

Dynamic prediction using joint models for recurrent  
and terminal events:  
*Evolution after a breast cancer*

*A. Mauguen \**, *B. Rachet \*\**, *S. Mathoulin-Pélissier \**,  
*S. Siesling\*\*\**, *G. MacGrogan \*\*\*\**, *A. Laurent \**, *V.*  
*Rondeau\**

*\* INSERM U897, Bordeaux*

*\*\* London School of Hygiene and Tropical Medicine, London*

*\*\*\* Integraal Kankercentrum Netherlands*

*\*\*\*\* Institut Bergonié, Bordeaux*

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# Introduction

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  - single or multiple events  
(recurrences, metastases, death)

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- clinical therapeutic decisions, and patient monitoring
- patient information
- trials : defining patient subpopulations

# Introduction

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- **Prediction of death**

- clinical therapeutic decisions, and patient monitoring
- patient information
- trials : defining patient subpopulations

- **Account for**

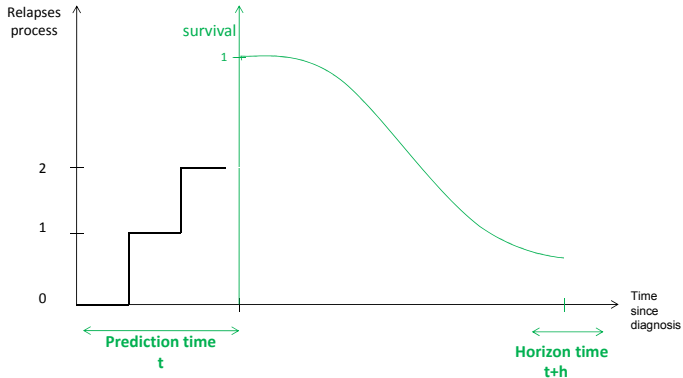
- individual characteristics
- tumour characteristics
- previous treatments
- evolution of longitudinal markers (*Rizopoulos, 2011 ; Proust-Lima 2009*)

# Introduction : Motivating example

- Cohort of patients with **operable breast cancer**
- Treated in a **comprehensive cancer centre** and followed 13.9 years (median)
- **Recurrent events** observed : loco-regional relapses, distant metastases ; until 3 events per patient
- Hypothesis : individual covariates but also **recurrent event process** may improve prediction of death risk

# Objective

**To predict** the risk of death between time  $t$  and  $t + h$  given the recurrent event process before time  $t$  in the context of joint modelling



# Joint Models

- Recurrent events and death **processes** are potentially **correlated**
- Standard (naive) approach of Cox with time-dependent covariate only for **external covariates** !
- Interest :
  - investigating the **strength of association** between recurrent events and death
  - allows to study impact of **covariates both** on recurrent events and death
  - treat **informative censoring** by death

## Joint models : some notations

- $t$  time of prediction and  $h$  window of prediction
- $D_i$  time of death for subject  $i$ ,  $i = 1, \dots, n$
- $X_{ij}$  time of the  $j$ th recurrence for subject  $i$
- $Z_{ij}^R$  and  $Z_i^D$  covariates vectors for recurrence and death
- $\lambda_{ij}^R$  and  $\lambda_i^D$  baseline hazards for risk of recurrence or death



# Joint models

Joint modelling for the risk of recurrent event (disease relapses) and terminal event (death)

$$\begin{cases} \lambda_{ij}^R(t|u_i) = u_i \lambda_0^R(t) \exp(\beta_1' Z_{ij}^R) \\ \lambda_i^D(t|u_i) = u_i^\alpha \lambda_0^D(t) \exp(\beta_2' Z_i^D) \end{cases}$$

- calendar timescale (time from origin)
- $u_i \sim \Gamma(1/\theta; 1/\theta)$ , i.e.  $E(u_i) = 1$  and  $\text{var}(u_i) = \theta$
- $\theta$  dependency between recurrent events and death
- $\alpha$  sense and strength of the association (more flexibility)

*Liu et al. Biometrics 2004; Rondeau et al. Biostatistics 2007*

# Inference in the joint model

## Penalized log-likelihood :

- smooth baseline hazard functions
- approximated by cubic M-splines

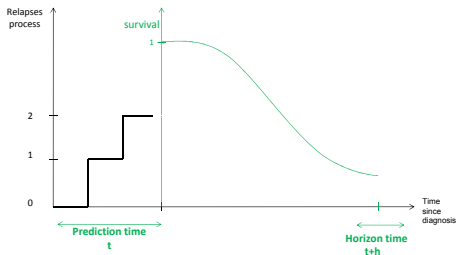
$$pl(\xi) = l(\xi) - \kappa_1 \int_0^\infty (\lambda_0^R(t))''^2 dt - \kappa_2 \int_0^\infty (\lambda_0^D(t))''^2 dt$$

