Human Survivorship Curves: Graveyard Lab

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Contents

1 Purpose

The purpose of this lab is to:

1. Collect demographic data and learn to describe age-structured populations.
2. Compare and explain differences in the survivorship curves and life-tables in a community with respect to gender and historical trends.
3. Incorporate age-structure to estimate **generation time**, **intrinsic rate of increase**, and **net reproductive rate** of the local community.
4. Consider forces that shape human populations and how this compares to other age-structured populations.

2   Scenario

Today we will be looking at local human demographics and population dynamics by collecting information from tombstones. Humans experience age-structured population growth, meaning birth rates and death rates depend on the age of the individual. In simple exponential and logistic growth models, we assumed that birth rates and death rates are constant with age. Now we will incorporate age-structure to estimate **generation time** (G), **intrinsic rate of increase** (r), and **net reproductive rate** (R_0). From this information, we will be able to identify some basic population data as well as compare characteristics of age-classes or chorts. For our graveyard study, our age-classes will consist of 10-year intervals, for which we will collect birth and death dates from tombstones in a local cemetery.

We will be investigating the hypothesis that there are differences in survivorship of individuals who lived in the 19$^{\text{th}}$ century (1801-1900) compared to individuals who lived in the 20$^{\text{th}}$ century (1901-2000). We will also be examining the data to see if gender plays a role in survivorship both as a whole and between the two time periods.

Please note, "sex" is a biological concept regarding gamets at birth, while "gender" is a social concept and refers to the social and cultural differences a society assigns to people based on their sex or an individual assings themselves. We will be catergorizing individual's gender based on their names only as we do not have information about their biological condition.

3   Background

3.0.1   Demography

Demography is the descriptive study of biological populations, including human populations. Demography includes the study of birth rates, death rates, immigration, and emigration patterns (sometimes referred to as vital statistics). Ecologists have perfected the analysis of demography because the vital statistics of a population tell us if the population is growing or declining, what will be the stable age distribution of the population, and how natural selection might work on individuals of each age class.

Human population dynamics can be particularly interesting because of how events or trends in human history affect them. Everyone has heard the term "Baby Boomers", which refers to the generation that was born after WWII when the economy was strong and soldiers returning from the war were getting married or were reunited with their spouses. This socio-political-economic event is observable in records of human populations via increased birthrate, life expectancy, increased total population, and changes in sex ratios in countries affected by the war. Other global events that are evident in population data are the flu pandemic of 1918, which killed between 50 and 100 million people in only 18 months. In the US, this was followed shortly by the Great Depression, which added to the dip in population growth.

There are many such events in human history that have impacted populations, some global and some local. An event that changes a particular population could be as seemingly insignificant as the closing of a mine in a small West Virginia town, closing of a tobacco farm in Virginia, or increasing housing prices in inner city Boston. Advances in healthcare have also significantly altered demographics in populations. In the early 1800s, one of every five women died during childbirth, and infant mortality was much higher than it is today. Fortunately, childbirth is not nearly as fatal today. These changes have been at least partially attributed to medical breakthroughs such as the discovery of antibiotics in the 1930s and the polio vaccine in the 1950s.

