# **Examples and Exercises from Think Stats, 2nd Edition**

http://thinkstats2.com (http://thinkstats2.com)

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# Survival analysis

If we have an unbiased sample of complete lifetimes, we can compute the survival function from the CDF and the hazard function from the survival function.

Here's the distribution of pregnancy length in the NSFG dataset.

```
In [2]: import nsfg

preg = nsfg.ReadFemPreg()
complete = preg.query('outcome in [1, 3, 4]').prglngth
cdf = thinkstats2.Cdf(complete, label='cdf')
```

The survival function is just the complementary CDF.

```
In [3]: import survival

def MakeSurvivalFromCdf(cdf, label=''):
    """Makes a survival function based on a CDF.

cdf: Cdf

returns: SurvivalFunction
    """

ts = cdf.xs
    ss = 1 - cdf.ps
    return survival.SurvivalFunction(ts, ss, label)
```

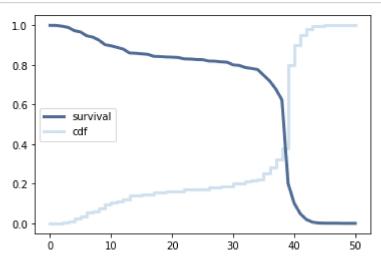
```
In [4]: sf = MakeSurvivalFromCdf(cdf, label='survival')
```

```
In [5]: print(cdf[13])
print(sf[13])
```

- 0.1397801412101171
- 0.8602198587898829

Here's the CDF and SF.

```
In [6]: thinkplot.Plot(sf)
    thinkplot.Cdf(cdf, alpha=0.2)
    thinkplot.Config(loc='center left')
```

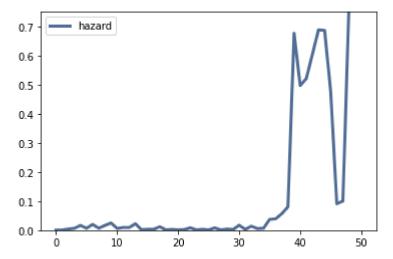


And here's the hazard function.

```
In [7]: hf = sf.MakeHazardFunction(label='hazard')
print(hf[39])
```

0.6767068273092369

```
In [8]: thinkplot.Plot(hf)
thinkplot.Config(ylim=[0, 0.75], loc='upper left')
```



# Age at first marriage

We'll use the NSFG respondent file to estimate the hazard function and survival function for age at first marriage.

```
In [9]: resp6 = nsfg.ReadFemResp()
```

We have to clean up a few variables.

```
In [10]: resp6.cmmarrhx.replace([9997, 9998, 9999], np.nan, inplace=True)
    resp6['agemarry'] = (resp6.cmmarrhx - resp6.cmbirth) / 12.0
    resp6['age'] = (resp6.cmintvw - resp6.cmbirth) / 12.0
```

And the extract the age at first marriage for people who are married, and the age at time of interview for people who are not.

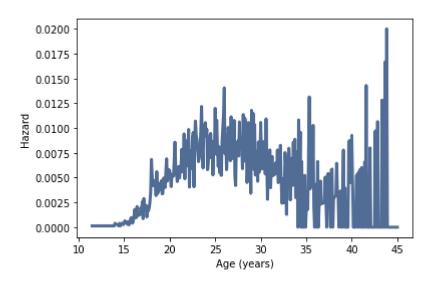
```
In [11]: complete = resp6[resp6.evrmarry==1].agemarry.dropna()
    ongoing = resp6[resp6.evrmarry==0].age
```

