# Sequential Monte Carlo: introduction, recent advances

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# Motivation: Feynman-Kac models, particle filtering

A Feynman-Kac model is made of:

- A Markov chain in X: initial law is m<sub>0</sub>(dx<sub>0</sub>), Markov kernel at iteration t is m<sub>t</sub>(x<sub>t-1</sub>, dx<sub>t</sub>)
- A sequence of potential functions  $G_0 : \mathcal{X} \to \mathbb{R}^+$ ,  $G_t : \mathcal{X} \times \mathcal{X} \to \mathbb{R}^+$

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- A sequence of potential functions  $G_0 : \mathcal{X} \to \mathbb{R}^+$ ,  $G_t : \mathcal{X} \times \mathcal{X} \to \mathbb{R}^+$

Aim is to compute sequentially quantities such as

$$\mathbb{Q}_t(\varphi) = \frac{1}{Z_t} \mathbb{E}\left[\varphi(X_t) G_0(X_0) \prod_{s=1}^t G_s(X_{s-1}, X_s)\right],$$
  
with  $Z_t = \mathbb{E}\left[G_0(X_0) \prod_{s=1}^t G_s(X_{s-1}, X_s)\right].$ 

 $\Rightarrow$  change of measure.

Take for instance

$$G_t(x_{t-1}, x_t) = \mathbb{1}_{A_t}(x_t)$$

then  $Z_t$  is the probability that the  $X_s \in A_s$  for all  $s \le t$ ,  $\mathbb{Q}_t$  is the dist' of  $X_t$  conditional on  $X_s \in A_s$  for  $s \le t$  and so on.

#### Application to HMMs (hidden Markov models)

Imagine a model for a Markov chain  $(X_t)$  that is not observed directly, but through

$$Y_t = h(X_t) + \text{noise}$$

and let  $g(y_t|x_t)$  be the density of  $Y_t$  conditional on  $X_t = x_t$ . Then, taking

$$G_t(x_{t-1}, x_t) = g(y_t | x_t)$$

turns  $\mathbb{Q}_t$  into the filtering distribution (the law of  $X_t$  conditional on data  $y_{0:t}$ ), and  $Z_t$  into the likelihood of the data (the marginal density of  $y_{0:t}$ ).

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Applications in signal processing, Ecology, neurosciences...

Vehicle moves in 2D space, acquires its speeds every  $T_s$  seconds, and receives  $d_v$  radio signals. Model is:

$$Y_{ti} = 10 \log_{10} \left( \frac{P_{i0}}{\|r_i - X_t\|^{\alpha_i}} \right) + \nu_{it}, \quad i = 1, \dots, d_y$$
$$X_t = X_{t-1} + T_s V_t + T_s \epsilon_t$$

and noise terms  $\epsilon_t$ ,  $\nu_t$  are Laplace-distributed.

#### Simulated data

#### $T_s = 1$ s, $d_y = 5$ (5 emiters), $\alpha_i = 0.95$ .



Figure 1: Simulated trajectory (15 min)



For a given Feynman-Kac model, a possible approach to approximate  $\mathbb{Q}_t$  sequentially would be (sequential) importance sampling:

- 1. At time t, simulate N copies  $X_t^n$  of Markov chain  $(X_t)$ ;
- 2. reweight according to function  $G_t$ .

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Problem: variance of cumulative weigts:

$$w(x_{0:t}^{n}) = \prod_{s=0}^{t} G_{s}(x_{s-1}^{n}, x_{s}^{n})$$

increases over time (at exponential rate).

At time 0, use importance sampling, to go from  $m_0(dx_0)$  to  $\mathbb{Q}_0(dx_0) \propto m_0(dx_0)G_0(x_0)$ . We thus obtain the following approximation of  $\mathbb{Q}_0$ :

$$\mathbb{Q}_0^N(\mathrm{d} x_0) = \frac{1}{\sum_{n=1}^N G_0(X_0^n)} \sum_{n=1}^N G_0(X_0^n) \delta_{X_0^n}(\mathrm{d} x_0)$$

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To progress to time 1:

- 1. Choose one 'ancestor'  $X_0^n$  with probability  $\propto G_0(X_0^n)$ ; call  $A_0^n$  the index of the selected ancestor.
- 2. Simulate  $X_1^n \sim m_1(X_0^{A_0^n}, dx_1)$
- 3. Reweight, with weight  $G_1(X_0^{A_0^n}, X_1^n)$

Operations must be be performed for all  $n \in 1 : N$ . At time 0,

> (a) Generate  $X_0^n \sim m_0(dx_0)$ . (b) Compute  $W_0^n = G_0(X_0^n) / \sum_{m=1}^N G_0(X_0^m)$ .

