Individual Prediction and Validation Using Joint Longitudinal-Survival Models in Prostate Cancer Studies

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1. INTRODUCTION

- Prostate Cancer
- Motivation; Individual Predictions
- Joint Longitudinal and Survival Models

2. PROSTATE CANCER APPLICATION

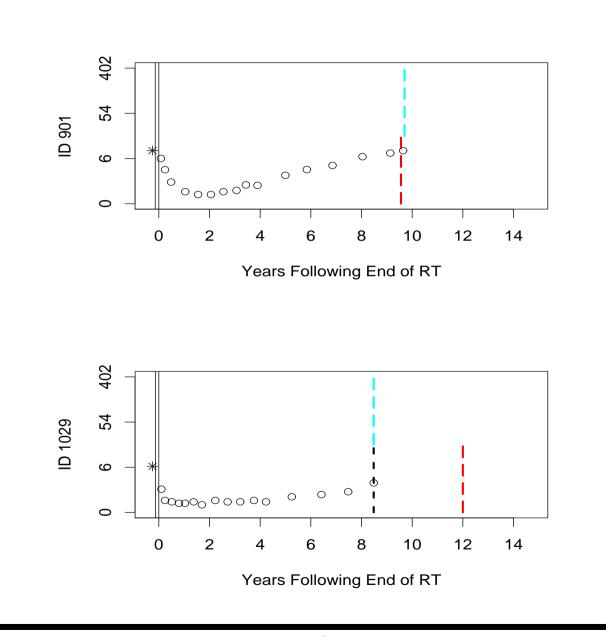
- Datasets, Models and Estimation
- Individual predictions, longitudinal and survival

3. WEBSITE

4. VALIDATION

PROSTATE CANCER

- Common cancer in older men
- Usually growing slowly, most people diagnosed with prostate cancer die of something else
- Treatment for localised disease
 - Radiation therapy (plus or minus hormones)
 - Surgery
- Following radiation PSA rise suggests cancer is regrowing
- Biochemical recurrence
 - Based on PSA
 - Not the real thing
- Clinical recurrence is the real thing (but PSA is useful)



GOAL

- Develop a website for patients and their physicians, psacalc.sph.umich.edu
- The patients were previously treated with radiation therapy for localised prostate cancer
- The patient inputs individual characteristics (stage of disease, treatment dose) and post-treatment measures of health
- The website provides quantitative information about future disease progression

MOCK EXAMPLE

- Patient treated in Oct 2003 for prostate cancer
- Pre-treatment characteristics
 - PSA = 10.3
 - T-stage = 3
 - Gleason grade = 8
 - Treatment dose was 74 Gy
- Patient has not experienced any clinical recurrence of prostate cancer

Table 1: Post treatment PSA measurements

Date	PSA
29 Feb 2004	2.1
1 May 2004	1.5
25 Dec 2004	1.1
4 July 2006	1.3
29 Feb 2008	1.7
1 Jan 2010	2.1

• What is the probability of the prostate cancer coming back within 3 years of today?

- Joint model trained on a large dataset
- Parameter estimates applied to this patient
- P(prostate cancer recurrence within 3 years) = 0.22

Prob(clinical recurrence within 3 years) = 0.22

- What should you do?
 - Intervene with salvage hormone therapy?
 - Order another PSA test for X months in the future?
 - Don't change the original plan
- This talk
 - How do we get 0.22
 - Attempts to validate the prediction

JOINT MODELS FOR LONGITUDINAL AND SURVIVAL DATA

- Setting: clinical trial or observational study
- Data
 - $-(t_i, \delta_i)$, censored event time
 - $-X_i$, time-independent covariates
 - $-Y_{ij}$, time-dependent covariate, biomarker
- Both T and Y are response variables

- Modelling choices for joint distribution of T and Y- [T, Y|X]
 - Factor as [T|X] and [Y|X,T]
 - Factor as [Y|X] and [T|Y,X]

- [Y|X] and [T|Y,X]
 - Faucett and Thomas (1996), Wulfsohn and Tsiatis (1997), and others
 - Most popular
 - Usually involves latent variables, R_i

$$- [Y_{ij}|X_i, R_i]$$

 $- [T_i|Y_i, X_i, R_i] = [T_i|X_i, R_i]$

- Factor $[T, Y \mid X]$ as $[Y \mid X][T \mid Y, X]$
- [Y | X], longitudinal model

- longitudinal random effects model

- $[T \mid Y, X]$
 - time-dependent proportional hazards model
- Use joint model for prediction of future longitudinal and event times for individual patients

