Life tables in R using the `tidyverse`

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Contents

Life tables are a fundamental tool in demography. A life table describes the mortality experiences for a certain population. Usually a life table is composed of sets of values showing the mortality experience of a hypothetical group of infants born at the same time and subject throughout their lifetime to the specific mortality rates of a given year. Life tables are how we calculate **life expectancy**, probably one of the most common mortality summary measures. They are useful to compare populations and also tells us something about the implied stationary population. Each column refers to a different measure of survivorship. There are different ways of describing survivorship; for example, probability still alive, life expectancy, etc, so a life table has many different columns.

This module explains the main columns of a lifetable and demonstrates how to construct a lifetable in R using the `tidyverse` syntax.

Let's load in the packages we need:

```
library(tidyverse) # data manipulation and ggplot functions
library(kableExtra) # format tables
library(janitor) # to easily clean up column names
```

1 Columns of the lifetable

1.1 Survivorship l_x

Every row of a life table refers to a different age or age group: if the later, the table is referred to as an **abridged** life table. We will define x to be age and n to be the length of the interval.

A usual place to start is survivorship, l_x, which is defined as the number of people still left alive at age x. The value of l_0 is the starting size of the population, and is called the **radix**. In practice, the radix is usually equal to 1, 100, or 100,000. If $l_0 = 1$ then then l_x is a probability of survival to age x. Note that for now we are implicitly assuming this l_0 relates to a **cohort** of people moving through time, so the life table documents **cohort** mortality. However, later on we will look at period mortality.

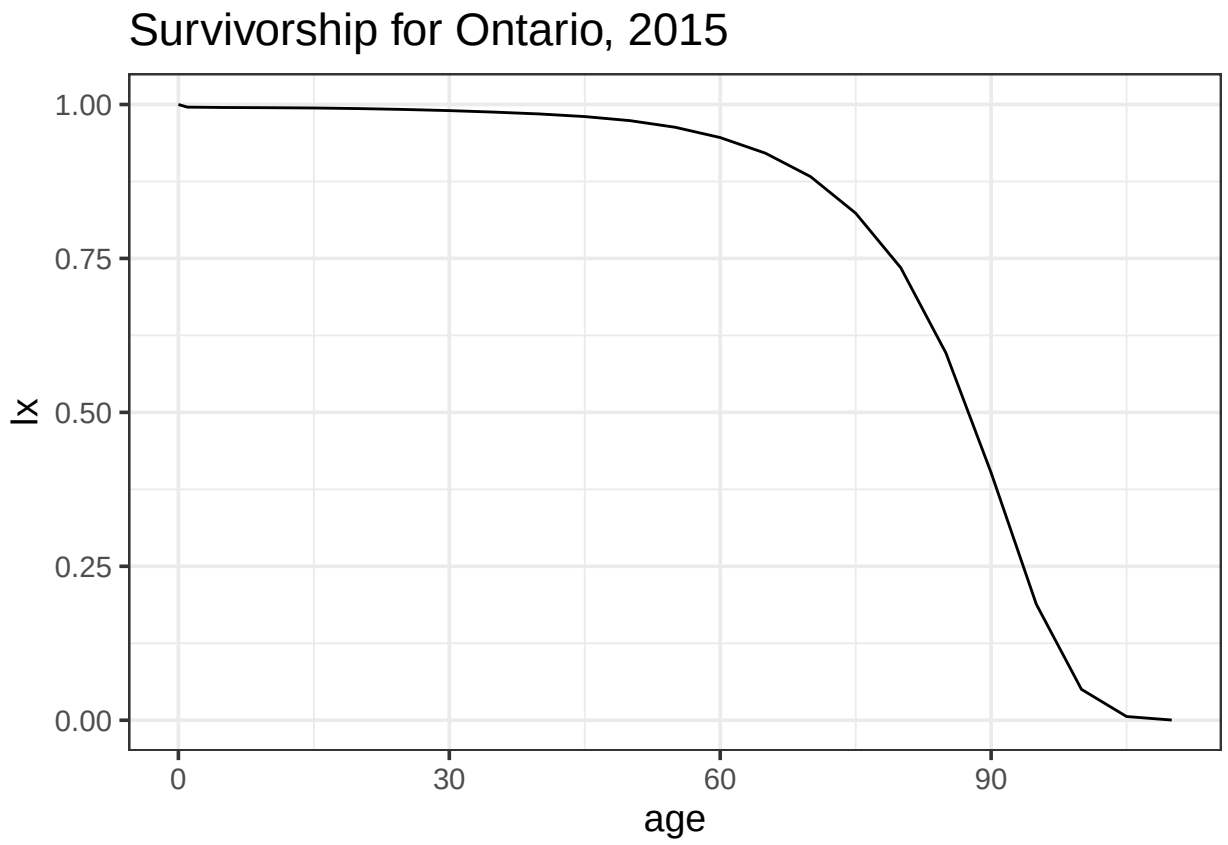
Here's the estimated l_x values for females in Ontario in 2015. The data are from the Canadian Human Mortality Database. Here, the radix is 100,000. By age 110, out of the original population of 100,000, it is estimated that 28 will survive.

```
lt <- read_table("http://www.prdh.umontreal.ca/BDLC/data/ont/fltper_5x5.txt", skip = 2)
lt <- lt |>
  filter(Year=="2015-2019") |>
  mutate(x = c(0,1,seq(5, 110, by = 5)),
         n = lead(x, default = Inf)-x)

lt |>
  select(x,n, lx) |>
  kable()
```