Recursively, for time t = 1 : T,

(a) Generate  $A_{t-1}^n \sim \mathcal{M}(W_{t-1}^{1:N})$ . (b) Generate  $X_t^n \sim m_t(X_{t-1}^{A_{t-1}^n}, dx_t)$ . (c) Compute  $W_t^n = G_t(X_{t-1}^{A_{t-1}^n}, X_t^n) / \sum_{m=1}^N G_t(X_{t-1}^{A_{t-1}^m}, X_t^m)$ .

### **Cartoon representation**



Source: Chris Steinruecken

At iteration t, compute

$$\mathbb{Q}_t^N(\varphi) = \sum_{n=1}^N W_t^n \varphi(X_t^n)$$

to approximate  $\mathbb{Q}_t(\varphi)$  (the filtering expectation of  $\varphi$ ).

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In addition, compute

$$Z_t^N = \prod_{s=0}^t \left\{ \frac{1}{N} \sum_{n=1}^N G_t(X_{t-1}^{A_{t-1}^n}, X_t^n) \right\}$$

as an approximation of  $Z_t$  (the likelihood of the data in a HMM).

#### Beyond boostrap filters: guided proposals

A PF such that  $m_t(x_{t-1}, dx_t)$  (the kernel used to simulate particles) matches  $f_t(x_{t-1}, dx_t)$  (the Markov kernel of  $(X_t)$  for the considered HMM) is called a bootstrap filter. However, it is possible, and often useful, to take  $m_t \neq f_t$ . Provided

$$G_t(x_{t-1}, x_t) = \frac{f_t(x_{t-1}, \mathrm{d}x_t)g(y_t|x_t)}{m_t(x_{t-1}, \mathrm{d}x_t)},$$

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The idea is to choose  $m_t$  so that the variance of  $G_t$  is as small as possible. The 'optimal' choice is the distribution of  $X_t$  conditional on  $X_{t-1}$  and  $Y_t$  (usually intractable).

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Notice how  $G_t$  depends on both  $x_{t-1}$  and  $x_t$  in this case.

#### Simple example of a guided proposal

$$\begin{aligned} X_t | X_{t-1} &= x_{t-1} \sim \mathcal{N}(x_{t-1}, 1) \\ Y_t &= \mathbbm{1}_{[0,\varepsilon]}(X_t) \end{aligned}$$

and assume data such that  $y_t = 1$  for all t.

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The bootstrap PF simulates particles from  $N(x_{t-1}, 1)$ , and kill particles that fall outside  $[0, \varepsilon]$ .

Instead, take  $m_t(x_{t-1}, dx_t)$  to be  $N(x_{t-1}, 1)$  conditional on  $x_t \in [0, \varepsilon]$ . Then

$$G_t(x_{t-1}, x_t) = \Phi(\varepsilon - x_{t-1}) - \Phi(-x_{t-1})$$

and all particles fall in  $[0, \varepsilon]$ .

### Resampling

A resampling scheme is a randomization procedure that takes as an input a weighted sample  $\{(X^n, W^n)\}_{n=1}^N$  and returns as an output resampled variables  $\{X^{A^n}\}_{n=1}^N$ , where  $A^n$  is a random index in  $\{1, \ldots, N\}$ .

A good resampling scheme should be such that

$$\frac{1}{N}\sum_{n=1}^N \delta(X^{A^n}) \approx \sum_{n=1}^N W^n \delta(X^n)$$

or, in words, the empirical probability measure of the resampled variables should remain close (in some sense) to the weighted empirical measure of the input variables.

It is well known that particle filters 'collapse' if the particles are not resampled from time to time.

(Other applications of resampling algorithms include e.g. survey sampling and weighted bootstrap.)

