Sequential Monte Carlo methods in Bayesian joint models for longitudinal and time-to-event data

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Statistical Modelling xxxx; **xx(x)**: 1–21

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Abstract: The statistical analysis of the information generated by medical follow-up is a very important challenge in the field of personalized medicine. As the evolutionary course of a patient's disease progresses, his/her medical follow-up generates more and more information that should be processed immediately in order to review and update his/her prognosis and treatment. Hence, we focus on this update process through sequential inference methods for joint models of longitudinal and time-to-event data from a Bayesian perspective. More specifically, we propose the use of sequential Monte Carlo (SMC) methods for static parameter joint models with the intention of reducing computational time in each update of the full Bayesian inferential process. Our proposal is very general and can be easily applied to most popular joint models approaches. We illustrate the use of the presented sequential methodology in a joint model with competing risk events for a real scenario involving patients on mechanical ventilation in intensive care units (ICUs).

Key words: Bayesian analysis, IBIS algorithm, joint models, sequential inference.

Received May 2019; **revised** February 2020; **accepted** March 2020

 10.1177/1471082X20916088

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Definition (National Academy of Science)

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Literature

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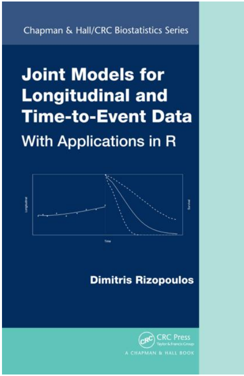

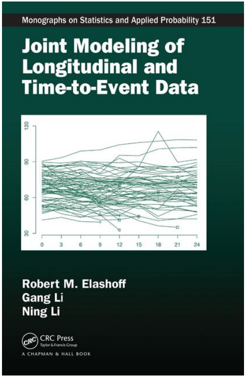

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3. Full joint probability distribution [Armero et al., 2018]:

$$f(\boldsymbol{y}, \boldsymbol{s}, \boldsymbol{b}, \theta) = f(\boldsymbol{y}, \boldsymbol{s} \mid \boldsymbol{b}, \theta)\, f(\boldsymbol{b} \mid \theta)\, \pi(\theta)$$

- $\boldsymbol{y}$: longitudinal; $\boldsymbol{s}$: survival; $\boldsymbol{b}$: random-effects; θ: parameters.
- $f(\boldsymbol{y}, \boldsymbol{s} \mid \boldsymbol{b}, \theta)$: conditional joint distribution of $(\boldsymbol{y}, \boldsymbol{s})$ given $\boldsymbol{b}$ and θ.
- $f(\boldsymbol{b} \mid \theta)$: conditional distribution of $\boldsymbol{b}$ given θ.
- $\pi(\theta)$: prior distribution of θ.

Connection structures for joint models [Alvares, 2017]

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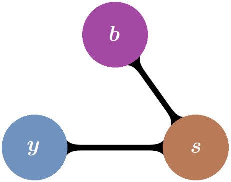

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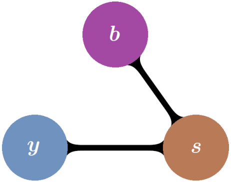
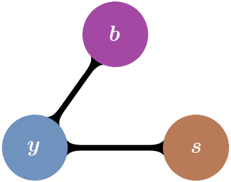


Selection models

$$f\left(\boldsymbol{y}, \boldsymbol{s} \mid \boldsymbol{b}, \boldsymbol{\theta}\right) = f\left(\boldsymbol{s} \mid \boldsymbol{y}, \theta\right) f\left(\boldsymbol{y} \mid \boldsymbol{b}, \theta\right)$$



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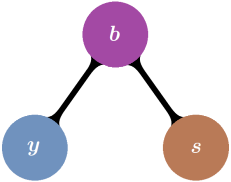

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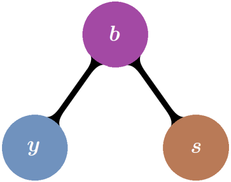
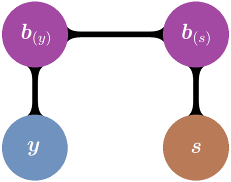


Random-effects models

$$f(\boldsymbol{y}, \boldsymbol{s} \mid \boldsymbol{b}, \theta) = f\left(\boldsymbol{y} \mid \boldsymbol{b}_{(y)}, \theta\right) f\left(\boldsymbol{s} \mid \boldsymbol{b}_{(s)}, \theta\right)$$



Motivation - Dynamic update

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We propose and implement dynamic procedures based on sequential Monte Carlo methods to make quick inference and prediction

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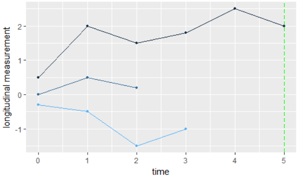

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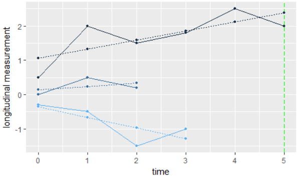

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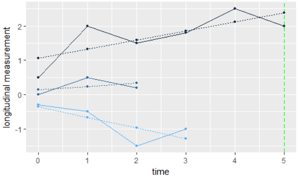

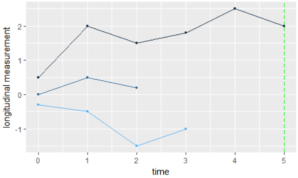

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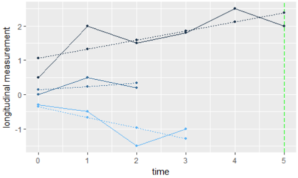

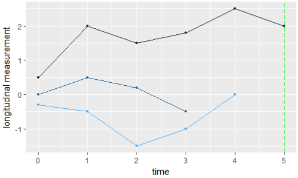

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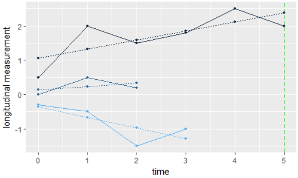