x	n	lx
0	1	100000
1	4	99569
5	5	99515
10	5	99478
15	5	99430
20	5	99334
25	5	99192
30	5	99008
35	5	98759
40	5	98461
45	5	98036
50	5	97380
55	5	96304
60	5	94626
65	5	92094
70	5	88287
75	5	82345
80	5	73473
85	5	59620
90	5	40198
95	5	18841
100	5	5017
105	5	599
110	Inf	28

Let's also plot the l_x and divide through by 100,000 so the l_x can be interpreted as the proportion of the population surviving at age x.

```
lt |>
  mutate(lx = lx/100000) |>
  ggplot(aes(x, lx)) +
  geom_line() +
  xlab("age") +
  theme_bw(base_size = 14) +
  ggtitle("Survivorship for Ontario, 2015")
```



1.2 Deaths ${}_nd_x$

The next column, ${}_nd_x$, is the number of deaths between ages x and $x+n$. Note that we using the 'duration-age' notation, because it refers to deaths over an interval. In contrast, l_x refers to survivors at a certain age x.

By definition, the number of deaths over an interval must be the number of survivors at the start of the interval, minus the number of survivors at the end, i.e.

$$ {}_nd_x = l_x - l_{x+n}. $$

Let's look at the estimated ${}_nd_x$ values for Ontario in 2015:

```
lt |>
  select(x,n, lx, dx) |>
  kable()
```

x	n	lx	dx
0	1	100000	431
1	4	99569	54
5	5	99515	37
10	5	99478	48
15	5	99430	96
20	5	99334	142
25	5	99192	184
30	5	99008	248
35	5	98759	298
40	5	98461	426
45	5	98036	655
50	5	97380	1077
55	5	96304	1677
60	5	94626	2533
65	5	92094	3807
70	5	88287	5942
75	5	82345	8873
80	5	73473	13853
85	5	59620	19422
90	5	40198	21356
95	5	18841	13824
100	5	5017	4419
105	5	599	571
110	Inf	28	28

Notice the structure of the life table in terms of where the the values of l_x and ${}_nd_x$ line up within the rows. l_x always starts at the radix, so the first row represents the total population before any deaths. The first row of ${}_nd_x$ represents the deaths in the first interval. So the second row of l_x is equal to the previous row of l_x minus the previous row of ${}_nd_x$, and so on. Note also the last interval: everyone who survived to the last age group must die.[1]

1.3 Probability of dying, ${}_nq_x$, and of surviving, ${}_np_x$

The next column, ${}_nq_x$ is the probability of dying between ages x and $x+n$. Note that this is a conditional probability, so it's the probability of dying in that interval given you survived to age x. ${}_nq_x$ can be calculated as

$$ {}_nq_x = \frac{{}_nd_x}{l_x} $$

The complement of ${}_nq_x$ is the probability of survival, ${}_np_x$

$$ {}_np_x = 1 - {}_nq_x $$

Again, this is a conditional probability, so it's the probability of survival between ages x and $x+n$ given you survived to age x. Given the relationship for ${}_nq_x$ and ${}_nd_x$, we can also calculate ${}_np_x$ as

$$ {}_np_x = 1 - {}_nq_x = 1 - \frac{{}_nd_x}{l_x} = \frac{l_x - l_x + l_{x+n}}{l_x} = \frac{l_{x+n}}{l_x} $$

i.e. the probability of survival is the ratio of the the survivors at the end and start of the interval.

Looking again at the data for Ontario in 2015, notice the probability of death in the last age group is 1, because again, everyone must die eventually.

