## Association between tumor size kinetics and survival in urothelial carcinoma patients treated with atezolizumab: implication for patient's follow-up

## <u>C. Tardivon<sup>1</sup></u>, S. Desmée<sup>2</sup>, M. Kerioui<sup>1,2</sup>, R. Bruno<sup>3</sup>, B. Wu<sup>4</sup>, F. Mentré<sup>1</sup>, F. Mercier<sup>5</sup>, J. Guedj<sup>1</sup>

IAME, UMR 1137, INSERM, Université Paris Diderot, Sorbonne Paris Cité Paris, France.
 Université de Tours, Université de Nantes, Inserm SPHERE, UMR 1246, Tours, France.
 Clinical Pharmacology, Roche/Genentech, Marseille, France.

 $^{4}$  Clinical Pharmacology, Genentech Inc, South San Francisco, CA, USA.

<sup>5</sup> Clinical Pharmacology, Roche Innovation Center, Basel, Switzerland.

PAGE Meeting - Oncology session

June 14<sup>th</sup> 2019





La science pour la sante From science to health



Infection • Antimicrobials • Modelling • Evolution



INTRODUCTION
000
CONTEVI

Phase 2 - Model Building 00000 Phase 3 - Model Validation 00000 Discussion 00

#### Atezolizumab in metastatic urothelial carcinoma (mUC)

- mUC is the 10<sup>th</sup> most common form of cancer worldwide <sup>1</sup>
- platinum-based chemotherapy is the standard of care<sup>2</sup>
- poor prognosis for patients progressing after a first line of chemotherapy <sup>3</sup>
- immune-oncology opens a new way in cancer : "Immune checkpoint inhibitors"
   → atezolizumab approved by FDA in 2016 for mUC patients not responding to
   chemotherapy

#### Treatment evaluation usually relies on the analysis of both

- overall survival
- response to treatment → guided by the longitudinal evolution of a biomarker (e.g. tumor size with RECIST)

#### Analyzing a biomarker kinetics can provide a better understanding of survival

The association between the tumor size dynamics and the survival is particularly complex and remains poorly characterized <sup>4, 5</sup>



<sup>1.</sup> Bray et al. (2018) CA Cancer J Clin

<sup>2.</sup> Von der Maase (2005) J Clin Oncol

<sup>3.</sup> Bellmunt et al. (2009) J Clin Oncol

<sup>4.</sup> Bellmunt et al. (2017) N Engl J Med

<sup>5.</sup> Powles et al. (2018) Lancet

INTRODUCTION

Phase 2 - Model Bui 00000 Phase 3 - Model Validati 00000

# JOINT MODELS IN ANALYZING THE ASSOCIATION BETWEEN TUMOR SIZE DYNAMICS AND OVERALL SURVIVAL

## Introducing a biomarker kinetics as a time-dependent covariate in a survival model can lead to methodological issues

- bias generated by the inclusion of an endogenous covariate → subject to informative censoring<sup>1, 2</sup>
- measurements made with error, and variation over time considered piecewise constant  $^3$



#### A proper way to overcome these issues is to use a JOINT MODELING approach

- longitudinal estimation
- survival estimation
- account for the correlation between those two processes
- 1. Rizopoulos (2012) Joint Models for Longitudinal and Time-to-Event Data
- 2. Hu and Sale (2003) J Pharmacokinet Pharmacodyn
- 3. Tsiatis, DeGruttola and Wulfsohn (1995) J Am Stat Assoc

INTRODUCTION	Strategy
000	00
<b>STUDY OBJECTIVES</b>	

- To characterize the association between tumor size kinetics, baseline covariates and overall survival using a nonlinear joint model
- **9** To evaluate the possibility to characterize "in real time" patient's profile of response and early detect patients most-at-risk of death or progression

INTRODUCTION	
000	

#### STRATEGY FOR MODEL BUILDING AND MODEL VALIDATION

#### PHASE 2 - Learning dataset (N=309)

## Nonlinear mixed-effects model to describe tumor size kinetics

- structural model selection
- covariate selection

#### Parametric model for survival

covariate selection

#### JOINT MODELING

- link function selection
- Goodness-of-fit assessment

Lancet, 2016 May 7;387(10031):1909-20. doi: 10.1016/S0140-6736(16)00561-4. Epub 2016 Mar 4.