### Most commonly used resampling methods (in PF)

• Multinomial resampling:

$$A^n = F_N^-(U^n), \quad n = 1, \dots, N, \quad F_N(x) = \sum_{n=1}^N W^n \mathbb{I}(n \le x)$$

where  $\{U^n\}_{n=1}^N$  are i.i.d.  $\mathcal{U}(0,1)$  random variables.

• Stratified resampling (Kitagawa, 1996):

$$A^n = F_N^- \left(\frac{n-1+U^n}{N}\right), \quad n = 1, \dots, N$$

where  $\{U^n\}_{n=1}^N$  are i.i.d.  $\mathcal{U}(0,1)$  random variables.

• Systematic resampling (Carpenter et al., 1999):

$$A^n = F_N^-\left(\frac{n-1+U}{N}\right), \quad n = 1, \dots, N$$

where  $U \sim \mathcal{U}(0, 1)$ .

#### Inverse CDF plot



**Figure 2:** Function  $F_N(x) = \sum_{n=1}^N W^n \mathbb{I}(n \le x)$ 

In practice, We use stratified/systematic (rather than multinomial) resampling, because these schemes are (a) a bit faster, and (b) leads to lower-variance estimates numerically. (See next slide)

In theory, we only consider multinomial resampling, as it is so much easier to study; indeed, resampled particles are IID, from distribution

$$\sum_{n=1}^{N} W^n \delta(X^n).$$

As a result, little is known about stratified/systematic; even wether they are consistent or not.

#### Numerical comparison of resampling schemes



**Figure 3:** TV distance between empirical distributions of weighted particles, and resampled particles as a function of  $\tau$ ; particles are  $\sim N(0, 1)$ , weight function is  $w(x) = exp(-\tau x^2/2)$ .

## Consistency results for unordered resampling schemes

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- Random variables (Z<sup>n</sup>)<sup>N</sup><sub>n=1</sub> are negatively associated (NA) if, for every pair of disjoint subsets I<sub>1</sub> and I<sub>2</sub> of {1,...N},

$$\operatorname{Cov}\Big(\varphi_1(Z^n, n \in I_1), \varphi_2(Z^n, n \in I_2)\Big) \leq 0$$

for all coordinatewise non-decreasing functions  $\varphi_1$  and  $\varphi_2$ , such that for  $k \in \{1, 2\}$ ,  $\varphi_k : \mathbb{R}^{|I_k|} \to \mathbb{R}$  and such that the covariance is well-defined.

We have a theorem that says that an unbiased resampling scheme is consistent if the collection of variables

$$\left\{\#_{\rho,z}^{n} := \sum_{m=1}^{N} \mathbb{I}(A^{m} = n)\right\}_{n=1}^{N}$$

is negatively associated (plus other conditions).

From the previous theorem we deduce that the following resampling schemes are consistent:

- Multinomial resampling (not new);
- Residual resampling (not new):
- Stratified resampling (new);
- Residual/Stratified resampling (new)
- SSP resampling (new, see next slide)

Unfortunately, the theorem does not apply to systematic resampling.

Start with  $Y^n = NW^n$  for n = 1, ..., N. Take a pair, say  $Y^1 = 3.7$ ,  $Y^2 = 2.2$ .

- With probability *p*, increase both, by amount 0.3: then *Y*<sup>1</sup> is 4.
- With probablity (1 p), decrease both, by amount 0.2; then  $Y^2$  is 2.

(Choose p so that the scheme remains unbiased: p = 2/5.)

Pair the particle with a fractional weight with another particle, and start over.
In a first step, we show that consistency is equivalent to a certain condition on the set of points, when ordered through the Hilbert curve.

In a second step, we use the NA condition to show that the same technical condition holds whatever the order of the input points.



The Hilbert curve is the limit of this sequence. Note the locality property of the Hilbert curve: if two points are close in [0, 1], then the the corresponding transformed points remains close in  $[0, 1]^d$ . (Source for the plot: Marc van Dongen)

# Analysis of Hilbert-ordered resampling schemes

Using simulations, Kitagawa (1996) noticed the following. [Kitagawa, 1996] Assume  $\mathcal{X} = \mathbb{R}$  (i.e. d = 1). Then, if the  $X_t^{n'}$ s are ordered before the resampling, The approximation error of stratified resampling is of size  $\mathcal{O}_{\mathbb{P}}(N^{-1})$ ;

Is this true? does it generalize to d > 1?