PROSTATE CANCER DATASETS

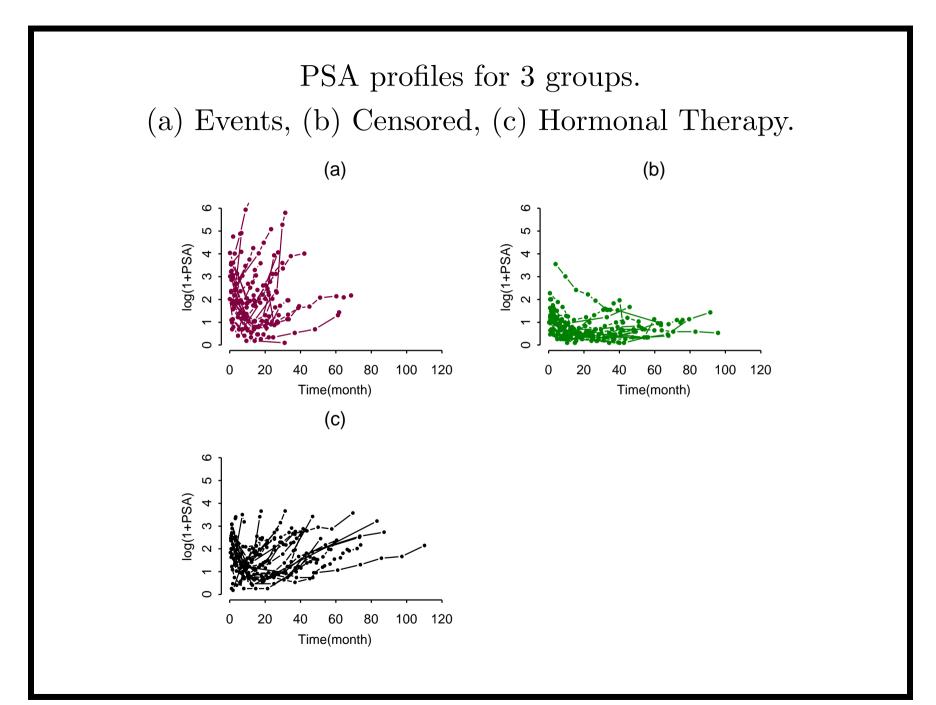
- Prostate cancer patients treated with radiation therapy.
- Training data
 - RTOG, n=615
 - Detroit, n=1268
 - Univ Michigan, n=503
- Testing data
 - Melbourne, n=395
 - Vancouver, n=846

Longitudinal Data (Y). Post-treatment PSA

- measured approximately every 6 months
- a total of 46,000 post-treatment PSA values
- median no. of PSA per patient is 8
- 10 year follow-up

Endpoints and Censoring (T)

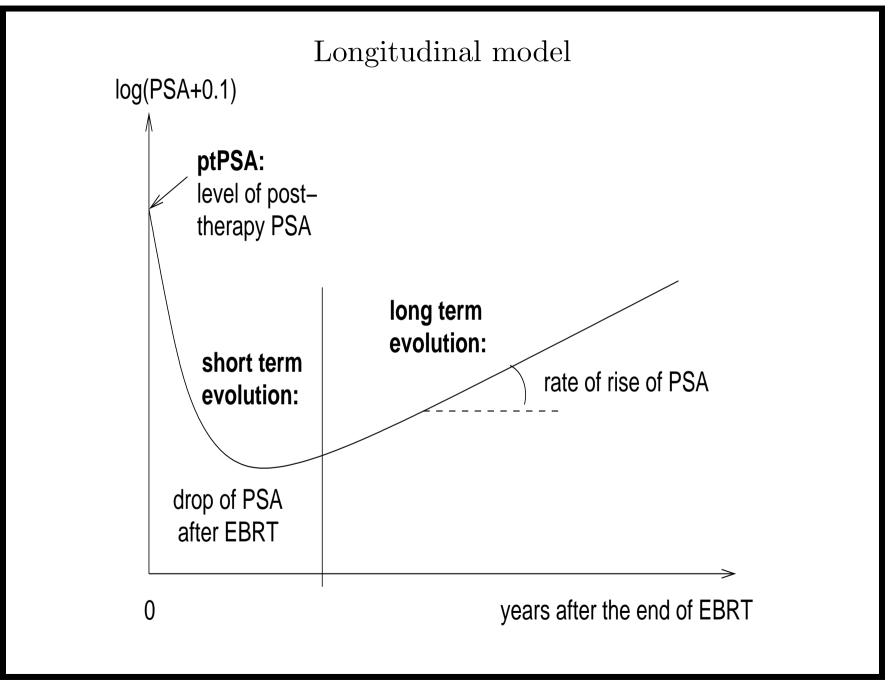
- $\bullet~15\%$ events: local/regional recurrence, distant metastasis
- 85% censored patients:
 - 20% are dead not from prostate cancer.
 - 65% are lost to follow-up or censored by the end of the study
- 10% of patients received salvage hormone therapy (HT) prior to recurrence (because of rising PSA).