[1] *memento mori*.

```
lt |>
  mutate(px = 1- qx) |>
  select(x, n, lx, dx, qx, px) |>
  kable()
```

x	n	lx	dx	qx	px
0	1	100000	431	0.00431	0.99569
1	4	99569	54	0.00054	0.99946
5	5	99515	37	0.00037	0.99963
10	5	99478	48	0.00049	0.99951
15	5	99430	96	0.00096	0.99904
20	5	99334	142	0.00143	0.99857
25	5	99192	184	0.00186	0.99814
30	5	99008	248	0.00251	0.99749
35	5	98759	298	0.00302	0.99698
40	5	98461	426	0.00432	0.99568
45	5	98036	655	0.00668	0.99332
50	5	97380	1077	0.01106	0.98894
55	5	96304	1677	0.01742	0.98258
60	5	94626	2533	0.02676	0.97324
65	5	92094	3807	0.04134	0.95866
70	5	88287	5942	0.06730	0.93270
75	5	82345	8873	0.10775	0.89225
80	5	73473	13853	0.18854	0.81146
85	5	59620	19422	0.32576	0.67424
90	5	40198	21356	0.53129	0.46871
95	5	18841	13824	0.73370	0.26630
100	5	5017	4419	0.88066	0.11934
105	5	599	571	0.95283	0.04717
110	Inf	28	28	1.00000	0.00000

1.4 Average years lived, ${}_na_x$

${}_na_x$ is the number of years lived by those who died between ages x and $x+n$. So for example, if ${}_1a_0 = 0.25$, then for that population, those infants who died in the first year on average died after 0.25 years = 3 months. To calculate the exact value for ${}_na_x$ requires a lot of data: you would need to know the exact lengths of life for each individual in the cohort. Approximations to ${}_na_x$ are discussed below in the period life table section.

1.5 Person-years lived, ${}_nL_x$

${}_nL_x$ is the number of person-years lived between ages x and $x+n$. The total number of person-years lived (PYL) in an interval is the sum of

1. the PYL by those who survived and
2. the PYL by those who died in the interval.

The first piece is just the interval length, n multiplied by the number of survivors at the end of the intervals, l_{x+n}. The second piece is the average time spent alive in the interval by those who died, ${}_na_x$ multiplied by the number of people who died in the interval, ${}_nd_x$. So

$$ {}_nL_x = n \cdot l_{x+n} +_n a_x \cdot_n d_x.$$

Note for the last interval there are no survivors, so ${}_\infty L_x = {}_\infty a_x \cdot {}_\infty d_x$.

Adding ${}_n a_x$ and ${}_n L_x$ to the Ontario life table:

```
lt |>
  select(x,n, lx, dx, ax, Lx) |>
  kable()
```

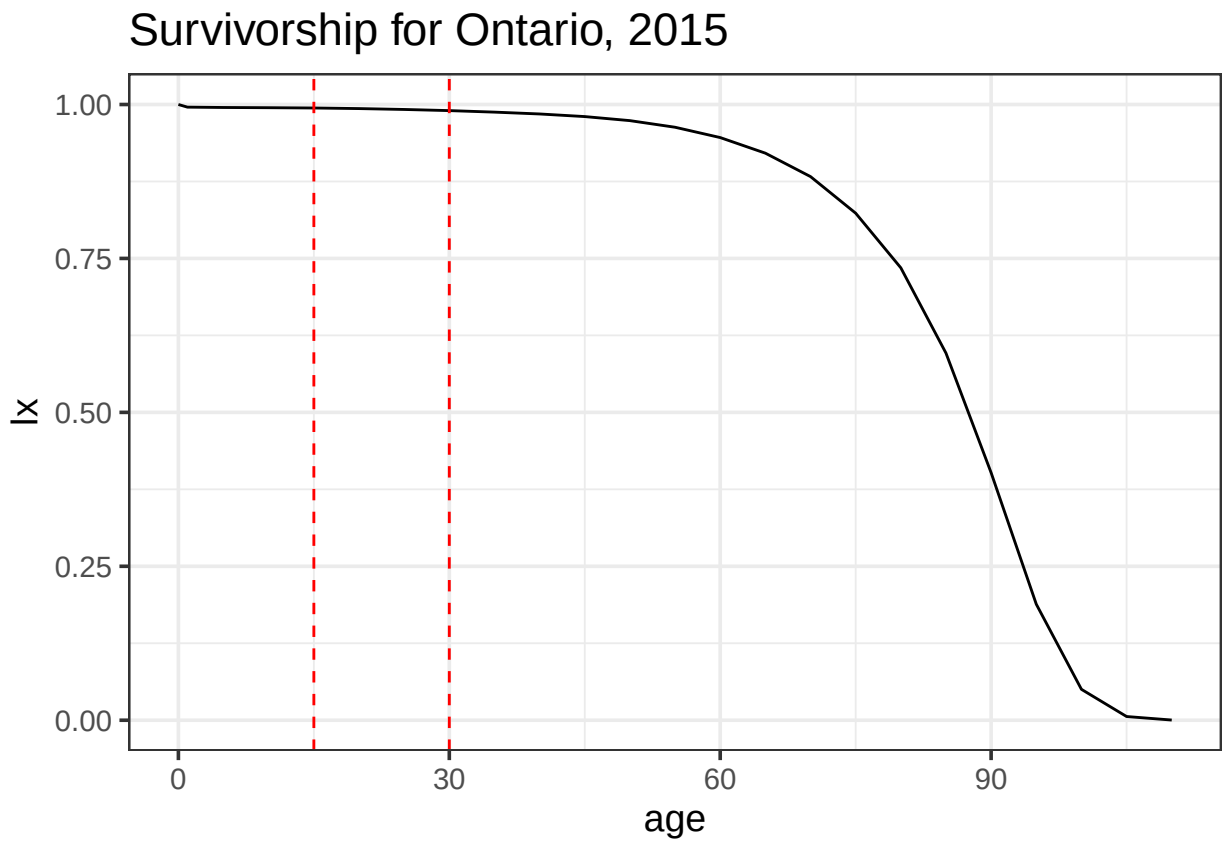
x	n	lx	dx	ax	Lx
0	1	100000	431	0.14	99629
1	4	99569	54	1.62	398147
5	5	99515	37	2.34	497476
10	5	99478	48	2.78	497283
15	5	99430	96	2.90	496947
20	5	99334	142	2.60	496329
25	5	99192	184	2.53	495505
30	5	99008	248	2.57	494435
35	5	98759	298	2.63	493089
40	5	98461	426	2.69	491321
45	5	98036	655	2.69	488665
50	5	97380	1077	2.72	484445
55	5	96304	1677	2.68	477626
60	5	94626	2533	2.68	467245
65	5	92094	3807	2.67	451612
70	5	88287	5942	2.67	427608
75	5	82345	8873	2.67	391032
80	5	73473	13853	2.67	335135
85	5	59620	19422	2.62	251897
90	5	40198	21356	2.44	146361
95	5	18841	13824	2.19	55428
100	5	5017	4419	1.87	11261
105	5	599	571	1.55	1025
110	Inf	28	28	1.45	41

