

thursday class notes

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Balancing equation

The change in population size can be reduced entirely to the initial population size, and the numbers of births, deaths, in-migrations, and out-migrations in the intermediate period.

$$N(T) = N(0) + B(0, T) - D(0, T) + I(0, T) - E(0, T)$$

Right about here I took a break to give an overarching warning about the broader context and history of population growth models have been abused. It's not the kind of thing that should be treated as an objective that can be *gamed*.

Crude indicators

$$CBR(0, T) = \frac{B(0, T)}{PY(0, T)}$$

Note, this can be positive or negative

$$CNMR(0, T) = \frac{I(0, T) - E(0, T)}{PY(0, T)}$$

Crude growth rate

$$CGR(0, T) = CBR(0, T) - CDR(0, T) + CNMR(0, T)$$

read in the data

```
#setwd()
library(tidyverse)
library(readr)
#Birth counts in 2014
B_url <- "https://raw.githubusercontent.com/timriffe/BSSD2021Module2/master/04_thursday/BirthsSpain2014
B2014 <- read_delim(B_url,
                    delim = " ",
                    trim_ws = TRUE) %>%
  mutate(Sex = "Total") %>%
  select(Age, Sex, Births = Total) %>%
  mutate(Age = parse_number(Age))

# Death counts in 2014
D_url <- "https://raw.githubusercontent.com/timriffe/BSSD2021Module2/master/04_thursday/DeathsSpain2014
D2014 <- read_delim(D_url,
```

```

      delim = " ",
      trim_ws = TRUE) %>%
pivot_longer(Female:Total,
              names_to = "Sex",
              values_to = "Deaths") %>%
mutate(Age = parse_number(Age))

# Population counts on January 1st, 2014
P1_url <- "https://raw.githubusercontent.com/timriffe/BSSD2021Module2/master/04_thursday/PopulationSpain2014.txt"
P2014 <- read_delim(P1_url,
                    delim = " ",
                    trim_ws = TRUE) %>%
pivot_longer(Female:Total,
              names_to = "Sex",
              values_to = "Population") %>%
mutate(Age = parse_number(Age))

# Population counts on January 1st, 2015
P2_url <- "https://raw.githubusercontent.com/timriffe/BSSD2021Module2/master/04_thursday/PopulationSpain2015.txt"
P2015 <- read_delim(P2_url,
                    delim = " ",
                    trim_ws = TRUE) %>%
pivot_longer(Female:Total,
              names_to = "Sex",
              values_to = "Population") %>%
mutate(Age = parse_number(Age))

ES2014 <-
  P2014 %>%
  bind_rows(P2015) %>%
  pivot_wider(names_from = Year,
              values_from = Population,
              names_prefix = "P") %>%
  left_join(D2014, by = c("Age", "Sex")) %>%
  left_join(B2014, by = c("Age", "Sex")) %>%
  arrange(Sex, Age)
#Births in 2014

# 2014 Life table (calculated in class 2)
LT_url <- "https://raw.githubusercontent.com/timriffe/BSSD2021Module2/master/04_thursday/LTSpain2014.txt"
LT <- read_delim(LT_url, delim = " ")

```

calculate crude growth

Components of change:

```

Components <-
  ES2014 %>%
  filter(Sex == "Total") %>%
  summarize(P1 = sum(P2014),
            P2 = sum(P2015),
            B = sum(Births, na.rm = TRUE),

```

```

      D = sum(Deaths)) %>%
mutate(PY = (P1 + P2) / 2,
      Nmig = P2 - (P1 + B - D))

CrudeRates <-
  Components %>%
  mutate(CGR = (P2 - P1) / PY,
         CBR = B / PY,
         CDR = D / PY,
         CNMR = Nmig / PY,
         CRNI = CBR - CDR,
         .keep = "none")
CrudeRates

## # A tibble: 1 x 5
##       CGR      CBR      CDR      CNMR      CRNI
##   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>
## 1 -0.00135 0.00917 0.00847 -0.00205 0.000696

```

geometric versus exponential / instantaneous growth

Geometric growth is the change in population size divided by what you started with.