Statistical Model

Notation

- $\mathbf{X}_{\mathbf{i}}$ baseline covariates.
- $Y_i(t) = PSA_i(t)$ longitudinal PSA data
- $\mathbf{T_i}$ time of recurrence.
- $\mathbf{R_i}$ random effects.
- Assumption Y_i and T_i conditionally independent given R_i and X_i .



Longitudinal. Non-linear random effects models.

$$\log \left[PSA_i(t) + 0.1 \right] = Z_i(t) + \epsilon_{it}$$

$$Z_i(t) = r_{i0} + r_{i1}f(t) + r_{i2}t$$

where $f(t) = ((1+t)^{-1.5} - 1)$, $\epsilon_{it} \sim$ t-distribution and $R_i = (r_{i0}, r_{i1}, r_{i2})$ are random effects for subject *i*.

 $[R_i \mid X_i] \sim N(\mu X_i, \Sigma)$

$$X_i = (bPSA_i, Tstage_i, Gleason_i)$$

<u>Hazard model</u>. Time-dependent proportional hazards.

$$\lambda_i(t \mid X_i, Z_i, sl_i, HT_i)$$

= $\lambda_0(t)$
exp[$\eta g(Z_i(t)) + \omega sl_i(t) + \gamma X_i + \phi HT_i(t)$]

 $sl_i(t) = slope of Z_i(t)$

$$HT_i(t) = \begin{cases} 0 & \text{if} \quad t < S_i \\ 1 & \text{if} \quad t > S_i \end{cases}$$

 $\lambda_0(t)$ is a step function.

- Estimation via MCMC
 - parameters θ
 - latent variables R_i
 - draws of θ, R_i , save for later use
 - over 12 hours of computing to obtain estimates
- Likelihood

 $\prod_{i} \int [\prod_{j} P(Y_{ij}|\theta, X_i, R_i)] P(T_i, \delta_i|\theta, X_i, R_i) f(R_i) dR_i$

PREDICT FUTURE PSA VALUES.

From model

$$\log \left[PSA_i(t) + 0.1 \right] = Z_i(t) + \epsilon_{it}$$

$$Z_i^k(t) = r_{i0}^k + r_{i1}^k f(t) + r_{i2}^k t$$

where k denotes k^{th} draw from posterior distribution (MCMC)

PREDICT RECURRENCE FOR CENSORED PATIENTS IN DATASET

• For patient *i*, the conditional probability of recurrence within *a* months

$$P[T < t_i + a | T > t_i, Y_i, X_i]$$

= (1/K) $\sum_k P[T < t_i + a | T > t_i, X_i, \theta^k, R_i^k]$

where θ^k, R_i^k are draws from the posterior distribution

Residual time distribution

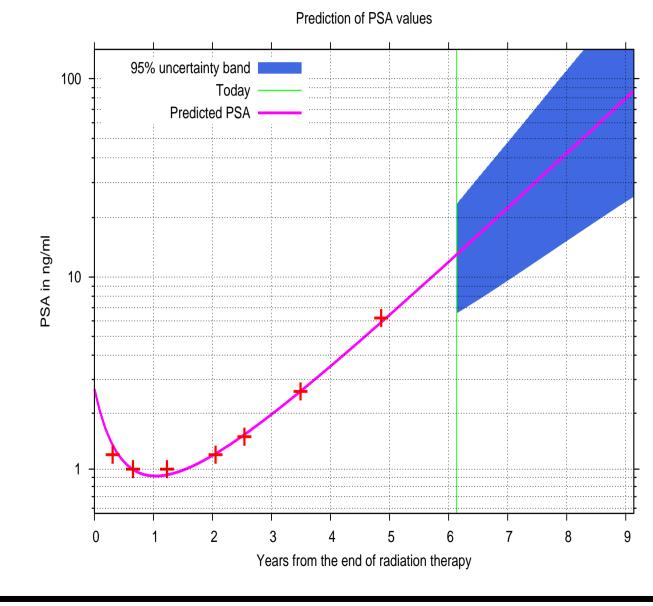
$$P[T > t_i + a \mid T > t_i, X_i, \theta, R_i]$$