Atezolizumab in patients with locally advanced and metastatic urothelial carcinoma who have progressed following treatment with platinum-based chemotherapy: a single-arm, multicentre, phase 2 trial.

Rosenbero JE<sup>1</sup>, Hoffman-Censits J<sup>2</sup>, Powies T<sup>3</sup>, van der Heijden MS<sup>4</sup>, Balar AV<sup>5</sup>, Netchi A<sup>6</sup>, Dawson N<sup>7</sup>, O'Donnell PH<sup>8</sup>, Balmanoukian A<sup>9</sup>, Loriot X<sup>10</sup>, Sminkas S<sup>11</sup>, Retz Min<sup>12</sup>, Grinxa E<sup>13</sup>, Jasenb RW<sup>14</sup>, Galsky MB<sup>15</sup>, Elemino JM<sup>16</sup>, Petrolak DP<sup>17</sup>, Peterz Carcia JL<sup>18</sup>, Burnit HA<sup>47</sup>, Gastellano D<sup>22</sup>, Canil C<sup>21</sup>, Bellmunt J<sup>22</sup>, Biogenin D<sup>22</sup>, Micken D<sup>24</sup>, Baurogen R<sup>34</sup>, Hammoto GM<sup>26</sup>, Gull<sup>24</sup>, Maintahasan S<sup>24</sup>, Adobyo C<sup>24</sup>, Fine GD<sup>24</sup>, Direice R<sup>26</sup>,

▲□▶ <圖▶ < ≣▶ < ≣▶ < ■■ <1</li>



Atezoilzumao versus chemotherapy in patients with platinum-treated locally advanced or metastatic urothelial carcinoma (IMvigor211): a multicentre, open-label, phase 3 randomised controlled trial.

Pendes 11 Duran 17, vana der Heisten MS<sup>3</sup>, Lond X<sup>4</sup>, Vorgetann MF<sup>5</sup>, Da Greip U<sup>6</sup>, Oudrad S<sup>7</sup>, Reiz MM<sup>4</sup>, Castellano D<sup>8</sup>, Bamias A<sup>10</sup>, Fichon A<sup>11</sup>, Grein MC<sup>15</sup>, G<sup>12</sup>, Hussan S<sup>13</sup>, Talamo T<sup>14</sup>, Leng M<sup>6</sup>, Kadel EE 2nd<sup>16</sup>, Banchereau R<sup>15</sup>, Heode PS<sup>16</sup>, Mariathasan S<sup>15</sup>, Cui N<sup>15</sup>, Shen X<sup>15</sup>, Dericht Cl<sup>15</sup>, Green MC<sup>15</sup>, Ranaud A<sup>16</sup>. Strategy

Phase 2 - Model Building 00000 Phase 3 - Model Validatio

#### BASELINE CHARACTERISTICS

	Learning dataset	Validation dataset
	PHASE 2	PHASE 3
Number of patients	309	457
Categorical covariates	%	(N)
Presence of baseline liver metastasis	31 (95)	30 (136)
Female sex	22 (69)	23 (107)
Baseline ECOG score = $1$	62 (192)	53 (242)
$\geq$ 5% of PD-L1 positive immune cells	32 (100)	25 (113)
>1 prior line of systemic therapies in the metastatic setting	52 (162)	29 (133)
>1 metastatic sites at baseline	67 (208)	62 (283)
Previous therapy with platinum-based regimen		
Cisplatin-based	73 (226)	56 (255)
Carboplatin-based	26 (80)	42 (192)
Other platinum combination	1 (3)	2 (9)
$\geq$ 1% of PD-L1 positive tumour cells	20 (61)	27 (123)
Continuous covariates	Median (min - max)	
Age	66 (32 - 91)	67 (33 - 88)
Baseline albumin concentration $(g.L^{-1})$	37 (27 - 49)	39 (20 - 54)
Baseline alkaline phosphatase value $(U.L^{-1})$	96 (34 - 612)	96 (36 - 1409)
Baseline lactate dehydrogenase value $(U.L^{-1})$	216.5 (107 - 1642)	221.5 (0.8 - 1603)
Baseline neutrophil-to-lymphocyte ratio	5.6 (1.5 - 69)	3.5 (0.6 - 60)
Baseline C-reactive protein concentration $(mg.L^{-1})$	26.7 (0.83 - 288)	15.2 (0.21 - 318)
Baseline hemoglobin concentration $(g.L^{-1})$	109 (85 - 150)	82 (79 - 162)
Baseline sum of target lesions diameters (mm)	64 (10 - 329)	53 (10 - 301)
Median overall survival (days)	243	272

