept = 1, col = "gray") +
  geom_line() +
  facet_grid(country_area ~ .) +
```

```
  theme(strip.text.y = element_text(angle = 0, hjust = 0))

g
```

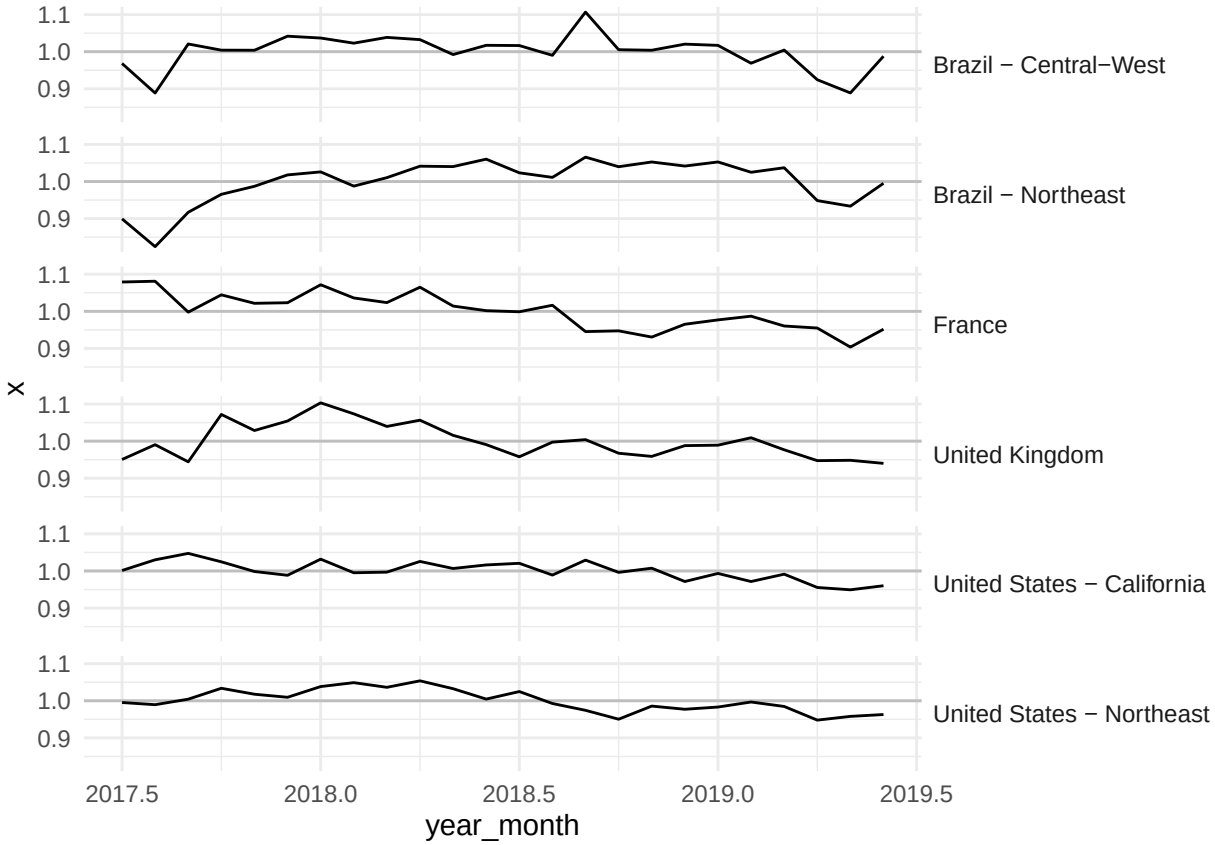


Figure 27: Relative sexual activity in each location, aggregated monthly.

4.3.2 Sexual activity model (weekdays-seasons-holidays)

In figure 18, one can observe a strong weekly trend, a mild seasonal trend (e.g. stronger in France) and peaks on holidays.

Consequently, sexual activity is here modeled as a combination of these trends. A generalized linear model (`glm`, family `gaussian`, identity link function) is used to model and predict the relative sexual behavior from the two following categorical input variables:

- **Weekly-monthly trend**: because the seasonal trend is weak and seems to primarily affect the amplitude of the weekly trend, the weekly and seasonal trends are modeled as an interaction between the weekdays and the month. The input corresponding to this trend is a categorical variable with 7x12 levels for the combination of each weekday (Mon-Sun) with each month (Jan - Dec). In addition to these 7x12 levels, a "reference day" (`ref_day`) is added as the reference (first) level of this categorical variable. A synthetic datapoint, in which the relative sexual frequency (output) is set to 1, is added to the training data ensuring that the model intercept value is 1, the average sexual frequency.
- **Holiday peaks**: the effects of holidays on the sexual frequency is modeled as a peak response for each holiday. The input variable is also a categorical variable in which the reference (and most common) level is `normal_day`, i.e. days in which there is no holiday or celebration. The other levels of this categorical variable are the holiday/celebration names (e.g. Labor day or National day). Additionally, each holiday is padded by 3 days so that we can account for the effect of holidays on the surrounding days (e.g. Christmas +1,2,3). These padding days are distinct levels of the holiday variable.

Finally, for some holidays, the "context", i.e. the day of the week at which they happened mattered, while for others, it didn't make a difference. The main consequence is that some holidays, such as Valentine's day, impact

the sexual frequency *additively* to the weekday variation, while other holidays, such as New Year, lead to an increased absolute level in sexual frequency that is the always the same, independent of the weekday. The reason for this is that, at New Year for example, most people are already on a lighter schedule at their work/school around the New Year and the exact day the New Year happens does not matter. For other such holidays, it does not matter because the weekday is always the same (e.g. Thanksgiving is always on Thursday).

To account for these differences in holiday, we replaced the value of the weekday_month variable by ref_day when the holiday impact on sexual frequency is not additive to the weekday variation.

Finally, because the number of users changes over time and that our trust in the data increases with the number of users, the model coefficients are fitted on weighted data: time-points with more users have more weight than time-points with less users.

```
clue_sex_agg = clue_sex_agg %>%
  arrange(country_area, BC, age_cat, sex_type, date)

clue_sex_agg = clue_sex_agg %>%
  mutate(cat = interaction(country_area, BC, age_cat, sex_type))
```

```
# for each category of users
sex_models =
  purrr::map(
    .x = unique(clue_sex_agg$cat),
    .f = function(category){
      # cat(category %>%  as.character(),"\n")
      # retrieve and augment the data
      this_cat_sex_data = clue_sex_agg %>% filter(cat == category)
      this_cat_sex_data = augment_with_weekdays_months_and_holidays(
        this_cat_sex_data,
        verbose = FALSE) # see Scripts/00_functions.R

      # the following lines add a fictive reference day to ensure the intercept = 1
      # and thus that the coefficients of the models are comparable between categories
      ref_day = this_cat_sex_data[1,] %>%
        mutate(
          weekday_month = factor("ref_day", levels =
                                   levels(this_cat_sex_data$weekday_month)),
          weekday_month_x = factor("ref_day", levels =
                                     levels(this_cat_sex_data$weekday_month_x)),
          holiday_ID  = factor("normal day", levels =
                                 levels(this_cat_sex_data$holiday_ID)),
          x = 1,
          n_users = max(this_cat_sex_data$n_users))
      this_cat_sex_data = bind_rows(ref_day, this_cat_sex_data)


      this_cat_sex_data = this_cat_sex_data %>%
        mutate(weight = n_users/max(n_users))

      # fit the model without contextual holidays
      formula = "x ~ weekday_month + holiday_ID"
      glm_sex_behavior_1 = glm(data = this_cat_sex_data,
                               formula = formula,
                               family = "gaussian",
                               weights = weight)

      # fit the model with contextual holidays (performs better, see below)
      formula = "x ~ weekday_month_x + holiday_ID"
      glm_sex_behavior = glm(data = this_cat_sex_data,
                             formula = formula,
                             family = "gaussian",
```

```
                    weights = weight)

    glm_sex_behavior = reduce_storage_size_of_glm_model(model = glm_sex_behavior)

    # results
    res = list(country_area = unique(this_cat_sex_data$country_area),
               BC = unique(this_cat_sex_data$BC),
               age_cat = unique(this_cat_sex_data$age_cat),
               sex_type = unique(this_cat_sex_data$sex_type),
               model = glm_sex_behavior,
               intercept = glm_sex_behavior$coefficients[1],
               ssr = sum(glm_sex_behavior$residuals^2),
               ssr_not_contextual = sum(glm_sex_behavior_1$residuals^2))

    res
  }
 )


# to retrieve the models based on the values of the list elements, we can use:
# sapply(sex_models, "[[","country_area")
# sapply(sex_models, "[[","BC")
# sapply(sex_models, "[[","sex_type")
```

```
sex_models_df = data.frame(
  country_area = sapply(sex_models, "[[","country_area"),
  BC = sapply(sex_models, "[[","BC"),
  age_cat = sapply(sex_models, "[[","age_cat"),
  sex_type = sapply(sex_models, "[[","sex_type"),
  SSR = sapply(sex_models, "[[","ssr"),
  SSR_not_contextual =  sapply(sex_models, "[[","ssr_not_contextual"),
  intercept = sapply(sex_models, "[[","intercept")
)

sex_models_df = sex_models_df %>%
  left_join(.,dict$country_area, by = "country_area") %>%
  left_join(.,dict$BC, by = "BC")
```

```
# for(ca in unique(sex_models_df$country_area)){
#   j = which(sex_models_df$country_area == ca)
#   sex_models_this_location = list()
#   for(i in 1:length(j)){sex_models_this_location[[i]] = sex_models[[j[i]]]}
#   save(sex_models_this_location, file = str_c(IO$out_Rdata,"sex_models_",ca,".Rdata"))
# }

sex_models_directory = str_c(IO$p_outputs, "sex_models/")

if(!dir.exists(sex_models_directory))
  dir.create(sex_models_directory)

for(i in 1:nrow(sex_models_df)){
  this_sex_model = sex_models[[i]]
  save(this_sex_model,
       file = str_c(sex_models_directory,
                    "sex_model_",sex_models_df$country_area[i],
                    "_BC_",sex_models_df$BC[i],
                    "_age_cat_",sex_models_df$age_cat[i],
                    "_sex_type_",sex_models_df$sex_type[i],
                    ".Rdata"))
```

```
}

save(sex_models_df, file = str_c(IO$p_outputs,"sex_models_df.Rdata"))
```

First, looking at the values of the residuals on the training set (no test set was used here because we only had two years of data and preferred to use both years rather than using one year as the training set and the other year as the test/validation set), we observe large differences between categories, despite the fact that each time-series has the same number of time-point (i.e. 2 years of data = 730 data-point).

```
ggplot(sex_models_df, aes(x = BC, y = SSR, fill =  BC_col))+
 # geom_bar(stat = "identity", aes(y = SSR_not_contextual), fill = "red")+
  geom_bar(stat = "identity")+
  scale_fill_identity()+
  facet_grid(country_area ~ age_cat + sex_type)+
  theme(strip.text.y = element_text(angle = 0, hjust = 0))
```

Figure 28: Sex models residuals on the training data

These differences can mostly be explained by the number of users that contributed to the aggregated time-series.

```
df_agg = clue_sex_agg %>%
  group_by(cat) %>%
  summarize(min_n_users = min(n_users),
            max_n_users = max(n_users),
            median_n_users = median(n_users))

tmp = full_join(
  sex_models_df %>%  mutate(cat = interaction(country_area, BC, age_cat, sex_type)),
  df_agg,
  by = "cat")

ggplot(tmp, aes(x = median_n_users, y = SSR, col =  country_area))+
  geom_point()+ scale_x_log10()+
  xlab("median # of users (log scale)")
```

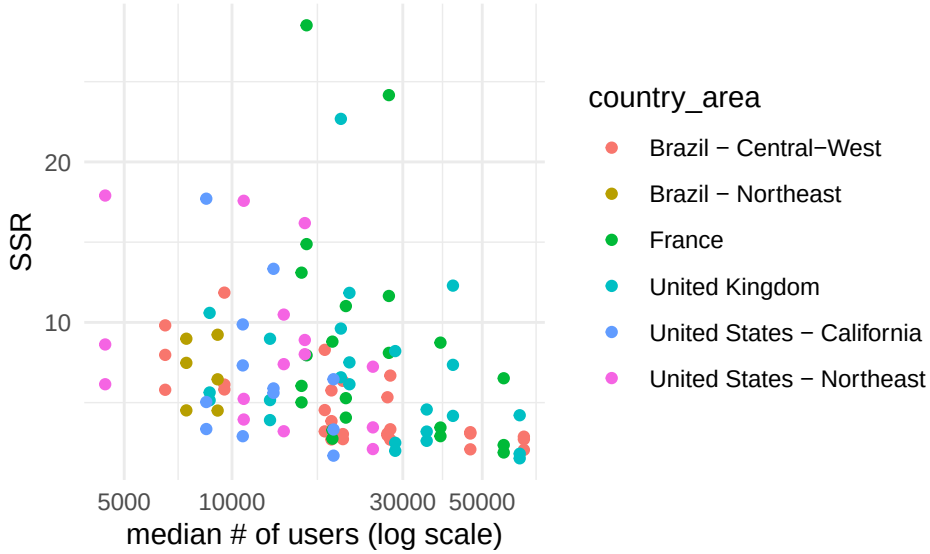


Figure 29: Residuals as a function of the median number of users that contributed to the aggregated time-series

The more users that were part of a category, the more the sexual behavior is accurately modeled as a weekly-seasonal trend + a holiday response. Categories with less users to build the time-series are more sensitive to individual variations in reported sexual intercourse.

```
ggplot(sex_models_df, aes(x = BC, y = (SSR - SSR_not_contextual)/SSR*100, fill =  BC_col))+
  geom_hline(yintercept = 0)+
  geom_bar(stat = "identity")+
  scale_fill_identity()+
  ylab("% change in SSR (SSR_context - SSR_additive)")+
  facet_grid(country_area ~ age_cat + sex_type)+
  theme(strip.text.y = element_text(angle = 0, hjust = 0))
```

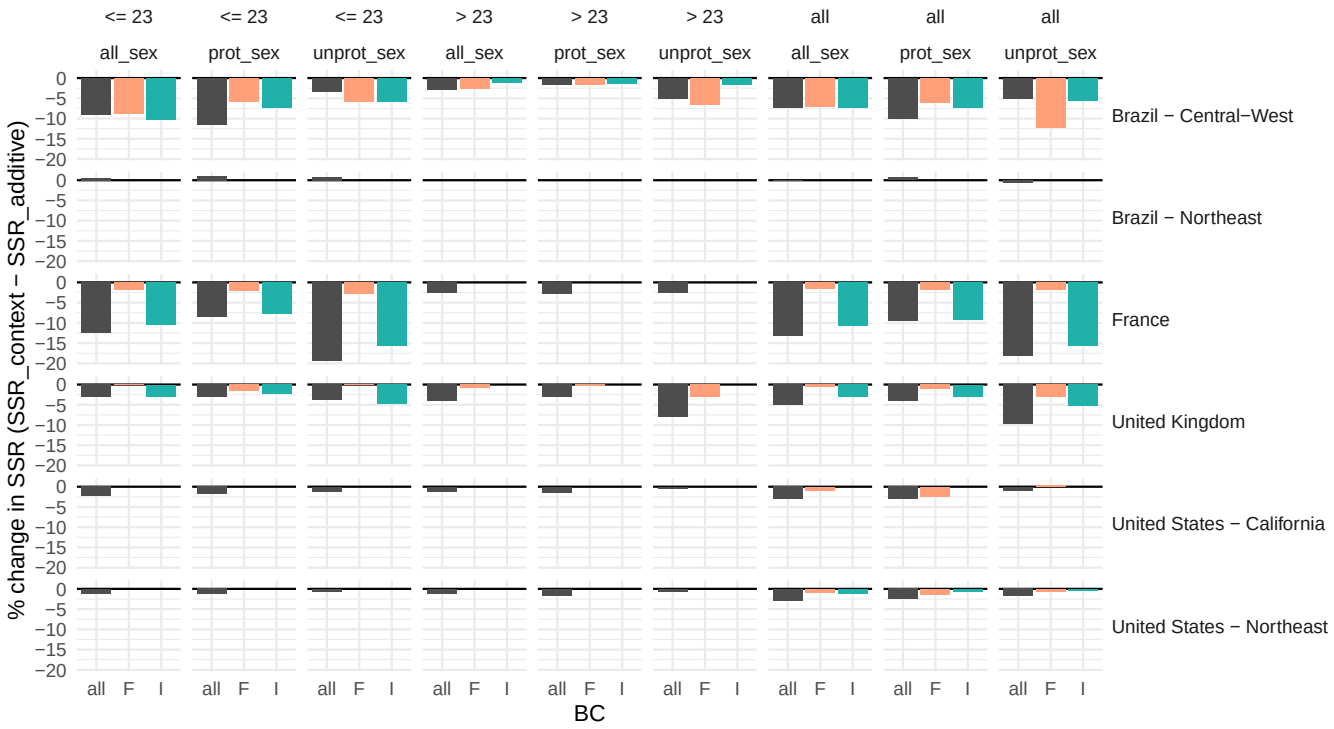


Figure 30: Percent change in residuals from sex models with contextual holidays vs strictly additive model

In figure 30 the residuals of the "contextual holiday model" are compared with the residuals of a strictly additive

model (see explanations earlier). In general, the "contextual holiday model" performs better and is used for the sexual behavior predictions from now on.

4.3.2.1 Visualization of the model coefficient and of the residuals

We show here the coefficient of the glm model and the fitted time-series as well as the residuals for the 6 countries/areas of interest. For each country/area, we display these coefficients and residuals for the timeseries of users from any age group (age_cat = "all"), any birth-control type (BC = "all") and for the sum of all sexual intercourse (sex_type = "all").

The models are saved on the github repo so these plots can be reproduced for any other category.

```
ok = foreach(ca = unique(sex_models_df$country_area)) %do% {

 # retrieving the model for this country and only plotting for BC all and sex_type all
 j = which(
   (sex_models_df$country_area == ca) &
     (sex_models_df$BC == "all") &
     (sex_models_df$sex_type == "all_sex") &
     (sex_models_df$age_cat == "all") )
 glm_sex_behavior = sex_models[[j]]$model

 # Visualization of the coefficient
 g_coef = ggplot_sex_activity_glm_coefficient(model = glm_sex_behavior,
                                              show_weekly_patterns = TRUE)
 g_coef = g_coef +
   ggtitle(str_c(ca," - BC: all - age_cat: all - sex type: all_sex"))

 # Visualization of the training + fitted time-series  # TO DO: plot the two years above each other.
 g_residuals = ggplot_sex_activity_data_fitted_and_residuals(model = glm_sex_behavior)

 g = suppressWarnings(cowplot::plot_grid(plotlist = list(g_coef, g_residuals), ncol = 1, heights = c(1.2,1)))
 print(g)
 return()
}
```

```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.
```

```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.
```

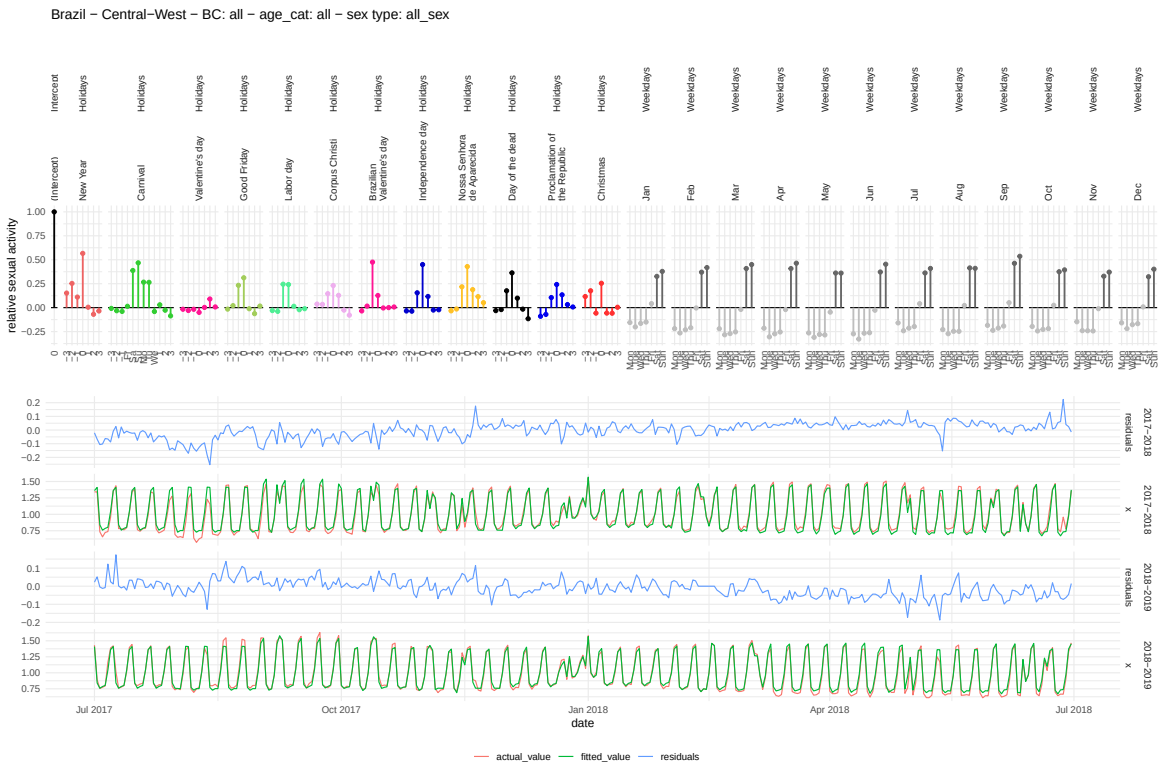


Figure 31: (Top) Coefficients of the generalized linear models used to predict relative sexual behavior changes. (Bottom) Actual vs Fitted and Residuals (squared difference between the actual and fitted values) over the two years of data used as training set.

Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
"none")` instead.

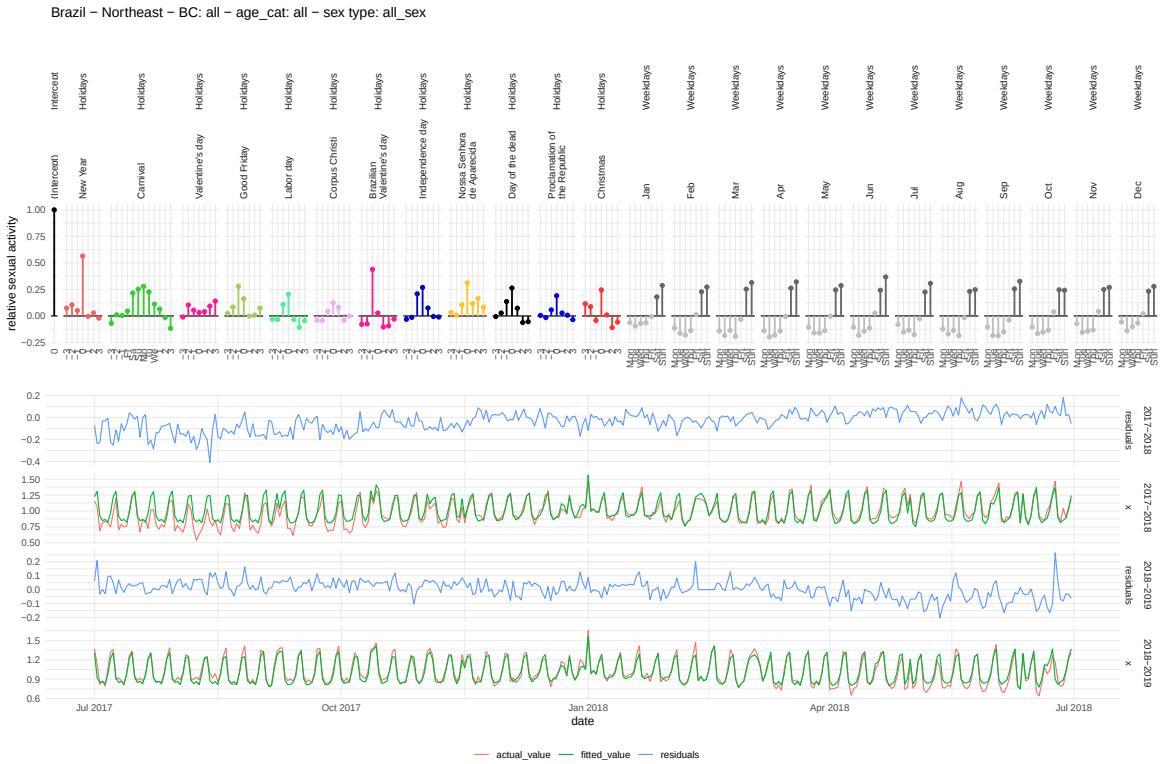


Figure 32: (Top) Coefficients of the generalized linear models used to predict relative sexual behavior changes. (Bottom) Actual vs Fitted and Residuals (squared difference between the actual and fitted values) over the two years of data used as training set.

Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
"none")` instead.

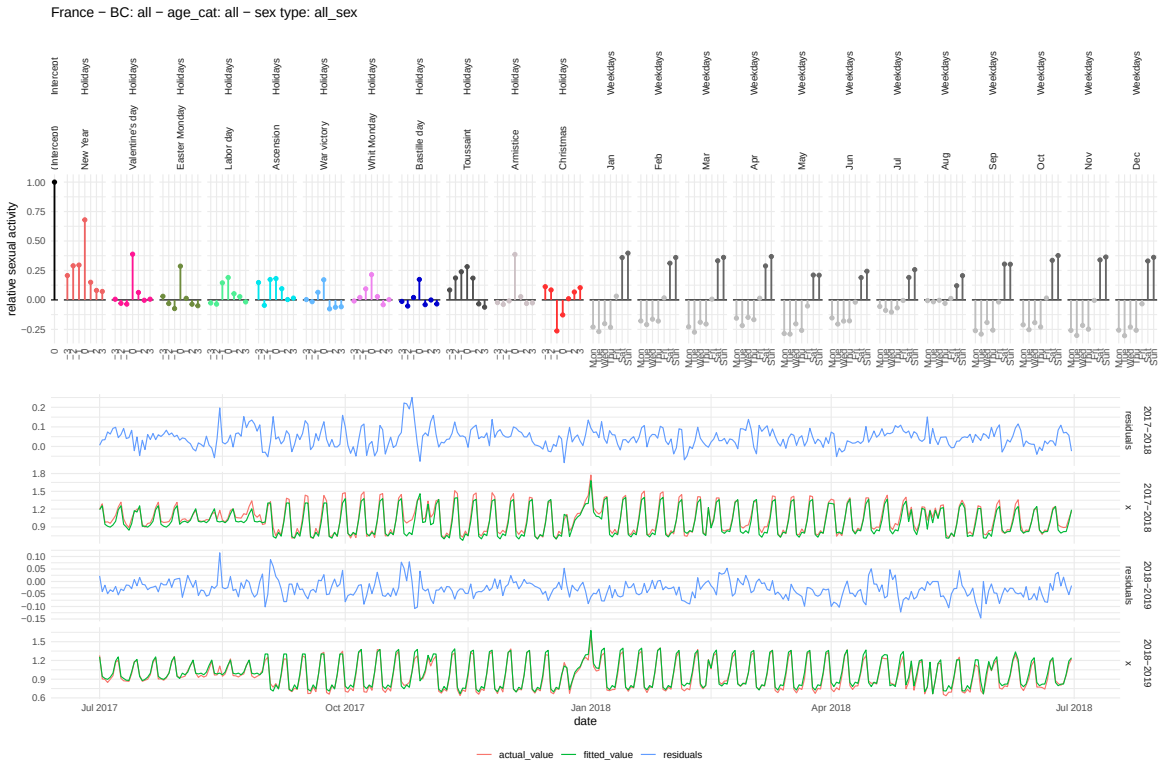


Figure 33: (Top) Coefficients of the generalized linear models used to predict relative sexual behavior changes. (Bottom) Actual vs Fitted and Residuals (squared difference between the actual and fitted values) over the two years of data used as training set.

Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
"none")` instead.

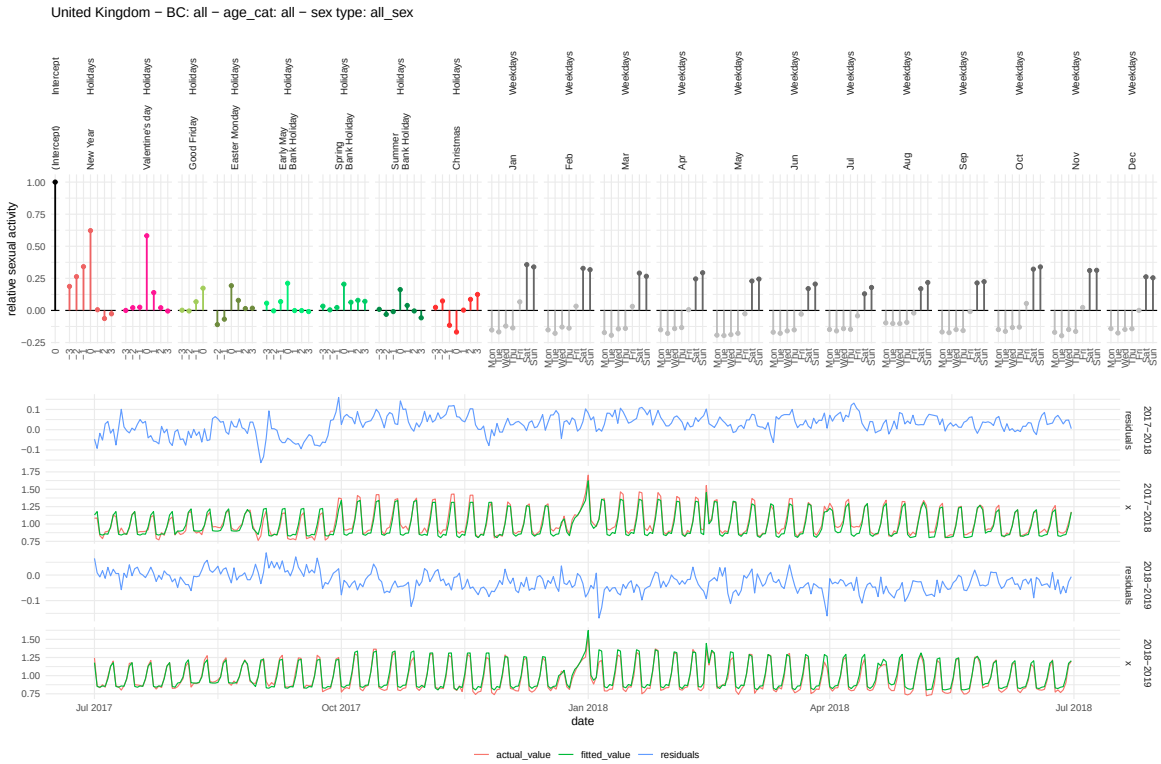


Figure 34: (Top) Coefficients of the generalized linear models used to predict relative sexual behavior changes. (Bottom) Actual vs Fitted and Residuals (squared difference between the actual and fitted values) over the two years of data used as training set.

Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
"none")` instead.

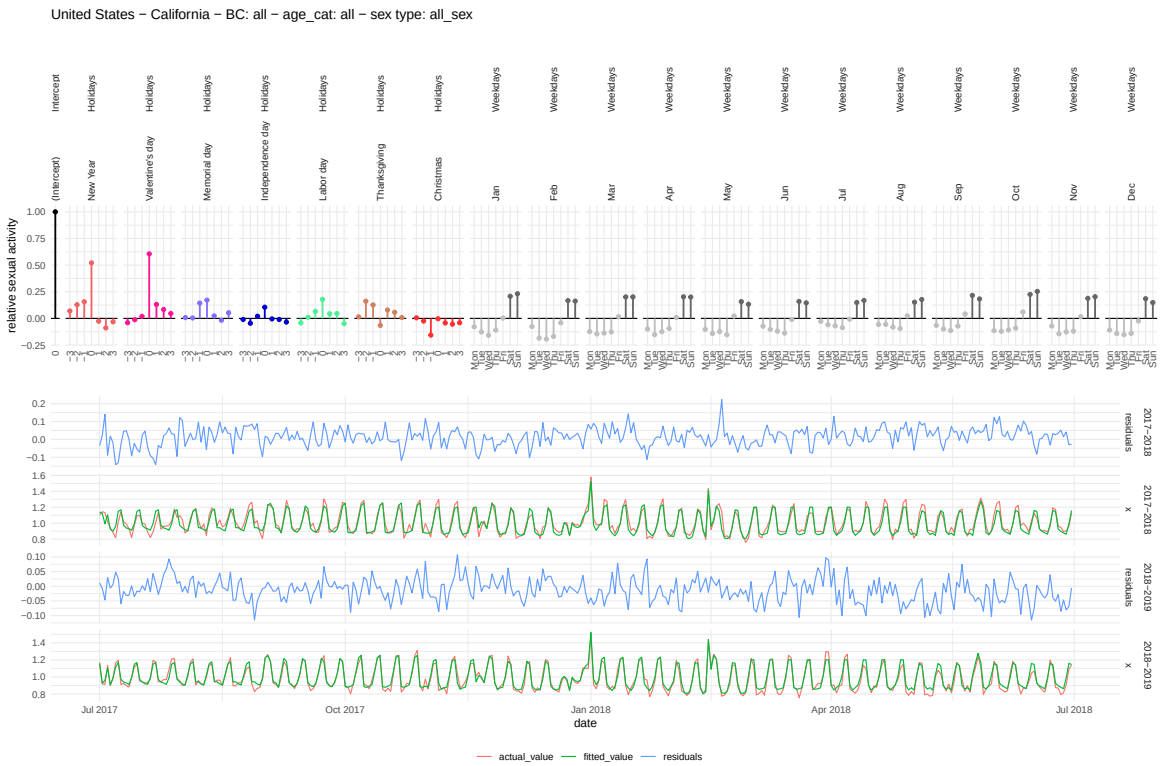


Figure 35: (Top) Coefficients of the generalized linear models used to predict relative sexual behavior changes. (Bottom) Actual vs Fitted and Residuals (squared difference between the actual and fitted values) over the two years of data used as training set.

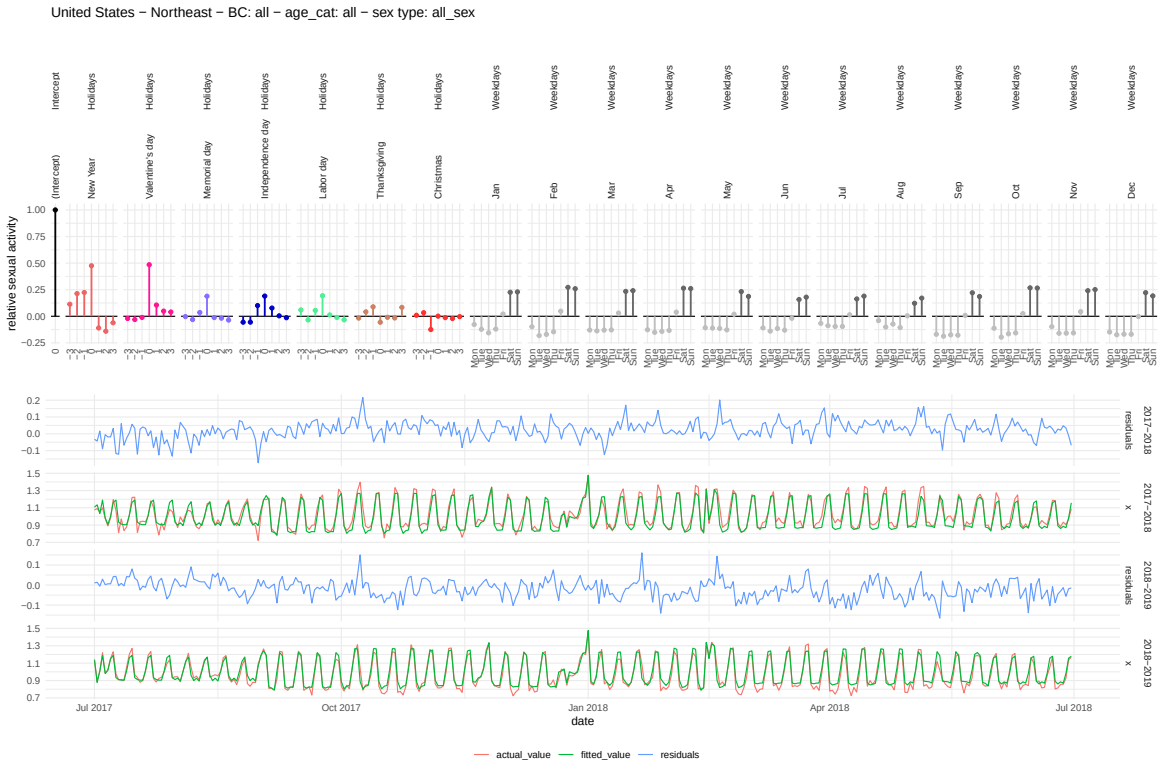


Figure 36: (Top) Coefficients of the generalized linear models used to predict relative sexual behavior changes. (Bottom) Actual vs Fitted and Residuals (squared difference between the actual and fitted values) over the two years of data used as training set.

Comparison of the coefficients per user categories (age, BC) and sex type