= $exp[-\int_{u=t}^{t+a} \lambda_i(u \mid X_i, \theta, Z_i(u), sl_i(u))du]$

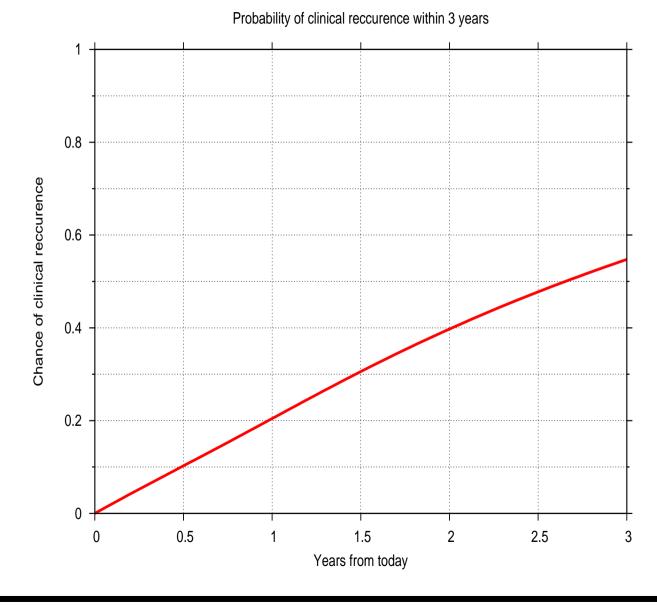
$$\lambda_i(u \mid X_i, \theta, Z_i(u), sl_i(u))$$

= $\lambda_0(t) \exp[\eta g(Z_i(u)) + \omega sl_i(u) + \gamma X_i]$

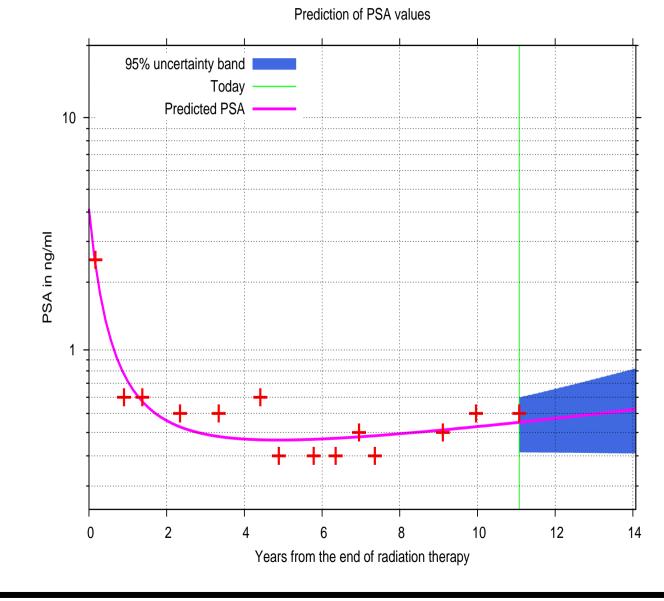
Predictions of PSA for Censored Subject



Residual Time Distribution for Censored Subject



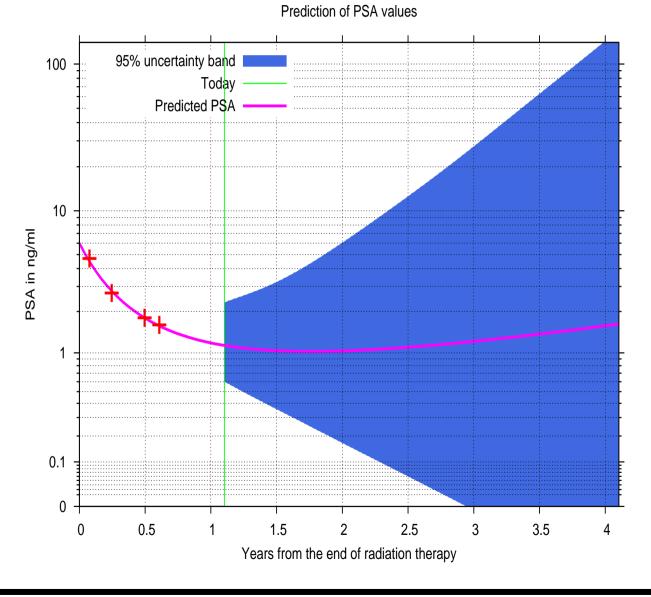
Predictions of PSA for Censored Subjects



Residual Time Distribution for Censored Subject

Probability of clinical reccurence within 3 years 0.8 Chance of clinical reccurence 0.6 0.4 0.2 0 + 1.5 0.5 2.5 0 2 3 1 Years from today

Predictions of PSA for Censored Subjects



Residual Time Distribution for Censored Subjects

Probability of clinical reccurence within 3 years 0.8 Chance of clinical reccurence 0.6 0.4 0.2 0 -1.5 0.5 2.5 0 2 3 Years from today

Predict Recurrence for New Censored Patient (m)

- Want $P[T < t_m + a | T > t_m, Y_m, X_m]$
- Obtain by averaging

$$P[T < t_m + a \mid T > t_m, X_m, \theta^k, R_m^k]$$

- Don't want to add new subject to dataset
- Have draws of θ from converged chain, needs draws of R_m
- For each θ^k run quick MCMC to get a draw of R_m^k .
- Draw R_m from $P(R_m | \theta^k, T_m > t_m, Y_m, X_m)$
- Use likelihood contribution from subject m $P(Y_m | \theta^k, X_m, R_m) P(T_m, \delta_m = 0 | \theta^k, X_m, R_m)$

Website for the public to use

psacalc.sph.umich.edu.