- Yes.
- Use the Hilbert curve.

$$N^{1/2}\left(\sum_{n=1}^{N}W_{t}^{n}\varphi(X_{t}^{n})-\mathbb{Q}_{t}(\varphi)\right)\Rightarrow N(0,\mathcal{V}_{t}(\varphi))$$

where the asymptotic variances are defined recursively:

$$\mathcal{V}_{t}[\varphi] = \frac{1}{\ell_{t}^{2}} \widetilde{\mathcal{V}}_{t} \left[ G_{t} \left\{ \varphi - \pi_{t}(\varphi) \right\} \right]$$
$$\widehat{\mathcal{V}}_{t}[\varphi] = \mathcal{V}_{t}[\varphi] + R_{t}(\rho, \varphi)$$
$$\widetilde{\mathcal{V}}_{t+1}[\varphi] = \widehat{\mathcal{V}}_{t} \left[ M_{t+1}(\varphi) \right] + \pi_{t} \left[ V_{t+1}(\varphi) \right]$$

We proved that  $R_t(\varphi) = 0$  for the Hilbert-ordered version of stratified resampling. (It is > 0 for multinomial and residual, see C, 2004).

Note: also optimality results for the auxiliary weight function of the APF, where the optimal function depends on the resampling scheme.

## Quick introduction to QMC

Consider the standard MC approximation

$$\frac{1}{N}\sum_{n=1}^{N}\varphi(\mathbf{u}^n)\approx\int_{[0,1]^d}\varphi(\mathbf{u})\mathrm{d}\mathbf{u}$$

where the *N* vectors  $\mathbf{u}^n$  are IID variables simulated from  $\mathcal{U}([0,1]^d)$ .

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QMC replaces  $\mathbf{u}^{1:N}$  by a set of N points that are more evenly distributed on the hyper-cube  $[0,1]^d$ . This idea is formalised through the notion of discrepancy.

QMC versus MC: N = 256 points sampled independently and uniformly in  $[0,1]^2$  (left); QMC sequence (Sobol) in  $[0,1]^2$  of the same length (right)

Koksma-Hlawka inequality:

$$\left|\frac{1}{N}\sum_{n=1}^{N}\varphi(\mathbf{u}^n)-\int_{[0,1]^d}\varphi(\mathbf{u})\,\mathrm{d}\mathbf{u}\right|\leq V(\varphi)D^{\star}(\mathbf{u}^{1:N})$$

where  $V(\varphi)$  depends only on  $\varphi$ , and the star discrepancy is defined as:

$$D^{\star}(\mathbf{u}^{1:N}) = \sup_{[\mathbf{0},\mathbf{b}]} \left| \frac{1}{N} \sum_{n=1}^{N} \mathbb{1} \left( \mathbf{u}^{n} \in [\mathbf{0},\mathbf{b}] \right) - \prod_{i=1}^{d} b_{i} \right|.$$

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There are various ways to construct point sets  $P_N = \{\mathbf{u}^{1:N}\}$  so that  $D^*(\mathbf{u}^{1:N}) = \mathcal{O}(N^{-1+\epsilon})$ .

## SQMC

We can formalise the succession of Steps (a), (b) and (c) at iteration t as an importance sampling step from random probability measure

$$\sum_{n=1}^{N} W_{t-1}^{n} \delta_{X_{t-1}^{n}} (\mathrm{d}\widetilde{X}_{t-1}) m_{t}(\widetilde{X}_{t-1}, \mathrm{d}x_{t})$$
(1)

to

 $\{\text{same thing}\} \times G_t(\widetilde{x}_{t-1}, x_t).$ 

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Idea: use QMC instead of MC to sample N points from (1); i.e. rewrite sampling from (1) this as a function of uniform variables, and use low-discrepancy sequences instead.