```
sex_models_df = sex_models_df %>%
  mutate(category = interaction(country_area, BC, age_cat, sex_type))

sex_models_coefficients_df = foreach(j = 1:nrow(sex_models_df), .combine = bind_rows) %do% {
  glm_sex_behavior = sex_models[[j]]$model
  coef_df = get_model_coeficient_df(model = glm_sex_behavior) %>%
    select(category, name, subcat, x, value)
  coef_df = bind_cols(
    coef_df,
    sex_models_df[rep(j,nrow(coef_df)),] %>%  select(country_area, BC, age_cat, sex_type, SSR)
  )
  coef_df
}
```

```
compare_model_coef_weekdays(sex_models_coefficients_df, var = "age_cat", var_name = "age group")
```

```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.
```

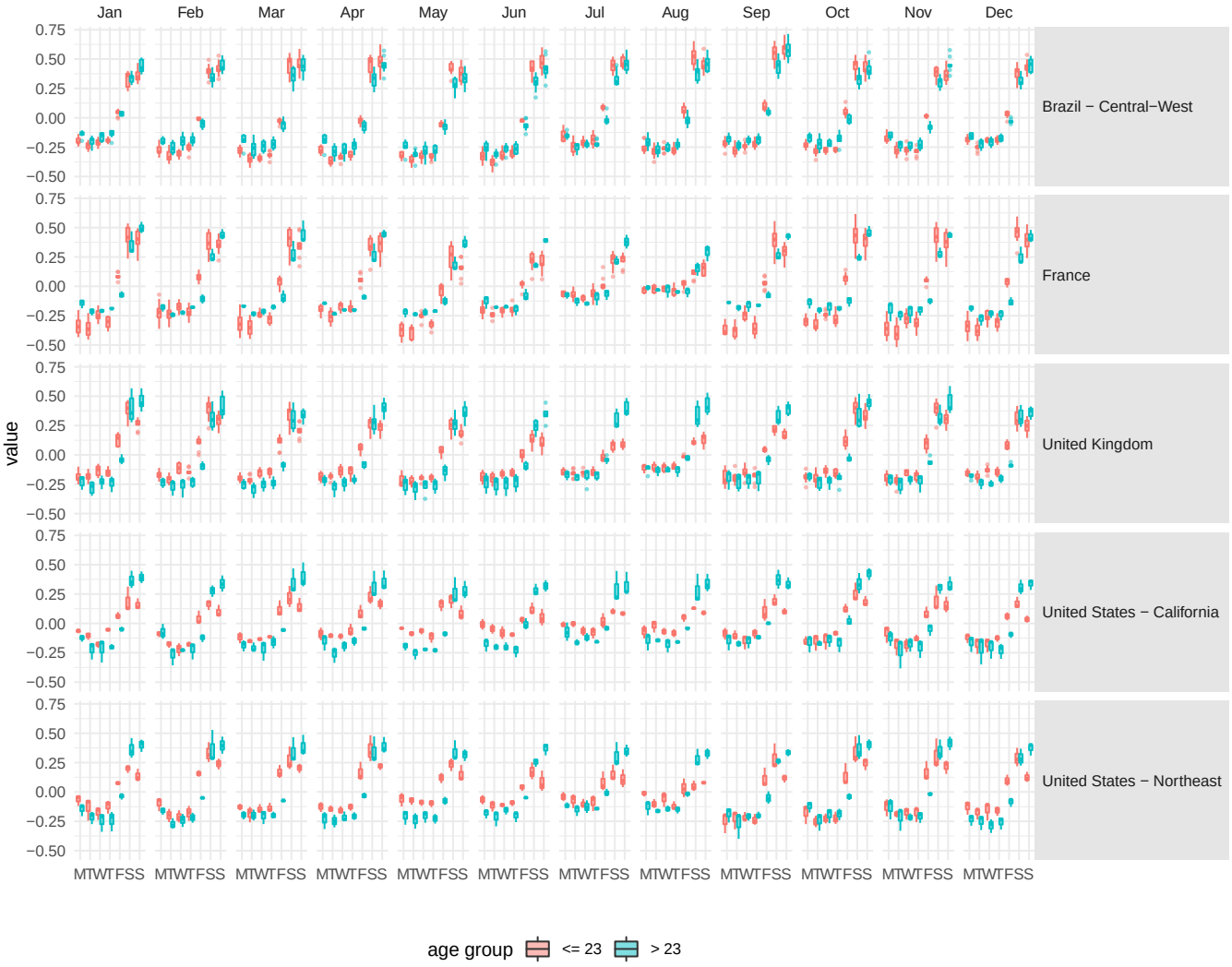


Figure 37: Comparison of the sex model coefficient for weekdays across age group.

```
compare_model_coef_weekdays(sex_models_coefficients_df, var = "BC", var_name = "birth control")
```

```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
```

"none")` instead.

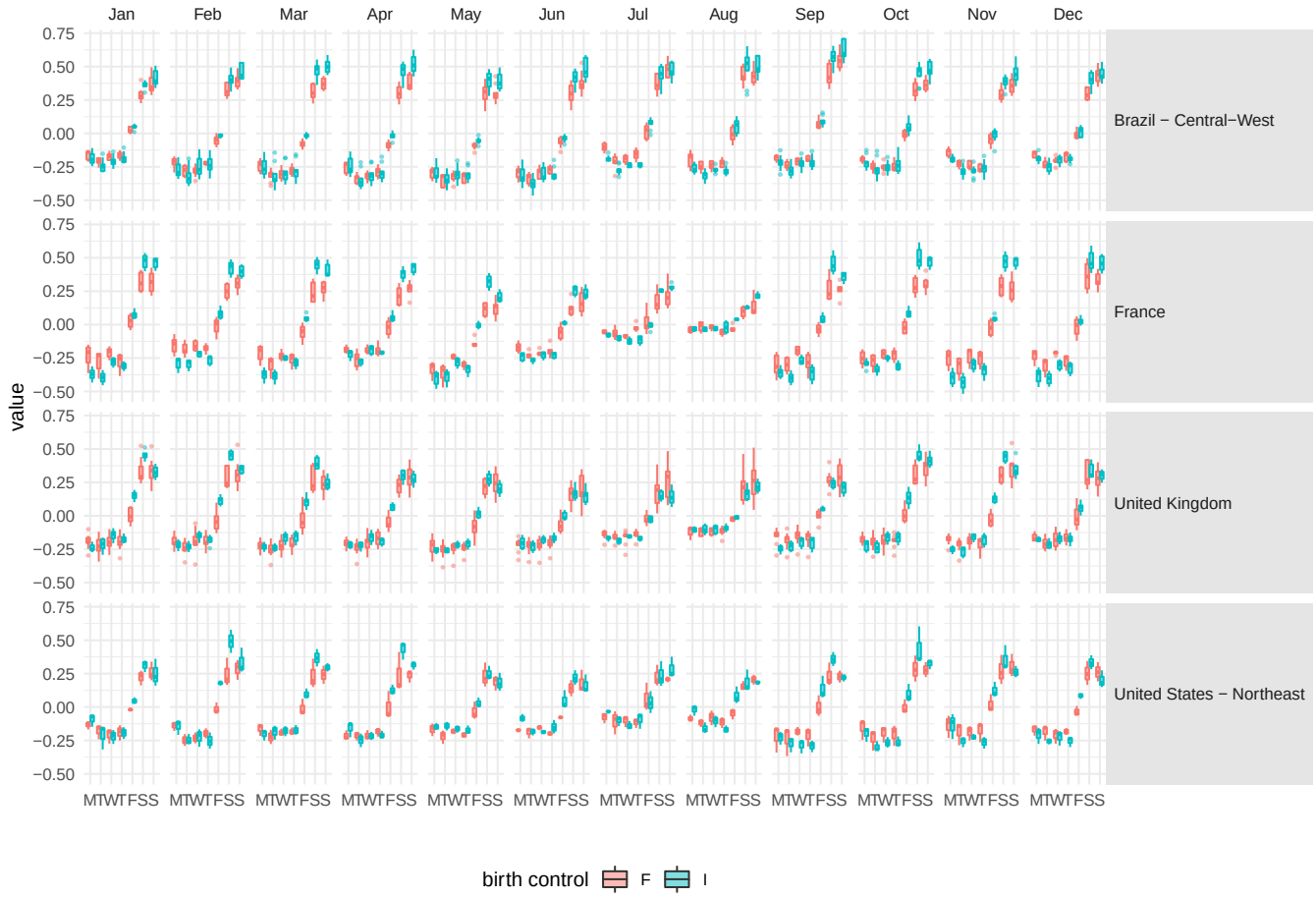


Figure 38: Comparison of the sex model coefficient for weekdays across birth control.

```
compare_model_coef_weekdays(sex_models_coefficients_df, var = "sex_type", var_name = "sex type")
```

Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
"none")` instead.

Figure 39: Comparison of the sex model coefficient for weekdays across sex type.

```
compare_model_coef_holidays(sex_models_coefficients_df, var = "age_cat", var_name = "age group")
```

```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.

## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.

## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.

## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.

## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.
```

Figure 40: Comparison of the sex model coefficient for the holidays across age group.

```
compare_model_coef_holidays(sex_models_coefficients_df, var = "BC", var_name = "birth control type")
```

```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.

## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.

## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.

## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.
```

Figure 41: Comparison of the sex model coefficient for the holidays across birth control type.

```
compare_model_coef_holidays(sex_models_coefficients_df, var = "sex_type", var_name = "sex type")
```

```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.

## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.

## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.

## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.

## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.

## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.
```

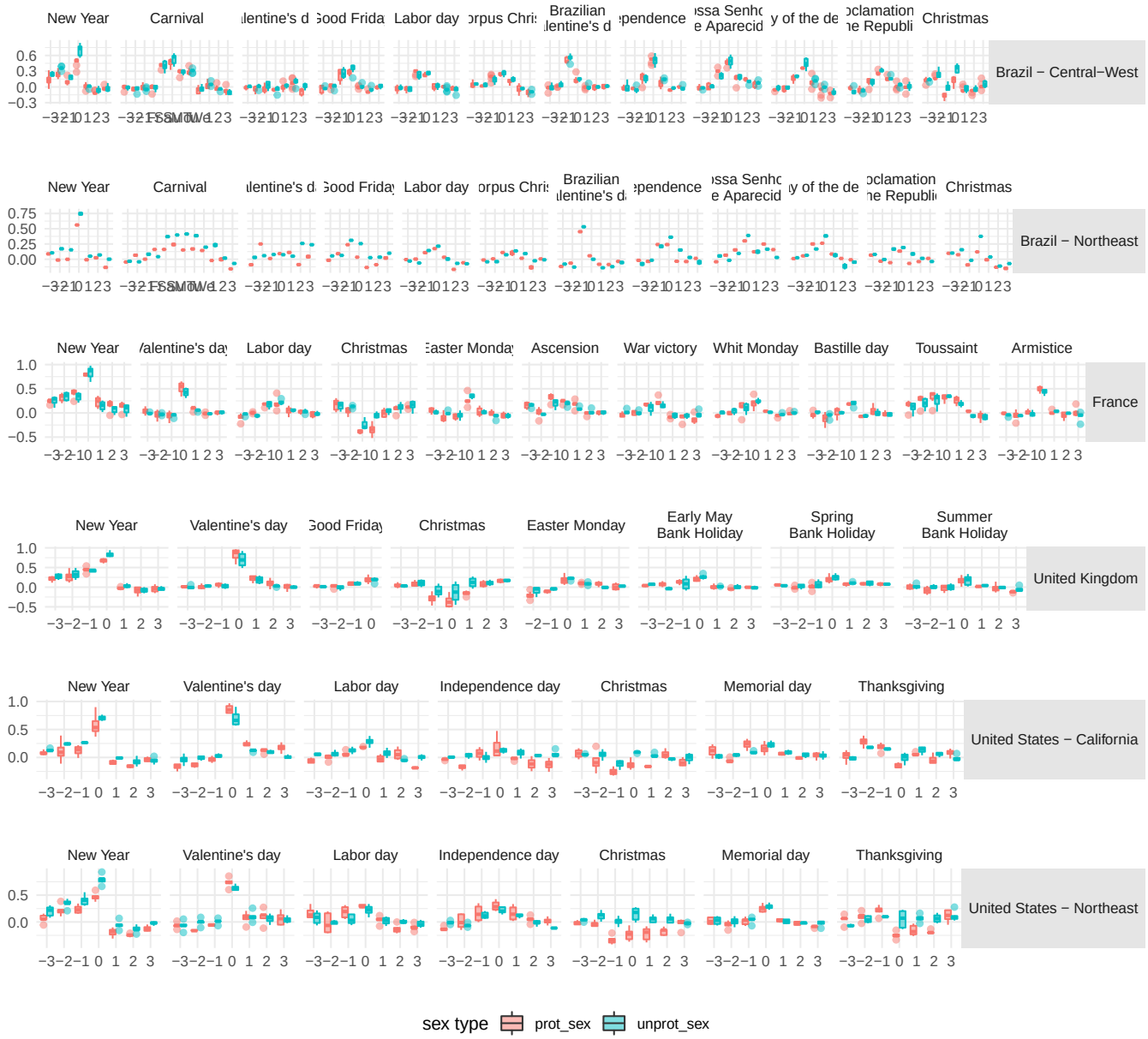


Figure 42: Comparison of the sex model coefficient for the holidays across sex type.

4.4 Official birth records

```
load("../Data/2_births_processed/birth_data.Rdata", verbose = TRUE)
```

```
## Loading objects:
##   birth
```

```
official_birth_records = birth %>% dplyr::filter(country_area %in% clue_sex_agg$country_area)
rm(birth)

official_birth_records = official_birth_records %>%
  mutate(country_area = factor(country_area, levels = dict$country_area$country_area))

official_birth_records = official_birth_records %>%
  left_join(., dict$country_area %>% dplyr::select(country_area, country_area_col), by = "country_area")
```

```
ggplot(official_birth_records, aes(x = date, y = births, col = country_area_col))+
  geom_line()+
  scale_color_identity()+
  facet_grid(country_area ~ ., scale = "free_y")+
  theme(strip.text.y = element_text(angle = 0, hjust = 0))
```

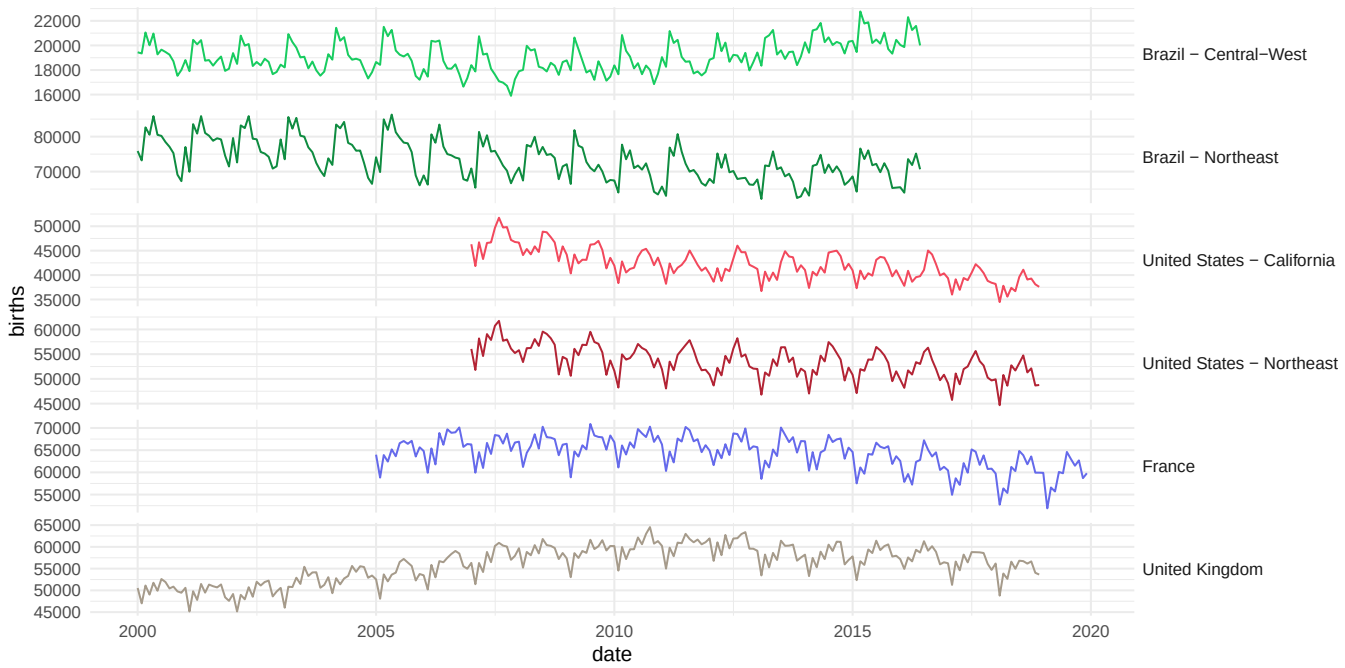


Figure 43: Official birth records - raw monthly data

4.4.1 Correcting for the number of days in each months

```
official_birth_records = official_birth_records %>%
  mutate(births_original_numbers = births,
         year_month = year + (month_num-1)/12)

# preparing a data.frame that has the number of day in each month
date_seq = seq(min(official_birth_records$date), max(official_birth_records$date) + days(365), by = 1)
date_seq = data.frame(date = date_seq, year = year(date_seq), month_num = month(date_seq))
date_seq = date_seq %>%  mutate(year_month = year + (month_num-1)/12)
n_days_per_month = date_seq %>% group_by(year_month) %>% dplyr::summarise(n_days = n(), .groups = "drop")

# joining with births table
official_birth_records = left_join(official_birth_records, n_days_per_month, by = "year_month")

# correcting
official_birth_records = official_birth_records %>%
  mutate(births = births_original_numbers/n_days*30)
```

```
# visualization
ggplot(official_birth_records, aes(x = date, y = births, col = country_area_col))+
  # uncorrected births
  #geom_point(aes(y = births_original_numbers), size = 0.5,  col = "gray")+
  geom_line(aes(y = births_original_numbers), col = "gray")+
  #corrected births
  #geom_point(size = 0.5)+
  geom_line()+
```

```
# settings
scale_color_identity()+
facet_grid(country_area ~., scale = "free")+
theme(strip.text.y = element_text(angle = 0, hjust = 0))
```

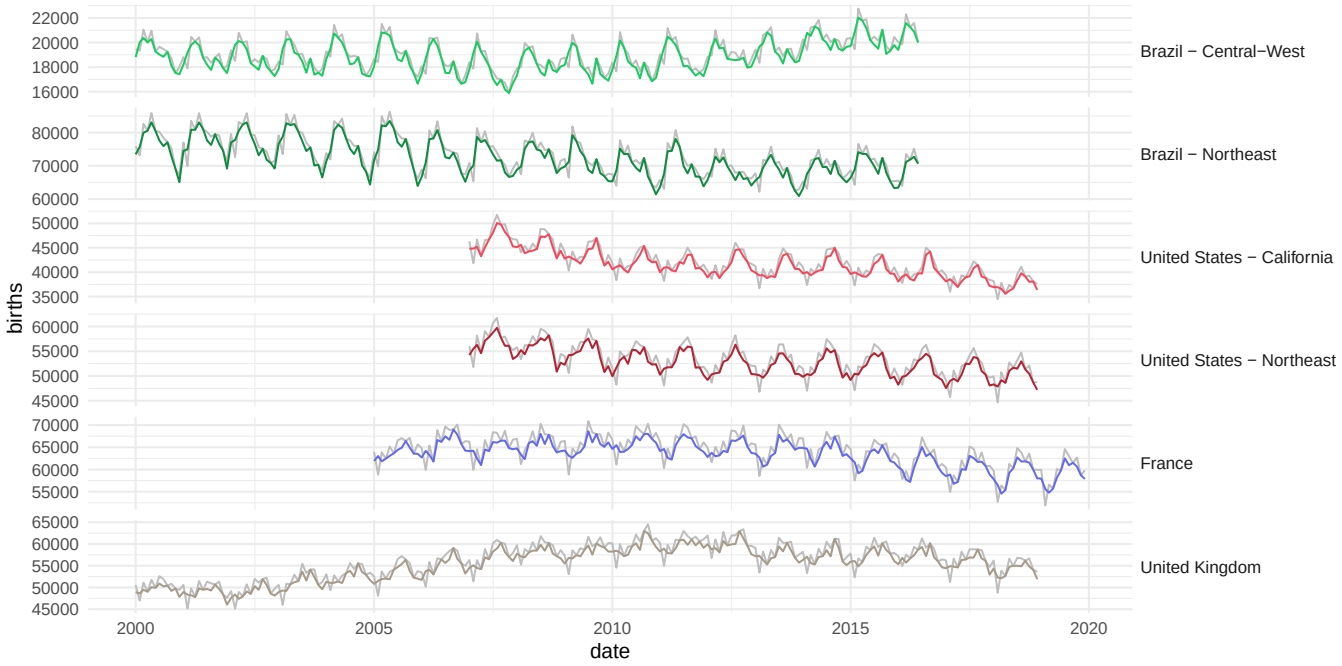


Figure 44: Official birth records: corrected for the number of days in each month (colored lines) and raw (light gray lines) monthly data

The gray lines under the colored lines are the actual (non-corrected) birth records. We can see that February is often associated with a local minima, which disappear when we correct for the month duration.

```
write_feather(official_birth_records, path = str_c(IO$p_outputs,"official_birth_records.feather"))
```

4.4.2 Average daily births

```
average_daily_births_df = foreach(ca = unique(official_birth_records$country_area), .combine = bind_rows) %do%{
 this_ca_births = official_birth_records %>%  filter(country_area == ca)

 date_seq = seq(min(this_ca_births$date), max(this_ca_births$date) + months(1), by = 1)
 date_seq = data.frame(date = date_seq, year = year(date_seq), month_num = month(date_seq))
 date_seq = date_seq %>%
  mutate(
   country_area = ca,
   year_month = year + (month_num-1)/12
  )

 this_ca_ave_daily_births = date_seq %>%
  full_join(.,
         this_ca_births %>%  select(country_area, date, births),
         by = c("country_area","date"))

 this_ca_ave_daily_births = this_ca_ave_daily_births %>%
  mutate(m_ave_daily_births = births/30)
 this_ca_ave_daily_births$m_ave_daily_births[this_ca_ave_daily_births$date == max(date_seq$date)] =
  this_ca_ave_daily_births$m_ave_daily_births[this_ca_ave_daily_births$date == max(this_ca_births$date)]
```

```
  this_ca_ave_daily_births = this_ca_ave_daily_births %>%
    mutate(daily_births = na.spline(m_ave_daily_births, method = "natural"),
           t = row_number())
  this_ca_ave_daily_births$ave_daily_births = predict(loess(daily_births ~ t, data = this_ca_ave_daily_births, span = 0.5))

  g = ggplot(this_ca_ave_daily_births, aes(x = date))+
    geom_point(aes(y = m_ave_daily_births), col = "black")+
    geom_line(aes(y = daily_births), col = "gray")+
    geom_line(aes(y = ave_daily_births), col = "blue")+
    ggtitle(ca)
  print(g)