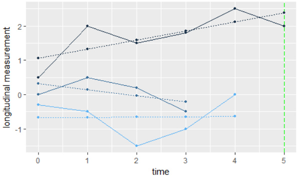

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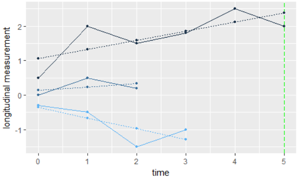

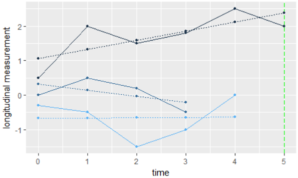

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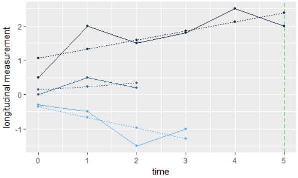

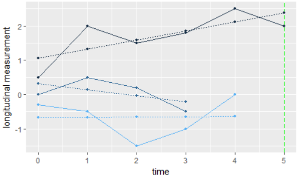

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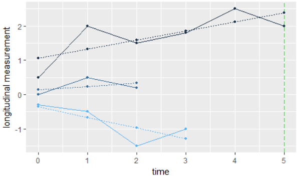

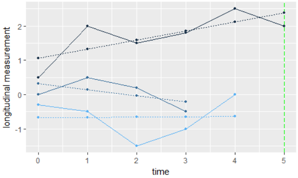

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It becomes advisable to use the Bayes' theorem to update the relevant information as it is recorded:

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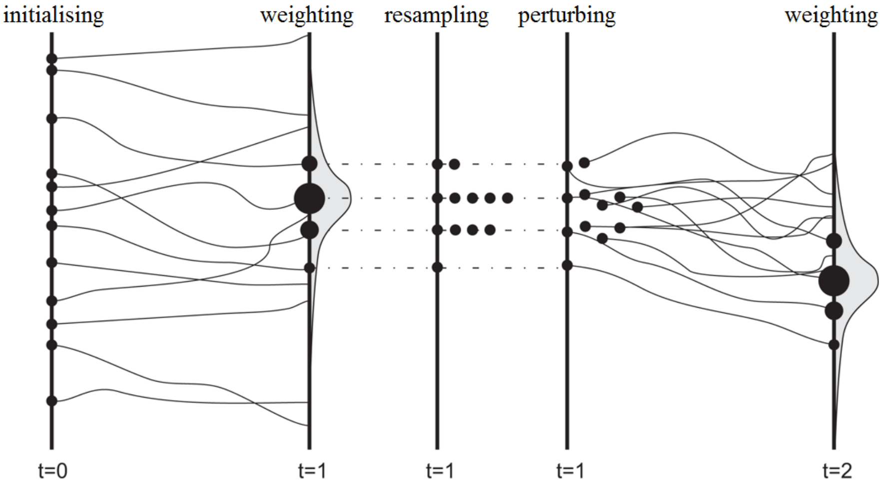
Other related names: particle filtering, Monte Carlo filter, survival of the fittest, sequential imputations, condensation, bootstrap filter, sequential importance resampling [Cappé et al., 2007].

Sequential Monte Carlo scheme



Source: C. Montzka, V. R. N. Pauwels, H. J. H. Franssen, X. Han, and H. Vereecken. Multivariate and multiscale data assimilation in terrestrial systems: a review. Sensors, 12(12): 16291 - 16333, 2012.

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Iterated Batch Importance Sampling (IBIS) [Chopin, 2002]

SMC algorithm for models of static parameters

Iterated Batch Importance Sampling (IBIS) algorithm

Step 1. Draw $\boldsymbol{\theta}^{(k)} \sim \pi(\boldsymbol{\theta} \mid \mathcal{D}_1)$ and set $w^{(k)} \leftarrow 1/K,\ k = 1, \ldots, K$.

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$$\widetilde{w}^{(k)} \leftarrow f\left(\mathcal{D}_2 \mid \mathcal{D}_1, \boldsymbol{\theta}^{(k)}\right) w^{(k)},$$

and normalise the weights $w^{(k)} \leftarrow \dfrac{\widetilde{w}^{(k)}}{\sum_{l=1}^{K} \widetilde{w}^{(l)}},\ k = 1, \ldots, K$.

if $(ESS < K_T)$ **then**

> **Step 3.** Draw $(\widetilde{\boldsymbol{\theta}}^{(1)}, \ldots, \widetilde{\boldsymbol{\theta}}^{(M)})$ from $(\boldsymbol{\theta}^{(1)}, \ldots, \boldsymbol{\theta}^{(K)})$ with probabilities proportional to the normalised weights $(M \leq K)$. Update $w^{(r)} \leftarrow 1/M,\ r = 1, \ldots, M$.
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Step 2. From new data $\mathcal{D}_2$, calculate

$$\widetilde{w}^{(k)} \leftarrow f\left(\mathcal{D}_2 \mid \mathcal{D}_1, \boldsymbol{\theta}^{(k)}\right) w^{(k)},$$

and normalise the weights $w^{(k)} \leftarrow \dfrac{\widetilde{w}^{(k)}}{\sum_{l=1}^{K} \widetilde{w}^{(l)}}, \ k = 1, \ldots, K.$

if $(ESS < K_T)$ **then**

> **Step 3.** Draw $(\widetilde{\boldsymbol{\theta}}^{(1)}, \ldots, \widetilde{\boldsymbol{\theta}}^{(M)})$ from $(\boldsymbol{\theta}^{(1)}, \ldots, \boldsymbol{\theta}^{(K)})$ with probabilities proportional to the normalised weights $(M \leq K)$. Update $w^{(r)} \leftarrow 1/M, \ r = 1, \ldots, M$.
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> **Step 4.** Draw $\check{\boldsymbol{\theta}}^{(r)}$ from an independent Metropolis-Hastings kernel of invariant distribution $\pi(\boldsymbol{\theta} \mid \mathcal{D}_1, \mathcal{D}_2), \ r = 1, \ldots, M$. Update $\boldsymbol{\theta}^{(r)} \leftarrow \check{\boldsymbol{\theta}}^{(r)}, \ r = 1, \ldots, M$ and $K \leftarrow M$.