With the vector of parameters :  $\zeta = (\lambda_0^D(\cdot), \lambda_0^R(\cdot), \beta, \alpha, \theta)$   
and  $\kappa_1$  and  $\kappa_2$  two smoothing parameters for the baseline hazard functions

# Dynamic prediction

- Consider a new subject  $i$  **free of death at time  $t$**  (i.e.  $D > t$ ), for whom we observe  $j$  recurrences before  $t$  and for whom the vector of covariates  $Z_{ij}^R$  and  $Z_{ij}^D$  are available at time of prediction
- The history of recurrences for patient  $i$  until time  $t$  is :

$$\mathcal{H}_i^j(t) = \{N_i^R(t) = J, X_{i1} < \dots < X_{iJ} \leq t\}$$



# Dynamic prediction

Distinguish **two settings** for the probability of death

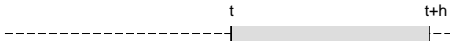
## Setting 1

Exactly 3 recurrent events before  $t$



## Setting 2

Whatever the history of recurrent events before  $t$



X Recurrent event

— Period where we consider what happens

■ Window of prediction of death

--- Period where we do not consider what happens

# Dynamic prediction

Setting 1 : with exactly  $j$  recurrences before  $t$

$$P^1(t, t+h; \xi) = P(D_i \leq t+h | D_i > t, \mathcal{H}_i^{j,1}(t), Z_{ij}^R, Z_i^D, \xi)$$
$$= \frac{\int_0^\infty [S_i^D(t|Z_i^D, u_i, \xi) - S_i^D(t+h|Z_i^D, u_i, \xi)] (u_i)^j S_{i(j+1)}^R(t|Z_{ij}^R, u_i, \xi) g(u_i) du_i}{\int_0^\infty S_i^D(t|Z_i^D, u_i, \xi) (u_i)^j S_{i(j+1)}^R(t|Z_{ij}^R, u_i, \xi) g(u_i) du_i}$$

and  $\mathcal{H}_i^{j,1}(t) = \{N_i^R(t) = j, X_{i1} < \dots < X_{ij} \leq t\}$ , with  $X_{i0} = 0$  and  $X_{i(j+1)} > t$

# Dynamic prediction

Setting 1 : with exactly  $j$  recurrences before  $t$

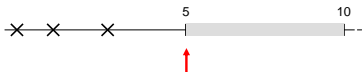
$$P^1(t, t+h; \xi) = P(D_i \leq t+h | D_i > t, \mathcal{H}_i^{j,1}(t), Z_{ij}^R, Z_i^D, \xi)$$
$$= \frac{\int_0^\infty [S_i^D(t|Z_i^D, u_i, \xi) - S_i^D(t+h|Z_i^D, u_i, \xi)] (u_i)^J S_{i(j+1)}^R(t|Z_{ij}^R, u_i, \xi) g(u_i) du_i}{\int_0^\infty S_i^D(t|Z_i^D, u_i, \xi) (u_i)^J S_{i(j+1)}^R(t|Z_{ij}^R, u_i, \xi) g(u_i) du_i}$$

and  $\mathcal{H}_i^{j,1}(t) = \{N_i^R(t) = j, X_{i1} < \dots < X_{ij} \leq t\}$ , with  $X_{i0} = 0$  and  $X_{i(j+1)} > t$

**Example :**

*"Up to now Mrs Martin has developed 3 recurrences of her initial cancer, her probability of dying in the next 5 years is  $x\%$ "*

Exactly 3 recurrent events before  $t$



# Dynamic prediction

Setting 2 : considering the recurrence history only in the parameters estimation

$$\begin{aligned} P^2(t, t+h; \xi) &= P(D_i \leq t+h | D_i > t, Z_i^D, \xi) \\ &= \frac{\int_0^\infty [S_i^D(t | Z_i^D, u_i, \xi) - S_i^D(t+h | Z_i^D, u_i, \xi)] g(u_i) du_i}{\int_0^\infty S_i^D(t | Z_i^D, \xi, u_i) g(u_i) du_i} \end{aligned}$$

# Dynamic prediction

Setting 2 : considering the recurrence history only in the parameters estimation

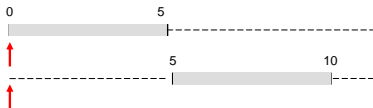
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## Example :

*" her probability of dying in the next 5 years is x% "*

*" if still alive in 5 years, her probability of dying over the next 5 years will be x% "*