  res = this_ca_ave_daily_births %>% select(country_area, date, ave_daily_births)
  return(res)
}
```

Warning: Removed 6712 rows containing missing values (geom_point).

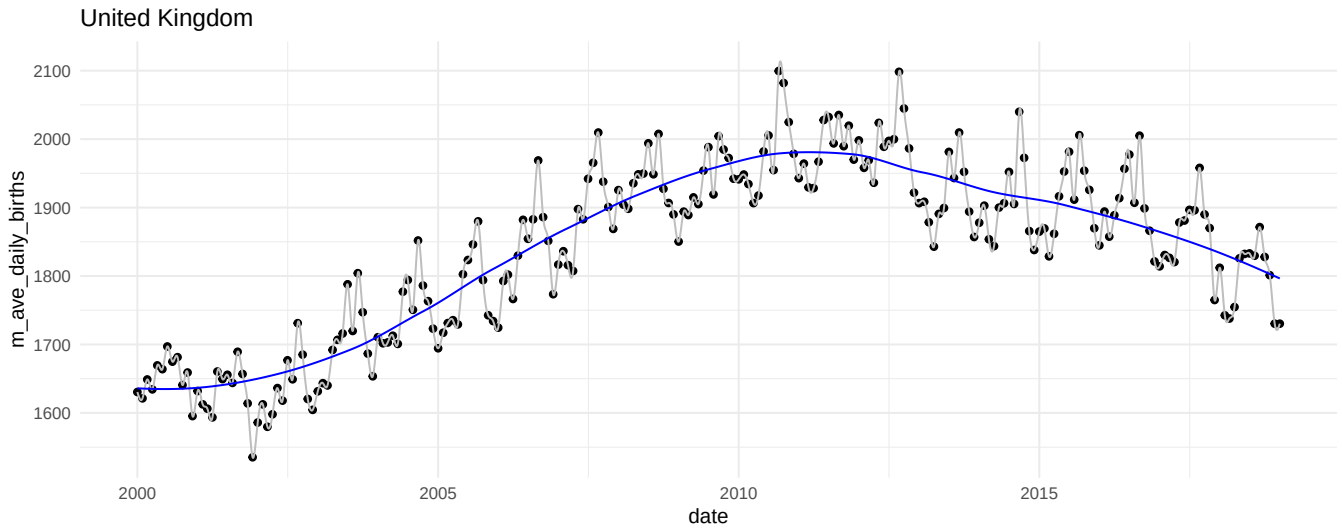


Figure 45: Average daily births (birth long-term trend).

Warning: Removed 5298 rows containing missing values (geom_point).

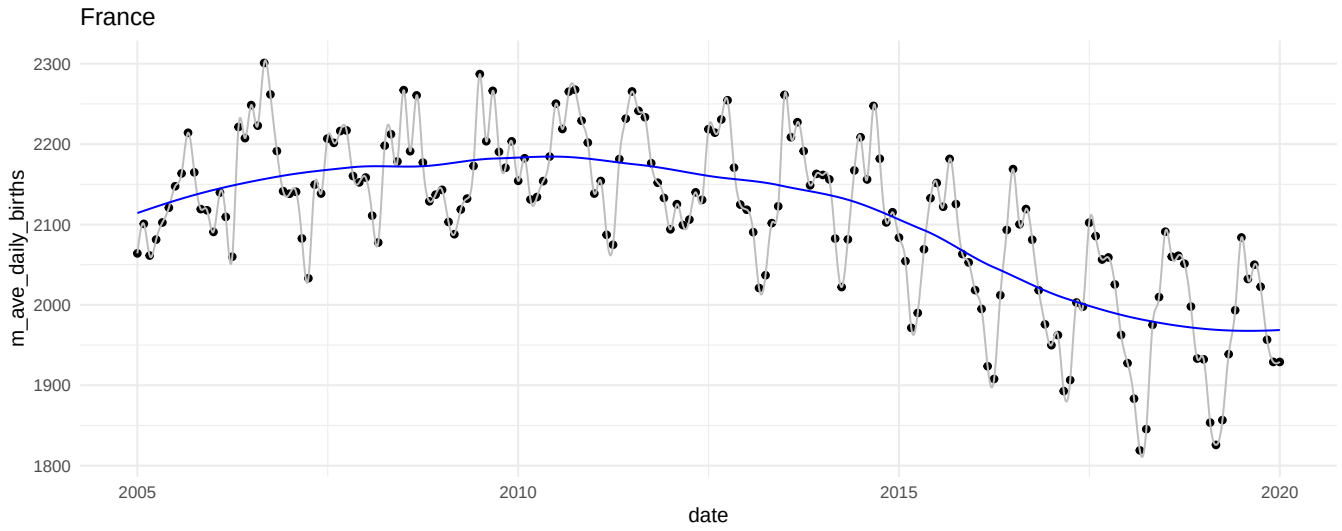


Figure 46: Average daily births (birth long-term trend).

Warning: Removed 4239 rows containing missing values (geom_point).

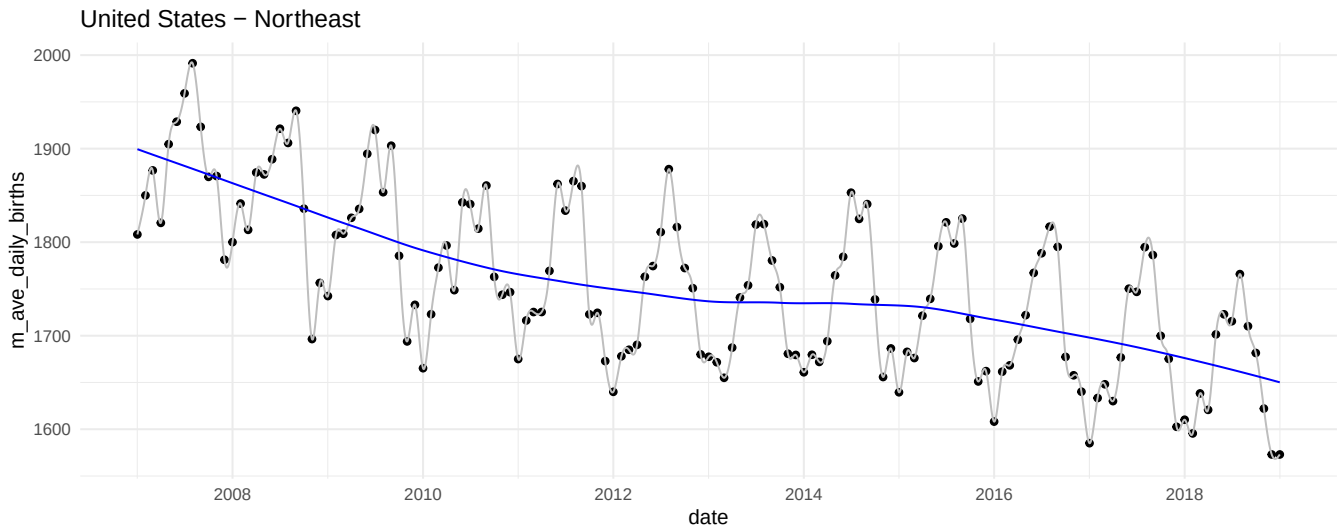


Figure 47: Average daily births (birth long-term trend).

Warning: Removed 4239 rows containing missing values (geom_point).

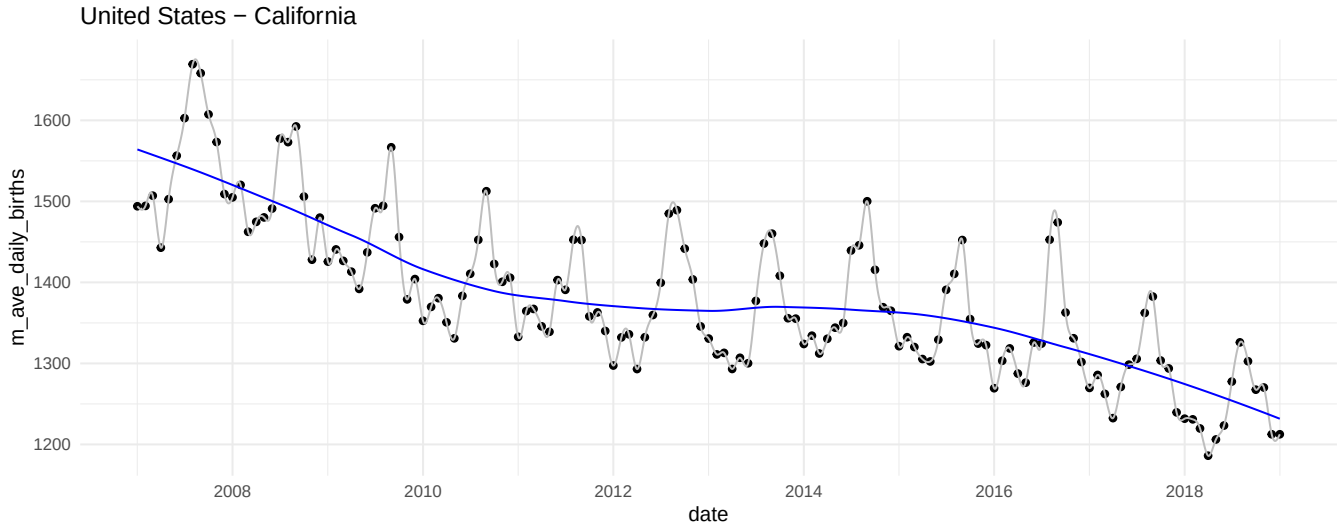


Figure 48: Average daily births (birth long-term trend).

Warning: Removed 5828 rows containing missing values (geom_point).

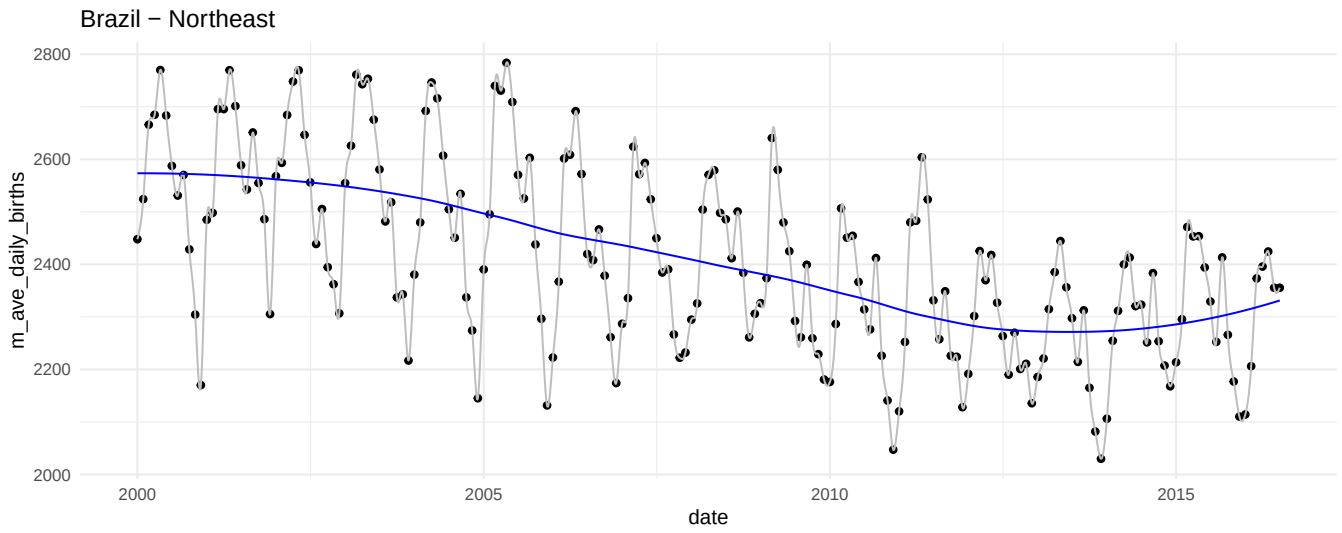


Figure 49: Average daily births (birth long-term trend).

Warning: Removed 5828 rows containing missing values (geom_point).

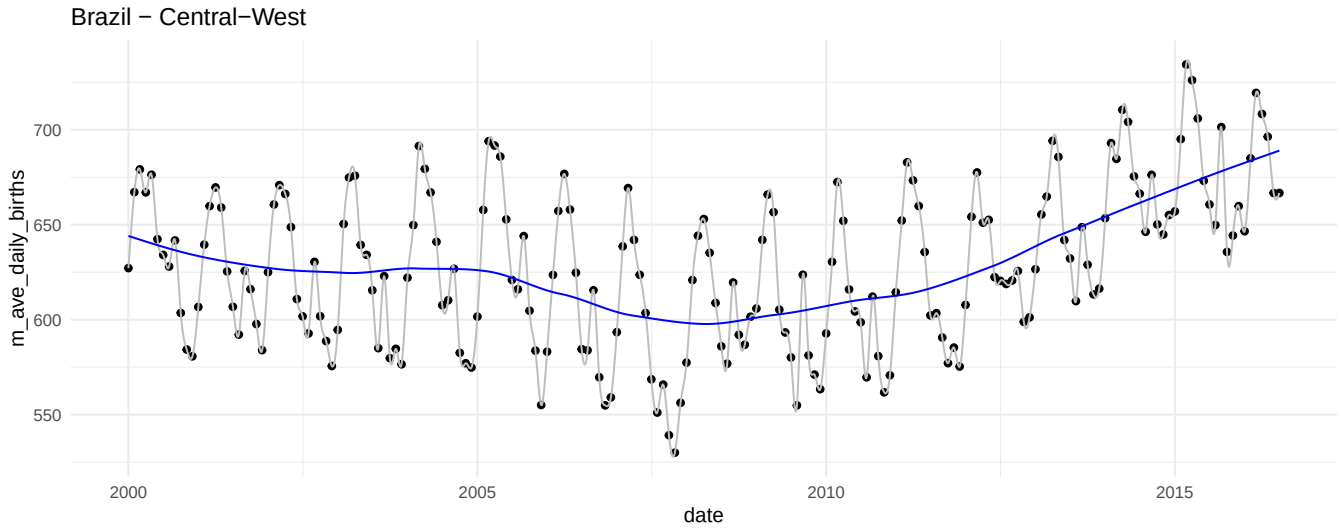


Figure 50: Average daily births (birth long-term trend).

4.5 Model parameters optimization

In this section, the fertility parameters α (relative amplitude) and T (peak fertility time) are optimized for model B and C and for each category independently.

4.5.1 Optimization functions

We first define the functions needed to optimize the parameters and simulate the daily and monthly births.

```
optimize_birth_param = function(varying_par = c(),
                                varying_par_prior = list(),
                                fixed_par = list(),
                                n_init = 10,
                                sex_df,
                                ave_daily_birth_df,
                                actual_monthly_birth_df,
                                verbose = FALSE){

 par_names = c("alpha","Tp", "beta","G","Gsd")
 # alpha is the fertility amplitude,
 # Tp is the peak time of fertility
 # beta is the amplitude (i.e the difference between the highest value and the mean, divided by the mean) of the sex curve
 # G is the average gestation period
 # Gsd is the standard deviation of the gestation period

 if((length(varying_par) == 0) & (length(fixed_par) == 0)){
  warning("varying_par and fixed_par are empty. All parameters will be optimized.")
  varying_par = par_names
 }

 if(! all(varying_par %in% par_names)) stop(paste("Parameters must be any of :",par_names))
 if(! all(names(fixed_par) %in% par_names)) stop(paste("Parameters must be any of :",par_names))

 if(length(varying_par) == 0){
  if(verbose) cat("nothing to optimize\n")
  # we don't need to optimize anything; we just compute the residuals
  par = c(0,0)

  SSR = residuals_simulated_vs_actual_monthly_birth(par = c(),
                                                    sex_df = sex_df,
                                                    ave_daily_birth_df= ave_daily_birth_df,
                                                    actual_monthly_birth_df = actual_monthly_birth_df,
                                                    alpha = 0, Tp = 0, beta = fixed_par[["beta"]], G = fixed_par[["G"]], Gsd = fixed_par[["Gsd"]])

  optimized_par = data.frame(SSR = SSR,
                             alpha = fixed_par[["alpha"]], Tp = fixed_par[["Tp"]],
                             beta = fixed_par[["beta"]],
                             G = fixed_par[["G"]],  Gsd = fixed_par[["Gsd"]],
                             stringsAsFactors = FALSE)
 }else{
  if(verbose) cat("Optimizing ",varying_par,"\n")

  # we run n_init optimization with different initial conditions
  res = foreach(i = 1:n_init, .combine = bind_rows)%do%{
   if(verbose) cat("\t",i,"\n")


   # initial values of the parameters
```

```
  par_init =
    c(runif(1, min = 0.01, max = 0.1), # alpha
      i/n_init, # Tp
      runif(1,min = 0.01, max = 1), # beta
      G0 + sample(-Gsd0:Gsd0,1), # G
      runif(1, min =  Gsd0/2, max = 2*Gsd0) # Gsd
    )
  lower = c(0, 0, 0, G0-Gsd0, Gsd0/2);
  upper = c(1, 1, 2, G0+Gsd0, Gsd0*2);

  if(length(varying_par_prior) > 0){
    for(par_name in par_names){
      if(par_name %in% names(varying_par_prior)){
        par_init[which(par_name == par_names)] = sample(varying_par_prior[[par_name]],1)
      }
    }
  }

  ix = c()
  for(par_name in par_names){
    if(par_name %in% varying_par){
      ix = c(ix, which(par_names == par_name))
      eval(parse(text = paste0(par_name," = NULL")))
    }else{
      if(! par_name %in% names(fixed_par))
        stop(paste("If",par_name,"is not varying, its value needs to be specified in 'fixed_par"))
      eval(parse(text = paste0(par_name," = fixed_par[['",par_name,"']]")))
    }
  }
  par_init = par_init[ix]
  lower = lower[ix]
  upper = upper[ix]

  if(verbose) cat(par_init, "\n")
  # optimization
  optimized_par = optim(par = par_init, lower = lower, upper = upper,
                        fn = residuals_simulated_vs_actual_monthly_birth,
                        sex_df = sex_df,
                        ave_daily_birth_df = ave_daily_birth_df,
                        actual_monthly_birth_df = actual_monthly_birth_df,
                        alpha = alpha, Tp = Tp, beta = beta, G = G, Gsd = Gsd,
                        method = "L-BFGS-B")

  opt_alpha = ifelse("alpha" %in% varying_par, optimized_par$par[which(ix == 1)],alpha)
  opt_Tp = ifelse("Tp" %in% varying_par, optimized_par$par[which(ix == 2)], Tp)
  opt_beta = ifelse("beta" %in% varying_par, optimized_par$par[which(ix == 3)], beta)
  opt_G = ifelse("G" %in% varying_par, optimized_par$par[which(ix == 4)],G)
  opt_Gsd = ifelse("Gsd" %in% varying_par, optimized_par$par[which(ix == 5)], Gsd)
  df = data.frame(value = optimized_par$value,
                  alpha = opt_alpha, Tp = opt_Tp,
                  beta = opt_beta,
                  G = opt_G, Gsd = opt_Gsd)

  return(df)
}
opt = which.min(res$value)
optimized_par = data.frame(SSR = res$value[opt],
                           alpha = res$alpha[opt], Tp = res$Tp[opt],
```

```
                    beta = res$beta[opt], G = res$G[opt], Gsd = res$Gsd[opt],
                    stringsAsFactors = FALSE)
  }

  return(optimized_par)
}



residuals_simulated_vs_actual_monthly_birth = function(
  par = c(alpha, Tp, beta, G, Gsd),
  sex_df,
  ave_daily_birth_df,
  actual_monthly_birth_df,
  alpha = NULL, Tp = NULL, beta = NULL, G = NULL, Gsd = NULL
){

  if(is.null(alpha)) alpha = par[1]
  if(is.null(Tp)) Tp = par[2]
  if(is.null(beta)) beta = par[3]
  if(is.null(G)) G = par[4]
  if(is.null(Gsd)) Gsd = par[5]

  df = simulated_vs_actual_monthly_birth(alpha = alpha, Tp = Tp, beta = beta, G = G, Gsd = Gsd,
                                         sex_df = sex_df,
                                         ave_daily_birth_df = ave_daily_birth_df,
                                         actual_monthly_birth_df = actual_monthly_birth_df)
  SSR = sum(df$sq_residuals)
  return(SSR)
}



simulated_vs_actual_monthly_birth = function(alpha, Tp, beta , G, Gsd,
                                             sex_df,
                                             ave_daily_birth_df,
                                             actual_monthly_birth_df){

  simulated_daily_births = simulate_daily_births(alpha = alpha, Tp = Tp, beta = beta, G = G, Gsd = Gsd,
                                                 sex_df = sex_df,
                                                 ave_daily_birth_df = ave_daily_birth_df )
  simulated_monthly_births = aggregate_monthly_births(simulated_daily_births)
  df = inner_join(simulated_monthly_births %>% select(year_month, births) %>% rename(sim_births = births),
                  actual_monthly_birth_df %>%  select(year_month, births),
                  by = "year_month")
  df = df %>% mutate(
    residuals = sim_births - births,
    sq_residuals = residuals^2
  )
  # we remove the first and last 6 months of data
  df = df %>% arrange(year_month) %>%
    head(.,-6) %>% tail(.,-6)
  return(df)
}



aggregate_monthly_births = function(daily_births){
```

```
  df = daily_births %>%
    mutate(year_month = year(date_births) + (month(date_births)-1)/12) %>%
    group_by(year_month) %>%
    summarize(n_days = n(),
              uncorrected_births = sum(births),
              births = uncorrected_births/n_days*30,
              .groups = "drop")
  return(df)
}



simulate_daily_births = function(alpha, Tp, beta, G, Gsd,
                                 sex_df,
                                 ave_daily_birth_df){

  beta_o = max(sex_df$sex - 1)
  if(beta_o != 0) sex_df = sex_df %>% mutate(sex_o = sex,
                                             rel_sex = (sex-1)/max(sex-1),
                                             sex = 1 + beta * rel_sex,
                                             sex = sex %>% pmax(.,0))

  df = inner_join(sex_df %>% select(date, sex),
                  ave_daily_birth_df , by = "date")

  df = df %>%
    mutate(
      year_day = year(date)+(yday(date)-1)/ifelse(leap_year(date),366,365),
      fertility = 1 + alpha*cos( (year_day - Tp) * (2 * pi)),
      conceptions = sex * fertility,
      smoothed_conceptions = smooth_conceptions(conceptions, sd_gestation = Gsd),
      date_conceptions = date,
      date_births = date + days(round(G)),
      births = ave_daily_births * smoothed_conceptions)

  df = df %>%
    select(country_area, date, date_births,
           ave_daily_births, sex, fertility,
           conceptions, smoothed_conceptions,
           births) %>%
    rename(date_conceptions = date)

  return(df)
}



smooth_conceptions = function(conceptions, sd_gestation = 9){
  x = conceptions
  if(all(is.na(x))){stop("conceptions can't be only NAs")}
  N = (sd_gestation*3.5) %>% round()
  gestation_distribution = dnorm(-N:N,mean = 0, sd = sd_gestation)
  xx = c(rev(x[1:N]),x, rev(x[(length(x)-N+1):length(x)]))
  y = stats::filter(x = xx, filter = gestation_distribution)
  y = y[!is.na(y)]
  return(y)
}
```

```r
predict_daily_sex_behavior = function(model , date_range, country_area){
  date_seq = seq(min(date_range), max(date_range), by = 1)
  df = data.frame(date = date_seq)
  df = df %>% mutate(country_area = country_area)

  df = augment_with_weekdays_months_and_holidays(df)
  df$sex = predict(object = model, newdata = df, type = "response")
  return(df)
}
```

4.5.2 Parameters optimization

```r
official_birth_records = official_birth_records %>%
  arrange(country_area, date) %>%
  group_by(country_area) %>%
  mutate(trend = predict(loess(births ~ year_month, span = 0.6)),
         detrended_births = births / trend,
         mean_detrended_birth = mean(detrended_births),
         centered_detrended_births = detrended_births - mean_detrended_birth)%>%
  ungroup()

fourier_transform = official_birth_records %>%
  group_by(country_area,year) %>%
  mutate(n_months = n()) %>%
  filter(n_months == 12) %>%
  ungroup() %>%
  group_by(country_area) %>%
  mutate(ft = fft(centered_detrended_births))

model_B_param_rough_estimates = fourier_transform %>%
  group_by(country_area) %>%
  mutate(
    i = row_number(),
    n_tp = n(),
    f_index = (n_tp %/% 12) + 1,
    amplitude_raw = max(ifelse(i == f_index, abs(ft), 0)),
    amplitude = amplitude_raw/n_tp * 2,
    angle = max(ifelse(i == f_index, -atan2(Im(ft), Re(ft)), -Inf))  %% (2*pi),
    birth_peak = angle / (2*pi),
    fertility_peak = (birth_peak + 1/3.5) %% 1)  %>%
  ungroup() %>%
  select(country_area, amplitude, birth_peak, fertility_peak) %>%  distinct()
```

```r
source("Scripts/00_functions_optim_each_model.R")


optimize_params_for_each_model = function(location, categories){
  cat(location,"\n")

  # optimization for model A: needs to be done for each sub-category in that location
  cat("\t model A\n")
  optimized_params_A =
    purrr::map_dfr(
      .x = categories$cat[categories$country_area == location],
      .f = optimize_params_for_model_A,
```

```
    categories = categories)


  # optimization for model B: only needs to be done once for the location
  cat("\t model B\n")
  optimized_params_B = optimize_params_for_model_B(location, categories = categories)

  # optimization for model C: needs to be done for each sub-category in that location
  cat("\t model C\n\t")
  optimized_params_C =
    purrr::map_dfr(
      .x = categories$cat[categories$country_area == location],
      .f = optimize_params_for_model_C,
      categories = categories,
      optimized_params_B = optimized_params_B[1,])
  cat("\n\t done\n")

  optimized_par_this_loc = bind_rows(optimized_params_A, optimized_params_B, optimized_params_C)
  optimized_par_this_loc
}
```

The parameters are now being optimized for each category of users (combination of location, birth control and age group) and sex type.

```
G_table = read_feather(path = str_c(IO$p_outputs,"Gestation_par_table.feather"))
categories = clue_sex_agg %>% select(country_area, BC, age_cat, sex_type, cat) %>%  distinct()

if(!file.exists(str_c(IO$p_outputs,"optimized_fertility_parameters.feather"))){

  tic()
  opt_par_df = purrr::map_dfr(.x = unique(categories$country_area),
                              .f = optimize_params_for_each_model, categories = categories)
  toc()

  write_feather(opt_par_df, path = str_c(IO$p_outputs,"optimized_fertility_parameters.feather"))
}else{
  warning("Fertility parameters were not optimized at this execution.\nLoading values from a previous execution.")
  opt_par_df = read_feather(path = str_c(IO$p_outputs,"optimized_fertility_parameters.feather"))
}
```

```
## Warning: Fertility parameters were not optimized at this execution.
## Loading values from a previous execution.
```

```
# opt_par_df_Brazil_Northeast = optimize_params_for_each_model(location = "Brazil - Northeast", categories = categories)
```

Computing beta_eff

```
beta_eff = purrr::map_dfr(.x = unique(categories$country_area), .f = function(location){

  j = which((sex_models_df$country_area == location) & (sex_models_df$BC == "all") & (sex_models_df$age_cat == "all") & (sex_models_df$sex_type == "unprot_sex"))
  this_cat_predicted_sex = predict_daily_sex_behavior(model = sex_models[[j]]$model, date_range = c(as.Date("2000-01-01"),as.Date("2015-12-31")), country_area = lo

  beta_C = opt_par_df %>% ungroup() %>%  filter(model == "C", country_area == location, BC == "all", age_cat == "all", sex_type == "unprot_sex") %>% select(beta) %>

  this_cat_monthly_sex = this_cat_predicted_sex %>%
    mutate(
      sex_A = sex,
      beta_A = max(sex_A - 1),
      beta_C = beta_C,
      sex_C = 1 + beta_C * (sex_A - 1)/beta_A,
      year = year(date)) %>%
```

```
  group_by(month, year, beta_A, beta_C) %>%
  summarize(sex_A = sum(sex_A),
            sex_C = sum(sex_C),
            n = n(),
            sex_A = sex_A/n*30,
            sex_C = sex_C/n*30,
            .groups = "drop") %>%
  filter(n > 20) %>%
  arrange(year, month) %>%
  mutate(beta_eff_A = (max(sex_A)-mean(sex_A))/mean(sex_A),
         beta_eff_C = (max(sex_C)-mean(sex_C))/mean(sex_C),
         country_area = location
  )

 betas = this_cat_monthly_sex %>%
  select(country_area, beta_A, beta_C, beta_eff_A, beta_eff_C) %>%
  distinct() %>%
  pivot_longer(cols = starts_with("beta"), names_to = c(".value","model"), names_pattern =  "(.*)_([AC])")

 betas

})

opt_par_df %>% ungroup() %>%  filter(BC == "all", age_cat == "all", sex_type == "unprot_sex") %>%
 select(country_area, model, alpha) %>%
 left_join(., beta_eff, by = c("country_area", "model")) %>%
 mutate(beta = beta %>% replace_na(0),
        beta_eff = beta_eff %>% replace_na(0))
```

4.5.3 Optimized parameters visualization

```
opt_par_df = opt_par_df %>%
 mutate(country_area_col = dict$country_area$country_area_col[match(country_area, dict$country_area$country_area)])


ggplot(opt_par_df %>% filter( ( (model %in% c("A","B")) & (BC=="all") & (age_cat=="all") & (sex_type == "all_sex") ) | (model == "C") ) ,
       aes(y = SSR, x = interaction(age_cat, BC, sex_type), fill = country_area_col)) +
 geom_bar(stat = "identity", col = "white")+
 xlab("")+
 scale_fill_identity()+
 facet_grid(country_area ~  model , scale = "free", space = "free_x")+
 theme(axis.text.x = element_text(angle = 90, hjust = 1),
       strip.text.y = element_text(angle = 0, hjust = 0))
```

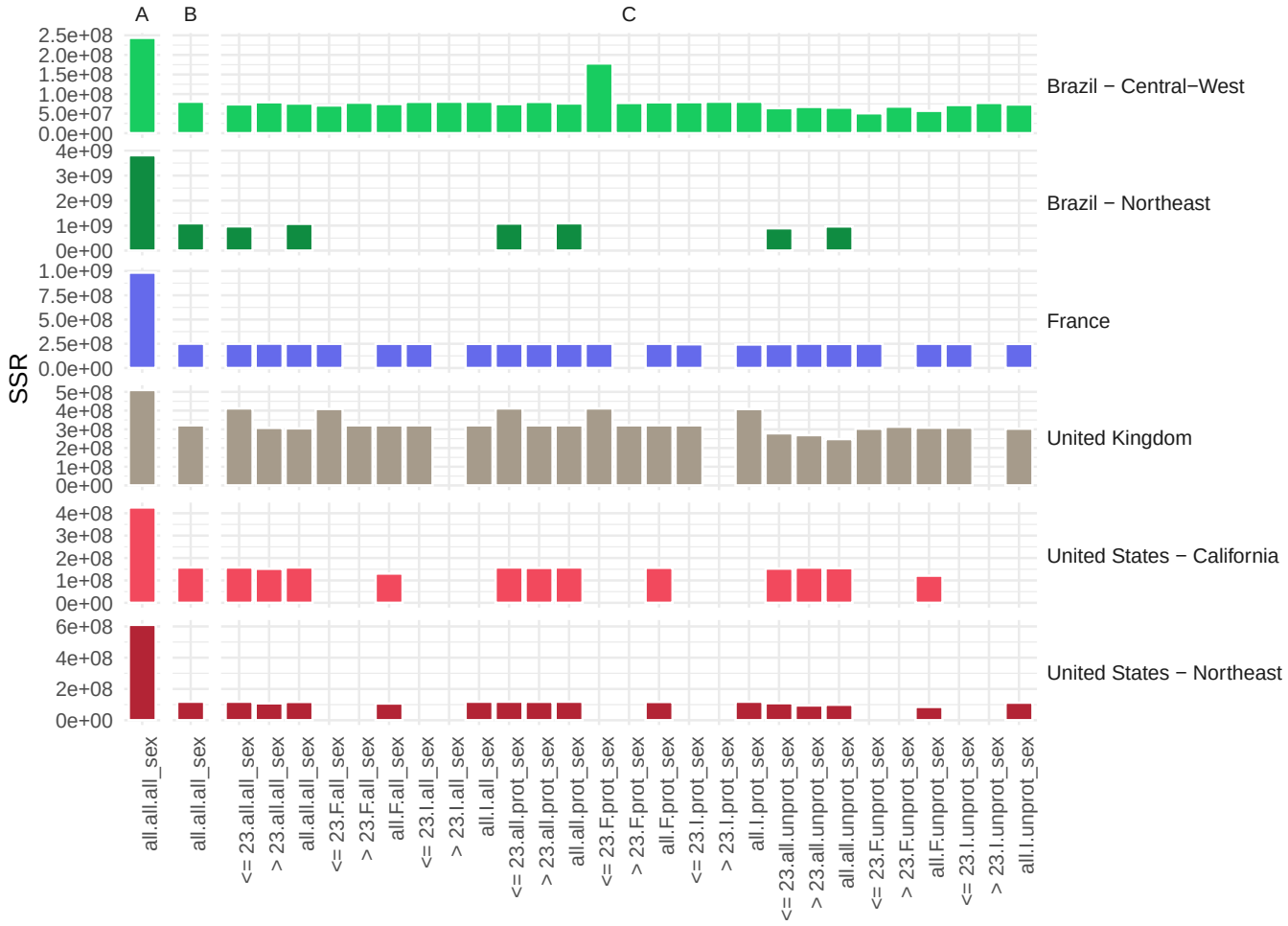


Figure 51: Comparison of the residuals for each model and each user category (model C)

```
opt_par_df = opt_par_df %>%
  mutate(country_area_wrapped =
           country_area %>%
           str_replace(.," - ","\n") %>%
           factor(., levels = dict$country_area$country_area  %>% str_replace(.," - ","\n")))

ggplot(opt_par_df %>%
         filter(model != "A",
                ((model == "B")&(BC=="all")&(age_cat=="all")&(sex_type == "all_sex")) |
                  (model == "C") ) ,
       aes(y = alpha, x = interaction(BC, sex_type, age_cat), fill = country_area_col)) +
  geom_bar(stat = "identity", col = NA)+
  scale_fill_identity()+
  xlab("")+
  facet_grid(. ~ country_area_wrapped + model , scale = "free", space = "free")+
  theme(axis.text.x = element_text(angle = 90, hjust = 1))
```

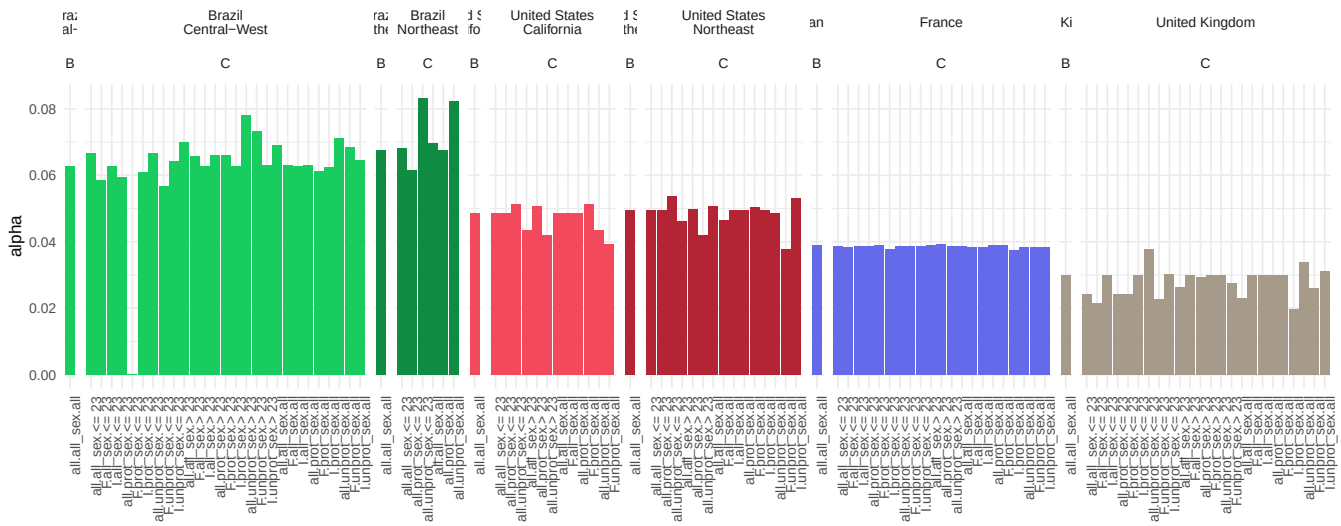


Figure 52: Relative amplitude of the fertility curve (optimized value)

```
ggplot(opt_par_df %>%
       filter(model != "A",
              ((model == "B")&(BC=="all")&(age_cat=="all")&(sex_type == "all_sex")) |
                (model == "C") ) ,
     aes(y = 12*(Tp %% 1), x = interaction(BC, sex_type, age_cat), col = country_area_col)) +
 geom_point()+
 scale_color_identity()+
 scale_y_continuous(breaks = seq(0,12,by = 2),limits = c(0,12))+
 ylab("Peak time of fertility [months]")+
 facet_grid(. ~ country_area_wrapped + model , scale = "free", space = "free")+
 theme(axis.text.x = element_text(angle = 90, hjust = 1))
```

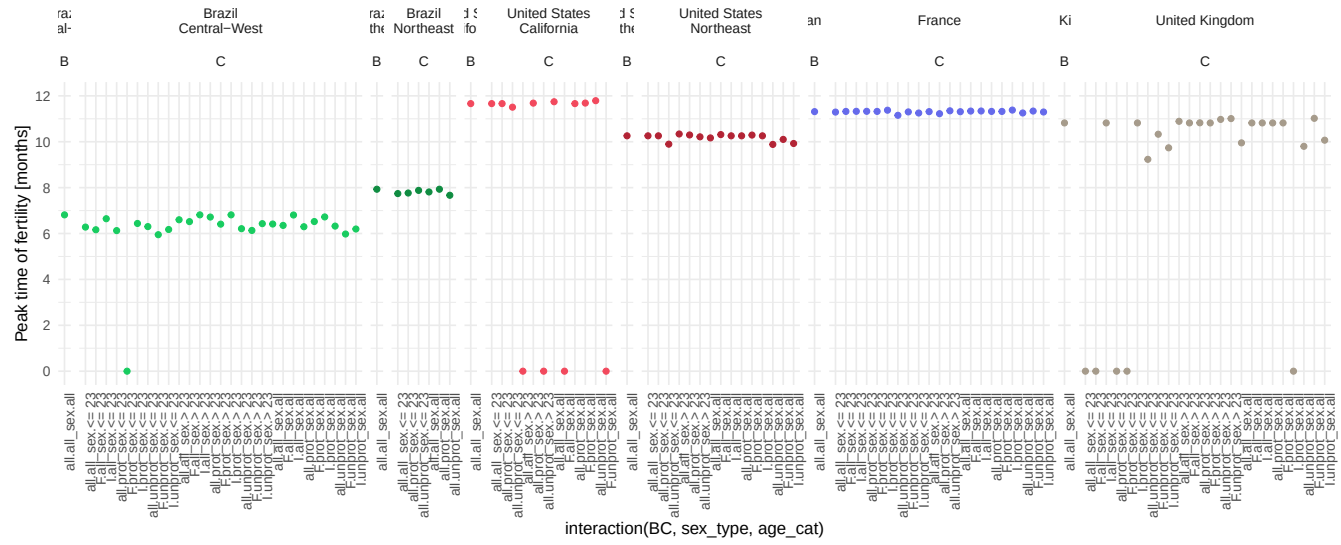


Figure 53: Peak time of fertility (optimized value). The y-axis shows the time of the year, expressed in month, at which fertility is the highest. A value of 0 (or 12) corresponds to January 1st.

4.6 Simulating monthly births

```
births = foreach(category = unique(clue_sex_agg$cat), .combine = bind_rows) %do%{

 this_cat_sex_data = clue_sex_agg %>%  filter(cat == category)
```

```
ca = unique(this_cat_sex_data$country_area)
bc = unique(this_cat_sex_data$BC)
ac = unique(this_cat_sex_data$age_cat)
st = unique(this_cat_sex_data$sex_type)
#cat(ca," - BC: ",bc," - age_cat: ",ac," - ",st, "\n")

# average daily births
this_cat_ave_daily_births = average_daily_births_df %>% filter(country_area == ca)

# actual births
this_ca_births = official_birth_records %>% filter(country_area == ca)

# predicting sex
j = which(
  (sex_models_df$country_area == ca) & (sex_models_df$BC == bc) &
    (sex_models_df$age_cat == ac) & (sex_models_df$sex_type == st))
this_cat_model = sex_models[[j]]$model
this_cat_predicted_sex = predict_daily_sex_behavior(
  model = this_cat_model,
  date_range = range(this_cat_ave_daily_births$date),
  country_area = ca)


# model A
this_cat_opt_par = opt_par_df %>%
  filter(model == "A",
         country_area == ca, age_cat == ac, BC == bc, sex_type == st)
beta = this_cat_opt_par$beta
G = this_cat_opt_par$G
Gsd = this_cat_opt_par$Gsd
monthly_births_A = simulated_vs_actual_monthly_birth(
  alpha = 0, Tp = 0, beta = beta, G = G, Gsd = Gsd,
  sex_df = this_cat_predicted_sex,
  ave_daily_birth_df = this_cat_ave_daily_births,
  actual_monthly_birth_df = this_ca_births)
monthly_births_A$model = "A"


# model B
this_cat_opt_par = opt_par_df %>%
  filter(model == "B",
         country_area == ca, age_cat == ac, BC == bc, sex_type == st)
alpha = this_cat_opt_par$alpha
Tp = this_cat_opt_par$Tp
G = this_cat_opt_par$G
Gsd = this_cat_opt_par$Gsd

sex_model_B = this_cat_predicted_sex %>%  mutate(sex = 1)

monthly_births_B = simulated_vs_actual_monthly_birth(
  alpha = alpha, Tp = Tp, beta = 0, G = G, Gsd = Gsd,
  sex_df = sex_model_B,
  ave_daily_birth_df = this_cat_ave_daily_births,
  actual_monthly_birth_df = this_ca_births)
monthly_births_B$model = "B"


# model C
```

```
  this_cat_opt_par = opt_par_df %>%
    filter(model == "C",
           age_cat == ac, country_area == ca, BC == bc, sex_type == st)
  alpha = this_cat_opt_par$alpha
  Tp = this_cat_opt_par$Tp
  beta = this_cat_opt_par$beta
  G = this_cat_opt_par$G
  Gsd = this_cat_opt_par$Gsd
  monthly_births_C = simulated_vs_actual_monthly_birth(
    alpha = alpha, Tp = Tp, beta = beta, G = G, Gsd = Gsd,
    sex_df = this_cat_predicted_sex,
    ave_daily_birth_df = this_cat_ave_daily_births,
    actual_monthly_birth_df = this_ca_births)
  monthly_births_C$model = "C"

  # Putting them together
  monthly_births = bind_rows(
    monthly_births_A,
    monthly_births_B,
    monthly_births_C)
  monthly_births = monthly_births %>%
    mutate(
      country_area = ca,
      BC = bc,
      age_cat = ac,
      sex_type = st,
      cat = category
    ) %>%
    select(country_area, BC, age_cat, sex_type, cat,
           model, year_month, sim_births, births,
           residuals, sq_residuals)
  return(monthly_births)
}
```

```
write_feather(births, path = str_c(IO$p_outputs, "simulated_births.feather"))
```

4.6.1 Time-series visualization

Time series are visualized only for BC = "all" and sex_type = "unprot_sex". Data for all simulated time-series are available on the github repo and can be visualized using the same script.