More precisely, we are going to write the simulation from

$$\sum_{n=1}^{N} W_{t-1}^{n} \delta_{X_{t-1}^{n}} (\mathrm{d} \widetilde{X}_{t-1}) m_{t} (\widetilde{X}_{t-1}, \mathrm{d} x_{t})$$

as a function of  $\mathbf{u}_t^n = (u_t^n, \mathbf{v}_t^n)$ ,  $u_t^n \in [0, 1]$ ,  $\mathbf{v}_t^n \in [0, 1]^d$ , such that:

- 1. We will use the scalar  $u_t^n$  to choose the ancestor  $\widetilde{X}_{t-1}$ .
- 2. We will use  $\mathbf{v}_t^n$  to generate  $X_t^n$  as

$$X_t^n = \Gamma_t(\widetilde{X}_{t-1}, \mathbf{v}_t^n)$$

where  $\Gamma_t$  is a deterministic function such that, for  $\mathbf{v}_t^n \sim \mathcal{U}[0,1]^d$ ,  $\Gamma_t(\widetilde{X}_{t-1},\mathbf{v}_t^n) \sim m_t(\widetilde{X}_{t-1},\mathrm{d}x_t)$ .

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The main problem is point 1.

Simply use the inverse transform method:  $\tilde{X}_{t-1}^n = \hat{F}^{-1}(u_t^n)$ , where  $\hat{F}$  is the empirical cdf of

$$\sum_{n=1}^{N} W_{t-1}^{n} \delta_{X_{t-1}^{n}} (\mathrm{d} \widetilde{X}_{t-1}).$$

When d > 1, we cannot use the inverse CDF method to sample from the empirical distribution

$$\sum_{n=1}^{N} W_{t-1}^{n} \delta_{X_{t-1}^{n}} (\mathrm{d} \widetilde{X}_{t-1}).$$

Idea: we "project" the  $X_{t-1}^n$ 's into [0,1] through the (generalised) inverse of the Hilbert curve.

At time 0,

(a) Generate a QMC point set u<sub>0</sub><sup>1:N</sup> in [0, 1]<sup>d</sup>, and compute X<sub>0</sub><sup>n</sup> = Γ<sub>0</sub>(u<sub>0</sub><sup>n</sup>). (e.g. Γ<sub>0</sub> = F<sub>m<sub>0</sub></sub><sup>-1</sup>)
(b) Compute W<sub>0</sub><sup>n</sup> = G<sub>0</sub>(X<sub>0</sub><sup>n</sup>) / Σ<sub>m=1</sub><sup>N</sup> G<sub>0</sub>(X<sub>0</sub><sup>m</sup>).

Recursively, for time t = 1 : T,

(a) Generate QMC ps u<sub>t</sub><sup>1:N</sup> in [0, 1]<sup>d+1</sup>; let u<sub>t</sub><sup>n</sup> = (u<sub>t</sub><sup>n</sup>, v<sub>t</sub><sup>n</sup>).
(b) Hilbert sort: find permutation σ such that h ∘ ψ(X<sub>t-1</sub><sup>σ(1)</sup>) ≤ ... ≤ h ∘ ψ(X<sub>t-1</sub><sup>σ(N)</sup>).
(c) Generate a<sub>t-1</sub><sup>1:N</sup> using inverse CDF Algorithm, with inputs sort(u<sub>t</sub><sup>1:N</sup>) and W<sub>t-1</sub><sup>σ(1:N)</sup>, and compute X<sub>t</sub><sup>n</sup> = Γ<sub>t</sub>(X<sub>t-1</sub><sup>σ(a<sub>t-1</sub><sup>n</sup>)</sup>, v<sub>t</sub><sup>σ(n)</sup>). (e.g. Γ<sub>t</sub> = F<sub>mt</sub><sup>-1</sup>)
(e) Compute W<sub>t</sub><sup>n</sup> ∝ G<sub>t</sub>(X<sub>t-1</sub><sup>σ(a<sub>t-1</sub>)</sup>, X<sub>t</sub><sup>n</sup>).

### Some remarks

- Related to array-RQMC (L'Ecuyer et al, 2006): same idea of using (T + 1) RQMC sequences of dimension d + 1, rather than a single sequence of dimension (T + 1)d.
- Because two sort operations are performed, the complexity of SQMC is O(N log N) (while SMC is O(N)).

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- The main requirement to implement SQMC is that one may simulate from Markov kernel m<sub>t</sub>(x<sub>t-1</sub>, dx<sub>t</sub>) by computing X<sub>t</sub> = Γ<sub>t</sub>(X<sub>t-1</sub>, u<sub>t</sub>), where u<sub>t</sub> ~ U[0,1]<sup>d</sup>, for some deterministic function Γ<sub>t</sub> (e.g. multivariate inverse CDF).