Public = cancer patients and their doctors

Issues

- What to present?
- How to present it?
- A lot of clinical information is required as input
- Needs to run fast
- Aid in clinical decision making
- Could present predictions if salvage HT is started
- How to publicize it
- How much validation needs to be done and shown

Possible uses

- Individual patient monitoring
- Definition of an endpoint
 - Taylor definition:
 - 1st time Pr(Clinical Recurrence within 3 years) > 0.1
- Entry criteria for clinical study
 - eg Pr(Clinical Recurrence within 3 years) > 0.1

Statistical Issues

- Death from other causes is regarded as censored
- Gives "pure risk", assuming no deaths from other causes
- Very parametric approach
 - Use spline type of longitudinal model
- How to calculate P(Recurrence) if someone started HT today

ISSUES IN VALIDATION

- Training data, External validation data
- Prediction at time t about an event in (t, t + a)
- Prediction is a distribution function, data is censored

SIMPLE GRAPHICAL APPROACH FOR BINARY Y (Hosmer-Lemeshow)

- $\hat{P}_i = \hat{P}(X_i)$ = predicted probability $P(Y = 1|X_i)$
- Create homogeneous groups of people with similar \hat{P}_i
- Estimate proportion for people in group g, \hat{P}_g
- Compare \hat{P}_i with \hat{P}_g

ALTERNATIVE APPROACHES WHEN Y IS BINARY

- ROC curves, AUC
 - Popular and familiar
 - Change \hat{P}_i to $\hat{P}_i/2$ would give same ROC curve.

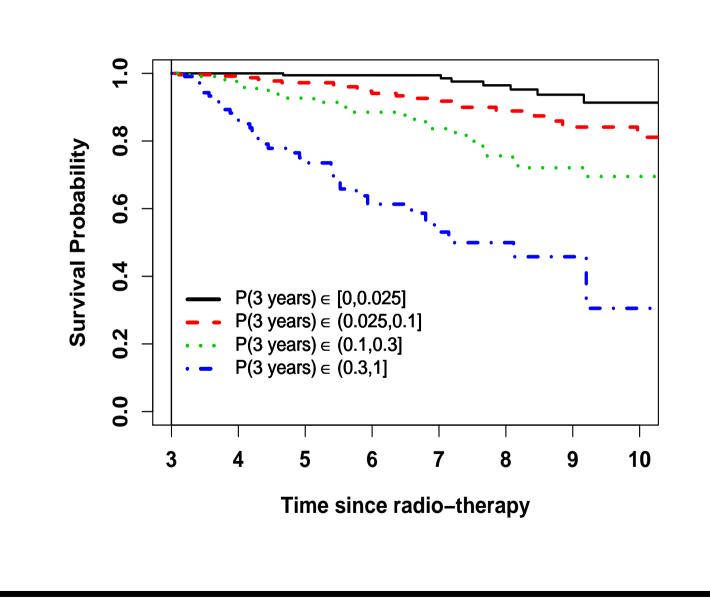
SIMPLE GRAPHICAL APPROACH FOR SURVIVAL DATA (like Hosmer-Lemeshow)

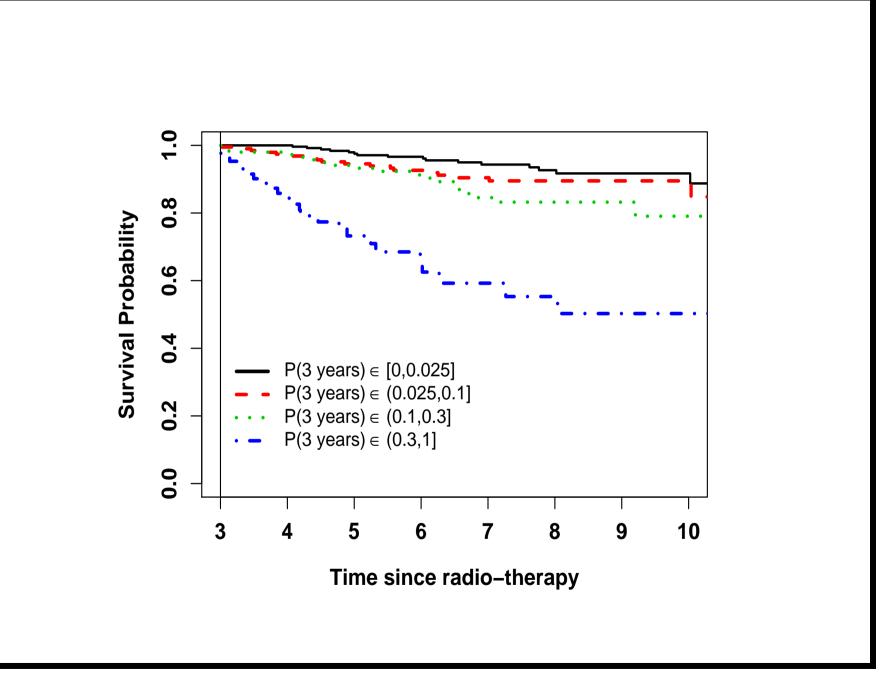
- Create homogeneous groups with "similar" $\hat{S}(t+a|T_i > t, H_i)$
- Estimate empirical survival distribution for people in group g, $\hat{S}_g(a)$
- Compare $\hat{S}(t+a|T_i > t, H_i)$ with $\hat{S}_g(a)$
 - Calibration

