

JPSurv - A Tool to Analyze and Estimate Cancer Survival Trends

September 29, 2022

NCI Analytic Tools SEERies

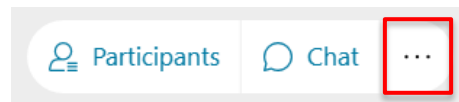
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Using WebEx and Webinar Logistics

The screenshot shows the WebEx interface with two panels highlighted by red boxes. The top panel is labeled 'Participants (1)' and contains a 'Chat' button. Below it is a dropdown menu set to 'All Panelists' and a text input field with the placeholder 'Enter chat message here'. The bottom panel is labeled 'Q & A' and shows 'All (0)' questions. Below the Q & A panel is a text input field with the placeholder 'Select a question and then type your answer here. There's a 512-character limit.' and two buttons: 'Send' and 'Send Privately'.

- All lines will be in listen-only mode
- Submit questions at any time using the **Q&A** or **Chat** Panel and select “All Panelists”
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- During the Live Demo- put your screen layout in “Full Screen” mode for a better viewing experience
- Closed Captioning is available
- This webinar is being recorded

Speakers:



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JPSurv: a web tool to estimate trends in survival

Angela Mariotto, PhD, NCI
Theresa Devasia, PhD, NCI

September 29, 2022

SEER*Stat Tools Webinar Series



Agenda

1. *Part 1: PowerPoint presentation*
 - *Background*
 - *JoinPoint model for Survival: JPSurv*
 - *Non-Hodgkin Lymphoma application*
 - *Measures to summarize survival trend*
 - *Proportionality assumption: Chronic Myeloid Leukemia example*
 - *Discussion/Conclusions*
 - *Q&A*
2. *Part 2: JPSurv demo (Dr. Theresa Devasia)*
3. *Q&A*

Sometimes the simplest questions are the hardest to answer!

NCI Director: Does this represent a significant change in the trend?



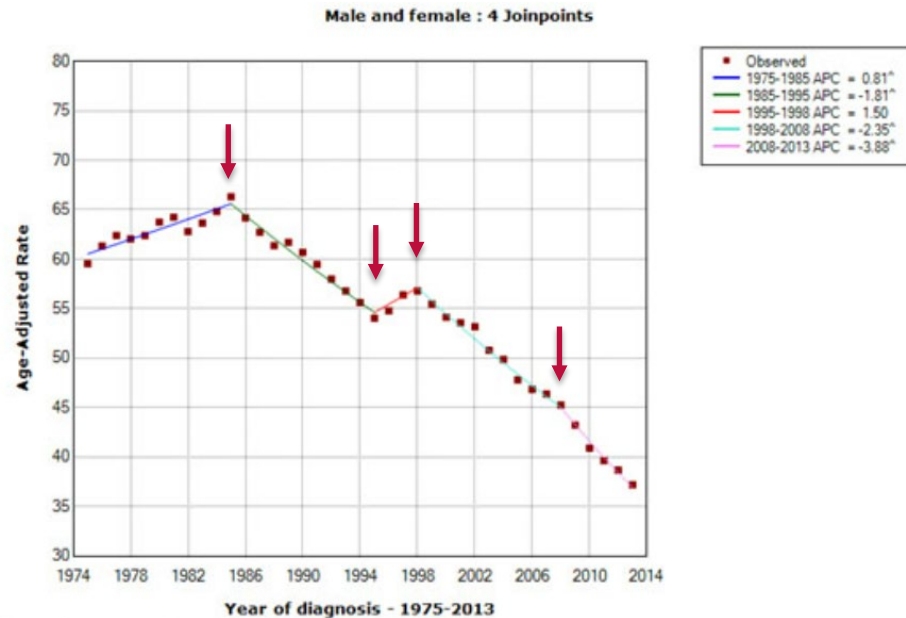
"This is where things started getting really weird."

Joinpoint

- Joinpoint is statistical software for the analysis of trends in rates (incidence or mortality) using joinpoint models, i.e., models like the figure where several different lines are connected together at the "joinpoints"
- Estimates the number and location of joinpoints, i.e., calendar years where trends changed
- Kim HJ, Fay MP, Feuer EJ, Midthune DN. Permutation tests for joinpoint regression with applications to cancer rates. *Stat Med* 2000;19:335-51.



Sample Joinpoint Graph



^ The Annual Percent Change (APC) is significantly different from zero at alpha = 0.05

Why do we need a different joinpoint model for survival data?

- Survival has an extra dimension compared to rate (in addition to calendar year at diagnosis):
 - Time since diagnosis
- To answer questions such as
 - At which years at diagnosis there is significant changes in survival?
 - How much survival (or probabilities of cancer death) are changing annually between joinpoints?
 - Are the changes similar for different time since diagnosis?

Joinpoint model for survival: JPSurv

- Analyze trends in survival with respect to year of diagnosis
- JPSurv estimates the number and location of joinpoints, i.e. calendar years at diagnosis where the probabilities of dying of cancer (hazard) have shown change in trends
- It also summarizes trends between joinpoints

Joinpoint model for survival: JPSurv



- The joinpoint survival model is an extension of the proportional hazards (Cox) model for survival (1-3)
- It can be applied to both Relative Survival or Cause Specific Survival (1)

1. Hakulinen T, Tenkanen L. Regression analysis of relative survival rates. *Appl Stat* 1987;36:309–17.

2. Yu et al. *JRSS-A* 2009;172:405-25.


3. Mariotto et al, *CEBP* 2021; 30 (11): 2001–2009.

Joinpoint survival model

- Let x be calendar year of diagnosis and t time since diagnosis
- We assume that the hazard rate of dying at time t follows a proportional hazard model:

$$\lambda(t | x) = \lambda_0(t) \exp\{h(x)\} = \exp\{\alpha_0(t) + h(x)\}$$


Baseline
hazard


The joinpoint model: linear segments
between joinpoints, describing trends
with respect to *year at diagnosis* x

$$S(t | x) = S_0(t) \exp\{h(x)\}$$


Baseline
survival

Joinpoint model $h(x)$ on calendar year x

- Let K be the number of joinpoints and t_1, \dots, t_K the position of the joinpoints

$$h(x) = \beta x + \sum_{j=1}^K \delta_k (x - t_j)^+ \quad u^+ = \begin{cases} u, & u > 0 \\ 0, & u \leq 0 \end{cases}$$

- $K+1$ linear segments connected at the joinpoints at t_1, \dots, t_K
- When there is no joinpoint ($K=0$), the model is a Cox proportional hazards model and the proportionality function is a linear function βx , i.e.

$$h(x) = \beta x$$

- β is the slope of the segment

Model estimation and selection: example 1975-2015 data

- For a fixed number of joinpoints K (up to 5) JPSurv fits a joinpoint model to each possible joinpoint location
- Example: User chooses maximum number of joinpoints $K=2$
 - $K=0 \rightarrow$ Fit one model with no joinpoint
 - $K=1 \rightarrow$ Fit models with 1 joinpoint at possible locations: 1978,..., 2010
 - Advanced options provide control of the minimum number of years required between joinpoints (2 years) , first (3 years) and last intervals (5 years)
 - $K=2 \rightarrow$ Fit models with combinations of 2 joinpoints (obeying restriction in Advanced Options)