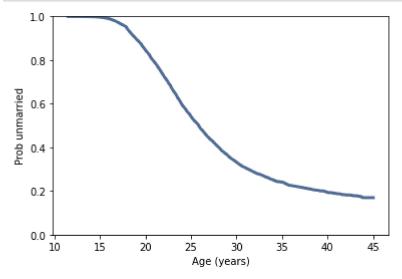
The following function uses Kaplan-Meier to estimate the hazard function.

```
In [12]: from collections import Counter
         def EstimateHazardFunction(complete, ongoing, label='', verbose=False):
             """Estimates the hazard function by Kaplan-Meier.
             http://en.wikipedia.org/wiki/Kaplan%E2%80%93Meier_estimator
             complete: list of complete lifetimes
             ongoing: list of ongoing lifetimes
             label: string
             verbose: whether to display intermediate results
             if np.sum(np.isnan(complete)):
                 raise ValueError("complete contains NaNs")
             if np.sum(np.isnan(ongoing)):
                 raise ValueError("ongoing contains NaNs")
             hist_complete = Counter(complete)
             hist_ongoing = Counter(ongoing)
             ts = list(hist_complete | hist_ongoing)
             ts.sort()
             at_risk = len(complete) + len(ongoing)
             lams = pd.Series(index=ts)
             for t in ts:
                 ended = hist_complete[t]
                 censored = hist_ongoing[t]
                 lams[t] = ended / at risk
                 if verbose:
                     print(t, at risk, ended, censored, lams[t])
                 at risk -= ended + censored
             return survival.HazardFunction(lams, label=label)
```

Here is the hazard function and corresponding survival function.

C:\Users\qvant\AppData\Local\Temp/ipykernel\_24864/1298931125.py:26: Deprecation
Warning: The default dtype for empty Series will be 'object' instead of 'float6
4' in a future version. Specify a dtype explicitly to silence this warning.
lams = pd.Series(index=ts)





### **Quantifying uncertainty**

To see how much the results depend on random sampling, we'll use a resampling process again.

```
In [16]: def EstimateMarriageSurvival(resp):
    """Estimates the survival curve.

    resp: DataFrame of respondents

    returns: pair of HazardFunction, SurvivalFunction
    """

    complete = resp[resp.evrmarry == 1].agemarry.dropna()
    ongoing = resp[resp.evrmarry == 0].age

    hf = EstimateHazardFunction(complete, ongoing)
    sf = hf.MakeSurvival()

    return hf, sf
```

```
In [17]: def ResampleSurvival(resp, iters=101):
    """Resamples respondents and estimates the survival function.

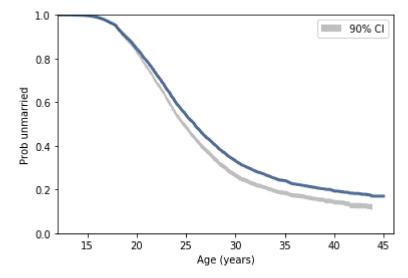
    resp: DataFrame of respondents
    iters: number of resamples
    """
    _, sf = EstimateMarriageSurvival(resp)
    thinkplot.Plot(sf)

    low, high = resp.agemarry.min(), resp.agemarry.max()
    ts = np.arange(low, high, 1/12.0)

    ss_seq = []
    for _ in range(iters):
        sample = thinkstats2.ResampleRowsWeighted(resp)
        _, sf = EstimateMarriageSurvival(sample)
        ss_seq.append(sf.Probs(ts))

    low, high = thinkstats2.PercentileRows(ss_seq, [5, 95])
    thinkplot.FillBetween(ts, low, high, color='gray', label='90% CI')
```

The following plot shows the survival function based on the raw data and a 90% CI based on resampling.



The SF based on the raw data falls outside the 90% CI because the CI is based on weighted resampling, and the raw data is not. You can confirm that by replacing ResampleRowsWeighted with ResampleRows in ResampleSurvival.

#### More data

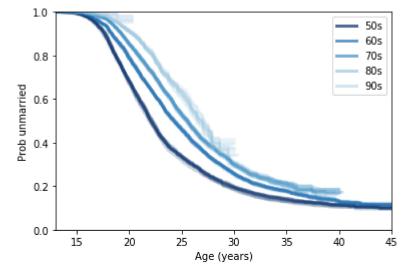
To generate survivial curves for each birth cohort, we need more data, which we can get by combining data from several NSFG cycles.

```
In [18]: resp5 = survival.ReadFemResp1995()
    resp6 = survival.ReadFemResp2002()
    resp7 = survival.ReadFemResp2010()
In [19]: resps = [resp5, resp6, resp7]
```