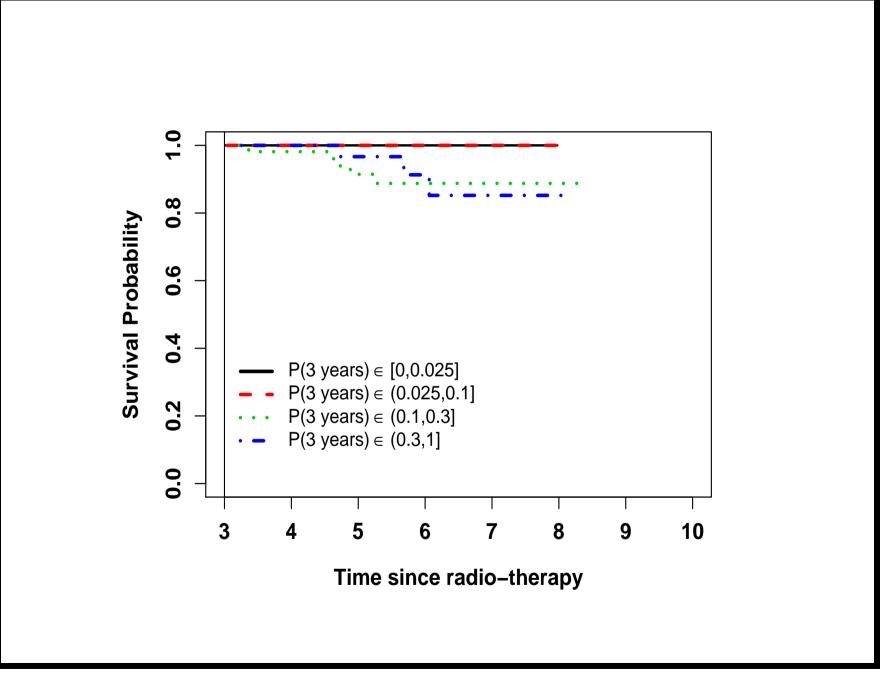
- Estimation on training data (3 cohort of patients):
 2386 patients
- 2. Predict on training data
- 3. Prediction on 2 independent cohorts:
 - . 846 patients from Vancouver cohort
 - . 395 patients from Melbourne

Graphical validation

- 4 groups based on $\hat{P}(T_i < 3 + a | T_i > 3, H_i(t))$
 - $-\hat{P} \in (0.0, 0.025)$
 - $-\hat{P} \in (0.025, 0.10)$
 - $-\hat{P} \in (0.1, 0.3)$
 - $-\hat{P} \in (0.3, 1.0)$
- Make predictions for everyone in testing datasets who are at risk at 3 years based on their PSA data prior to 3 years
- Place person into group
- Kaplan-Meier curve of what happened to them after 3 years