Model estimation and selection

- For each fitted model JPSurv calculates:
 - Bayesian Information Criterion (BIC)
 - Akaike Information Criterion (AIC)
 - Log-likelihood
- **Selected model is the model that minimizes BIC**

- When maximum no. of joinpoints is large (>2) →
 - Long time to run all models
 - User is required to provide an e-mail to retrieve results



Example: Non-Hodgkin Lymphoma (NHL) Data

- Cancer patients diagnosed with NHL between 1975-2015
- Complete follow-up through 2016
- 10 years of follow-up

Year	since diagnosis				Observed (%)		Expected (%)		Relative (%)	
		Alive	Died	Lost	Interval	Cumul.	Interval	Cumul.	Interval	Cumul.
1975	< 1 yr	1,731	577	0	66.7	66.7	96.9	96.9	68.8	68.8
1975	1-<2 yr	1,154	202	0	82.5	55.0	97.6	94.6	84.6	58.1
1975	2-<3 yr	952	94	0	90.1	49.6	97.5	92.2	92.4	53.8
1975	3-<4 yr	858	83	0	90.3	44.8	97.5	89.9	92.7	49.8
1975	4-<5 yr	775	76	1	90.2	40.4	97.6	87.7	92.4	46.0
1975	5-<6 yr	698	84	0	88.0	35.5	97.6	85.6	90.2	41.5
...
1975	9-<10 yr	483	34	1	93.0	26.0	97.4	77.4	95.4	33.6
...
...
2015	< 1 yr	5,081	876	76	82.6	82.6	97.4	97.4	84.8	84.8
2015	1-<2 yr	4,129	275	87	93.3	77.1	97.7	95.2	95.5	81.0

Specifying Data and Parameters in JPSurv

JPSurv
JoinPoint Survival Model

Dictionary File: NHL_CML_1.dic
Data File: NHL_CML_1.txt
Data Type: Relative Survival in Percents

Cohort and Model Specifications

Year of Diagnosis*: Year of diagnosis 1975+
Year of Diagnosis Range: 1975 to 2015
Max No. of Years from Diagnosis (follow-up) to include: <= 10

Site recode NHL and CML:
 Non-Hodgkin Lymphoma
 Chronic Myeloid Leukemia

Maximum Joinpoints: 5 ?

Multiple Cohorts or single cohort with maximum Joinpoints greater than 2 will require additional computing time. When computation is completed, a notification will be sent to the e-mail entered above.

E-mail: mariotta@mail.nih.gov

Advanced Options

Reset **Submit**

Data

Specifying the calendar years and follow-up time to fit the model

Selecting the cohort

Max. # JP to test

E-mail to retrieve results

Controls restriction on Joinpoints

Run

JPSurv
JoinPoint Survival Model

Advanced Options

Delete Last Interval:

Yes No

Minimum Number of Years between
Joinpoints (Excluding Joinpoints):

Minimum Number of Years before First
Joinpoint (Excluding Joinpoint):

Minimum Number of Years after Last
Joinpoint (Excluding Joinpoint):

Number of Calendar Years of Projected
Survival:

[Reset Advanced Options](#)

[Hide](#)

Reset

Calculate

Balance between finding “true”
joinpoints and joinpoints because of
random variability

Provides more stable survival
projections not dependent on
fluctuations at the last calendar
years

Non-Hodgkin Lymphoma- Testing up to 5 Joinpoints

Analysis Help

Cohort: Non-Hodgkin Lymphoma Number of Decimal Places: 2 [Download Full Dataset](#) [Export Workspace](#)

Model #	Number of Joinpoints	Location	Bayesian Information Criterion (BIC)	Akaike Information Criterion (AIC)	Log Likelihood	Converged
1	0	None	1542.01	1414.55	-696.27	Yes
2	1	1991	1123.45	984.40	-480.20	Yes
3	2	1995, 2002	984.96	834.33	-404.16	Yes
4	3	1983, 1994, 2003	983.27	821.04	-396.52	Yes
5 (final selected model)	4	1983, 1990, 1995, 2003	982.74	808.93	-389.47	Yes
6	5	1983, 1990, 1995, 2002, 2010	987.81	802.41	-385.21	Yes

Best model has 4 Joinpoints at: 1983, 1990, 1995 & 2003

Cohort Number of Decimal Places [Download Full Dataset](#)[Export Workspace](#)

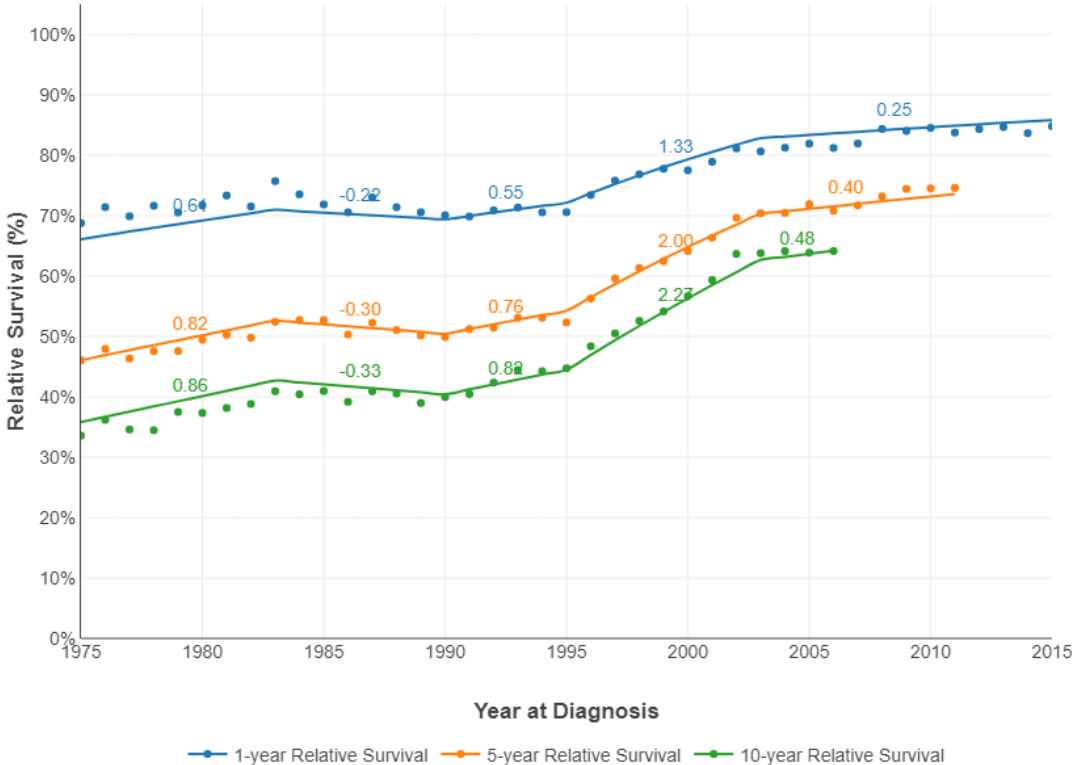
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[Survival vs. Year at Diagnosis](#)[Death vs. Year at Diagnosis](#)[Survival vs. Time Since Diagnosis](#)[Model Estimates](#)