The following is the code from survival.py that generates SFs broken down by decade of birth.

```
In [20]: def AddLabelsByDecade(groups, **options):
             """Draws fake points in order to add labels to the legend.
             groups: GroupBy object
             thinkplot.PrePlot(len(groups))
             for name, _ in groups:
                 label = '%d0s' % name
                 thinkplot.Plot([15], [1], label=label, **options)
         def EstimateMarriageSurvivalByDecade(groups, **options):
             """Groups respondents by decade and plots survival curves.
             groups: GroupBy object
             thinkplot.PrePlot(len(groups))
             for , group in groups:
                 _, sf = EstimateMarriageSurvival(group)
                 thinkplot.Plot(sf, **options)
         def PlotResampledByDecade(resps, iters=11, predict_flag=False, omit=None):
             """Plots survival curves for resampled data.
             resps: list of DataFrames
             iters: number of resamples to plot
             predict flag: whether to also plot predictions
             for i in range(iters):
                 samples = [thinkstats2.ResampleRowsWeighted(resp)
                            for resp in resps]
                 sample = pd.concat(samples, ignore_index=True)
                 groups = sample.groupby('decade')
                 if omit:
                     groups = [(name, group) for name, group in groups
                                if name not in omit]
                 # TODO: refactor this to collect resampled estimates and
                 # plot shaded areas
                 if i == 0:
                     AddLabelsByDecade(groups, alpha=0.7)
                 if predict flag:
                     PlotPredictionsByDecade(groups, alpha=0.1)
                     EstimateMarriageSurvivalByDecade(groups, alpha=0.1)
                 else:
                     EstimateMarriageSurvivalByDecade(groups, alpha=0.2)
```

Here are the results for the combined data.



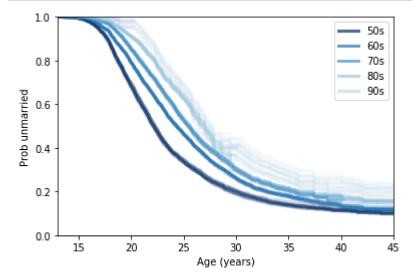
We can generate predictions by assuming that the hazard function of each generation will be the same as for the previous generation.

```
In [22]: def PlotPredictionsByDecade(groups, **options):
    """Groups respondents by decade and plots survival curves.

    groups: GroupBy object
    """
    hfs = []
    for _, group in groups:
        hf, sf = EstimateMarriageSurvival(group)
        hfs.append(hf)

    thinkplot.PrePlot(len(hfs))
    for i, hf in enumerate(hfs):
        if i > 0:
              hf.Extend(hfs[i-1])
        sf = hf.MakeSurvival()
              thinkplot.Plot(sf, **options)
```

And here's what that looks like.



## **Remaining lifetime**

Distributions with difference shapes yield different behavior for remaining lifetime as a function of age.

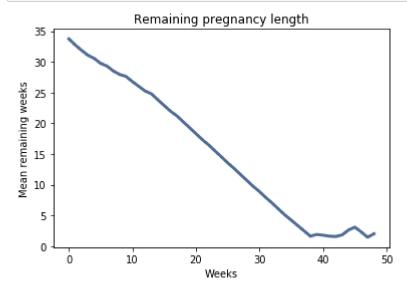
```
In [24]: preg = nsfg.ReadFemPreg()

complete = preg.query('outcome in [1, 3, 4]').prglngth
    print('Number of complete pregnancies', len(complete))
    ongoing = preg[preg.outcome == 6].prglngth
    print('Number of ongoing pregnancies', len(ongoing))

hf = EstimateHazardFunction(complete, ongoing)
    sf1 = hf.MakeSurvival()
```

Number of complete pregnancies 11189 Number of ongoing pregnancies 352

Here's the expected remaining duration of a pregnancy as a function of the number of weeks elapsed. After week 36, the process becomes "memoryless".



And here's the median remaining time until first marriage as a function of age.

```
In [26]: hf, sf2 = EstimateMarriageSurvival(resp6)
```



#### **Exercises**

**Exercise:** In NSFG Cycles 6 and 7, the variable cmdivorcx contains the date of divorce for the respondent's first marriage, if applicable, encoded in century-months.

Compute the duration of marriages that have ended in divorce, and the duration, so far, of marriages that are ongoing. Estimate the hazard and survival curve for the duration of marriage.