$$r^{geometric} = \frac{P2 - P1}{P1}$$

$$P(t) = P(0) \cdot (1 + r^{geometric})^t$$

$$P(t) = P(0) * e^{r * t}$$

$$r^{continuous} = \frac{\ln(\frac{P(T)}{P(0)})}{T}$$

So, let's do a hypothetical projection, holding the crude geometric growth rates constant for something like 10 years.

```

growth <-
  Components %>%
  mutate(r_geom = (P2 - P1) / P1,
         r_nat = (B - D) / P1,
         r_cont = log(P2 / P1),
         r_cont_nat = log((P1 + B - D) / P1)) %>%
  right_join(tibble(t = 0:10),
            by = character()) %>%
  mutate(Pt_geom = P1 * (1 + r_geom) ^ t,
         Pt_nat = P1 * (1 + r_nat) ^ t,
         Pt_cont = P1 * exp(r_cont * t),
         Pt_cont_nat = P1 * exp(r_cont_nat * t)) %>%
  select(t, Pt_geom, Pt_nat, Pt_cont, Pt_cont_nat)

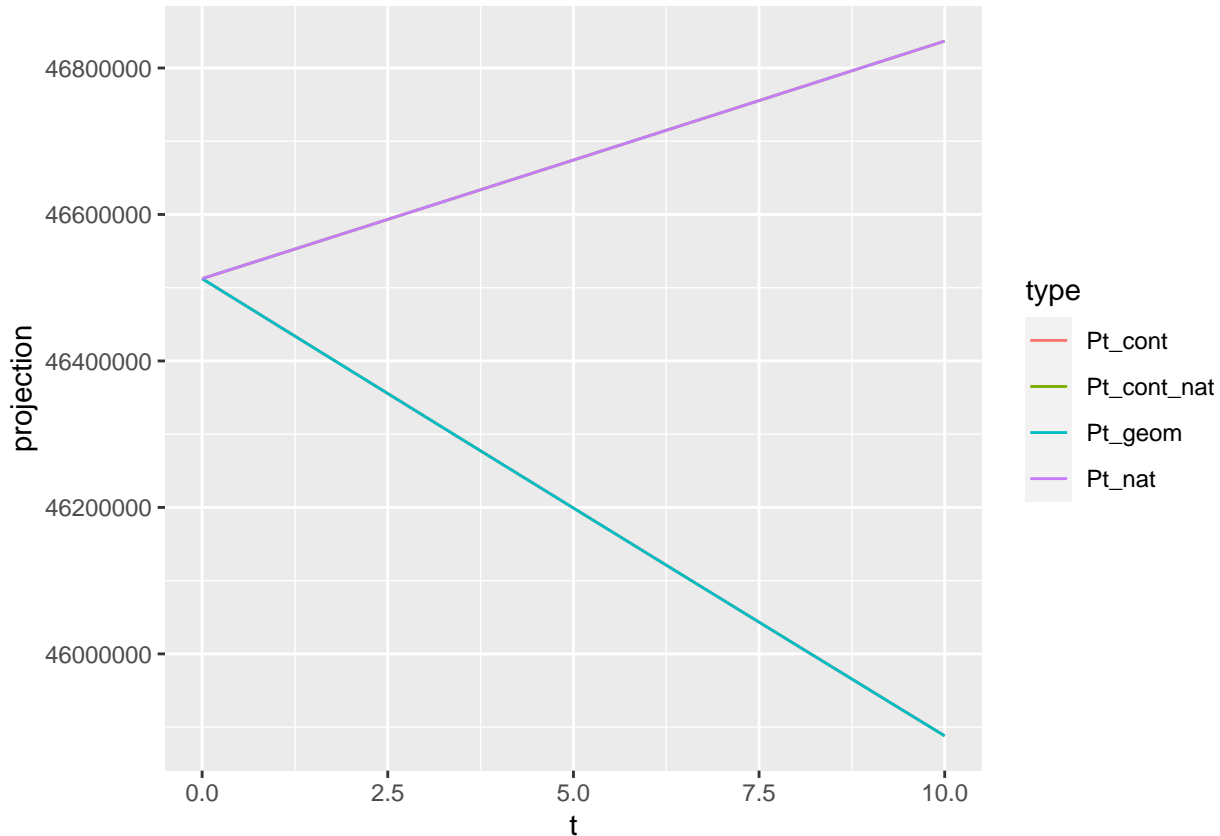
growth %>%

```

```

pivot_longer(Pt_geom:Pt_cont_nat,
              names_to = "type",
              values_to = "projection") %>%
ggplot(aes(x = t, y = projection, color = type)) +
geom_line()

```



stationary vs stable populations

The life table L_x is a kind of stationary population. Or at least it can be convenient to think of it as one. Namely, in a *stationary* population, 1. the rates of mortality and fertility are unchanging 2. the numbers of births and deaths each year are the same 3. the number of births and deaths are equal 4. the population structure is proportional to the life table L_x and is unchanging 5. the period population population structure is equal to the cohort population structure.

a stable population is the same in that: 1. the rates of mortality and fertility are unchanging 2. the period population structure is unchanging (proportionally equal) 3. cohort cross-sections of the Lexis diagram remain proportional to the life table L_x

a stable population is different in that: 1. the numbers of births and deaths in each year can be different 2. period and cohort population structure are not proportional to one another (unless $r = 0$)