Graphs

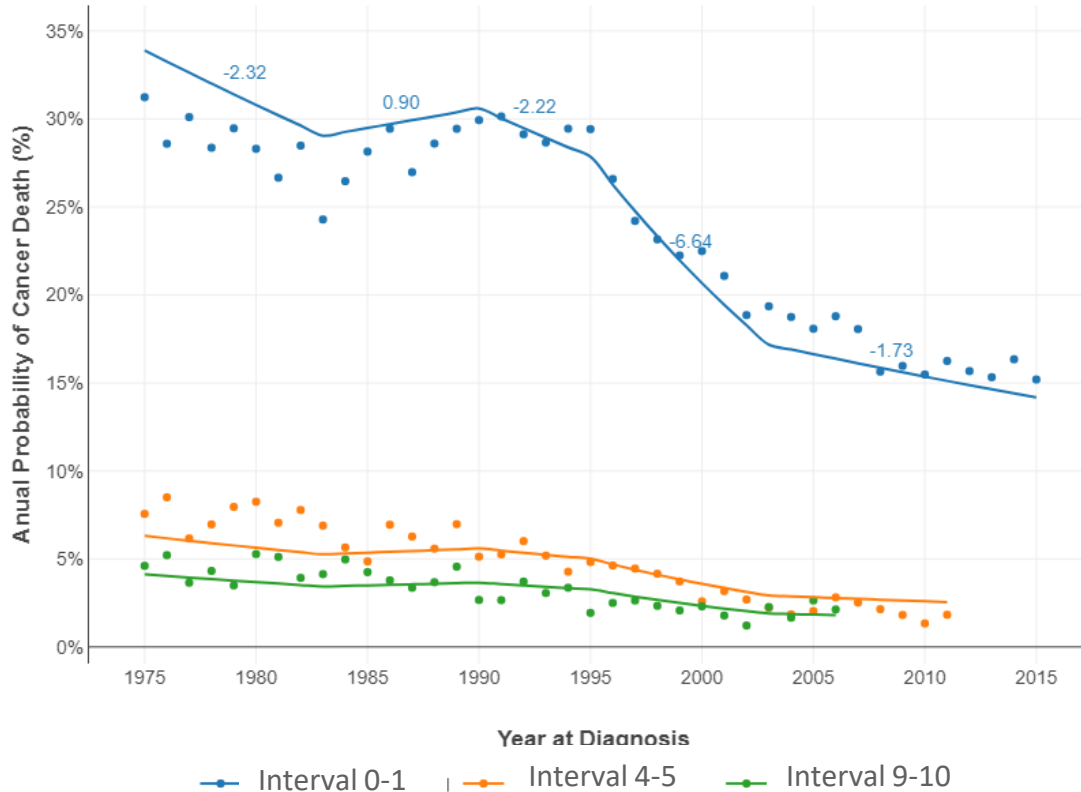
Survival vs. Year at Diagnosis

Relative Survival by Diagnosis Year
Non-Hodgkin Lymphoma - Joinpoint 4 (1983, 1990, 1995, 2003)



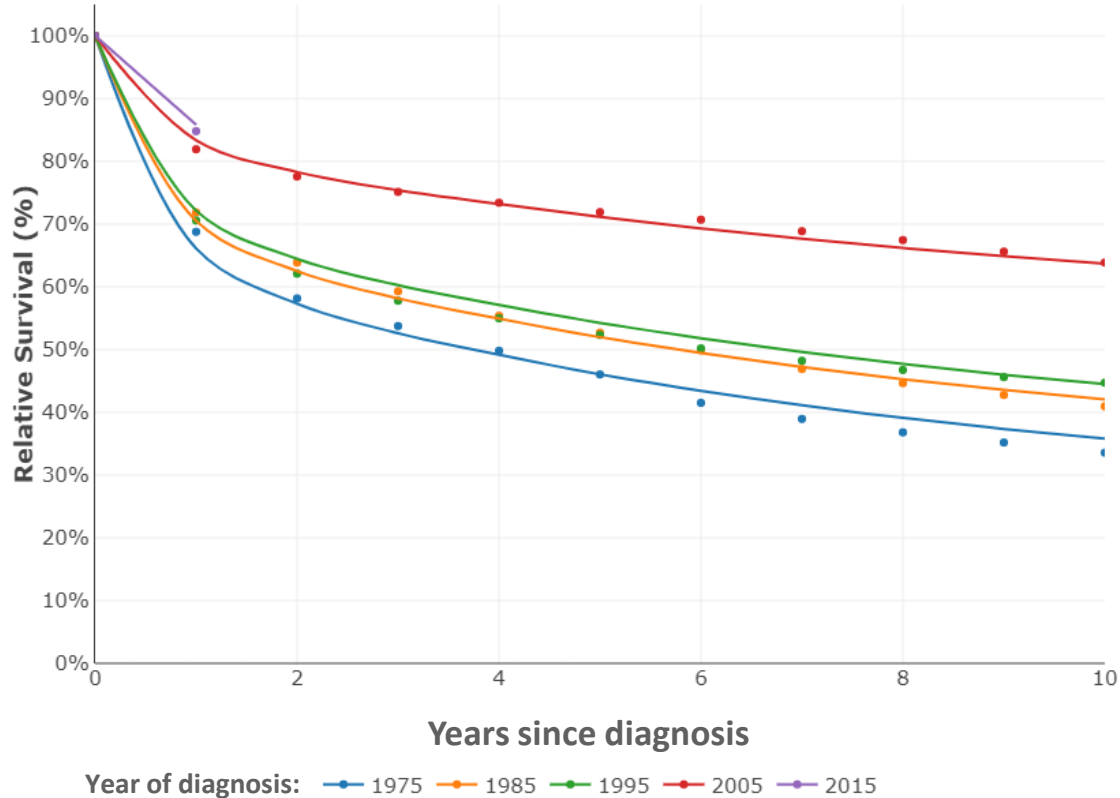
Death vs. Year at Diagnosis

Annual Probability of Dying of Cancer by Diagnosis Year
Non-Hodgkin Lymphoma - Joinpoint 4 (1983, 1990, 1995, 2003)



Survival vs. Time Since Diagnosis

Relative Survival by Year Since Diagnosis for Selected Diagnosis Year
Non-Hodgkin Lymphoma - Joinpoint 4 (1983, 1990, 1995, 2003)



*How do we summarize survival trends
between joinpoints?*

Trends in Joinpoint Model for Analysis of Rates

- Annual Percent Change (APC) is used to describe trends between joinpoints
- Interpretation: if the APC is 1%, and the rate in 1990 is 50 per 100,000
 - In 1991 the rate is $50 \times 1.01 = 50.5$ per 100,000
 - In 1992 the rate is $50.5 \times 1.01 = 51.005$ per 100,000



Two summary trend measures in JPSurv

- Probability of Cancer Death Scale
 - Annual Percent Change in the Probability of Cancer Death¹: APC_D
- Cumulative Survival Scale
 - Motivation for developing a measure in the survival scale is because prognosis is usually reported as cumulative survival
 - Average Absolute Change in Survival²: AAC_S