▲□▶ < ⓓ▶</li>
 ▲ 邑▶ < 邑▶</li>
 ▲ 邑▶
 ▲ □▶

INTRODUCTION		
000		

Phase 2 - Model Building 0000

Phase 3 - Model Validation 00000

#### NONLINEAR JOINT MODELS

 $\rightarrow$  2 sub-models

LONGITUDINAL PART - Nonlinear mixed-effects model (NLMEM)

$$y_{ij} = b(t_{ij}, \psi_i) + \left(\sigma_{inter} + \sigma_{slope} \ b(t_{ij}, \psi_i)\right) \epsilon_{ij}$$

- **b** : process of interest (tumor size) **possibly non-linear**
- $\psi_i$ : individual longitudinal parameters as a function of fixed effects  $\mu$ , random effects  $\eta_i \sim \mathcal{N}(0, \Omega)$  and covariates  $z_i$  $\hookrightarrow$  e.g. log-normal distribution for  $\psi_i \Rightarrow \psi_i = \mu \times e^{\eta_i + c \cdot z_i}$

• 
$$\epsilon_{ij}$$
 : residual error with  $\epsilon_{ij} \sim \mathcal{N}(0, 1)$ 

#### SURVIVAL PART

- $T_i$  : observed event time
- $\delta_i$ : event indicator =  $\begin{cases}
  1 & \text{if event observed} \\
  0 & \text{if event not observed}
  \end{cases}$



Hazard function for patient i:

$$h_i(t|\psi_i) = h_0(t) \exp(\beta \times \boldsymbol{f}(t,\psi_i)) \quad \text{ for } t \geq 0$$

$$\hookrightarrow S_i(t|\psi_i) = P(T_i \ge t) = \exp\left[-\int_0^t h_i(u|\psi_i) du\right]$$

• Link function f depends on  $\psi_i$ 

INTRODUCTION	Strategy
000	00

Phase 2 - Model Building

Phase 3 - Model Validation 00000 Discussion 00

#### LONGITUDINAL SUB-MODEL

#### LONGITUDINAL PART

Structural model selection by BIC

Wang model<sup>1</sup>  $SLD(t) = \begin{cases} BSLD e^{g t} & \text{if } t < tx \\ BSLD e^{g tx} \cdot (e^{-d(t-tx)+g \cdot tx} + g(t-tx)) & \text{if } t \ge tx \end{cases}$ 

## Stein-Fojo model<sup>2</sup> $SLD(t) = \begin{cases} BSLD \ e^{g \ t} & \text{if } t < tx \\ BSLD \ e^{g \ tx} \cdot (e^{-d(t-tx)} + e^{g(t-tx)} - 1) & \text{if } t \ge tx \end{cases}$

### Tumor size model with parameter $\phi$ for proportion of cells sensitive to treatment <sup>3</sup>

 $SLD(t) = \begin{cases} BSLD \ e^{g \ t} & \text{if } t < tx \\ BSLD \ e^{g \ tx} \times (\phi e^{-d(t-tx)} + (1-\phi)e^{g(t-tx)}) & \text{if } t \ge tx \end{cases}$ 

1. Wang et al. (2009) Clin Pharmacol Ther

2. Stein et al. (2008) Oncologist

3. Chatterjee et al. (2017) CPT Pharmacomet Syst Pharmacol

Strate
00

rategy O Phase 2 - Model Building

Phase 3 - Model Validation

Discussion 00

#### LONGITUDINAL SUB-MODEL

#### LONGITUDINAL PART





*t* : time since inclusion (days) *tx* : time elapsed between inclusion and treatment onset

SLD : Sum of target lesions diameters (mm)BSLD : SLD at inclusion time (mm)d : tumor shrinkage parameterg : tumor growth parameter