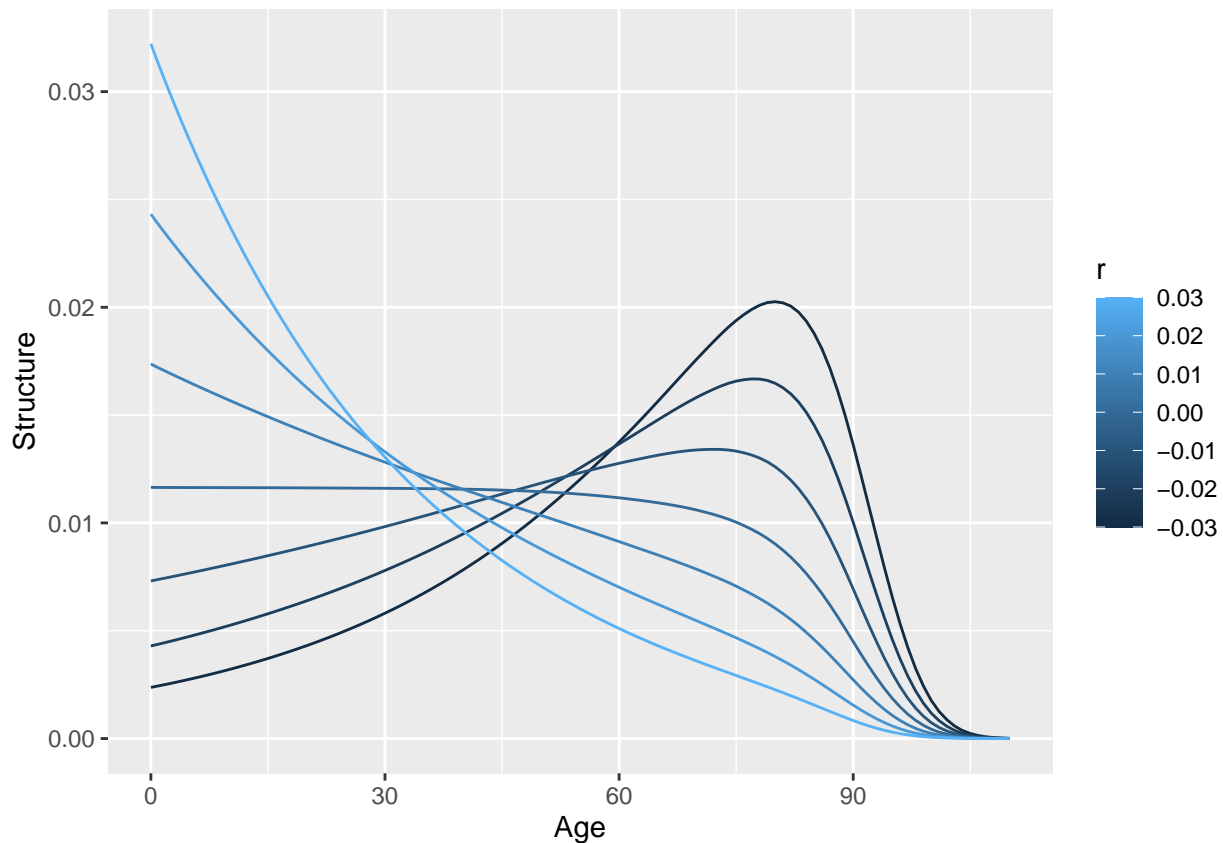
detour for intuition

The stable population structure is mapped from something proportional to life table exposure L_x . If the population is growing then it can expand at the base and shrink at the top. if the population is shrinking

then it can bulge at the top.

```
r      <- seq(-.03,.03, by = .01)
r_thing <- expand_grid(r, Age = 0:110)

LT %>%
  select(Age, Lx) %>%
  mutate(Age_mid = Age + .5) %>%
  right_join(
    r_thing, by = "Age"
  ) %>%
  arrange(r, Age) %>%
  mutate(Structure = Lx * exp(-r * Age_mid)) %>%
  group_by(r) %>%
  mutate(Structure = Structure / sum(Structure)) %>%
  ggplot(aes(x = Age, y = Structure, color = r, group = r)) +
  geom_line()
```



Deriving r empirially.

the napkin approach

```
G <- 30
BF <-
B2014 %>%
```

```

select(-Sex)

# this has all 3 sexes, so we filter down

StableComponents <-
  ES2014 %>%
  filter(Sex == "Female") %>%
  # remove Births col so we can add it back right
  select(-Births) %>%
  # add on Births
  left_join(BF, by = "Age") %>%
  # add on the lifetable
  left_join(LT, by = "Age") %>%
  mutate(
    Exposure = (P2014 + P2015) / 2,
    Fxf = Births / Exposure * .4886,
    Lx = Lx / 1e5,
    Fxf = ifelse(is.na(Fxf), 0, Fxf)) %>%
  select(Age, Lx, Fxf)

# NRR
NRR <-
StableComponents %>%
  summarize(NRR = sum(Lx * Fxf)) %>%
  pull(NRR)

```

Here's a parlor trick, back of the envelope calculation of r , just guess the mean length of the generation in the stable population, it ought to be sort of close to MAB , which we calculated earlier in this module.

$$\begin{aligned}
 NRR &= e^{rT} \\
 \log(NRR) &= rT \\
 \frac{\log(NRR)}{T} &= r
 \end{aligned}$$

```
log(NRR) / 33
```

```
## [1] -0.01351271
```

So, this estimate is going to be my guess!