Whatever the history of recurrent events before t





# Dynamic prediction : variability of the probability estimators

by **Monte Carlo** :

- at each  $b$  step ( $b=1, \dots, B=1000$ ) :  
 $\hat{\xi} = (\widehat{\lambda_0^R(\cdot)}, \widehat{\lambda_0^D(\cdot)}, \hat{\beta}, \hat{\alpha}, \hat{\theta})$  from  $\mathcal{MN}(\hat{\xi}, \hat{\Sigma}_\xi)$ .  
estimate  $P^b(t, t+h; \hat{\xi})$
- Percentile confidence interval : using the 2.5<sup>th</sup> and the 97.5<sup>th</sup> percentiles

# Dynamic prediction : Error of prediction

Based on a **weighted estimator of a time-dependent Brier Score (IPCW error)**

$$Err_{t+h} = \frac{1}{N_t} \sum_{i=1}^{N_t} [I(T_i^D > t+h) - (1 - \hat{P}(t, t+h; \hat{\xi}))]^2 \hat{w}_i(t+h, \hat{G}_N(.))$$

with

$$w_i(t+h, \hat{G}_N(.)) = \frac{I(T_i^D \leq t+h)\delta_i^D}{\hat{G}_N(T_i^D)/\hat{G}_N(t)} + \frac{I(T_i^D > t+h)}{\hat{G}_N(t+h)/\hat{G}_N(t)}$$

$T_i^D$  = observed survival time ;  $\delta_i$  = event indicator

$N_t$  = patients alive and uncensored at  $t$

$\hat{G}_N(t)$  = KM estimate or adjusted Cox estimate of the censoring distribution

Validated by a 10-fold cross-validation

*Brier. Monthly Weather Review 1950 - Gerds et al. Biometrical J 2006*

# Dynamic prediction : Error of prediction

To be able to compare different populations : residual error  
 $R^2$

$$R^2 = 1 - Err_{t+h} / Err_{t+h}^0$$

with  $Err_{t+h}$  as previously defined  
 $Err_{t+h}^0$  the prediction error from a Kaplan-Meier model  
(average survival predicted for each patient)

*Graf. Stat Med 1999*

# Application

## *1. On the French cohort*

# Development cohort

- Model development
  - Variable selection
  - Parameters estimation
- Internal validation of the prediction
  - Apparent error
  - Cross-validated error

# French cohort

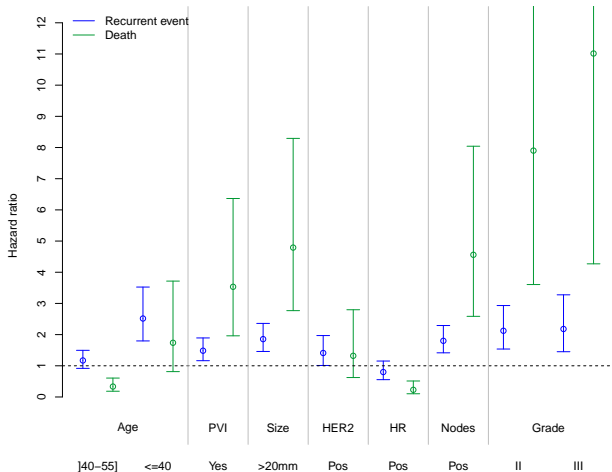
- 1067 patients
- median follow-up : 13.8 years (min=5 months)
- 427 recurrent events (locoregional relapses and distant metastases) in 362 patients (mean 0.40)

N events	0	1	2	3	All
Alive	600	114	20	3	737
Died	105	187	37	1	330
All	705	301	57	4	1067

with the R package **frailtypack**

<http://cran.r-project.org/web/packages/frailtypack/>

# Prognostic joint model



$\theta=1.03$  (se=0.06) and  $\alpha=4.66$  (se=0.28)

## Prediction values between 5 and 10 years

Recurrence history	$P^{Recurrence}(5, 10; \hat{\xi})$	$P^{Ignoring}(5, 10; \hat{\xi})$
No recurrence	10.8 (4.2)	12.7 (4.5)
One recurrence	30.3 (8.9)	12.7 (4.5)
Two recurrences	50.6 (11.4)	12.7 (4.5)
Three recurrences	67.4 (11.9)	12.7 (4.5)

For a given patient : age > 55y, no PVI, size  $\leq$  20mm, HER2 negative, HR positive, no lymph node involvement, grade II.