```
#births = read_feather(path = str_c(IO$out_Rdata, "simulated_births.feather"))

ok = foreach(ca = unique(clue_sex_agg$country_area)) %do% {

  this_cat_births = births %>%  filter(country_area == ca, BC == "all", sex_type == "unprot_sex")
  g = ggplot(this_cat_births, aes(x = year_month, y = sim_births/1000 , col = model))
  g = g+
    geom_line(aes(y = births/1000), col = "black", size = 1)+
    geom_line()+
    guides(col = FALSE)+
    ylab("Actual (black) and simulated (colored) births (thousands)")+
    xlab("date")+
    facet_grid(age_cat ~  model)+
    ggtitle(str_c(ca," | BC = all | sex = unprotected sex"))+
    theme(strip.background = element_rect(fill = "gray90", color = NA))
  print(g)
```

```
}
```

```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.
```

```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.
```

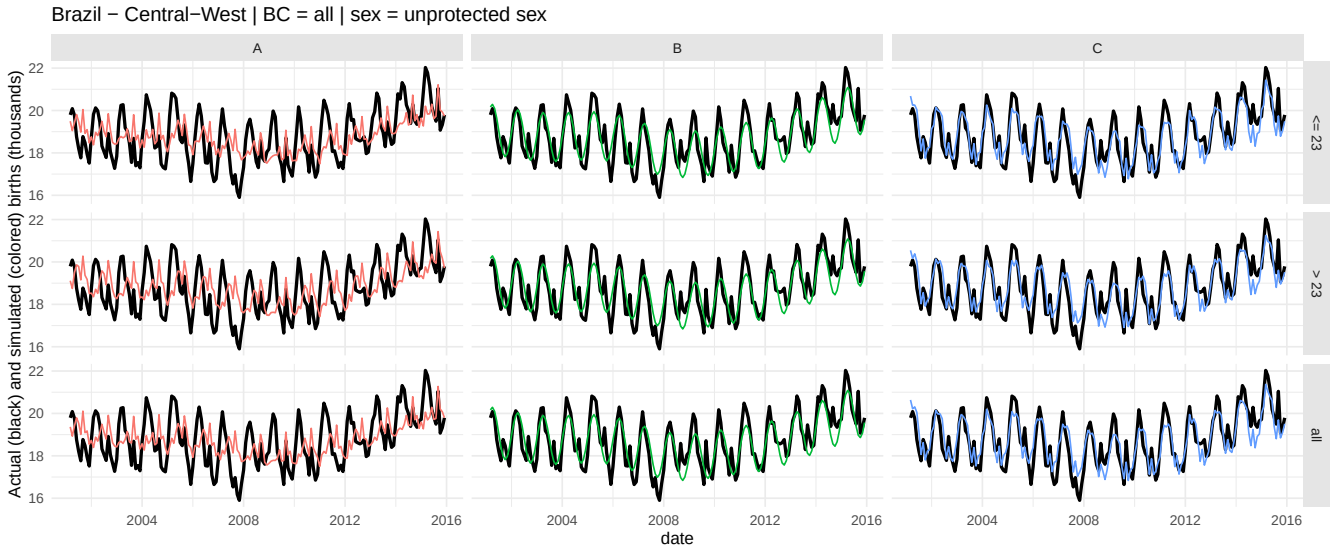


Figure 54: Simulated vs actual births.

```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.
```

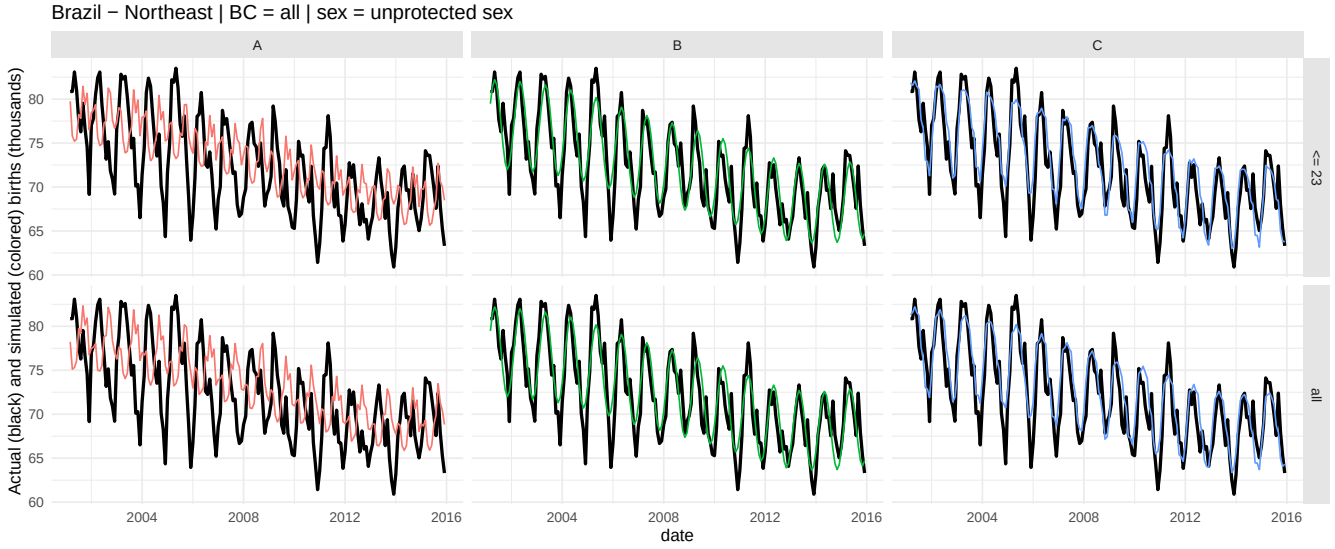


Figure 55: Simulated vs actual births.

```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.
```

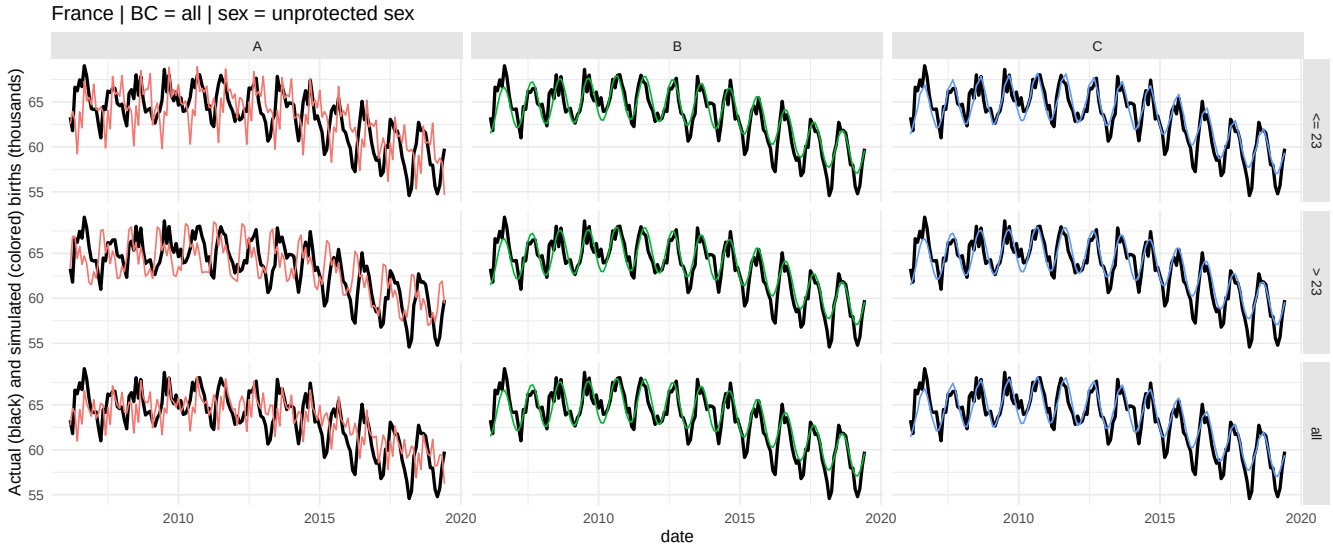


Figure 56: Simulated vs actual births.

Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
"none")` instead.

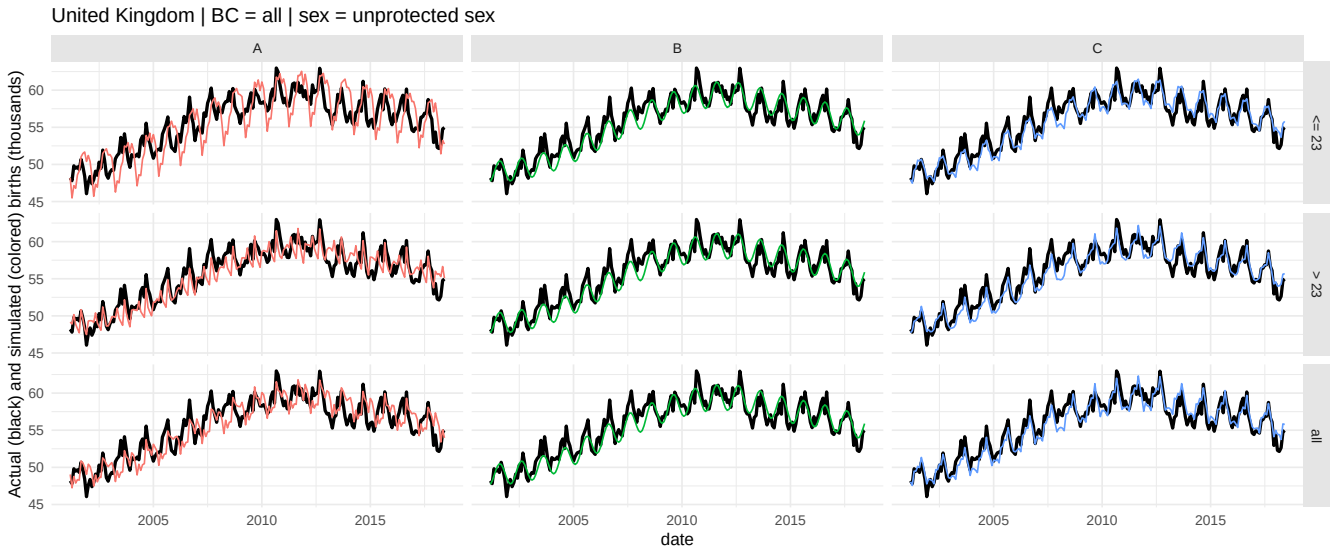


Figure 57: Simulated vs actual births.

Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
"none")` instead.

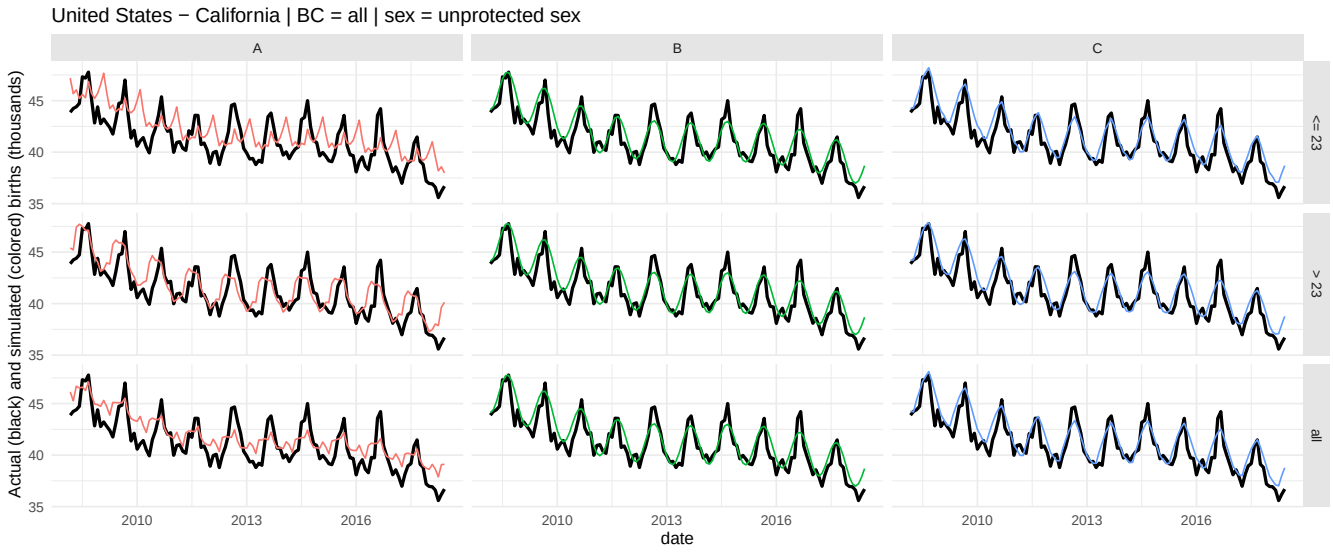


Figure 58: Simulated vs actual births.

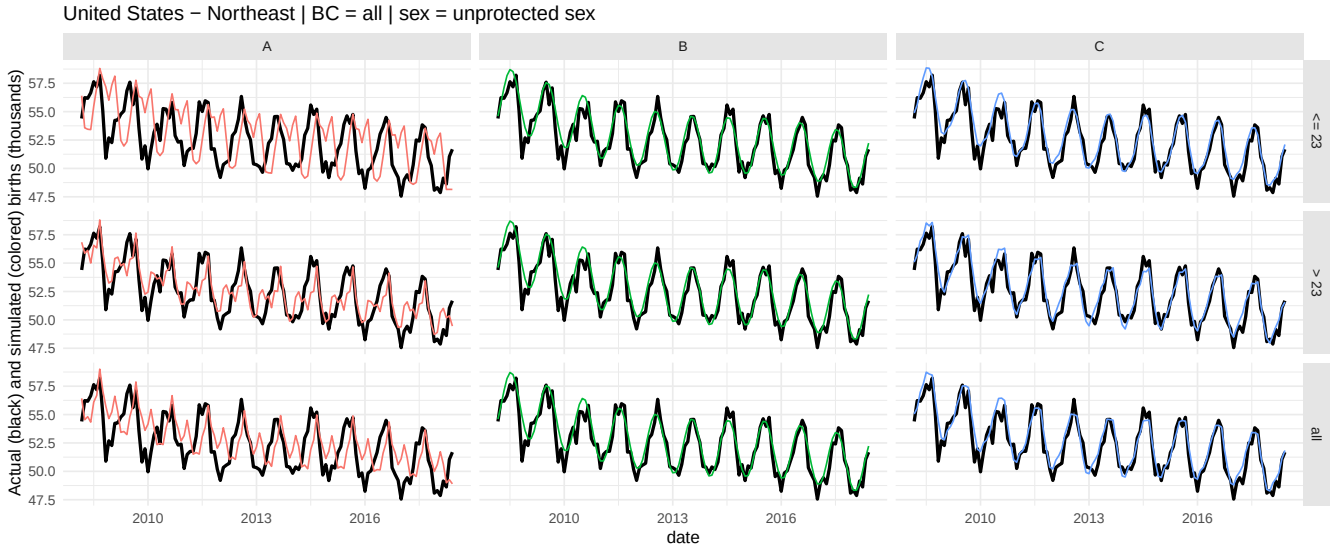


Figure 59: Simulated vs actual births.

4.7 Determining best model (A, B or C)

To understand if the seasonal sexual variations are (partially) driving seasonal birth patterns, the AIC (Akaike Information Criteria) is used to compare the three models.(*12*)

4.7.1 Residuals and AIC

```
opt_par_df = opt_par_df %>% mutate(sex_type_short = sex_type %>% str_remove(.,"_sex"))

ggplot(opt_par_df, aes(x = model, y = SSR , fill = model))+ #
  geom_bar(stat = "identity")+
  guides(fill = FALSE)+
  facet_grid(country_area ~ age_cat + BC + sex_type_short, scale = "free_y")+
  theme(strip.text.y = element_text(angle = 0, hjust = 0))
```

```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
```

"none")` instead.

Figure 60: Residuals for each model and each category of users.

We compute the AIC for each category of users.

```
# first we need to get the number of data point for each time-series
n_tp = births %>%
  group_by(country_area, age_cat, BC, sex_type, model) %>%
  summarize(n = n(),
            sigmasq = var(births), #residuals
            .groups = "drop")

opt_par_df = full_join(opt_par_df, n_tp, by = c("country_area", "BC","age_cat", "sex_type", "model"))

opt_par_df = opt_par_df %>%
  mutate(n_par = case_when(
    model == "A" ~ 0,
    model == "B" ~ 2,
    model == "C" ~ 3),
    lL = n * log(1/sqrt(2*pi*sigmasq)) - 1/(2*sigmasq)*SSR,
    AIC = 2*n_par - 2*lL
  )
```

```
ggplot(opt_par_df, aes(x = model, y = AIC , col = model))+ #
  geom_point(size = 3)+
  facet_grid(country_area ~ sex_type_short + BC + age_cat , scale = "free_y")+
  theme(strip.text.y = element_text(angle = 0, hjust = 0))
```

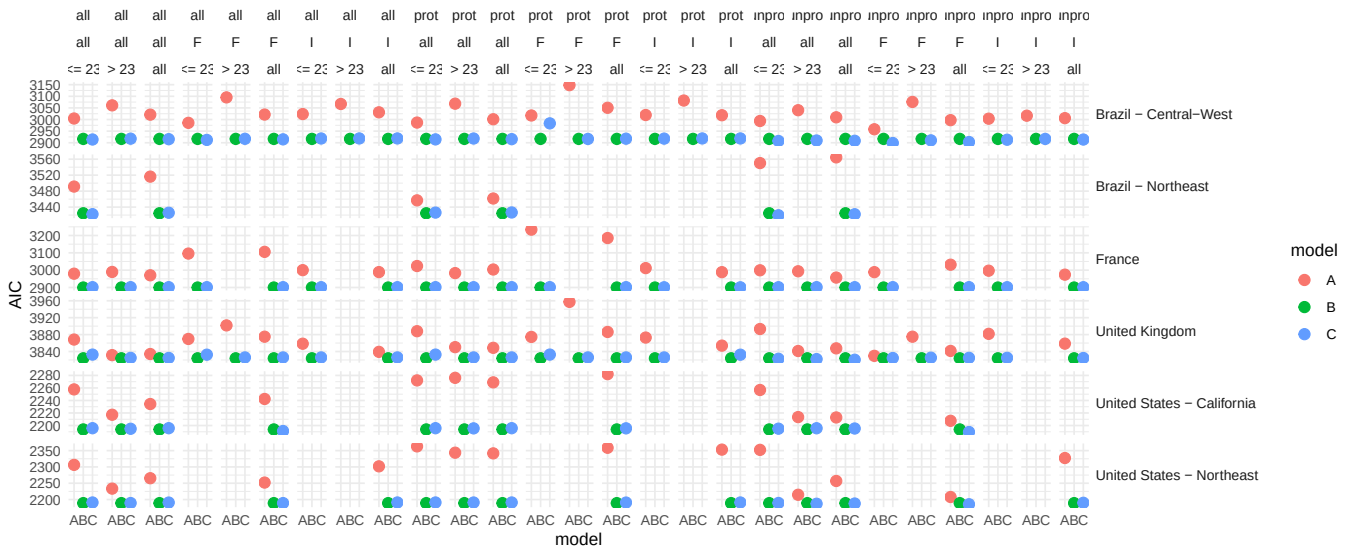


Figure 61: AIC for each model and each category of users.

```
ggplot(opt_par_df, aes(x = AIC, fill = model))+
  geom_histogram(position = "identity", bins = 50, aes(y = ..ndensity..))+
  facet_grid(model ~ country_area, scale = "free")+ # age_cat + BC + sex_type
  theme(legend.position = "bottom")
```

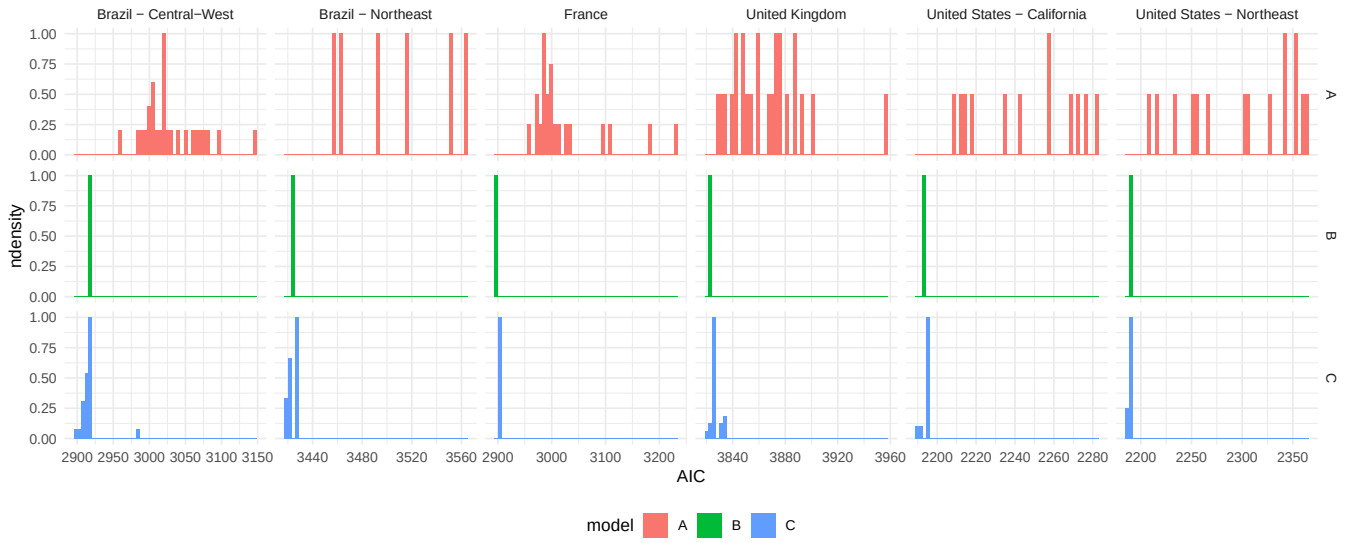


Figure 62: AIC distributions for each model and country/area.

The first observation, is that the AIC values of model A are always much higher than those of models B or C. The conclusion of this observation is that variations in sexual behavior alone do not explain seasonal births.

```
AIC_table = opt_par_df %>%
  select(country_area, sex_type, BC, age_cat, model, AIC) %>%
  arrange(country_area, sex_type, BC, age_cat, model) %>%
  mutate(AIC = round(AIC, 1)) %>%
  pivot_wider(id_cols = c(country_area, BC, age_cat),
              values_from = AIC,
              names_from = c("sex_type","model"))


colnames(AIC_table) = colnames(AIC_table) %>%
  str_remove("all_sex_") %>% str_remove("unprot_sex_") %>% str_remove("prot_sex_")
```

Table 10: AIC values for each country/area, sex type and user category

			Total sex			Protected sex			Unrotected sex		
country_area	BC	age_cat	A	B	C	A	B	C	A	B	C
Brazil - Central-West	all	<= 23	3004.4	2916.6	2914.1	2986.9	2916.6	2914.5	2993.7	2916.6	2907.6
Brazil - Central-West	all	> 23	3061.0	2916.6	2917.6	3068.2	2916.6	2918.2	3040.1	2916.6	2909.8
Brazil - Central-West	all	all	3021.0	2916.6	2915.5	3001.1	2916.6	2915.6	3009.5	2916.6	2908.5
Brazil - Central-West	F	<= 23	2985.6	2916.6	2912.2	3017.4	2916.6	2983.5	2958.1	2916.6	2898.9
Brazil - Central-West	F	> 23	3095.3	2916.6	2917.0	3148.0	2916.6	2916.4	3075.7	2916.6	2910.3
Brazil - Central-West	F	all	3021.4	2916.6	2914.7	3050.5	2916.6	2917.5	2997.3	2916.6	2903.1
Brazil - Central-West	I	<= 23	3023.5	2916.6	2918.4	3019.4	2916.6	2917.8	3003.6	2916.6	2913.0
Brazil - Central-West	I	> 23	3066.9	2916.6	2918.6	3081.7	2916.6	2918.6	3016.4	2916.6	2916.5
Brazil - Central-West	I	all	3031.0	2916.6	2918.6	3018.5	2916.6	2918.5	3005.9	2916.6	2913.9
Brazil - Northeast	all	<= 23	3491.4	3424.6	3422.3	3456.9	3424.6	3426.3	3550.2	3424.6	3419.6
Brazil - Northeast	all	all	3516.3	3424.6	3425.9	3461.5	3424.6	3426.6	3564.5	3424.6	3422.2
France	all	<= 23	2979.6	2899.9	2901.7	3023.8	2899.9	2901.8	2999.3	2899.9	2901.5
France	all	> 23	2989.7	2899.9	2901.9	2983.0	2899.9	2901.6	2993.5	2899.9	2901.9
France	all	all	2970.3	2899.9	2901.8	3003.7	2899.9	2901.7	2957.2	2899.9	2901.6
France	F	<= 23	3095.7	2899.9	2901.7	3233.9	2899.9	2901.8	2988.5	2899.9	2901.9
France	F	all	3105.6	2899.9	2901.8	3185.4	2899.9	2901.8	3031.4	2899.9	2901.8
France	I	<= 23	3000.1	2899.9	2901.6	3011.8	2899.9	2901.2	2996.9	2899.9	2901.5
France	I	all	2988.8	2899.9	2901.7	2988.5	2899.9	2901.0	2974.0	2899.9	2901.6
United Kingdom	all	<= 23	3868.3	3824.0	3832.7	3888.0	3824.0	3832.7	3893.2	3824.0	3822.8
United Kingdom	all	> 23	3831.5	3824.0	3825.0	3850.3	3824.0	3826.0	3841.2	3824.0	3822.1
United Kingdom	all	all	3834.1	3824.0	3824.8	3848.7	3824.0	3826.0	3847.5	3824.0	3820.5
United Kingdom	F	<= 23	3869.7	3824.0	3832.5	3874.5	3824.0	3832.7	3829.7	3824.0	3824.7
United Kingdom	F	> 23	3901.7	3824.0	3826.0	3957.4	3824.0	3826.0	3875.0	3824.0	3825.5
United Kingdom	F	all	3875.0	3824.0	3826.0	3886.2	3824.0	3826.0	3841.4	3824.0	3825.1
United Kingdom	I	<= 23	3858.4	3824.0	3826.0	3873.0	3824.0	3826.0	3881.8	3824.0	3825.1
United Kingdom	I	all	3839.2	3824.0	3826.0	3853.9	3824.0	3832.5	3858.6	3824.0	3824.7
United States - California	all	<= 23	2257.7	2193.8	2195.8	2272.0	2193.8	2195.8	2256.7	2193.8	2194.9
United States - California	all	> 23	2217.2	2193.8	2194.8	2276.1	2193.8	2195.4	2213.5	2193.8	2195.7
United States - California	all	all	2234.3	2193.8	2195.7	2268.9	2193.8	2195.8	2212.9	2193.8	2195.2
United States - California	F	all	2242.4	2193.8	2191.2	2282.1	2193.8	2195.5	2207.5	2193.8	2189.6
United States - Northeast	all	<= 23	2306.3	2189.0	2191.0	2363.0	2189.0	2191.0	2352.3	2189.0	2189.5
United States - Northeast	all	> 23	2233.5	2189.0	2189.3	2343.6	2189.0	2191.0	2214.7	2189.0	2187.1
United States - Northeast	all	all	2265.4	2189.0	2190.8	2341.6	2189.0	2191.0	2256.9	2189.0	2187.9
United States - Northeast	F	all	2252.1	2189.0	2189.2	2358.7	2189.0	2190.8	2207.8	2189.0	2185.6
United States - Northeast	I	all	2301.8	2189.0	2191.0	2353.1	2189.0	2191.0	2327.3	2189.0	2190.1

```
kable(
  AIC_table,
  format = "latex",
  booktabs = "T",
  linesep = "",
  caption = "AIC values for each country/area, sex type and user category"
  ) %>%
  kable_styling(
    latex_options = c("striped","scale_down"),
    stripe_index = rep(1:3, 3)+ rep(c(0,6,12), each = 6),
    font_size = 8) %>%
add_header_above(c(" " = 3, "Total sex" = 3, "Protected sex" = 3, "Unrotected sex" = 3))
```

```
best_models = opt_par_df %>%
  arrange(country_area, BC, age_cat, sex_type, AIC) %>%
  group_by(country_area, BC, age_cat, sex_type) %>%
  top_n(n = 1, wt = desc(AIC)) %>%
  rename(best_model = model) %>%
  ungroup()

best_models_table = best_models %>%
  select(country_area, BC, age_cat , sex_type, best_model) %>%
```

Table 11: Best Models (i.e. with the lowest AIC) for each country/area, user category and sex type

		BC: all			BC: F			BC: I		
country_area	age_cat	all_sex	prot_sex	unprot_sex	all_sex	prot_sex	unprot_sex	all_sex	prot_sex	unprot_sex
Brazil - Central-West	<= 23	C	C	C	C	B	C	B	B	C
Brazil - Central-West	> 23	B	B	C	B	C	C	B	B	C
Brazil - Central-West	all	C	C	C	C	B	C	B	B	C
Brazil - Northeast	<= 23	C	B	C	NA	NA	NA	NA	NA	NA
Brazil - Northeast	all	B	B	C	NA	NA	NA	NA	NA	NA
France	<= 23	B	B	B	B	B	B	B	B	B
France	> 23	B	B	B	NA	NA	NA	NA	NA	NA
France	all	B	B	B	B	B	B	B	B	B
United Kingdom	<= 23	B	B	C	B	B	B	B	B	B
United Kingdom	> 23	B	B	C	B	B	B	NA	NA	NA
United Kingdom	all	B	B	C	B	B	B	B	B	B
United States - California	<= 23	B	B	B	NA	NA	NA	NA	NA	NA
United States - California	> 23	B	B	B	NA	NA	NA	NA	NA	NA
United States - California	all	B	B	B	C	B	C	NA	NA	NA
United States - Northeast	<= 23	B	B	B	NA	NA	NA	NA	NA	NA
United States - Northeast	> 23	B	B	C	NA	NA	NA	NA	NA	NA
United States - Northeast	all	B	B	C	B	B	C	B	B	B

```
  pivot_wider(names_from = c("BC", "sex_type"), values_from = "best_model", names_prefix = "BC: ", names_sep = " - ")

colnames(best_models_table) = colnames(best_models_table) %>%
  str_remove("BC: all") %>% str_remove("BC: F") %>% str_remove("BC: I") %>%
  str_remove(" - ")
```

```
kable(best_models_table, format = "latex", booktabs = T, linesep = "",
      caption = "Best Models (i.e. with the lowest AIC) for each country/area, user category and sex type") %>%
  kable_styling(
    latex_options = c("striped","scale_down"),
    stripe_index = c(1,2,3,6,7,8,12,13,14),
    font_size = 8) %>%
add_header_above(c(" " = 2, "BC: all" = 3, "BC: F" = 3, "BC: I" = 3))
```

In table 11, model B is predominantly the best model for most countries/areas and users category. However, the differences in AIC are sometimes very mild, as shown in fig 63. In this figure, to understand if sexual variations contribute to seasonal birth together with seasonal fertility, we display the AIC difference between model B and model C.