3.0.2   Survivorship Curves

Survivorship curves are representations of population mortality over a lifespan. They illustrate the proportion of an initial cohort that is alive at age x. There are three common forms that these curves can take that represent different life history strategies. It is easy to forget that demography includes all biological populations, not just humans.
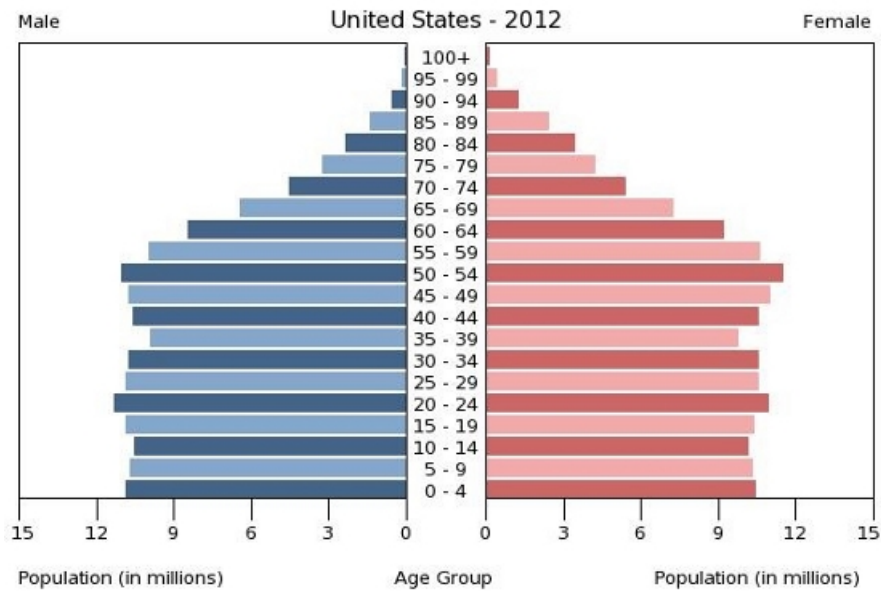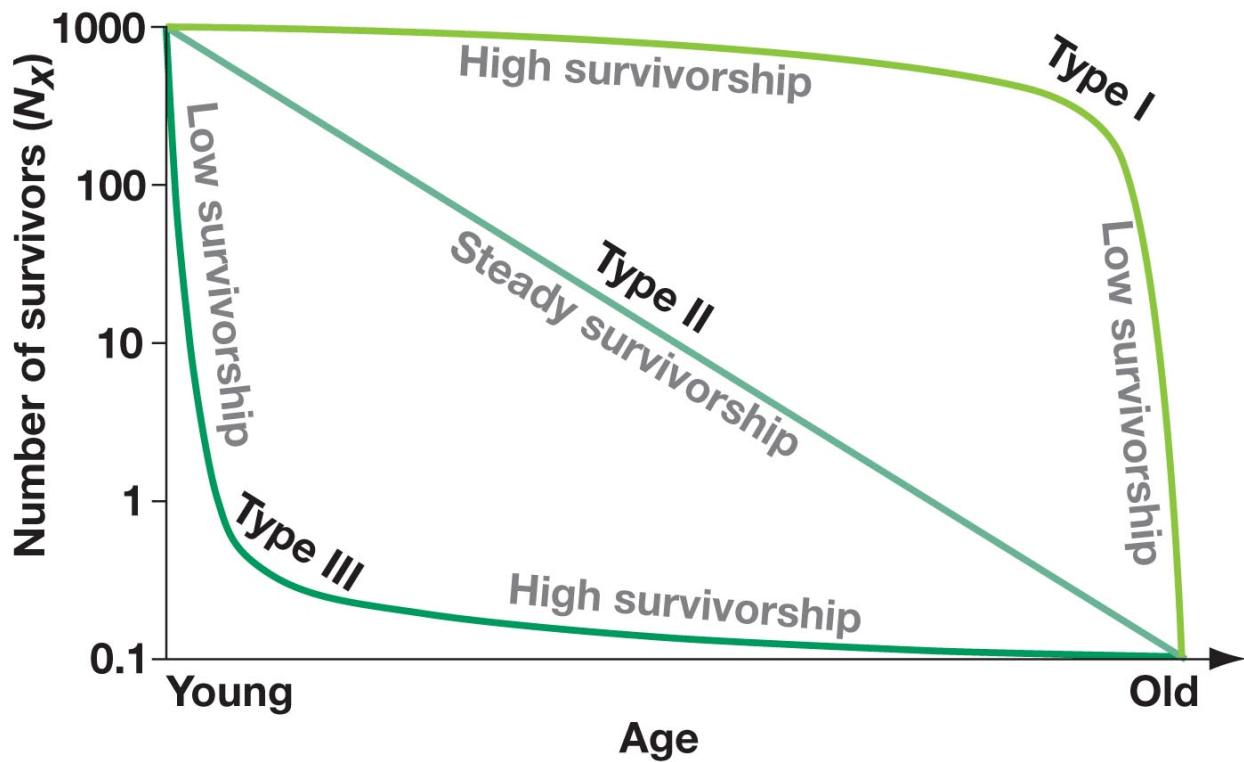
Figure 1: usa

(a) Three general types of survivorship curves

Figure 2: survivorship

1. **Type I** survivorship is characterized by relatively low mortality rates for young age classes, but high mortality rates for old age classes. Species that follow this type of curve often have few offspring and provide parental care for the younger age classes. Large-bodied animals and ones in the higher trophic levels, such as lions, whales, and apes, often exhibit Type I survivorship. In developed nations with good health care, human populations also have survivorship curves that appear most like Type I. Survivorship curves are often described as properties of a species, but they actually depend on the local conditions in a particular environment. In many places in the world, human infant mortality is still high, and the survivorship curve will not look like an idealized Type I curve.

2. **Type II** survivorship is characterized by nearly constant mortality over all age classes, leading to a linear decline in survivorship with age. This type of curve is fairly uncommon in nature, because most species and populations exhibit some differences in mortality rates as they age.

3. **Type III** survivorship is characterized by relatively high mortality rates for young age classes, but low mortality rates for old age classes. In this kind of life history, organisms produce many offspring and provide little or no parental care. As a consequence, mortality in young age classes is very high, and very few offspring will survive to reproduce. Some examples of these types of species might include organisms such as octopi, which can lay up to 200,000 eggs. Many plant species also exhibit Type III survivorship curves. Maple trees, for example, can drop thousands of seeds of which only a handful may ever make it to reproductive maturity. However, once they get past the recruitment stage, the survivorship rate of large old trees is relatively high.

3.0.3 Graveyards

Graveyards are interesting in themselves because they reflect social change and attitudes toward death. Prior to the Revolutionary War era, many European and New England gravestones were decorated with grinning skulls and cross-bones, stressing the inevitability of death and the relatively brief time of life. Cemeteries were muddy and unkempt, reinforcing this grim message. By the late 1700s, death was viewed more as a release from earthly suffering, and white marble, a symbol of purity, became common for grave markers. They were often shaped like headboards of beds and the size indicated the age of the deceased.