end

If new data available, return to **Step 2.**

SMC algorithm for models of static parameters

Iterated Batch Importance Sampling (IBIS) algorithm

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LIMITATION: standard IBIS does not work for random effects models

Outline

Updating the inference on $\boldsymbol{\theta}$

Standard IBIS works

$$\pi(\boldsymbol{\theta} \mid \mathcal{D}_1, \mathcal{D}_2) \propto f(\mathcal{D}_1, \mathcal{D}_2 \mid \boldsymbol{\theta})\, \pi(\boldsymbol{\theta})$$

Updating the inference on $\boldsymbol{\theta}$

Standard IBIS works

$$\pi(\boldsymbol{\theta} \mid \mathcal{D}_1, \mathcal{D}_2) \propto f(\mathcal{D}_1, \mathcal{D}_2 \mid \boldsymbol{\theta})\, \pi(\boldsymbol{\theta})$$

Standard IBIS does not work

$$\pi(\boldsymbol{b}, \boldsymbol{\theta} \mid \mathcal{D}_1, \mathcal{D}_2) \propto f(\mathcal{D}_1, \mathcal{D}_2 \mid \boldsymbol{b}, \boldsymbol{\theta})\, f(\boldsymbol{b} \mid \boldsymbol{\theta})\, \pi(\boldsymbol{\theta})$$

Updating the inference on θ

Standard IBIS works

$$\pi(\boldsymbol{\theta} \mid \mathcal{D}_1, \mathcal{D}_2) \propto f(\mathcal{D}_1, \mathcal{D}_2 \mid \boldsymbol{\theta})\, \pi(\boldsymbol{\theta})$$

Standard IBIS does not work

$$\pi(\boldsymbol{b}, \theta \mid \mathcal{D}_1, \mathcal{D}_2) \propto f(\mathcal{D}_1, \mathcal{D}_2 \mid \boldsymbol{b}, \theta)\, f(\boldsymbol{b} \mid \theta)\, \pi(\theta)$$

$$f\left(\mathcal{D}_1, \mathcal{D}_2 \mid \theta\right) = \int f\left(\mathcal{D}_1, \mathcal{D}_2 \mid \boldsymbol{b}, \theta\right) f\left(\boldsymbol{b} \mid \theta\right) \mathrm{d}\boldsymbol{b}$$

Updating the inference on $\boldsymbol{\theta}$

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$$\pi(\boldsymbol{\theta} \mid \mathcal{D}_1, \mathcal{D}_2) \propto f(\mathcal{D}_1, \mathcal{D}_2 \mid \boldsymbol{\theta})\, \pi(\boldsymbol{\theta})$$

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$$\pi(\boldsymbol{b}, \boldsymbol{\theta} \mid \mathcal{D}_1, \mathcal{D}_2) \propto f(\mathcal{D}_1, \mathcal{D}_2 \mid \boldsymbol{b}, \boldsymbol{\theta})\, f(\boldsymbol{b} \mid \boldsymbol{\theta})\, \pi(\boldsymbol{\theta})$$

$$\begin{aligned} f\left(\mathcal{D}_1, \mathcal{D}_2 \mid \boldsymbol{\theta}\right) &= \int f\left(\mathcal{D}_1, \mathcal{D}_2 \mid \boldsymbol{b}, \boldsymbol{\theta}\right) f\left(\boldsymbol{b} \mid \boldsymbol{\theta}\right) \mathrm{d}\boldsymbol{b} \\ &\approx \frac{1}{L} \sum_{l=1}^{L} f\left(\mathcal{D}_1, \mathcal{D}_2 \mid \boldsymbol{b}^{(l)}, \boldsymbol{\theta}\right) \end{aligned}$$

where $\boldsymbol{b}^{(l)}$ is simulated from $f\left(\boldsymbol{b} \mid \boldsymbol{\theta}\right)$ for $l = 1, \ldots, L$.

Updating the inference on $\boldsymbol{\theta}$

Standard IBIS works

$$\pi(\boldsymbol{\theta} \mid \mathcal{D}_1, \mathcal{D}_2) \propto f(\mathcal{D}_1, \mathcal{D}_2 \mid \boldsymbol{\theta})\, \pi(\boldsymbol{\theta})$$

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where $\boldsymbol{b}^{(l)}$ is simulated from $f\left(\boldsymbol{b} \mid \boldsymbol{\theta}\right)$ for $l = 1, \ldots, L$.

Updating the inference on θ

Standard IBIS works

$$\pi(\boldsymbol{\theta} \mid \mathcal{D}_1, \mathcal{D}_2) \propto f(\mathcal{D}_1, \mathcal{D}_2 \mid \boldsymbol{\theta})\, \pi(\boldsymbol{\theta})$$

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Updating the inference on $\boldsymbol{\theta}$

Standard IBIS works

$$\pi(\boldsymbol{\theta} \mid \mathcal{D}_1, \mathcal{D}_2) \propto f(\mathcal{D}_1, \mathcal{D}_2 \mid \boldsymbol{\theta})\, \pi(\boldsymbol{\theta})$$

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Integration methods used:

- Monte Carlo
- Quasi-Monte Carlo

Updating the inference on $\boldsymbol{b}$

Standard IBIS works

$$\pi(\boldsymbol{\theta} \mid \mathcal{D}_1, \mathcal{D}_2)$$

Standard IBIS does not work

$$\pi(\boldsymbol{b}, \boldsymbol{\theta} \mid \mathcal{D}_1, \mathcal{D}_2) \propto f(\mathcal{D}_1, \mathcal{D}_2 \mid \boldsymbol{b}, \boldsymbol{\theta})\, f(\boldsymbol{b} \mid \boldsymbol{\theta})\, \pi(\boldsymbol{\theta})$$

Updating the inference on $\boldsymbol{b}$

Standard IBIS works

$$\pi(\boldsymbol{\theta} \mid \mathcal{D}_1, \mathcal{D}_2)$$

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$$\pi(\boldsymbol{b}, \boldsymbol{\theta} \mid \mathcal{D}_1, \mathcal{D}_2) \propto f(\mathcal{D}_1, \mathcal{D}_2 \mid \boldsymbol{b}, \boldsymbol{\theta}) \, f(\boldsymbol{b} \mid \boldsymbol{\theta}) \, \pi(\boldsymbol{\theta})$$

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Updating the inference on $\boldsymbol{b}$

Standard IBIS works

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Metropolis-Hastings algorithm based on posterior samples of $\boldsymbol{\theta}$

Sequential Monte Carlo algorithm for joint models

SMC-JM algorithm [Alvares et al., 2020]

Step 1. Draw $\boldsymbol{\theta}^{(k)} \sim \pi(\boldsymbol{\theta} \mid \mathcal{D}_1)$ and set $w^{(k)} \leftarrow 1/K,\ k = 1, \ldots, K$.