### Some remarks

- Related to array-RQMC (L'Ecuyer et al, 2006): same idea of using (T + 1) RQMC sequences of dimension d + 1, rather than a single sequence of dimension (T + 1)d.
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- The dimension of the point sets u<sup>1:N</sup><sub>t</sub> is 1 + d: first component is for selecting the parent particle, the d remaining components is for sampling X<sup>n</sup><sub>t</sub> given X<sup>a<sup>n</sup><sub>t-1</sub></sup><sub>t-1</sub>.

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We were able to establish the following types of results: consistency

$$\mathbb{Q}_t^N(arphi) - \mathbb{Q}_t(arphi) o 0, \quad ext{as } N o +\infty$$

for certain functions  $\varphi$ , and rate of convergence

$$\mathrm{MSE}\left[\mathbb{Q}_t^N(\varphi)\right] = o(N^{-1})$$

(under technical conditions, and for certain types of RQMC point sets).

Theory is non-standard and borrows heavily from QMC concepts.

Let  $\mathcal{X} = [0,1]^d$ . Consistency results are expressed in terms of the star norm

$$\|\mathbb{Q}_t^N - \mathbb{Q}_t\|_{\star} = \sup_{[\mathbf{0}, \mathbf{b}] \subset [\mathbf{0}, 1)^d} \left| \left( \mathbb{Q}_t^N - \mathbb{Q}_t \right) (B) \right| \to 0.$$

This implies consistency for bounded functions  $\varphi$ ,  $\mathbb{Q}_t^N(\varphi) - \mathbb{Q}_t(\varphi) \to 0.$ 

The Hilbert curve conserves discrepancy:

$$\|\pi^{N} - \pi\|_{\star} \to 0 \quad \Rightarrow \quad \|\pi_{h}^{N} - \pi_{h}\|_{\star} \to 0$$

where  $\pi \in \mathcal{P}([0,1]^d)$ ,  $h: [0,1]^d \to [0,1]$  is the (pseudo-)inverse of the Hilbert curve, and  $\pi_h$  is the image of  $\pi$  through  $\pi$ .

## **Examples**

Well known toy example (Kitagawa, 1998):

$$\begin{cases} Y_t = \frac{X_t^2}{a} + \epsilon_t \\ X_t = b_1 X_{t-1} + b_2 \frac{X_{t-1}}{1 + X_{t-1}^2} + b_3 \cos(b_4 t) + \sigma \nu_t \end{cases}$$

No paramater estimation (parameters are set to their true value). We compare SQMC with SMC (based on systematic resampling) both in terms of N, and in terms of CPU time.

Log-likelihood evaluation (based on T = 100 data point and 500 independent SMC and SQMC runs).

Filtering: computing  $\mathbb{E}(X_t | \mathbf{y}_{0:t})$  at each iteration *t*. Gain factor is MSE(SMC)/MSE(SQMC).

### Autonomous positioning: results



**Figure 4:** Left: Gain factor vs time (PF MSE/SQMC MSE); Right: number of time steps such that  $MSE(\hat{x}_{t1}) > 0.01Var(x_{t1}|y_{0:t})$ , as a function of CPU time



#### Model is

$$\left\{ egin{aligned} \mathbf{y}_t &= S_t^{rac{1}{2}} \boldsymbol{\epsilon}_t \ X_t &= \boldsymbol{\mu} + \Phi(X_{t-1} - \boldsymbol{\mu}) + \Psi^{rac{1}{2}} \boldsymbol{
u}_t \end{aligned} 
ight.$$

where  $S_t = \text{diag}(e^{x_{t1}}, \dots, e^{x_{td}})$ , with correlated noise terms:  $(\epsilon_t, \nu_t) \sim N_{2d}(\mathbf{0}, \mathbf{C})$ .

Log-likelihood evaluation (based on T = 400 data points and 200 independent runs).
Log-likelihood evaluation (left) and filtering (right) as a function of t.

Log-likelihood estimation (based on T = 400 data points and 200 independent runs)

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Increasing the dimension has two effects:

- 1. The Hilbert curve is less and less smooth (See also He and Owen, 2015)
- 2. The proportion of particles with non-negligible weights get small.

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- 1. The Hilbert curve is less and less smooth (See also He and Owen, 2015)
- 2. The proportion of particles with non-negligible weights get small.

