The Survival Function $S(t)$ and Hazard Function $h(t)$

- In survival analysis, the outcome is either the survival proportion or the event rate (the proportion who do not experience the event)

$$h(t) = f'(x) / f(x) = -\frac{d}{dt} \ln S(t) = \frac{f(t)}{S(t)}$$

- Which indicates that the event rate is proportional to the rate at which the survival function decreases

- Strictly, the hazard is the rate of change of $\ln S(t)$ but we can think of it as being proportional to the rate of change of $S(t)$
Prognosis of Cancer Patients

- Total mortality (among the patients)
- Net mortality (mortality associated with a diagnosis of cancer)
- Cause-specific mortality (an estimate of net mortality under certain assumptions)
- When estimating cause-specific mortality, only those deaths which can be attributed to the cancer in question are considered to be events
Cause-specific mortality

- Cause-specific mortality = number of death due to cancer/person-time at risk
- The survival times of patients who die of causes other than cancer are censored
- Need reliably coded information on cause of death
- Even when cause of death information is available to the cancer registry via death certificates, it is often vague and difficult to determine whether or not cancer is the primary cause of death
How do we classify, for example, death due to treatment complications?

Consider a patient treated with radiation therapy and chemotherapy, who dies of cardiovascular disease. Do we classify this death as “due entirely to cancer” or “due entirely to other causes”?

Some of the researcher developed an improved cause-of-death indicator.
Relative Survival

- Instead of cause-specific mortality, we can estimate excess mortality: the difference between observed (all-cause) and expected mortality
  - Excess mortality = Observed mortality – Expected mortality
Relative survival is the survival analog of excess mortality – the relative survival ratio is defined as the observed survival in the patient group divided by the expected survival of a comparable group from the general population.

- Relative survival ratio = observed survival proportion/expected survival proportion
It is usual to estimate the expected survival proportion from nationwide (or state/province wide) population life tables stratified by age, sex, calendar time, and where applicable, race.

Several different methods exist for estimating expected survival, the most commonly used: Ederer I, Ederer II, and Hakulinen.
Advantages

- Information on cause of death is not required
- Obtain a measure of the excess mortality experienced by patients diagnosed with cancer, irrespective of whether the excess mortality is directly or indirectly attributable to the cancer
- Deaths due to treatment complications or suicide are examples of deaths which may be considered indirectly attributable to cancer
Estimating Relative Survival

- The relative survival ratio (RSR) is estimating using life table methods.
- The cumulative RSR is estimate at discrete points in the follow-up by taking the product of interval-specific estimates over sub-intervals of the follow-up.
- Sample data set containing information on colon carcinoma diagnosed in Finland.
In general, two data files are required to estimate relative survival;

- A file contain individual level data on the patient (colon)
- A file contain expected probabilities of death for a comparable general population (popmort)
- Running the SAS code in survival.sas will produce the life table estimates of relative survival stratified by sex, age, and calendar period of diagnosis
Cont..

- In addition, two output data sets are created;
  - One contains grouped data
  - One contains individual patient data
- These two files are used for input data sets for modeling
- The SAS code in models.sas estimates a relative survival regression model using several different approaches (Described in Dickman et al.)
Overview in SAS

- Split the observation time
- To split the data, use the SAS macro ‘lexis’ (written by Bendix Carstensen)
- The general approach is as follows:
  - Use the lexis macro to split the observation time
  - Ensure each record has the correct value for attained age and attained calendar period
  - Merge from an external file (the so-called ‘popmort’ file), expected probabilities of surviving the interval
The general approach (Cont...)