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Step 5. Simulate $\boldsymbol{b}^{(k)} \sim \pi\left(\boldsymbol{b} \mid \mathcal{D}_1, \mathcal{D}_2, \boldsymbol{\theta}^{(k)}\right),\ k = 1, \ldots, K$.

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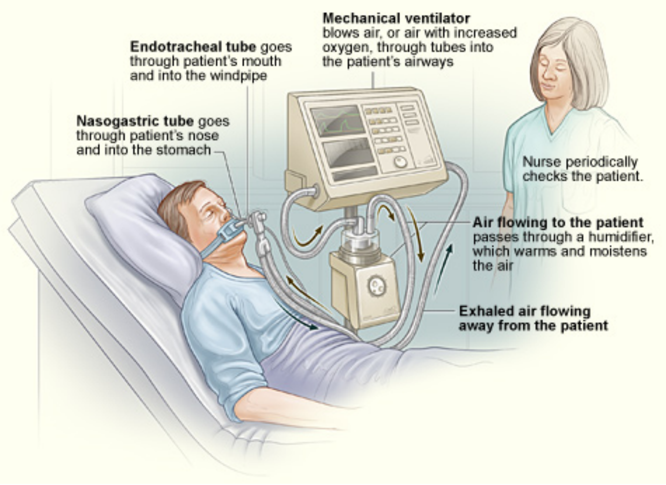
Outline

Context



Source: `http://www.dentistryiq.com/articles/2014/03/boomers-and-the-greatest-generation.html`

Goal

Analysis of the association between a severity marker and the events *alive discharge* and *death* for patients receiving mechanical ventilation in intensive care units (ICU) during 30 days

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Information:

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Analysis of the association between a severity marker and the events *alive discharge* and *death* for patients receiving mechanical ventilation in intensive care units (ICU) during 30 days

Information:

1. Based on the work of [Rué et al., 2017]
2. 139 patients: 97 (69.8%) were discharged alive, 28 (20.1%) died, and 14 (10.1%) were administratively censored
3. Covariate: Age
4. Biomarker: Sequential Organ Failure Assessment (SOFA) score

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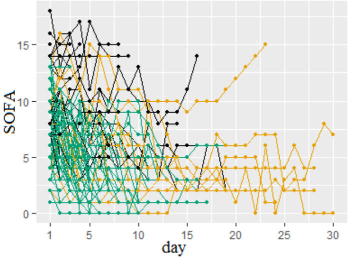
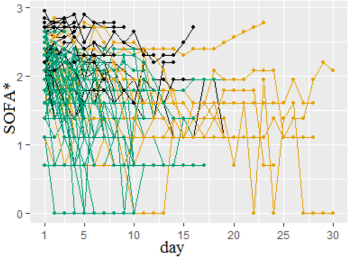
4. Biomarker: Sequential Organ Failure Assessment (SOFA) score
    - Six organ systems: respiratory, cardiovascular, renal, coagulation, hepatic, and neurological systems.
    - Organ dysfunction: scores of 0 (normal) to 4 (most abnormal).

Data description

$$\text{SOFA}^* = \log(\text{SOFA} + 1)$$





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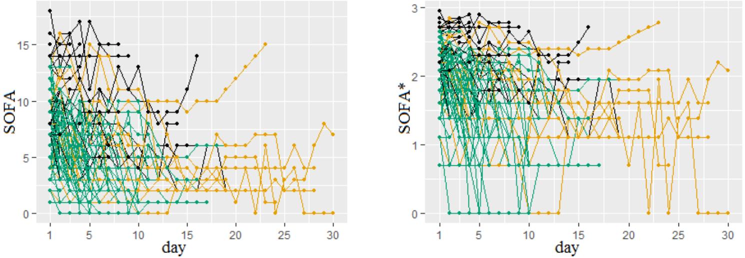
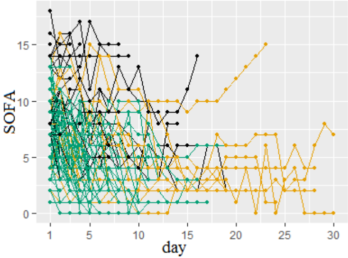
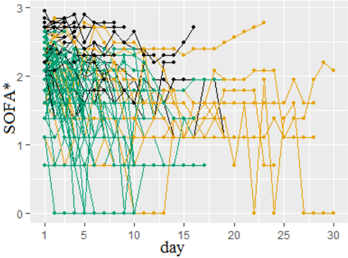


Removing observations:

Data description

$$\text{SOFA}^* = \log(\text{SOFA} + 1)$$



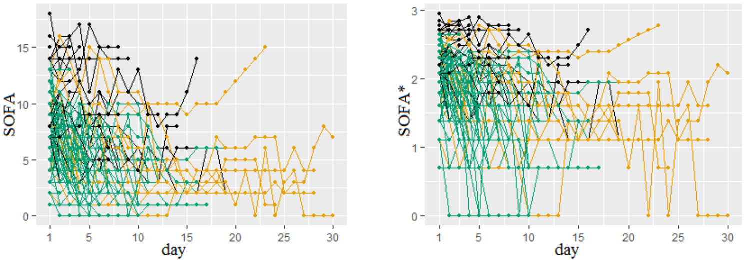


Removing observations:

1. **Patient 12**: 71 years old, discharged alive from the ICU at day 6, and its SOFA scores, from day 1 to 6, were 9, 9, 9, 4, 2, and 2.
2. **Patient 131**: 63 years old, died in the ICU at day 5, and its SOFA scores, from day 1 to 3, were 16, 15, and 15.