```
tmp = opt_par_df  %>% filter(model != "A") %>%
   select(country_area, age_cat, BC, sex_type, model, AIC) %>%
   pivot_wider(names_from = model, values_from = AIC) %>%
   mutate(AIC_diff_B_minus_C = B-C,
          cat = interaction(country_area, BC, age_cat, sex_type))

tmp = full_join(tmp, df_agg, by = "cat") %>%
  mutate(sex_type_short = sex_type %>% str_remove(.,"_sex"))

age_df = purrr::map_dfr(.x = unique(tmp$country_area),
                        .f = function(x) tmp %>% filter(country_area == x, age_cat == get_age_cat(x), BC == "all", sex_type == "unprot_sex"))

ggplot(tmp, aes(ymin = 0, ymax = median_n_users, xmin = 0, xmax = 1))+
  geom_rect(aes(fill = AIC_diff_B_minus_C))+
  geom_rect(data = age_df, fill = "transparent", color = "black")+
  scale_x_continuous(breaks = NULL) +  #scale_y_continuous(breaks = NULL) +
  xlab("") +
  ylab("Median number of users \n contributing to the aggregated time-series") +
  scale_fill_gradient2(name = "Difference in AIC:  AIC(B) - AIC(C)", low = "red", high = "blue", mid = "gray90", midpoint = 0)+
  facet_grid(country_area ~ age_cat + BC + sex_type_short , scale = "free_y")+
```

```
theme(legend.position = "bottom",
    strip.text.y = element_text(angle = 0, hjust = 0, vjust = 0))
```

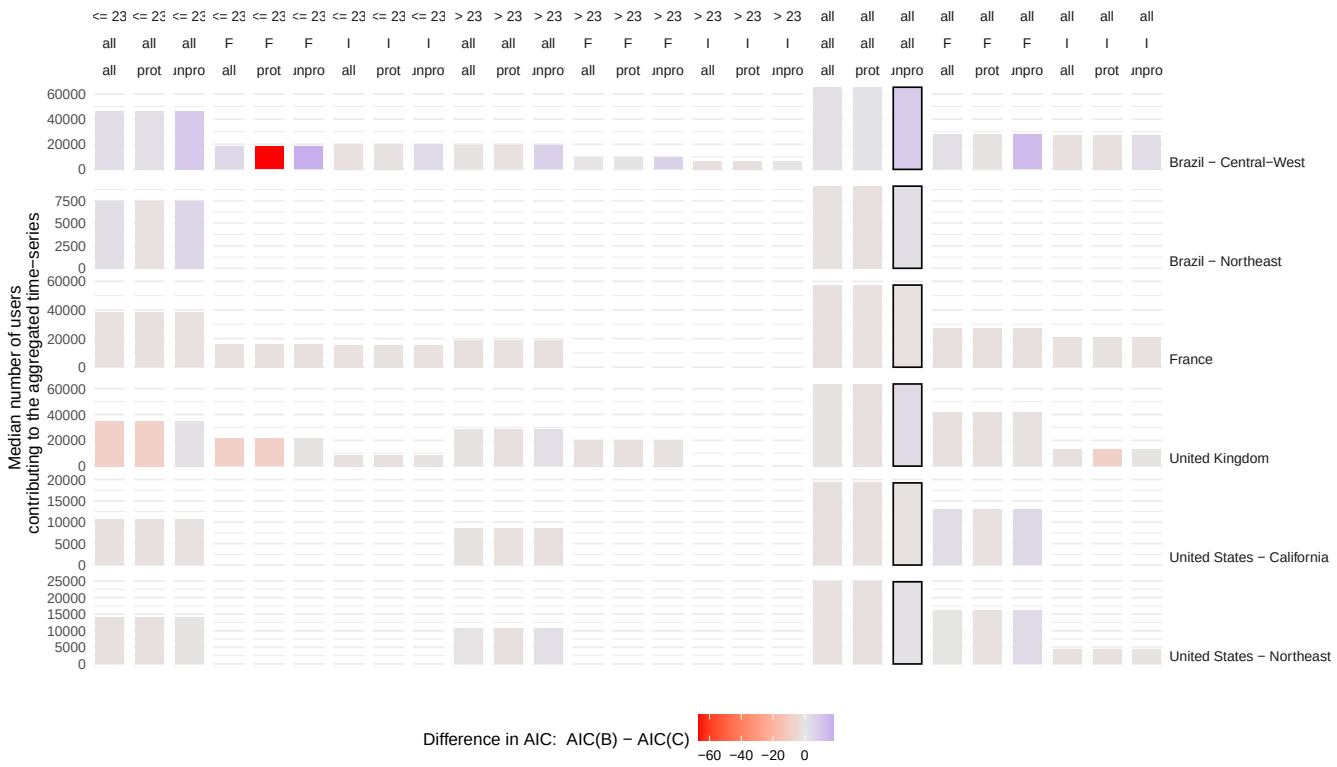


Figure 63: Difference in AIC between model B and model C. A positive (blue-ish) value indicated that sexual frequency variations contribute to explaining the seasonal birth patterns. Rectangle height is proportional to the median number of app users who contributed to the aggregated time-series of sexual frequency. The black rectangles indicates the categories of users used for the rest of the analysis (see text)

In fig 63, the black rectangles show the categories of users selected for the rest of the analysis. These categories correspond to sex_type = 'unprotected sex' (which is most likely to lead to a pregnancy), includes all users on any kind of birth control (incl. no birth control at all) and for most countries/areas, users of all age groups were considered.

```
write_feather(opt_par_df, path = str_c(IO$p_outputs, "optimal_parameters_and_AIC.feather"))
```

4.7.2 Impact of age, birth control and sex type on simulated births with model C

```
for(ca in unique(births$country_area)){

 # ggplot(births %>% filter(model == "C", country_area == ca, sex_type != "all_sex"),
 #       aes(x = year_month)) +
 #  geom_line(aes(y = births)) +
 #  geom_line(aes(y = sim_births, col = age_cat, linetype = BC)) +
 #  facet_grid(sex_type ~ .) +
 #  xlab("time (year)") +
 #  theme(strip.background.y = element_rect(fill = "gray90", color = "transparent")) +
 #  ggtitle(ca)

 g = ggplot(births %>% filter(model == "C", country_area == ca),
         aes(x = year_month)) +
  geom_line(aes(y = births)) +
  geom_line(aes(y = sim_births, col = sex_type, linetype = BC)) +
```

```
  facet_grid(age_cat ~ ., labeller = label_both) +
  xlab("time (year)") +
  theme(strip.background.y = element_rect(fill = "gray90", color = "transparent"),
        legend.position = "bottom") +
  ggtitle(ca)

 # g = ggplot(births %>% filter(model == "C", country_area == ca),
 #            aes(x = year_month - floor(year_month))) +
 #   geom_line(aes(y = births)) +
 #   geom_line(aes(y = sim_births, col = sex_type)) +
 #   facet_grid(floor(year_month) ~ age_cat + BC, labeller = label_context) +
 #   xlab("time (year)") +
 #   theme(strip.background.y = element_rect(fill = "gray90", color = "transparent"),
 #         legend.position = "right") +
 #   ggtitle(ca)

  print(g)
}
```

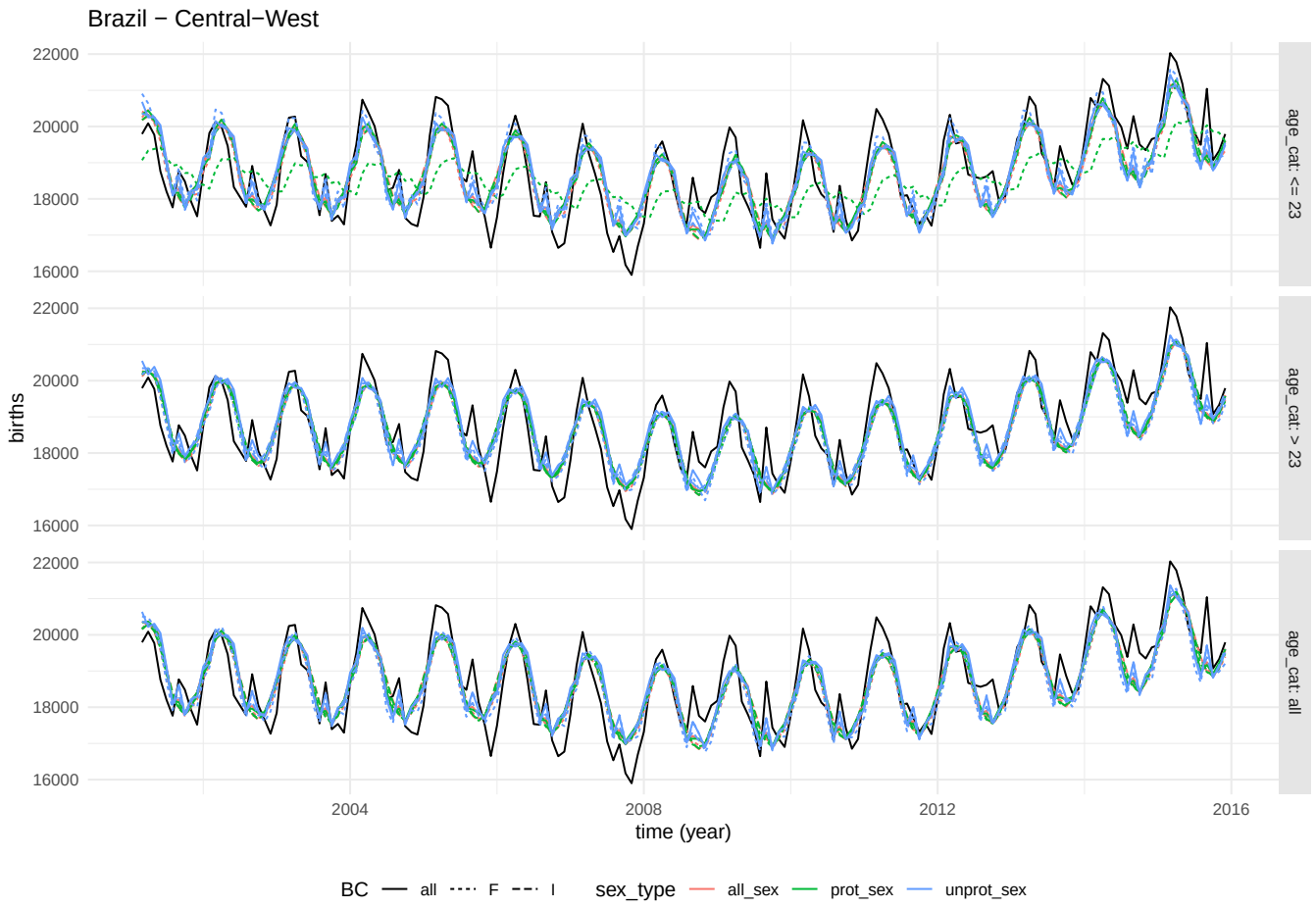


Figure 64: Impact of age, birth control and sex type on simulated births with model C.

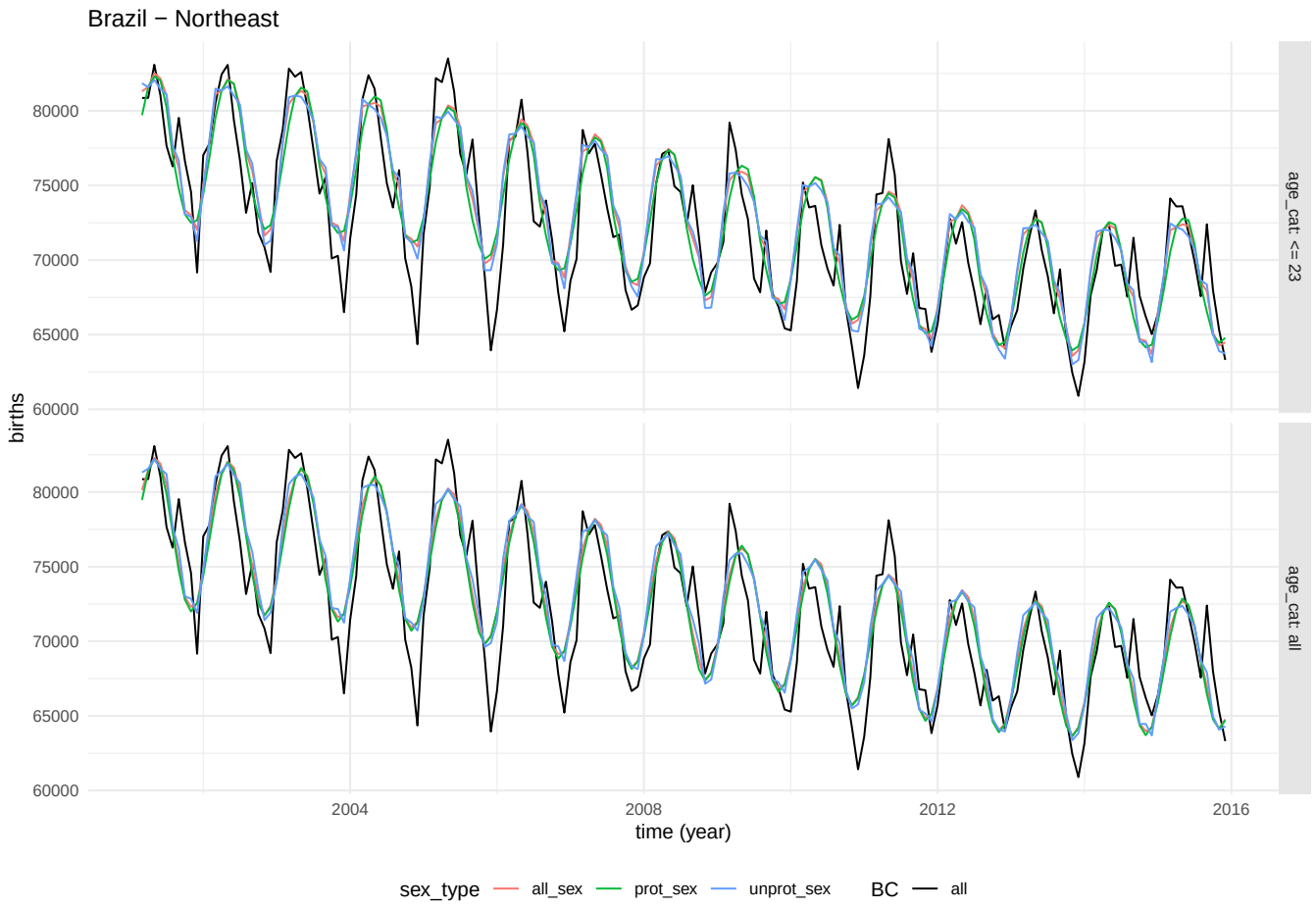


Figure 65: Impact of age, birth control and sex type on simulated births with model C.

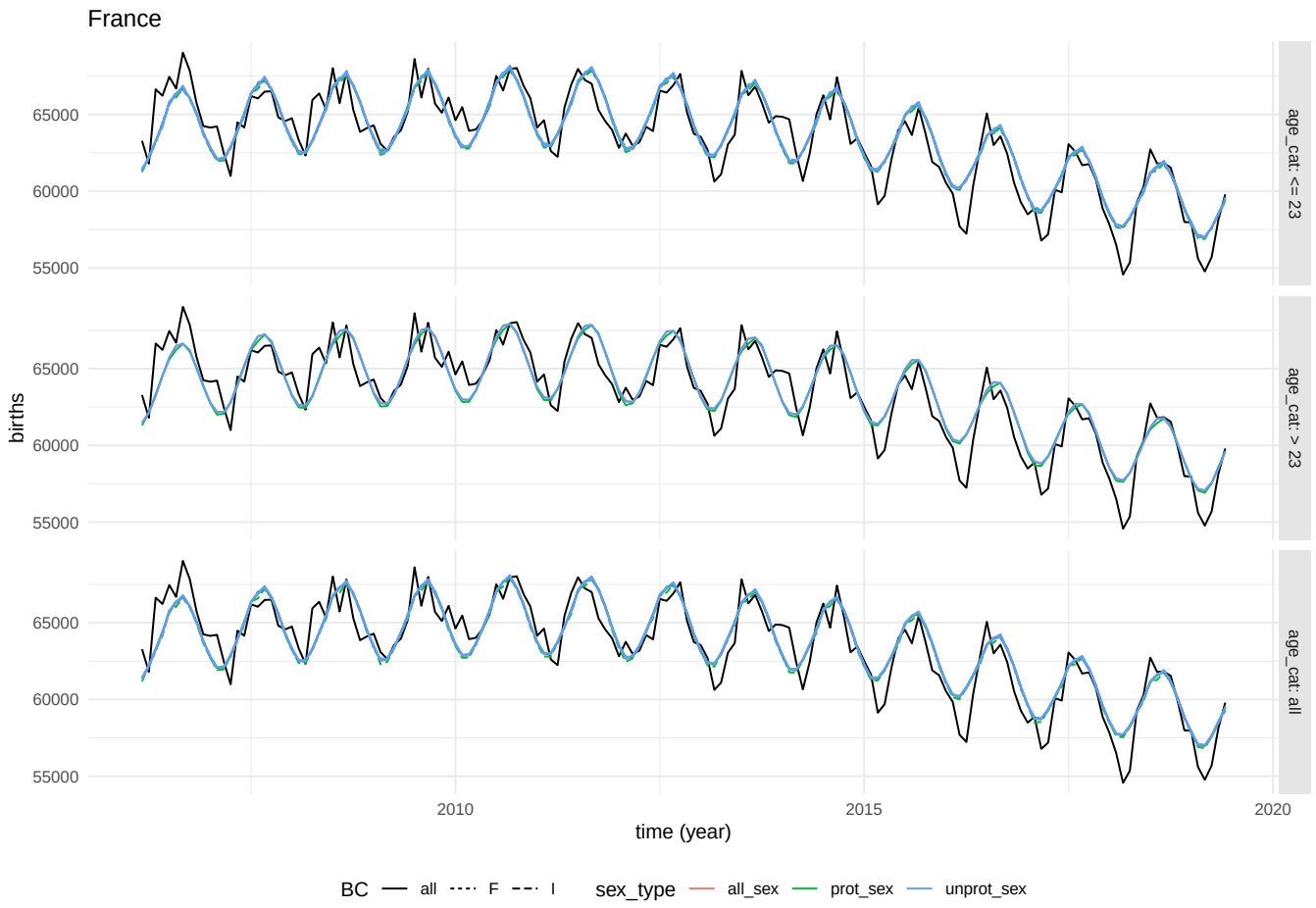


Figure 66: Impact of age, birth control and sex type on simulated births with model C.

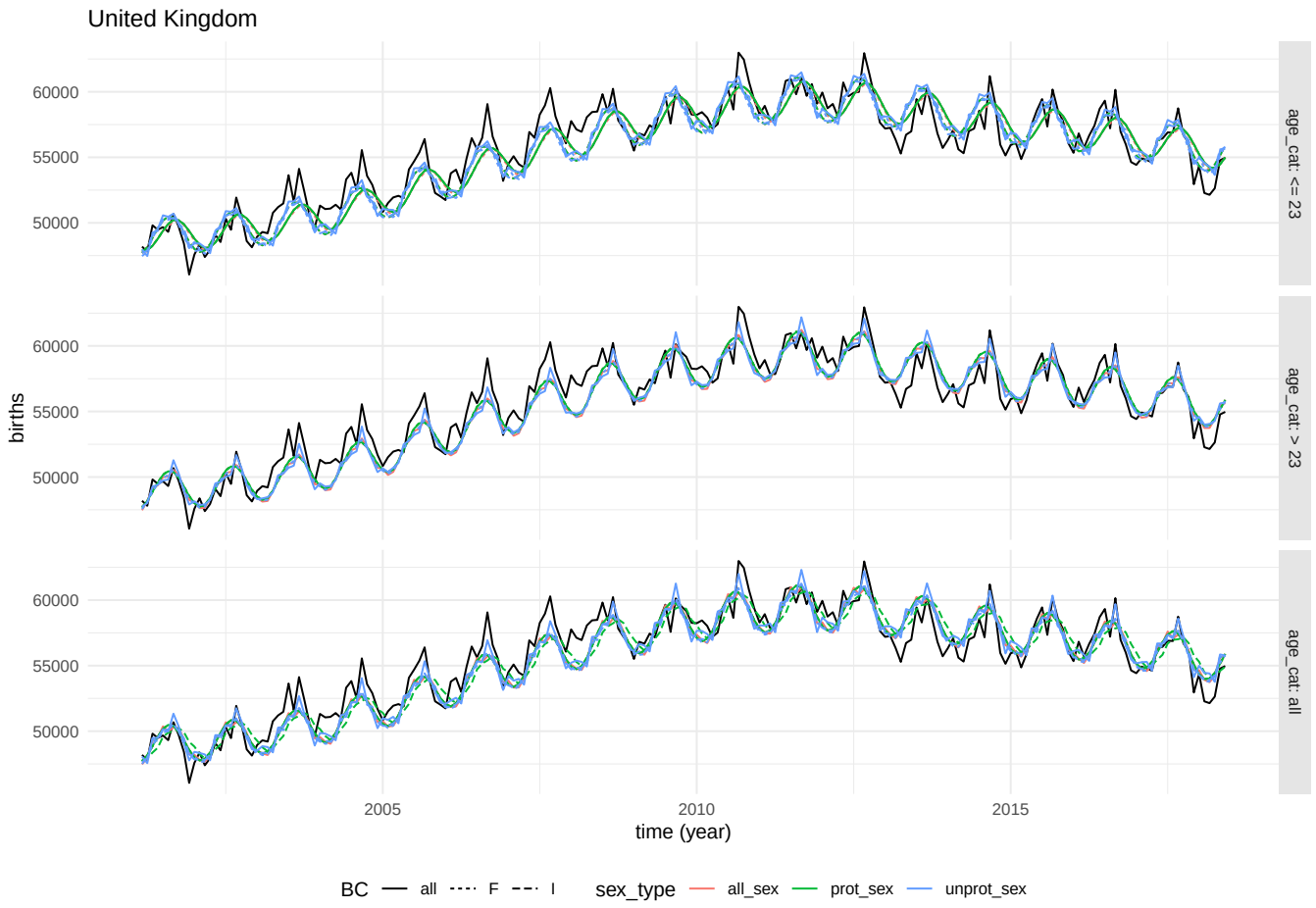


Figure 67: Impact of age, birth control and sex type on simulated births with model C.

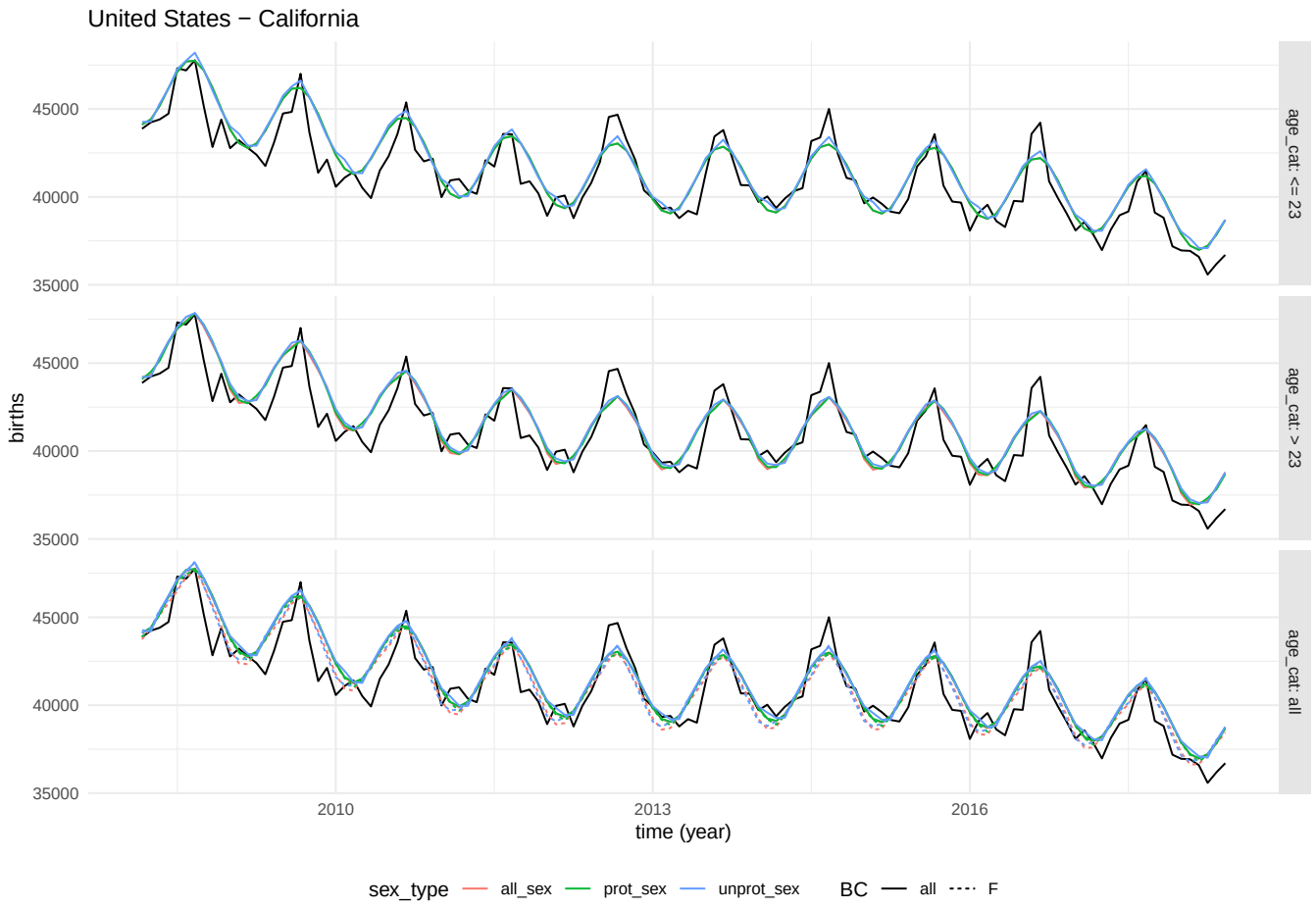


Figure 68: Impact of age, birth control and sex type on simulated births with model C.

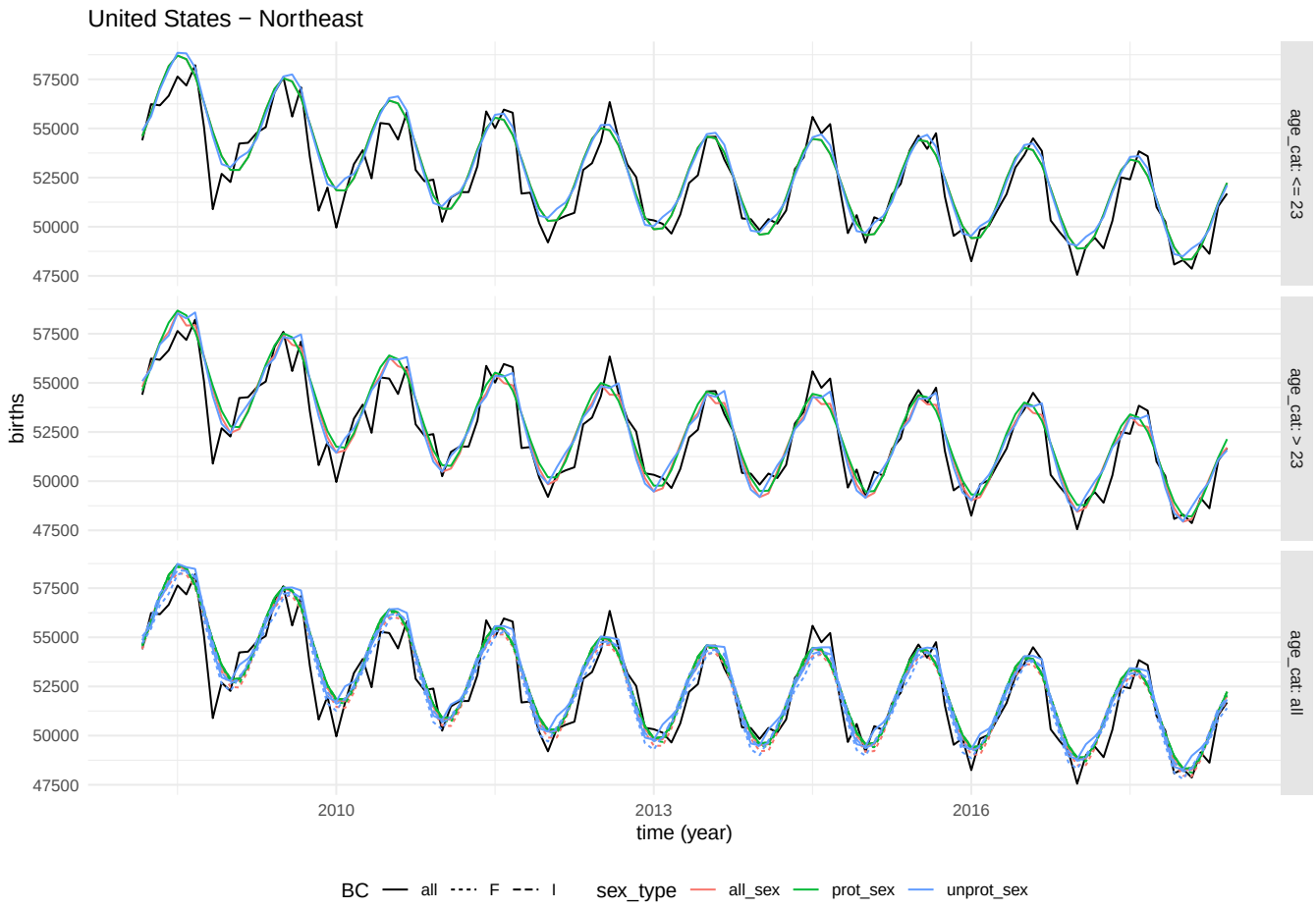


Figure 69: Impact of age, birth control and sex type on simulated births with model C.

4.7.3 Seasonal decomposition and seasonal trends comparisons

Before doing a seasonal decomposition of the actual vs simulated births, a visualization of the time-series with the months stacked on top of each other for each year of simulated data helps understand where the variability in high-frequency changes in births patterns and how model A and model C, by accounting for non-fixed holidays, correlates with these high-frequency changes or minor peaks.