1. Yu et al. *JRSS-A* 2009;172:405-25.

2. Mariotto et al, *CEBP* 2021; 30 (11): 2001–2009.

Annual Percent Change in the Probability of Cancer Death (APC_D)

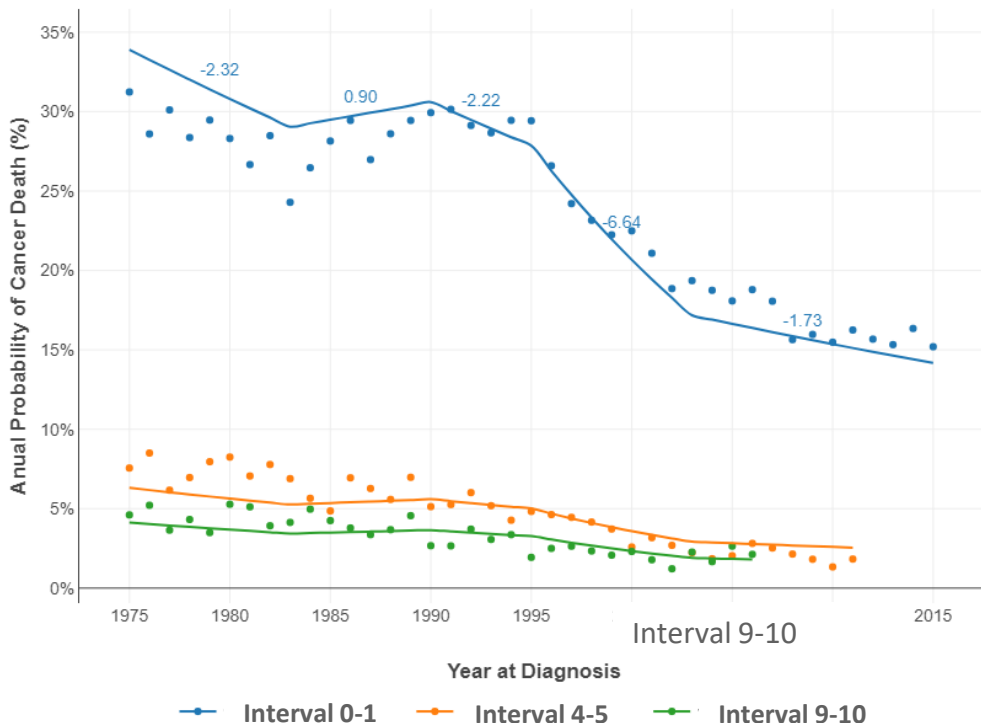
- $P(i,y)$: Conditional probability of dying of cancer in interval i given alive at the beginning of the interval, for patients diagnosed in year y
- *Example $i=1$ and $y=1996$*

$$APC_D = 100 * \frac{P(1,1996) - P(1,1995)}{P(1,1995)} = 100 \times \{\exp(\beta) - 1\}$$

- It does not depend on interval i nor the calendar year y at the joinpoint segment but only on the β the coefficient in the joinpoint segment

Numbers are the Annual Percent Change in the Probabilities of Cancer Death

Annual Probability of Dying of Cancer by Diagnosis Year
Non-Hodgkin Lymphoma - Joinpoint 4 (1983, 1990, 1995, 2003)



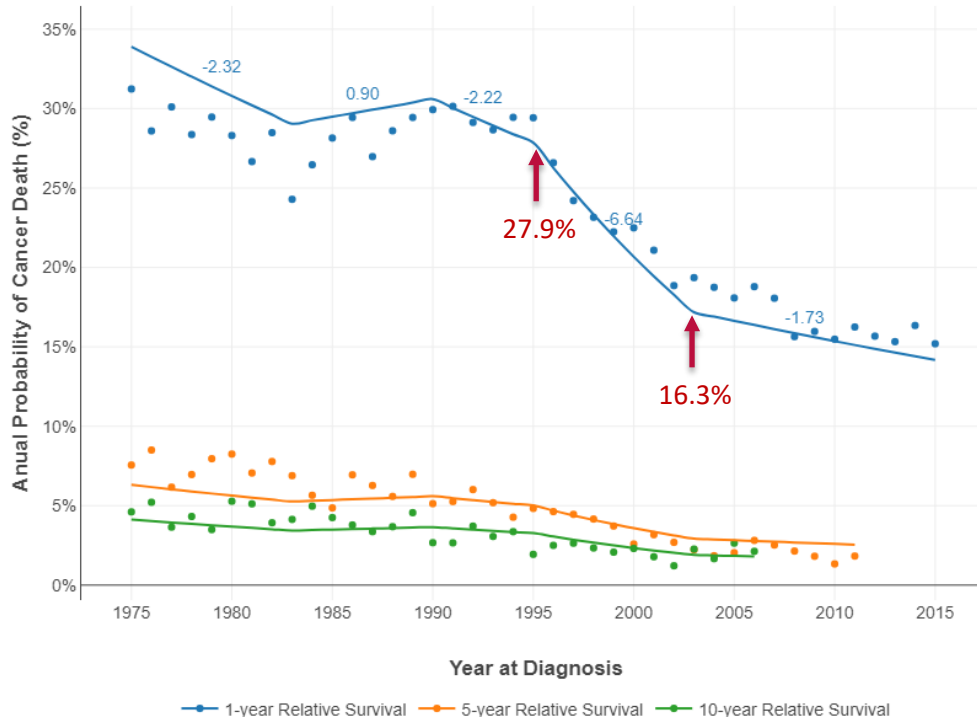
Start Year	End Year	Prob death in interval 0-1			Prob death in interval 5				
		APC_D	Lower 95% C.I.	Upper 95% C.I.	nifi can ce	APC_D	Lower 95% C.I.	Upper 95% C.I.	nifi can ce
1975	1983	-2.32	0.51	-3.31	↓	-2.32	0.51	-3.31	↓
1983	1990	0.90	0.48	-0.05	n.s.	0.90	0.48	-0.05	n.s.
1990	1995	-2.22	0.59	-3.39	↓	-2.22	0.59	-3.39	↓
1995	2003	-6.64	0.35	-7.33	↓	-6.64	0.35	-7.33	↓
2003	2015	-1.73	0.30	-2.32	↓	-1.73	0.30	-2.32	↓

- Largest decrease in the Prob of cancer death occurred between 1995-2003: 6.64% annual percentage decrease
- The estimate is independent of the interval