In the 1830s, cemeteries began to be run by towns rather than churches and it became necessary to buy plots. Grave markers became more ornate, and, for wealthy families, mausoleums were popular. By the late 1800s, family memorials had a central marker for the head of the family (usually an adult male), with smaller stones around it representing family members.

At this time, one out of five women died during childbirth, and many children died before the age of five. Thus, death in the immediate family was fairly frequent. Because cemeteries held those recently deceased individuals, families would often make weekend excursions to the cemetery and took along picnic lunches. The atmosphere of graveyards reflected such social patterns, and graveyards were landscaped and groomed for a park-like effect. During this century, the trend is for spouses to have equal and side-by-side headstones stressing the marital bond, rather than the supremacy of the husband.

I am sure you do not have to be reminded, but cemeteries are places of honor for those who went before us. Please remember to show respect for the dead and for any other people who may be visiting their loved ones in the cemetery while we gather the data. Please respect the privacy of any people visiting graves by avoiding those areas.

4 Methods

4.0.1 Location

Today we will be working in a local cemetery with 19th and 20th century graves..

4.0.2 Team Work

Work in pairs to collect data in the area of the graveyard you are assigned. Record the year of birth, death, and gender for 50 individuals from each century cohort.

4.0.3 Standarized Collection

Each group will collect data from 50 gravestones; 25 from each treatment (the 19th century and 25 from the 20th century). Data collection best practices for this lab:

1. If the gender of the name is too ambiguous to infer sex, omit that individual.
2. Be sure not to focus exclusively on large tombstones, because tombstone size is influenced by wealth and selecting large (or small) tombstones will bias the data by introducing differences in quality of health care.
3. Choose data for individuals who lived primarily in one century or the other to avoid overlap of the two categories.
4. If the name or date on a gravestone is illegible, make a rubbing using blank paper and the side of a dark crayon. Rubbings can greatly enhance legibility.

4.0.4 Preparing Data on Your CSV File (in Excel)

Before you start analyzing your data, you first need to format it in a way that R can read it. For this lab, you need to input your data into Excel first. Please see associated `.csv` file. You should have 6 columns that MUST BE LABELED THE SAME WAY OR THE SCRIPT WILL NOT WORK! *There is a template for you*

Date = Date of collection

SiteID = The site where you collected your data (IE. National Cemetery)

GroupID = Your group (IE Group 1 or "Team Ramrod")

Gender = The infered sex of the individual based on the gender of the name

Birth_Year = Date of birth (year only)

Death_Year = Date of death (year only)

```
##      TaID SiteID GroupID Gender Birth_Year Death_Year
## [1,]  NA    NA      NA     NA       NA         NA
```

Once you are finished entering your data, save your *Excel* document as a `.csv` file (Comma Separated).

4.0.5 Importing Data

Here you are importing your dataset from your `.csv` file to your R script. There are TWO csv files needed for this script.

1. The class raw data (we will name this csv file *survival*). This dataset has all observations you recorded from the tombstones (gender, year of birth, year of death).

2. The birth schedule (we will name this csv file *birth*) and will be provided. This information was made based off of the historical census data, and provides a typical birth schedule (average number of offspring per female of each age class) for the 19th and 20th centuries.

```
# remember you can set the working directory
# use the file.choose() to select both csv files

survival <-read.csv(file ="Graveyard_Survival_Manual.csv")

birth <-read.csv(file = "Graveyard_Birth.csv")
```

4.0.6 Example Data

This section is an example from your text book (Gotelli *A Primer of Ecology* pg 52; Table 3.1). We will be making a similar table with our *survival* and *birth* data.

4.0.7 Visualize Datasets

- Here you can check if you imported the data correctly

```
head(survival)
```

```
##    SiteID GroupID Gender Birth_Year Death_Year
## 1 Sample       1      M       1884       1885
## 2 Sample       1      M       1821       1886
## 3 Sample       1      F       1826       1888
## 4 Sample       1      F       1857       1883
## 5 Sample       1      M       1815       1891
## 6 Sample       1      F       1827       1864
```

```
head(birth)
```

```
##   Age bx_19 bx_20
## 1   0     0     0
## 2   1     0     0
## 3   2     0     0
## 4   3     0     0
## 5   4     0     0
## 6   5     0     0
```

4.0.8 Attach Primary Datasets

You have seen before how you can extract a column from a dataset and save it as an object in R. This can be tedious when you have datasets with several columns. This also creates several objects in R that just use extra space. R has a nice function called **attach**. This function allows you to attach a dataframe and then call each column later as if it was an independent object. In the end of your script you can just **detach** your dataframe, and these columns will no longer be recognized as separate objects. You have already attached the two csv files (*survival* and *birth*), but we should recall them using the **attach** ().

```
attach(survival)
attach(birth)
 # Each column can be used as an object in R (remember to detach in the end
```