```
ok = foreach(ca = unique(clue_sex_agg$country_area)) %do% {

  ac = get_age_cat(country_area = ca)

  bc = "all"

  this_cat_births = births %>%  filter(country_area == ca,  BC == bc, age_cat == ac, sex_type == "unprot_sex")
  aic = opt_par_df %>% filter(country_area == ca,  BC == bc, age_cat == ac, sex_type == "unprot_sex")
  best_model_df = best_models %>% filter(country_area == ca,  BC == bc, age_cat == ac, sex_type == "unprot_sex")

  g = ggplot(this_cat_births, aes(x = month, y = sim_births/1000 , col = model))
  g = g+
    geom_line(aes(y = births/1000), col = "black", size = 1.2)+
    geom_line()+
    guides(col = FALSE)+
    ylab("Births (thousands)")+
    facet_grid(year ~ model, scale = "free_y")+
    scale_x_continuous(breaks = seq(1,12,by = 3), labels = c("Jan","Apr","Jul","Oct"))+
    ggtitle(str_c(ca, " / BC : all / age_cat : ",ac," /sex : unprotected \n BEST MODEL = ",best_model_df$best_model))+
    theme(strip.text.y = element_text(angle = 0, hjust = 0))
  print(g)

}
```

```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.
```

```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.
```

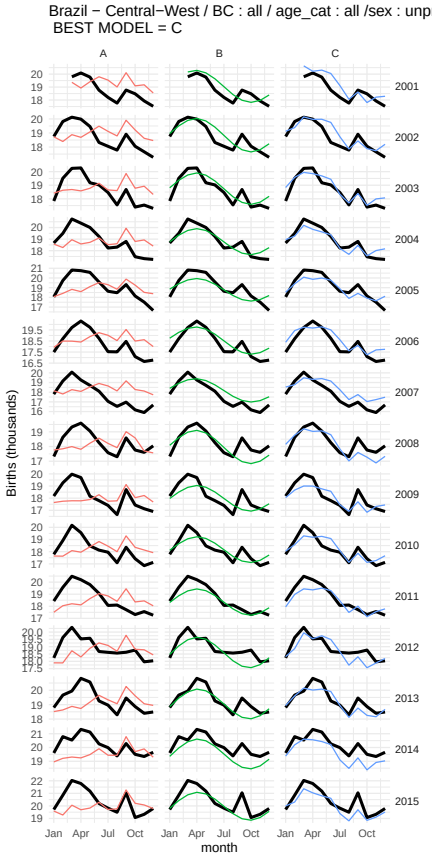


Figure 70: Actual (black lines) and simulated (colored lines) births.

Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
"none")` instead.

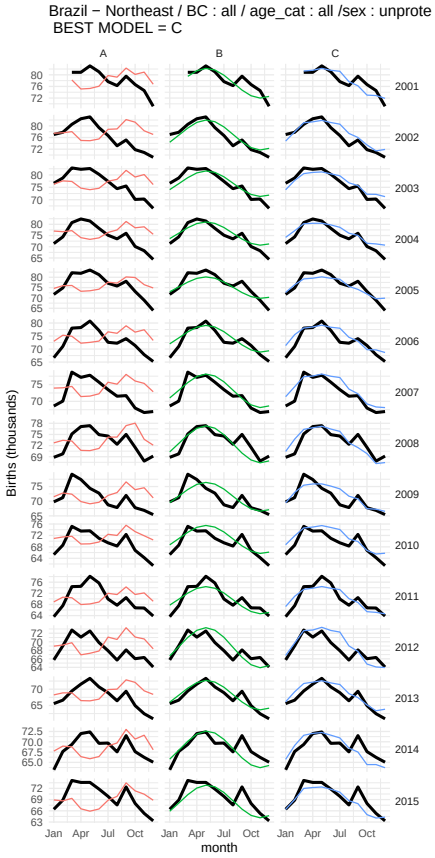


Figure 71: Actual (black lines) and simulated (colored lines) births.

Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
"none")` instead.

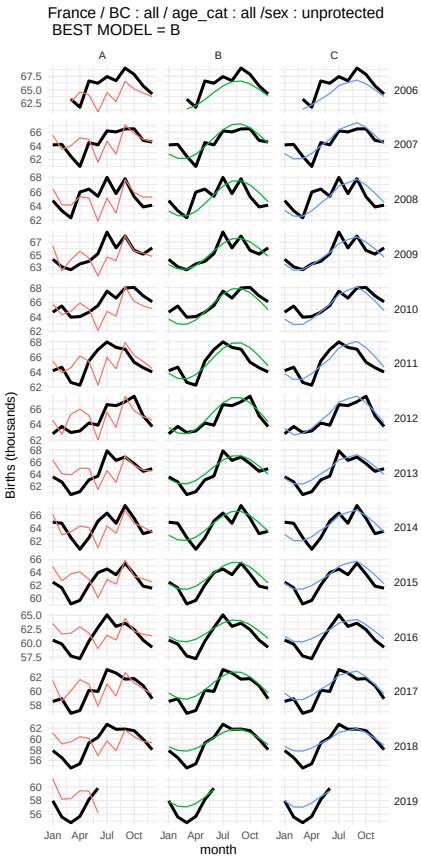


Figure 72: Actual (black lines) and simulated (colored lines) births.

Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
"none")` instead.

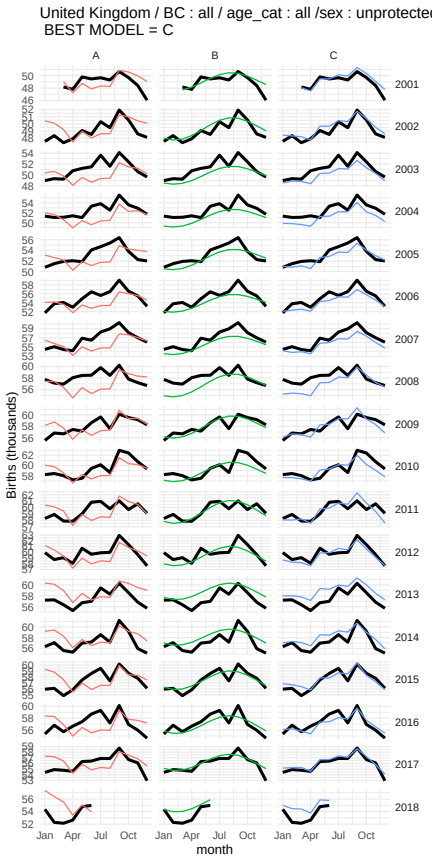


Figure 73: Actual (black lines) and simulated (colored lines) births.

Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
"none")` instead.

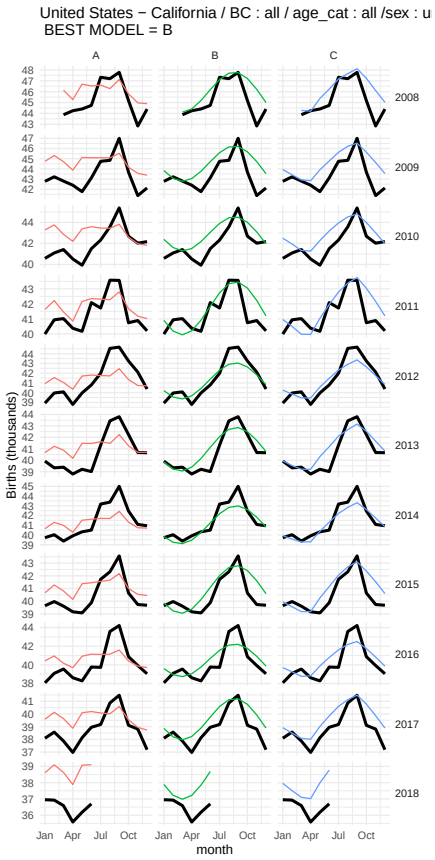


Figure 74: Actual (black lines) and simulated (colored lines) births.

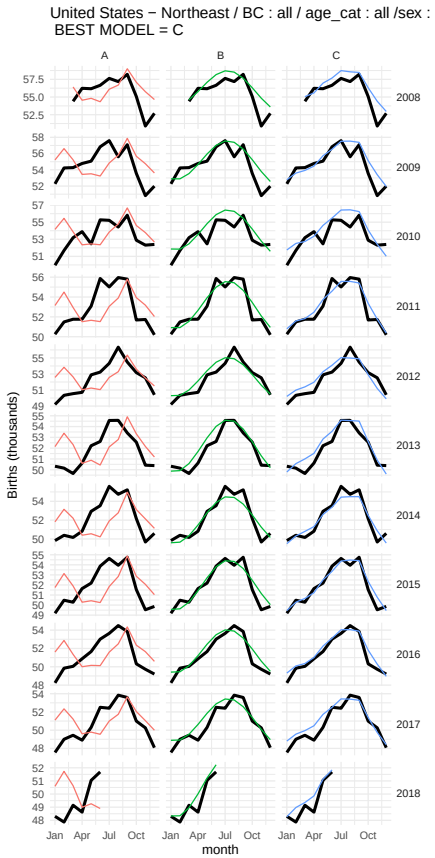


Figure 75: Actual (black lines) and simulated (colored lines) births.

```
births_STL = foreach(ca = unique(births$country_area), .combine = function(x,y) suppressWarnings(bind_rows(x,y))) %do% {

 ac = get_age_cat(country_area = ca)

 this_ca_births = births %>% filter(country_area == ca, age_cat == ac, sex_type == "unprot_sex", BC == "all")

 ### seasonal decomposition sim births
 this_ca_births_STL = foreach(m = c("A","B","C"), .combine = function(x,y) suppressWarnings(bind_rows(x,y))) %do% {
  this_ca_births_M = this_ca_births %>% filter(model == m)
  sb_ts = ts(this_ca_births_M$sim_births,
             start = c(this_ca_births_M$year[1],this_ca_births_M$month[1]),
             end = c(last(this_ca_births_M$year),last(this_ca_births_M$month)),
             frequency = 12)
  sb_stl = stl(sb_ts, s.window = "periodic")
  this_ca_births_M = this_ca_births_M %>% mutate(
    sim_births_trend = sb_stl$time.series[,2],
    sim_births_seasonal = sb_stl$time.series[,1],
    sim_births_remainder = sb_stl$time.series[,3]
  )
  this_ca_births_M
 }

 ### seasonal decomposition births
 this_ca_births_ = this_ca_births %>% filter(model == "A")
 b_ts = ts(this_ca_births_$births,
           start = c(this_ca_births_$year[1],this_ca_births_$month[1]),
           end = c(last(this_ca_births_$year),last(this_ca_births_$month)),
           frequency = 12)
 b_stl = stl(b_ts, s.window = "periodic")
 this_ca_births_ = this_ca_births_ %>% mutate(
   births_trend = b_stl$time.series[,2],
   births_seasonal = b_stl$time.series[,1],
   births_remainder = b_stl$time.series[,3]
 ) %>% select(country_area, BC, sex_type, year_month, births_trend, births_seasonal, births_remainder)

 # joining sim births all models with measured births
 this_ca_births_STL = full_join(this_ca_births_STL, this_ca_births_, by = c("country_area", "BC", "sex_type", "year_month"))

 # return
 this_ca_births_STL
}
```

```
write_feather(births_STL, path = str_c(IO$p_outputs, "simulated_births_seasonal_trends.feather"))
```

```
g = ggplot(births_STL, aes(x = month, y = sim_births_seasonal, col = model))
g = g +
  geom_hline(yintercept = 0, col = "gray80")+
  geom_line(aes(y = births_seasonal), col = "black", size = 1.2)+
  geom_line()+
  guides(col = FALSE)+
  scale_x_continuous(breaks = seq(0,12, by = 3))+
  facet_grid(country_area ~ model, scale = "free_y")+
  theme(strip.text.y = element_text(angle = 0, hjust = 0))
```

```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.
```

```
g
```

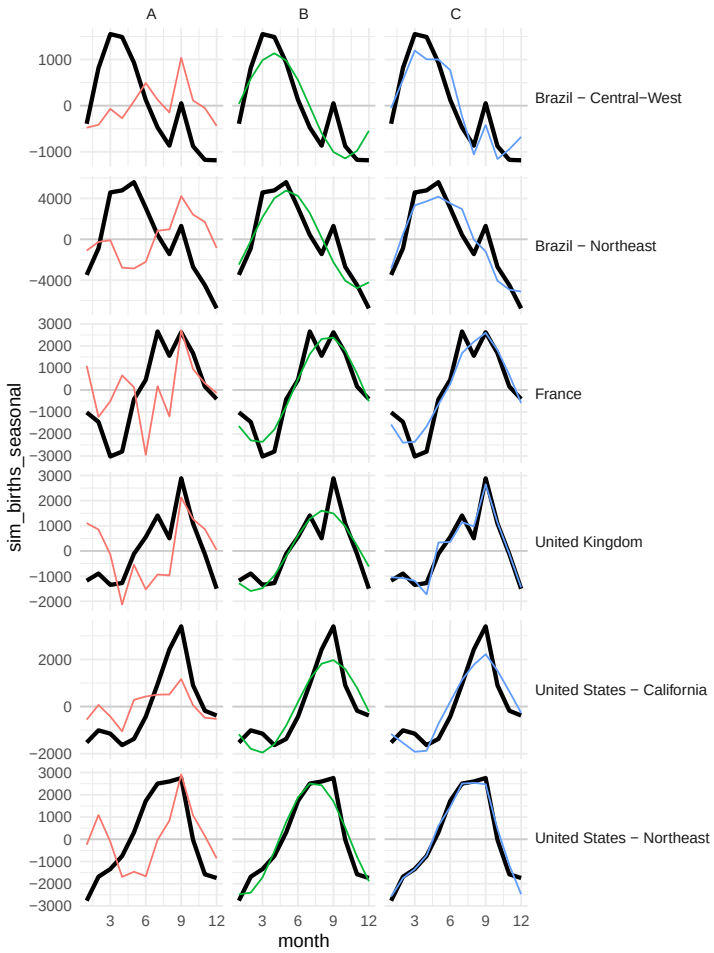


Figure 76: Seasonal trends of actual (black lines) and simulated (colored lines) births.

```
g = ggplot(births_STL %>% filter(model != "A"), aes(x = year_month, y = sim_births_remainder, col = model))
g = g +
  geom_hline(yintercept = 0, col = "gray80")+
  geom_line(aes(y = births_remainder), col = "black")+
  geom_line()+
  guides(col = FALSE)+
  ylab("Remainders of the seasonal decompositions")+ xlab("date")+
  facet_grid(country_area ~ model, scale = "free", labeller = label_both)+
  ggtitle("Remainders")+
  theme(strip.text.y = element_text(angle = 0, hjust = 0))
```

```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.
```

```
g
```

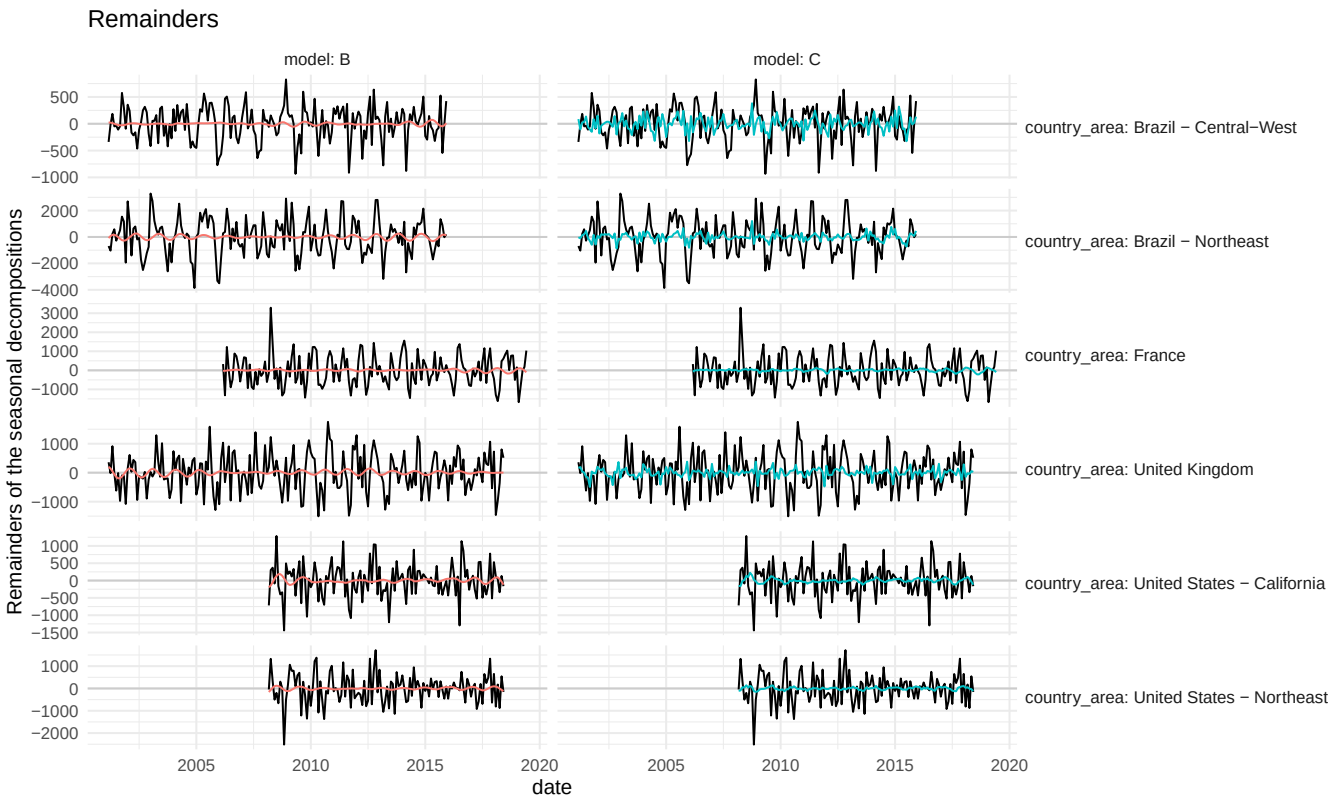


Figure 77: Remainders of the seasonal decompositions on actual (black lines) and simulated (colored lines) births.

The Remainders of the actual births are a lot larger than the Remainders of the simulated births, which means that the variability in the actual births is larger than the variation in the simulated births. In our model, the year-to-year variability in the simulated birth is driven by the non-fixed holidays. This seems to not be a sufficient source of variation to explain the variability in the actual births.

4.7.4 Year-to-year variability in holiday day-of-year.

```
holidays_flex = get_extended_holidays(countries = unique(official_birth_records$country),
                                      year_range = range(official_birth_records$year),
                                      hdict = dict$holidays,
                                      n_days = 0)

holidays_flex = holidays_flex %>%
  mutate(
    day_of_year = as.Date("2020-01-01") + days(date - floor_date(date, unit = "year")),
    color = dict$holidays$color[match(holiday_name, dict$holidays$holiday_name)])

g = ggplot(holidays_flex, aes(x = day_of_year, y = year(date), col = color))
g = g +
  geom_point()+
  ylab("Year")+ xlab("Holiday date")+
  scale_x_date(date_labels = "%b %d")+
  scale_color_identity(name = "", guide = "legend", labels = dict$holidays$holiday_name_wrapped, breaks = dict$holidays$color)+
  facet_grid(country ~ .)+
  theme(legend.position = "bottom")
g
```

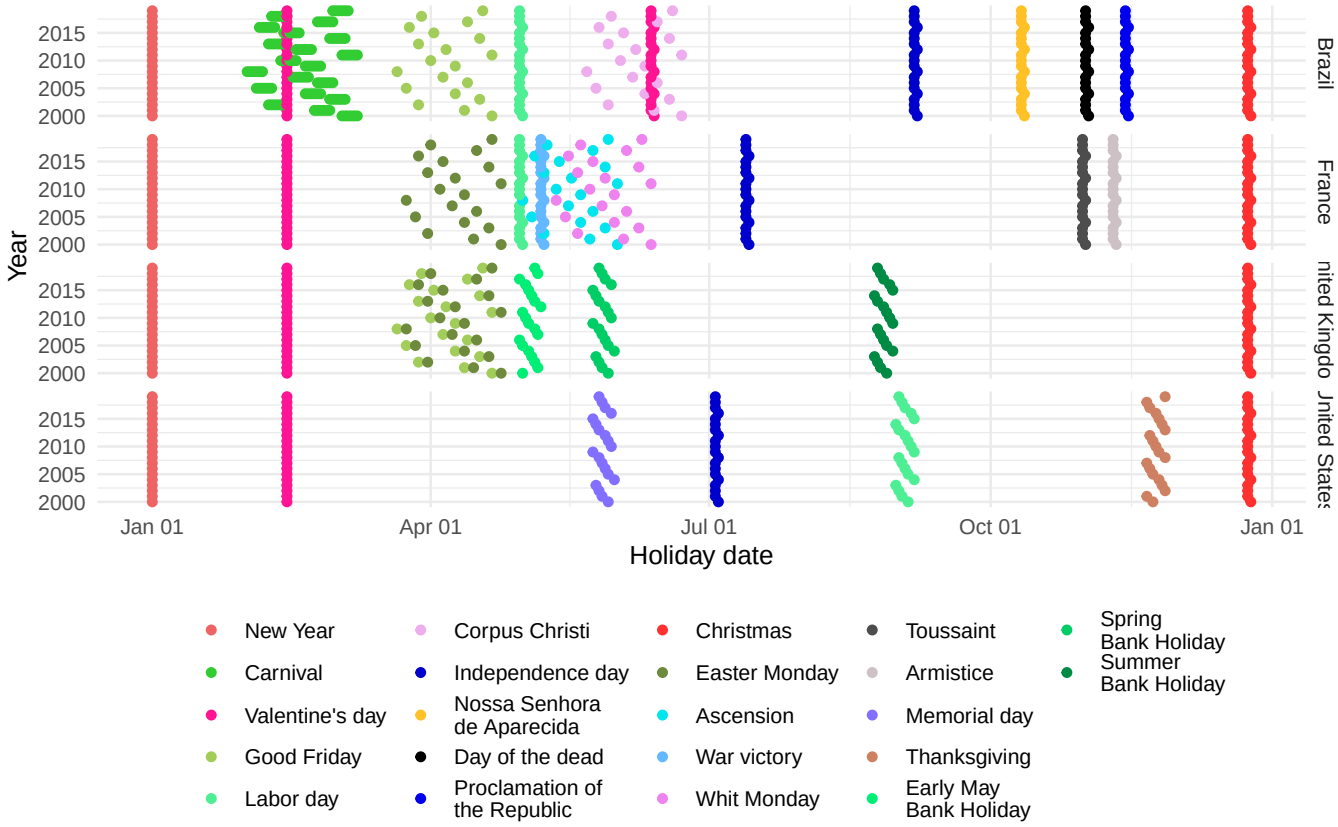


Figure 78: Holidays in considered countries

4.8 Varying average gestation duration and the spread of the gestation duration distribution

Here, we investigate the impact of changing the gestation duration distribution by changing the average and the standard deviation.

```
Gs = c(37:39)*7
Gsds = c(5,10,20)

sim_births_G = foreach(ca = unique(clue_sex_agg$country_area), .combine = bind_rows) %do%{
 res = foreach(G = Gs, .combine = bind_rows) %do% {
  r = foreach(Gsd = Gsds, .combine = bind_rows) %do% {

   #cat(ca,"\n")
   #cat("\tG: ",G,"\n")
   #cat("\tGsd: ",Gsd,"\n")

   bc = "all"; st = "unprot_sex"; ac = get_age_cat(country_area = ca)

   # average daily births
   this_cat_ave_daily_births = average_daily_births_df %>% filter(country_area == ca)

   # actual births
   this_ca_births = official_birth_records %>% filter(country_area == ca) %>% arrange(date)

   # predicting sex
   j = which((sex_models_df$country_area == ca) & (sex_models_df$BC == bc) & (sex_models_df$age_cat == ac) & (sex_models_df$sex_type == st))
   this_cat_model = sex_models[[j]]$model
   this_cat_predicted_sex = predict_daily_sex_behavior(model = this_cat_model,
                                       date_range = range(this_cat_ave_daily_births$date),
                                       country_area = ca)



   #  model parameters
   pars = opt_par_df %>%  filter(country_area == ca, BC == bc, age_cat == ac, sex_type == st, model == "C")
   alpha = pars$alpha;
   Tp = pars$Tp
   beta = pars$beta

   # simulating births
   monthly_births_C = simulated_vs_actual_monthly_birth(alpha = alpha, Tp = Tp, beta = beta, G = G, Gsd = Gsd,
                                       sex_df = this_cat_predicted_sex,
                                       ave_daily_birth_df = this_cat_ave_daily_births,
                                       actual_monthly_birth_df = this_ca_births)
   monthly_births_C = monthly_births_C %>%
    mutate(model = "C",
           G = G,
           Gsd = Gsd,
           country_area = ca,
           sex_type = st,
           BC = bc)

   #SSR = monthly_births_C$sq_residuals %>%  sum()
   #cat("\t\t\t",round(100*SSR/pars$SSR), "\n")

   return(monthly_births_C)
  }
}
```

```
}
```

```
SSR_df = sim_births_G %>%
  group_by(country_area, BC, sex_type, model, G, Gsd ) %>%
  summarize(SSR = sum(sq_residuals)) %>%
  mutate(color = dict$country_area$country_area_col[match(country_area, dict$country_area$country_area)])
```

```
## `summarise()` has grouped output by 'country_area', 'BC', 'sex_type', 'model', 'G'. You can override using the `.groups` argument.
```

```
model_B_SSR = opt_par_df %>% filter(model == "B", BC == "all", sex_type == "unprot_sex") %>%  select(country_area, SSR)

g = ggplot(SSR_df, aes(x = as.factor(G), y = SSR, fill = color))+
  scale_fill_identity()+
  geom_bar(stat = "identity")+
  geom_hline(data = model_B_SSR, aes(yintercept = SSR), col = "black")+
  facet_grid(country_area ~ Gsd, scale = "free_y")
print(g)
```

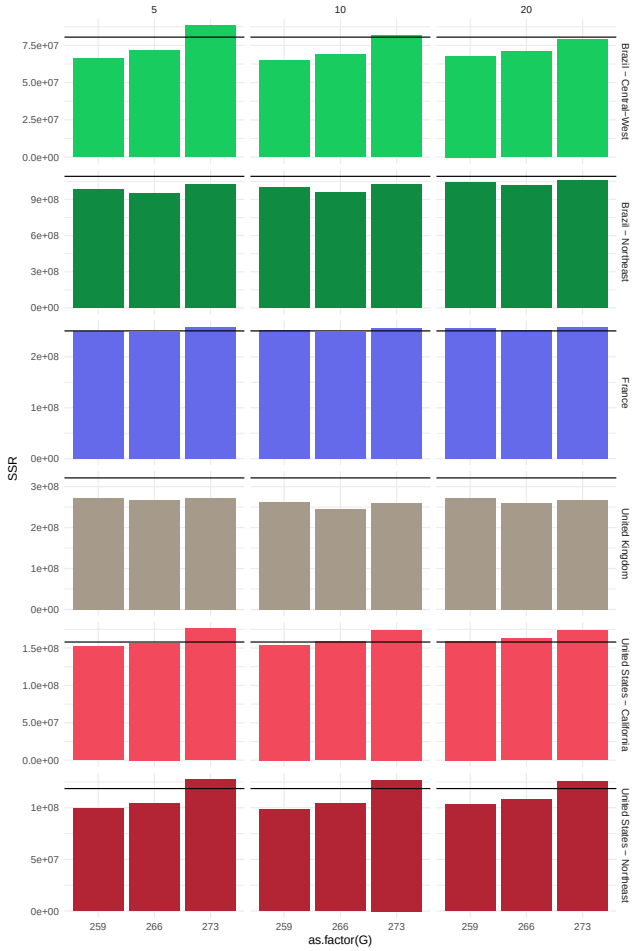


Figure 79: Model C residuals for various values of G (x axis) and Gsd (vertical panels). The black horizontal lines are at the values of the model B residuals.

```
for(ca in unique(SSR_df$country_area)){

  this_ca_births_G = sim_births_G %>% filter(country_area == ca, Gsd == 10)
  ref_line = min(this_ca_births_G$births)-max(this_ca_births_G$residuals)

  g = ggplot(this_ca_births_G , aes(x = year_month))
  g = g+
```

```
  geom_segment(aes(y = ref_line, yend = ref_line + residuals, x = year_month, xend = year_month, col = sq_residuals), #
               size = 1.2)+
  geom_hline(yintercept = ref_line, col = "gray")+
  scale_color_gradient(low = "white", high = "red")+
  geom_line(aes(y = births), col = "black",size = 1.2)+
  geom_line(aes(y = sim_births), col = "indianred1")+
  facet_grid( G  ~ ., scale = "free_y")+
  guides(col = FALSE)+
  ggtitle(ca)

 model_B_SSR = opt_par_df %>%
  filter(country_area == ca, model == "B", BC == "all", sex_type == "unprot_sex", Gsd == 10) %>%  select(SSR) %>% unlist()
 g_bar =  ggplot(SSR_df %>% filter(country_area == ca, Gsd == 10), aes(x = 1, y = SSR))+
  coord_flip()+
  geom_bar(stat = "identity")+
  geom_hline(yintercept = model_B_SSR, col = "cadetblue1")+
  facet_grid(G ~ ., scale = "free_y")+
  xlab("")+scale_x_continuous(breaks = NULL)+
  ggtitle(ca)

 g_combined = plot_grid(g,g_bar, ncol = 2, nrow = 1, rel_widths = c(3,1), align = "v" )
 print(g_combined)

}
```

```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.
```

```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.
```

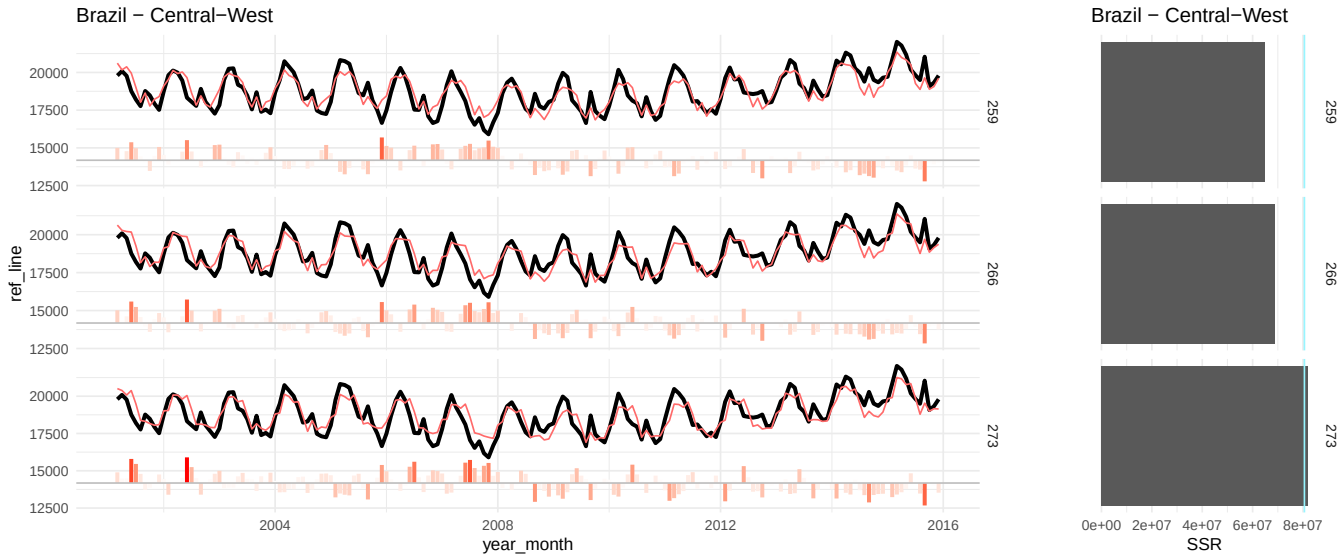


Figure 80: [main panel - left] Actual (black) and simulated (with model B, red) births with different average gestation durations. [side panel - right] SSR (sum of square of the residuals) for each different average gestation duration.