Use resampling to take into account sampling weights, and plot data from several resamples to visualize sampling error.

Consider dividing the respondents into groups by decade of birth, and possibly by age at first marriage.

```
In [33]: def CleanData(resp):
             """Cleans respondent data.
             resp: DataFrame
             resp.cmdivorcx.replace([9998, 9999], np.nan, inplace=True)
             resp['notdivorced'] = resp.cmdivorcx.isnull().astype(int)
             resp['duration'] = (resp.cmdivorcx - resp.cmmarrhx) / 12.0
             resp['durationsofar'] = (resp.cmintvw - resp.cmmarrhx) / 12.0
             month0 = pd.to_datetime('1899-12-15')
             dates = [month0 + pd.DateOffset(months=cm)
                      for cm in resp.cmbirth]
             resp['decade'] = (pd.DatetimeIndex(dates).year - 1900) // 10
In [34]: CleanData(resp6)
         married6 = resp6[resp6.evrmarry==1]
         CleanData(resp7)
         married7 = resp7[resp7.evrmarry==1]
In [35]: def CleanData(resp):
             """Cleans respondent data.
             resp: DataFrame
             resp.cmdivorcx.replace([9998, 9999], np.nan, inplace=True)
             resp['notdivorced'] = resp.cmdivorcx.isnull().astype(int)
             resp['duration'] = (resp.cmdivorcx - resp.cmmarrhx) / 12.0
             resp['durationsofar'] = (resp.cmintvw - resp.cmmarrhx) / 12.0
             month0 = pd.to datetime('1899-12-15')
             dates = [month0 + pd.DateOffset(months=cm)
                      for cm in resp.cmbirth]
             resp['decade'] = (pd.DatetimeIndex(dates).year - 1900) // 10
In [36]: CleanData(resp6)
         married6 = resp6[resp6.evrmarry==1]
```

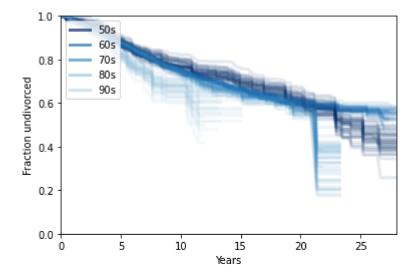
married7 = resp7[resp7.evrmarry==1]

CleanData(resp7)

```
In [37]: ## Divorce Cruve vs sample data
         def ResampleDivorceCurve(resps):
             for in range(11):
                 samples = [thinkstats2.ResampleRowsWeighted(resp)
                            for resp in resps]
                 sample = pd.concat(samples, ignore index=True)
                 PlotDivorceCurveByDecade(sample, color='#225EA8', alpha=0.1)
             thinkplot.Show(xlabel='years',
                            axis=[0, 28, 0, 1])
In [38]: ## Divoice Curve vs Birth Cohort
         def ResampleDivorceCurveByDecade(resps):
             for i in range(41):
                 samples = [thinkstats2.ResampleRowsWeighted(resp)
                            for resp in resps]
                 sample = pd.concat(samples, ignore_index=True)
                 groups = sample.groupby('decade')
                 if i == 0:
                     survival.AddLabelsByDecade(groups, alpha=0.7)
                 EstimateSurvivalByDecade(groups, alpha=0.1)
             thinkplot.Config(xlabel='Years',
                              ylabel='Fraction undivorced',
                              axis=[0, 28, 0, 1])
In [39]: ## Estimates survival by decade
         def EstimateSurvivalByDecade(groups, **options):
             thinkplot.PrePlot(len(groups))
             for name, group in groups:
                 _, sf = EstimateSurvival(group)
                 thinkplot.Plot(sf, **options)
In [40]: ## Estimates survival code
         def EstimateSurvival(resp):
             complete = resp[resp.notdivorced == 0].duration.dropna()
             ongoing = resp[resp.notdivorced == 1].durationsofar.dropna()
             hf = survival.EstimateHazardFunction(complete, ongoing)
             sf = hf.MakeSurvival()
```

return hf, sf

In [41]: ResampleDivorceCurveByDecade([married6, married7])



In [ ]:
---------