1.5.1 ${}_n L_x$ graphically and the relationship with l_x

${}_n L_x$ is essentially the number of survivors times the average length of time they survived in a particular interval. For a given radix l_0 and interval length n, the maximum ${}_n L_x$ could be is $l_0 \cdot n$, if everyone survived.

How does ${}_n L_x$ relate to l_x? It is the area under the l_x curve for the interval $[x, x+n]$, as illustrated below by the red dashed lines, for ${}_{15}L_{15}$. It may help to think about the units here: ${}_n L_x$ has units person-years. l_x has units of persons. The x-axis on the graph below has units years.

```
lt |>
  mutate(lx = lx/100000) |>
  ggplot(aes(x, lx)) +
  geom_line() +
  xlab("age") +
  theme_bw(base_size = 14) +
  geom_vline(xintercept = 15, lty = 2, color = "red")+
  geom_vline(xintercept = 30, lty = 2, color = "red")+
  ggtitle("Survivorship for Ontario, 2015")
```



With this in mind, we can represent ${}_nL_x$ in continuous form as

$$ {}_nL_x = \frac{1}{l_0}\int_x^{x+n} l_x dx $$

In practice we usually have to calculate ${}_nL_x$ in the discrete form, but it's often useful to think about it in continuous form, i.e. the area under the survivorship curve.

1.6 Person-years lived above age x, T_x

Whereas ${}_nL_x$ is the person-years lived in a specific interval, T_x is the person-years lived above a specific age x (so notice it does not have the duration/age notation). It is defined as the sum of the relevant ${}_nL_x$:

$$ T_x = \sum_x^{\infty} {}_nL_x $$

In a similar fashion to ${}_nL_x$, T_x can be thought of as the area under the l_x curve above age x. In addition, We can write T_x in continuous form as

$$ T_x = \frac{1}{l_0}\int_x^{\infty} l_x dx $$

1.7 Life expectancy at age x, e_x

The final column we will introduce for now is probably the most well-known: e_x, the average number of remaining years of life for those who reach age x, or the **life expectancy** at age x. Note that the 'expectancy'

terminology is related to the expected value in the statistical sense. e_x is calculated as

$$e_x = \frac{T_x}{l_x}$$

We can do a quick check of the units here to make sure it makes sense: T_x has units person-years, l_x has units persons, so e_x has units of years.

You are probably most familiar with life expectancy at birth, e_0. Note that it is again a conditional measure, that is, it's the average number of remaining years **given** a person has already survived to age x. As such, the value of e_x need not decrease monotonically over age. In practice it usually does, unless infant mortality is relatively high.