#### Tumor size model with parameter $\phi$ for proportion of cells sensitive to treatment <sup>1</sup>

$$SLD(t) = \begin{cases} BSLD \ e^{g \ t} & \text{if } t < tx \\ BSLD \ e^{g \ tx} \times (\phi e^{-d(t-tx)} + (1-\phi)e^{g(t-tx)}) & \text{if } t \ge tx \end{cases}$$

$$\Rightarrow \text{TTG} = \frac{\log\left(\frac{d\phi}{g(1-\phi)}\right)}{g+d} + tx$$

#### Forward covariate selection by BIC

1. Chatterjee et al. (2017) CPT Pharmacomet Syst Pharmacol

INTRODUCTION	5
000	

Phase 2 - Model Building

Phase 3 - Model Validatio

Discussion 00

#### SURVIVAL SUB-MODEL AND LINK FUNCTION SELECTION

#### SURVIVAL PART

$$h_i(t|\psi_i) = h_0(t) \exp(\gamma^T z_i + \beta^T f(t, \psi_i))$$

Weibull baseline hazard function  $h_0(t) = \frac{k}{\lambda} \left( \frac{t}{\lambda} \right)^{k-1}$ 

#### Forward covariate selection by BIC : $z_i$

Link function f depends on SLD kinetics of patient i through the true longitudinal process

( d.d.)

 $\Rightarrow$  Forward selection by BIC :

- Baseline covariates :  $f(t, \psi_i) = 0$
- Current SLD :  $f(t, \psi_i) = SLD(t, \psi_i)$

• Current SLD slope : 
$$f(t, \psi_i) = \frac{d SLD(t, \psi_i)}{dt}, t \ge tx_i$$

• Time-to-growth (TTG): 
$$f(t, \psi_i) = \frac{\log\left(\frac{d_i}{g_i - \phi_i}\right)}{g_i + d_i} + tx_i$$

INTROD	UCTION
000	

Phase 2 - Model Building

Phase 3 - Model Validatio

## JOINT MODEL RESULTS

#### BIC and parameters estimates (R.S.E. (%)) of tumor size kinetics and survival

MODELS	<b>Baseline covariates</b>	Current SLD	Current SLD slope	TTG	TTG and current SLD slope
BIC	12525	12463	12456	12442	12416
LONGITUDINAL SUB-MODEL					
BSLD (mm)	53.7 (4)	53.6 (4)	53.4 (4)	53.8 (4)	53.5 (4)
Presence of baseline liver metastasis	0.47 (16)	0.47 (16)	0.47 (16)	0.47 (16)	0.47 (16)
Hemoglobin at baseline $(g.L^{-1})$	-0.01 (20)	-0.01 (29)	-0.01 (20)	-0.01 (20)	-0.01 (20)
$d (day^{-1})$	0.00667 (18)	0.00675 (17)	0.00669 (17)	0.00923 (13)	0.00881 (14)
$g (day^{-1})$	0.0012 (17)	0.0013 (17)	0.0015 (17)	0.0011 (16)	0.0013 (17)
Presence of baseline liver metastasis	0.917 (23)	0.965 (23)	0.873 (23)	0.936 (22)	0.901 (23)
$\phi$	0.104 (53)	0.089 (53)	0.104 (49)	0.0352 (53)	0.0421 (59)
Alkaline phosphatase at baseline $(U.L^{-1})$	-0.0283 (28)	-0.0285 (27)	-0.0281 (26)	-0.0273 (23)	-0.0268 (29)
SURVIVAL SUB-MODEL					
$\lambda ({\rm day}^{-1})$	546 (15)	922 (18)	733 (16)	288 (14)	368 (15)
≥ 5% of PD-L1-positive immune cells	-0.59 (26)	-0.51 (32)	-0.57 (31)	-0.32 (53)	-0.34 (53)
Baseline ECOG score = 1	0.604 (26)	0.57 (30)	0.72 (25)	0.36 (46)	0.453 (40)
Alkaline phosphatase at baseline $(U.L^{-1})$	0.0038 (17)	0.0027 (26)	0.0039 (19)	0.0034 (20)	0.0036 (21)
Baseline neutrophil-to-lymphocyte ratio	0.0503 (17)	0.055 (17)	0.053 (20)	0.0496 (20)	0.0509 (21)
Hemoglobin at baseline $(g.L^{-1})$	-0.0131 (34)	-0.0105 (47)	-0.0124 (41)	-0.0152 (31)	-0.0145 (35)
>1 metastatic sites at baseline	0.41 (39)	0.22 (81)	0.38 (49)	0.35 (50)	0.30 (62)
k	1.2 (5)	1.19 (4)	1.31 (4)	1.45 (6)	1.5 (5)
$\beta_{\rm current \ SLD} \ (\rm mm^{-1})$	-	0.00732 (15)	-	-	-
$\beta_{\rm TTG}  ({\rm day}^{-1})$	-	-	-	-0.00758 (17)	-0.0064 (20)
$\beta_{\text{current SLD slope}} (\text{mm}^{-1}.\text{day})$	-	-	1.1 (10)	-	<b>0.697</b> (13)