## Prediction values between 5 and 15 years

Recurrence history	$P^{Recurrence}(5, 15; \hat{\xi})$	$P^{Ignoring}(5, 15; \hat{\xi})$
No recurrence	22.7 (4.8)	25.6 (4.7)
One recurrence	53.0 (6.9)	25.6 (4.7)
Two recurrences	75.6 (6.0)	25.6 (4.7)
Three recurrences	88.4 (4.1)	25.6 (4.7)

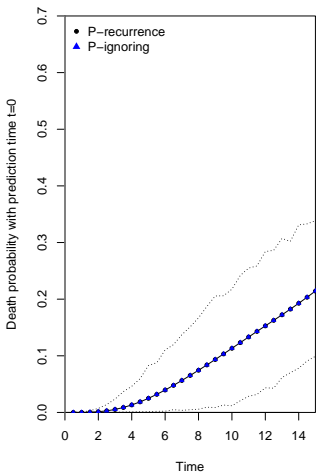
For a given patient : age > 55y, no PVI, size  $\leq$  20mm, HER2 negative, HR positive, no lymph node involvement, grade II.

# Death prediction for 2 particular cases

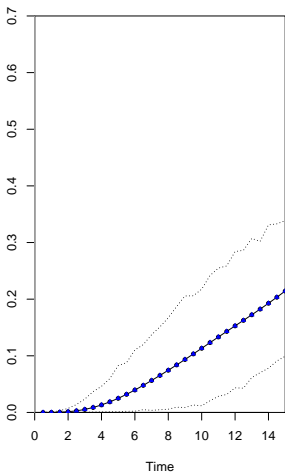
## Baseline prediction

between 40 and 55 y, no peritum. vasc. invasion, tumour size  $\leq 20$  mm, HER2 -, HR +, no lymph node invol., grade II

**Patient 1**  
With recurrences



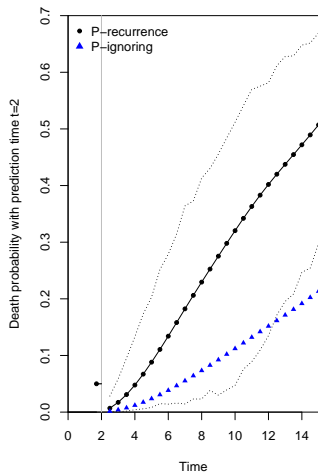
**Patient 2**  
Without recurrence



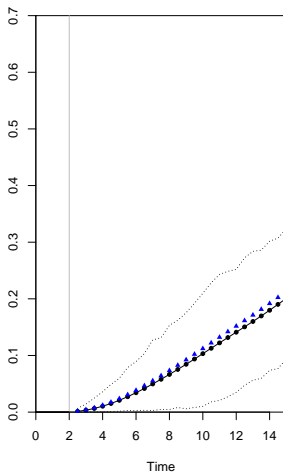
# Death prediction for 2 particular cases

Prediction time  $t=2$  years

**Patient 1**  
With recurrences



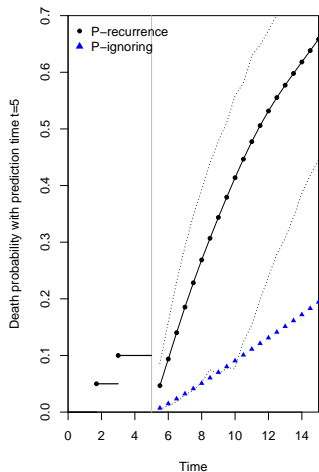
**Patient 2**  
Without recurrence



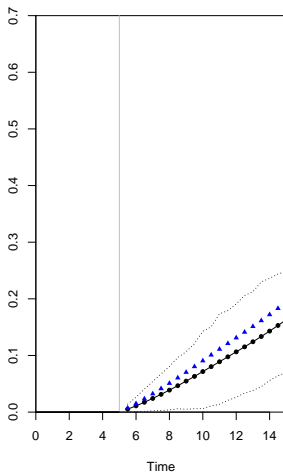
# Death prediction for 2 particular cases

Prediction time  $t=5$  years

**Patient 1**  
With recurrences



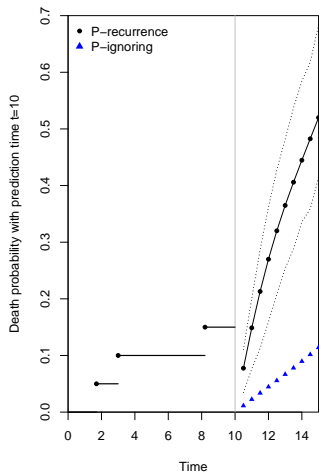
**Patient 2**  
Without recurrence



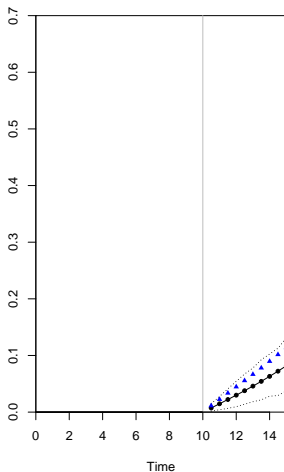
# Death prediction for 2 particular cases