The filled-in life table with all columns discussed:

```
lt |>
  select(x,n, lx, dx, ax, Lx, Tx, ex) |>
  kable()
```

x	n	lx	dx	ax	Lx	Tx	ex
0	1	100000	431	0.14	99629	8449540	84.50
1	4	99569	54	1.62	398147	8349911	83.86
5	5	99515	37	2.34	497476	7951764	79.91
10	5	99478	48	2.78	497283	7454288	74.93
15	5	99430	96	2.90	496947	6957006	69.97
20	5	99334	142	2.60	496329	6460059	65.03
25	5	99192	184	2.53	495505	5963730	60.12
30	5	99008	248	2.57	494435	5468225	55.23
35	5	98759	298	2.63	493089	4973790	50.36
40	5	98461	426	2.69	491321	4480701	45.51
45	5	98036	655	2.69	488665	3989380	40.69
50	5	97380	1077	2.72	484445	3500715	35.95
55	5	96304	1677	2.68	477626	3016271	31.32
60	5	94626	2533	2.68	467245	2538645	26.83
65	5	92094	3807	2.67	451612	2071400	22.49
70	5	88287	5942	2.67	427608	1619788	18.35
75	5	82345	8873	2.67	391032	1192180	14.48
80	5	73473	13853	2.67	335135	801148	10.90
85	5	59620	19422	2.62	251897	466013	7.82
90	5	40198	21356	2.44	146361	214115	5.33
95	5	18841	13824	2.19	55428	67755	3.60
100	5	5017	4419	1.87	11261	12326	2.46
105	5	599	571	1.55	1025	1066	1.78
110	Inf	28	28	1.45	41	41	1.45

2 Period life tables

A life table as defined above refers to tracking the mortality of a **cohort** of people as they age. However, it is often not practical or useful just to consider the mortality of a cohort, because in order to to build a complete table, we have to wait to observe everyone in the cohort die. So for the 1990 birth cohort, for example, we would probably have to wait around until at least 2090 before a reasonable cohort life table could be built. This is not very useful to study current mortality conditions.

In addition to constructing cohort life tables, we can construct **period** life tables. They refer to the period in the sense that they are constructed using mortality conditions in a particular period. This means the lifetable refers to a **synthetic cohort**, a hypothetical group of people that experience the mortality conditions of the period of interest throughout their entire life. Why is this hypothetical and potentially unrealistic? Because mortality conditions change over time (and in general, are getting better). So for example, if I live until I'm 70, the mortality conditions I am subject to in the future are likely to be different to the mortality conditions that a current 70-year-old is being subjected to. However, period life tables are still useful to compare mortality outcomes for different populations in a more up-to-date way.

2.1 Construction from period mortality rates

The key to constructing period life tables is converting the observed period mortality rates ${}_nM_x$ to probabilities of death, ${}_nq_x$. The mortality rate is the number deaths divided by person years lived, so in life table notation this is:

$$ {}_nM_x = \frac{{}_ndx}{{}_nLx} $$

We can use the following ${}_nM_x$ **to** ${}_nq_x$ **conversion formula** to get the ${}_nq_x$ column, after which all other columns can be derived based on the relationships discussed above (and choosing a radix). The formula is:

$$ {}_nq_x = \frac{n \cdot {}_nM_x}{1 + (n - {}_na_x) \cdot {}_nM_x} $$

How did this come about? By rewriting

$$ {}_nL_x = n \cdot l_{x+n} + {}_na_x \cdot {}_nd_x = n(l_n - {}_nd_x) + {}_na_x \cdot {}_nd_x $$

rearranging to get l_x and rewriting ${}_nq_x$ with this denominator.

2.2 Getting values for ${}_na_x$

The conversion formula requires information only on period mortality rates and values of the average number of years lived for those who died, ${}_na_x$. How do we get these values? As mentioned above, the data required to calculate ${}_na_x$ exactly is usually not available, so we need to approximate it somehow. Preston, Heuveline and Guilot (2000) has a good overview of the options here (section 3.2, page 44), but the most common and easiest approach is, for **most** age groups, assume

$$ {}_na_x = n/2 $$

that is, on average those who die, die half-way through the interval. So for an abridged life table with five-year intervals, ${}_na_x = 2.5$. This assumption is fine for most age groups, except for the very young and very old ages.

At younger ages, typically in abridged life tables the first five years is split out into the first year, and years 1-5, so we need values for ${}_1a_0$ and ${}_4a_1$. For mortality at younger ages, we expected comparatively more deaths to occur at the start of the interval, so ${}_na_x < n/2$. The following two approximations are common, and used e.g. by Wachter in Essential Demographic Methods (2014):

$$ {}_1a_0 = 0.07 + 1.7{}_1M_0 $$

and

$$ {}_4a_1 = 1.5 $$

The equation for ${}_1a_0$ says that infants who die on average die at about 1 month plus a bit, where the bit depends on the over level of infant mortality. This is based on the observation that as infant mortality declines, infants that are dying are more likely to die from pre-existing conditions rather than exogenous factors, so deaths occur relatively early.