- For each observation, create indicator variables for death and censoring
- Create life tables for each desired combination of covariates by collapsing over relevant records
- For each life table interval, calculate interval-specific and cumulative observed, expected, and relative survival with corresponding standard errors and confidence intervals
- Print the life table (using Proc Print)
Models for Relative Survival

- Models for relative survival can be estimated based on either individual (subject-specific) or grouped/collapsed (i.e. life table) data
- A copy of data is saved before collapsing (the default data set name is individ) and after collapsing (the default data set name is grouped)
The patient data file (colon)

- A file containing information on individuals diagnosed with cancer is required and must contain, at a minimum, the following information:
  - Survival time (time at risk)
  - Indicator for vital status (dead/alive)
  - Variables upon which expected survival depends – typically age, sex, and period.
# Alphabetic List of Variables and Attributes

<table>
<thead>
<tr>
<th>#</th>
<th>Variable</th>
<th>Type</th>
<th>Len</th>
<th>Format</th>
<th>Label</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>AGE</td>
<td>Num</td>
<td>4</td>
<td></td>
<td>Age at diagnosis</td>
</tr>
<tr>
<td>11</td>
<td>DX</td>
<td>Num</td>
<td>8</td>
<td>DATE.</td>
<td>Date of diagnosis</td>
</tr>
<tr>
<td>12</td>
<td>EXIT</td>
<td>Num</td>
<td>8</td>
<td>DATE.</td>
<td>Date of exit</td>
</tr>
<tr>
<td>4</td>
<td>MMDX</td>
<td>Num</td>
<td>4</td>
<td></td>
<td>Month of diagnosis</td>
</tr>
<tr>
<td>1</td>
<td>SEX</td>
<td>Num</td>
<td>4</td>
<td>SEX.</td>
<td>Sex</td>
</tr>
<tr>
<td>3</td>
<td>STAGE</td>
<td>Num</td>
<td>4</td>
<td>STAGE.</td>
<td>Clinical stage at diagnosis</td>
</tr>
<tr>
<td>8</td>
<td>STATUS</td>
<td>Num</td>
<td>4</td>
<td>STATUS.</td>
<td>Vital status at last date of contact</td>
</tr>
<tr>
<td>9</td>
<td>SUBSITE</td>
<td>Num</td>
<td>4</td>
<td>COLONSUB.</td>
<td>Anatomical subsite of tumour</td>
</tr>
<tr>
<td>6</td>
<td>SURV_MM</td>
<td>Num</td>
<td>4</td>
<td></td>
<td>Survival time in completed months</td>
</tr>
<tr>
<td>7</td>
<td>SURV_YY</td>
<td>Num</td>
<td>4</td>
<td></td>
<td>Survival time in completed years</td>
</tr>
<tr>
<td>10</td>
<td>YEAR8594</td>
<td>Num</td>
<td>4</td>
<td></td>
<td>Indicator for year of dx 1985-94</td>
</tr>
<tr>
<td>5</td>
<td>YYDX</td>
<td>Num</td>
<td>4</td>
<td></td>
<td>Year of diagnosis</td>
</tr>
</tbody>
</table>
The population mortality file (popmort)

- Contains expected survival probabilities (PROB) for the Finnish general population stratified by age, calendar year, and sex for the years 1951 to 2000
- Calculated by the central statistical office (Statistics Finland)
# Popmort Data

<table>
<thead>
<tr>
<th>Ob</th>
<th>SEX</th>
<th>YEAR</th>
<th>AGE</th>
<th>PROB</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1</td>
<td>1951</td>
<td>0</td>
<td>0.96429</td>
</tr>
<tr>
<td>2</td>
<td>1</td>
<td>1951</td>
<td>1</td>
<td>0.99639</td>
</tr>
<tr>
<td>3</td>
<td>1</td>
<td>1951</td>
<td>2</td>
<td>0.99783</td>
</tr>
<tr>
<td>4</td>
<td>1</td>
<td>1951</td>
<td>3</td>
<td>0.99842</td>
</tr>
<tr>
<td>5</td>
<td>1</td>
<td>1951</td>
<td>4</td>
<td>0.99882</td>
</tr>
<tr>
<td>6</td>
<td>1</td>
<td>1951</td>
<td>5</td>
<td>0.99893</td>
</tr>
<tr>
<td>7</td>
<td>1</td>
<td>1951</td>
<td>6</td>
<td>0.99913</td>
</tr>
<tr>
<td>8</td>
<td>1</td>
<td>1951</td>
<td>7</td>
<td>0.99905</td>
</tr>
<tr>
<td>9</td>
<td>1</td>
<td>1951</td>
<td>8</td>
<td>0.99920</td>
</tr>
<tr>
<td>10</td>
<td>1</td>
<td>1951</td>
<td>9</td>
<td>0.99931</td>
</tr>
</tbody>
</table>
SAS Code