Prediction time  $t=10$  years

**Patient 1**  
With recurrences

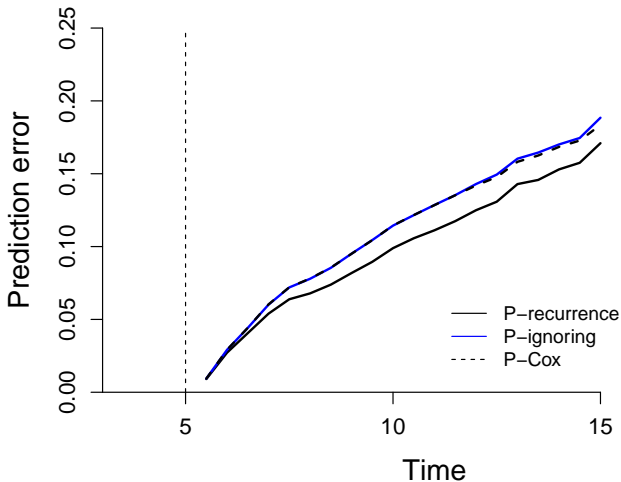


**Patient 2**  
Without recurrence



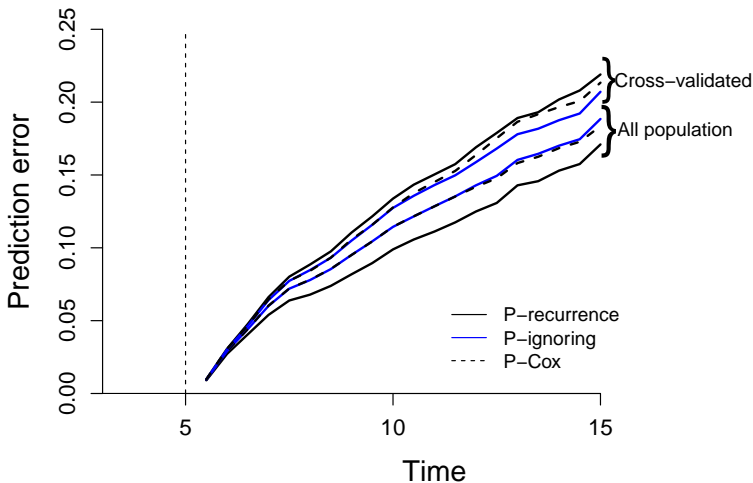
# Death prediction error

Prediction at 5 years (949 patients alive)



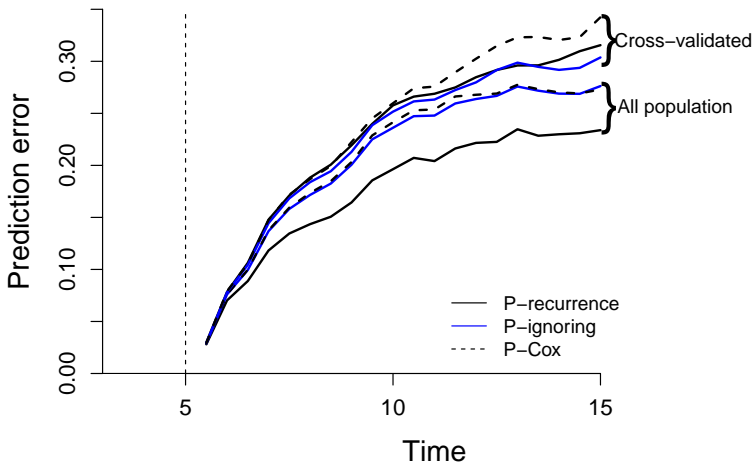
# Prediction error

Prediction at 5 years (949 patients alive), with 10-fold cross-validation



# Prediction error

Prediction at 5 years (267 patients alive with recurrence),  
with 10-fold cross-validation





## At this step

- Found the prognostic factors of interest
- Estimated parameters (factor effects, correlation between the two endpoints)
- Were able to account for relapses in the prediction of the risk of death
- Not clear whether accounting for relapses has an interest for prediction

# Application

## *2. External validation*

# External validation - why ?

- Model designed to perform well on development data
  - problem with the design or methods
  - absence of an important predictor
- To check the **reproducibility** of the model and predictions
  - overfitting
    - correct for optimism
  - difference case-mix
- To update the proposed prognostic model