INTRODUCTION	Strat
000	00

rategy D Phase 2 - Model Building

Phase 3 - Model Validation 00000

#### Model illustration



- $\beta_{\rm TTG} < 0 \Rightarrow$  durable response associated with extended OS
- $\beta_{\text{current SLD slope}} > 0 \Rightarrow$  instantaneous response to treatment (i.e. pace of tumor growth during relapse) directly related to OS

 $\Rightarrow$  need to rapidly identify the time of tumor relapse in order to minimize the time window where the tumor will grow  $\Rightarrow$ 

INTRODUCTION	Strategy	Phase 2 - Model Building
000	00	00000
DYNAMIC PREDICTIC	ONS OF A NEW INDI	VIDUAL <sup>1, 2, 3</sup>



#### • Landmark time *s*

• Horizon time window *t* 

Assumption : *true* joint model is known → *Population parameters used as priors* 



1. Rizopoulos (2011) Biometrics

- 2. Rizopoulos (2012) Joint Models for Longitudinal and Time-to-Event Data
- Desmée et al. (2017) BMC Med Res Methodol

INTRODUCTION	Strategy	Phase 2 - Model Building	Phase 3 - Model Validation	Discussion
000	00	00000	0000	00
Dynamic pred	ICTIONS OF A NEV	V INDIVIDUAL <sup>1, 2, 3</sup>		

→ Predict  $S_i(s + t|s) = \mathbb{P}(X_i > s + t|X_i > s, \mathcal{Y}_i(s))$  the conditional survival probability up to the prediction horizon s + t with t > 0

- Landmark time s
- Horizon time window *t*

Assumption : *true* joint model is known → *Population parameters used as priors* 



1. Rizopoulos (2011) Biometrics

12/0

<sup>2.</sup> Rizopoulos (2012) Joint Models for Longitudinal and Time-to-Event Data

<sup>3.</sup> Desmée et al. (2017) BMC Med Res Methodol



→ Predict  $S_i(s + t|s) = \mathbb{P}(X_i > s + t|X_i > s, \mathscr{Y}_i(s))$  the conditional survival probability up to the prediction horizon s + t with t > 0

- Landmark time s
- Horizon time window *t*

Assumption : *true* joint model is known → *Population parameters used as priors* 

For  $\ell = 1, ..., L$ :

- Draw in the *a posteriori* distribution of the individual parameters ψ<sup>(ℓ)</sup><sub>i</sub>
- **2** Compute  $S_i^{\ell}(s+t|s) + 90\%$  credibility interval



イロト スポト イヨト イヨト

<sup>1.</sup> Rizopoulos (2011) Biometrics

<sup>2.</sup> Rizopoulos (2012) Joint Models for Longitudinal and Time-to-Event Data

<sup>3.</sup> Desmée et al. (2017) BMC Med Res Methodol

 Introduction
 Strattegy
 Phase 2 - Model Building
 Phase 3 - Model Validation

 000
 00
 00000
 00000

 DISCRIMINATION AND CALIBRATION METRICS 1, 2

Discrimination - ability of the model to distinguish patients of low and high risk of death

Area under the ROC curve (AUC)

$$AUC(s,t) = \mathbb{P}(S_i(s+t|s) < S_j(s+t|s)|\mathbf{1}_{\{X_i < s+t\}} = 1, \mathbf{1}_{\{X_j < s+t\}} = 0, X_i > s, X_j > s)$$

The higher the better

#### Discrimination

+

Calibration - ability of the model to predict future events

→ Brier score (BS)