- The approach is implemented as SAS code, rather than as a SAS macro, in order to make it more transparent and easier to customize.
- The main parameters are, however, defined as macro variables at the top of the file: Two input data files and two output data files –
SAS Code: Cont...

- title; footnote;
- title1 'Colon carcinoma diagnosed in Finland 1975-1994 (follow-up to 1995)';

- libname colon 'H:\rsmodel';

- options fmtsearch=(colon work library)
  orientation=landscape pageno=1;
SAS Code: Cont...

- Define the input and output files.
- `%let popmort=colon.popmort ;`
- `%let patdata=colon.colon ;`
- `%let individ=colon.individ ;`
- `%let grouped=colon.grouped ;`
The macro variable “vars” stores the variables over which the life tables are stratified:

```sas
%let vars = sex yydx age;
%let formats = sex sex. age age. yydx yydx. ;
```

The lifetable may be estimated for each combination of sex, yydx (year of diagnosis), and age.

If, for example, the variable age contains age at diagnosis in years then categories can be constructed using a format.

Formats can be used to group metric variables into categories.
The next step is a data step where housekeeping on the patient data file is performed:

```sas
data &individ;
length id 5;
set &patdata;
```

Restrict to localized stage: local, distant, regional, unknown:

```sas
if stage=1;
```

Create a unique ID for each individual:

```sas
id+1;
```
SAS Code: Cont...

- The variable SURV_MM contains survival time in completed months.
- We will add 0.5 to all survival times, both to avoid problems with individuals with time=0 (who are theoretically never at risk and may be excluded from some analyses) and because this provides a more accurate estimate of person-time at risk (for Poisson regression analyses).

\[
\text{surv\_mm} = \text{surv\_mm} + 0.5;
\]
The lexis macro requires a variable containing the time at entry:
   entry=0;

Create an indicator variable for death due to any cause (Dead: Cancer, other) -
   if status in (1,2) then d=1;
   else d=0;
   drop stage subsite status;
   label id='Unique subject ID';
run;
Portion of the outputs:

<table>
<thead>
<tr>
<th>id</th>
<th>SEX</th>
<th>AGE</th>
<th>YYDX</th>
<th>SURV_MM</th>
<th>d</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Female</td>
<td>78</td>
<td>78</td>
<td>82.5</td>
<td>1</td>
</tr>
<tr>
<td>2</td>
<td>Male</td>
<td>80</td>
<td>80</td>
<td>8.5</td>
<td>1</td>
</tr>
<tr>
<td>3</td>
<td>Female</td>
<td>75</td>
<td>75</td>
<td>23.5</td>
<td>1</td>
</tr>
<tr>
<td>4</td>
<td>Male</td>
<td>77</td>
<td>77</td>
<td>85.5</td>
<td>1</td>
</tr>
<tr>
<td>5</td>
<td>Female</td>
<td>76</td>
<td>76</td>
<td>32.5</td>
<td>1</td>
</tr>
</tbody>
</table>
SAS Code: Cont...

- Splitting the time at risk using the lexis macro
  - Use the lexis macro to split the observation time for each individual into multiple observations, one for each band to follow-up (1-year interval, maximum 10-year for this example).

    %include 'H:\~\lexis.sas';

- Split the data to obtain one observation for each life table interval for each individual. The scale must be transformed to years.