For the last age group, we can assume ${}_na_x$ is the inverse of the mortality rate:

$$ {}_\infty a_\omega = 1/{}_\infty M_\omega $$

where ${}_\infty M_\omega$ is the age-specific mortality rate for the last age interval; ω refers to the last age. The smaller the interval of the open-ended age group, the better approximation.

2.3 Interpretation of period life table measures

As mentioned at the start of this section, period life tables are constructed from a synthetic cohort of people that hypothetically would go through life experiencing the age-specific mortality conditions of the current period. Period life table measures, and in particular, period life expectancy at birth, are the most commonly published and discussed. However, period measures of life expectancy are often misinterpreted. The technical definition is the expected number of years of live for a newborn who would be subject to the current mortality conditions for their entire life. But life expectancy is usually just talked about as 'how long you're expected to live for'. Part of the confusion comes from the name, but the 'expected' part refers to the fact that it is an expected value in the statistical sense; in particular, $E[T_x] = e_x$.

3 R: Make your own life table

Let's make a period life table for females in Quebec in 2015 using data from the Canadian Human Mortality Database. Read in the data directly from the website, and filter out what we need:

```
Mx <- read_table("http://www.prdh.umontreal.ca/BDLC/data/que/Mx_5x5.txt", skip = 2, col_types = 'ccddd')

d <- Mx |>
  mutate(year = as.numeric(substr(Year, 1, 4))) |>
  select(year, Age, Total) |>
  clean_names() |>
  rename(Mx = total)

head(d)
```

```
## # A tibble: 6 x 3
##    year age        Mx
##   <dbl> <chr>   <dbl>
## 1  1921 0     0.163
## 2  1921 1-4   0.0129
## 3  1921 5-9   0.00302
## 4  1921 10-14 0.00224
## 5  1921 15-19 0.00357
## 6  1921 20-24 0.00481
```

The `age` column is a character, so let's make and age `x` and interval length `n` column:

```
d <- d |>
  mutate(x = as.numeric(str_remove(age, "-.*|\\+")),
         n = lead(x, default = Inf) - x) |>
  filter(x<105) |> # remove older ages that have varying data availability
  select(year, age, x, n, Mx)
head(d)
```

```
## # A tibble: 6 x 5
##    year age       x     n      Mx
##   <dbl> <chr> <dbl> <dbl>   <dbl>
## 1  1921 0         0     1 0.163
## 2  1921 1-4       1     4 0.0129
## 3  1921 5-9       5     5 0.00302
## 4  1921 10-14    10     5 0.00224
## 5  1921 15-19    15     5 0.00357
## 6  1921 20-24    20     5 0.00481
```

Now we can use `tidyverse` to calculate the columns in the life table, based on the equations presented in previous sections. I set the radix l_0 to be zero and filter to just include the year 2015. This code makes use of the `case_when` function, which allows to define different values of ${}_na_x$ based on age group. Formulas for other columns are based on equations stated above. The formula for T_x is implemented by first reversing the ${}_nL_x$ column, taking the cumulative sum, and then reversing the result.

```
lt_2015 <- d |>
  filter(year==2015) |>
  mutate(
       ax = case_when(
       x==0 ~ 0.07 + 1.7*Mx,
       x==1 ~ 1.5,
       x==110 ~ 1/Mx,
       TRUE ~ 2.5
     ),
      qx = n * Mx / (1 + (n - ax)* Mx),
      px = 1 - qx,
      lx = lag(cumprod(px), default = 1),
      dx = lx - lead(lx, default = 0),
      Lx = n * lead(lx, default = 0) + (ax* dx),
      Tx = rev(cumsum(rev(Lx))),
      ex = Tx / lx
      )

head(lt_2015)
```

```
## # A tibble: 6 x 13
##    year age       x     n      Mx     ax      qx    px    lx      dx    Lx    Tx
##   <dbl> <chr> <dbl> <dbl>   <dbl>  <dbl>   <dbl> <dbl> <dbl>   <dbl> <dbl> <dbl>
## 1  2015 0         0     1 4.21e-3 0.0772 4.19e-3 0.996 1     4.19e-3 0.996  82.7
## 2  2015 1-4       1     4 1.35e-4 1.5    5.40e-4 0.999 0.996 5.38e-4 3.98   81.7
## 3  2015 5-9       5     5 6.70e-5 2.5    3.35e-4 1.00  0.995 3.33e-4 4.98   77.7
## 4  2015 10-14    10     5 8.40e-5 2.5    4.20e-4 1.00  0.995 4.18e-4 4.97   72.8
## 5  2015 15-19    15     5 2.21e-4 2.5    1.10e-3 0.999 0.995 1.10e-3 4.97   67.8
## 6  2015 20-24    20     5 3.42e-4 2.5    1.71e-3 0.998 0.993 1.70e-3 4.96   62.8
## # i 1 more variable: ex <dbl>
```