4.0.9 Manipulating Datasets

Now it is time to start working with the data you have collected from the Cemetery. We have a lot of calculations to do! * Calculate age of death (life span) * Calculate Cohort Survival (S_x) * Calculate Survivorship Schedule (l_x) * Calculate Survival Probability (g_x) * Calculate $l_x * b_x$ * Calculate $l_x * b_x$ (x) * Calculate Net Reproductive Rate (R_0) * Calculate Generation Time (G_x) * Estimate the Intrinsic Rate of Increase (r) * Plot Survivorship Curves

4.0.10 Calculate Age of Death

Calculate the age of death for all individuals by subtracting the year of birth from the year of death. Note that the age of death is equivalent to the lifespan of the individual.

```
Death_Age <- Death_Year-Birth_Year
  # This subtracts the year of birth from death

Ages<- min(birth$Age):max(birth$Age)
  # This is the range of ages to be included in tables and calculation
  # Just like we did before we build histograms! Remeber the bin sizes?

Death_Age <- factor(Death_Age,levels=Ages)
  # This transforms the Death_Age into a "factor" for later convenience.
  # R likes working with factors.


### Here we start selecting Death_Age by century
Death_Age_19 <- Death_Age[ Birth_Year < 1901 ]
  # Selects individuals born before 1901 (19th Century)
Death_Age_20 <- Death_Age[ Birth_Year >= 1901 ]
  # Select only individuals born after or in 1901 (20th Century)

### Here we start to filter between genders
Death_Age_19M <- Death_Age[Birth_Year<1901&Gender=="M"]
   # Selects individuals MALES in the 19th Century
Death_Age_19F <- Death_Age[Birth_Year<1901&Gender=="F"]
   # Selects individuals FEMALES in the 19th Century
Death_Age_20M <- Death_Age[Birth_Year>=1901&Gender=="M"]
   # Selects individuals MALES in the 20th Century
Death_Age_20F <- Death_Age[Birth_Year>=1901&Gender=="F"]
   # Selects individuals FEMALES in the 20th Century
```

4.0.11 Calculate Chorot Survival (S_x)

S_x and (S0...s10) is the Cohort Survival. Remember that this means we are calculating the survival of individuals born at the same time (a cohort). But before we make a S_x table, we need to calculated the life span for males and females in both 19th and 20th Centuries.

This is taking the cumulative sum of Deaths by century and then by century and gender. We use length() for counts because it counts the number of rows. The (-) before length means that it is ignoring the previous row. That is because the first row is actually the headings and there are no numerical values associated with the first row and therefore, not needed for calculation.

```r
S0_19<-sum(Birth_Year<1901)
  # Adds the number of people (males and females) togehter in 19th century
  # In this example s0 = 75
S0_20<-sum(Birth_Year>=1901)
  # Adds the number of people (males and females) togehter in 20th century
  # In this example s0 = 75


#### s0 for the Genders ####
S0_19M <- sum(Birth_Year<1901&Gender=="M")
  # Adds the number of MALES togehter in 19th century
  # In this example s0 = 37

S0_19F <- sum(Birth_Year<1901&Gender=="F")
  # Adds the number of FEMALES togehter in 19th century
  # In this example s0 = 38

S0_20M <- sum(Birth_Year>1901&Gender=="M")
  # Adds the number of MALES togehter in 20th century
  # In this example s0 = 36
S0_20F <- sum(Birth_Year>1901&Gender=="F")
  # Adds the number of FEMALES togehter in 20th century
  # In this example s0 = 39

##### Now we can make tables for the age of deaths (or life span)
Deaths_19 <- table(Death_Age_19)
  # table for the age of death for people (males and females) in the 19th century
Deaths_20 <- table(Death_Age_19)
  # table for the age of death for people (males and females) in the 20th century
Deaths_19M<-table(Death_Age_19M)
  # table for the age of death for people (males and females) in the 20th century
Deaths_19F<-table(Death_Age_19F)
  # table for the age of death for people (males and females) in the 20th century
Deaths_20M<-table(Death_Age_20M)
  # table for the age of death for people (males and females) in the 20th century
Deaths_20F<-table(Death_Age_20F)
  # table for the age of death for people (males and females) in the 20th century


#### Now we can make the cohort survival tables
Sx_19 <- c(S0_19, S0_19 - cumsum(Deaths_19[-length(Deaths_19)]))
  # Survival by age in the 19th century
Sx_20 <- c(S0_20 , S0_20 - cumsum(Deaths_20[-length(Deaths_20)]))
  # Survival by age in the 20th century
Sx_19M <- c(S0_19M, S0_19M - cumsum(Deaths_19M[-length(Deaths_19M)]))
  # Survival of MALES by age in the 19th century
Sx_19F <- c(S0_19F, S0_19F - cumsum(Deaths_19F[-length(Deaths_19F)]))
  # Survival of FEMALES by age in the 19th century
Sx_20M <- c(S0_20M, S0_20M - cumsum(Deaths_20M[-length(Deaths_20M)]))
  # Survival of MALES by age in the 20th century
Sx_20F <- c(S0_20F, S0_20F - cumsum(Deaths_20F[-length(Deaths_20F)]))
  # Survival of FEMALES by age in the 20th century
```

