Detecting sparse and weak deviations of non-proportional hazard in survival analysis

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Session: Detection and Estimation of Sparse and Weak Signals Joint Statistical Meeting August 2023 Toronto

- Existing methods for comparing the survival of two groups are generally ineffective against differences in **hazard** occurring in a **few time instances** when those instances are **unknown** to us in advance
- We propose a method that is effective against such differences

Survival Data and Analysis

	Control (X)		Treatment (<mark>Y</mark>)	
t	at risk	events	at risk	events
0	1000	29	1000	17
1	971	25	983	24
2	946	21	959	26
3	925	15	933	15
4	910	15	918	26
5	894	17	891	16
6	877	24	875	34
7	853	24	841	17
8	829	23	823	16
:	:	:	:	:
•	•	•	•	
48	365	11	338	8
49	354	6	330	7
50	348		323	

Survival Data and Analysis

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48	365	11	338	8	0.4
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Survival Data and Analysis



The goal of the analysis:

Determine whether the treatment has a non-null effect.

• Mantel-Cox log-rank test [Mantel 1966]

EVALUATION OF SURVIVAL DATA AND TWO NEW RANK ORDER STATISTICS ARISING IN ITS CONSIDERATION¹

Nathan Mantel²

[PDF] Evaluation of survival data and two new rank order statistics arising in its consideration

N Mantel - Cancer Chemother Rep, 1966 - medicine.mcgill.ca

Survival-time patterns should be compared properly in their entirety rather than at isolated points only. Such overall comparison would require a value function for rating particular durations of survival, but no such function exists. A chi-square procedure is proposed for comparing two sets of life-table data in their entirety. The implicit value function for the pro cedure is reasonable in that it gives greater weight to earlier deaths. By considering the case in which the life-table intervals are arbitrarily short, it is seen to be essentially a rank order ...

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	Control	(X)	Treatment (Y)		
	at risk	events	at risk	events	
: t :	$\frac{1}{n_{x}(t-1)}$: o _x (t)	: n _y (t-1) :	: o _y (t) :	

[total	Group X	Group Y
\Rightarrow	M k	$n_x(t-1)$ $o_x(t)$	$\overbrace{n_y(t-1)}^{\mathcal{K}}_{o_y(t)}$
-		\Downarrow	
	$H_{0,t}$:	$O_y(t) \sim H_z$	yG(M, K, k)

4

	Control	(X)	Treatment (<mark>Y</mark>)		
	at risk	t risk events at risk		events	
t	$\begin{vmatrix} \vdots \\ n_x(t-1) \\ \vdots \\ \vdots \end{vmatrix}$: o _x (t) :	: n y(t-1) :	: <mark>o</mark> y(t) :	⇒

$$\begin{array}{||c|c|c|c|}\hline total & Group X & Group Y \\\hline M & n_{x}(t-1) & \overbrace{n_{y}(t-1)}^{K} \\ & o_{x}(t) & o_{y}(t) \\\hline \\ & \downarrow \\\hline \end{array}$$

 $H_{0,t}\,:\, \textcolor{black}{O_y}(t) \sim \mathrm{HyG}(M,K,k)$

 $\mu(t) := \mathbb{E}\left[\mathsf{O}_{\mathbf{y}}(t)|\mathsf{H}_{0,t}\right], \qquad \mathsf{V}(t) = \operatorname{Var}\left[\mathsf{O}_{\mathbf{y}}(t)|\mathsf{H}_{0,t}\right]$

$$\mathrm{LR}_{T} := \frac{\sum_{t=1}^{T} \left(\mathbf{o}_{\mathbf{y}}(t) - \boldsymbol{\mu}(t) \right)}{\sqrt{\sum_{t=1}^{T} \mathsf{V}(t)}}$$

 $\mathrm{LR}_{\mathrm{T}} \stackrel{\mathrm{D}}{pprox} \mathcal{N}(0,1)$ under the global null

The Log-Rank Test (cont'd)

• The log-rank test:

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- Asymptotically equivalent to the likelihood ratio test in a proportional hazard model [Breslow 1977]
- 🙁 Not sensitive to excessive hazard localized in time