    %lexis (data=&individ., out=&individ., breaks = %str(0 to 10 by 1), origin = 0, entry = entry, exit = surv_mm, fail = d, scale = 12, right = right, risk = y, lrisk = ln_y, lint = length, cint = w, nint = fu) ;
SAS Code: Cont..

In the previous code, instead of using the information on survival time in the variable `surv_mm` we may, alternatively, specify the date of diagnosis and exit:

```sas
%lexis (data=&individ., out=&individ., breaks = %str( 0 to 10 by 1 ),
origin = dx, entry = dx, exit = exit, fail = d, scale = 365.25,
right = right, risk = y, lrisk = ln_y, lint = length, cint = w, nint = fu );
```
Create variables for attained age and calendar year which are 'updated' for each observation for a single individual. These are the variables by which we will merge in the expected probabilities of death, so they must have the same names and same format as the variables indexing the POPMORT file (sex, _age, _year in this example).

```sas
data &individ;
 set &individ;
   _age=floor(age+left);
   _year=floor(1900+yydx+left);
run;
```

A variable to label the life table output

```sas
range=put(left,4.1) || ' - ' ||left(put(right,4.1));
drop entry left right;
run;
```
The output:

<table>
<thead>
<tr>
<th>id</th>
<th>SEX</th>
<th>AGE</th>
<th>_age</th>
<th>YYDX</th>
<th>_year</th>
<th>d</th>
<th>w</th>
<th>fu</th>
<th>y</th>
<th>length</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Female</td>
<td>78</td>
<td>78</td>
<td>78</td>
<td>1978</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>1</td>
<td>Female</td>
<td>78</td>
<td>79</td>
<td>78</td>
<td>1979</td>
<td>0</td>
<td>0</td>
<td>2</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>1</td>
<td>Female</td>
<td>78</td>
<td>80</td>
<td>78</td>
<td>1980</td>
<td>0</td>
<td>0</td>
<td>3</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>1</td>
<td>Female</td>
<td>78</td>
<td>81</td>
<td>78</td>
<td>1981</td>
<td>0</td>
<td>0</td>
<td>4</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>1</td>
<td>Female</td>
<td>78</td>
<td>82</td>
<td>78</td>
<td>1982</td>
<td>0</td>
<td>0</td>
<td>5</td>
<td>1</td>
<td>1</td>
</tr>
</tbody>
</table>
Now merge in the expected probabilities of death.
proc sort data=&individ;
  by sex _year _age;
run;
proc sort data=&popmort;
  by sex _year _age;
run;
data &individ;
    length d w fu 4 y ln_y length 5;
merge &individ(in=a) &popmort(in=b);
by sex _year _age;
if a;
• /* Need to adjust for interval lengths other than 1 year */
  p_star=prob**length;
• /* Expected number of deaths */
  d_star=-log(p_star)*(y/length);
keep &vars fu range length d w p_star y ln_y d_star;
SAS Code: Cont...

label
d_star='Expected number of deaths'
d='Indicator for death during interval'
w='Indicator for censored during interval'
y='Person-time (years) at risk during the interval'
length='Interval length (potential not actual)'
ln_y='ln(person-time at risk)'
p_star='Expected survival probability'
_age='Attained age'
_year='Attained calendar year'
range='Life table interval'
fu='Follow-up interval'
sex='Sex';

run;
SAS Code: Cont...

- After merging in the expected probabilities of surviving (p_star), we have the following:

<table>
<thead>
<tr>
<th>id</th>
<th>SEX</th>
<th>AGE</th>
<th>_age</th>
<th>YYDX</th>
<th>_year</th>
<th>d</th>
<th>w</th>
<th>fu</th>
<th>y</th>
<th>length</th>
<th>p_star</th>
</tr>
</thead>
<tbody>
<tr>
<td>1331</td>
<td>Male</td>
<td>22</td>
<td>22</td>
<td>75</td>
<td>1975</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>0.99836</td>
</tr>
<tr>
<td>1318</td>
<td>Male</td>
<td>27</td>
<td>27</td>
<td>75</td>
<td>1975</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>0.99830</td>
</tr>
<tr>
<td>1321</td>
<td>Male</td>
<td>27</td>
<td>27</td>
<td>75</td>
<td>1975</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>0.99830</td>
</tr>
<tr>
<td>1277</td>
<td>Male</td>
<td>36</td>
<td>36</td>
<td>75</td>
<td>1975</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>0.99700</td>
</tr>
<tr>
<td>1278</td>
<td>Male</td>
<td>36</td>
<td>36</td>
<td>75</td>
<td>1975</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>0.99700</td>
</tr>
</tbody>
</table>
Collapse the data to produce the life table:

```sas
proc summary data=&individ nway;
   var d w p_star y d_star;
   id range length;
   class &vars fu;
   /* Follow-up must be the last variable in this list */
   output out=&grouped(drop=_type_
      rename=( _freq_=l))
   sum(d w y d_star)=d w y d_star
   mean(p_star)=p_star;
   format &formats ;
run;
```
SAS Code: Cont...

Output from the group data:

<table>
<thead>
<tr>
<th>SEX</th>
<th>YYDX</th>
<th>AGE</th>
<th>fu</th>
<th>range</th>
<th>length</th>
<th>l</th>
<th>d</th>
<th>w</th>
<th>y</th>
<th>d_star</th>
<th>p_star</th>
</tr>
</thead>
<tbody>
<tr>
<td>M</td>
<td>1975-84</td>
<td>0-44</td>
<td>1</td>
<td>0.0</td>
<td>-1.0</td>
<td>1</td>
<td>75</td>
<td>4</td>
<td>0</td>
<td>73.42</td>
<td>0.22</td>
</tr>
<tr>
<td>M</td>
<td>1975-84</td>
<td>0-44</td>
<td>2</td>
<td>1.0</td>
<td>-2.0</td>
<td>1</td>
<td>71</td>
<td>8</td>
<td>0</td>
<td>66.33</td>
<td>0.21</td>
</tr>
<tr>
<td>M</td>
<td>1975-84</td>
<td>0-44</td>
<td>3</td>
<td>2.0</td>
<td>-3.0</td>
<td>1</td>
<td>63</td>
<td>1</td>
<td>1</td>
<td>62.50</td>
<td>0.22</td>
</tr>
<tr>
<td>M</td>
<td>1975-84</td>
<td>0-44</td>
<td>4</td>
<td>3.0</td>
<td>-4.0</td>
<td>1</td>
<td>61</td>
<td>3</td>
<td>0</td>
<td>59.46</td>
<td>0.22</td>
</tr>
<tr>
<td>M</td>
<td>1975-84</td>
<td>0-44</td>
<td>5</td>
<td>4.0</td>
<td>-5.0</td>
<td>1</td>
<td>58</td>
<td>3</td>
<td>0</td>
<td>56.54</td>
<td>0.23</td>
</tr>
</tbody>
</table>

l: # alive at the start of the interval

d: # of deaths during the interval

w: # of patients whose survival time was censored during the interval

p_star: Expected survival proportion for the interval

d_star: Expected number of deaths
Calculate the interval-specific observed and expected relative survival and then estimate cumulative survival:

data &grouped;
  retain cp cp_star cr 1;
  set &grouped;
  if fu=1 then do;
    cp=1; cp_star=1; cr=1; se_temp=0;
  end;
  l_prime=l-w/2;
  ns=l_prime-d;
/* Two alternative approaches to estimating interval-specific survival */
/* Must use the hazard approach for period analysis */
p=exp(-(d/y)*length); /* transforming the hazard */
p=1-d/l_prime; /* actuarial approach */
r=p/p_star;
cp=cp*p;
cp_star=cp_star*p_star;
cr=cp/cp_star;
ln_y_group=log(l_prime-d/2);
ln_y=log(y);
d_star_group = l_prime*(1-p_star);
excess = (d-d_star)/y;
se_p = sqrt(p*(1-p)/l_prime);
se_r = se_p/p_star;
se_temp + d/(l_prime*(l_prime-d)); /* Component of the SE of the cumulative survival */
se_cp = cp*sqrt(se_temp);
se_cr = se_cp/cp_star;
/* Calculate confidence intervals on the log-hazard scale and back transform */
/* First for the interval-specific estimates */
if se_p ne 0 then do;
    /* SE on the log-hazard scale using Taylor series approximation */
    se_lh_p=sqrt( se_p**2/(p*log(p))**2 );
    /* Confidence limits on the log-hazard scale */
    lo_lh_p=log(-log(p))+1.96*se_lh_p;
    hi_lh_p=log(-log(p))-1.96*se_lh_p;
SAS Code: Cont.....