```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.
```

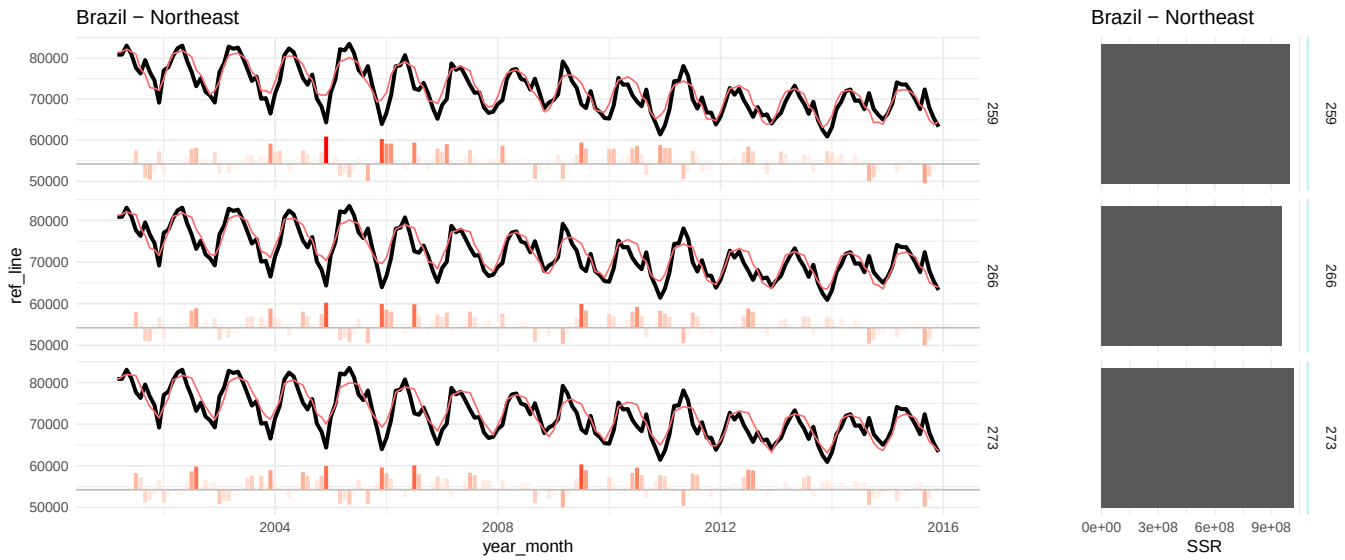


Figure 81: [main panel - left] Actual (black) and simulated (with model B, red) births with different average gestation durations. [side panel - right] SSR (sum of square of the residuals) for each different average gestation duration.

Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
"none")` instead.

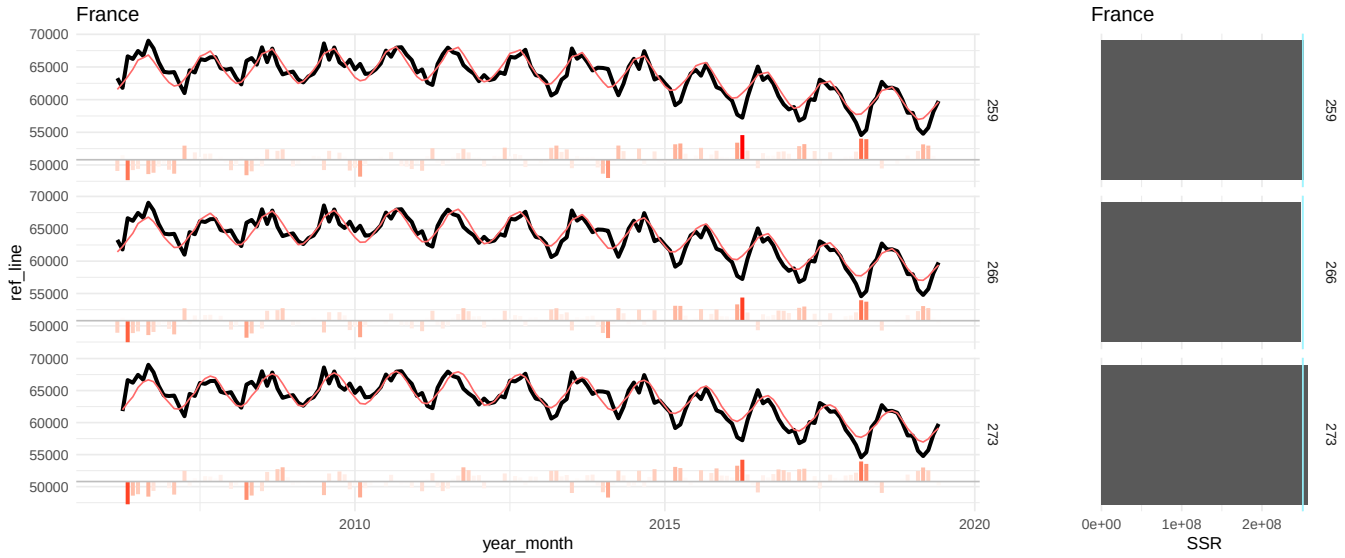


Figure 82: [main panel - left] Actual (black) and simulated (with model B, red) births with different average gestation durations. [side panel - right] SSR (sum of square of the residuals) for each different average gestation duration.

Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
"none")` instead.

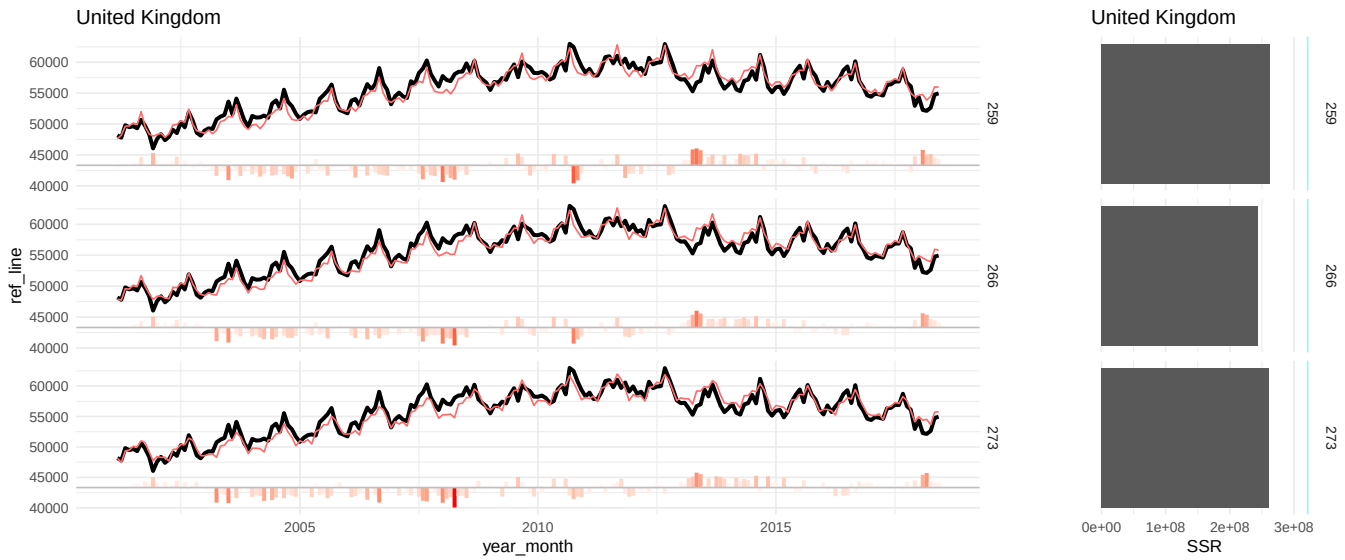


Figure 83: [main panel - left] Actual (black) and simulated (with model B, red) births with different average gestation durations. [side panel - right] SSR (sum of square of the residuals) for each different average gestation duration.

Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
"none")` instead.

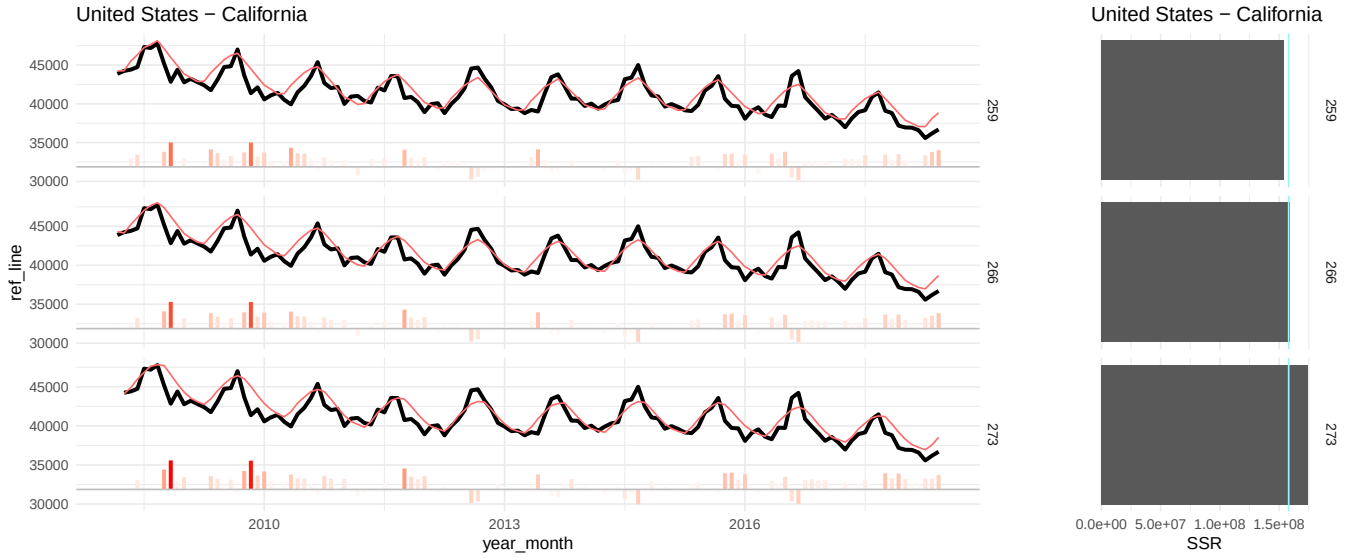


Figure 84: [main panel - left] Actual (black) and simulated (with model B, red) births with different average gestation durations. [side panel - right] SSR (sum of square of the residuals) for each different average gestation duration.

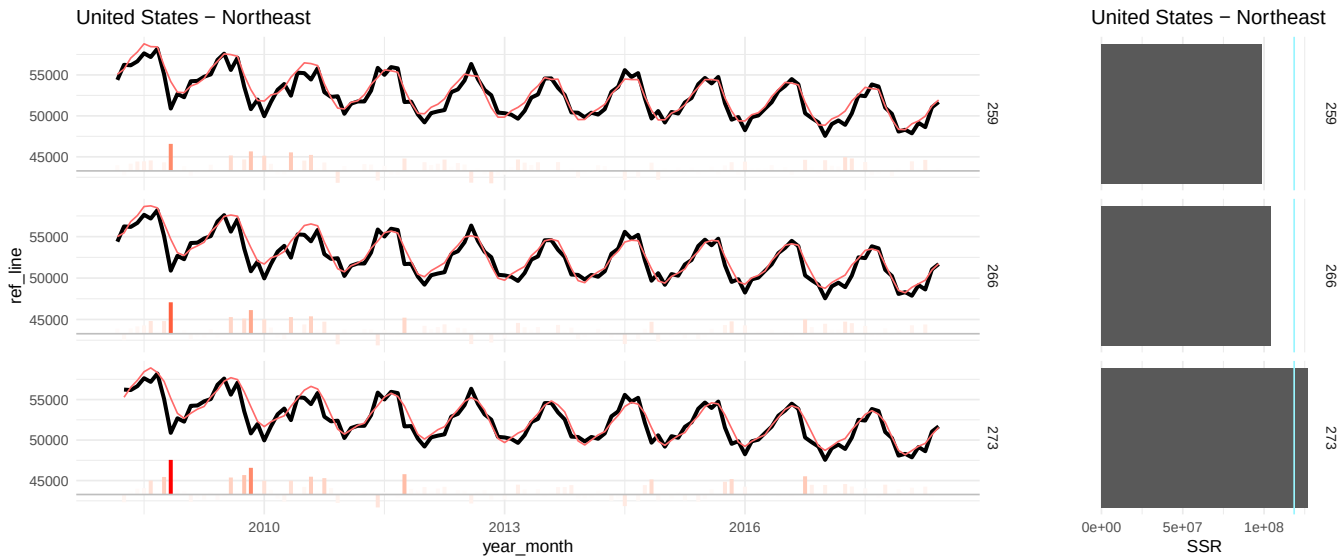


Figure 85: [main panel - left] Actual (black) and simulated (with model B, red) births with different average gestation durations. [side panel - right] SSR (sum of square of the residuals) for each different average gestation duration.

5 Checking for reporting biases from the app users

5.1 Loading data and detrending curves

Loading the aggregated logs

```
control_features_agg =
  read_feather(
    path = "../Data/4_clue_data_aggregated/aggregated_control_features_counts_clue_July2017-June2019_incl.feather"
    )
str(control_features_agg)
```

```
## tibble [102,200 x 9] (S3: tbl_df/tbl/data.frame)
##  $ country_area    : chr [1:102200] "Brazil - Central-West" "Brazil - Central-West" "Brazil - Central-West" "Brazil - Central-West" ...
##  $ BC              : chr [1:102200] "F" "F" "F" "F" ...
##  $ age_cat         : chr [1:102200] "<= 23" "<= 23" "<= 23" "<= 23" ...
##  $ date            : Date[1:102200], format: "2017-07-01" "2017-07-01" ...
##  $ n_users         : num [1:102200] 1855 1855 1855 1855 1898 ...
##  $ n_any           : num [1:102200] 540 540 540 540 588 588 588 588 583 583 ...
##  $ control_features: chr [1:102200] "medium_bleeding" "long_sleep" "exercise" "breast_pain" ...
##  $ n               : num [1:102200] 78 44 15 66 92 61 12 75 89 48 ...
##  $ x               : num [1:102200] 0.931 1.414 0.795 1.065 1.074 ...
```

```
clue_sex_agg =
  read_feather(
    "../Data/4_clue_data_aggregated/aggregated_sex_counts_clue_July2017-June2019_incl.feather"
    )
str(clue_sex_agg)
```

```
## tibble [76,650 x 9] (S3: tbl_df/tbl/data.frame)
##  $ country_area: chr [1:76650] "Brazil - Central-West" "Brazil - Central-West" "Brazil - Central-West" "Brazil - Central-West" ...
##  $ BC          : chr [1:76650] "F" "F" "F" "F" ...
##  $ age_cat     : chr [1:76650] "<= 23" "<= 23" "<= 23" "<= 23" ...
##  $ date        : Date[1:76650], format: "2017-07-01" "2017-07-01" ...
##  $ n_users     : num [1:76650] 1855 1855 1855 1898 1898 ...
##  $ n_any       : num [1:76650] 540 540 540 588 588 588 583 583 583 551 ...
##  $ sex_type    : chr [1:76650] "all_sex" "prot_sex" "unprot_sex" "all_sex" ...
##  $ n           : num [1:76650] 118 47 39 141 53 43 80 29 25 74 ...
##  $ x           : num [1:76650] 1.63 2.02 1.48 1.79 2.09 ...
```

We do this analysis for BC = "all" and age_cat = "all" and the last year of data (we only take the last year because some features are less reported and there were not enough logs to build meaningful time-series).

```
control_features_agg = control_features_agg %>%
  filter(BC == "all", age_cat == "all", date >= as.Date("2018-07-01"),
         control_features %in% c("exercise", "medium_bleeding", "breast_pain","long_sleep"))

clue_sex_agg = clue_sex_agg %>%
  filter(BC == "all", age_cat == "all", date >= as.Date("2018-07-01"), sex_type == "all_sex")
```

We compute the relatives changes and detrend the curves.

```
# relative change

control_features_agg = control_features_agg %>%
  mutate(r = n/n_users)

clue_sex_agg = clue_sex_agg %>%
  mutate(r = n/n_users)

# trend
```

```
control_features_agg = control_features_agg %>%
  arrange(country_area, BC, age_cat, control_features, date) %>%
  group_by(country_area, BC, age_cat, control_features) %>%
  mutate(t = row_number(),
         trend = predict(loess(r ~ t))) %>%
  ungroup() %>%  select(-t)


clue_sex_agg = clue_sex_agg %>%
  arrange(country_area, BC, age_cat, sex_type, date) %>%
  group_by(country_area, BC, age_cat, sex_type) %>%
  mutate(t = row_number(),
         trend = predict(loess(r ~ t))) %>%
  ungroup() %>%  select(-t)


# relative change

control_features_agg = control_features_agg %>% dplyr::mutate(x = r/trend)
clue_sex_agg = clue_sex_agg %>% dplyr::mutate(x = r/trend)
```

5.2 Comparison of the control feature logs with the sex logs

```
for(ca in unique(control_features_agg$country_area)){

  CF = control_features_agg %>%  filter(country_area == ca)
  S = clue_sex_agg %>%  filter(country_area == ca)

  g = ggplot(CF, aes(x = date, y = x, col = control_features))+
    geom_hline(yintercept = 1)+
    geom_line(data = S, aes(x = date, y = x), col = "gray50")+
    geom_line()+
    guides(col = FALSE)+
    facet_grid(control_features ~ ., scale = "free")+
    ggtitle(ca)


  J = full_join(CF, S, by = c("country_area", "BC", "age_cat", "date"), suffix = c(".CF",".S"))

  g2 = ggplot(J, aes(x = x.CF, y = x.S, col = control_features))+
    coord_fixed()+
    geom_abline(intercept = 0, slope = 1)+
    geom_point()+
    xlab("Control feature")+ylab("Sex")+
    guides(col = FALSE)+
    facet_wrap(control_features ~ .)+
    theme(strip.background = element_rect(fill = "gray80", color = "transparent"))+
    ggtitle(ca)


  g_combined = cowplot::plot_grid(g, g2, ncol = 1)
  print(g_combined)

}
```

```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
```

```
## "none")` instead.

## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.

## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.

## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.
```

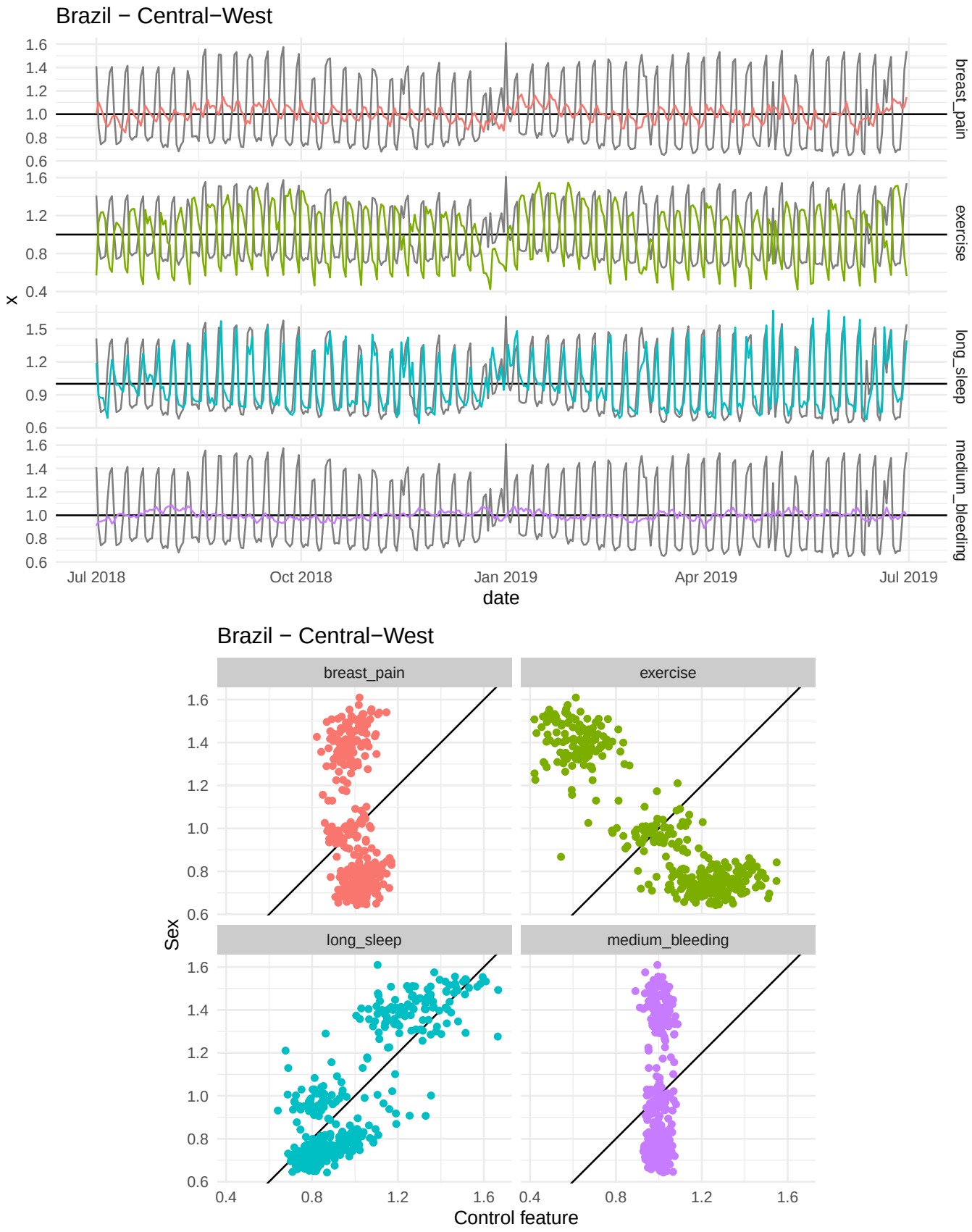


Figure 86: (Top) Detrended time-series for the control features (colored lines) and for sex (any sex type, gray line). (Bottom) Relative changes in the control features (x axis) vs the relative changes in sexual activity (y axis).

Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
"none")` instead.

```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.
```

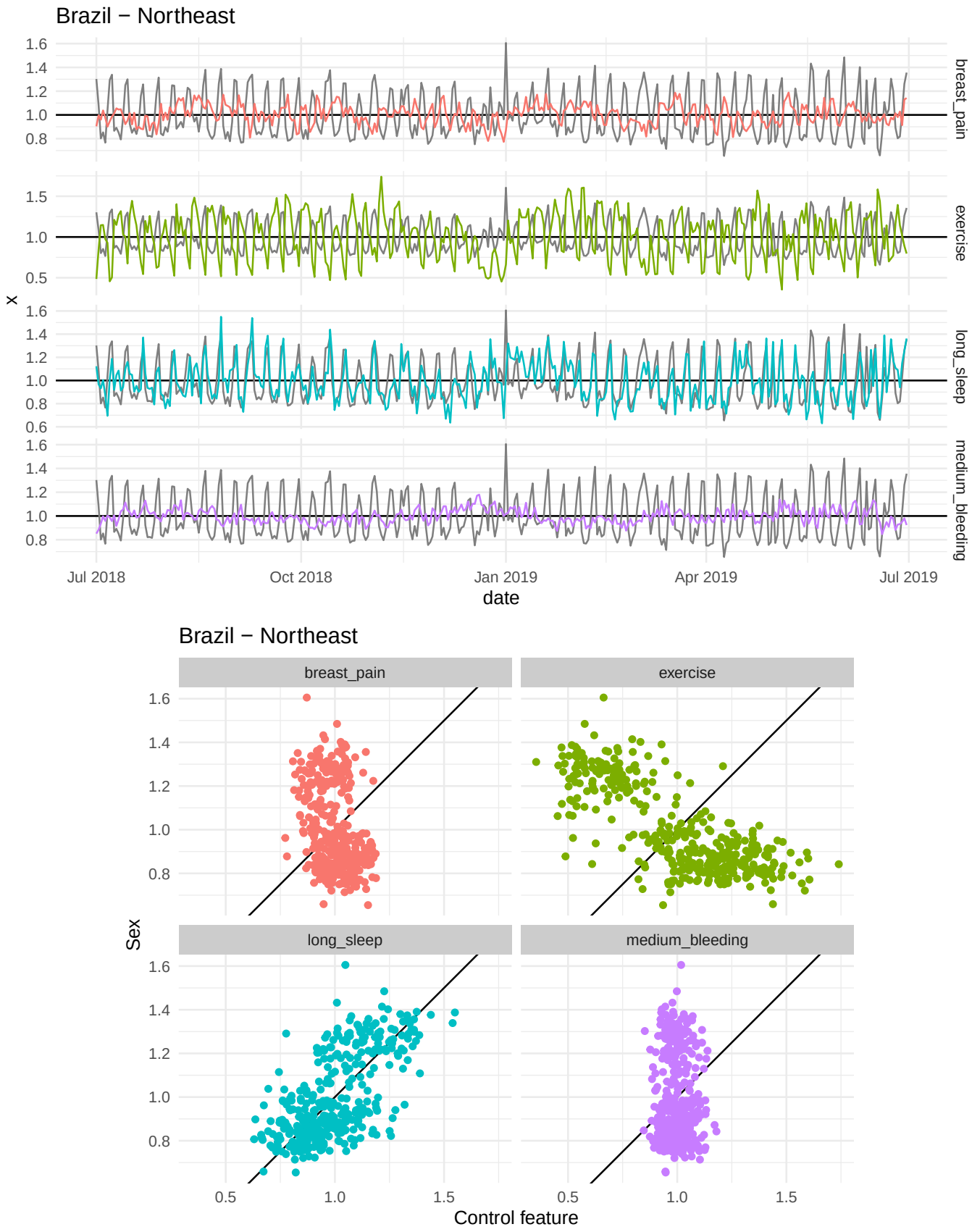


Figure 87: (Top) Detrended time-series for the control features (colored lines) and for sex (any sex type, gray line). (Bottom) Relative changes in the control features (x axis) vs the relative changes in sexual activity (y axis).

Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
"none")` instead.

```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.
```

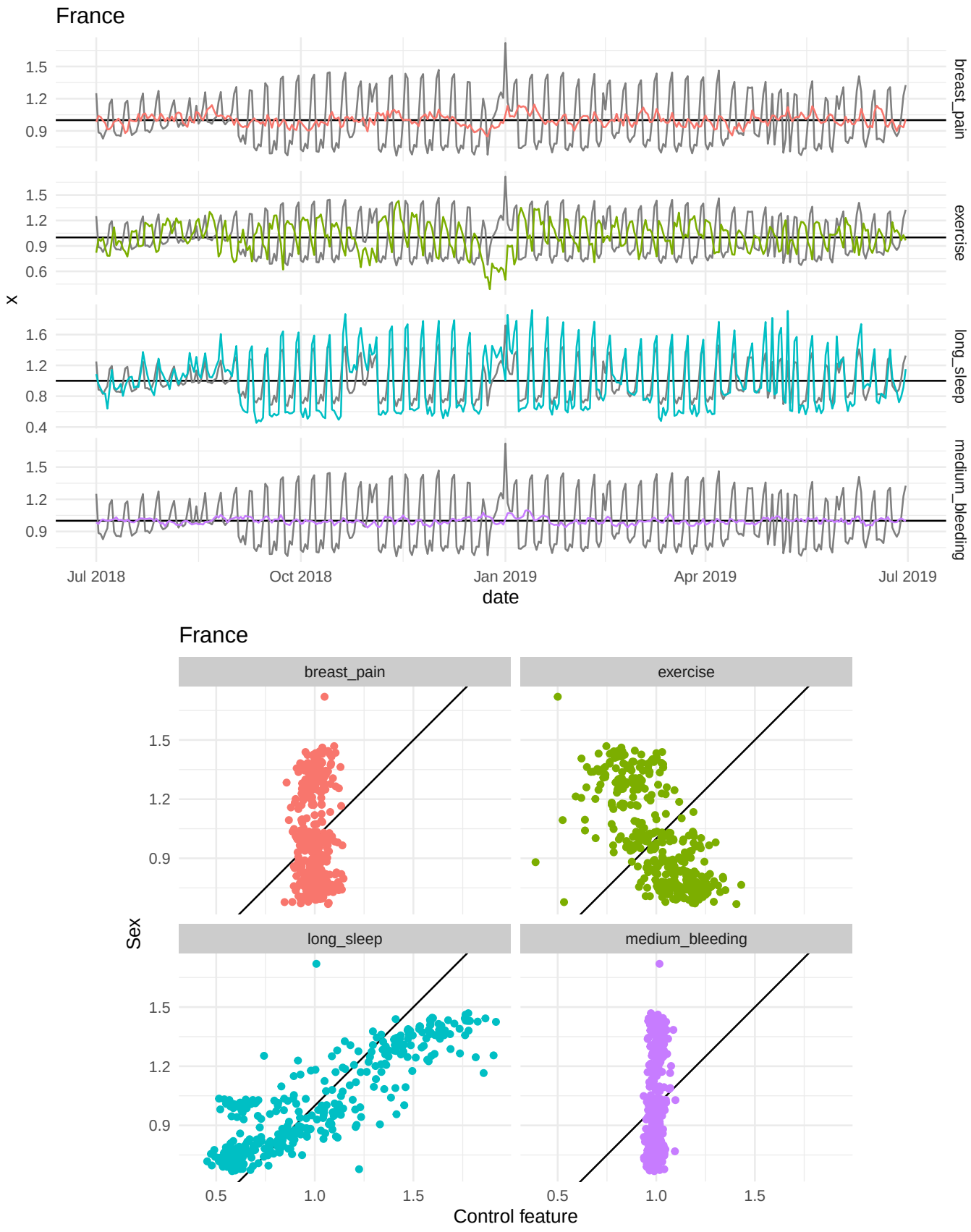


Figure 88: (Top) Detrended time-series for the control features (colored lines) and for sex (any sex type, gray line). (Bottom) Relative changes in the control features (x axis) vs the relative changes in sexual activity (y axis).

Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
"none")` instead.

```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.
```

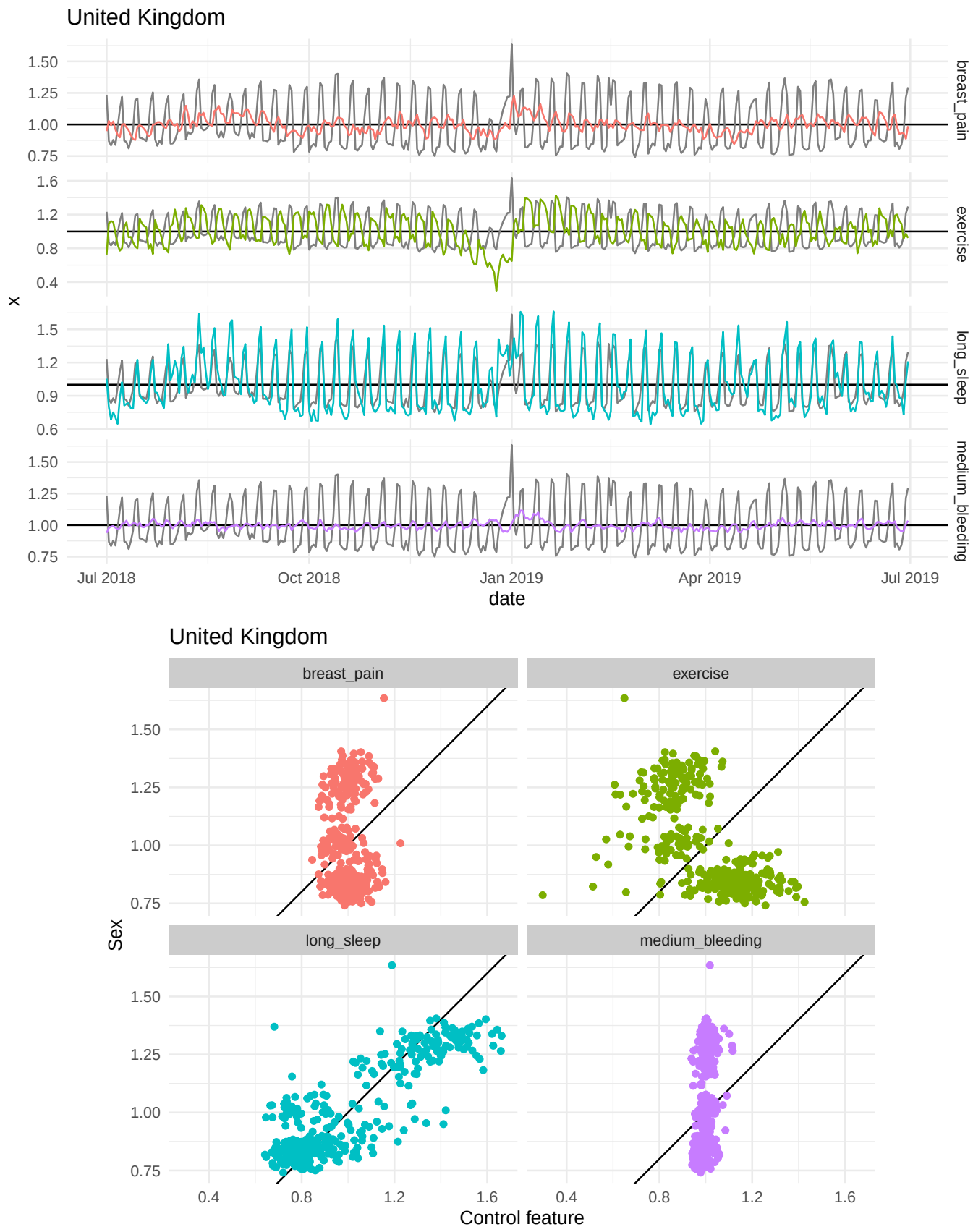


Figure 89: (Top) Detrended time-series for the control features (colored lines) and for sex (any sex type, gray line). (Bottom) Relative changes in the control features (x axis) vs the relative changes in sexual activity (y axis).

Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
"none")` instead.