4.0.12 Calcuate Survivorship Schedule (l_x)

Now we have the cohort survival (S_x) we need to make the Survivorship Schedule (l_x). The survivorship schedule (l_x) takes the cohort (S_x) and converts it to make a life table (l). The survivorship quantity l is defined as the proportion of the original cohort that survive to the next age class because not all individuals born survive to the next age class just as not all individuals survive until they are 100! l_x is calculated by dividing the S_x by the S_0! IE the current age class divided by the age class at birth.The following generates tables that calculate the proportion of individuals that survive to the next age class.

```
lx_19 = Sx_19/S0_19
  # the survivorship of the people (males and females) in the 19th century
lx_20 = Sx_20/S0_20
  # the survivorship of the people (males and femlaes) in the 20th century
lx_19M = Sx_19M/S0_19M
 # the survivorship of MALES in the 19th century
lx_19F = Sx_19F/S0_19F
 # the survivorship of FEMALES in the 19th century
lx_20M = Sx_20M/S0_20M
  # the survivorship of MALES in the 20th century
lx_20F = Sx_20F/S0_20F
  # the survivorship of FEMALES in the 20th century
```

4.0.13 Calculate Survival Probability (g_x)

Now we have the Survivorship Schedule (l_x) we need to calculate the Survival Probability(g_x). The Survival Probability(g_x) is the probability that an individual from $generation_x$ survives to age x+1. That survive to the next age class because not all individuals born survive to the next age class just as not all individuals survive until they are 100! The current survivorship at age x+1 divided by the survivorship at the present age x. g_x is calculated by $l_{(}x+1)/l_x$!

```
gx_19 = lx_19 [-1] / lx_19 [-length(lx_19)]
  # the Survival Probability of the people (males and females) in the 19th century
gx_20 = lx_20 [-1] / lx_20 [-length(lx_20)]
  # the Survival Probability of the people (males and females) in the 20th century
gx_19M = lx_19M [-1] / lx_19M [-length(lx_19M)]
  # the Survival Probability of MALES in the 19th century
gx_19F = lx_19F [-1] / lx_19F [-length(lx_19F)]
  # the Survival Probability of FEMALES in the 19th century
gx_20M = lx_20M [-1] / lx_20M [-length(lx_20M)]
# the Survival Probability of MALES in the 20th century
gx_20F = lx_20F [-1] / lx_20F [-length(lx_20F)]
# the Survival Probability of FEMALES in the 20th century
```

4.0.14 Calculate Survivorship by the Birth I ($l_x * b_x$)

Now we need to multiply the Survivorship Schedule (l_x) by the Birth Schedule (bx; from the *birth* csv file).

```
lxbx_19 = lx_19*bx_19
  # Males and females in the 19th century
lxbx_20 = lx_20*bx_20
  # Males and females in the 20th century
lxbx_19M = lx_19M*bx_19
```

```
  # MALES in the 19th century
lxbx_19F = lx_19F*bx_19
  # FEMALES in the 19th century
lxbx_20M = lx_20M*bx_20
  # MALES in the 20th century
lxbx_20F = lx_20F*bx_20
  # MALES in the 20th century
```

4.0.15 Calculate Survivorship by Birth II ($l_x*b_x(\mathbf{x})$)

Now we need to multiply the Survivorship Schedule (l_x) by the Birth Schedule (b_x) for each cohort (which is the AGE).

```
lxbxx_19 = lxbx_19*Ages
  # Males and females in the 19th century
lxbxx_20 = lxbx_20*Ages
  # Males and females in the 20th century
lxbxx_19M = lxbx_19M*Ages
  # MALES in the 19th century
lxbxx_19F = lxbx_19F*Ages
  # FEMALES in the 19th century
lxbxx_20M = lxbx_20M*Ages
  # MALES in the 20th century
lxbxx_20F = lxbx_20F*Ages
  # FEMALES in the 20th century
```

4.0.16 Calculate Net Reproducive Rate (R_0)

Now we can calculate the Net Reproductive Rate. Net Reproductive Rate (R_0) is the mean number of female offspring produced per female over her lifetime. (R_0) is the of the products of Survivorship Schedule (l_x) and Fecundity Schedule (bx; from the *birth* csv file) for each age class.

```
R0_19 = sum(lxbx_19,na.rm = T)
  # the Net Reproducive Rate of the people (males and females) in the 19th century
  # in this example R0_19 = 1.038
R0_20 = sum(lxbx_20,na.rm = T)
  # the Net Reproducive Rate of the people (males and females) in the 20th century
  # in this example R0_20 = 1.765
R0_19M = sum(lxbx_19M,na.rm = T)
  # the Net Reproducive Rate of MALES in the 19th century
  # in this example R0_19M = 1.157
R0_19F = sum(lxbx_19F,na.rm = T)
  # the Net Reproducive Rate of FEMALES in the 19th century
  # in this example R0_19F = .922
R0_20M = sum(lxbx_20M,na.rm = T)
  # the Net Reproducive Rate of MALES in the 20th century
  # in this example R0_20M = 2.544
R0_20F = sum(lxbx_20F,na.rm = T)
  # the Net Reproducive Rate of FEMALES in the 20th century
  # in this example R0_20F = 2.688
```