Interpretation for the trends between 1995-2003

Annual Percent Change in the Probabilities of Cancer Death

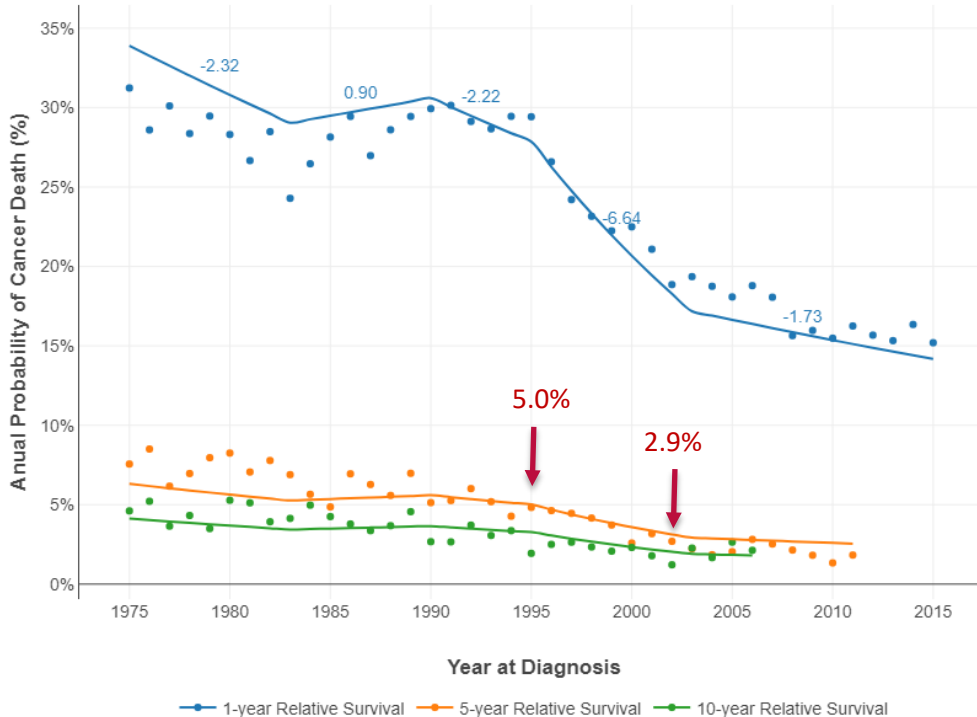
Annual Probability of Dying of Cancer by Diagnosis Year
 Non-Hodgkin Lymphoma - Joinpoint 4 (1983, 1990, 1995, 2003)



- APC_D = -6.64% and P(1,1995)=27.9% then
 - P(1, 1996)=27.9% x 0.9336 = 26.0%
 - P(1, 1997)=26.0% x 0.9336 = 24.3%
 -
 - P(1,2003)=P(1,2002) x 0.9336 =16.3%

Interpretation

Annual Probability of Dying of Cancer by Diagnosis Year
Non-Hodgkin Lymphoma - Joinpoint 4 (1983, 1990, 1995, 2003)



- if the APC_D is -6.64%
- and the annual prob. of cancer death in the 5 year after diagnosis in 1995 is $P(5,1995)=5.0\%$ then
 - $P(5,1996)=5.0\% \times 0.9336 = 4.7\%$
 - $P(5,1997)=4.7\% \times 0.9336 = 4.4\%$
 -
 - $P(5,2003)=P(5,2002) \times 0.9336 = 2.9\%$
- The annual probability of dying of cancer is decreasing by 6.64% for each subsequent year of diagnosis.

Average Absolute Change in Survival (AAC_S)

- $S(i,y)$: i -year Cumulative Survival for patients diagnosed in year y
- Average of $\{S(j,y+1)-S(j,y)\}$ over calendar years y in the joinpoint segment
- Example $i=1$ and segment 1995 to 2003, 8 years

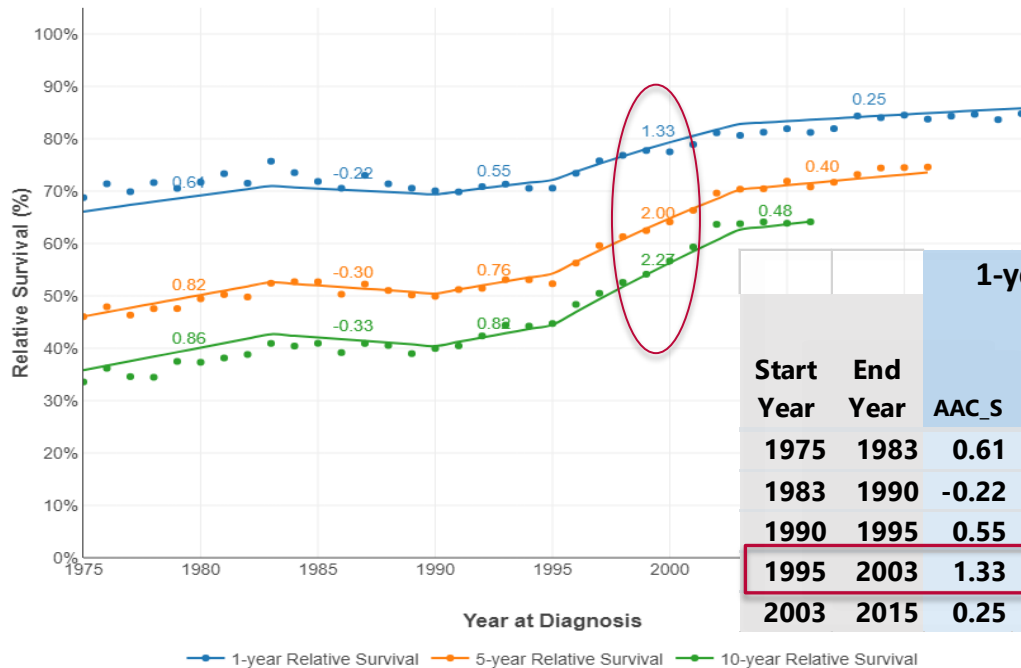
$$AAC_S(1) = \sum_{y=1995}^{2003} \frac{S(1, y+1) - S(1, y)}{8}$$

- Measured in **survival “percentage points (pp)”**
- Depends on time since diagnosis and is averaged on the calendar years at the segment

Numbers are the Average Absolute Change in Survival (AAC_S)

Relative Survival by Diagnosis Year

Non-Hodgkin Lymphoma - Joinpoint 4 (1983, 1990, 1995, 2003)



Start Year	End Year	1-year Survival			5-year Survival			10-year Survival					
		AAC_S	Lower 95% C.I.	Upper 95% C.I.	Sig nifi can ce	AAC_S	Lower 95% C.I.	Upper 95% C.I.	Sig nifi can ce	AAC_S	Lower 95% C.I.	Upper 95% C.I.	Sig nifi can ce
1975	1983	0.61	0.34	0.87	↑	0.82	0.45	1.18	↑	0.86	0.48	1.24	↑
1983	1990	-0.22	-0.45	0.01	n.s.	-0.30	-0.63	0.02	n.s.	-0.33	-0.67	0.02	n.s.
1990	1995	0.55	0.26	0.84	↑	0.76	0.36	1.17	↑	0.82	0.38	1.25	↑
1995	2003	1.33	1.19	1.48	↑	2.00	1.79	2.22	↑	2.27	2.03	2.51	↑
2003	2015	0.25	0.16	0.34	↑	0.40	0.27	0.54	↑	0.48	0.32	0.65	↑