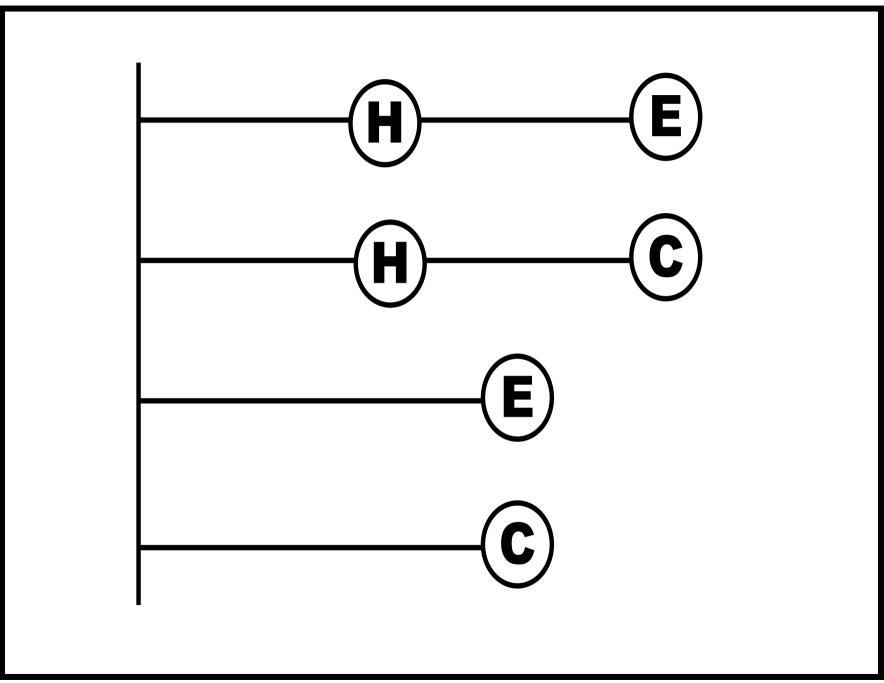


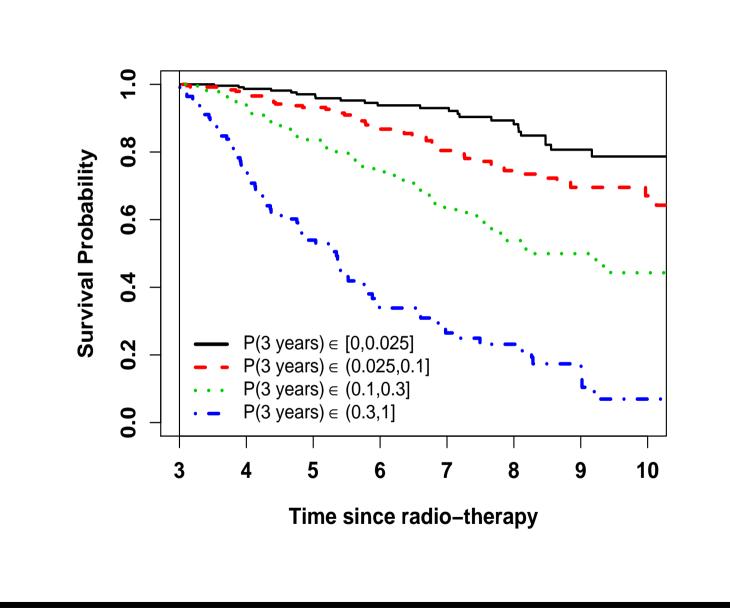


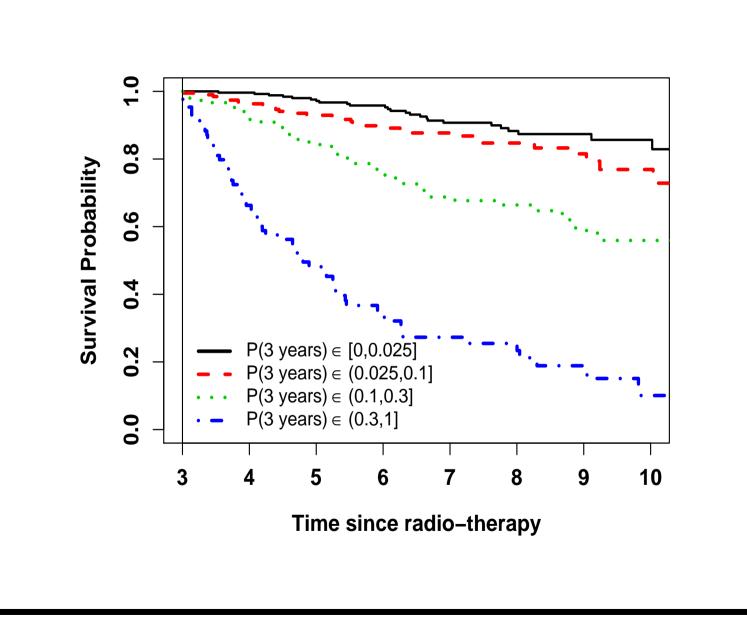


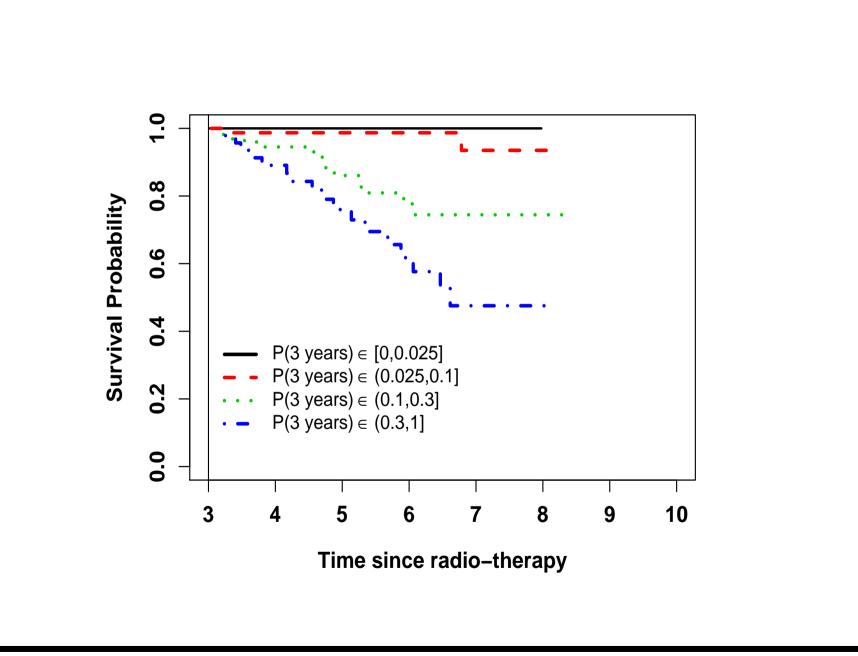
A complication with Kaplan-Meier estimate, dependent censoring