We managed recently to obtain reasonable gains even for d = 10 for a multivariate linear Gaussian model (using the optimal proposal).

#### Diffusion-driven SV model ( $d = \infty$ )

$$\begin{cases} \mathrm{d}Y_t = \{\mu_P + \beta e^{X_t}\} \mathrm{d}t + e^{X_t/2} \mathrm{d}B_t \\ \mathrm{d}\tilde{X}_t = \mu(\tilde{X}_t) \mathrm{d}t + \omega(\tilde{X}_t) \mathrm{d}W_t \end{cases}$$

where  $(B_t)_{t\geq 0}$  and  $(W_t)_{t\geq 0}$  are Brownian motions with correlation coefficient  $\rho \in (-1, 1)$  and

$$\mu(x) = \kappa(\mu - e^x)e^{-x} - 0.5\omega^2 e^{-x}$$
$$\omega(x) = \omega e^{-x/2}$$

The  $Y_t$  are observed at times  $t = 0, 1, \ldots, T$ .

For  $M \geq 1$  (with  $\delta = M^{-1}$ ), let  $\mathbf{x}_t \in \mathbb{R}^M$  be such that:

$$\begin{cases} Y_t | Y_{t-1}, X_t \sim \mathcal{N}_1 \Big( Y_{t-1} + \mu_P + \beta \sigma_t^2 + \rho Z_t, \ (1 - \rho^2) \sigma_t^2 \Big) \\ X_t(1) = X_{t-1}(M) + \delta \mu (X_{t-1}(M)) + \omega (X_{t-1}(M)) (W_{t-1+\delta} - W_{t-1}) \\ \vdots \\ X_t(M) = X_{t-1}(M - 1) + \delta \mu (X_{t-1}(M - 1)) \\ + \omega (X_{t-1}(M - 1)) (W_t - W_{t-\delta}) \end{cases}$$

and

$$\sigma_t^2 = \frac{1}{M} \sum_{m=1}^M e^{X_{t-1}(m)}, \quad Z_t = \sum_{m=1}^M e^{X_{t-1}(m)} (W_{t+m\delta} - W_{t+(m-1)\delta}).$$

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For this model, M = 10 is a reasonable choice (Chib et al., 2004).

A naive application of SQMC would imply working in dimension M = 10, in particular for the Hilbert ordering.

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However, if we implement a bootstrap filter, we notice that (a)  $G_t$  depends only on  $X_t$ ; and (b) the simulation of  $\tilde{X}_t$  depends only on  $X_{t-1}(M)$  (the last component of  $X_{t-1}$ ), because process  $(X_t)$  is Markov. Thus we can collapse the choice of the ancestor to the choice of a scalar.

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More generally, notion of effective dimension for the choice of the ancestors.

To simulate  $X_t^n$  given  $X_{t-1}^n(M)$ , we must simulate the innovation terms  $W_{t+m\delta} - W_{t+(m-1)\delta}$ .

• Forward approach: simulate the consecutive

$$W_{t+m\delta}^n - W_{t+(m-1)\delta}^n$$

as IID  $N(0, \delta)$  variates.

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• Brownian bridge: Simulate  $W_{t+m\delta}$  (cond. on the previous ones) in the following order: m = M, m = M/2, m = M/4, m = 3M/4, ...

The parameters of the model are set to their estimated values for the daily return data on the closing price of the S&P 500 index from 5/5/1995 to 4/14/2003 (Chib et al., 2004).

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Estimation of  $\mathbb{E}[X_t|Y_{0:T}]$  for  $t \in \{1, ..., T\}$  and for different values of N (and based 100 independent SMC and SQMC runs). SQMC is implemented with the forward method (left) and with the Brownian Bridge method (right).

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Estimation of the log-likelihood for different values of N (and based 100 independent SMC and SQMC runs). SQMC is implemented with the forward method (left) and with the Brownian Bridge method (right).

### Conclusion

- Only requirement to replace SMC with SQMC is that the simulation of  $X_t^n | X_{t-1}^n$  may be written as a  $X_t^n = \Gamma_t(X_{t-1}^n, \mathbf{u}_t^n)$  where  $\mathbf{u}_t^n \sim U[0, 1]^d$ .
- impressive gains in performance (even for small N and moderate d).
- Supporting theory.
- C++ package by Mathieu (improved), Python library coming soon.

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