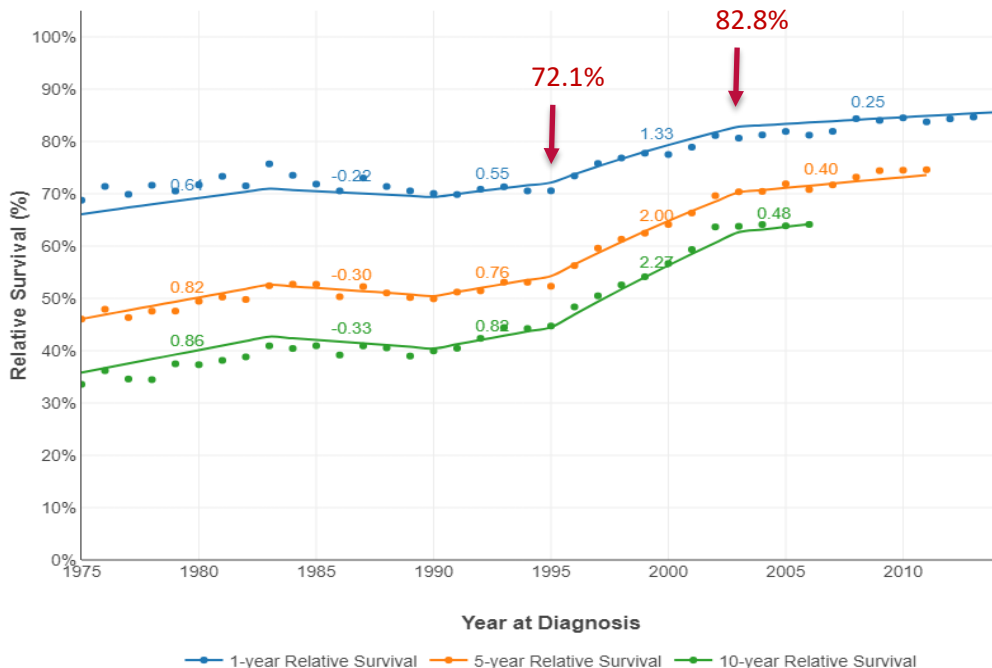
Largest increases in relative survival (RS) occurred between 1995-2003:

1.33 percentage points (pp) in 1-year RS, 2 pp in 5-year RS and 2.27 pp in 10-year RS

Interpretation for the trends between 1995-2003

Average Absolute Change in Survival (AAC_S)

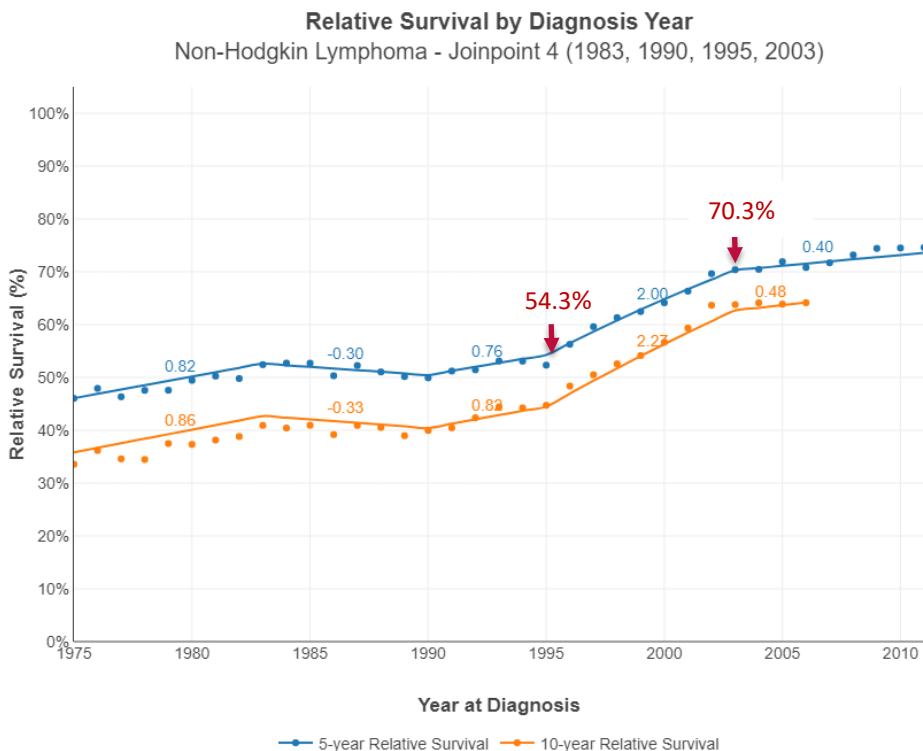
Relative Survival by Diagnosis Year
Non-Hodgkin Lymphoma - Joinpoint 4 (1983, 1990, 1995, 2003)



- The AAC_S(1) is 1.33 survival percentage points for the 1-year survival trends
- The 1-year relative survival in 1995 is $S(1,1995)=72.1\%$
 - $S(1, 1996)=72.1\% + 1.33\% = 73.5\%$
 - $S(1, 1997)=73.5\% + 1.33\% = 74.8\%$
 -
 - $P(1,2003)=P(1,2002) + 1.33\% = 82.8\%$

Interpretation for the trends between 1995-2003

Average Absolute Change in Survival (AAC_S)



- The AAC_S(5) is 2.00 survival percentage points for the 5-year survival trends
- The 5-year relative survival in 1995 is $S(5,1995)=54.3\%$
 - $S(5,1996)=72.1\% + 2.00\% = 56.3\%$
 - $S(5,1997)=73.5\% + 2.00\% = 58.3\%$
 -
 - $S(5,2003)=S(5,2002) + 2.00\% = 70.3\%$
- The 5-year cancer survival is increasing on average 2 percentage points for each subsequent year of diagnosis

AAC_S: Average Absolute Change in Survival

APC_D: Annual Percent Change in the Conditional Probability of Death

Interpretation

AAC_S(5)=2%: The 5-year cancer survival is increasing on average 2 percentage points for each subsequent year of diagnosis

APC_D=-2%: The annual probability of dying of cancer is decreasing by 2% for each subsequent year of diagnosis. This measure is similar to APC

Does it vary by time since diagnosis?

Yes
AAC_S(1) \neq AAC_S(5)

No
APC_D is the same for 0-1 year, 1-2 years, ... from diagnosis.