- people are given salvage hormone therapy (HT) prior to an event, because of rising PSA
- Options
 - censor at time of HT
 - call HT an event
 - ignore HT
 - something fancier









Is this worth all the trouble? Simpler approaches:

- . Cox model (PHM) with baseline variables: $P(T_i \leq t + a | T_i \geq t, X_i; \hat{\theta_0})$
- . PHM with baseline variables & the last PSA (landmark analysis) $P(T_i \leq t + a | T_i \geq t, Y_i(t); \hat{\theta}_t)$

References

- Yu et al, 2004, Statistica Sinica
- Taylor et al, 2005, J Clin Oncol
- Yu et al, 2007, JASA
- Pauler and Finkelstein, 2002, Stat in Med
- Proust-Lima et al, 2008, Int J Rad Oncol Biol Phys
- Proust-Lima et al, 2009, Biostatistics

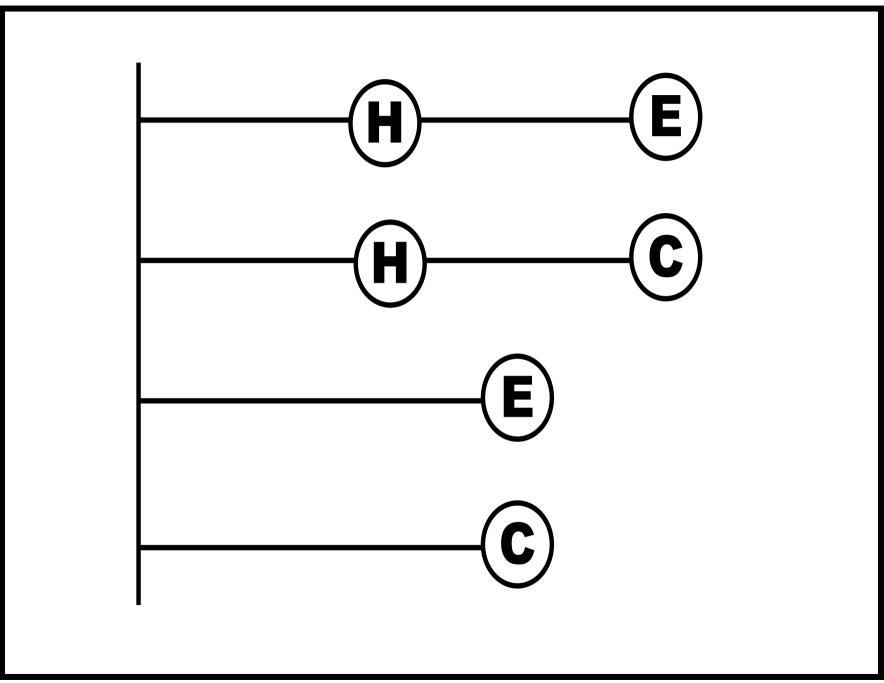
Collaborators and funding

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Hormonal therapy and dependent censoring

- Salvage hormonal therapy (HT) is sometimes given when a patient exhibits a rising trend in PSA, before a clinical event.
- HT delays occurrence of the clinical event
- HT is a nuisance factor present in the data.
- A different problem would be estimating the effect of HT.



 $\lambda_i(t \mid X_i, Z_i, sl_i, HT_i)$ = $\lambda_0(t)$ exp[$\eta g(Z_i(t)) + \omega sl_i(t) + \gamma X_i + \phi HT_i(t)$]

 $sl_i(t) = slope of Z_i(t)$

$$HT_i(t) = \begin{cases} 0 & \text{if} \quad t < S_i \\ 1 & \text{if} \quad t > S_i \end{cases}$$

Sensitivity analyses suggests estimates of η, ω, γ are stable

Using model to estimate effect of salvage hormonal therapy

- When PSA starts to rise some patients receive an intervention, which is thought to delay recurrence
- Level and slope of PSA are the important factors associated with the decision to initiate salvage therapy
- Of all patients about 10% receive salvage therapy prior to any recurrence
- Of all recurrences about 75% are before salvage therapy and 25% are after salvage therapy