# Models to be compared

- Joint frailty model
  - + One model  $\rightarrow$  dynamic prediction
  - + Correlation between the two processes fully accounted for
  - more parameters  $\rightarrow$  less stability
  
- Landmark Cox model
  - + Robust and simple model
  - + Time-dependent effects
  - One model for each prediction time  $t$
  - Information about recurrent events : number of recurrent events

# Populations - description

## West Midlands

- 1196 subjects
- Diagnosed in 1996
- Follow-up : 16 years
- 376 relapses in 301 patients (mean=0.31)
- 613 deaths (51%)

## Dutch registry

- 31,075 subjects
- Diagnosed in 2003-2006
- median follow-up : 7.7 y
- 3854 relapses in 3844 patients (mean=0.12)
- 7162 deaths (23%)

# Populations - missing data

- Missing data problem not much discussed in the literature in that context
- Not an effect estimation problem
- Clinical point of view  
→ complete case analysis

## West Midlands

- 1196 subjects
- from 3168 cases (38%)
- HER2 and hormonal receptor unavailable

## Dutch registry

- 31,075 subjects
- from 41,676 cases (75%)
- HER2 and hormonal receptor unavailable
- Perivascular invasion unavailable

# Populations - Relapses definitions

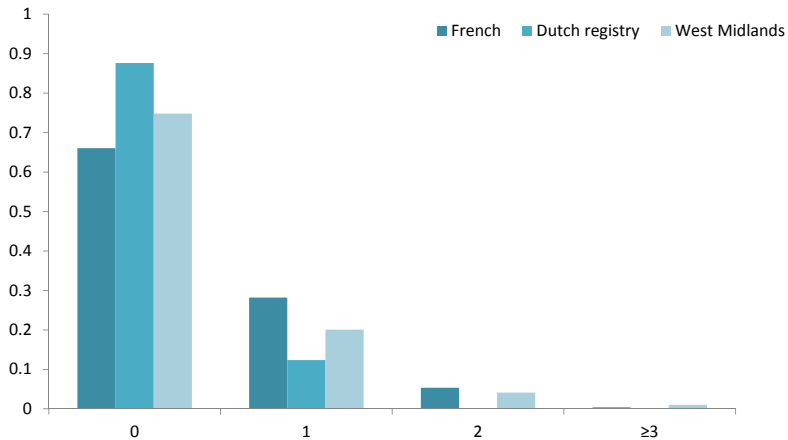
## West Midlands

- Recurrence defined from treatment
- 376 relapses
  - 22% <2 years
  - 59% <5 years

## Dutch registry

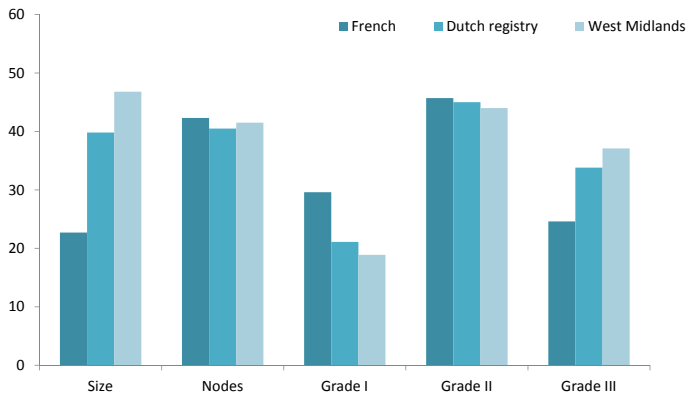
- Recurrences recorded (only the 1<sup>st</sup> one of each type)
- 3854 relapses
  - 41% <2 years
  - 93% <5 years