We can extend this to calculate life tables for every year using the `group_by` function

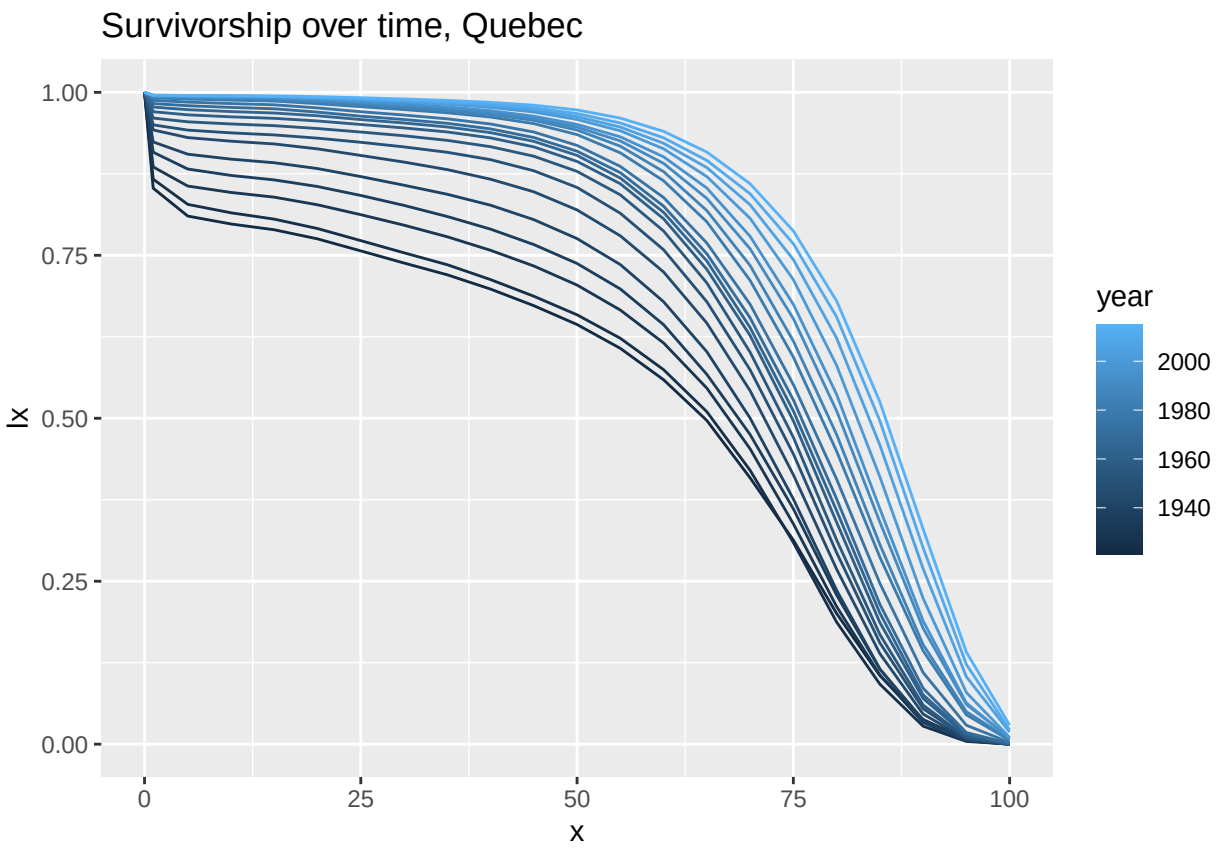
```
lt_all_years <- d |>
  group_by(year) |>
  mutate(
       ax = case_when(
       x==0 ~ 0.07 + 1.7*Mx,
       x==1 ~ 1.5,
       x==110 ~ 1/Mx,
       TRUE ~ 2.5
     ),
      qx = n * Mx / (1 + (n - ax)* Mx),
      px = 1 - qx,
      lx = lag(cumprod(px), default = 1),
      dx = lx - lead(lx, default = 0),
      Lx = n * lead(lx, default = 0) + (ax* dx),
      Tx = rev(cumsum(rev(Lx))),
      ex = Tx / lx
      )

head(lt_all_years)
```

```
## # A tibble: 6 x 13
## # Groups:   year [1]
##    year age       x     n      Mx    ax     qx    px    lx      dx    Lx    Tx
##   <dbl> <chr> <dbl> <dbl>   <dbl> <dbl>  <dbl> <dbl> <dbl>   <dbl> <dbl> <dbl>
## 1  1921 0         0     1 0.163   0.347 0.147  0.853 1     0.147   0.904  52.9
## 2  1921 1-4       1     4 0.0129  1.5   0.0501 0.950 0.853 0.0428  3.30   52.0
## 3  1921 5-9       5     5 0.00302 2.5   0.0150 0.985 0.810 0.0121  4.02   48.7
## 4  1921 10-14    10     5 0.00224 2.5   0.0111 0.989 0.798 0.00889 3.97   44.6
## 5  1921 15-19    15     5 0.00357 2.5   0.0177 0.982 0.789 0.0140  3.91   40.7
## 6  1921 20-24    20     5 0.00481 2.5   0.0238 0.976 0.775 0.0184  3.83   36.8
## # i 1 more variable: ex <dbl>
```