Motivation/Summary

- More clear interpretation in terms of cumulative survival (prognosis)
- Vary by time since diagnosis

- More challenging prognosis interpretation
- Do not vary by time versus
- More elegant mathematical derivation

Notes about trend survival measures

- The standard errors for trends measures are obtained using the delta method
- The trend measures in the probability of death (APC_D) and survival have opposite signs
 - Increasing survival: APC_D is negative vs AAC_S is positive
 - Decreasing survival: APC_D is positive vs AAC_S is negative

Proportionality assumption: Example of survival for patients diagnosed with Chronic Myeloid Leukemia

Proportionality assumption

- JPsurv assumes that the probabilities of cancer death (hazard) by time since diagnosis are proportional (in the log scale)
 - Changes are “similar” in the first versus later years after diagnosis
- Works well for most cancer sites and applications
- In some exception cancer sites proportionality assumption does not hold:
Example Chronic Myeloid Leukemia¹

1. Mariotto et al, *CEBP* 2021; 30 (11): 2001–2009.

Proportionality Assumption

- If t is time since diagnosis and y is the year at diagnosis a proportional survival model is:

$$S(t | y) = S_0(t)^{\exp[h(y)]}$$

- Which translate into a proportional survival model at the log scale

- $$\log[S(t | y)] = \exp[h(y)] + \log[S_0(t)]$$

↓

Proportionality
constant depends on
year of diagnosis y

↘

Common
baseline survival
(depends on time
since diagnosis t)

Model Selection Using up to 10 years Survival Data

Cohort

Number of Decimal Places

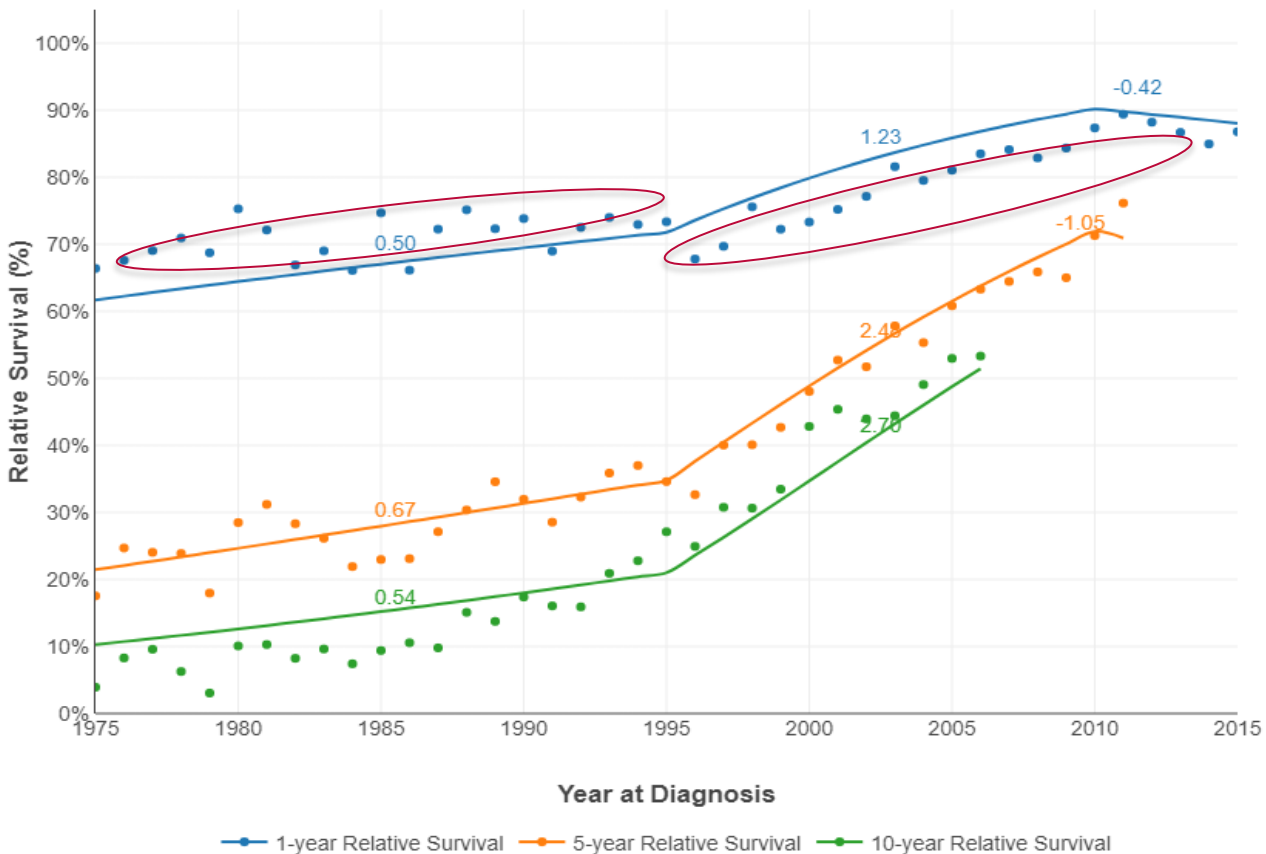
[Download Full Dataset](#)

[Export Workspace](#)

Model #	Number of Joinpoints	Location	Bayesian Information Criterion (BIC)	Akaike Information Criterion (AIC)	Log Likelihood	Converged
1	0	None	1086.93	987.16	-482.58	Yes
2	1	1992	963.43	854.58	-415.29	Yes
3 (final selected model)	2	1995, 2010	950.47	832.55	-403.27	Yes
4	3	1986, 1996, 2010	954.08	827.09	-399.55	Yes
5	4	1981, 1984, 1996, 2010	959.84	823.78	-396.89	Yes
6	5	1981, 1984, 1988, 1996, 2010	969.88	824.75	-396.38	Yes

Relative Survival by Diagnosis Year

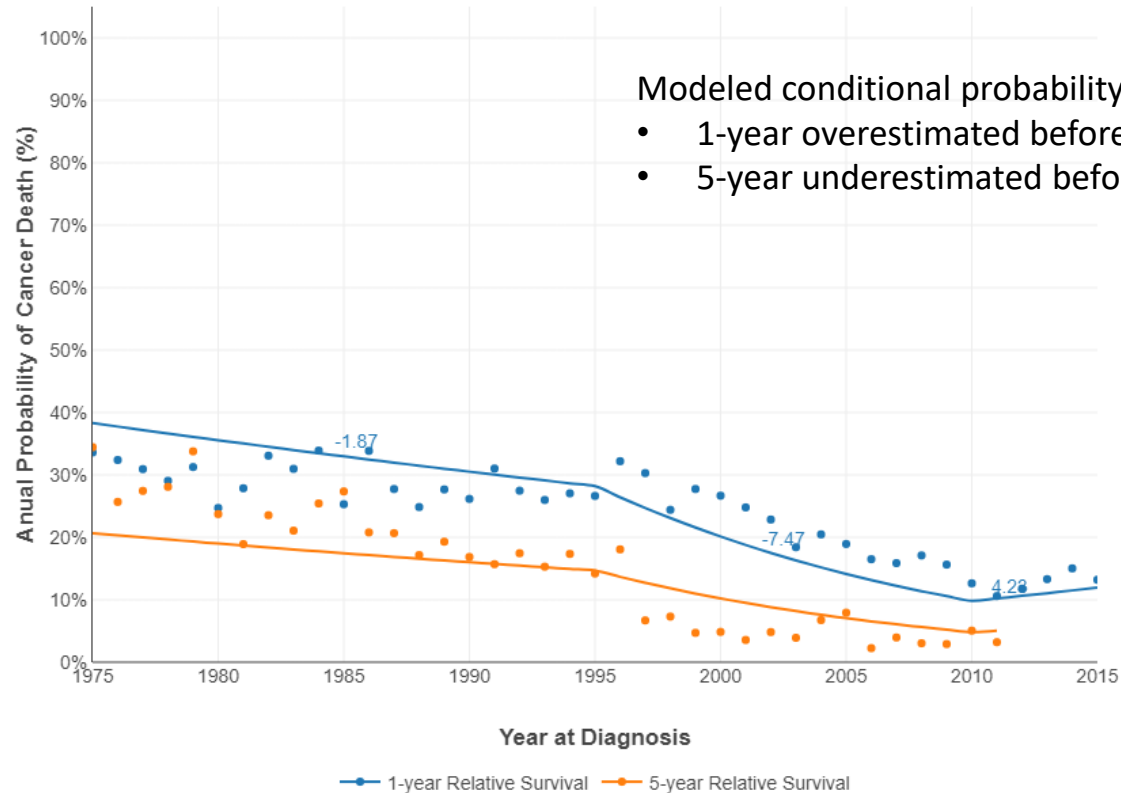
Chronic Myeloid Leukemia - Joinpoint 2 (1995, 2010)