```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.
```

Figure 90: (Top) Detrended time-series for the control features (colored lines) and for sex (any sex type, gray line). (Bottom) Relative changes in the control features (x axis) vs the relative changes in sexual activity (y axis).

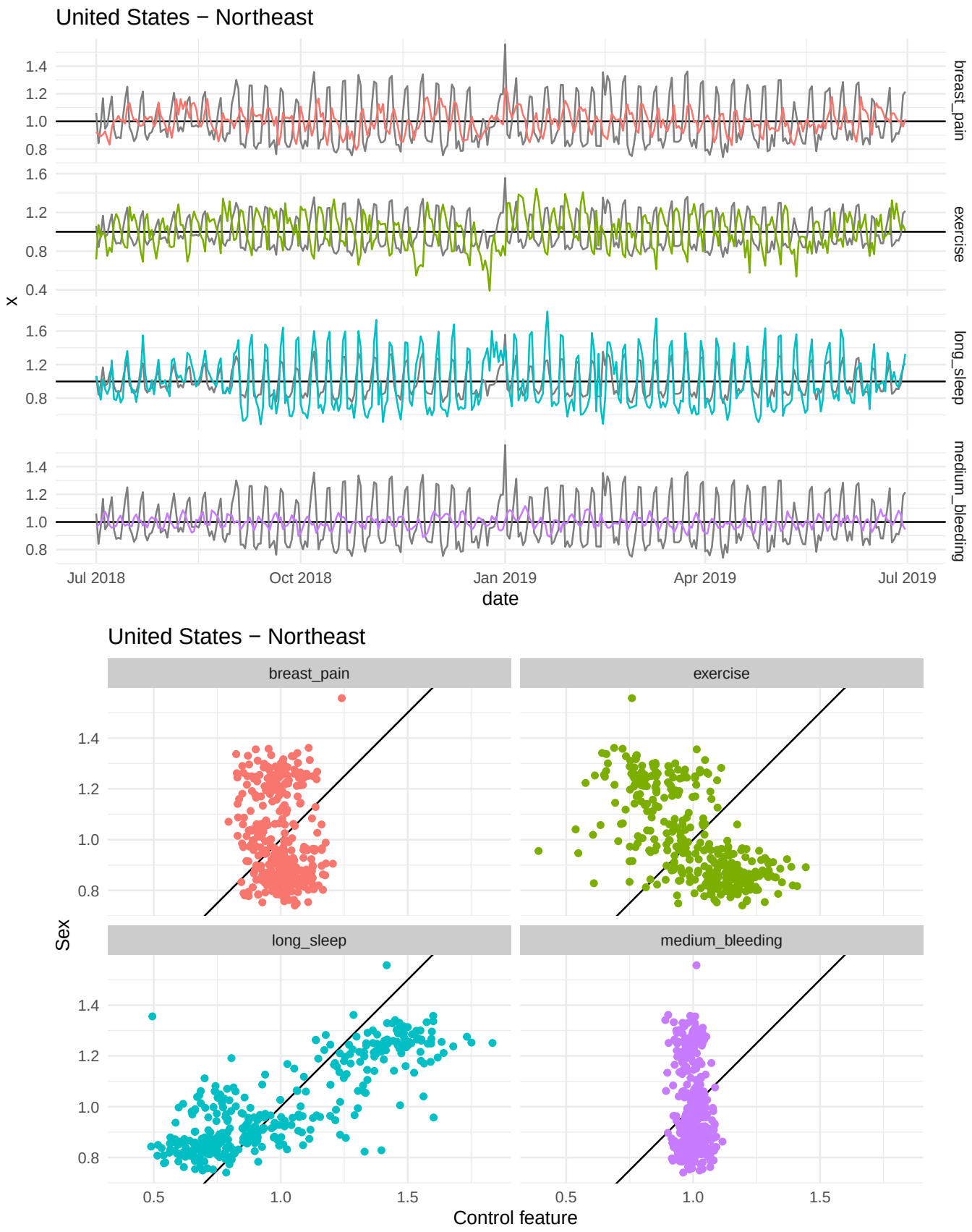


Figure 91: (Top) Detrended time-series for the control features (colored lines) and for sex (any sex type, gray line). (Bottom) Relative changes in the control features (x axis) vs the relative changes in sexual activity (y axis).

From these figures, we observe that there is a positive correlation between the sexual activity and sleeping over

9h; both of these self-reported variables have their peaks during week-ends and holidays. Reported breast pain and medium bleeding do not appear to have any temporal structure and are thus not correlated with sexual activity. Exercise is negatively correlated with sexual activity in most locations (Clue users report exercising more during week-days than during week-ends). In California, the negative correlation is not as strong as in other locations such as the Central-West region in Brazil. Altogether, these observations are matching expected patterns and likely indicate that the temporal patterns in sexual activity are not driven by reporting biases but rather reflect actual variations in sexual activity of the app users.

6 Main and Supplementary Figures

6.1 Figure 1: Datasets (births data and sex data)

6.1.1 Births data

```
official_birth_records =
  read_feather(
    path =
      str_c("../Data/5_outputs/official_birth_records.feather")
  )
```

```
official_birth_records = official_birth_records %>%
  mutate(births_thousands = births/1000)

official_births_summary = official_birth_records %>%
  group_by(country_area, country_area_col) %>%
  summarize(min_births = min(births_thousands),
            max_births = max(births_thousands),
            mean_births = mean(births_thousands),
            max_date = max(date))
```

```
## `summarise()` has grouped output by 'country_area'. You can override using the `.groups` argument.
```

```
ref_date = as.Date("2020-01-01")

g_births = ggplot(official_birth_records,
                  aes(x = date, y = births_thousands,
                      col = country_area_col))

g_births = g_births +
  #### reference for variations
  geom_segment(data = official_births_summary,
               aes(x = ref_date, xend = ref_date,
                   y = mean_births, yend = mean_births-5*mean_births/100),
               size = 1.5, alpha = 0.7)+
  # geom_text(data = official_births_summary, aes(x = ref_date, y = min_births-5*mean_births/100), label = "5% change from the mean",
  #           hjust = 0, vjust = 0, nudge_x = 100)+
  #### uncorrected births
  geom_line(aes(y = births_original_numbers/1000), col = "gray80")+
  #### corrected births
  geom_line()+   #geom_point(size = 0.5)+
  #### COUNTRIES
  geom_text(data = official_births_summary,
            aes(x = ref_date, y = max_births *1.05,
                label = country_area, fontface = 2),
            vjust = 0, hjust = 1)+
  #### settings
  scale_color_identity()+
  scale_x_date(date_minor_breaks = "1 year", date_labels = "%Y")+
  scale_y_continuous(expand = expansion(mult = c(0,0.2)))+
  # sec.axis = sec_axis(~ (. - max(.))/max(.)*100, breaks = seq(-30,30,by = 10), name = "% change from the max")
  ylab("Births (monthly in thousands)") +
  xlab("Date")+
  facet_grid(country_area ~., scale = "free") +
  theme(strip.text.y = element_blank())

# g_births
```

6.1.2 App data (sexual activity data)

```
pp = read_feather(path = "../Data/4_clue_data_aggregated/aggregated_sex_counts_clue_July2017-June2019_incl.feather")

pp_sum = pp %>%
  filter(BC == "all", age_cat == "all") %>%
  mutate(sex_type_str =
           case_when(
             sex_type == "all_sex" ~ "Total Sex",
             sex_type == "prot_sex" ~ "Protected Sex",
             sex_type == "unprot_sex" ~ "Unprotected Sex")) %>%
  group_by(date, sex_type, sex_type_str) %>%
  summarize(n_users = sum(n_users),
            n_any  = sum(n_any),
            n_log = sum(n),
            .groups = "drop") %>%
  group_by(sex_type) %>%
  mutate(relative_frequency = n_log / n_any,
         relative_frequency = relative_frequency/mean(relative_frequency)) %>%
  arrange(sex_type , date) %>% ungroup() %>%
  mutate(
    sex_type_str = sex_type_str %>%
      factor(., levels = c("Total Sex","Protected Sex","Unprotected Sex"))
    )

sex_colors = c("gray40","steelblue2","yellow3")

g_sex_freq =
  ggplot(pp_sum,
         aes(x = date, y = relative_frequency,
             col = sex_type_str))+
  geom_line()+
  ylab("Relative sex frequency (daily)")+xlab("Date")+
  #expand_limits(y = 0)+
  scale_color_manual(name = "", values = sex_colors)+
  facet_grid(sex_type_str ~ .)+
  guides(col = FALSE) +
  theme(legend.position = "top",
        legend.direction = "horizontal",
        legend.title = element_blank(),
        legend.background =
          element_rect(fill = "white",
                       color = "transparent",
                       size = 0.5))
```

```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.
```

```
# g_sex_freq
```

6.1.3 Clue tracking screen

```
# import png
clue_screen = image_read("../Figures Tables Media/Media/Clue_app_screens.png")

clue_screen_ratio = image_info(clue_screen)$height / image_info(clue_screen)$width
padding = 20
```

```
g_clue_screen = ggplot()+ coord_fixed(ratio = clue_screen_ratio)+
  background_image(clue_screen)+theme(plot.margin = margin(t=padding, l=padding, r=padding, b=padding, unit = "pt"))
```

6.1.4 Assembled Figure 1

```
fig_1 = arrangeGrob(
  g_births,
  g_clue_screen,
  g_sex_freq,
  ncol = 2, nrow = 2,
  widths = c(1.5, 1),
  heights = c(0.55,0.45),
  layout_matrix = cbind(c(1,1), c(3,4)))

fig_1 = as_ggplot(fig_1) +
  draw_plot_label(label = letters[1:3], size = 15,
                  x = c(0, 0.6, 0.6), y = c(1, 1, 0.45))

# fig_1
```

6.2 Supplementary Figure 1: Sex data for each location separately

```
pp = pp %>%
  mutate(Sex_type =
           sex_type %>%
           str_replace(.,"_","\n") %>%
           str_replace(., "prot", "protected") %>%
           str_to_sentence())

suppl_fig_1_plotlist =
  map(
    .x = unique(pp$country_area) %>% sort(),
    .f = function(loc){

      this_loc_sex =
        pp %>% filter(country_area == loc)

      this_loc_holidays =
        get_holidays(
          countries = loc %>% str_split_fixed(.," - ",2) %>% first(),
          year_range = c(2017,2019),
          hdict = dict$holidays) %>%
        filter(date %in% this_loc_sex$date)

      ggplot(this_loc_sex,
             aes(x = date)) +
        geom_point(
          data = this_loc_holidays,
          aes(y = min(this_loc_sex$x)-0.05),
          shape = 17, col = "gray"
        ) +
        geom_line(aes(y = x, col = sex_type)) +
        guides(col = FALSE) +
        scale_color_manual(values = sex_colors) +
        facet_grid(Sex_type ~ ., scale = "free_y") +
```

```
    ggtitle(loc) +
    xlab("Date") +
    ylab("Relative sexual frequency")

  }
)
```

```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.

## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.

## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.

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## "none")` instead.

## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.

## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.
```

```
suppl_fig_1 =
  ggarrange(plotlist = suppl_fig_1_plotlist,
            ncol = 2, nrow = 3,
            labels = "auto")

# suppl_fig_1
```

6.3 Figure 2 and Suppl. Figure 2: Sexual activity model coefficients

```
# load Figure 2 data

load(file = str_c(IO$p_outputs,"sex_models_df.Rdata"), verbose = TRUE)
```

```
## Loading objects:
##   sex_models_df
```

```
plotlist = list()
n_items = c()
cas = unique(sex_models_df$country_area)
ok = foreach(ca = cas) %do% {
  cat(ca, "\n")

  # retrieving the model for this country and only plotting for BC all and sex_type all
  load(
    file = str_c(
      "../Data/5_outputs/sex_models/",
      "sex_model_",ca,
      "_BC_all_age_cat_all_sex_type_all_sex.Rdata"
    ),
    verbose = TRUE
  )
  glm_sex_behavior = this_sex_model$model
```

```
  # Visualisation of the coefficient
  g_coef = ggplot_sex_activity_glm_coefficient(
    model = glm_sex_behavior,
    show_intercept = FALSE,
    show_weekly_patterns = FALSE,
    ylim = c(-0.4, 1))
  g_coef = g_coef +
    ggtitle(ca)+
    theme(axis.text.x = element_text(size = 7))
  # print(g_coef)

  plotlist[[ca]] = g_coef
  n_items = c(n_items, nrow(g_coef$data))
}
```

```
## Brazil - Central-West
## Loading objects:
##   this_sex_model
```

```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.
```

```
## Brazil - Northeast
## Loading objects:
##   this_sex_model
```

```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.
```

```
## France
## Loading objects:
##   this_sex_model
```

```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.
```

```
## United Kingdom
## Loading objects:
##   this_sex_model
```

```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.
```

```
## United States - California
## Loading objects:
##   this_sex_model
```

```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.
```

```
## United States - Northeast
## Loading objects:
##   this_sex_model
```

```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.
```

```
fig_2 = ggarrange(
  ggarrange(
    plotlist[[which(cas == "Brazil - Central-West")]],
    plotlist[[which(cas == "United States - Northeast")]],
    labels = c("a","b"),
    ncol = 2, nrow = 1,
    widths = n_items[which(cas %in% c("Brazil - Central-West","United States - Northeast"))] /
      sum(n_items[which(cas %in% c("Brazil - Central-West","United States - Northeast"))])
```

```
  ),
  ggarrange(
    plotlist[[which(cas == "France")]],
    plotlist[[which(cas == "United Kingdom")]],
    labels = c("c","d"),
    ncol = 2, nrow = 1,
    widths = n_items[which(cas %in% c("France","United Kingdom"))] /
      sum(n_items[which(cas %in% c("France","United Kingdom"))])
  ),
  nrow = 2, ncol = 1
)

# fig_2
```

```
suppl_fig_2 =
  ggarrange(
    plotlist = plotlist,
    nrow = 3, ncol = 2,
    labels = "auto"
)

# suppl_fig_2
```

6.4 Figure 3, Suppl. Figures 3, 4 and 5: Mathematical models, seasonal fertility and simulated births

6.4.1 Model schematics

```
model = image_read("../Figures Tables Media/Media/Figure 3-01.png")
model_ratio =  image_info(model)$height / image_info(model)$width
g_model = ggplot()+ coord_fixed(ratio = model_ratio)+
  background_image(model)



models = image_read("../Figures Tables Media/Media/Figure 3-04.png")
models_ratio = image_info(models)$height / image_info(models)$width
g_models = ggplot()+ coord_fixed(ratio = models_ratio)+
  background_image(models)
```

6.4.2 Seasonal trends

```
# model_colors = c("turquoise3","sienna3","maroon3")

model_colors = c(
  hsv(h = 41.45/360, s = 1, v = 0.98),
  hsv(h = 188/360, s = 1, v = 0.7882),
  hsv(h = 17.94/360, s = 0.8392, v = 1)
)


ca_levels = dict$country_area$country_area


# we load the seasonal trend data
```

```
births_STL = read_feather(path = str_c(IO$p_outputs, "simulated_births_seasonal_trends.feather"))
births_STL = births_STL %>% mutate(country_area = factor(country_area, levels = ca_levels))


# we also load the AIC values
opt_par_df = read_feather(path = str_c(IO$p_outputs, "optimal_parameters_and_AIC.feather"))
opt_par_df = opt_par_df %>% mutate(country_area = factor(country_area, levels = ca_levels))
AIC =
  opt_par_df %>%
  filter(age_cat == "all",
         BC == "all",
         sex_type == "unprot_sex") %>%
  select(country_area, model, AIC)


# we create one ggplot object per country

g_st_list = map(
  .x = ca_levels,
  .f = function(ca){

    this_ca_births_STL =
      births_STL %>%
      filter(country_area == ca)

    yaxis_lim =
      c(this_ca_births_STL$births_seasonal,
        this_ca_births_STL$sim_births_seasonal) %>%
      range() %>% abs() %>% min() %>%
      divide_by(1000) %>% round()
    yaxis = c(-yaxis_lim, 0, yaxis_lim)

    yaxis_limits =
      c(this_ca_births_STL$births_seasonal,
        this_ca_births_STL$sim_births_seasonal) %>%
      range() %>% abs() %>% max() %>%
      multiply_by(c(-1.04,1.04)) %>% divide_by(1000)


    g = ggplot(this_ca_births_STL, aes(x = month))
    g +
      geom_text(
        data = AIC %>% filter(country_area == ca),
        aes(x = ifelse(str_detect(ca, "Brazil"),1.5, 12),
            y = -Inf,
            hjust = ifelse(str_detect(ca, "Brazil"),0, 1),
            vjust = 0,
            label = str_c(model, " : ",AIC %>% round()),
            col = model),
        size = 3
      ) +
      geom_hline(yintercept = 0, col = "gray80") +
      geom_line(aes(y = births_seasonal/1000), col = "black", size = 1) +
      geom_line(aes(y = sim_births_seasonal/1000, col = model),) +
      scale_x_continuous(breaks = seq(0,12,by = 3), minor_breaks = 0:12) +
      scale_y_continuous(breaks = yaxis, minor_breaks = -10:10, limits = yaxis_limits) +
      scale_color_manual(values = model_colors) +
      guides(col = FALSE)+
```

```
    xlab(ifelse(ca == ca_levels[3],"Calendar months","")) +
    ylab(ifelse(ca == ca_levels[1],"Seasonal trends [births, thousands]","")) +
    facet_grid(model ~ .) +
    ggtitle(ca %>%
              str_replace(.," - ","\n") %>%
              str_replace(., "United States", "US") %>%
              str_replace(., "United Kingdom", "UK")) +
    theme(strip.text.y = element_blank(),
          plot.title  = element_text(hjust = 0.5, size = 10))
  }
)
```

```
## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.

## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.

## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.

## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.

## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.

## Warning: `guides(<scale> = FALSE)` is deprecated. Please use `guides(<scale> =
## "none")` instead.
```

```
g_st = ggarrange(plotlist = g_st_list, ncol = 6, nrow = 1, align = "h")

# g_st
```

6.4.3 Time-series

```
births = read_feather(path = str_c(IO$p_outputs, "simulated_births.feather"))

g_b_list =
  map(
    .x = ca_levels[c(1,4,2,3,5,6)],
    .f = function(ca){
      g = ggplot(births %>%
                   filter(country_area == ca,
                          model == "C",
                          age_cat == "all",
                          sex_type == "unprot_sex",
                          BC == "all"),
                 aes(x = year_month))
      g +
        geom_line(aes(y = births/1000), size = 1, col = "black") +
        geom_line(aes(y = sim_births/1000), col = model_colors[3]) +
        ylab(ifelse(ca == "Brazil - Northeast", "Births (thousands)","")) +
        xlab(ifelse(ca %in% c("France","United Kingdom"),"Date","")) +
        ggtitle(ca) +
        theme(plot.title = element_text(size = 10))
    }
  )
```

```
g_b = ggarrange(plotlist = g_b_list, ncol = 2, nrow = 3, align = "hv")

# g_b
```

```
g_all_mod_b_list =
  map(
    .x = ca_levels,
    .f = function(ca){
      g = ggplot(births %>%
                   filter(country_area == ca,
                          age_cat == "all",
                          sex_type == "unprot_sex",
                          BC == "all"),
                 aes(x = year_month))
      g +
        geom_line(aes(y = births/1000), size = 1, col = "black") +
        geom_line(aes(y = sim_births/1000, col = model)) +
        scale_color_manual(values = model_colors, guide = "none") +
        ylab(ifelse(ca == "Brazil - Northeast", "Births (thousands)","")) +
        xlab(ifelse(ca %in% c("France","United Kingdom"),"Date","")) +
        ggtitle(ca) +
        facet_grid(model ~ ., labeller = label_both) +
        theme(plot.title = element_text(size = 10))
    }
  )


suppl_fig_3 = ggarrange(plotlist = g_all_mod_b_list, ncol = 2, nrow = 3, align = "hv", labels = "auto")

# suppl_fig_3
```

6.4.4 Fertility phase and amplitude

```
ca_wrapped_levels = dict$country_area$country_area %>% str_replace(.," - ","\n")

opt_par_df = read_feather(path = str_c(IO$p_outputs, "optimal_parameters_and_AIC.feather"))
opt_par_df =
  opt_par_df %>%
  mutate(
    country_area = factor(country_area, levels = ca_levels),
    country_area_wrapped = str_replace(country_area," - ","\n") %>%
      factor(., levels = ca_wrapped_levels),
    Amplitude = 100*alpha
  )


DF = opt_par_df %>%
  filter(model != "A",
         sex_type == "unprot_sex",
         BC == "all",
         age_cat == "all")

g_F = ggplot(DF, aes(x = Tp, y = Amplitude, col = country_area_col))
g_F = g_F +
  geom_segment(aes(xend = Tp, yend = 0, linetype = model))+
  geom_point()+
```

```
  scale_color_identity(guide = "legend",
                       labels = ca_wrapped_levels,
                       name = "location" )+
  scale_x_continuous(limits = c(0,1),breaks = seq(0,3/4,by = 1/4), labels = c("Jan","Apr","Jul","Oct"))+
  ylab("Amplitude (% from mean)")+ xlab("Fertility peak time")+
  coord_polar(theta = "x", start = 0)+
  ggtitle("Calendar year")
# g_F


DF = DF %>%
  mutate(
    country = str_split_fixed(country_area, " - ",2)[,1],
    Tp_seas = (Tp-10/365 - 0.5*(country == "Brazil"))%%1)

g_F_seas = ggplot(DF,
                  aes(x = Tp_seas,
                      y = Amplitude,
                      col = country_area_wrapped))
g_F_seas = g_F_seas +
  geom_segment(aes(xend = Tp_seas, yend = 0, linetype = model))+
  geom_point()+
  scale_color_manual(values = dict$country_area$country_area_col,
                     name = "location" )+
  scale_y_continuous(position = "left", breaks = seq(2, 6, by = 2))+
  scale_x_continuous(limits = c(0,1), breaks = seq(0,3/4,by = 1/4),
                     labels = c("Winter\nSolstice",
                                "Spring\nEquinox",
                                "Summer\nSolstice",
                                "Autumn\nEquinox")) +
  ylab("Amplitude (% of mean)") + xlab("Fertility peak time") +
  coord_polar(theta = "x", start = 0, clip = "off") +
  ggtitle("Solar year") +
  theme(
    plot.title = element_text(hjust = 0.5),
    legend.position = "bottom",
    legend.direction = "vertical",
    legend.key.height = unit(22,"pt")
  )
# g_F_seas
```

```
df_sine_curves = expand.grid(t = seq(0,12,by = 0.1), country_area = DF$country_area)
df_sine_curves = left_join(df_sine_curves,
                           DF %>%
                             filter(sex_type == "unprot_sex", BC == "all", model == "C") %>%
                             select(country_area, country_area_col, country_area_wrapped,  alpha, Amplitude, Tp, Tp_seas) %>%
                             ungroup(),
                           by = "country_area")

df_sine_curves = df_sine_curves %>%
  mutate(
    Fertility_calendar = 100 + Amplitude * cos(t/12*2*pi - Tp*2*pi),
    Fertility_solar = 100 + Amplitude * cos(t/12*2*pi - Tp_seas*2*pi)
  )


g_fert = ggplot(df_sine_curves, aes(x = t, y = Fertility_calendar, col = country_area_col))+
  geom_hline(yintercept = 100, col = "gray75")+
  geom_line(size = 0.8)+
```

```
  scale_color_identity()+
  scale_x_continuous(breaks = seq(0,12,by = 3), minor_breaks = 0:12, labels = c("Jan","Apr","Jul","Oct","Jan"))+
  xlab("Calendar months")+
  ylab("Relative changes in fertility (%)")
# g_fert

g_fert_solar = ggplot(df_sine_curves, aes(x = t, y = Fertility_solar, col = country_area_col))+
  geom_hline(yintercept = 100, col = "gray75")+
  geom_line(size = 0.8)+
  scale_color_identity()+
  scale_x_continuous(breaks = seq(0,12,by = 3), minor_breaks = 0:12,
                     labels = c("Winter\nSolstice","Spring\nEquinox","Summer\nSolstice","Autumn\nEquinox","Winter\nSolstice"))+
  xlab("Solar time")+
  ylab("Relative changes in fertility (%)")
# g_fert_solar
```

6.4.5 Amplitude comparison in model C (sex vs fertility)

```
suppl_fig_4_list =
  map(
    .x = unique(births_STL$country_area),
    .f = function(loc){

      opt_par_model_C =
        opt_par_df %>%
        filter(country_area == loc,
               model == "C",
               sex_type == "unprot_sex",
               age_cat == "all",
               BC == "all")

      opt_par_model_B =
        opt_par_df %>%
        filter(country_area == loc,
               model == "B",
               sex_type == "unprot_sex",
               age_cat == "all",
               BC == "all")



      seas_trend =
        births_STL %>%
        filter(country_area == loc,
               sex_type == "unprot_sex",
               age_cat == "all",
               BC == "all") %>%
        group_by(model, month) %>%
        slice_head(n = 1) %>%  ungroup()

      coef_A = opt_par_model_C$beta
      ratio_B = opt_par_model_C$alpha/opt_par_model_B$alpha

      amplitudes_df =
        bind_rows(
          seas_trend %>%
            filter(model == "A") %>%
```

```
        select(month, sim_births_seasonal)  %>%
        rename(value = sim_births_seasonal) %>%
        mutate(value = value * coef_A,
               variable  = "Sex",
               group = "A"),
      seas_trend %>%
        filter(model == "B") %>%
        select(month, sim_births_seasonal)  %>%
        rename(value = sim_births_seasonal) %>%
        mutate(value = value * ratio_B,
               variable  = "Fertility",
               group = "A"),
      seas_trend %>%
        filter(model == "C") %>%
        select(month, sim_births_seasonal)  %>%
        rename(value = sim_births_seasonal) %>%
        mutate(variable  = "Simulated births",
               group = "B"),
      seas_trend %>%
        filter(model == "C") %>%
        select(month, births_seasonal)  %>%
        rename(value = births_seasonal) %>%
        mutate(variable  = "Actual births",
               group = "B")
    ) %>%
    mutate(
      variable = variable %>%
        factor(., levels = c("Sex", "Fertility","Simulated births", "Actual births"))
    ) %>%
    rename(Month = month)

  ggplot(amplitudes_df,
         aes(x = Month, y = value, col = variable)) +
    geom_line() +
    geom_point() +
    facet_grid(group ~ ., scale = "free") +
    ggtitle(loc %>%  str_replace(., " - ","\n")) +
    scale_color_manual("",values = c(model_colors, "black")) +
    scale_y_continuous(breaks = 0, minor_breaks = 10) +
    scale_x_continuous(breaks = seq(0,12,by = 3), minor_breaks = 1:12) +
    theme(strip.text.y = element_blank()) +
    ylab("Seasonal trends")

  }
)

suppl_fig_4 = ggarrange(
  plotlist = suppl_fig_4_list,
  ncol = 6, nrow = 1,
  common.legend = TRUE, legend = "bottom",
  labels = "auto",
  align = "hv"
)
```

6.4.6 Assembling figure panels

```
fig_3 =
 ggarrange(
  ggarrange(g_models, g_st, nrow = 1, widths = c(3,5.5), labels = "auto"),
  ggarrange(g_b, g_F_seas, ncol = 2, nrow = 1, widths = c(10,3), labels = c("c","d")),
  nrow = 2,
  ncol = 1,
  heights = c(1,2)
 )
```

```
suppl_fig_5 =
 ggarrange(
  g_F + theme(plot.title = element_blank(), legend.key.height = unit(30, "pt")),
  g_fert,
  g_fert_solar,
  nrow = 1, ncol = 3,
  widths = c(3,2,2),
  labels = "auto"
 )
```

6.5 Saving figures and suppl. figures as pdf and png files

```
Figures_path = "../Figures Tables Media/Figures/"
scale = 2

# Figure 1

ggsave(plot = fig_1, filename = str_c(Figures_path, "F1.pdf"),
       width = 17.5, height = 12, units = "cm", scale = scale)

ggsave(plot = fig_1, filename = str_c(Figures_path, "F1.png"),
       width = 17.5, height = 12, units = "cm", scale = scale)

# Supplementary Figure 1

ggsave(plot = suppl_fig_1, filename = str_c(Figures_path, "F1S.pdf"),
       width = 17.5, height = 15, units = "cm", scale = scale)

ggsave(plot = suppl_fig_1, filename = str_c(Figures_path, "F1S.png"),
       width = 17.5, height = 15, units = "cm", scale = scale)

# Figure 2

ggsave(plot = fig_2, filename = str_c(Figures_path, "F2.pdf"),
       width = 17.5, height = 10, units = "cm", scale = scale)

ggsave(plot = fig_2, filename = str_c(Figures_path, "F2.png"),
       width = 17.5, height = 10, units = "cm", scale = scale)

# Supplementary Figure 2

ggsave(plot = suppl_fig_2, filename = str_c(Figures_path, "F2S.pdf"),
       width = 17.5, height = 14, units = "cm", scale = scale)

ggsave(plot = suppl_fig_2, filename = str_c(Figures_path, "F2S.png"),
       width = 17.5, height = 14, units = "cm", scale = scale)
```

```r
# Figure 3

ggsave(plot = fig_3, filename = str_c(Figures_path, "F3.pdf"),
       width = 17.5, height = 12, units = "cm", scale = scale)

ggsave(plot = fig_3, filename = str_c(Figures_path, "F3.png"),
       width = 17.5, height = 12, units = "cm", scale = scale)


# Supplementary Figure 3

ggsave(plot = suppl_fig_3, filename = str_c(Figures_path, "F3S.pdf"),
       width = 17.5, height = 14, units = "cm", scale = scale)

ggsave(plot = suppl_fig_3, filename = str_c(Figures_path, "F3S.png"),
       width = 17.5, height = 14, units = "cm", scale = scale)


# Supplementary Figure 4

ggsave(plot = suppl_fig_4, filename = str_c(Figures_path, "F4S.pdf"),
       width = 17.5, height = 6, units = "cm", scale = scale)

ggsave(plot = suppl_fig_4, filename = str_c(Figures_path, "F4S.png"),
       width = 17.5, height = 6, units = "cm", scale = scale)


# Supplementary Figure 5

ggsave(plot = suppl_fig_5, filename = str_c(Figures_path, "F5S.pdf"),
       width = 17.5, height = 6, units = "cm", scale = scale)

ggsave(plot = suppl_fig_5, filename = str_c(Figures_path, "F5S.png"),
       width = 17.5, height = 6, units = "cm", scale = scale)
```

Reproducibility receipt

```
## Execution datetime:

## [1] "2022-01-21 08:51:32 PST"

## ------------------------------

## sessionInfo :

## R version 4.0.5 (2021-03-31)
## Platform: x86_64-apple-darwin17.0 (64-bit)
## Running under: macOS Big Sur 10.16
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/4.0/Resources/lib/libRblas.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.0/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] parallel  stats     graphics  grDevices utils     datasets  methods
## [8] base
##
## other attached packages:
##  [1] magrittr_2.0.1    forcats_0.5.1     stringr_1.4.0     purrr_0.3.4
##  [5] tidyr_1.1.4       tibble_3.1.6      tidyverse_1.3.1   forecast_8.15
##  [9] biwavelet_0.20.21 bookdown_0.24     styler_1.6.2      tictoc_1.0.1
## [13] doParallel_1.0.16 iterators_1.0.13  foreach_1.5.1     dplyr_1.0.7
## [17] plyr_1.8.6        timeDate_3043.102 lubridate_1.8.0   chron_2.3-56
## [21] reshape_0.8.8     scales_1.1.1      ggmap_3.0.0       rworldmap_1.3-6
## [25] sp_1.4-6          magick_2.7.3      ggpubr_0.4.0      cowplot_1.1.1
## [29] kableExtra_1.3.4  hexbin_1.28.2     quantreg_5.86     SparseM_1.81
## [33] gridExtra_2.3     mapdata_2.3.0     maps_3.4.0        ggthemes_4.2.4
## [37] ggplot2_3.3.5     zoo_1.8-9         MASS_7.3-54       feather_0.3.5
## [41] readr_2.1.1       knitr_1.37
##
## loaded via a namespace (and not attached):
##   [1] readxl_1.3.1         backports_1.4.1      spam_2.7-0
##   [4] systemfonts_1.0.3    splines_4.0.5        listenv_0.8.0
##   [7] digest_0.6.29        htmltools_0.5.2      viridis_0.6.2
##  [10] fansi_0.5.0          tzdb_0.2.0           recipes_0.1.17
##  [13] globals_0.14.0       modelr_0.1.8         gower_0.2.2
##  [16] matrixStats_0.61.0   vroom_1.5.7          R.utils_2.11.0
##  [19] xts_0.12.1           svglite_2.0.0        tseries_0.10-49
##  [22] jpeg_0.1-9           colorspace_2.0-2     rvest_1.0.2
##  [25] textshaping_0.3.6    haven_2.4.3          xfun_0.29
##  [28] jsonlite_1.7.2       crayon_1.4.2         survival_3.2-13
##  [31] glue_1.6.0           gtable_0.3.0         ipred_0.9-12
##  [34] webshot_0.5.2        MatrixModels_0.5-0   R.cache_0.15.0
##  [37] car_3.0-12           future.apply_1.8.1   quantmod_0.4.18
##  [40] abind_1.4-5          DBI_1.1.2            rstatix_0.7.0
##  [43] Rcpp_1.0.7           viridisLite_0.4.0    bit_4.0.4
##  [46] foreign_0.8-81       dotCall64_1.0-1      stats4_4.0.5
##  [49] lava_1.6.10          prodlim_2019.11.13   httr_1.4.2
##  [52] ellipsis_0.3.2       farver_2.1.0         pkgconfig_2.0.3
##  [55] R.methodsS3_1.8.1    dbplyr_2.1.1         nnet_7.3-16
##  [58] utf8_1.2.2           caret_6.0-90         labeling_0.4.2
##  [61] tidyselect_1.1.1     rlang_0.4.12         reshape2_1.4.4
```

```
##  [64] cellranger_1.1.0     munsell_0.5.0        tools_4.0.5
##  [67] cli_3.1.0            generics_0.1.1       broom_0.7.10
##  [70] evaluate_0.14        fastmap_1.1.0        ragg_1.2.1
##  [73] yaml_2.2.1           bit64_4.0.5          fs_1.5.2
##  [76] ModelMetrics_1.2.2.2 RgoogleMaps_1.4.5.3  future_1.23.0
##  [79] nlme_3.1-153         R.oo_1.24.0          xml2_1.3.3
##  [82] compiler_4.0.5       rstudioapi_0.13      curl_4.3.2
##  [85] png_0.1-7            ggsignif_0.6.3       reprex_2.0.1
##  [88] stringi_1.7.6        fields_13.3          lattice_0.20-45
##  [91] Matrix_1.4-0         urca_1.3-0           vctrs_0.3.8
##  [94] pillar_1.6.4         lifecycle_1.0.1      lmtest_0.9-39
##  [97] data.table_1.14.2    bitops_1.0-7         maptools_1.1-2
## [100] conquer_1.2.1        R6_2.5.1             parallelly_1.30.0
## [103] codetools_0.2-18     assertthat_0.2.1     rjson_0.2.20
## [106] withr_2.4.3          fracdiff_1.5-1       hms_1.1.1
## [109] quadprog_1.5-8       grid_4.0.5           rpart_4.1-15
## [112] class_7.3-19         rmarkdown_2.11       carData_3.0-4
## [115] TTR_0.24.3           pROC_1.18.0
```

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