Data description

$$\text{SOFA}^* = \log(\text{SOFA} + 1)$$



Removing observations:

1. **Patient 12**: 71 years old, discharged alive from the ICU at day 6, and its SOFA scores, from day 1 to 6, were 9, 9, 9, ~~4, 2, and 2.~~
2. ~~**Patient 131**~~: ~~63 years old, died in the ICU at day 5, and its SOFA scores, from day 1 to 3, were 16, 15, and 15.~~

Bayesian joint modeling and preliminary results

- T_{iv}: time to event v for patient i.
- $v = 1$: *alive discharge*, $v = 2$: *death*, and $i = 1, \ldots, 138$.
- $y_i(t)$: log(SOFA+1) of patient i at time t.
- $\boldsymbol{\theta} = (\boldsymbol{\alpha}_1, \boldsymbol{\alpha}_2, \lambda_1, \lambda_2, \nu_1, \nu_2, \gamma_1, \gamma_2, \boldsymbol{\beta}, \sigma, \sigma_0, \sigma_1)^\top$.

Bayesian joint modeling and preliminary results

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Competing risks submodel

$$h_{iv}(t \mid b_{0i}, b_{1i}, \boldsymbol{\theta}) = \lambda_v \nu_v t^{\nu_v - 1} \exp\left[\gamma_v \mathrm{age}_i + \alpha_{0v} b_{0i} + \alpha_{1v} b_{1i} t\right]$$

$$(b_{0i}, b_{1i} \mid \sigma_0, \sigma_1) \sim \mathcal{N}\left((0, 0)^\top, \mathrm{diag}\left(\sigma_0^2, \sigma_1^2\right)\right)$$

Bayesian joint modeling and preliminary results

- T_{iv}: time to event v for patient i.
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$$(b_{0i}, b_{1i} \mid \sigma_0, \sigma_1) \sim \mathcal{N}\left((0, 0)^\top, \text{diag}\left(\sigma_0^2, \sigma_1^2\right)\right)$$

Longitudinal submodel

$$(y_i(t) \mid b_{0i}, b_{1i}, \boldsymbol{\theta}) \sim \mathcal{N}\left(\mu_i(t), \sigma^2\right)$$

$$\mu_i(t) = \beta_0 + b_{0i} + (\beta_1 + b_{1i})\, t + \beta_2 \text{age}_i$$

Bayesian joint modeling and preliminary results

- T_{iv}: time to event v for patient i.
- $v = 1$: *alive discharge*, $v = 2$: *death*, and $i = 1, \ldots, 138$.
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$$\mu_i(t) = \beta_0 + b_{0i} + (\beta_1 + b_{1i})\, t + \beta_2 \text{age}_i$$

Prior distribution

$$\pi(\alpha_{01}) = \pi(\alpha_{02}) = \pi(\alpha_{11}) = \pi(\alpha_{12}) = \mathcal{N}(0, 1000)$$
$$\pi(\log(\lambda_1)) = \pi(\log(\lambda_2)) = \mathcal{N}(0, 1000)$$
$$\pi(\nu_1) = \pi(\nu_2) = \mathcal{G}(0.01, 0.01)$$
$$\pi(\gamma_1) = \pi(\gamma_2) = \mathcal{N}(0, 1000)$$
$$\pi(\beta_0) = \pi(\beta_1) = \pi(\beta_2) = \mathcal{N}(0, 1000)$$
$$\pi(\sigma) = \pi(\sigma_0) = \pi(\sigma_1) = \mathcal{U}(0, 100)$$

Bayesian joint modeling and preliminary results

$\boldsymbol{\theta}$	Mean	SD	2.5%	50%	97.5%	$P(\cdot > 0 \mid \mathcal{D})$
	Competing risks process - Alive					
γ_1	0.001	0.007	-0.012	0.001	0.016	0.563
α_{01}	-0.203	0.323	-0.846	-0.208	0.468	0.259
α_{11}	-1.012	0.256	-1.582	-0.998	-0.549	0.000
ν_1	1.525	0.151	1.247	1.516	1.834	—
λ_1	0.015	0.009	0.004	0.013	0.040	—
	Competing risks process - Death					
γ_2	0.022	0.017	-0.009	0.021	0.058	0.917
α_{02}	3.367	0.948	1.756	3.307	5.456	1.000
α_{12}	0.745	0.472	-0.173	0.750	1.605	0.943
ν_2	1.172	0.250	0.740	1.157	1.733	—
λ_2	0.002	0.004	0.000	0.001	0.012	—
	*Longitudinal process - SOFA**					
β_0	1.844	0.155	1.537	1.844	2.141	1.000
β_1	-0.086	0.009	-0.105	-0.086	-0.067	0.000
β_2	0.005	0.002	0.000	0.005	0.009	0.973
σ	0.311	0.008	0.295	0.310	0.328	—
σ_0	0.407	0.032	0.349	0.405	0.476	—
σ_1	0.067	0.008	0.052	0.066	0.084	—

Conditional cumulative incidence function (CIF)

$$P(T_i \leq t, \delta_i = v \mid y_{i,1:n_i+g}, T_i \geq t_{i,n_i+g}, \boldsymbol{b}_i, \theta), \quad t > t_{i,n_i+g}$$

Conditional cumulative incidence function (CIF)

$$P(T_i \leq t, \delta_i = v \mid \cancel{y_{i,1:n_i+g}}, T_i \geq t_{i,n_i+g}, \boldsymbol{b}_i, \theta), \quad t > t_{i,n_i+g}$$

Conditional cumulative incidence function (CIF)

$$\begin{aligned} P(T_i \leq t, \delta_i = v \mid \cancel{y_{i,1:n_i+g}}, T_i \geq t_{i,n_i+g}, \boldsymbol{b}_i, \theta) \\ = F_{iv}(t \mid T_i \geq t_{i,n_i+g}, \boldsymbol{b}_i, \theta), \quad t > t_{i,n_i+g} \end{aligned}$$