4.0.17 Calculate Generation Time (G_x)

Now that we have the Net Reproductive Rate R_0, we can calculate the Generation Time (G). Generation Time is the average age of parents of all the offspring produced by a single cohort.This is the sum of $l_x*b_x(\mathrm{x})$.

```
G_19 = sum(lxbxx_19,na.rm = T)/RO_19
  # Generation time for the people (males and females) in the 19th century
  # in this example G_19 = 26.63
G_20 = sum(lxbxx_20,na.rm = T)/RO_20
  # Generation time for the people (males and females) in the 20th century
  # in this example G_20 = 26.63
G_19M = sum(lxbxx_19M,na.rm = T)/RO_19M
  # Generation time for MALES in the 19th century
  # in this example G_19M = 26.15
G_19F = sum(lxbxx_19F,na.rm = T)/RO_19F
  # Generation time for FEMALES in the 19th century
  # in this example G_19F = 27.21
G_20M = sum(lxbxx_20M,na.rm = T)/RO_20M
  # Generation time for MALES in the 20th century
  # in this example G_19M = 26.70
G_20F = sum(lxbxx_20F,na.rm = T)/RO_20F
  # Generation time for MALES in the 20th century
  # in this example G_19M = 27.14
```

4.0.18 Estimate the Intrinsic Rate of Increase (r)

Now it is time to calculate the Intrinsic Rate of Increase (r). Intrinsic Rate of Increase is the difference between the instantaneous birth rate (b) and the instantaneous death rate (d). We have calculated the birth rate and death rates based of the data we collected. The Intrinsic Rate of Increase is the natural logarithm (ln) of Net Reproductive Rate (R_0) divided by the Generation Time (G_x). So, $r = \log(R_0)/G_x$.

*Please note that the natural logarithm function in R is **ln()**.*

```
r_19 = log(RO_19)/G_19
  # for the people (Males and Females) for the 19th century
  # in this example r_19 = 0.0014
r_20 = log(RO_20)/G_20
  # for the people (Males and Females) for the 20th century
  # in this example r_20 = 0.0213
r_19M = log(RO_19M)/G_19M
  # for the MALE in the 19th century
  # in this example r_19M = 0.0056
r_19F = log(RO_19F)/G_19F
  # for the FEMALE in the 19th century
  # in this example r_19F = -0.0030
r_20M = log(RO_20M)/G_20M
  # for the MALE in the 20th century
  # in this example r_20M = 0.0350
r_20F = log(RO_20F)/G_20F
  # for the MALE in the 20th century
  # in this example r_20F = 0.0364
```

4.0.19 Making Tables

Next you calculate the **generation time** (G), **intrinsic rate of increase** (r), and **net reproductive rate** (R_0) of males and females from the 19th and 20th century, and assemble these numbers in tables.

```r
# 19th Century Summary

# cbind combines columns
CenturySummary19 = cbind(R0_19,G_19,r_19)
CenturySummary19F= cbind(R0_19F,G_19F,r_19F)
CenturySummary19M= cbind(R0_19M,G_19M,r_19M)

# rbind combines the rows
CenturySummaryTable19 = rbind(CenturySummary19, CenturySummary19F, CenturySummary19M)

# rownames allows you to name the rows
rownames(CenturySummaryTable19) = c("Male + Female","Female", "Male")

# colnames allows you to name the columns
colnames(CenturySummaryTable19) = c("R0_19M","G_19M","r_19M")


# 20th Century Summary
CenturySummary20 = cbind(R0_20,G_20,r_20)
CenturySummary20F= cbind(R0_20F,G_20F,r_20F)
CenturySummary20M= cbind(R0_20M,G_20M,r_20M)
CenturySummaryTable20 = rbind(CenturySummary20, CenturySummary20F, CenturySummary20M)
rownames(CenturySummaryTable20) = c("Male + Female","Female", "Male")
colnames(CenturySummaryTable20) = c("R0_20M","G_20M","r_20M")
```

You will need to install the PerformanceAnalytics package if you want to create a table in the plot panel. You have seen this function before.

```r
PerformanceAnalytics:::textplot(CenturySummaryTable19,
                                halign = "center",
                                valign = "center",
                                max.cex = 2,
                                cmar = 3,
                                rmar = 3,
                                hadj = 1,
                                vadj = 1,
                                row.valign = "center",
                                heading.valign = "center",
                                mar = c(0, 0, 0, 0) + 0.5,
                                col.data = par("col"),
                                col.rownames = par("col"),
                                col.colnames = par("col"),
                                wrap = TRUE,
                                wrap.colnames = 20,
                                wrap.rownames = 20)
```