# Populations - recurrent event

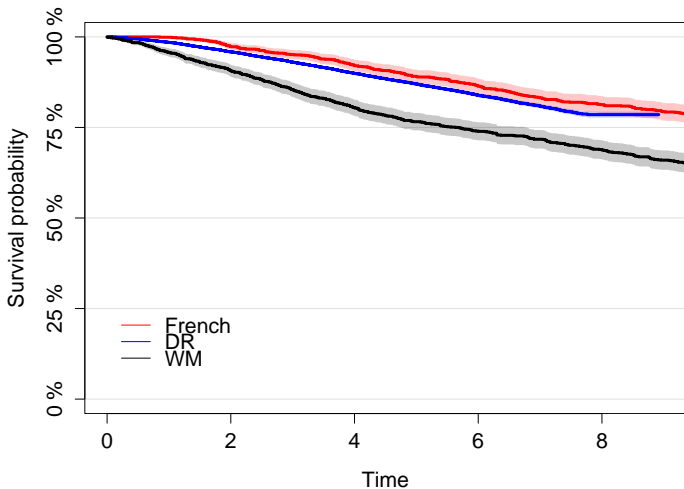




# Populations - prognostic factors



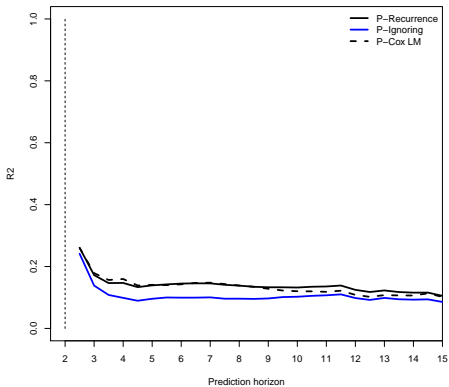
# Populations - overall survival



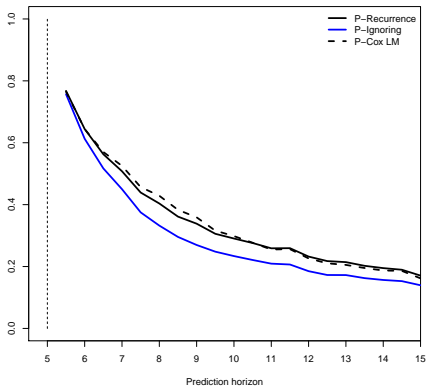
[n.risk] 1067 1065 1049 1019 999 966 940 907 874 841 815