- /* Confidence limits on the survival scale (observed survival) */
  lo_p=exp(-exp(lo_lh_p));
  hi_p=exp(-exp(hi_lh_p));

- /* Confidence limits for the corresponding relative survival rate */
  lo_r=lo_p/p_star;
  hi_r=hi_p/p_star;

- /* Drop temporary variables */
  drop se_lh_p lo_lh_p hi_lh_p;
SAS Code: Cont....

- /* Formats and labels */
  format lo_p hi_p lo_r hi_r 8.5;
  label
  lo_p='Lower 95% CI for P'
  hi_p='Upper 95% CI for P'
  lo_r='Lower 95% CI for R'
  hi_r='Upper 95% CI for R'
  ;
  end;
/* Now for the cumulative estimates */
if se_cp ne 0 then do;
/* SE on the log-hazard scale using Taylor series approximation */
   se_lh_cp=sqrt( se_cp**2/(cp*log(cp))**2 );
/* Confidence limits on the log-hazard scale */
   lo_lh_cp=log(-log(cp))+1.96*se_lh_cp;
   hi_lh_cp=log(-log(cp))-1.96*se_lh_cp;
/* Confidence limits on the survival scale (observed survival) */

lo_cp=exp(-exp(lo_lh_cp));
hi_cp=exp(-exp(hi_lh_cp));

/* Confidence limits for the corresponding relative survival rate */

lo_cr=lo_cp/cp_star;
hi_cr=hi_cp/cp_star;
SAS Code: Cont...

- /* Drop temporary variables */
  drop se_lh_cp lo_lh_cp hi_lh_cp;
- /* Formats and labels */
  format lo_cp hi_cp lo_cr hi_cr 8.5;
  label
    lo_cp='Lower 95% CI for CP'
    hi_cp='Upper 95% CI for CP'
    lo_cr='Lower 95% CI for CR'
    hi_cr='Upper 95% CI for CR'
  ;
  end;
  drop se_temp;
SAS Code: Cont...

label

range='Interval'
fu='Interval'
l='Alive at start'
l_prime='Effective number at risk'
ns='Number surviving the interval'
d='Deaths'
w='Withdrawals'
SAS Code: Cont..

p='Interval-specific observed survival'
cp='Cumulative observed survival'
r='Interval-specific relative survival'
cr='Cumulative relative survival'
p_star='Interval-specific expected survival'
cp_star='Cumulative expected survival'
SAS Code: Cont...

\[ \ln_{y\_group} = \ln(l\_prime - d/2) \]
\[ \ln_{y} = \ln(person\_time) \text{ (using exact times)} \]
\[ y = 'Person-time at risk (using exact times)' \]
\[ d\_star = 'Expected deaths (using exact times)' \]
\[ d\_star\_group = 'Expected deaths (approximate)' \]
\[ excess = 'Empirical excess hazard' \]
SAS Code: Cont...

se_p='Standard error of P'
se_r='Standard error of R'
se_cp='Standard error of CP'
se_cr='Standard error of CR'
;
run;
SAS Code: Cont...