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- 🙂 Can accommodate **censorship**
- Asymptotically equivalent to the likelihood ratio test in a proportional hazard model [Breslow 1977]
- 🙁 Not sensitive to excessive hazard localized in time
- Non-homogeneous Log-rank [Tarone & James 1977], [Lee 1996], [Liu et. al. 2022]
 - 🙂 Can be sensitive to non-proportional hazards, but
 - Not useful when time instances of excessive hazard are apriori unknown

Our goal:

Attain sensitivity to **excessive hazard** localized in a **few** time instances such that we do not know in advance where those instances might be

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Use cases:

- Identifying age-specific effects [Nuzhdin, Khazaeli, Curtsinger, 2005]
- Analyzing the effect of bursty "space weather" radiation on radioactive decay [Castro-Palacio et. al. 2020]

HCHG has two steps:

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1. Many exact hypergeometric (HG) tests:

$$p_t := \Pr\left[\operatorname{HyG}(M, K, k) \ge O_y(t)\right], \qquad t = 1, \dots, T,$$

$$M = n_x(t-1) + n_y(t-1), \quad K = n_y(t-1), \quad k = o_x(t) + o_y(t)$$

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2. Global testing with Higher Criticism (HC):

$$\mathrm{HC} := \mathrm{HC}(p_1, \dots, p_T) := \max_{i \leq T\gamma} \sqrt{T} \frac{i/T - p_{(i)}}{\sqrt{(i/T)(1 - i/T)}}$$

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Notable properties of HCHG:

- Can accommodate censorship
- More sensitive than **log-rank** when instances of excessive risk are **sparse and weak** (later)
- Has a built-in mechanism to identify instances of excessive risk...

Identifying instances of excessive risk

• Identifying instances of excessive risk via HC thresholding [Donoho & Jin 2008, 2009]:



$$\Delta^* = \{t, p_t \le p_{(i^\star)}\}, \qquad i^\star = \arg \max_{i \le i_0} \sqrt{N} \frac{I/I - p_{(i)}}{\sqrt{(i/T)(1 - i/T)}}$$

Analysis under Sparse and Weak Effect Model

• Piece-wise exponential decay model [Feigl & Zelen 1965], [Friedman 1982]:

$$\begin{split} N_{X}(0) &= x_{0}, \qquad N_{y}(0) = y_{0} \\ \text{for } t &= 1, \dots, T \\ \begin{cases} O_{x}(t) \sim \operatorname{Pois}(N_{x}(t-1)\bar{\lambda}_{x}(t)) \\ N_{x}(t) &= N_{x}(t-1) - O_{x}(t) \end{cases} \qquad \begin{cases} O_{y}(t) \sim \operatorname{Pois}(N_{y}(t-1)\bar{\lambda}_{y}(t)) \\ N_{y}(t) &= N_{y}(t-1) - O_{y}(t) \end{cases} \end{split}$$

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• Non-homogeneous hazard alternative:

$$H_0 : \bar{\lambda}_x(t) = \bar{\lambda}_y(t), \quad \forall t$$

$$H_1 : \bar{\lambda}_y(t) = \begin{cases} \bar{\lambda}_x(t) & \text{w.p. } 1 - \epsilon \\ \left(\sqrt{\bar{\lambda}_x(t)} + \sqrt{\delta(t)}\right)^2 & \text{w.p. } \epsilon \end{cases}$$

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for
$$t = 1, ..., T$$

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- Sparse and weak calibration:
 - Individual effects are sparse: $\epsilon = T^{-\beta}$, $\beta \in (0, 1)$
 - Individual effects are **weak**: $\delta(t)$ is small...

• Individual effects are weak: conditioned on $n_x(t-1)$, $n_y(t-1)$, $n_x(t) + o_y(t)$, hypergeometric P-values of non-null instances are asymptotically log-chisquared with a moderate location shift:

$$-2\log(p_t) \stackrel{\mathbb{D}}{\approx} \left(\mathcal{N}(\sqrt{r\log(T)}, 1) \right)^2, \qquad r > 0$$

[Kipnis 2023], [Donoho & Kipnis 2023]

Analysis under Sparse and Weak Effect Model (cont'd)

Theorem

HCHG is asymptotically powerful if

$$r > \rho(\beta) = \begin{cases} 2(\beta - 1/2) & \frac{1}{2} < \beta < \frac{3}{4} \\ 2\left(1 - \sqrt{1 - \beta}\right)^2 & \frac{3}{4} \le \beta < 1, \end{cases}$$

and asymptotically **powerless** if $r < \rho(\beta)$

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• $\rho(\beta)$ is the **two-sample sparse normal means** phase transition curve [Donoho & Kipnis 2023]. $\rho(\beta)/2$ is the **sparse normal means** phase transition curve [Ingster 1997], [Jin 2003], [Donoho & Jin 2004], [Mukherjee et. al 2015], [Arias-Castro & Wu 2015, 2018], [Jin & Ke 2016]...