Conditional cumulative incidence function (CIF)

$$P(T_i \leq t, \delta_i = v \mid \cancel{y_{i,1:n_i+g}}, T_i \geq t_{i,n_i+g}, \boldsymbol{b}_i, \boldsymbol{\theta}) \\ = F_{iv}(t \mid T_i \geq t_{i,n_i+g}, \boldsymbol{b}_i, \boldsymbol{\theta}), \quad t > t_{i,n_i+g}$$

Bayesian approach:

$$\mathrm{E}\left(F_{iv}\left(t \mid T_i \geq t_{i,n_i+g}, \boldsymbol{b}_i, \boldsymbol{\theta}\right) \mid \mathcal{D}\right) = \int F_{iv}\left(t \mid T_i \geq t_{i,n_i+g}, \boldsymbol{b}_i, \boldsymbol{\theta}\right) \pi\left(\boldsymbol{b}_i, \boldsymbol{\theta} \mid \mathcal{D}_i^g, \mathcal{D}\right) \mathrm{d}(\boldsymbol{b}_i, \boldsymbol{\theta}),$$

where $\mathcal{D}_i^g = \left[y_{i,n_i+1:n_i+g}, (t_{i,n_i+g}, \delta_i)\right]^\top$.

$$\mathrm{E}\left(F_{iv}\left(t \mid T_i \geq t_{i,n_i+g}, \boldsymbol{b}_i, \boldsymbol{\theta}\right) \mid \mathcal{D}\right) \approx \frac{1}{L} \sum_{l=1}^{L} F_{iv}\left(t \mid T_i \geq t_{i,n_i+g}, \boldsymbol{b}_i^{(l)}, \boldsymbol{\theta}^{(l)}\right),$$

where $\boldsymbol{b}_i^{(l)}$ and $\boldsymbol{\theta}^{(l)}$ are drawn from $\pi\left(\boldsymbol{b}_i, \boldsymbol{\theta} \mid \mathcal{D}_i^g, \mathcal{D}\right)$, for $l = 1, \ldots, L$ and $v = 1, 2$.

Individual estimation of the dynamic conditional CIF

SMC for Bayesian joint models

Step 1. INITIALIZING.

Step 2. WEIGHTING.

if ($ESS < K_T$) **then**

  Step 3. RESAMPLING.

  Step 4. MOVE.

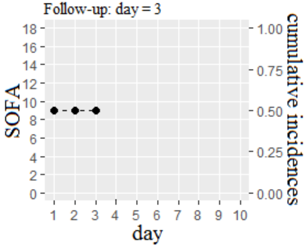
end

Step 5. PERSONALIZE.

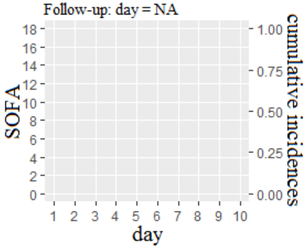
Update the conditional CIF.

If new data available, return to **Step 2.**

Patient 12



Patient 131



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SMC for Bayesian joint models

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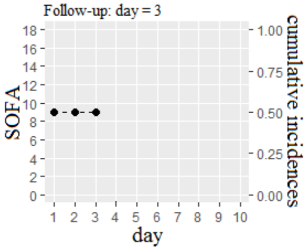
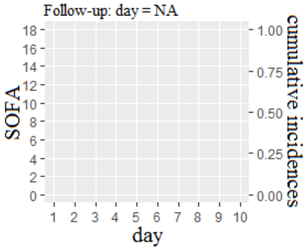


Patient 131



Individual estimation of the dynamic conditional CIF

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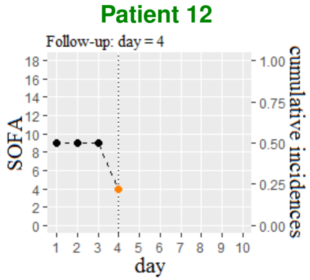

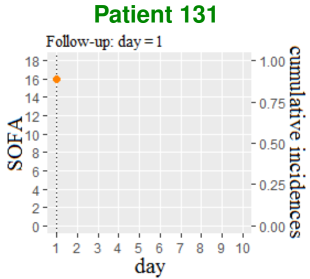

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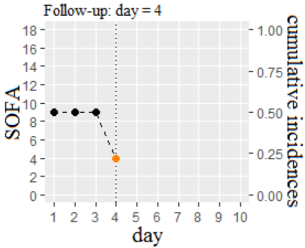
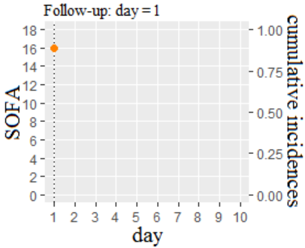


Patient 131



Individual estimation of the dynamic conditional CIF

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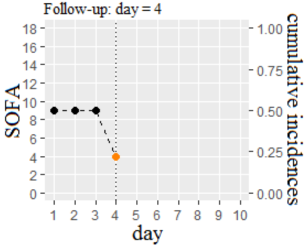
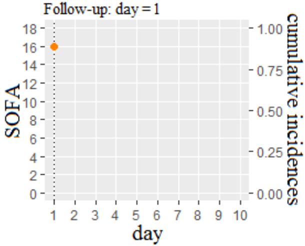


Patient 131



Individual estimation of the dynamic conditional CIF

SMC for Bayesian joint models

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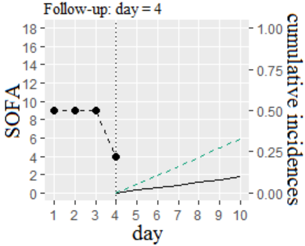
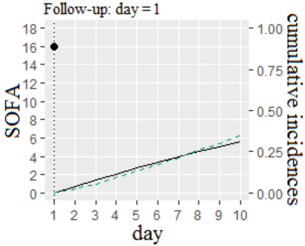


Patient 131



Individual estimation of the dynamic conditional CIF

SMC for Bayesian joint models

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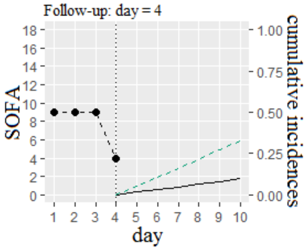
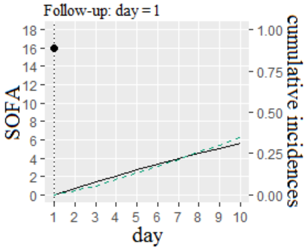
Patient 12