	R0_19M	G_19M	r_19M
Male + Female	1.29013215547703	28.0127751450669	0.00909387441670248
Female	1.39917166666667	28.1020824225762	0.0119521532176889
Male	1.22224967741935	27.9773954637852	0.00717340392935239

```
PerformanceAnalytics:::textplot(CenturySummaryTable20,
                                halign = "center",
                                valign = "center",
                                max.cex = 2,
                                cmar = 3,
                                rmar = 3,
                                hadj = 1,
                                vadj = 1,
                                row.valign = "center",
                                heading.valign = "center",
                                mar = c(0, 0, 0, 0) + 0.5,
                                col.data = par("col"),
                                col.rownames = par("col"),
                                col.colnames = par("col"),
                                wrap = TRUE,
                                wrap.colnames = 20,
                                wrap.rownames = 20)
```

	R0_20M	G_20M	r_20M
Male + Female	2.11561101503759	27.8891441856334	0.0268686504608019
Female	2.61228448275862	28.8796078541375	0.0332492436912589
Male	2.56531338582677	28.5839201853437	0.032958413078446

4.0.20 Plot Survivorship Curves

That was a lot of calculation, but now we have all the data we need to plot survivorship curves.

On the x-axis we will need the ages (Ages) and on the y-axis we need the logarithm of the elements in the Survivorship Schedule (l_x). We also need four lines on this graph (19th century females, 19th century males, 20th century females, 20th century males, . First we plot the data for the 19th Century Females with the `plot ()` function. We then add the other lines with the `point()` function.

1. Male Survivorship Curve in 19th century (blue dashed)
2. Male Survivorship Curve in 20th century (blue solid)
3. Female Survivorship Curve in 19th century (pink dashed)
4. Female Survivorship Curve in 20th century (pink solid)

```
# 19th Century Female
plot(lx_19F~Ages,
    type="l", # line plot
    col="hotpink",
    lwd=2,
    lty=2, # dashed line
    xlab="Age",
    ylab="ln [ l(x) ]",
    log = "y")
```

```
## Warning in xy.coords(x, y, xlabel, ylabel, log): 11 y values <= 0 omitted from
## logarithmic plot
```
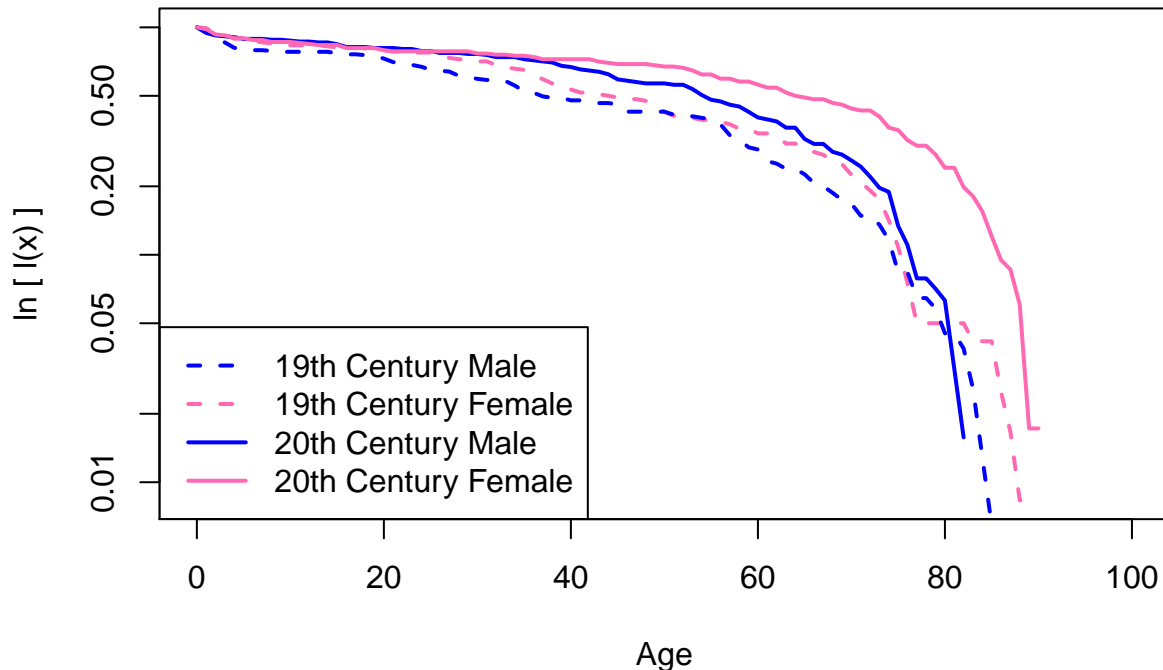
```r
# 19th Century Male
points(lx_19M~Ages,
       type="l",
       col="blue",
       lwd=2,
       lty=2)

# 20th Centruy Male
points(lx_20M~Ages,
       type="l",
       col="blue",
       lwd=2)

# 20th Century Female
points(lx_20F~Ages,type="l",
       col="hotpink",
       lwd=2)

# recall the legend function
legend("bottomleft",
       c("19th Century Male","19th Century Female",
         "20th Century Male","20th Century Female"),
      lty=c(2,2,1,1),
      lwd=2,
      col=c("blue","hotpink")
      )
```

```
detach(survival)
detach(birth)
```

5 Writing Your Paper

Now it's time to ask questions that will help you write your paper (meaning, the following questions should be answered in your paper). **You should check and follow the rubric for every paper before you start writing.**

1. Compare **generation time** (G), **intrinsic rate of increase** (r), and **net reproductive rate** (R_0) of males and females from the 19th and 20th century.
2. What biological mechanism(s) may cause these values to differ?
3. Which survivorship schedule curve (Type I, Type II, or Type III) do your data most closely match?
4. Are the survivorship curves different between centuries?
5. Are the survivorship curves different between gender and what can you infer about sex?
6. What biological, historical, or cultural mechanism(s) could explain the patterns you observe in your data?