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Also, when $\beta > 1/2$,

- Log-rank is asymptotically powerless
- Fisher's combination statistic of HG P-values is asymptotically powerless

Asymptotic Power and Phase Transition





Significant* empirical power* difference



* at level $\alpha=0.05$

Demonstration for Real Gene-Expression Data

- SCAN dataset [Saal et. al. 2015]:
 - 3,069 breast cancer patients
 - Expression level of 8,702 genes
- We partitioned each gene by its median expression level; yields $2 \times 8,702$ Control/Treatment assignments
- We consolidated events into $\approx 21~{\rm day}$ intervals (originally, $t\in[56,2474]~{\rm days})$
- Example:

Gen	Gene name: ADSS					
t	Below m at risk	nedian (X) events	Above n at risk	nedian (<mark>Y</mark>) events		
0	1534	0	1535	1		
1	1534	1	1534	1		
2	1533	0	1533	0		
3	1533	2	1533	1		
:	•	:	:	÷		
97	703	0	665	1		
98	693	0	653	0		
99	686	0	645	0		



Figure 1: Number of genes with expression levels significantly² associated with survival according to HCHG(**■**) and log-rank (**■**)

¹at level $\alpha = 0.05$

 $^{^2 {\}rm at} ~{\rm level} ~\alpha = 0.05$

Gene Name	HC (P-value)	Log-rank (P-value)	Increased Mortality
DCK	0.00010	0.35505	> med
ADSS	0.00005	0.0633	> med
KCTD9	0.01284	0.33369	> med
VAMP4	0.01271	0.20006	> med
TMEM38B	0.02857	0.41772	< med
HIST1H3G	0.02725	0.39828	< med
SIGMAR1	0.01180	0.16812	< med
POLDIP3	0.04683	0.33744	< med
SMG9	0.03775	0.22874	< med
FBXL12	0.01266	0.05641	> med
BTNL8	0.03934	0.05110	< med

Table 1: Some genes in which **HCHG** identified a significantly lower survival rate in one group than the other while log-rank failed to do so.

Demonstration for Real Gene-Expression Data - Results (cont'd)



t	$n_x(t-1)$	$n_y(t-1)$	$O_X(t)$	$o_y(t)$	pt
56.00	1203.00	1187.00	0.00	8.00	0.00
62.00	1120.00	1101.00	0.00	7.00	0.01

Demonstration for Real Gene-Expression Data - Results (cont'd)



t	$n_x(t-1)$	$n_y(t-1)$	$o_x(t)$	$o_y(t)$	p_t
9.00	1524.00	1528.00	0.00	5.00	0.03
38.00	1412.00	1404.00	0.00	5.00	0.03
49.00	1281.00	1275.00	0.00	5.00	0.03
50.00	1271.00	1261.00	0.00	5.00	0.03
66.00	1069.00	1041.00	0.00	5.00	0.03

Demonstration for Real Gene-Expression Data - Results (cont'd)



t	$n_x(t-1)$	$n_y(t-1)$	$o_x(t)$	$o_y(t)$	pt
29.00	1500.00	1475.00	0.00	6.00	0.01
35.00	1454.00	1439.00	0.00	6.00	0.02
62.00	1111.00	1116.00	0.00	7.00	0.01

- HCHG is based on:
 - 1. Many exact hypergeometric tests
 - 2. Global testing with Higher Criticism
- HCHG is sensitive to sparse and weak deviations of non-proportional hazard
 - Theoretically: **more powerful** than existing methods in exponential decay **sparse and weak hazard departures setting**
 - Empirically: finds many discoveries not reported by the log-rank test

References

- B. Galili, A. Kipnis and Z. Yakhini. (2023). Detecting rare and weak deviations of non-proportional hazard in survival analysis. (*on arxiv*)

The end.