Patient 131



Individual estimation of the dynamic conditional CIF

SMC for Bayesian joint models

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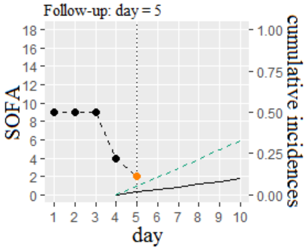
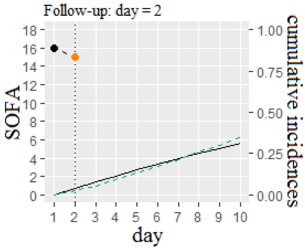
Update the conditional CIF.

If new data available, return to **Step 2.**

Patient 12



Patient 131



Individual estimation of the dynamic conditional CIF

SMC for Bayesian joint models

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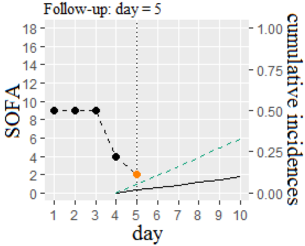
Step 5. PERSONALIZE.

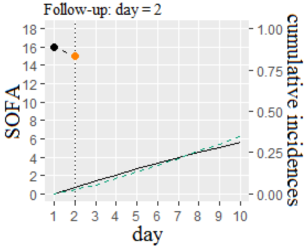
Update the conditional CIF.

If new data available, return to **Step 2.**

Patient 12



Patient 131



Individual estimation of the dynamic conditional CIF

SMC for Bayesian joint models

Step 1. Initializing.

Step 2. Weighting.

if $(ESS < K_T)$ **then**

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  Step 4. Move.

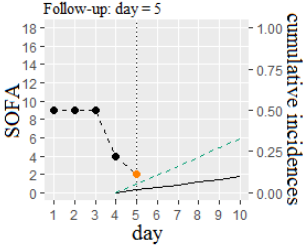
end

Step 5. Personalize.

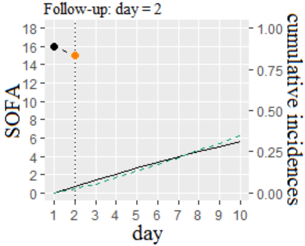
Update the conditional CIF.

If new data available, return to **Step 2.**

Patient 12



Patient 131



Individual estimation of the dynamic conditional CIF

SMC for Bayesian joint models

Step 1. INITIALIZING.

Step 2. WEIGHTING.

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end

Step 5. PERSONALIZE.

Update the conditional CIF.

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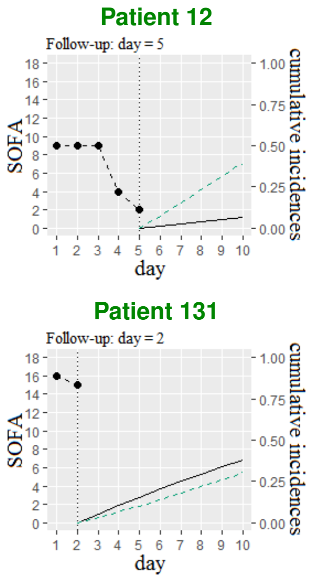

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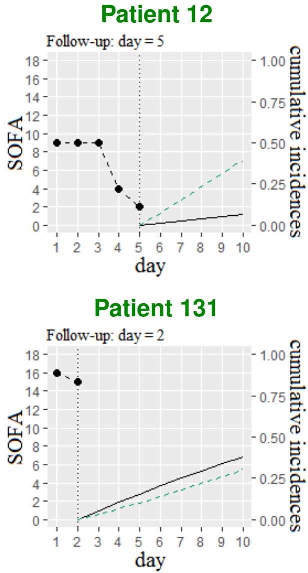

Individual estimation of the dynamic conditional CIF

SMC for Bayesian joint models

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Update the conditional CIF.

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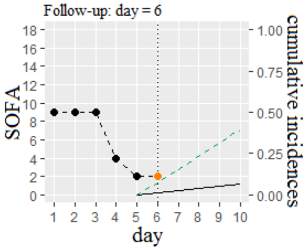
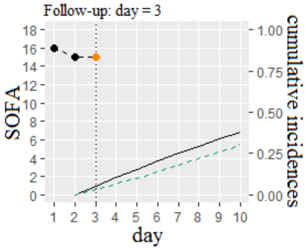
Patient 12



Patient 131



Individual estimation of the dynamic conditional CIF

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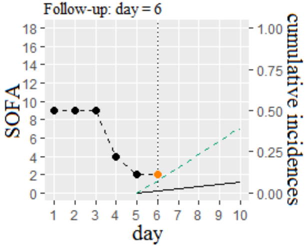
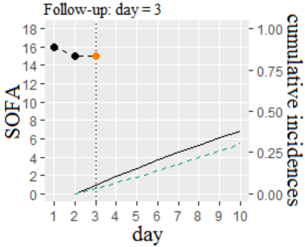
Patient 12



Patient 131



Individual estimation of the dynamic conditional CIF

SMC for Bayesian joint models

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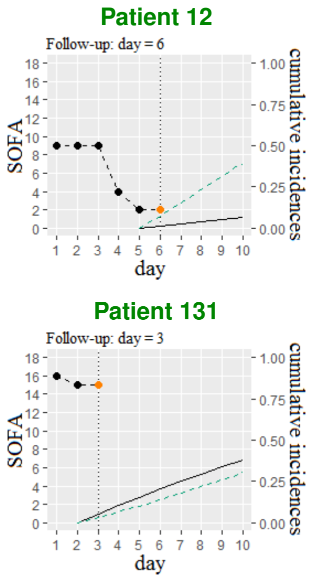
Update the conditional CIF.