Let's plot the l_x curve over time; notice as mortality improves, the drop in l_x after the first year of life becomes less noticeable, and the curve becomes more 'rectangular'[2]

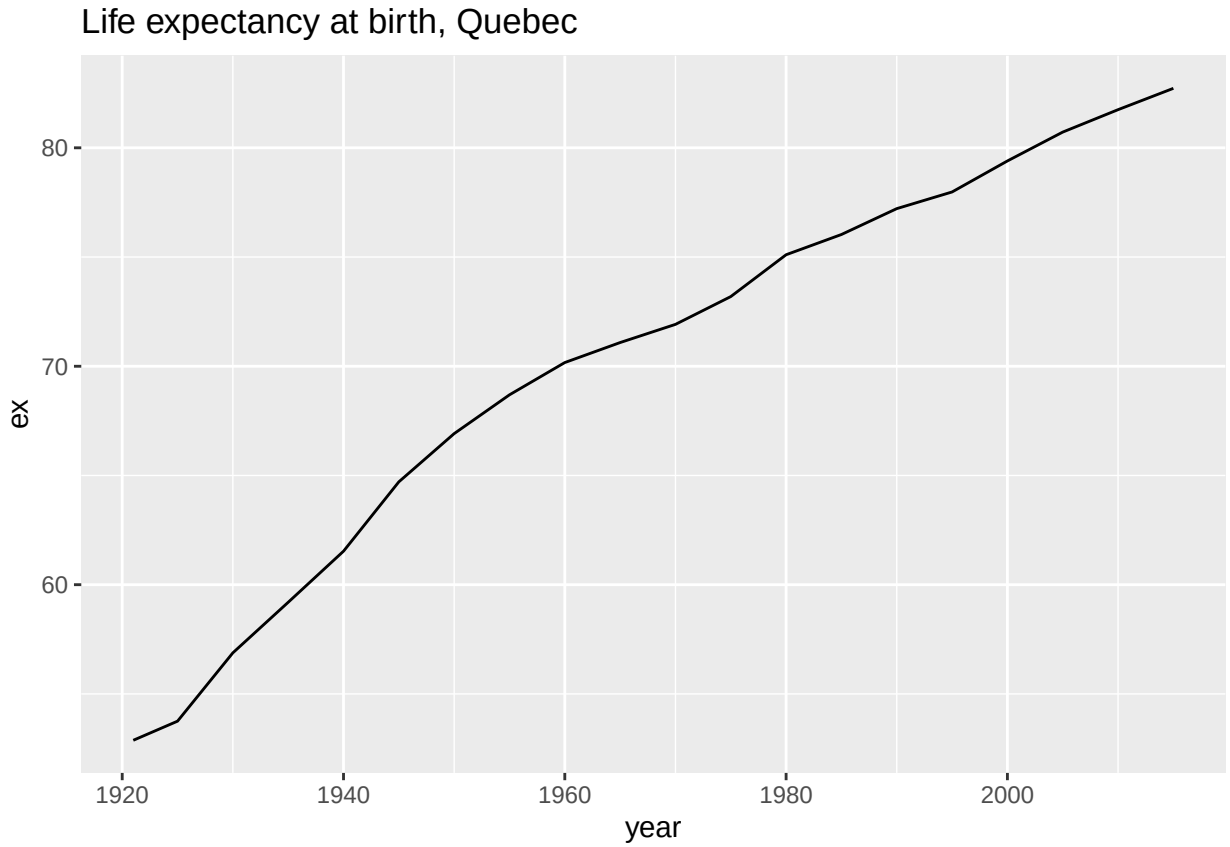
```
lt_all_years |>
  ggplot(aes(x, lx, color = year, group = year)) +
  geom_line()+
  ggtitle("Survivorship over time, Quebec")
```

[2]Indeed, this phenomenon is called 'the rectangularization of the survival curve' and is related to the study of 'compression' of mortality, meaning that deaths become more concentration at older ages. See for example Wilmoth and Horiuchi.



We can also plot life expectancy at birth over time:

```
lt_all_years |>
  filter(x==0) |>
  ggplot(aes(year, ex)) +
  geom_line() +
  ggtitle("Life expectancy at birth, Quebec")
```


Life expectancy at birth, Quebec
80
70
60
ex
1920
1940
1960
1980
2000
year