- Print the lifetables. We first need to extract the last variable in the varlist to use as the argument in the pageby command.

  \[ \%let lastvar = \%scan(&vars,-1); \]
SAS Code: Print

- proc print data=&grouped noobs label;
  title2 'Life table estimates of patient survival';
  title3 'The Ederer II method is used to estimate expected survival';
  by &vars;
  pageby &lastvar;
  var range l d w l_prime p cp p_star cp_star r cr;
  format fu 3.0 l d w 4.0 l_prime 8.1 p cp p_star cp_star r cr se_p se_r se_cp se_cr 8.5;
  label l='L' d='D' w='W';
  run;
Colon carcinoma diagnosed in Finland 1975-1994 (follow-up to 1995)

Life table estimates of patient

The Ederer II method is used to estimate expected survival

<table>
<thead>
<tr>
<th>Interval</th>
<th>L</th>
<th>D</th>
<th>W</th>
<th>at risk</th>
<th>survival</th>
<th>observed</th>
<th>expected</th>
<th>relative survival</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.0 - 1.0</td>
<td>75</td>
<td>4</td>
<td>0</td>
<td>75.0</td>
<td>0.94667</td>
<td>0.94667</td>
<td>0.99697</td>
<td>0.94954</td>
</tr>
<tr>
<td>1.0 - 2.0</td>
<td>71</td>
<td>8</td>
<td>0</td>
<td>71.0</td>
<td>0.88732</td>
<td>0.84000</td>
<td>0.99381</td>
<td>0.89015</td>
</tr>
<tr>
<td>2.0 - 3.0</td>
<td>63</td>
<td>1</td>
<td>1</td>
<td>62.5</td>
<td>0.98400</td>
<td>0.82656</td>
<td>0.99032</td>
<td>0.98747</td>
</tr>
<tr>
<td>3.0 - 4.0</td>
<td>61</td>
<td>3</td>
<td>0</td>
<td>61.0</td>
<td>0.95082</td>
<td>0.78591</td>
<td>0.98660</td>
<td>0.95440</td>
</tr>
<tr>
<td>4.0 - 5.0</td>
<td>58</td>
<td>3</td>
<td>0</td>
<td>58.0</td>
<td>0.94828</td>
<td>0.74526</td>
<td>0.98266</td>
<td>0.95208</td>
</tr>
<tr>
<td>5.0 - 6.0</td>
<td>55</td>
<td>2</td>
<td>0</td>
<td>55.0</td>
<td>0.96364</td>
<td>0.71816</td>
<td>0.97836</td>
<td>0.96787</td>
</tr>
<tr>
<td>6.0 - 7.0</td>
<td>53</td>
<td>0</td>
<td>0</td>
<td>53.0</td>
<td>1.00000</td>
<td>0.71816</td>
<td>0.97378</td>
<td>1.00470</td>
</tr>
<tr>
<td>7.0 - 8.0</td>
<td>53</td>
<td>0</td>
<td>0</td>
<td>53.0</td>
<td>1.00000</td>
<td>0.71816</td>
<td>0.96882</td>
<td>1.00512</td>
</tr>
<tr>
<td>8.0 - 9.0</td>
<td>53</td>
<td>1</td>
<td>0</td>
<td>53.0</td>
<td>0.98113</td>
<td>0.70461</td>
<td>0.96352</td>
<td>0.98653</td>
</tr>
<tr>
<td>9.0 - 10.0</td>
<td>52</td>
<td>2</td>
<td>0</td>
<td>52.0</td>
<td>0.96154</td>
<td>0.67751</td>
<td>0.95792</td>
<td>0.96717</td>
</tr>
</tbody>
</table>
Acknowledgement

- This presentation has been adapted from the website of Dr. Paul Dickman (www.pauldickman.com)
- Dr. Paul Dickman, Department of Medical Epidemiology and Biostatistics, Karolinska Institutet, Stockholm, Sweden
- Riaz Alvi, Saskatchewan Cancer Agency
- Tong Zhu, Saskatchewan Cancer Agency
- Gopinath Narasimhan, Saskatchewan Cancer Agency
Thank you