If new data available, return to **Step 2.**



Individual estimation of the dynamic conditional CIF

SMC for Bayesian joint models

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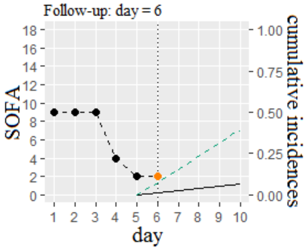
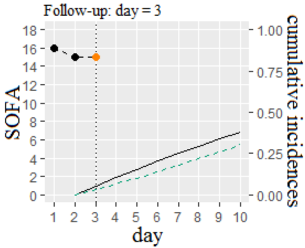
Patient 12



Patient 131



Individual estimation of the dynamic conditional CIF

SMC for Bayesian joint models

Step 1. INITIALIZING.

Step 2. WEIGHTING.

if $(ESS < K_T)$ **then**

> **Step 3.** RESAMPLING.
>
> **Step 4.** MOVE.

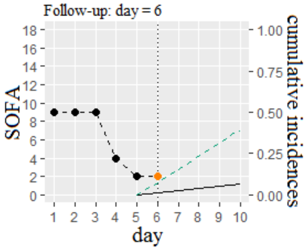
end

Step 5. PERSONALIZE.

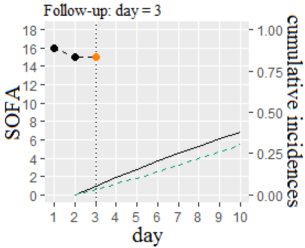
Update the conditional CIF.

If new data available, return to **Step 2.**

Patient 12



Patient 131



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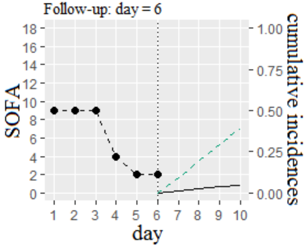
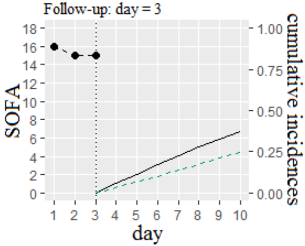
Patient 12



Patient 131



Individual estimation of the dynamic conditional CIF

SMC for Bayesian joint models

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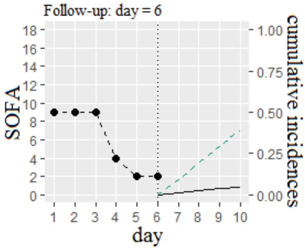
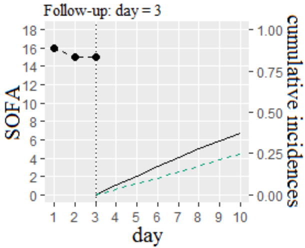
Patient 12



Patient 131



Updating the posterior information

θ	Initial		SMC-JM		JAGS	
	Mean	SD	Mean	SD	Mean	SD
	Competing risks process - Alive					
α_{01}	-0.203	0.323	-0.221	0.313	-0.222	0.316
α_{11}	-1.012	0.256	-0.998	0.253	-0.999	0.255
λ_1	0.015	0.009	0.015	0.009	0.015	0.009
ν_1	1.525	0.151	1.538	0.146	1.537	0.151
γ_1	0.001	0.007	0.002	0.007	0.002	0.007
	Competing risks process - Death					
α_{02}	3.367	0.948	3.272	0.858	3.278	0.861
α_{12}	0.745	0.472	0.717	0.453	0.716	0.454
λ_2	0.002	0.004	0.002	0.003	0.002	0.004
ν_2	1.172	0.250	1.176	0.248	1.178	0.249
γ_2	0.022	0.017	0.022	0.016	0.022	0.017
	*Longitudinal process - SOFA**					
β_0	1.844	0.155	1.851	0.149	1.851	0.154
β_1	-0.086	0.009	-0.088	0.009	-0.088	0.009
β_2	0.005	0.002	0.005	0.002	0.005	0.002
σ	0.311	0.008	0.311	0.007	0.311	0.008
σ_0	0.407	0.032	0.410	0.031	0.410	0.031
σ_1	0.067	0.008	0.069	0.009	0.068	0.009
Time (min)	867		121		869	

Outline

Conclusions

SMC methods in Bayesian joint models

- Improve statistical efficiency by using all the data simultaneously in a single model.
- “Complete” inference and quick update.
- Adaptations involving analytically intractable integrals.
- Incorporation of the step of update of the random effects.

Conclusions

SMC methods in Bayesian joint models

- Improve statistical efficiency by using all the data simultaneously in a single model.
- "Complete" inference and quick update.
- Adaptations involving analytically intractable integrals.
- Incorporation of the step of update of the random effects.

ICU discharge data:

- Individual estimation of the dynamic CIF of each event.
- Reduction of 867 minutes to 121 minutes.

References I

Alvares, D. (2017).
Sequential Monte Carlo methods in Bayesian joint models for longitudinal and time-to-event data.
PhD thesis, Universitat de València.

Alvares, D., Armero, C., Forte, A., and Chopin, N. (2020).
Sequential Monte Carlo methods in Bayesian joint models for longitudinal and time-to-event data.
Statistical Modelling, pages 1–21.

Armero, C., Forte, A., Perpiñán, H., Sanahuja, M. J., and Agustí, S. (2018).
Bayesian joint modeling for assessing the progression of chronic kidney disease in children.
Statistical Methods in Medical Research, 27(1):298 – 311.

Cappé, O., Godsill, S. J., and Moulines, E. (2007).
An overview of existing methods and recent advances in sequential Monte Carlo.
In *Proceedings of the Institute of Electrical and Electronics Engineers*, volume 95(5), pages 899 – 924.

Cappé, O., Moulines, E., and Ryden, T. (2005).
Inference in hidden Markov models.
Springer-Verlag, 1st edition.

Chopin, N. (2002).
A sequential particle filter for static models.
Biometrika, 89(3):539 – 551.

Rué, M., Andrinopoulou, E. R., Alvares, D., Armero, C., Forte, A., and Blanch, L. (2017).
Bayesian joint modeling of bivariate longitudinal and competing risks data: an application to study patient-ventilator asynchronies in critical care patients.
Biometrical Journal (In press).

Thank you for your attention