 $BS(s,t) = \mathbb{E}[(\mathbf{1}_{\{X > s+t\}} - S(s+t|s))^2 | X > s]$ 

The lower the better

13/0

<sup>1.</sup> Blanche et al. (2015) Biometrics

<sup>2.</sup> Desmée et al. (2017) BMC Med Res Methodol



Discrimination - ability of the model to distinguish patients of low and high risk of death

Area under the ROC curve (AUC)

 $AUC(s,t) = \mathbb{P}(S_i(s+t|s) < S_j(s+t|s) | \mathbf{1}_{\{X_i < s+t\}} = 1, \mathbf{1}_{\{X_j < s+t\}} = 0, X_i > s, X_j > s)$ 

The higher the better

Discrimination

+ Calibration - ability of the model to predict future events

**→ Brier score** (BS)

```
BS(s, t) = \mathbb{E}[(\mathbf{1}_{\{X > s+t\}} - S(s+t|s))^2 | X > s]
```

The lower the better

13/0

<sup>1.</sup> Blanche et al. (2015) Biometrics

<sup>2.</sup> Desmée et al. (2017) BMC Med Res Methodol

## AUC FOR VARIOUS LANDMARK AND HORIZON TIMES

95% CI based on the bootstrap percentile method  $^3$ 

			Horizon windows (months)			
AUC		Models	t = 3	t = 6	t = 9	t = 12
		Baseline covariates	0.73 (0.66 - 0.79)	0.76 (0.71 - 0.81)	0.75 (0.71 - 0.80)	0.73 (0.68 - 0.77)
	s = 0					
		TTG + Current SLD slope	0.76 (0.71 - 0.82)	0.79 (0.74 - 0.83)	0.77 (0.73 - 0.81)	0.74 (0.70 - 0.79)
		Baseline covariates	0.75 (0.70 - 0.81)	0.73 (0.67 - 0.78)	0.69 (0.64 - 0.74)	0.70 (0.64 - 0.76)
	s = 3					
					0.78 (0.74 - 0.83)	
		TTG + Current SLD slope	0.84 (0.79 - 0.89)	0.81 (0.77 - 0.85)	0.81 (0.77 - 0.85)	0.82 (0.77 - 0.86)
		Baseline covariates	0.65 (0.58 - 0.72)	0.62 (0.56 - 0.69)	0.64(0.57 - 0.71)	0.65 (0.58 - 0.73)
Landmark times	s = 6					
(months)						
		TTG + Current SLD slope	0.75 (0.69 - 0.82)	0.79 (0.73 - 0.84)	0.80 (0.75 - 0.85)	0.84 (0.79 - 0.89)
		Baseline covariates	0.55 (0.45 - 0.65)	0.60 (0.52 - 0.68)	0.63 (0.54 - 0.72)	-
	s = 9					
		TTG + Current SLD slope	0.76 (0.69 - 0.84)	0.76 (0.69 - 0.82)	0.82 (0.75 - 0.88)	-
		Baseline covariates	0.65 (0.53 - 0.75)	0.68 (0.58 - 0.77)	-	-
				0.82 (0.74 - 0.89)		
	s = 12					
		TTG + Current SLD slope	0.73 (0.63 - 0.82)	0.82 (0.75 - 0.89)	-	-