# West Midlands population

$t=2$  years

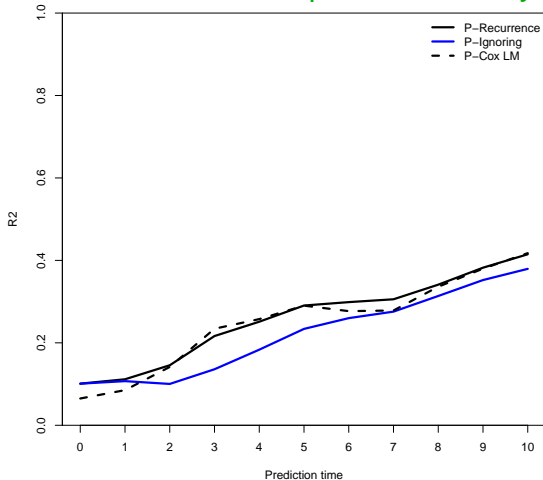


$t=5$  years

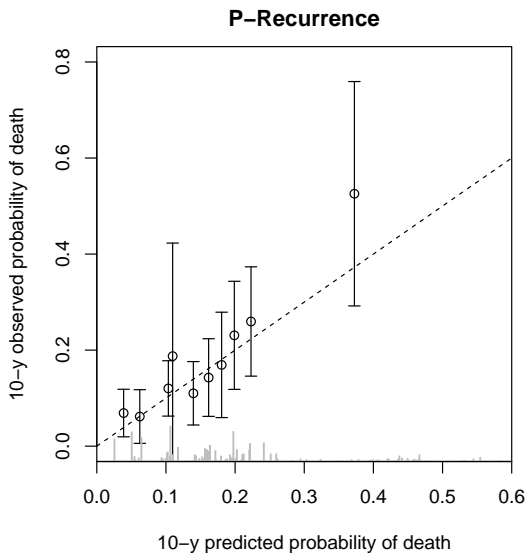


# West Midlands population

Fixed window of prediction  $h=5$  y

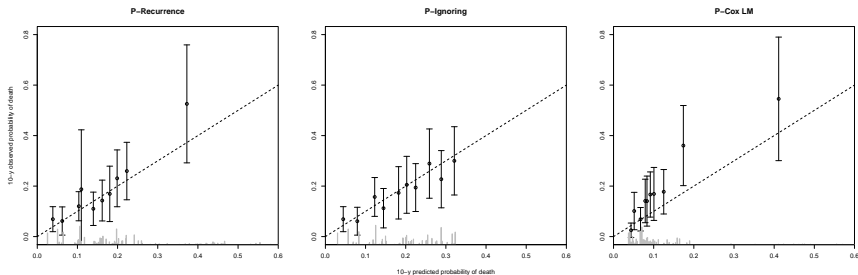


## West Midlands population - Calibration at 10 years ( $t=5$ years)



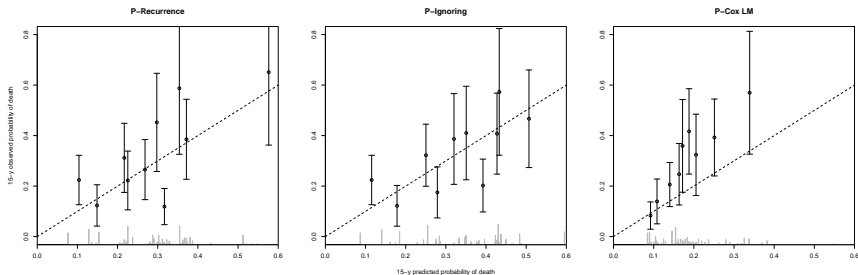
# West Midlands population

## Calibration at 10 years ( $t=5$ years)



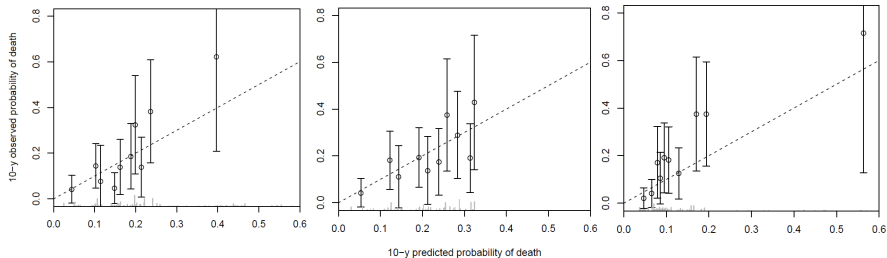
# West Midlands population

## Calibration at 15 years ( $t=5$ years)



# Subgroup analysis

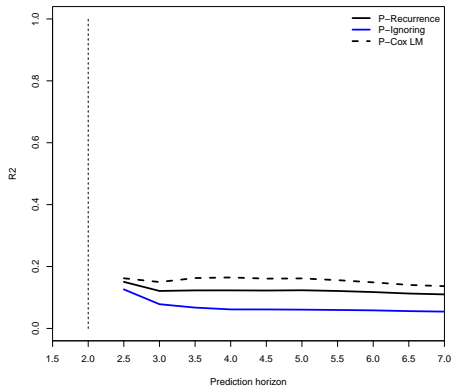
West Midlands population - operated patients



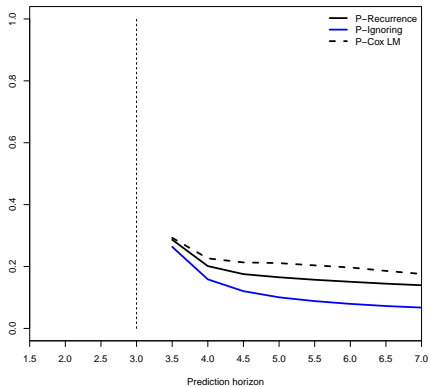


# Dutch population

$t=2$  years

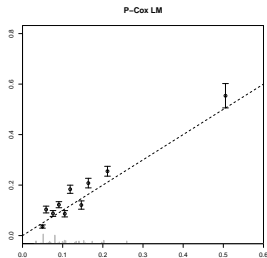
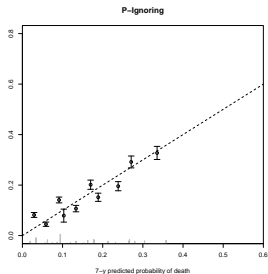
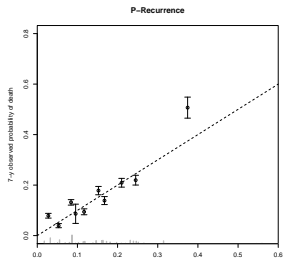


$t=3$  years



# Dutch population

## Calibration at 7 years ( $t=2$ years)



# At the end

- Relapses information is **useful to predict** the death of patients with breast cancer
- The **more information**, the better relapses information prior to 2-3 years not enough
- Two approaches (joint and landmark) give similar performance
  - Do not be afraid to use complex model (with more parameters) in prediction **if needed**

# At the end

- The model estimated on a **selected** cohort of patients can be useful in more general populations
  - Good performance in West Midlands population despite
    - a different survival in the population
    - a different period of inclusion
    - a different case-mix
  - Prediction not good in Dutch registry patients
    - Short follow-up
    - Patient recently diagnosed
    - impact of change in the clinical practice ?

## And then ?

- Considering the **type of recurrence**  
Different effect of loco-regional relapse and metastasis on the risk of death
  
- Predict the **risk of recurrence**  
For example, risk of metastasis considering the previous loco-regional relapses

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<http://cran.r-project.org/web/packages/frailtypack/>

<http://cran.r-project.org/web/packages/pec/>

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