5.0.1 Abstract (~300 words)

The abstract is the summary of the entire paper, so it is best to write it last. The abstract should address:

- What is the primary purpose of the study

- What are the biological, alternative, and null hypotheses?
- How were data collected?
- What methods were used to analyze the data?
- Was there a statistical difference between times or between genders?
- Was the null hypothesis accepted or rejected?
- What is the overall conclusion?

5.0.2 Introduction (1-2 pages)

Here you should look up some papers on survivorship curves in different species. Give examples from all III curves. Discuss human demography in the US and what you expect to see from your sample. You need to also *clearly* state your biological, alternate, and null hypothesis in this section. Also include the purpose of this study.

Hint: look at the questions above to help you search for papers

5.0.3 Methods (1-2 pages)

This will be a short section.

- Where was the study conducted?/ Where were data collected?
- How were data collected?
- How were data analyzed?

5.0.4 Results (~ 1 page of text, 2 tables, 1 graphs)

In the results section, describe the patterns in the graphs and tables that you have created. Make sure that you specifically cite each table or graph and tell what the result is. Just report the results in this section. You will interpret them in the discussion section.

- What does your table of values show?
- What patterns are present for the survivorship curves of males and females in the 19th and 20th centuries?

5.0.5 Discussion (~1-2 pages)

- What can you say about the demography in VT during the 19th and 20th century between males and females?
- Are you going to accept or reject your Null Hypothesis?
- Why or why not?
- What does your study say about human demography and using gravestones to collect this type of data?
- What are the potential sources of error and uncertainty in your estimates of the survivorship and birth schedules?

5.0.6 References

Must be in *Ecology* format

6 Definitions

6.0.1 Survivorship Schedule (l_x)

The l_x schedule gives the probability that an individual survives from birth to the start of age x. By definition, the survival of newborns is 100%, so l_0 always equals 1.0. The survival of the final age class is 0.0, because, by definition, there are no individuals left alive after the last age class.

6.0.2 Survival Probability (g_x)

The age-specific survival probability for individuals of age x is defined as the probability that an individual alive at age x will still be alive at age $x+1$.

6.0.3 Type I Survivorship Curve

A survivorship curve in which survival probabilities are relatively high for young individuals and relatively low for old individuals.

6.0.4 Type II Survivorship Curve

A survivorship curve in which survival probabilities are relatively constant across different ages.

6.0.5 Type III Survivorship Curve

A survivorship curve in which survival probabilities are relatively low for young individuals and relatively high for old individuals.

7 New R Functions

7.0.1 `attach()` & `detach()`

The `attach()` attaches the database to the R search path. This means that the database is searched by R when evaluating a variable, so objects in the database can be accessed by simply giving their names. Recall in previous script that we use the style $Dataset Column (IE : RawData Depth)$. With the `attach()`, you can attach the dataset, then call the column without the $. Do not forget to use the `detach()` at the end of your script.

8   Graveyard Demography Lab Rubric (15pts)

8.0.1   Drafts _____/ 4 points

1. Was your draft complete? (2 points)
2. Did you bring 2 copies? (2 points)

8.0.2   Overall _____ / 2 points

1. Is it clearly written and does it make sense?

8.0.3   Abstract _____ / 1 point

1. Complete with Main Idea? Hypothesis? Major Methods? Major Results? Hypothesis supported? Conclusion? (1pt)

8.0.4   Introduction _____ / 1 point

1. Provide background? (.75pts)
2. Hypothesis? (.25pts)

8.0.5   Material/Methods _____ / 2 points

1. What did you do? (.50pts)
2. Location? (.25pts)
3. What were you testing? (effects of century and gender on survivorship)? (.25pts)
4. What variables did you calculate from the data and what formulas did you use? (.75pts)
5. What software did you use? (.25pts)

8.0.6   Results _____ / 2 points

1. Written Results! Not just figures! (1pt)
2. Graphs and tables (.50pts)
3. Figure Captions (.50 pts)

8.0.7   Conclusion _____/ 2 points

1. Did you give a quick summary? (.25pts)
2. Do you accept/refute your statistical hypotheses? Why? (1 pt)
3. Did you relate your findings to biological hypothesis? (.50pts)
4. Do any treatments (century or gender) impact survivorship? (.25pts)

8.0.8   References _____ / 1 point

1. 3 references (.50pts)
2. Ecology Format -CSE (.50pts)