3. Qin and Hotilovac (2008) Stat Methods Med Res

## AUC FOR VARIOUS LANDMARK AND HORIZON TIMES

95% CI based on the bootstrap percentile method  $^3$ 

			Horizon windows (months)			
AUC		Models	t = 3	t = 6	t = 9	t = 12
		Baseline covariates	0.73 (0.66 - 0.79)	0.76 (0.71 - 0.81)	0.75 (0.71 - 0.80)	0.73 (0.68 - 0.77)
	s = 0					
		TTG + Current SLD slope	0.76 (0.71 - 0.82)	0.79 (0.74 - 0.83)	0.77 (0.73 - 0.81)	0.74 (0.70 - 0.79)
		Baseline covariates	0.75 (0.70 - 0.81)	0.73 (0.67 - 0.78)	0.69 (0.64 - 0.74)	0.70 (0.64 - 0.76)
					0.79 (0.74 - 0.83)	
	s = 3					
					0.78 (0.74 - 0.83)	
		TTG + Current SLD slope	0.84 (0.79 - 0.89)	0.81 (0.77 - 0.85)	0.81 (0.77 - 0.85)	0.82 (0.77 - 0.86)
		Baseline covariates	0.65 (0.58 - 0.72)	0.62 (0.56 - 0.69)	0.64 (0.57 - 0.71)	0.65 (0.58 - 0.73)
Landmark times	s = 6					
(months)						
		TTG + Current SLD slope	0.75 (0.69 - 0.82)	0.79 (0.73 - 0.84)	0.80 (0.75 - 0.85)	0.84 (0.79 - 0.89)
		Baseline covariates	0.55 (0.45 - 0.65)	0.60 (0.52 - 0.68)	0.63 (0.54 - 0.72)	-
	s = 9					
		TTG + Current SLD slope	0.76 (0.69 - 0.84)	0.76 (0.69 - 0.82)	0.82 (0.75 - 0.88)	-
		Baseline covariates	0.65 (0.53 - 0.75)	0.68 (0.58 - 0.77)	-	-
				0.82 (0.74 - 0.89)		
	s = 12					
		TTG + Current SLD slope	0.73 (0.63 - 0.82)	0.82 (0.75 - 0.89)	-	-

3. Qin and Hotilovac (2008) Stat Methods Med Res

## AUC FOR VARIOUS LANDMARK AND HORIZON TIMES

95% CI based on the bootstrap percentile method  $^3$ 

			Horizon windows (months)			
AUC		Models	t = 3	t = 6	t = 9	t = 12
		Baseline covariates	0.73 (0.66 - 0.79)	0.76 (0.71 - 0.81)	0.75 (0.71 - 0.80)	0.73 (0.68 - 0.77)
		Current SLD	0.75 (0.69 - 0.81)	0.79 (0.74 - 0.83)	0.78 (0.73 - 0.82)	0.74 (0.69 - 0.79)
	s = 0	Current SLD slope	0.74 (0.68 - 0.80)	0.79 (0.74 - 0.83)	0.77 (0.73 - 0.81)	0.74 (0.69 - 0.78)
		TTG	0.75 (0.69 - 0.81)	0.78 (0.73 - 0.82)	0.76 (0.71 - 0.80)	0.74 (0.69 - 0.78)
		TTG + Current SLD slope	0.76 (0.71 - 0.82)	0.79 (0.74 - 0.83)	0.77 (0.73 - 0.81)	0.74 (0.70 - 0.79)
		Baseline covariates	0.75 (0.70 - 0.81)	0.73 (0.67 - 0.78)	0.69 (0.64 - 0.74)	0.70 (0.64 - 0.76)
		Current SLD	0.84 (0.78 - 0.88)	0.80 (0.75 - 0.84)	0.79 (0.74 - 0.83)	0.80 (0.75 - 0.84)
	s = 3	Current SLD slope	0.84 (0.79 - 0.89)	0.78 (0.73 - 0.83)	0.76 (0.71 - 0.81)	0.78 (0.73 - 0.83)
		TTG	0.79 (0.75 - 0.84)	0.79 (0.74 - 0.83)	0.78 (0.74 - 0.83)	0.78 (0.72 - 0.83)
		TTG + Current SLD slope	0.84 (0.79 - 0.89)	0.81 (0.77 - 0.85)	0.81 (0.77 - 0.85)	0.82 (0.77 - 0.86)
	s = 6	Baseline covariates	0.65 (0.58 - 0.72)	0.62 (0.56 - 0.69)	0.64(0.57 - 0.71)	0.65 (0.58 - 0.73)
Landmark times		Current SLD	0.72 (0.65 - 0.79)	0.74 (0.68 - 0.79)	0.78 (0.72 - 0.83)	0.81 (0.75 - 0.87)
		Current SLD slope	0.69 (0.61 - 0.76)	0.70 (0.64 - 0.76)	0.74 (0.68 - 0.80)	0.76 (0.69 - 0.82)
(months)		TTG	0.75 (0.69 - 0.81)	0.78 (0.72 - 0.83)	0.78 (0.72 - 0.84)	0.83 (0.77 - 0.89)
		TTG + Current SLD slope	0.75 (0.69 - 0.82)	0.79 (0.73 - 0.84)	0.80 (0.75 - 0.85)	0.84 (0.79 - 0.89)
		Baseline covariates	0.55 (0.45 - 0.65)	0.60 (0.52 - 0.68)	0.63 (0.54 - 0.72)	-
		Current SLD	0.71 (0.62 - 0.79)	0.73 (0.65 - 0.80)	0.79 (0.72 - 0.86)	-
	s = 9	Current SLD slope	0.67 (0.57 - 0.77)	0.70 (0.61 - 0.77)	0.75 (0.66 - 0.82)	-
		TTG	0.74 (0.67 - 0.81)	0.75 (0.68 - 0.81)	0.82 (0.75 - 0.88)	-
		TTG + Current SLD slope	0.76 (0.69 - 0.84)	0.76 (0.69 - 0.82)	0.82 (0.75 - 0.88)	-
		Baseline covariates	0.65 (0.53 - 0.75)	0.68 (0.58 - 0.77)	-	-
		Current SLD	0.73 (0.64 - 0.82)	0.82 (0.74 - 0.89)	-	-
	s = 12	Current SLD slope	0.71 (0.61 - 0.81)	0.76 (0.68 - 0.85)	-	-
		TTG	0.72 (0.62 - 0.82)	0.82 (0.75 - 0.90)	-	-
		TTG + Current SLD slope	0.73 (0.63 - 0.82)	0.82 (0.75 - 0.89)	-	-