Indication that the model does not fit well the 1-year relative survival

Annual Probability of Dying of Cancer by Diagnosis Year

Chronic Myeloid Leukemia - Joinpoint 2 (1995, 2010)



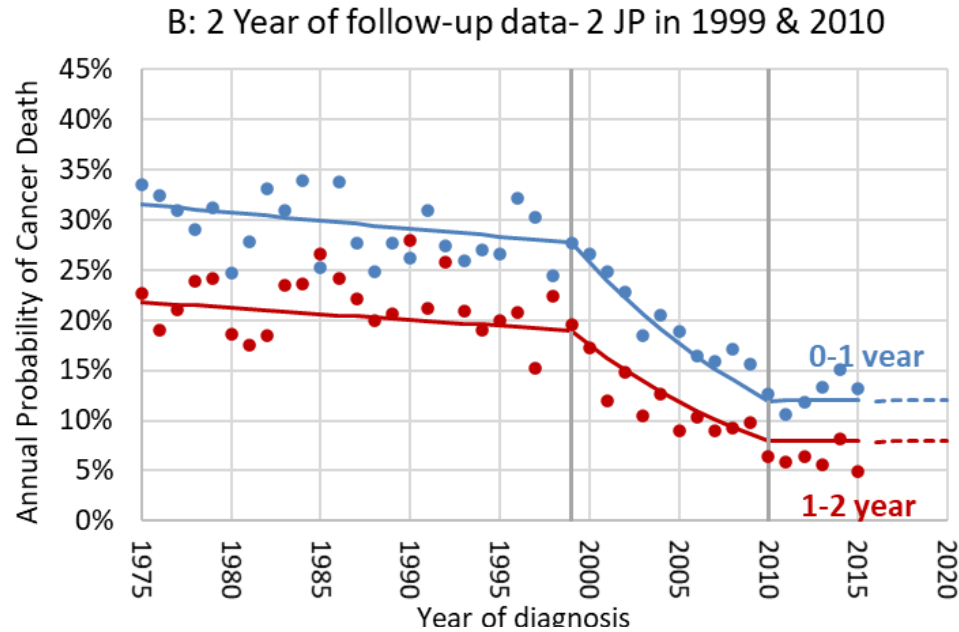


Figure 3. Observed (dots) and modeled (lines) annual probabilities of dying of cancer in the 0-1 and 1-2 annual intervals since diagnosis by year of diagnosis, for patients diagnosed with CML. The figures correspond to models using up to 2 years of follow-up (**A** and **B**) and 5 years of follow-up (**C**). **B** is the final model using the BIC criteria while **A** is the final model using the AIC criteria. The dashed lines are projections beyond available data. JP, jointpoints.

Interpretation for the Chronic Myeloid Leukemia example

- The Jpsurv model did not fit the data well
 - Probability of cancer death did not decrease proportionally for all years since diagnosis
 - The modeled 1-year survival overestimated observed survival after 1995
 - Restricting the data to 2 years of follow-up, improved the fit
- Suggests larger improvements in the chances of surviving CML for patients who had already survived 3+ years compared with the initial years after diagnosis after 1995
- The first tyrosine kinase inhibitor (TKI), Imatinib, was approved by the FDA in 2000 to treat patients with CML

Relaxing proportionality assumption in JPSurv

- Work in progress
- We will be implementing a more flexible joinpoint model in JPSurv that relax (somewhat) the proportionality assumption of year at diagnosis effect
- The new model will identify the best cut-point for time since diagnosis, e.g. 2 years from diagnosis and allow for two different joinpoint survival models:
 - A JPSurv model for the 0-<2 time since diagnosis
 - A PSurv model for the 2-<5 time since diagnosis



Discussion/Conclusions

Opportunities

- JPSurv webtool provides a suite of estimates and graphs for analyzing cancer survival trends
- Can be used with both relative survival and cause-specific survival
- Easier to use with data exported from SEER*Stat.
 - Improving the CSV functionality to read other survival data
- Trend measures available for trends of probability of cancer death and cumulative survival measures
- Can be used to **project** survival beyond the observed data, both in future calendar years as well as time since diagnosis.
 - Particularly useful in prevalence projections

Opportunities

- Different statistics to select best model are available: BIC, AIC and log-likelihood
 - BIC is the default and provide more parsimonious models
- Advanced options provide control of the minimum number of years required between joinpoints, first and last intervals and the number of years for projections
 - Last interval important for projections
- Graphs, trend measures and results are available and can be displayed for all tested models



Challenges

- The model and trend survival measures presents some challenges in understanding and interpretation
 - Trends in survival and probability of cancer death (hazard) measures
 - Two time scales: time since diagnosis and calendar year
- Assumes proportionality by time since diagnosis
 - Graphical display provides way of checking assumption

Summary

- The JPSurv webtool provides a suite of estimates for analyzing trends in cancer survival that complement traditional descriptive survival analyses
- Caution should still be used when interpreting survival trends for those cancer sites for which screening or early detection have been widely disseminated in the population
 - Survival increases may reflect biases (overdiagnosis, lead time and length biases) rather than real improvements
 - Looking at incidence and mortality trends (1,2) can help in the interpretation of survival trends

1. Cho H, et al . When do changes in cancer survival mean progress? The insight from population incidence and mortality. JNCI Monogr 2014;2014:187–97.
2. Dickman PW, Adami HO. Interpreting trends in cancer patient survival. J Intern Med 2006;260:103–17.

References

- Mariotto AB, Zhang F, Buckman DW, Miller D, Cho H, Feuer EJ. Characterizing Trends in Cancer Patients' Survival Using the JPSurv Software. *Cancer Epidemiol Biomarkers Prev.* 2021 Nov;30(11):2001-2009.
- Yu B, Huang L, Tiwari RC, Feuer EJ, Johnson KA. Modelling population-based cancer survival trends using joint point models for grouped survival data. *J R Stat Soc Ser A Stat Soc* 2009;172:405–25.
- Hakulinen T, Tenkanen L. Regression analysis of relative survival rates. *Appl Stat* 1987;36:309–17.
- Dickman PW, Adami HO. Interpreting trends in cancer patient survival. *J Intern Med* 2006;260:103–17.
- Cho H, Mariotto AB, Schwartz LM, Luo J, Woloshin S. When do changes in cancer survival mean progress? The insight from population incidence and mortality. *J Natl Cancer Inst Monogr* 2014;2014:187–97.

Thank you! Questions?

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Thursday, October 20 at 1:00-3:00 pm ET



Zaria Tatalovich, Ph.D.

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