3. Qin and Hotilovac (2008) Stat Methods Med Res

INTRODUCTION	
000	

Phase 2 - Model Building 00000 Phase 3 - Model Validation

#### Dynamic individual predictions

Example on 3 patients alive at 12 months

#### Landmark s=3 months



INTRODUCTION	
000	

Phase 2 - Model Building 00000 Phase 3 - Model Validation

#### DYNAMIC INDIVIDUAL PREDICTIONS

Example on 3 patients alive at 12 months

#### Landmark s=6 months



INTRODUCTION	
000	

Phase 2 - Model Building 00000 Phase 3 - Model Validation

#### DYNAMIC INDIVIDUAL PREDICTIONS

Example on 3 patients alive at 12 months

#### Landmark s=9 months



INTRODUCTION	Strategy	
000	00	

Phase 2 - Model Building

Phase 3 - Model Validation

#### Model predictions at the individual level



- Landmark s=6 months
- Horizon s+t=12 months

NTRODUCTION	STRATEGY	Phase 2 - Model Building	Phase 3 - Model Validation	DISCUSSION
Conclusion	00	00000	00000	•0
• We used	d a <b>joint modeling a</b> r	<b>proach</b> to characterize the relat	tionship between	
o tun	nor size kinetics	•	*	
o ove	erall survival			
o bas	senne covariates			

in mUC patients treated with atezolizumab.

- Time-to-growth (TTG) and the current SLD slope were identified as the best kinetic predictors of OS, in addition to baseline covariates.
- On-treatment tumor dynamic data included in a relevant statistical framework may be useful to identify most-at-risk patients in "real time".
- Nonlinear joint models pave the way to improve prediction at a population and individual level.

□ > < @ > < E > < E > E = <10,0</li>

INTRODUCTION	Strategy
000	00
LIMITS / PERSE	PECTIVES

Phase 2 - Model Building 00000

Our approach could be extended to increase the predictive ability of such models by including

- clinical events (e.g. our model did not account for other events associated to disease progression, like the apparition of new lesions)
- more frequent data, other longitudinal markers
- PK data to measure the impact of drug exposure on longitudinal kinetics and OS
- $\Rightarrow$  This will need the use of more complex and/or more mechanistic models

#### Acknowledgements

Clin Pharmacol Ther. 2019 Apr 15. doi: 10.1002/cpt.1450. [Epub ahead of print]

Association between tumor size kinetics and survival in urothelial carcinoma patients treated with atezolizumab: implication for patient's follow-up.

Tardivon C<sup>1</sup>, Desmée S<sup>2</sup>, Kerioui M<sup>1,2</sup>, Bruno R<sup>3</sup>, Wu B<sup>4</sup>, Mentré F<sup>1</sup>, Mercier F<sup>5</sup>, Guedj J<sup>1</sup>.



## Supervisor

## Jérémie Guedj

France Mentré Solène Desmée Marion Kerioui



**INSERM** colleagues



François Mercier René Bruno Benjamin Wu Thank you for your attention!

JUNE 14, 2019

★□ > ★□ > ★∃ > ★∃ > ★∃ = 410.00